

## **Supplementary Material**

### **Study sample**

The vervets used in this study are part of a pedigreed research colony that has included more than 2,000 monkeys since its founding. Briefly, the Vervet Research Colony (VRC) was established at UCLA during the 1970's and 1980's from 57 founder animals captured from wild populations on the adjacent Caribbean islands of St. Kitts and Nevis; Europeans brought the founders of these populations to the Caribbean from West Africa in the 17<sup>th</sup> Century <sup>1</sup>. The breeding strategy of the VRC has emphasized the promotion of diversity, the preservation of the founding matriline, and providing all females and most of the males an opportunity to breed. The colony design modeled natural vervet social groups to facilitate behavioral investigations in semi-natural conditions. Social groups were housed in large outdoor enclosures with adjacent indoor shelters. Each enclosure had chain link siding that provided visual access to the outside, with one or two large sitting platforms and numerous shelves, climbing structures and enrichment devices. The monkeys studied were members of 16 different social matrilineal groups, containing from 15 to 46 members per group. In 2008 the VRC was moved to Wake Forest School of Medicine's Center for Comparative Medicine Research, however the samples for gene expression measurements in Dataset 1 (see below) and the MRI assessments used in this study occurred when the colony was at UCLA.

### **Gene expression phenotypes**

Two sets of gene expression measurements were collected. Dataset 1 used RNA obtained from whole blood in 347 vervets, assayed by microarray (Illumina HumanRef-8 v2); Dataset 2 assayed gene expression by RNA-Seq, in RNA obtained from 58 animals, with seven tissues (adrenal, blood, Brodmann area 46 [BA46], caudate, fibroblast, hippocampus and pituitary) measured in each animal.

#### *Dataset 1: Microarray (blood)*

The microarray data set has been described in Jasinska et al. <sup>2</sup> and is available at NCBI at the BioProject PRJNA115831. Briefly, Total RNA from whole blood preserved in PaxGene RNA Blood tubes (PreAnalyticX) was extracted using PAXgene Blood RNA Kit (PreAnalyticX). The integrity of the extracted total RNA samples was assessed on the Agilent 2100 Bioanalyzer (Agilent Technologies) with the RNA 6000 Nano Assay Kit (Agilent Technologies), and sample concentrations were quantified with RiboGreen RNA (Invitrogen).

For assessing transcript levels, we used the Illumina HumanRef-8 v2 chip. This chip provides genome-wide transcriptional coverage of well-characterized genes and splice variants. This chip uses 22,184 probes representing 18,189 unique human genes (or 20,424 unique transcripts) from Reference Sequence (RefSeq) database1, Release 17. The Illumina gene expression platform utilizes 50-mer gene-specific probes that provide both good selectivity and sensitivity <sup>3</sup>. We expected that the long probes would also tolerate

sequence incompatibilities between human probe sequence and vervet target transcripts and be more robust than shorter probes to possible allelo-specific differences in hybridization efficiency due to vervet-specific SNP variants occurring in probe-interaction sites <sup>4</sup>.

cDNA was synthesized and *in vitro* transcribed into biotinylated cRNA using the Illumina Totalprep RNA amplification kit, following the manufacturer's instructions (Ambion). Labeled cRNA was hybridized to the HumanRef-8 version 2 (Illumina) gene expression bead-chip. A gene was called detectable by BeadStudio when the detection p-value was <0.01. The gene expression module of the BeadStudio software version 3.1 (Illumina) was used for initial data processing and background correction. Lumi software was also used to perform a variance-stabilizing transformation that takes advantage of the technical replicates available on every Illumina microarray (usually over 30 randomly distributed beads per probe), and subsequently performs robust spline normalization and quality control of gene expression measures <sup>5</sup>.

Probe filtering for eQTL analysis: The probes on the Illumina HumanRef-8 v2 microarray were originally developed for assaying gene expression in humans. We selected probes that were compatible with vervet genomic sequence based on the following criteria: contain no indels, up to a total of five mismatches in a probe, with maximum of one mismatch in the 16 nt central portion of the probe). To prevent expression measurement-bias due to SNP interference with the hybridization process, we excluded probes targeting sequences with high-quality common SNPs identified in the VRC pedigree. For this filtering step, we used a set of 3.45 Mln high-quality SNPs segregating in the VRC with MAF $\geq$ 10%. A total of 11,001 probes passed these filters (Supplementary Data 1). We then evaluated the detection levels of each probe in all animals, and retained for analysis 6,018 probes that were detected with Illumina p<0.05 in at least 5% of animals.

#### Dataset 2: RNA-Seq (seven tissues)

Below we describe sample collection and processing, and determination of expression counts for the RNA-Seq gene expression dataset.

Tissue collection for RNA: Tissues were obtained from 60 vervets during experimental necropsies. The vervets represented a range of developmental stages from neonates (7 days), infants (90 days and one year), young juveniles (1.25, 1.5, 1.75, 2 years old), peri-adolescents or subadults (2.5, 3 years old) to adults (4+ years old) with 6 vervets (3 males and 3 females) from each developmental time point. Two animals (a 1.75 year old female and a 7 day old male) were excluded for the eQTL study as they did not have WGS data, leaving a total of 58 monkeys with RNA-Seq and whole genome sequencing (WGS) data for eQTL analysis. Two samples (from caudate and BA46) from individual 2008147 were excluded after the PCA analysis suggested a sample mix-up between tissues.

Vervets were anesthetized with 10-15 mg/kg of ketamine administered intramuscularly followed by pentobarbital 100 mg/kg administered intravenously. After animals reached a deep plane of anesthesia, the abdominal and thoracic cavities were opened and the

vasculature was perfused with normal saline chilled to 4° C administered via the left cardiac ventricle until perfusate escaping through a cut in the inferior vena cava became blood free. After exsanguination, the head was then disarticulated and the top of the cranium removed using Ronjeurs to chip off small bone pieces. Keeping the Ronjeurs superficial to the dura, bone was first removed at the base of the skull, proceeding anteriorly just above the ear canal and across the brow ridge to fully encircle the entire head. The dura was then cut with scissors, and the top of the skull was removed with Ronjeurs. Scissors were used to cut cranial nerves II-XII to free the brain, keeping the olfactory nerve and olfactory bulb together with the brain when possible. After removal, the brain was weighed, and then hemisected with a scalpel. The right hemisphere was preserved in 10% neutral buffered formalin and the left hemisphere was dissected. Brain tissues were generally collected within 60-70 minutes of removal of the brain from the skull. All brain samples were placed immediately in RNAlater and refrigerated for 24 hours. The RNAlater was then removed and the tissue frozen at -80° C or below.

For 14 necropsies performed after August 4, 2010, the necropsy protocol was modified as follows: 1) 100% oxygen was delivered to the animal by face mask starting before pentobarbital administration and continuing until initiation of saline perfusion; 2) the animal was placed on a bed of ice prior to pentobarbital administration (but after ketamine administration) to accelerate cooling of tissues; 3) dissection protocols were streamlined to minimize the time elapsed between pentobarbital administration and removal of the brain from the skull and to minimize the time elapsed to the completion of brain dissection.

During necropsies of 30 vervets whose brain tissues were used in this study, a fresh frozen sample of occipital lobe was collected near the end of the dissection procedure to allow tissue pH to be measured. pH was measured in occipital lobe specimens as described by Harrison et al.<sup>6</sup>. pH ranged from 5.98 to 6.98 (mean pH 6.6, SD 0.2). These data were used to assess the potential effect of brain pH on gene expression PC patterns (see Possible Technical and Biological Covariates).

BA46: The samples were collected from both banks of the principal sulcus, bluntly dissecting downward with forceps inserted at the upper margin of each bank to free tissue to the floor of the principal sulcus. The midpoint of the principal sulcus along its length was used as the posterior margin for the collected samples, which extended anteriorly for the length of the sulcus. The samples collected from the two sulcal banks were pooled at the time of dissection and processed as a single sample.

Caudate: From the medial surface of the hemisected brain, forceps were inserted into the lateral ventricle and used to remove the overlying tissue, exposing the caudate. A coronally oriented cut was then made through the head of the caudate, and caudate tissue was pinched from the portion of the brain anterior to this cut using forceps.

Hippocampus: To obtain the hippocampal sample, a coronally oriented cut was made with a scalpel through the occipital pole, passing through the head and body of the hippocampus. Blunt dissection with forceps was used to isolate the hippocampus from surrounding tissue, extending approximately 2-3 mm into the exposed tissue face.

RNA collection: The following tissue preservation methods were used during the collection to maintain sample quality. Whole blood was drawn into PAXgene RNA Blood Tubes (PreAnalyticX) with reagent instantly stabilizing RNA profiles. Solid tissues were preserved in RNAlater reagent (Ambion) immediately after collection, protecting the integrity of RNA profiles.

To establish fibroblast cultures, skin biopsies were collected from shaved and cleaned skin from an area of the middle of the thigh (outer side) using a skin punch, after ketamine anesthesia but prior to euthanasia. Biopsies were placed in cell culture medium (79% Minimum Essential Media, CORNING Cellgro, 20% Fetal Bovine Serum, CORNING Cellgro, 1% Antibiotic-Antimycotic, Gibco) and shipped to UCLA at ambient temperature until the next day when the cultures were started from skin explants. Cell pellets from fibroblast cultures in the second passage were collected into Triazol reagent (Qiagen), immediately stabilizing RNA.

The following methods were used for RNA extraction for seven tissues used in this study, three brain tissues (BA46, caudate, and hippocampus), two endocrine tissues (adrenal and pituitary) and two peripheral tissues (blood and fibroblasts): PaxGene RNA Kit (Qiagen) for blood, miRNease (Qiagen) for fibroblast, PerfectPure RNA (5PRIME) or miRNeasy (Qiagen) for adrenal, BA46, caudate, hippocampus, and pituitary. RNA integrity was assessed via measuring RIN scores on either Bioanalyzer 2100 (Agilent) or 2200 TapeStation (Agilent), and RNA yield was determined with RiboGreen RNA (Invitrogen). RIN score values for each sample type were: 9.6 (SD=0.54) in cultured skin fibroblasts, 7.98 (SD=0.99) in blood, 8.22 (SD=0.54) in adrenal cortex, 8.05 (SD=0.61) in pituitary, 6.35 (SD=0.7) in caudate, 6.35 (SD=0.7) for hippocampus, and 6.04 (SD=0.5) in BA46.

RNA sequencing (RNA-Seq): We conducted RNA-Seq across the seven tissues, as follows:

From purified RNA, we created two types of cDNA libraries. For fibroblasts, adrenal and pituitary, we used poly-A RNA cDNA libraries, since that was the only protocol available at that time when we started working with these tissues. For BA46, blood, caudate, and hippocampus, we used more recently available total RNA cDNA libraries that allowed us to obtain data not only in polyadenylated transcripts but also non-coding RNAs. For all samples, for each tissue, only one type of library was created. For these library preps we used either the TruSeq RNA SamplePrep v2 kit (Illumina, [http://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry\\_documentation/samplepreps\\_truseq/truseq\\_rna/truseq-rna-sample-prep-v2-guide-15026495-f.pdf](http://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/samplepreps_truseq/truseq_rna/truseq-rna-sample-prep-v2-guide-15026495-f.pdf)) or this same kit mated to the standalone RiboZero Gold rRNA reduction kit (Epicentre, [http://www.epibio.com/docs/default-source/protocols/ribo-zero-magnetic-gold-kit-\(human-mouse-rat\).pdf?sfvrsn=16](http://www.epibio.com/docs/default-source/protocols/ribo-zero-magnetic-gold-kit-(human-mouse-rat).pdf?sfvrsn=16)). The preps that used poly-A selection used the standard TruSeq RNA SamplePrep protocol without changes. The preps that used RiboZero followed the stand-alone RiboZero protocol with a final cleanup with Ampure RNAClean XP beads (Appendix A). rRNA reduced RNA samples were eluted off of the Ampure beads in 11 ul resuspension buffer and 8.5 ul of the eluted product was combined with 8.5 ul of 2x EPF

buffer. At this point the samples were subjected to the TruSeq RNA SamplePrep v2 protocol at the "Incubate RFP" step, which was completed with no further changes.

To minimize lane effects, we multiplexed libraries into pools, where each library is indexed with a unique tag; we then split each pool between different sequencing lanes to generate technical replicates. Each pool was run in a minimum of three lanes on an Illumina HiSeq2500 HiSeq 4000 instrument. We generated paired end 100 bp reads, and paired and 120 bp reads from the project. On average, 56.6 Mln reads per sample were generated (Supplementary Table 20). The RNA-Seq reads data were made available through NCBI as BioProject PRJNA219198.

Determination of gene expression based on RNA-Seq read counts: RNA-Seq reads were aligned to the vervet genomic assembly *Chlorocebus\_sabeus* 1.1 [http://www.ncbi.nlm.nih.gov/assembly/GCF\\_000409795.2](http://www.ncbi.nlm.nih.gov/assembly/GCF_000409795.2) with gene name revisions provided by NCBI before Aug 10th 2016 by the ultrafast STAR aligner<sup>7</sup> using our standardized pipeline. STAR was run using default parameters that allow a maximum of ten mismatches. Gene expression was measured as total read counts per gene. For paired end experiments, total fragments are considered. Fragment counts that aligned to known exonic regions based on the NCBI *Chlorocebus\_sabeus* Annotation Release 100 were quantified using the HTSeq package<sup>8</sup>. The HTSeq-count script was executed using intersection\_nonempty mode, which excluded ambiguous reads that map to regions where there are multiple genes. All other reads mapping to a single gene were included in the corresponding gene counts. The counts for all 33,994 genes were then combined and lowly expressed genes, defined as genes with a mean count of less than 1 across all samples, as well as genes detected in fewer than 10% of samples, were filtered out. We set this threshold higher than that used in Dataset 1 (5% of samples with a given gene detected) because of the much smaller sample size in Dataset 2. Finally, quantile normalization was applied to the remaining genes to obtain normalized gene counts.

In Supplementary Table 2, we summarize biotypes of quantified RNAs. The overall number of genes as well as of protein-coding, non-coding and pseudogenes is the largest in blood and the smallest in fibroblasts. The difference in the number of expressed genes may stem from differences in cell composition: a high cellular heterogeneity in blood versus monoculture of skin fibroblasts. As expected given the differences in library generation protocols, fibroblasts, adrenal and pituitary (generated with the poly-A protocol) have lower numbers of non-coding genes than hippocampus, BA46, caudate and blood (generated with the total RNA protocol).

### **Comparative expression analysis using Allen Brain Atlas (ABA) datasets from human and rhesus macaque**

We compared gene expression in matched age categories between vervet (our data), human<sup>9</sup>, and rhesus macaque<sup>10</sup>. The comparison of vervet BA46 with rhesus macaque medial frontal cortex used 12 vervets (3 animals per time point). The comparison of vervet caudate with rhesus macaque basal ganglia used 11 animals: 2 animals for the first age category (age 7 days in vervet), 3 animals for remaining time points, and the comparison of

vervet and rhesus macaque hippocampus used 12 animals (3 animals per time point). The comparison of vervet BA46 with human BrainSpan DLPFC data used 18 vervets: 2 males at age 7 days, 1 male at age 90 days, 2 males and 2 females at age 1-1.25y, 2 males and 1 female at age 1.5-2.5y, 1 male and 2 females at age 3-4y. The comparison of vervet caudate with human BrainSpan striatum data used 14 vervets: 1 male at 7 days, 2 males and 1 female at age 1-1.25y, 1 male at age 1.5-2.5y, 2 females at age 3-4y, and 3 males and 3 females at age 5y or older. The comparison of vervet and human BrainSpan hippocampus data used, 17 samples: (T6: 2M, T7: 1F, T8: 1M + 1F, T9: 2M + 1F, T10: 2F + 1M, T11: 3F + 3M).

For each of the tissues in Supplementary Table 23, we identified the 1,000 most variable genes in each species and identified orthologous genes. We then ranked genes according to their mean expression, and compared ranks using the Spearman correlation ( $\rho$ ). Analysis was done separately by tissue and age group. We observed a moderate correlation between vervet and human ranked expression in hippocampus and between vervet BA46 and human DLPFC, with  $\rho$  for both comparisons averaging 0.62. We found a slightly lower correlation between vervet caudate and human striatum, with  $\rho$  averaging 0.56 (Supplementary Table 4). The comparisons of rank expression in vervet and rhesus macaque yielded smaller correlations than comparisons with human ( $\rho \sim 0.35$ ), probably due to the difference in gene expression platform (the rhesus macaque data are based on microarray, Supplementary Table 5). We also compared expression in adrenal, blood, caudate, hippocampus, and pituitary between vervet and GTEx<sup>11</sup> and observed ranked expression correlation ranging from  $\rho = 0.79$  for adrenal and pituitary and  $\rho = 0.68$  in caudate (Supplementary Table 6).

### **Evaluation of tissue specific gene expression in Dataset 2**

We identified 137 genes (27 in adrenal, 72 in blood, 3 in caudate, 22 in fibroblast, and 13 in pituitary) where mean normalized gene expression was  $>100$  cpm in one tissue, and  $<10$  cpm in all other tissues (Supplementary Table 3). Many of these genes have distinctive functions and/or expression patterns associated with a given tissue. For example, in adrenal this list includes numerous genes involved in steroid hormone metabolism, such as *STAR*, which regulates cholesterol metabolism and steroid production in adrenal cortex, and *MC2R*, which is a form of adrenocorticotrophic hormone receptor (*ACTH* receptor) acting in adrenal cortex. In pituitary this list includes *POMC*, a gene coding a precursor of adrenocorticotrophic hormone (*ACTH*) and *CGA*, a gene coding an alpha subunit of luteinizing hormone, follicle stimulating hormone, and thyroid stimulating hormone, all of which are hormones produced by pituitary. In blood the list includes several genes specific to different blood cell lineages; in fibroblasts, it includes *FAP*, a gene controlling fibroblast growth. In caudate, it includes *SYNDIG1L*, a gene known to be predominantly expressed in non-human primate (capuchin monkey) striatum.

### **Possible technical and biological covariates**

Several technical experimental variables are known to influence gene expression assays, including premortem acidosis (as reflected by tissue pH), RNA integrity (RIN), RNA

extraction protocols, and interval between death and tissue harvesting. Given the possible impact on this tissue of diurnal and seasonal variations in cortisol secretion, we considered two additional covariates for adrenal: time of day of necropsy and date of necropsy. None of these variables showed correlation with any PCs in any of the seven tissues that we examined, except RNA-Seq batch. Sample batch showed correlation with PC2 in adrenal and pituitary, and PC3 in caudate and pituitary (data not shown), and, therefore, was used as a covariate in eQTL analyses.

### **Genes with the highest loadings on the PCs associated with age and sex**

In each tissue, we examined the genes in the top and bottom 10% of the distribution of PC loadings on PCs 1, 2, or 3 (200 genes total per tissue, per PC), in relation to age (PC1 in BA46 and caudate) or sex (PC2 in caudate, BA46 and blood, PC1 in hippocampus and pituitary, and PC3 in adrenal) (Supplementary Tables 7, 8).

Genes with the highest loadings on PCs associated with age in BA46 and caudate The lists of genes with age-related expression patterns in BA46 and the caudate (Supplementary Table 8) includes several genes that are both essential for nervous system development and implicated in the causation of human disorders. Figure 2 and Supplementary Figure 2 show expression patterns by age-point of some notable examples.

In the main text we described the age-related PC1 variation in BA46 of thrombospondin genes. Among the other genes contributing to such age-related PC1 variation in BA46 are several genes involved in myelination (*MOG*, *MAG*, *OPALIN*, *MBP*), all of which show increased expression with age (Supplementary Figure 3). Similar age-related upregulation of these genes is observed in human DLPFC from ABA (Supplementary Figure 3). These genes are not represented in the rhesus macaque dataset in ABA. Coordinated increase of expression of genes regulating myelination suggests that the BA46 age-related expression pattern (PC1) at least partially reflects this process.

In vervet caudate, *ASPM*, which regulates neurogenesis in the cerebral cortex and, when mutated, results in primary microcephaly<sup>12</sup>, shows a systematic decrease across development that resembles the expression patterns of these gene in human and rhesus macaque datasets from ABA (Supplementary Figure 3). *NDRG1* displays an increasing expression pattern with age in vervet caudate that is concordant with the human expression profile in striatum in ABA (Supplementary Figure 3). This gene is not represented in rhesus macaque basal ganglia in ABA. *NDRG1* (i) stimulates cellular differentiation and proliferation, (ii) is commonly involved in somatic rearrangements leading to medulloblastoma (the most prevalent pediatric brain tumor<sup>13</sup>), and (iii) when mutated, causes a progressive peripheral neuropathy, Charcot-Marie-Tooth (CMT) disease Type 4d.

Genes with the highest loadings on PCs associated with sex Among genes contributing to the sex-related expression patterns in specific tissues, perhaps the most striking examples are genes encoding the receptors for two structurally similar neuropeptides, the oxytocin receptor *OXTR* (in caudate) and the vasopressin receptor *AVPR1A* (in hippocampus). These

two genes function in a sex specific manner mediated by the sex-steroids estrogen (for *OXTR*<sup>14</sup>) and androgen (for *AVPR1A*<sup>15</sup>). The distribution and function of these genes also differ dramatically between mammalian species, including among some that are closely related. For example, a polymorphism in the promoter of *Avpr1a* has been associated, in prairie voles, with inter-species differences in sex-related social behaviors, such as pair bonding<sup>16</sup>. In monogamous prairie vole males, additional polymorphisms in this region result in inter-individual variation in expression of *Avpr1a* in hippocampus and other tissues comprising a memory circuit, and these expression differences are related to sex-specific spatial behaviors<sup>17</sup>. Another notable example from the hippocampus gene list is *PDYN*, encoding the opioid peptide dynorphin, which modulates hippocampal synaptic plasticity<sup>18</sup> in a sex-specific manner, mediated by estrogen<sup>19</sup>.

The lists of genes with sex-related expression patterns in pituitary and adrenal overlap substantially (40 of the top 200 genes in common) and include several molecules with functions in reproduction or in biological processes with a marked sex bias. Tissue-specific examples include, for pituitary, *TAC1*, encoding substance P, which regulates puberty onset and fertility<sup>20</sup> and *PTGER2* which plays a role in ovulation and fertilization<sup>21</sup>, and, for adrenal, *PRL*, which stimulates lactation in new mothers, plays a role in social behaviors, and is regulated by adrenal steroids<sup>22</sup>.

### **Comparison to DLPFC eQTLs from CommonMind Consortium (CMC)**

We downloaded the Open Access version of the eQTL results from CMC (<https://www.synapse.org/#!/Synapse:syn5652289>) generated from n=467 genetically-inferred Caucasian samples (209 schizophrenia cases, 206 controls, and 52 affective disorder cases) using RNA-Seq data from DLPFC<sup>23</sup>. The eQTL results are provided with FDR summarized into significance bins: <0.01, <0.05, <0.1, and <0.2. We compare vervet local eQTLs from three brain regions (BA46, caudate, hippocampus) with FDR<0.2 and FDR<0.05 (used as significance threshold in the CMC dataset by Fromer et al.<sup>23</sup>). The results for comparison of Bonferroni-corrected and FDR-corrected vervet eQTL with the CMC eQTL are summarized in Supplementary Table 13.

For our Bonferroni corrected eQTL set, almost 100% of local eQTL genes with human orthologs that were analyzed in the CMC data were found to have an eQTL at FDR < 0.20 in the CMC. Using the FDR < 0.05 threshold employed by the CMC manuscript<sup>23</sup>, 88.59% of our local eQTL genes have a local association in CMC.

For our FDR corrected results, we observe similar numbers, with 99% of our local eQTL genes also found to have a local eQTL at FDR < 0.20, and 88.16% at an FDR < 0.05. We observe the largest overlap of local brain eQTL between BA46 in vervet and DLPFC in human.

### **Correlation of expression between *IFIT1B* and genes regulated by the distant eQTL on CAE9**

On CAE 9, 76 SNPs across a ~500 Kb region displayed, in Dataset 1, a genome-wide significant local eQTL signal, and also genome-wide significant distant eQTLs for probes



representing up to 14 genes (Figure 3, Supplementary Table 18) on different vervet chromosomes (*RANBP10*, *SUGT1*, *LCMT1*, *HMBS*, *ST7*, *TMEM57*, *YPEL4*, *NARF*, *UBALD1*, *THBS4*, *DEDD2*, *CNN3*, *STXBP1*, *UQCR10*). We observed a high degree of genetic correlation between expression of *IFIT1B* and expression of the distantly regulated genes (Supplementary Table 17). For most of these distantly regulated genes the genetic correlation with *IFIT1B* is significantly different from 1, indicating that their expression derives from a shared genetic causation as well as genetic contributions that are unique for each transcript (incomplete pleiotropy).

### **Quantitative real-time PCR (qRT-PCR)**

Hippocampal expression results for the non-coding lncRNA genes associated with hippocampal volume were validated via qRT-PCR using the following TaqMan® assays with a FAM reporter.

Custom primers and hydrolysis probes were designed using the Custom TaqMan® Assays Design Tool (Applied Biosystems) as presented in Supplementary Table 24. Target sequences for primer and probe design were based on the NCBI Reference Sequences of *LOC103222765*, *LOC103222769*, *LOC103222771*, *HPRT1*, *GAPDH*, and *B2M*.

Each reverse transcription reaction contained 250ng total RNA in a final volume of 20µL. The diluted RT products used to create the cDNA pool were diluted once more (1:5 relative to the high standard) to ensure that the amount of template would fall within the established linear dynamic range of each assay. The cycling parameters for real-time PCR amplification were as follows: 95°C for 30 seconds, followed by 40 cycles of 95°C for 15 seconds and 60°C for 1 minute, with the fluorescence signal acquired at 60°C. Each 10µL qPCR reaction contained 5µL of iTaq® Universal Probes Supermix (Bio-Rad), 0.5µL of the 20x Custom TaqMan® Gene Expression Assay (primer concentration: 900nm; probe concentration: 250nm), 0.5µL of nuclease-free water, and 4µL of the twice-diluted cDNA.

Target sequences for custom primer and hydrolysis probe design were evaluated bioinformatically prior to submission to ensure quality. NCBI Primer-BLAST® was used to ensure specificity and avoid low-complexity regions, and common genetic variants were masked to prevent primer or probe design at those sites. TaqMan® MGB probes were designed to span an exon-exon boundary. Multiple coordinates for probe design were submitted for consideration, and the optimal probe sequence was determined by the Primer Express® Software (Applied Biosystems). The suitability of three reference gene candidates (*HPRT1*, *B2M*, and *GAPDH*) for normalization was evaluated using the NormFinder software (v5) in R<sup>24</sup>. As both *GAPDH* and *HPRT1* show a high stability of expression across all 16 animals, we used them as endogenous controls. Amplification efficiency was evaluated by a relative standard curve. The expression of each lncRNA in each sample was compared with a calibrator sample. All qRT-PCR procedures were designed and carried out according to Minimum Information for Publication of Quantitative Real-Time PCR Experiments(MIQE) guidelines<sup>25</sup>.

### **Hippocampal volume phenotype**

Structural MRI of 347 vervets > age 2 provided estimates of hippocampal volume, as described previously<sup>26,27</sup>. Briefly, nine structural images were acquired from each animal as axial T1-weighted volumes with a 3D magnetization prepared rapid acquisition gradient echo (MPRAGE) using an 8-channel high-resolution knee array coil as a receiver in a 1.5 Tesla Siemens (Erlangen) Symphony unit (TR 1900 msec; TE 4.38 msec; TI 1100 msec; flip angle 15 degrees; voxel resolution 0.5 mm in all three planes). The nine separate images were aligned to each other in pair-wise rigid body registrations and averaged together to yield one high signal-to-noise image. An affine population atlas was created from the individual MRI images using methods described by Woods<sup>28</sup> and phenotypes were generated from images transformed into this space. Hippocampi were segmented using a combination of manual and automated delineation<sup>26</sup>. Briefly, forty images were manually segmented in duplicate by ten extensively trained research assistants and these segmentations were used to train a hybrid discriminative/generative-learning algorithm<sup>29</sup>, which, in turn, was used to segment the entire set of images to produce the final phenotype. Prior to genetic analysis, hippocampal volumes were log transformed, regressed on sex and age in SOLAR, and residuals used as the final phenotype.

In hippocampus, the genome-wide significant eQTL SNPs reside in, and regulate expression of, two long non-coding RNA genes (lncRNA), *LOC103222765* (nine associated local eQTL SNPs) and *LOC103222769* (three associated local eQTL SNPs) located at a distance of 168 Kb from each other in the central portion of the QTL region for hippocampal volume. All significant SNPs within each locus are in complete LD ( $r^2=1$ ), but we observe no LD between the loci. An additional lncRNA gene, *LOC103222771*, situated two bp from *LOC103222769*, shows hippocampal specific association to six SNPs at a level ( $p < 10^{-9}$ ) just above genome-wide significance. All six SNPs associated to *LOC103222771* are in strong LD ( $r^2 > 0.93$ ).

Given the physical proximity of these lncRNAs, we used multivariate conditional analyses to evaluate whether the regulation of these genes depends on a single eQTL or two or three independent ones. For each lncRNA we designated a “lead SNP” (the SNP most significantly associated to its expression, Supplementary Table 19). The lead SNP for *LOC103222765* shows little correlation with the lead SNPs for *LOC103222769* ( $r^2=0.07$ ) or *LOC103222771* ( $r^2=0.0034$ ), while the lead SNPs for *LOC103222769* and *LOC103222771* are moderately correlated ( $r^2=0.55$ ). The minor allele frequencies of the lead SNPs for *LOC103222765*, *LOC103222769*, and *LOC103222771* are 0.43, 0.46, and 0.31, respectively (estimated in the full set of 721 vervets with genotype data) and are similar to frequency of the same alleles in an independent sample of 31 vervets from St. Kitts, the island from which the founders of the VRC pedigree derive (0.48, 0.34, and 0.27, respectively<sup>30</sup>). Multivariate conditional analyses suggest two eQTLs in this region; one associated to *LOC103222765*, and the second associated to *LOC103222769* and *LOC103222771*

## References

- 1 McGuire, M. T. & Members of the Behavioral Sciences Foundation. *The St. Kitts vervet*. Vol. 1 (Karger, 1974).
- 2 Jasinska, A. J. *et al.* Identification of brain transcriptional variation reproduced in peripheral blood: an approach for mapping brain expression traits. *Human molecular genetics* **18**, 4415-4427, doi:10.1093/hmg/ddp397 (2009).
- 3 Kuhn, K. *et al.* A novel, high-performance random array platform for quantitative gene expression profiling. *Genome Res* **14**, 2347-2356, doi:10.1101/gr.2739104 (2004).
- 4 Jacquelin, B. *et al.* Long oligonucleotide microarrays for African green monkey gene expression profile analysis. *FASEB J* **21**, 3262-3271, doi:10.1096/fj.07-8271com (2007).
- 5 Du, P., Kibbe, W. A. & Lin, S. M. lumi: a pipeline for processing Illumina microarray. *Bioinformatics* **24**, 1547-1548, doi:10.1093/bioinformatics/btn224 (2008).
- 6 Harrison, P. J. *et al.* The relative importance of premortem acidosis and postmortem interval for human brain gene expression studies: selective mRNA vulnerability and comparison with their encoded proteins. *Neurosci Lett* **200**, 151-154 (1995).
- 7 Dobin, A. *et al.* STAR: ultrafast universal RNA-seq aligner. *Bioinformatics* **29**, 15-21, doi:10.1093/bioinformatics/bts635 (2013).
- 8 Anders, S., Pyl, P. T. & Huber, W. HTSeq—a Python framework to work with high-throughput sequencing data. *Bioinformatics* **31**, 166-169, doi:10.1093/bioinformatics/btu638 (2015).
- 9 Kang, H. J. *et al.* Spatio-temporal transcriptome of the human brain. *Nature* **478**, 483-489, doi:10.1038/nature10523 (2011).
- 10 Bakken, T. E. *et al.* A comprehensive transcriptional map of primate brain development. *Nature* **535**, 367-375, doi:10.1038/nature18637 (2016).
- 11 GTEx Consortium. Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. *Science* **348**, 648-660, doi:10.1126/science.1262110 (2015).
- 12 Bond, J. *et al.* ASPM is a major determinant of cerebral cortical size. *Nature genetics* **32**, 316-320, doi:10.1038/ng995 (2002).
- 13 Northcott, P. A. *et al.* Subgroup-specific structural variation across 1,000 medulloblastoma genomes. *Nature* **488**, 49-56, doi:10.1038/nature11327 (2012).
- 14 Welsh, T. *et al.* Estrogen receptor (ER) expression and function in the pregnant human myometrium: estradiol via ERalpha activates ERK1/2 signaling in term myometrium. *The Journal of endocrinology* **212**, 227-238, doi:10.1530/JOE-11-0358 (2012).
- 15 Insel, T. R. The challenge of translation in social neuroscience: a review of oxytocin, vasopressin, and affiliative behavior. *Neuron* **65**, 768-779, doi:10.1016/j.neuron.2010.03.005 (2010).
- 16 Young, L. J. & Hammock, E. A. On switches and knobs, microsatellites and monogamy. *Trends in genetics : TIG* **23**, 209-212, doi:10.1016/j.tig.2007.02.010 (2007).
- 17 Okhovat, M., Berrio, A., Wallace, G., Ophir, A. G. & Phelps, S. M. Sexual fidelity trade-offs promote regulatory variation in the prairie vole brain. *Science* **350**, 1371-1374, doi:10.1126/science.aac5791 (2015).
- 18 Weisskopf, M. G., Zalutsky, R. A. & Nicoll, R. A. The opioid peptide dynorphin mediates heterosynaptic depression of hippocampal mossy fibre synapses and modulates long-term potentiation. *Nature* **362**, 423-427, doi:10.1038/362423a0 (1993).
- 19 Harte-Hargrove, L. C., Varga-Wesson, A., Duffy, A. M., Milner, T. A. & Scharfman, H. E. Opioid receptor-dependent sex differences in synaptic plasticity in the hippocampal mossy fiber pathway of the adult rat. *The Journal of neuroscience : the official journal of the Society for Neuroscience* **35**, 1723-1738, doi:10.1523/JNEUROSCI.0820-14.2015 (2015).

- 20 Simavli, S. *et al.* Substance p regulates puberty onset and fertility in the female mouse. *Endocrinology* **156**, 2313-2322, doi:10.1210/en.2014-2012 (2015).
- 21 Tamba, S. *et al.* Timely interaction between prostaglandin and chemokine signaling is a prerequisite for successful fertilization. *Proc Natl Acad Sci U S A* **105**, 14539-14544, doi:10.1073/pnas.0805699105 (2008).
- 22 Egli, M., Leeners, B. & Kruger, T. H. Prolactin secretion patterns: basic mechanisms and clinical implications for reproduction. *Reproduction* **140**, 643-654, doi:10.1530/REP-10-0033 (2010).
- 23 Fromer, M. *et al.* Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nat Neurosci* **19**, 1442-1453, doi:10.1038/nn.4399 (2016).
- 24 Andersen, C. L., Jensen, J. L. & Orntoft, T. F. Normalization of real-time quantitative reverse transcription-PCR data: a model-based variance estimation approach to identify genes suited for normalization, applied to bladder and colon cancer data sets. *Cancer Res* **64**, 5245-5250, doi:10.1158/0008-5472.CAN-04-0496 (2004).
- 25 Bustin, S. A. *et al.* The MIQE guidelines: minimum information for publication of quantitative real-time PCR experiments. *Clin Chem* **55**, 611-622, doi:10.1373/clinchem.2008.112797 (2009).
- 26 Fears, S. C. *et al.* Identifying heritable brain phenotypes in an extended pedigree of vervet monkeys. *The Journal of neuroscience : the official journal of the Society for Neuroscience* **29**, 2867-2875, doi:10.1523/JNEUROSCI.5153-08.2009 (2009).
- 27 Fears, S. C. *et al.* Anatomic brain asymmetry in vervet monkeys. *PloS one* **6**, e28243, doi:10.1371/journal.pone.0028243 (2011).
- 28 Woods, R. P., Grafton, S. T., Watson, J. D., Sicotte, N. L. & Mazziotta, J. C. Automated image registration: II. Intersubject validation of linear and nonlinear models. *J Comput Assist Tomogr* **22**, 153-165 (1998).
- 29 Tu, Z. *et al.* Brain anatomical structure segmentation by hybrid discriminative/generative models. *IEEE Trans Med Imaging* **27**, 495-508, doi:10.1109/TMI.2007.908121 (2008).
- 30 Jasinska, A. J. *et al.* Systems biology of the vervet monkey. *ILAR J* **54**, 122-143, doi:10.1093/ilar/ilt049 (2013).

## Supplementary Figure Legends

Supplementary Figure 1. Principle components 1, 2, 3, and 6 from analysis of gene expression levels (RNA-seq) in seven tissues. PC1 (47.5% of total variance) separates fibroblast from brain tissues, PC2 (18.2% of variance) separates blood from all other tissues, while the three brain regions do not separate until PC6 (2% of variance).

Supplementary Figure 2. Vervet age related genes: in BA46 *MOG*, *MAG*, *OPALIN*, and *MBP* involved in myelination, and *ASPM* and *NDRG1* in caudate.

Supplementary Figure 3. Expression profiles of orthologs of vervet genes with clear developmental trajectories, in similar tissues from human and rhesus macaque in the Allen Brain Atlas (ABA) data. (A) Top row: *THBS1*, *THBS2*, *THBS4* in human DLPFC (N=18); Bottom row: *THBS1*, *THBS2*, *THBS4* in rhesus medial frontal cortex (N=12). (B) *MOG*, *MAG*, *OPALIN* and *MBP* in human DLPFC (N=18). (C) *ASPM* and *NDRG1* in human caudate (N=14, left and middle panels), and *ASPM* in rhesus macaque basal nuclei (N=11, right panel). Genes *MOG*, *MAG*, *OPALIN*, *MBP*, *NDRG1* were not represented in the rhesus macaque dataset in ABA.

Supplementary Figure 4. Deconvolution analysis in BA46. (A) cell type composition for each animal (B) distribution of cell type composition by age group.

Supplementary Figure 5. Deconvolution in caudate. (A) cell type composition for each animal (B) distribution of cell type composition by age group.

Supplementary Figure 6. Deconvolution in hippocampus. (A) cell type composition for each animal (B) distribution of cell type composition by age group.

Supplementary Figure 7. Deconvolution in blood. (A) cell type composition for each animal (B) distribution of cell type composition by age group.

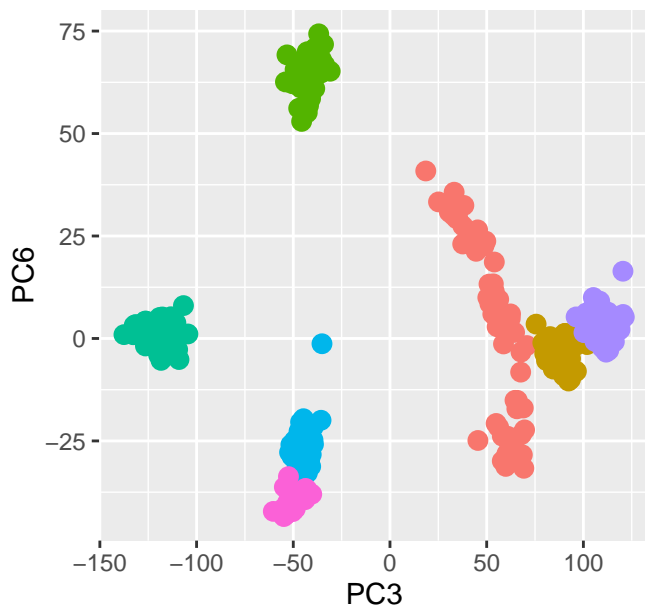
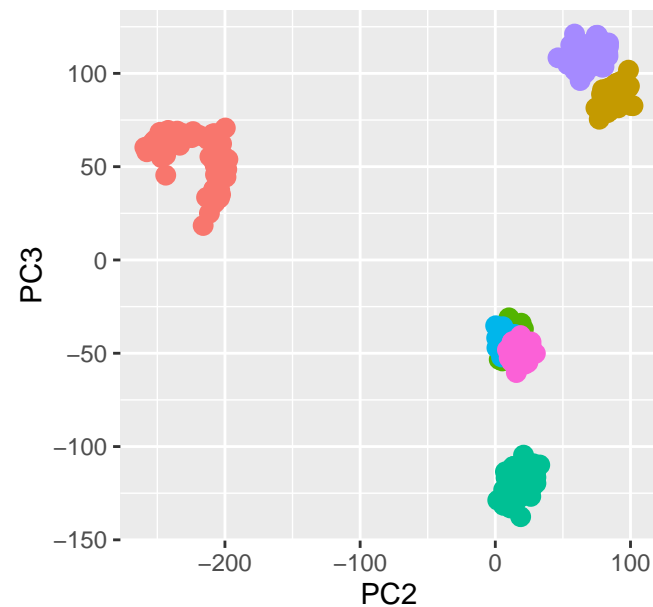
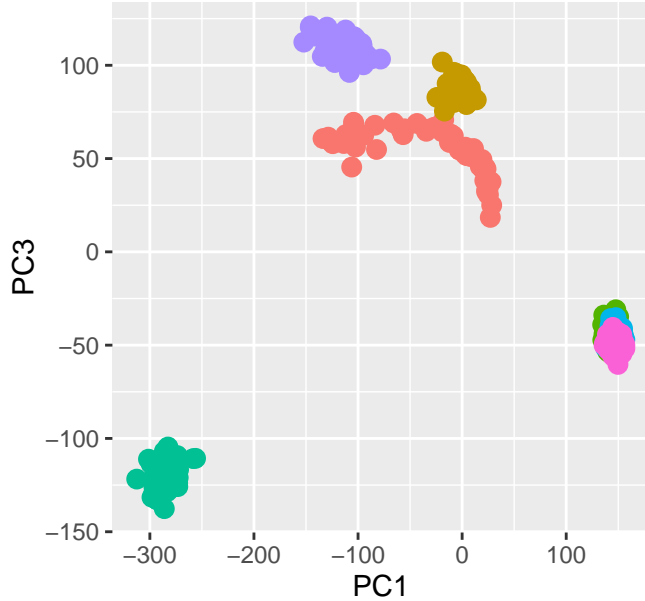
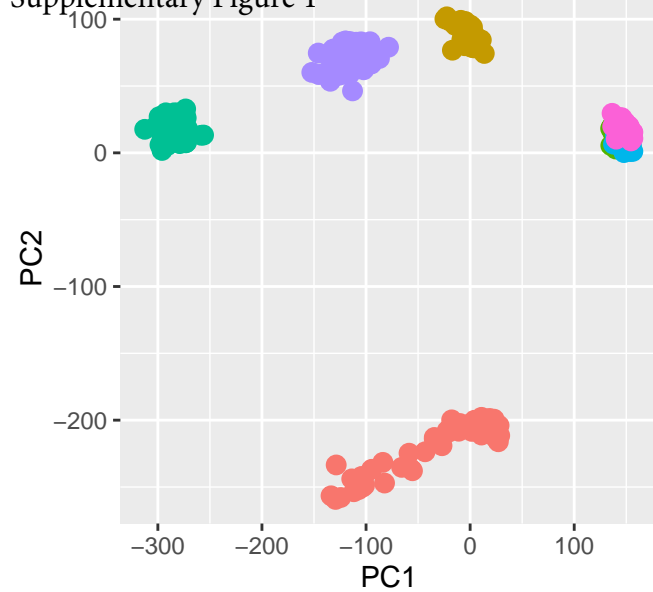
Supplementary Figure 8. Distribution, over 58 vervets, of entropy of cell type, for four tissues.

Supplementary Figure 9. eGene sharing among tissues. The intersection of FDR significant eGenes among the seven tested vervet tissues.

Supplementary Figure 10. Forest plot representing analysis of enrichment of eQTLs in genic and regulatory regions. Log odds-ratio is on the x-axis, and horizontal lines around each estimate represent the 95% confidence interval. Liver Me and Liver Ac stand for, respectively, H3K4me3 and H3K27ac marks in vervet liver. Rhesus caudate Ac and Rhesus prefrontal Ac stand for the vervet orthologous location of H3K27ac epigenetic marks in rhesus macaque caudate and prefrontal cortex, respectively.

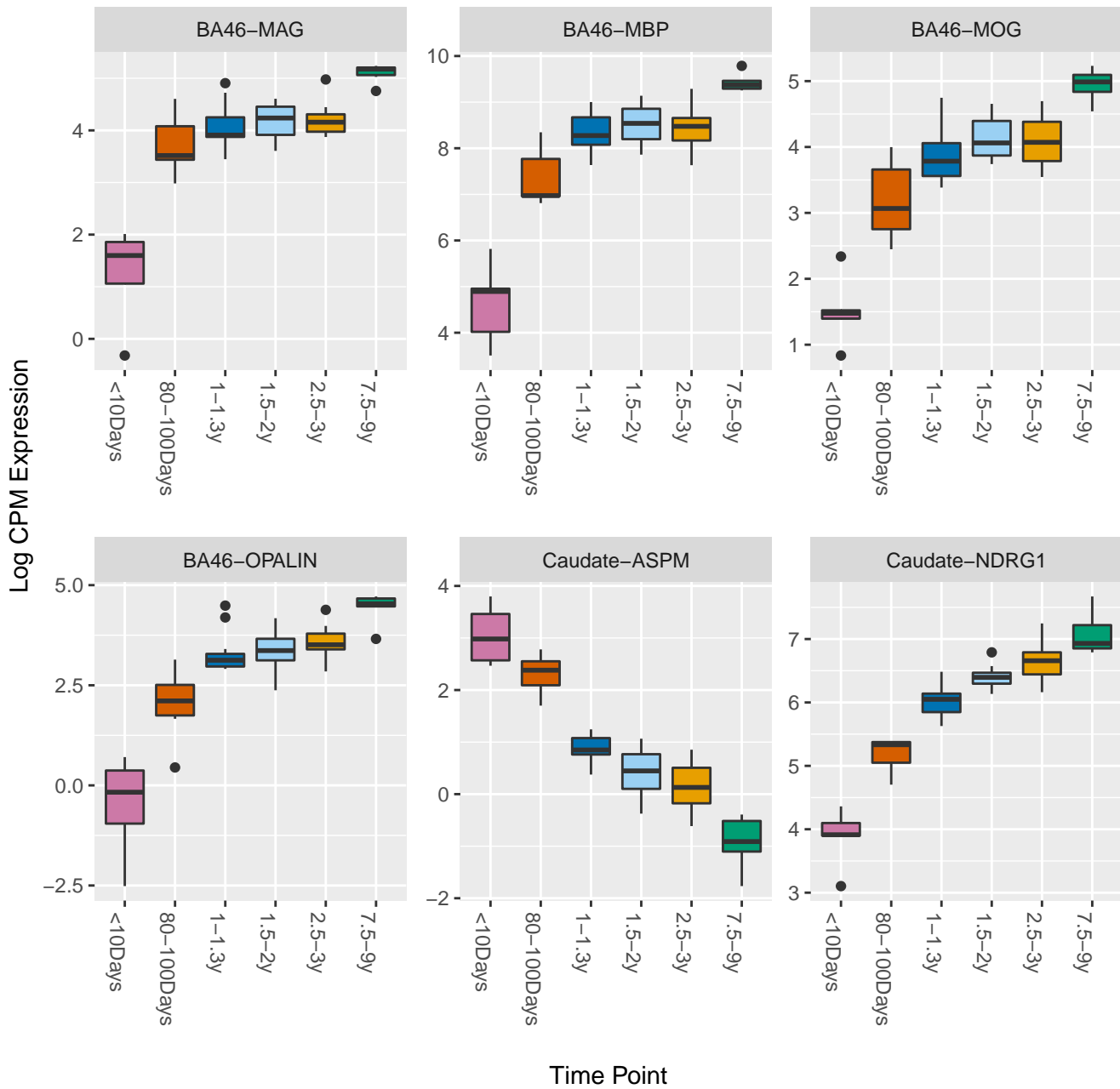
Supplementary Figure 11. Increase in the proportion of eQTL SNPs, compared to all SNPs, in the region of the TSS and TES. For each eQTL SNP, we note the location from the SNP to the TSS/TES of the gene to which it was associated. For non-eQTL SNPs, we note the locations of the SNP to the TSS/TES of all genes within 200 Kb of the SNP. Distances to the left and right of the TSS/TES are binned into 10 Kb intervals, and the number of SNPs in each distance bin recorded. As genes are of different sizes, for each gene the interval between the TSS and TES was divided into 10 equally sized intervals. The ratio of the number of eQTL to non-eQTL SNPs was noted for each distance bin. Supplementary Figure 9 represents a summation over the 27,196 genes; a formal statistical analysis of enrichment was not attempted because SNPs were oftentimes within 200kb of the TSS/TES of multiple genes.

Supplementary Figure 1

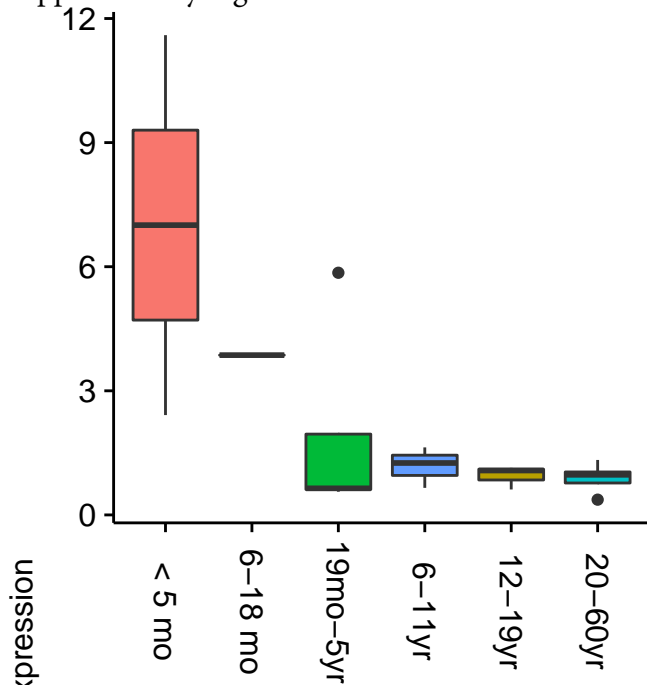


Tissue

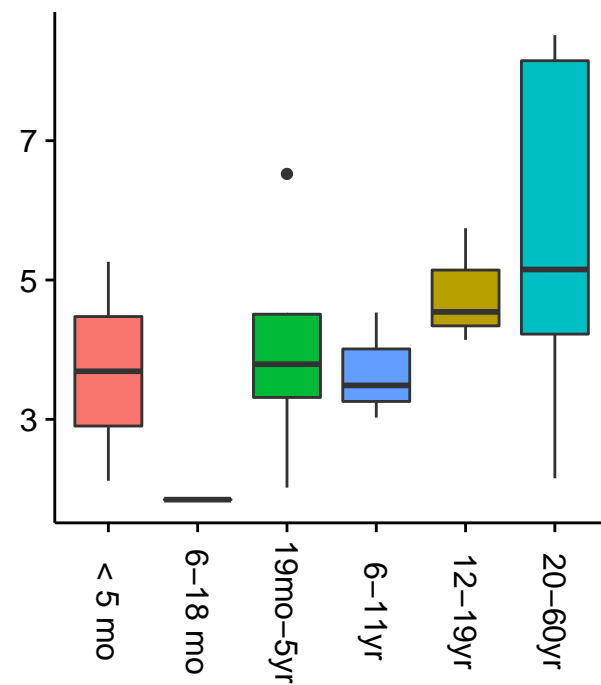
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<span style="color: yellow;">●</span> Pituitary	<span style="color: teal;">●</span> Fibroblast	<span style="color: purple;">●</span> Adrenal	



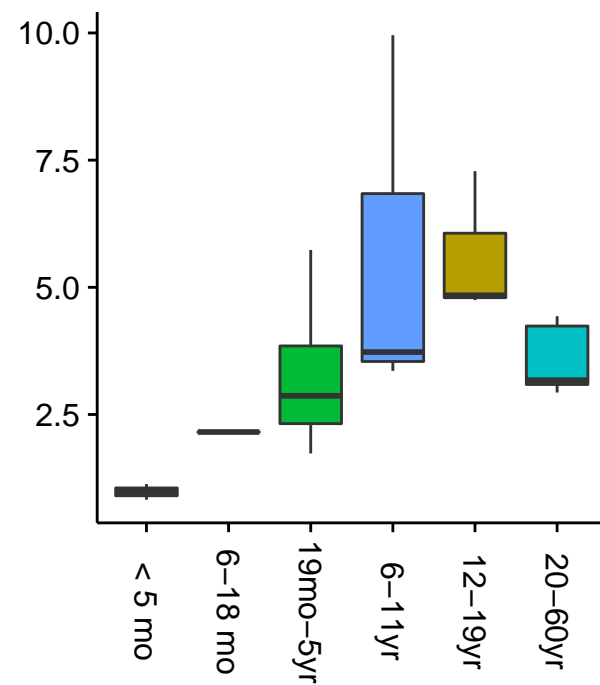
Supplementary Figure 3a **THBS1**



**THBS2**

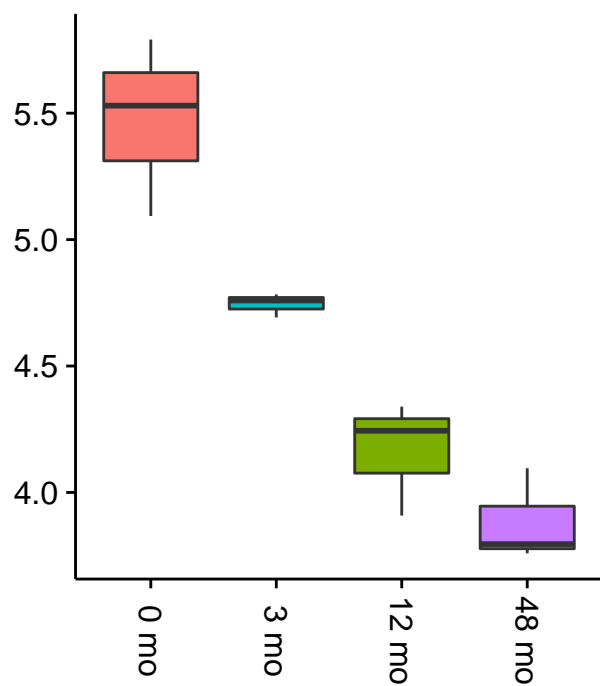


**THBS4**

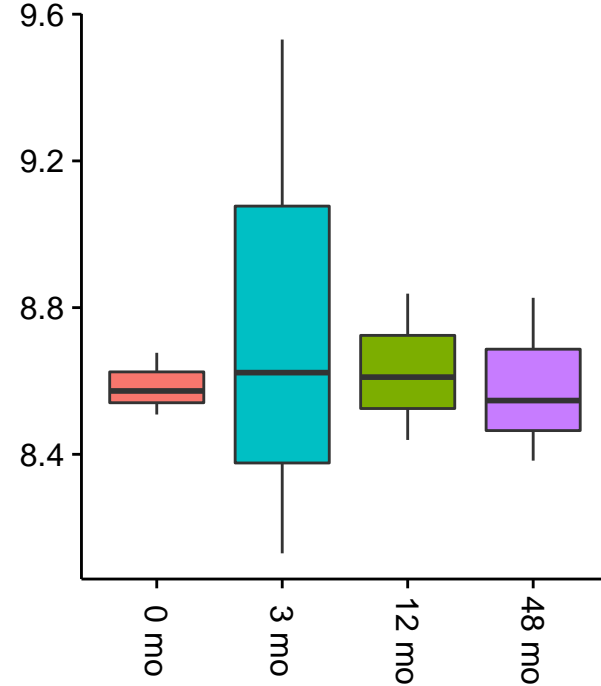


Normalized Expression

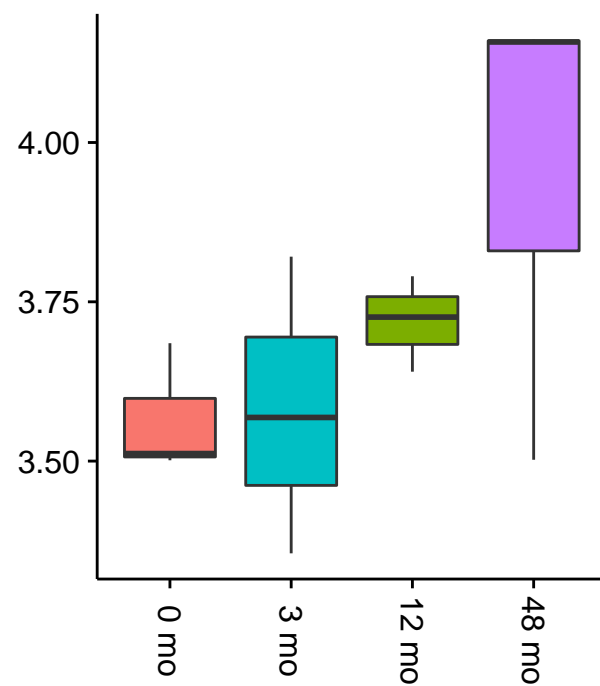
**THBS1**



**THBS2**



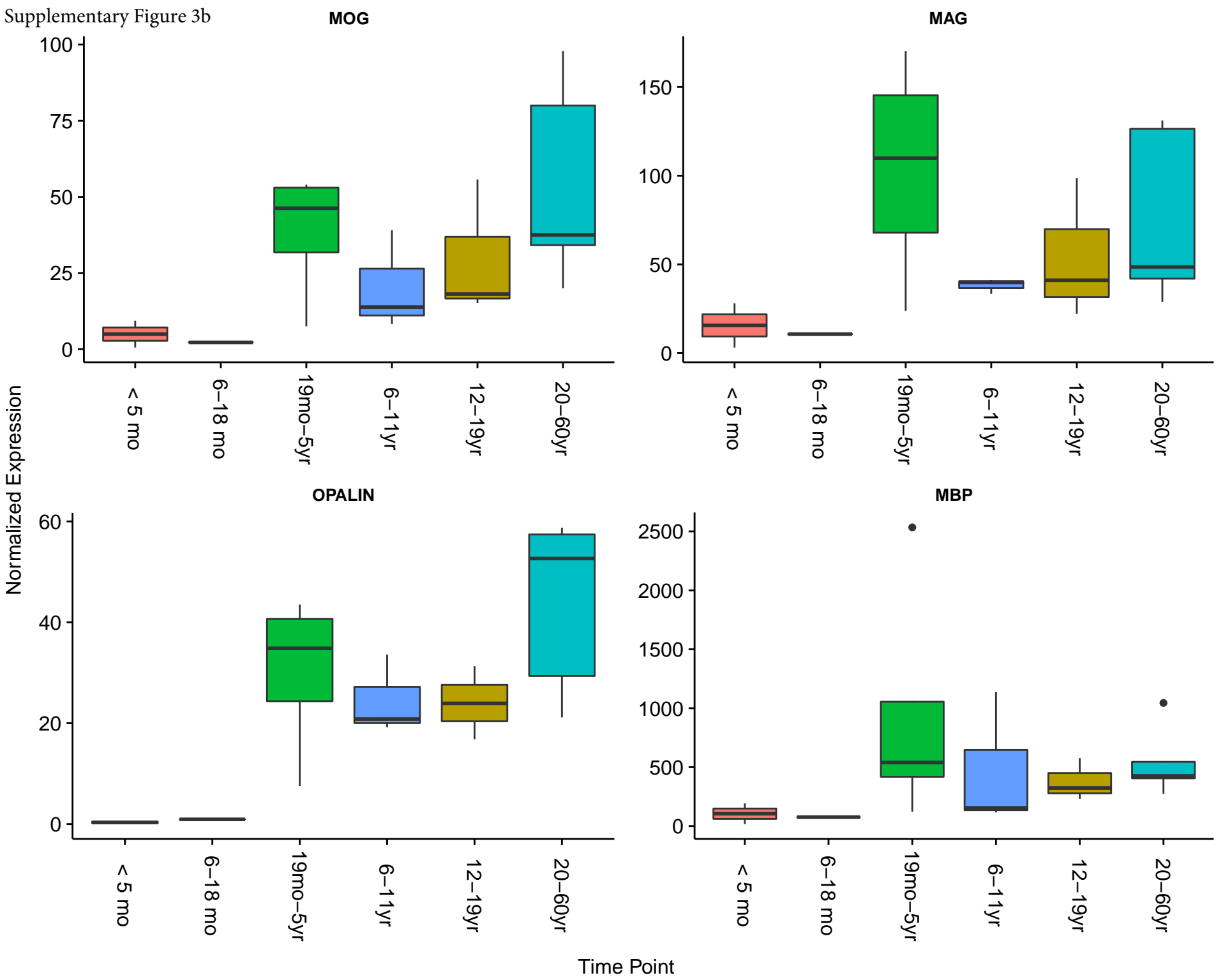
**THBS4**



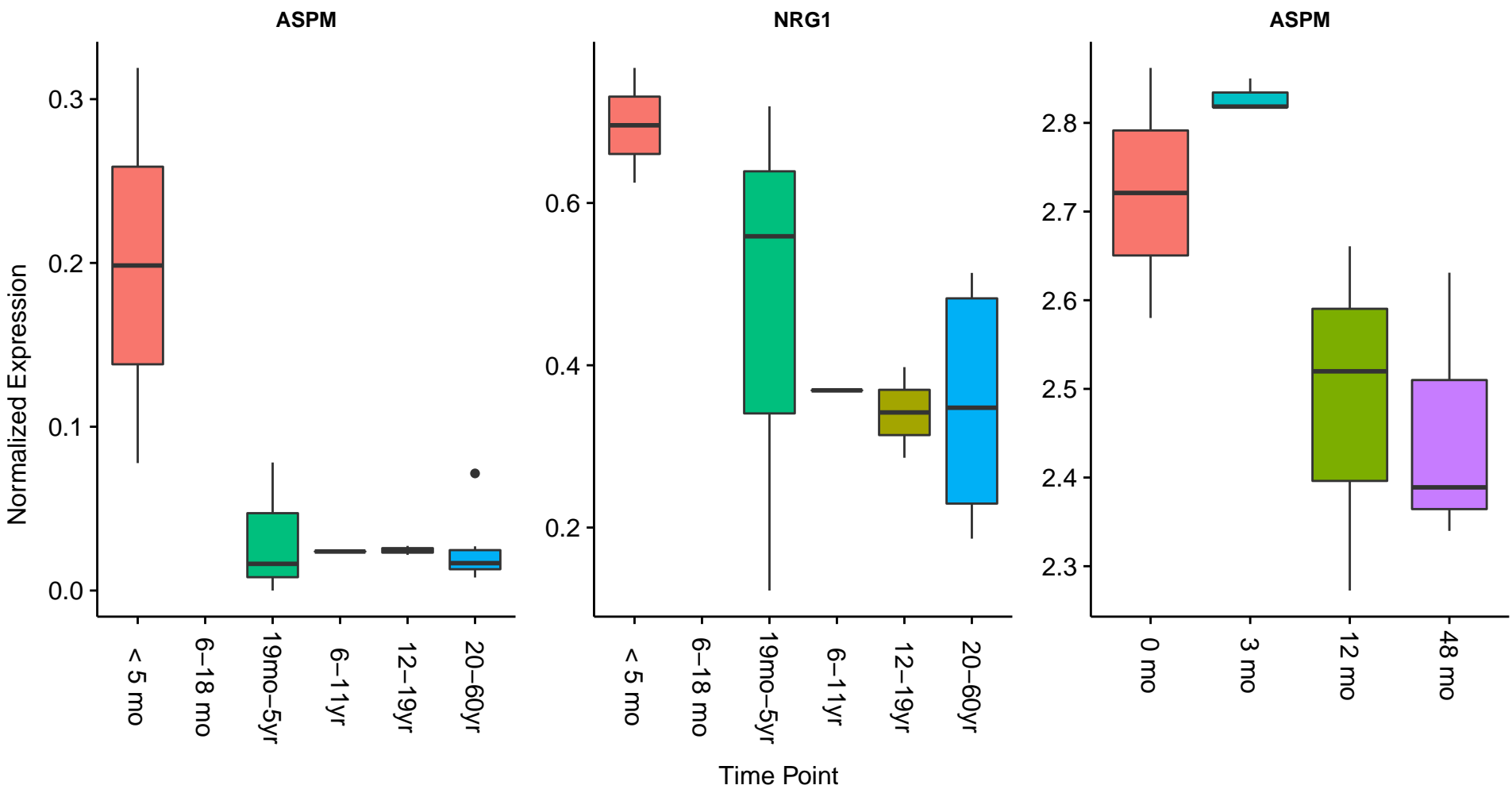
Time Point

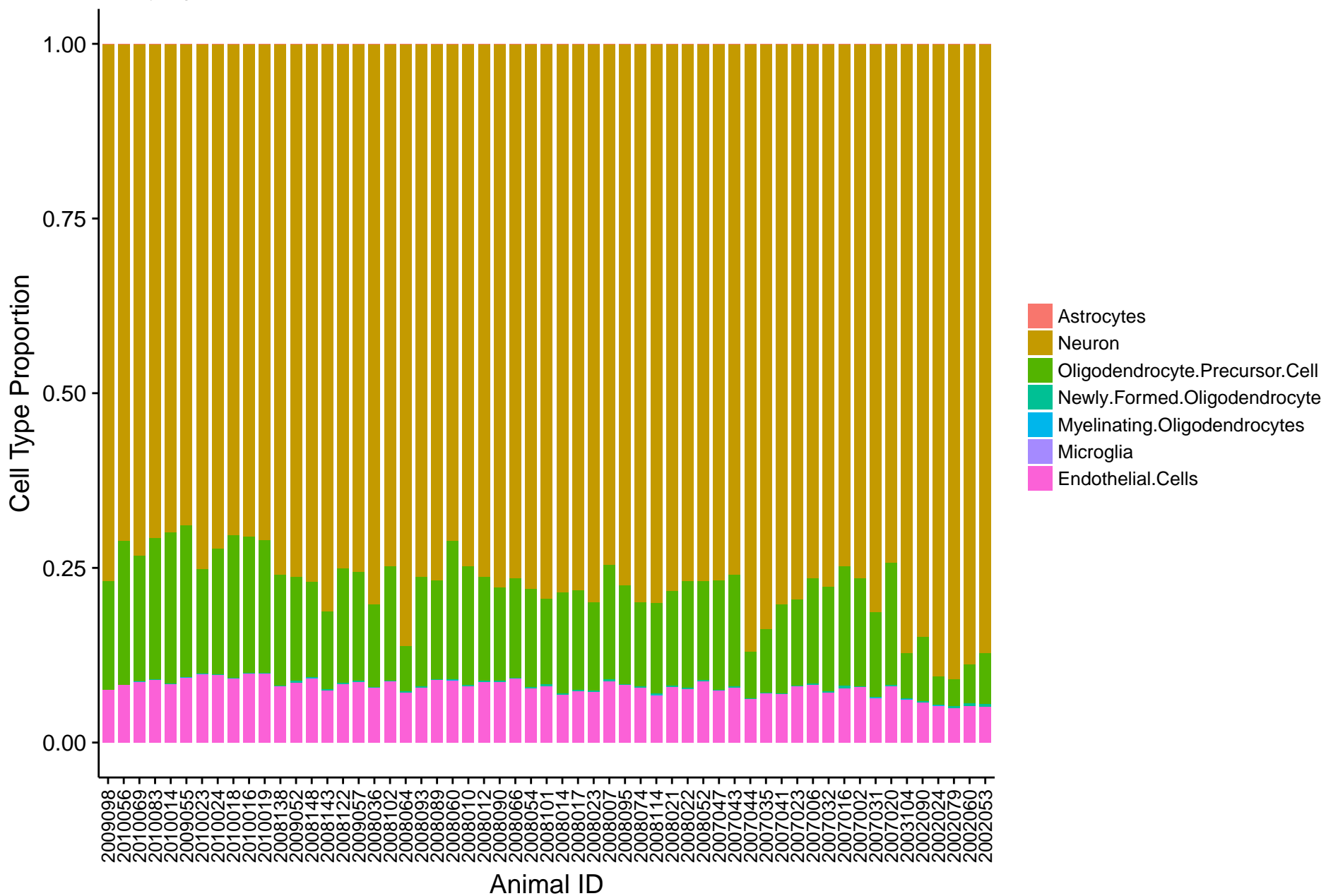


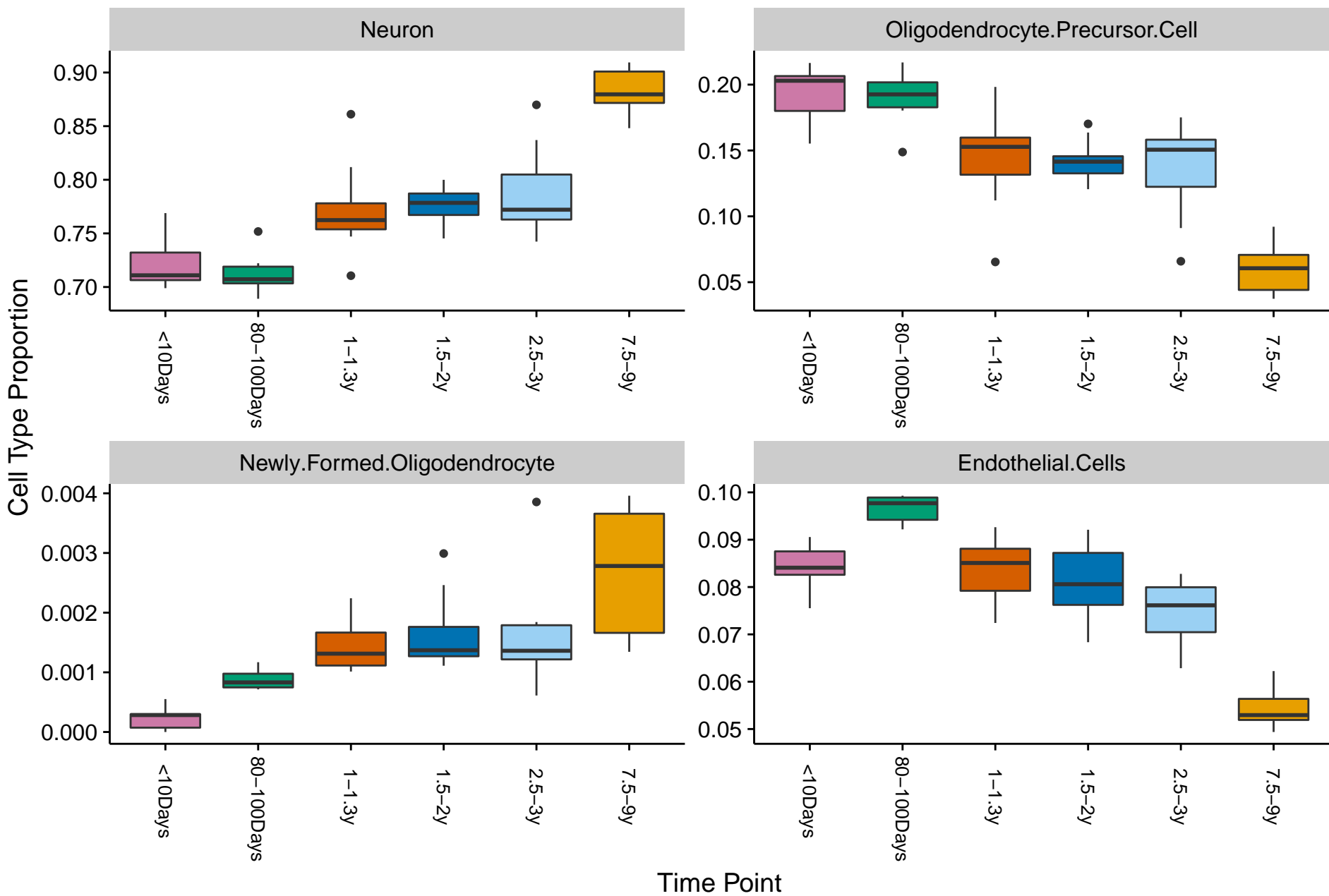
Supplementary Figure 3b



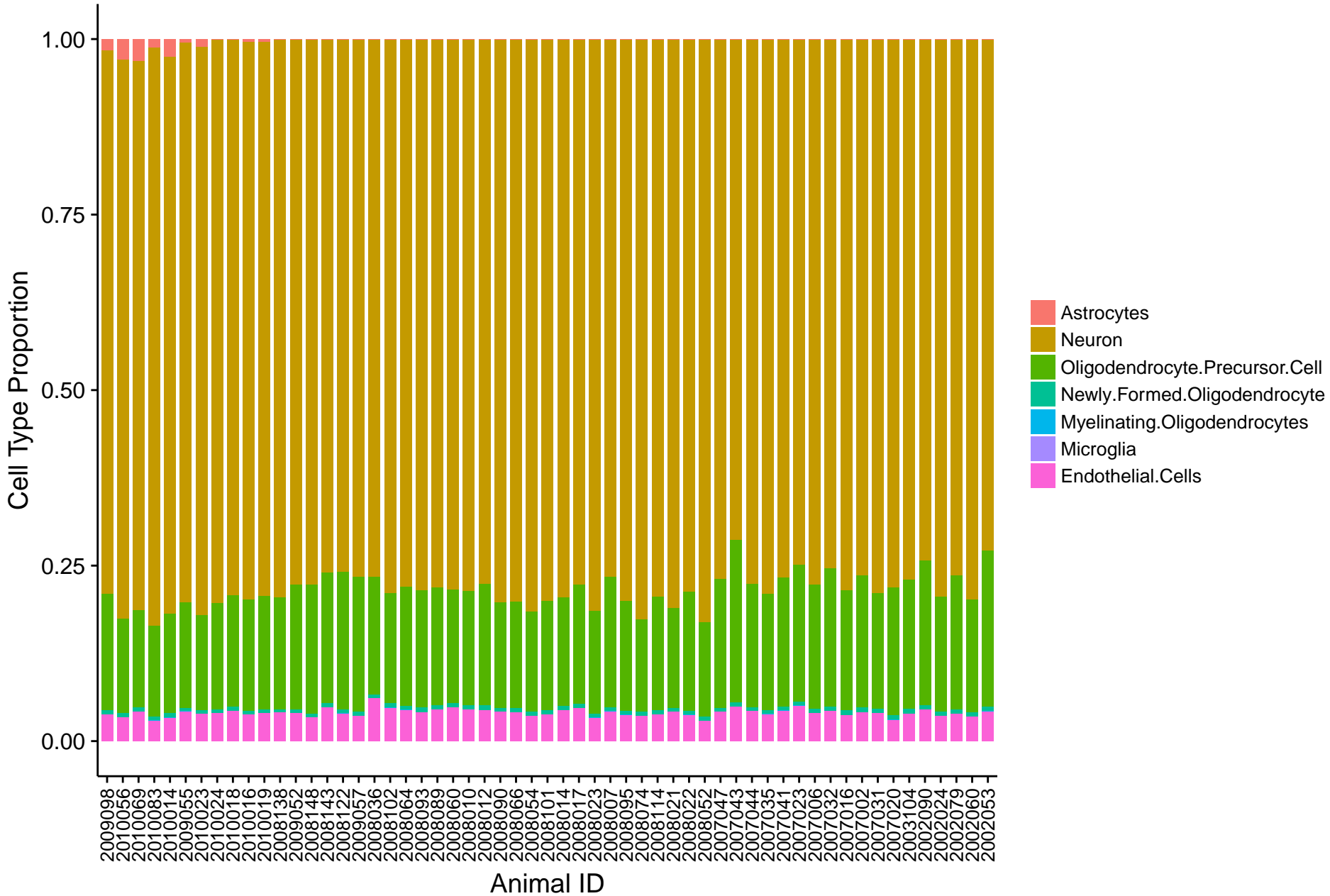
Supplementary Figure 3c





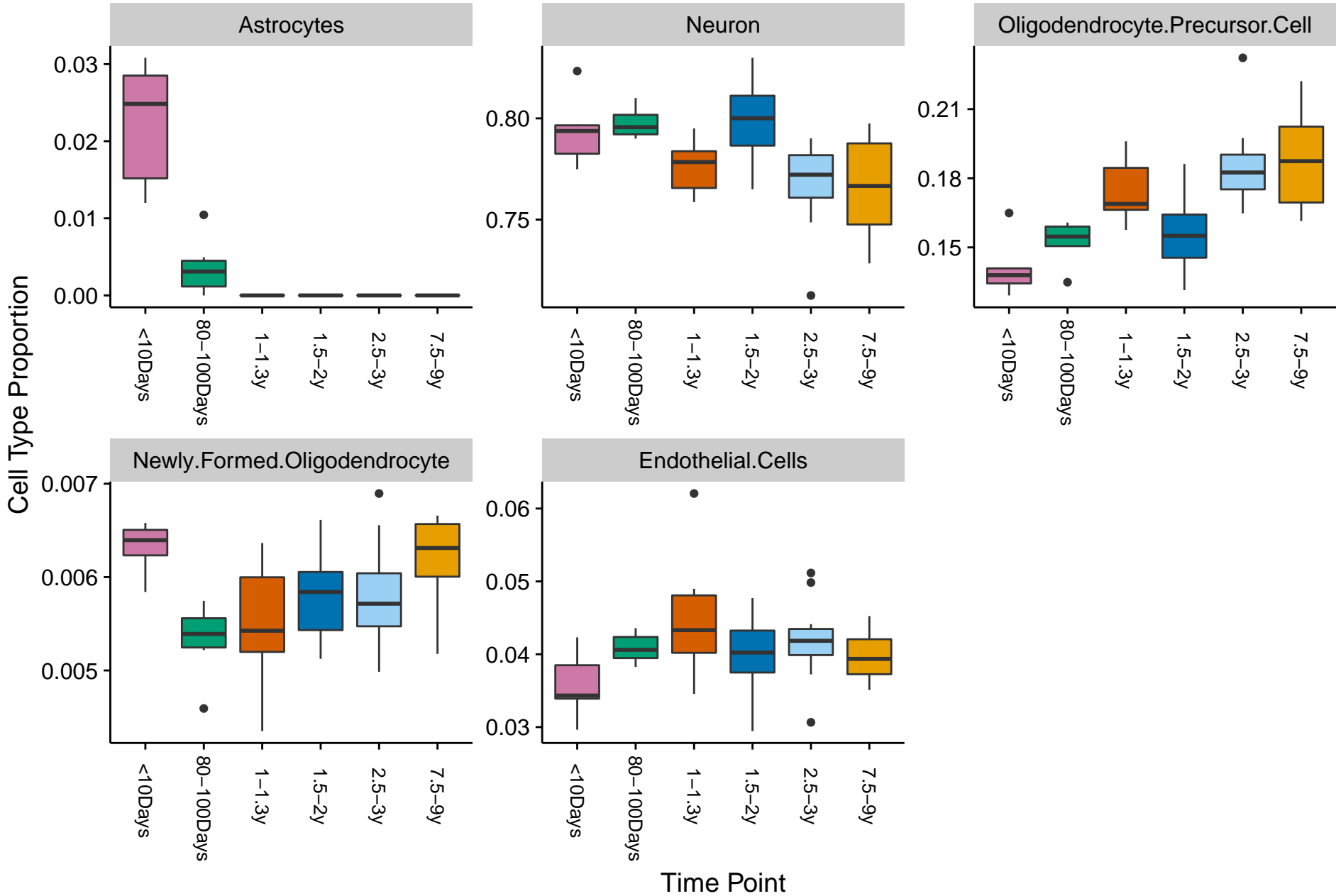


## Caudate

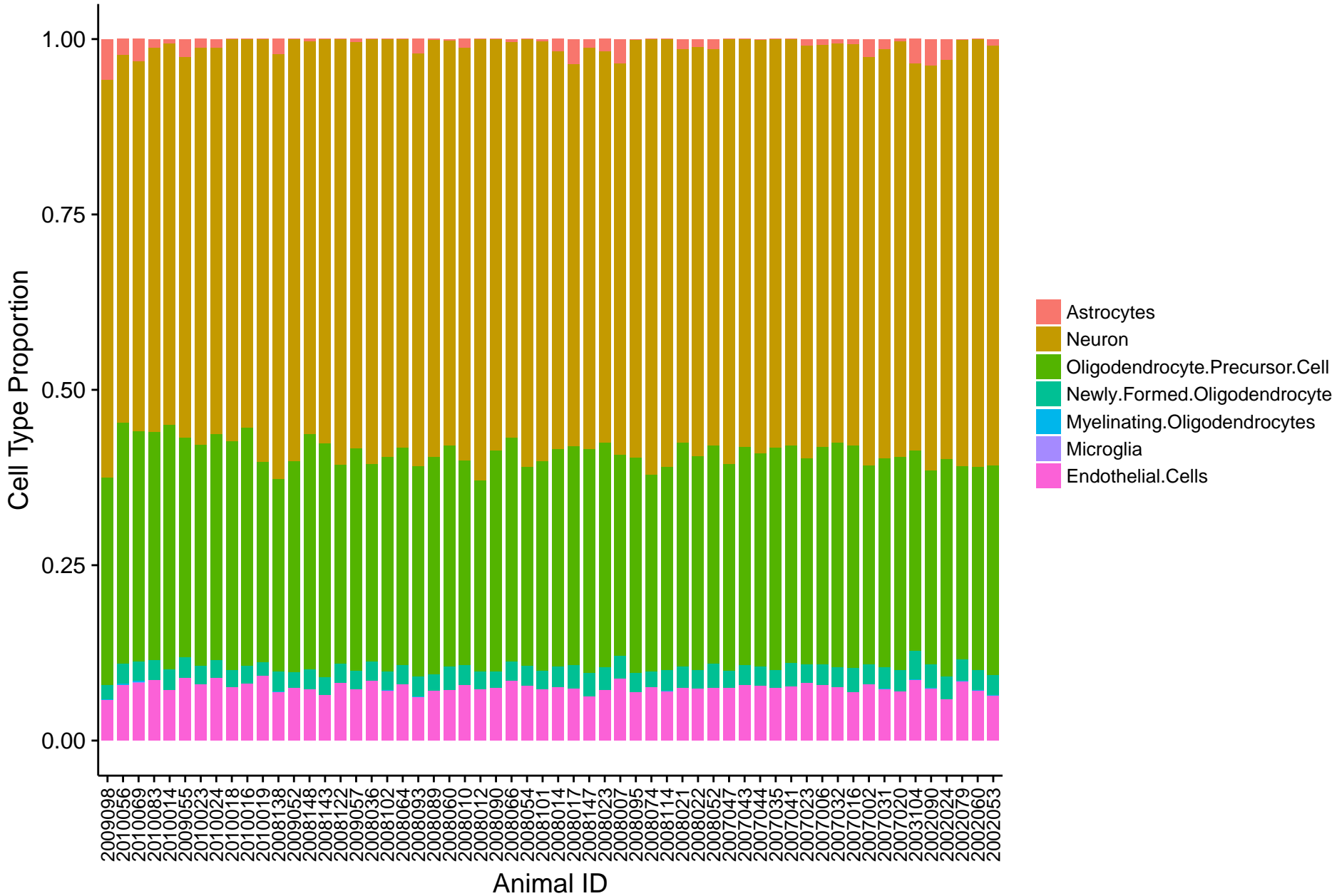


Supplementary Figure 5b

### Caudate

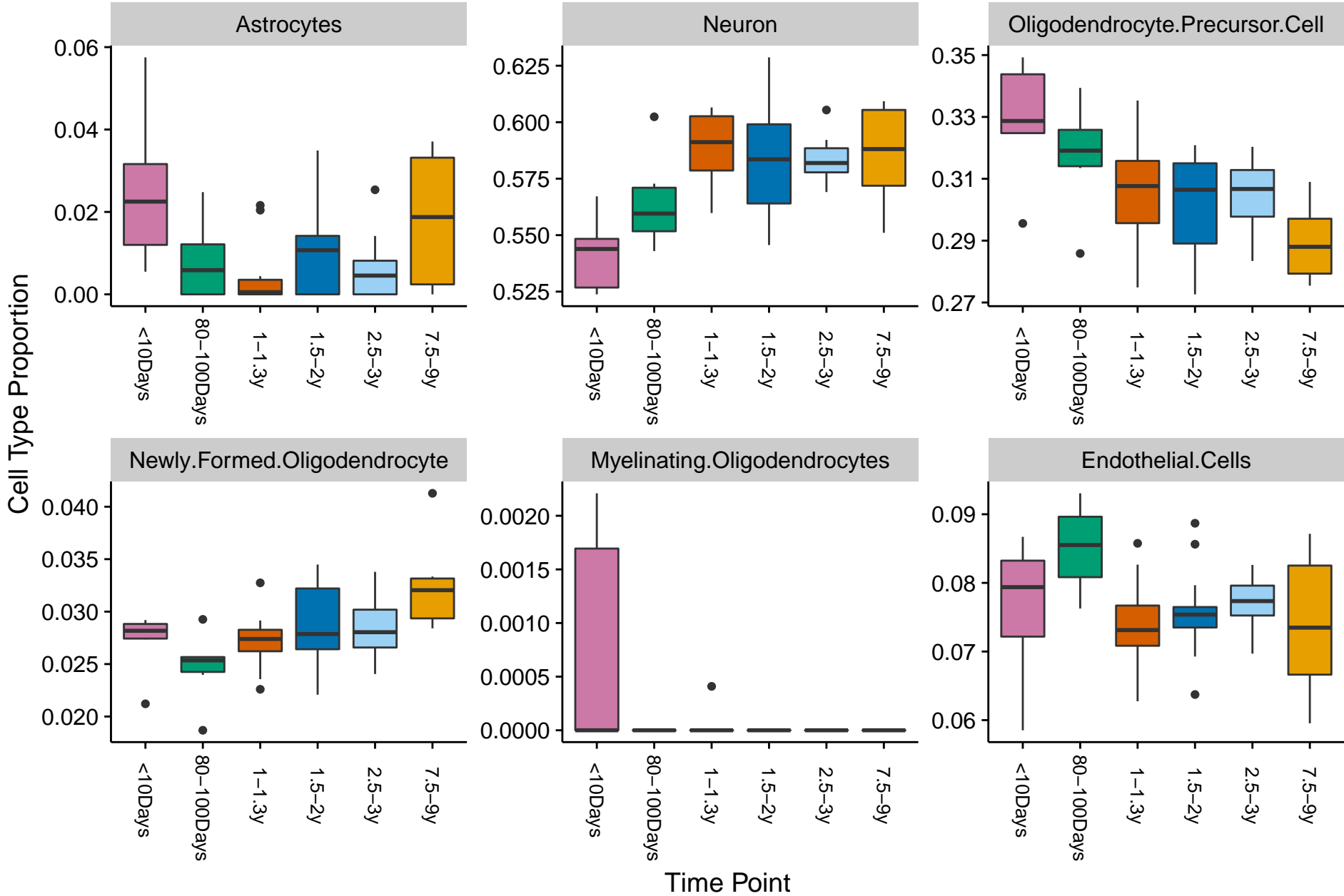


## Hippocampus



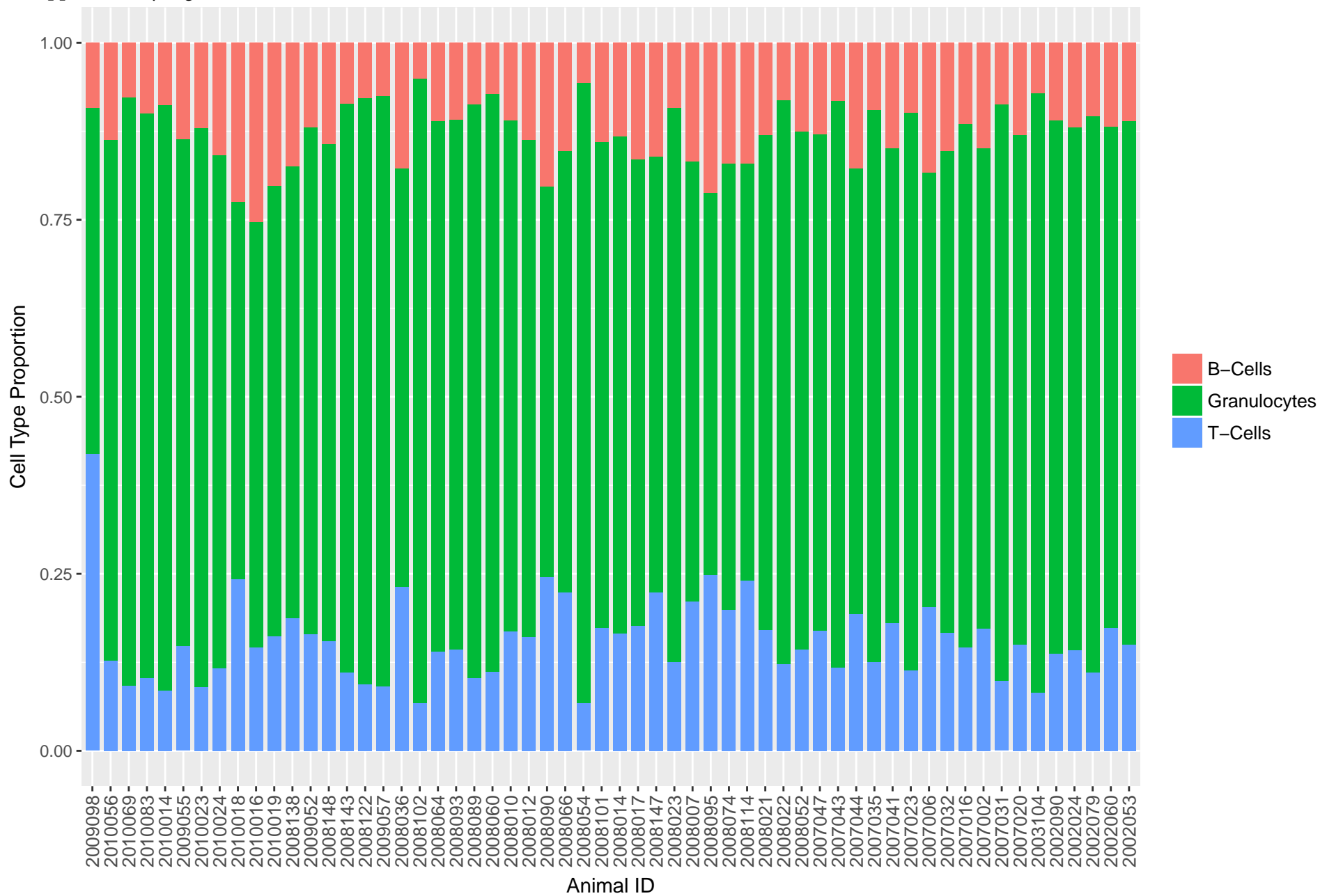
Supplementary Figure 6b

### Hippocampus

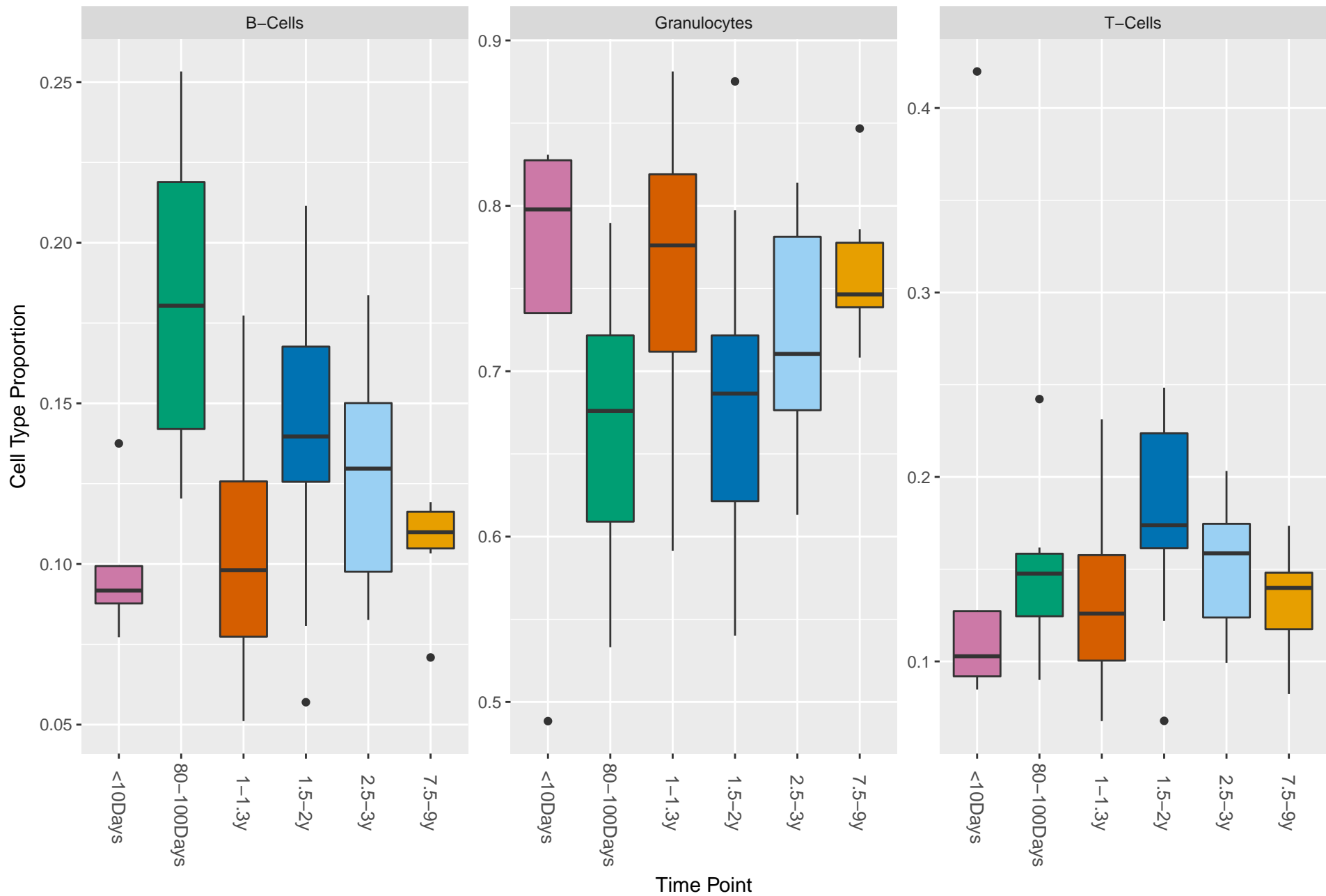


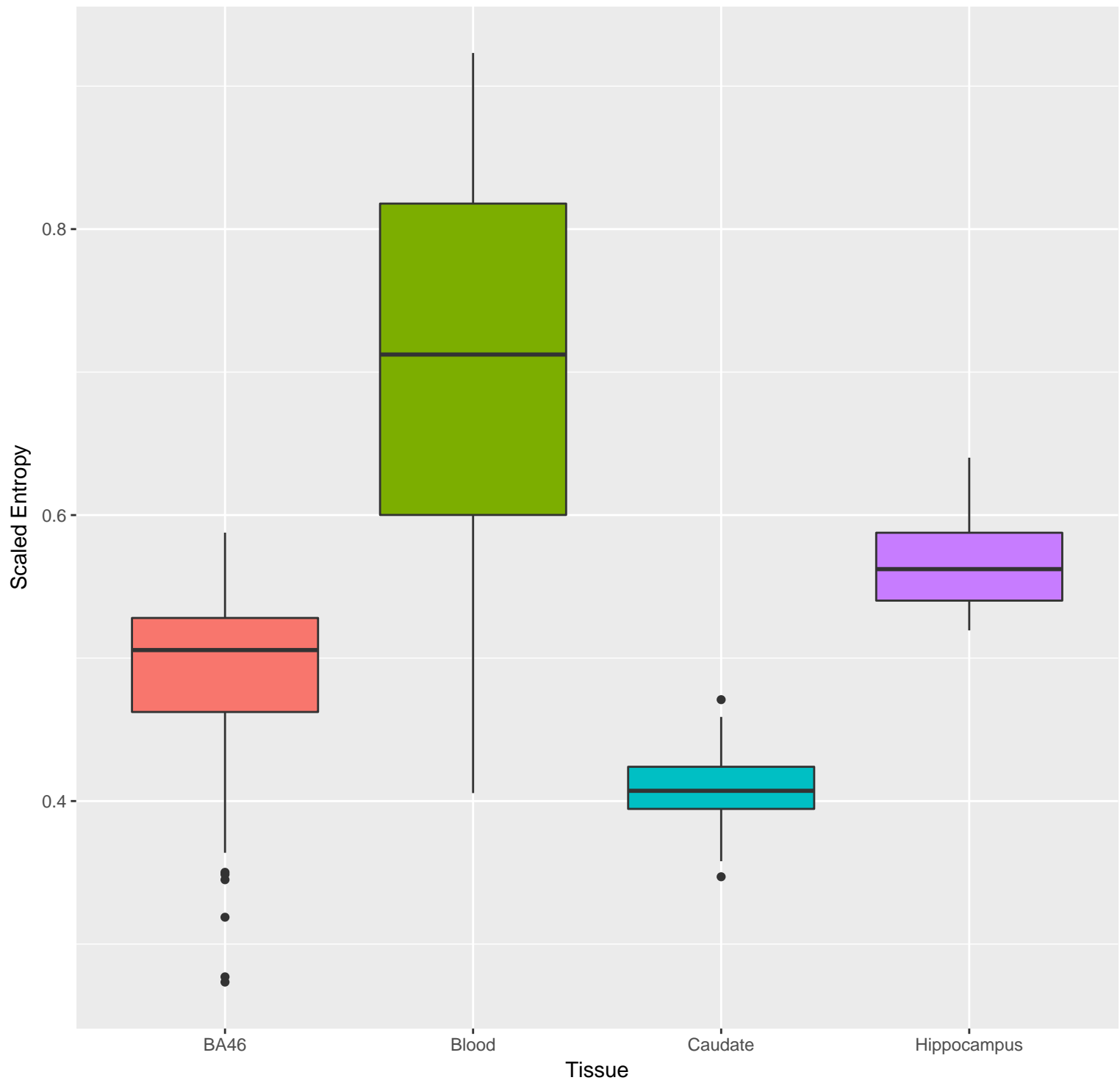
Time Point



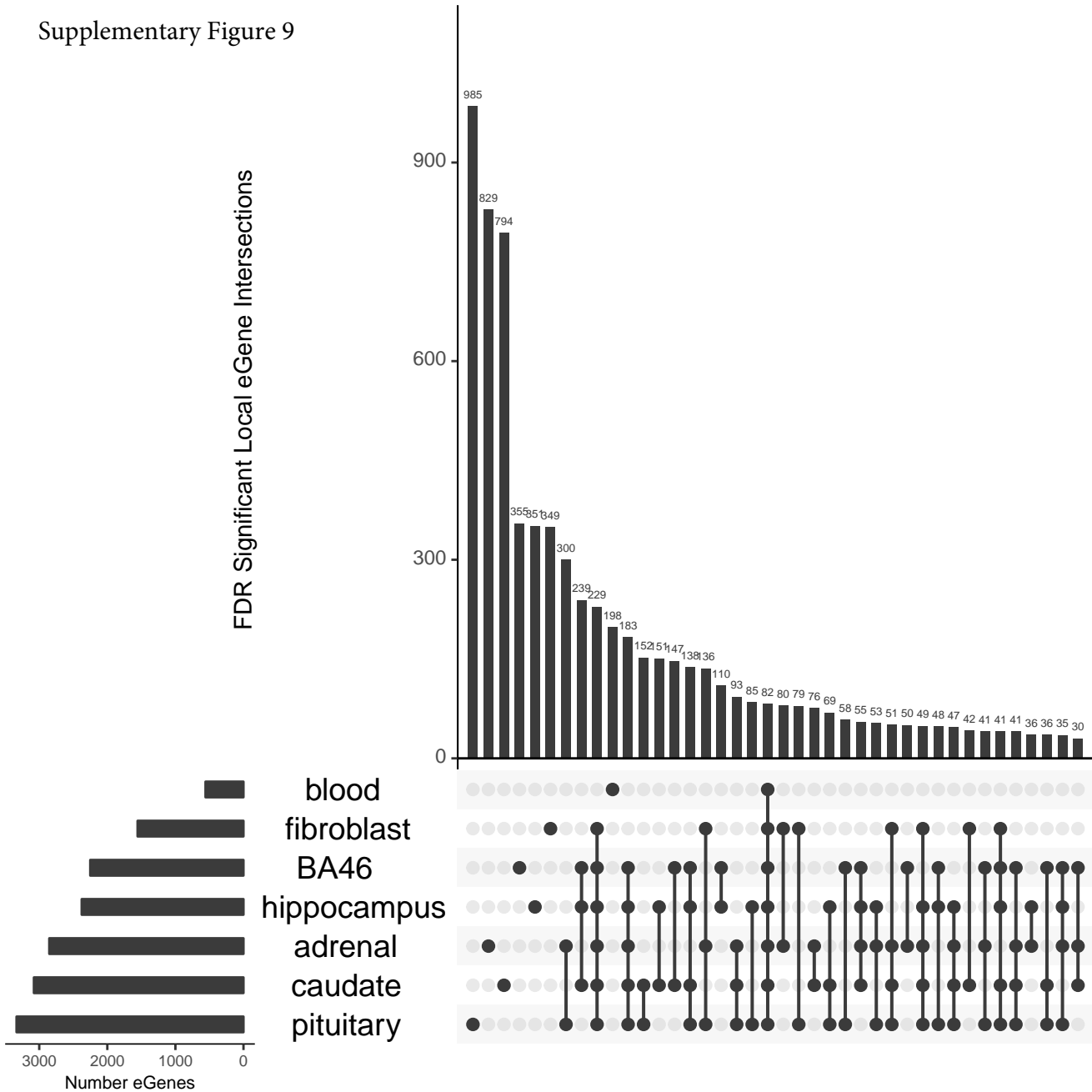


Supplementary Figure 7b

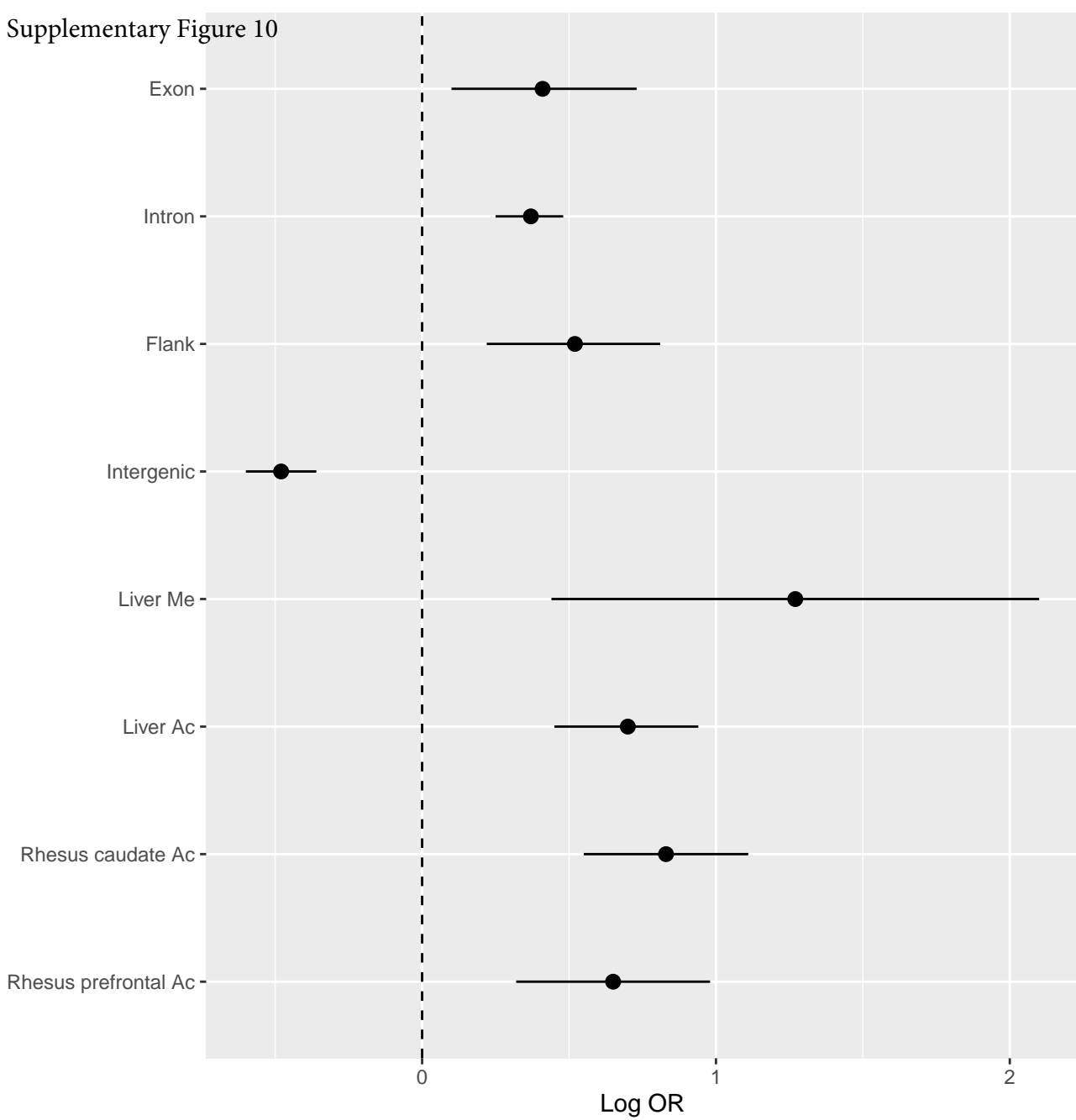




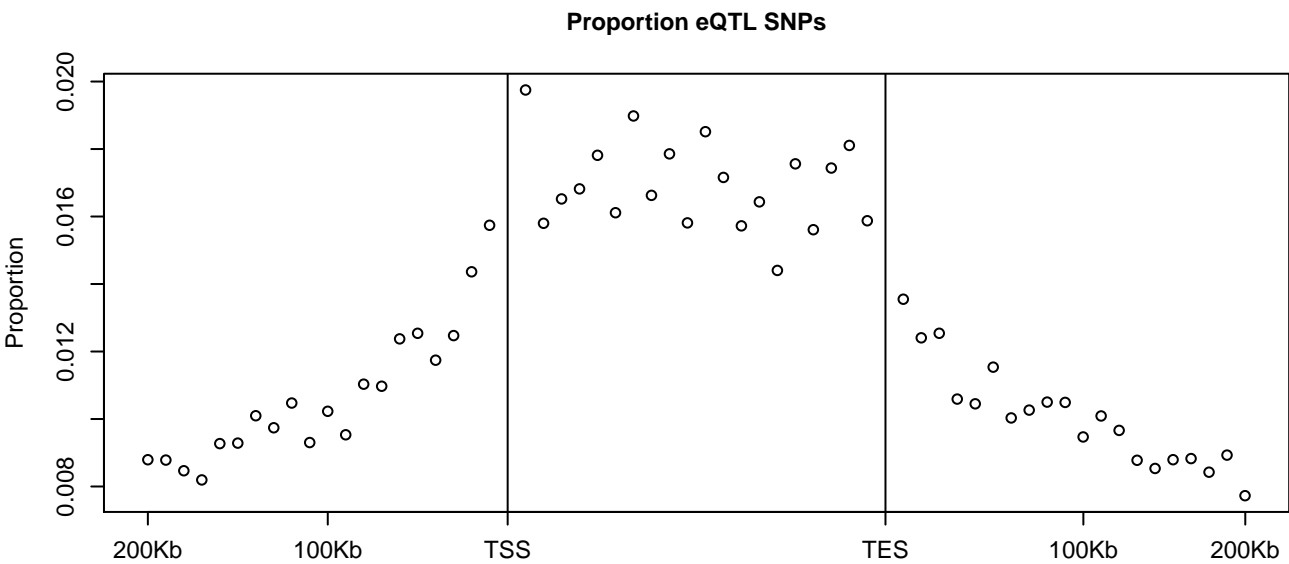
Supplementary Figure 9



Supplementary Figure 10



Supplementary Figure 11



**Supplementary Table 1. Summary of sequential probe filtering steps applied to HumanRef-8v2 array**

<b>Filtering Step</b>	<b>Number of probes excluded</b>	<b>Number of probes remaining</b>
Total Number of Probes on HumanRef-8v2		22,184
Align to vervet sequence	3581	18,603
No indels	4837	13,766
Unique hits to vervet sequence	461	13,305
Up to 5 mismatches in total probe sequence	207	13,098
Maximum 1 mismatch in central portion of probe	1563	11,535
Presence of common SNPs in probe sequence	434	11,101
Liftover from scaffold to vervet chromosome	100	11,001
Detected in at least 5% of animals at Illumina $p < 0.05$	4983	6,018

**Supplementary Table 2. Biotypes of genes analyzed in Dataset 2**

<b>Tissue</b>	<b>Protein_Coding</b>	<b>Non_Coding</b>	<b>Pseudo_Gene</b>	<b>Other/Unknown</b>	<b>Total_Genes</b>
Adrenal	18221	3898	3036	32	25187
BA46	18451	5656	3393	30	27530
Blood	20529	8112	5093	42	33776
Caudate	18695	5961	3559	34	28249
Fibroblast	16614	2913	2787	14	22328
Hippocampus	18290	5411	3223	33	26957
Pituitary	18879	4976	3344	37	27236



**Supplementary Table 3. Genes with high expression in one of the seven tissues evaluated with RNA-Seq. Presented are the means per tissue of CPM of TMM normalized count data. References are provided at the bottom of the table.**

VervetGeneSymbol	Description	Adrenal	Blood	Caudate	Fibroblast	Hippo	Pituitary	BA46	Max	Tissue.Max	Gene links to the tissue function*
<i>LOC103216445</i>	steroid 17-alpha-hydroxylase/17,20 lyase	14036.7	1.96902	0.96493	2.0436848	1.045	4.24694	1.0368	14036.7	Adrenal	
<i>STAR</i>	steroidogenic acute regulatory protein	10620.4	1.75588	0.99425	1.3615424	0.829	3.60259	0.8475	10620.4	Adrenal	a role in steroidogenesis in adrenals <sup>1</sup>
<i>LOC103237546</i>	cytochrome P450 11B1, mitochondrial	5682.77	1.17149	0.06733	0.7601465	0.088	1.56708	0.079	5682.77	Adrenal	
<i>LOC103245339</i>	cholesterol side-chain cleavage enzyme, mitochondrial	5274.27	1.83883	1.41084	0.8371132	0.479	5.55669	0.3911	5274.27	Adrenal	
<i>LOC103224109</i>	3 beta-hydroxysteroid dehydrogenase/Delta 5->4-isome	4620.16	1.02853	0.17528	0.6648728	0.13	1.60302	0.1659	4620.16	Adrenal	
<i>LOC103221724</i>	steroid 21-hydroxylase	4614.96	0.98424	0.37278	0.6002827	0.375	2.22281	0.2324	4614.96	Adrenal	
<i>LOC103221358</i>	glutathione S-transferase A3	2378.28	1.078	0.05385	0.3126857	0.033	0.83506	0.0281	2378.28	Adrenal	
<i>LOC103237547</i>	cytochrome P450 11B1, mitochondrial-like	1497.27	1.34717	0.08066	0.2068515	0.046	0.40351	0.0706	1497.27	Adrenal	
<i>LOC103221720</i>	tenascin-X-like	1099.93	0.96596	0.62226	0.714856	0.665	1.12399	0.8683	1099.93	Adrenal	
<i>LOC103221719</i>	steroid 21-hydroxylase-like	1080.27	0.48447	0.02674	0.1298478	0.02	0.29704	0.0172	1080.27	Adrenal	
<i>SERPINA5</i>	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, i	969.736	5.01123	0.32745	0.1265797	0.653	8.77306	0.2177	969.736	Adrenal	role in adrenal gland development and steroidogenesis <sup>2</sup>
<i>MC2R</i>	melanocortin 2 receptor (adrenocorticotrophic hormone)	677.134	1.49872	0.03163	0.0990165	0.024	0.66854	0.0143	677.134	Adrenal	
<i>LOC103221721</i>	serine/threonine-protein kinase 19-like	397.149	0.34683	0.02677	0.048376	0.029	0.1449	0.0459	397.149	Adrenal	
<i>AVPR1A</i>	arginine vasopressin receptor 1A	351.362	0.99528	0.24922	0.0540573	0.69	0.55493	2.2969	351.362	Adrenal	regulation of aldosterone secretion <sup>3</sup> , in brain (mostly in septal nucleus), V1A
<i>KRT80</i>	keratin 80	338.73	2.54884	0.03079	1.7058982	0.106	2.003	2.2695	338.73	Adrenal	
<i>SERPINF2</i>	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigr	293.858	2.14206	0.07687	2.2143439	0.667	2.2331	0.1015	293.858	Adrenal	
<i>VTN</i>	vitronectin	252.728	2.08564	2.89347	0.3577577	1.99	3.84988	2.6754	252.728	Adrenal	
<i>PON3</i>	paraoxonase 3	225.041	1.10187	2.12092	0.3979202	1.415	3.318	1.1356	225.041	Adrenal	
<i>LOC103236010</i>	alcohol dehydrogenase 1C	195.564	1.90079	0.10949	0.0388765	0.065	2.23227	0.0536	195.564	Adrenal	
<i>HOXA5</i>	homeobox A5	183.006	1.14667	0.00291	5.3960996	0.007	0.06456	0.0028	183.006	Adrenal	
<i>MAP3K15</i>	mitogen-activated protein kinase kinase kinase 15	180.401	9.59698	6.3744	0.5891424	7.887	2.66232	5.8447	180.401	Adrenal	
<i>LOC103221726</i>	uncharacterized LOC103221726	170.991	0.60676	0.26157	0.0586167	0.241	0.31083	0.2392	170.991	Adrenal	
<i>RGN</i>	regucalcin	170.15	1.14789	4.02933	0.0795482	6.108	7.38139	4.5735	170.15	Adrenal	
<i>LRRC38</i>	leucine rich repeat containing 38	167.802	1.05419	0.20054	0.030719	0.042	0.65828	0.7031	167.802	Adrenal	
<i>MRAP</i>	melanocortin 2 receptor accessory protein	154.064	1.18998	0.66305	0.2422359	0.572	0.28949	0.6347	154.064	Adrenal	
<i>CHAD</i>	chondroadherin	150.751	4.50058	2.47324	0.2957742	2.163	7.87485	2.5129	150.751	Adrenal	
<i>RBP5</i>	retinol binding protein 5, cellular	147.506	1.05587	0.87473	0.2071491	0.38	1.28551	0.8882	147.506	Adrenal	
<i>LOC103225291</i>	hemoglobin subunit alpha	0.99532	34787.8	3.05125	0.2085443	0.991	9.02605	0.6743	34787.8	Blood	
<i>ALAS2</i>	aminolevulinate, delta-, synthase 2	0.15539	14948.3	1.41916	0.1541252	0.175	2.86073	0.1311	14948.3	Blood	
<i>LOC103247904</i>	hemoglobin subunit gamma-1	0.81707	14228	3.11984	0.3912939	0.179	1.11515	0.1328	14228	Blood	
<i>C5</i>	complement component 5	1.61909	904.861	1.82808	0.139223	1.844	3.40081	0.9734	904.861	Blood	
<i>SELL</i>	selectin L	1.18212	696.891	0.40014	0.0213302	0.614	0.98613	0.6272	696.891	Blood	
<i>SLC4A1</i>	solute carrier family 4 (anion exchanger), member 1 (Diego I	0.53236	682.359	0.77049	0.007127	0.111	2.26319	0.044	682.359	Blood	
<i>CA1</i>	carbonic anhydrase I	0.13072	646.323	0.08292	0.0099249	0.02	0.85557	0.0198	646.323	Blood	
<i>CD52</i>	CD52 molecule	9.71651	610.509	2.08159	0.0129236	1.811	6.81823	2.8456	610.509	Blood	
<i>S100A9</i>	S100 calcium binding protein A9	0.40654	586.988	0.21593	0.0401566	0.125	6.39559	0.1844	586.988	Blood	
<i>DNAI2</i>	dynein, axonemal, intermediate chain 2	0.07174	427.83	2.9213	0.0064386	1.652	3.00147	0.1679	427.83	Blood	
<i>IFIT1B</i>	interferon-induced protein with tetratricopeptide repeats 1	0.15954	427.43	0.3951	0.0126759	0.297	0.38511	0.1095	427.43	Blood	
<i>MNDA</i>	myeloid cell nuclear differentiation antigen	9.78374	422.066	3.91453	0.0309068	4.273	7.98511	2.0923	422.066	Blood	
<i>GYPA</i>	glycophorin A (MNS blood group)	0.0166	333.829	0.09705	0.0082046	0.046	0.27031	0.0868	333.829	Blood	
<i>TUBB1</i>	tubulin, beta 1 class VI	2.86652	321.042	8.83069	0.2702692	9.062	7.0658	6.7667	321.042	Blood	granulocyte-specific expression profile <sup>5</sup>
<i>CSF3R</i>	colony stimulating factor 3 receptor (granulocyte)	1.86434	298.799	0.74464	0.0062131	0.647	2.10644	0.5129	298.799	Blood	
<i>PPBP</i>	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7	0.08841	293.199	0.03981	0.0054294	0.017	0.29933	0.0166	293.199	Blood	
<i>IKZF1</i>	IKAROS family zinc finger 1 (Ikaros)	5.69602	284.778	7.39798	0.0013347	6.907	5.0687	5.6931	284.778	Blood	
<i>FAIM3</i>	Fas apoptotic inhibitory molecule 3	4.4721	274.113	5.71989	4.2443931	4.704	3.427	4.6085	274.113	Blood	
<i>PHOSPHO1</i>	phosphatase, orphan 1	1.19298	259.229	3.84816	0.0813775	4.355	1.38958	4.1806	259.229	Blood	
<i>LOC103218320</i>	multidrug resistance-associated protein 1-like	0.0276	258.752	3.0322	0.0050187	3.573	0.6083	4.0503	258.752	Blood	
<i>PTPRCAP</i>	protein tyrosine phosphatase, receptor type, C-associated p	3.96477	247.138	1.88494	0.2962148	1.441	3.51085	1.5907	247.138	Blood	
<i>SAMD9</i>	sterile alpha motif domain containing 9	7.67217	241.471	5.60187	0.728545	7.457	3.67927	2.8625	241.471	Blood	
<i>FYB</i>	FYN binding protein	6.60373	240.504	7.37868	0.2835352	8.762	6.89427	5.5687	240.504	Blood	
<i>TAGAP</i>	T-cell activation RhoGTPase activating protein	3.1357	221.868	5.36609	0.7699518	5.603	2.2658	3.8776	221.868	Blood	
<i>RGS18</i>	regulator of G-protein signaling 18	1.92409	214.933	3.81188	0.0085742	5.112	1.51364	3.7099	214.933	Blood	

**Supplementary Table 3. Genes with high expression in one of the seven tissues evaluated with RNA-Seq. Presented are the means per tissue of CPM of TMM normalized count data. References are provided at the bottom of the table.**

VervetGeneSymbol	Description	Adrenal	Blood	Caudate	Fibroblast	Hippo	Pituitary	BA46	Max	Tissue.Max	Gene links to the tissue function*
<i>CSF2RB</i>	colony stimulating factor 2 receptor, beta, low-affinity (gran	5.76557	212.738	2.41002	0.2373445	2.453	4.27773	2.2889	212.738	Blood	granulocyte-specific expression profile <sup>5</sup>
<i>WDFY4</i>	WDFY family member 4	9.0863	211.01	8.28788	0.1456566	8.052	4.06722	6.1162	211.01	Blood	
<i>HCLS1</i>	hematopoietic cell-specific Lyn substrate 1	9.85568	210.45	5.04323	0.3959009	5.299	7.93302	4.0685	210.45	Blood	
<i>CCR7</i>	chemokine (C-C motif) receptor 7	0.90704	210.431	0.1255	1.1361711	0.151	0.521	0.1869	210.431	Blood	
<i>ITK</i>	IL2-inducible T-cell kinase	1.20429	207.227	1.29309	0.004317	0.116	0.60054	0.1465	207.227	Blood	
<i>LCK</i>	lymphocyte-specific protein tyrosine kinase	3.22682	206.222	0.17094	0.0051783	0.558	1.4517	0.2232	206.222	Blood	
<i>SYK</i>	spleen tyrosine kinase	5.36424	202.679	6.13767	0.0092155	6.222	4.91539	5.8755	202.679	Blood	B-lymphocytes-specific expression profile <sup>5</sup>
<i>ICAM4</i>	intercellular adhesion molecule 4 (Landsteiner-Wiener bloo	0.58076	202.447	0.36422	0.5094981	1.455	0.45466	1.3257	202.447	Blood	
<i>SLA</i>	Src-like-adaptor	4.55569	201.596	4.93429	0.6827327	4.81	4.65201	7.6022	201.596	Blood	
<i>BIN2</i>	bridging integrator 2	8.56543	197.903	9.19053	0.0103679	9.271	6.77759	7.4435	197.903	Blood	
<i>ITGB7</i>	integrin, beta 7	2.26861	192.36	1.39781	0.2896981	1.11	1.25833	1.1638	192.36	Blood	
<i>EPB42</i>	erythrocyte membrane protein band 4.2	0.17348	185.244	0.54186	0.0146697	0.643	0.5039	0.7406	185.244	Blood	
<i>RAC2</i>	ras-related C3 botulinum toxin substrate 2 (rho family, smal	8.47778	182.007	0.34371	0.1670654	0.362	4.07683	0.3183	182.007	Blood	a crucial role in T-cell development <sup>6</sup>
<i>ARHGAP15</i>	Rho GTPase activating protein 15	2.48094	180.697	2.07022	0.0134773	4.871	1.44684	3.8718	180.697	Blood	
<i>SPTA1</i>	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	0.0703	176.331	0.62955	0.0169989	0.027	1.06831	0.0547	176.331	Blood	
<i>TNFRSF10C</i>	tumor necrosis factor receptor superfamily, member 10c, de	0.156	175.366	0.09162	0.0214552	0.046	0.47142	0.0613	175.366	Blood	
<i>GPR160</i>	G protein-coupled receptor 160	0.37351	172.74	1.84634	2.0446647	4.499	1.51714	2.3069	172.74	Blood	
<i>TMEM154</i>	transmembrane protein 154	0.75609	171.639	0.83376	4.1035227	1.347	1.57482	1.5051	171.639	Blood	
<i>TRIM58</i>	tripartite motif containing 58	1.3372	169.446	1.31528	2.3272836	8.429	3.29084	6.0942	169.446	Blood	granulocyte-specific expression profile <sup>5</sup>
<i>MYO1G</i>	myosin IG	4.87605	167.294	1.3589	0.0335384	0.31	2.13445	0.7187	167.294	Blood	
<i>NCF2</i>	neutrophil cytosolic factor 2	6.94626	160.915	6.36527	0.1752165	6.585	6.59206	4.2583	160.915	Blood	
<i>CXCR2</i>	chemokine (C-X-C motif) receptor 2	0.37292	160.77	0.45831	0.0063517	0.475	0.7306	0.3963	160.77	Blood	
<i>HBM</i>	hemoglobin, mu	0.01872	158.583	0.16214	0.004093	0.146	0.49123	0.0233	158.583	Blood	
<i>NFE2</i>	nuclear factor, erythroid 2	0.12315	150.242	0.11881	0.0996207	0.138	3.65572	0.0624	150.242	Blood	
<i>TBC1D10C</i>	TBC1 domain family, member 10C	2.46192	149.682	2.04228	0.1177031	0.686	2.65843	0.8981	149.682	Blood	a component of T-cell receptor complex on the surface of T-cell lymphocytes
<i>DPEP2</i>	dipeptidase 2	4.1437	149.173	0.46393	0.0519735	0.52	1.75374	0.368	149.173	Blood	
<i>NLRP12</i>	NLR family, pyrin domain containing 12	0.71242	146.294	0.14345	0.0972757	0.44	0.25348	0.2669	146.294	Blood	
<i>IL16</i>	interleukin 16	9.05422	141.607	4.35364	1.9403878	3.384	4.54366	2.3579	141.607	Blood	
<i>CD247</i>	CD247 molecule	1.49865	139.885	0.39725	0.0440795	0.271	1.94811	0.3561	139.885	Blood	
<i>GIMAP7</i>	GTPase, IMAP family member 7	8.44495	139.628	2.53748	0.0055401	2.104	5.47873	1.806	139.628	Blood	
<i>IDO1</i>	indoleamine 2,3-dioxygenase 1	4.72264	134.578	0.09899	0.0168587	0.154	1.35854	0.1319	134.578	Blood	expressed in T-lymphocytes <sup>8</sup>
<i>SASH3</i>	SAM and SH3 domain containing 3	4.94053	129.76	3.51595	0.0578001	3.67	4.07672	2.9602	129.76	Blood	
<i>ITGAL</i>	integrin, alpha L (antigen CD11A (p180), lymphocyte functio	3.5473	125.127	1.46544	0.0330256	0.965	2.22777	0.9641	125.127	Blood	
<i>CD28</i>	CD28 molecule	0.64319	123.58	0.37204	0.0074687	0.563	0.5559	0.4777	123.58	Blood	
<i>GRAP</i>	GRB2-related adaptor protein	4.61528	123.495	3.82252	0.0293726	2.915	3.10314	3.3656	123.495	Blood	
<i>ACAP1</i>	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	4.49456	122.338	5.16906	0.6244673	2.891	3.96063	5.2017	122.338	Blood	
<i>PIK3CG</i>	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic su	3.96204	120.873	4.66636	0.0187881	4.481	3.02214	3.834	120.873	Blood	plays a crucial role in the blood coagulation system and is involved in bleedin highly expressed in primate caudate <sup>11</sup>
<i>ARHGAP25</i>	Rho GTPase activating protein 25	5.56771	120.404	3.09473	0.0910841	3.375	4.67395	4.3869	120.404	Blood	
<i>C5H16orf54</i>	chromosome 5 open reading frame, human C16orf54	1.76697	120.069	1.78915	0.0017853	1.399	1.45079	0.9107	120.069	Blood	
<i>GRAP2</i>	GRB2-related adaptor protein 2	0.67118	115.758	9.2738	0.2629744	1.858	1.6753	4.4376	115.758	Blood	
<i>SLFN14</i>	schlafen family member 14	0.50108	112.603	0.11824	0.0124975	0.073	0.12506	0.088	112.603	Blood	
<i>CEACAM8</i>	carcinoembryonic antigen-related cell adhesion molecule 8	0.9532	110.705	0.61223	2.0276954	0.779	0.56339	1.6412	110.705	Blood	
<i>HCK</i>	hemopoietic cell kinase	6.67133	105.138	4.50921	0.0072104	4.085	4.25221	3.3802	105.138	Blood	highly expressed in primate caudate <sup>11</sup>
<i>FGR</i>	feline Gardner-Rasheed sarcoma viral oncogene homolog	6.85491	104.652	2.99501	0.0379101	2.199	2.46274	3.1518	104.652	Blood	
<i>FCN1</i>	ficolin (collagen/fibrinogen domain containing) 1	0.35937	104.334	0.02149	0.0037023	0.007	0.35056	0.019	104.334	Blood	
<i>ARHGAP9</i>	Rho GTPase activating protein 9	3.61136	104.314	3.6441	0.5965154	2.546	2.98619	3.3161	104.314	Blood	
<i>ITGA2B</i>	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa comple	2.54366	100.039	0.89719	0.2402636	0.927	4.22703	3.3328	100.039	Blood	
<i>SYNDIG1L</i>	synapse differentiation inducing 1-like	0.00695	1.65544	1643.46	0.0062972	8.388	0.14088	6.9838	1643.46	Caudate	
<i>ANKRD34B</i>	ankyrin repeat domain 34B	0.1371	0.8741	131.476	0.6091162	5.926	0.77101	6.0818	131.476	Caudate	highly expressed in primate caudate <sup>11</sup>
<i>GPR149</i>	G protein-coupled receptor 149	0.14648	2.05913	100.111	0.0047378	1.301	0.22843	2.5745	100.111	Caudate	
<i>GREM1</i>	gremlin 1, DAN family BMP antagonist	0.85543	2.73165	6.95508	2717.083	6.603	7.19289	3.5768	2717.08	Fibroblast	
<i>LRRC15</i>	leucine rich repeat containing 15	1.46922	3.19143	0.37839	1326.0936	0.104	0.13224	0.021	1326.09	Fibroblast	
<i>MFAP5</i>	microfibrillar associated protein 5	3.64449	1.45438	0.0605	576.90715	2.437	2.40718	0.036	576.907	Fibroblast	

**Supplementary Table 3. Genes with high expression in one of the seven tissues evaluated with RNA-Seq. Presented are the means per tissue of CPM of TMM normalized count data. References are provided at the bottom of the table.**

VervetGeneSymbol	Description	Adrenal	Blood	Caudate	Fibroblast	Hippo	Pituitary	BA46	Max	Tissue.Max	Gene links to the tissue function*
ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif	6.26744	5.88702	0.81667	483.66447	1.797	1.78261	5.3783	483.664	Fibroblast	
KRT7	keratin 7	0.98287	1.8237	0.04404	436.75437	0.331	8.12842	1.6153	436.754	Fibroblast	
LOX	lysyl oxidase	6.87638	2.48235	0.76194	360.80632	5.541	3.24337	2.1599	360.806	Fibroblast	involved in connective tissues functions <sup>12</sup>
DKK1	dickkopf WNT signaling pathway inhibitor 1	2.68719	0.66992	0.17735	323.48887	0.349	3.1234	2.2633	323.489	Fibroblast	expressed in fibroblasts <sup>13</sup>
CREB3L1	cAMP responsive element binding protein 3-like 1	8.11879	2.45756	0.76705	251.01609	1.278	8.83631	1.3623	251.016	Fibroblast	
FAP	fibroblast activation protein, alpha	5.42582	2.06841	0.27513	223.92162	0.311	1.66847	3.054	223.922	Fibroblast	control of fibroblast growth <sup>14</sup>
LOC103228547	uncharacterized LOC103228547	8.02166	0.73147	0.95235	221.78529	7.085	1.70055	0.9114	221.785	Fibroblast	
PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.36117	4.57555	4.5746	186.49797	2.617	1.70006	5.8793	186.498	Fibroblast	
CTHRC1	collagen triple helix repeat containing 1	0.91535	1.79414	4.84924	176.73317	5.407	9.40576	5.3876	176.733	Fibroblast	
AHRR	aryl-hydrocarbon receptor repressor	2.68431	6.08175	8.62163	164.03714	6.492	6.49391	9.4615	164.037	Fibroblast	
LOC103246059	A disintegrin and metalloproteinase with thrombospondin r	2.48844	1.54259	0.6998	141.3365	1.329	1.33267	0.9723	141.336	Fibroblast	
MXRA5	matrix-remodelling associated 5	1.35586	0.7689	0.8753	140.49966	2.537	2.42318	1.7359	140.5	Fibroblast	fibroblast functions <sup>15</sup>
STC2	stanniocalcin 2	1.71629	3.0736	0.48159	136.16403	0.657	2.45464	1.37	136.164	Fibroblast	
NUPR1	nuclear protein, transcriptional regulator, 1	7.87828	2.41962	1.69673	128.36354	3.753	5.78662	1.5071	128.364	Fibroblast	
VGLL3	vestigial-like family member 3	2.24105	1.2349	0.43655	127.56238	3.172	0.52289	0.5052	127.562	Fibroblast	
PTGDR2	prostaglandin D2 receptor 2	4.27626	7.10525	2.56264	123.25984	2.289	4.57497	1.9674	123.26	Fibroblast	
WISP1	WNT1 inducible signaling pathway protein 1	1.15569	1.57859	0.32221	118.57036	0.46	1.2281	0.4115	118.57	Fibroblast	
GDF15	growth differentiation factor 15	1.59988	1.8955	0.55922	110.46743	1.086	0.31309	1.3943	110.467	Fibroblast	
CKAP2	cytoskeleton associated protein 2	4.03398	5.53649	3.62243	106.7829	9.4	7.68669	6.0167	106.783	Fibroblast	
POMC	proopiomelanocortin	9.13195	0.91481	2.56866	1.5617152	1.013	22141.6	1.68	22141.6	Pituitary	coding a precursor of ACTH synthesized mainly in the anterior lobe of the pituitary growth hormone <sup>17</sup>
LOC103243211	somatotropin	2.25858	0.27496	0.06203	0.4746679	0.008	8700.7	0	8700.7	Pituitary	glycoprotein hormone coding a subunit alpha of luteinizing hormone (LH), fo
CGA	glycoprotein hormones, alpha polypeptide	1.17134	1.63155	0.20511	0.1448983	0.158	2333.25	0.2254	2333.25	Pituitary	
GPR50	G protein-coupled receptor 50	0.38016	1.64213	0.06901	0.039129	0.303	402.89	0.0854	402.89	Pituitary	
PITX1	paired-like homeodomain 1	0.15652	2.62771	0.13069	2.2180586	0.428	368.347	0.0868	368.347	Pituitary	involvement in pituitary development <sup>19</sup>
LOC103244205	nose resistant to fluoxetine protein 6-like	0.24848	2.40042	0.19456	2.6695869	0.448	366.005	0.4421	366.005	Pituitary	
LHX3	LIM homeobox 3	0.0998	1.8607	0.17645	0.0285294	0.134	323.719	0.0869	323.719	Pituitary	transcription factor in pituitary development mutated in combined pituitary I
SIX2	SIX homeobox 2	0.4951	2.80929	0.20709	0.5668065	0.016	221.262	0.5097	221.262	Pituitary	
TBX19	T-box 19	3.93586	5.73745	1.81374	1.0612523	3.157	174.514	0.9303	174.514	Pituitary	pituitary expression <sup>22</sup>
IRS4	insulin receptor substrate 4	0.12948	1.71543	3.18921	0.0189929	3.671	149.549	1.9885	149.549	Pituitary	IRS-4 is restricted almost exclusively to the pituitary gland and brain <sup>23</sup>
CITED1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carb	4.32754	1.58345	4.40898	0.0547896	8.745	131.987	4.9819	131.987	Pituitary	
PAX7	paired box 7	0.07404	3.99654	0.02562	0.0303716	0.314	123.632	0.3955	123.632	Pituitary	pituitary expression <sup>24</sup> involved in pituitary organogenesis <sup>25</sup>
PITX2	paired-like homeodomain 2	2.3887	3.51857	0.00565	2.8584209	0.002	100.327	0.0012	100.327	Pituitary	

\*References:

- Lin, D., Sugawara, T., Strauss, J.F., 3rd, Clark, B.J., Stocco, D.M., Saenger, P., Rogol, A., and Miller, W.L. (1995). Role of steroidogenic acute regulatory protein in adrenal and gonadal steroidogenesis. *Science* 267, 1828-1831.
- Chida, D., Nakagawa, S., Nagai, S., Sagara, H., Katsumata, H., Imaki, T., Suzuki, H., Mitani, F., Ogishima, T., Shimizu, C., et al. (2007). Melanocortin 2 receptor is required for adrenal gland development, steroidogenesis, and neonatal gluconeogenesis. *J Biol Chem* 282, 1151-1157.
- Birumachi, J., Hiroshima, M., Fujiwara, Y., Aoyagi, T., Sanbe, A., and Tanoue, A. (2007). Impaired arginine-vasopressin-induced aldosterone release from adrenal gland cells in mice lacking the vasopressin V1A receptor. *Eur J Pharmacol* 557, 105-112.
- Insel, T.R. (2010). The challenge of translation in social neuroscience: a review of oxytocin, vasopressin, and affiliative behavior. *Neuron* 65, 768-779.
- Palmer, C., Diehn, M., Alizadeh, A.A., and Brown, P.O. (2006). Cell-type specific gene expression profiles of leukocytes in human peripheral blood. *BMC Genomics* 7, 115.
- Guo F., Cancelas J. A., Hildeman D., Williams D. A., and Zheng Y. (2008) Rac GTPase isoforms Rac1 and Rac2 play a redundant and crucial role in T-cell development. *Blood* 112, 1767-1775.
- Call, M.E., Schnell, J.R., Xu, C., Lutz, R.A., Chou, J.J., and Wucherpfennig, K.W. (2006). The structure of the zeta-zeta transmembrane dimer reveals features essential for its assembly with the T cell receptor. *Cell* 127, 355-368.
- Jenkins, M.K., Taylor, P.S., Norton, S.D., and Urdahl, K.B. (1991). CD28 delivers a costimulatory signal involved in antigen-specific IL-2 production by human T cells. *Journal of immunology* 147, 2461-2466.
- Prandini, M. H., Denarier, E., Frachet, P., Uzan, G., Marguerie, G. (1988) Isolation of the human platelet glycoprotein IIb gene and characterization of the 5-prime flanking region. *Biochem. Biophys. Res. Commun.* 156: 595-601.
- Ferrer, M., Tao, J., Iruin, G., Sanchez-Ayuso, M., Gonzalez-Rodriguez, J., Parrilla, R., Gonzalez-Manchon, C. Truncation of glycoprotein (GP) IIIa (delta 616-762) prevents complex formation with GPIIb: novel mutation in exon 11 of GPIIIa associated with thrombasthenia. *Blood* 97: 1007-1012.
- de Chaldée M, Brochier C, Van de Vel A, Caudy N, Luthi-Carter R, Gaillard MC, Elalouf JM. (2006) Capucin: a novel striatal marker down-regulated in rodent models of Huntington disease. *Genomics*. Feb;87(2):200-7.
- Ryan T, Kendall and Carol A. Feghali-Bostwick (2014) Fibroblasts in fibrosis: novel roles and mediators. *Front Pharmacol*. 2014; 5: 123.
- Yamaguchi, Y., Itami, S., Watabe, H., Yasumoto, K., Abdel-Malek, Z.A., Kubo, T., Rouzaud, F., Tanemura, A., Yoshikawa, K., and Hearing, V.J. (2004). Mesenchymal-epithelial interactions in the skin: increased expression of dickkopf1 by palmoplantar keratoderma. *J Biol Chem* 279, 1010-1016.
- Huber, M.A., Kraut, N., Park, J.E., Schubert, R.D., Rettig, W.J., Peter, R.U., and Garin-Chesa, P. (2003). Fibroblast activation protein: differential expression and serine protease activity in reactive stromal fibroblasts of melanocytic skin tumors. *J Biol Chem* 278, 1010-1016.
- Zhang, C. et al. (2009) Fibroblast growth factor receptor 2-positive fibroblasts provide a suitable microenvironment for tumor development and progression in esophageal carcinoma. *Clin Cancer Res* 15, 4017-4027.
- Herbert, E. & Uhler, M. Biosynthesis of polyprotein precursors to regulatory peptides. *Cell* 30, 1-2 (1982).
- Daughaday, W.H., and Parker, M.L. (1965). Human Pituitary Growth Hormone. *Annual Review of Medicine* 16, 47-66.
- Fiddes, J.C., and Goodman, H.M. (1981). The gene encoding the common alpha subunit of the four human glycoprotein hormones. *Journal of Molecular and Applied Genetics* 1, 3-18.
- Szeto, D.P., Ryan, A.K., O'Connell, S.M., and Rosenfeld, M.G. (1996). P-OTX: a PIT-1-interacting homeodomain factor expressed during anterior pituitary gland development. *Proc Natl Acad Sci U S A* 93, 7706-7710.
- Colvin, S.C., Mullen, R.D., Pfaeffle, R.W., and Rhodes, S.J. (2009). LHX3 and LHX4 transcription factors in pituitary development and disease. *Pediatric Endocrinology Reviews: PER* 6 Suppl 2, 283-290.



**Supplementary Table 4. Rank correlation values ( $\rho$ ) for expression comparison between vervet and human data from ABA.**

**V=Vervet; H=Human. d=days, y=years, m=months**

Age (V)	Age (H)	BA46 (V) vs DLPFC (H)			Caudate (V) vs Striatum (H)			Hippocampus (V) vs Hippocampus (H)		
		# of samples (V)	# of samples (H)	Rho	# of samples (V)	# of samples (H)	Rho	# of samples (V)	# of samples (H)	Rho
7 d	<=5 m	5	2	0.638	5	2	0.548	5	2	0.628
90 d	6-18 m	6	2	0.618	6	1	0.537	6	1	0.615
1-1.25 y	19m-5y	12	3	0.544	12	2	0.539	12	2	0.552
1.5-2.5 y	6-11y	22	3	0.599	22	1	0.567	23	3	0.66
3-4y	12-19y	6	3	0.603	6	2	0.512	6	3	0.601
>=5y	20-60+ y	6	5	0.591	6	5	0.549	6	5	0.622

**Supplementary Table 5. Rank correlation values (rho) for expression comparison between vervet and rhesus data from ABA. V=Vervet; R=Rhesus. d=days, m=months, y=years**

Age(V)	Age®	BA46 (V) vs Medial Frontal Cortex (R)			Caudate (V) vs Basal ganglia (R)			Hippocampus (V) vs Hippocampal Cortex (R)		
		# of samples (V)	# of samples (R)	Rho	# of samples (V)	# of samples (R)	Rho	# of samples (V)	# of samples (R)	Rho
7 d	0 m	2	3	0.381	2	2	0.274	2	3	0.379
90 d	3 m	3	3	0.349	3	3	0.287	3	3	0.372
1-1.25y	12 m	6	3	0.326	6	3	0.303	6	3	0.371
>=4 y	48 m	3	3	0.339	3	3	0.288	3	3	0.376

**Supplementary Table 6. Rank correlation values ( $\rho$ ) for expression comparison between vervet and human GTEx**

<b>Vervet-GTEx Comparison</b>				
<b>Vervet</b>		<b>Human</b>		<b>Correlation (<math>\rho</math>)</b>
Tissue	# of Samples	Tissue	# of Samples	
Adrenal	58	Adrenal	126	0.794
Blood	58	Blood	338	0.78
Caudate	57	Caudate	100	0.683
Hippocampus	58	Hippocampus	81	0.717
Pituitary	58	Pituitary	87	0.795

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
ADAD1	adenosine deaminase domain containing 1	Adrenal	3
AGXT2	alanine--glyoxylate aminotransferase 2	Adrenal	3
ARHGAP36	Rho GTPase activating protein 36	Adrenal	3
ARHGAP8	Rho GTPase activating protein 8	Adrenal	3
B4GALNT2	beta-1,4-N-acetyl-galactosaminyltransferase 2	Adrenal	3
C16H17orf107	chromosome 16 open reading frame, human C17orf107	Adrenal	3
C23H5orf46	chromosome 23 open reading frame, human C5orf46	Adrenal	3
C26H15orf43	telomere repeat binding bouquet formation protein 2	Adrenal	3
C6H19orf26	CACN beta subunit associated regulatory protein	Adrenal	3
C9H10orf82	chromosome 9 open reading frame, human C10orf82	Adrenal	3
CADM2	cell adhesion molecule 2	Adrenal	3
CCDC33	coiled-coil domain containing 33	Adrenal	3
CGA	glycoprotein hormones, alpha polypeptide	Adrenal	3
CKM	creatine kinase, M-type	Adrenal	3
CNTNAP2	contactin associated protein-like 2	Adrenal	3
COCH	cochlin	Adrenal	3
CPN2	carboxypeptidase N subunit 2	Adrenal	3
CPNE4	copine 4	Adrenal	3
CYR61	cysteine rich angiogenic inducer 61	Adrenal	3
DDX3Y	DEAD-box helicase 3, Y-linked	Adrenal	3
DNER	delta/notch like EGF repeat containing	Adrenal	3
DPEP1	dipeptidase 1 (renal)	Adrenal	3
DUSP9	dual specificity phosphatase 9	Adrenal	3
EGR3	early growth response 3	Adrenal	3
EVX1	even-skipped homeobox 1	Adrenal	3
FERMT1	fermitin family member 1	Adrenal	3
FOSB	FosB proto-oncogene, AP-1 transcription factor subunit	Adrenal	3
FTHL17	ferritin heavy chain like 17	Adrenal	3
GIPC2	GIPC PDZ domain containing family member 2	Adrenal	3
GJC2	gap junction protein gamma 2	Adrenal	3
GPR101	G protein-coupled receptor 101	Adrenal	3
GPR149	G protein-coupled receptor 149	Adrenal	3
GPR22	G protein-coupled receptor 22	Adrenal	3
GRIN3B	glutamate ionotropic receptor NMDA type subunit 3B	Adrenal	3
HAND1	heart and neural crest derivatives expressed 1	Adrenal	3
HP	haptoglobin	Adrenal	3
IFI6	interferon alpha inducible protein 6	Adrenal	3
IRX2	iroquois homeobox 2	Adrenal	3
ISG15	ISG15 ubiquitin-like modifier	Adrenal	3
KCNC2	potassium voltage-gated channel subfamily C member 2	Adrenal	3
KDM5D	lysine demethylase 5D	Adrenal	3
KLK3	kallikrein related peptidase 3	Adrenal	3
KRBOX1	KRAB box domain containing 1	Adrenal	3
LOC103214525	steroidogenic acute regulatory protein, mitochondrial-like	Adrenal	3
LOC103214550	ferritin heavy chain pseudogene	Adrenal	3
LOC103214638	uncharacterized LOC103214638	Adrenal	3
LOC103214639	probable ATP-dependent RNA helicase DDX6	Adrenal	3
LOC103214682	uncharacterized LOC103214682	Adrenal	3
LOC103214794	uncharacterized LOC103214794	Adrenal	3
LOC103215213	spermine synthase pseudogene	Adrenal	3
LOC103215237	uncharacterized LOC103215237	Adrenal	3
LOC103215347	uncharacterized LOC103215347	Adrenal	3
LOC103215782	60S ribosomal protein L9 pseudogene	Adrenal	3
LOC103216847	uncharacterized LOC103216847	Adrenal	3
LOC103216848	uncharacterized LOC103216848	Adrenal	3
LOC103217010	60S ribosomal protein L12 pseudogene	Adrenal	3
LOC103217729	gamma-crystallin D	Adrenal	3
LOC103217948	uncharacterized LOC103217948	Adrenal	3
LOC103218076	alkaline phosphatase, placental-like	Adrenal	3
LOC103218078	uncharacterized LOC103218078	Adrenal	3
LOC103218277	endothelin-converting enzyme-like 1	Adrenal	3
LOC103218335	endothelin-converting enzyme-like 1	Adrenal	3
LOC103218363	uncharacterized LOC103218363	Adrenal	3
LOC103218706	elongation factor 1-alpha 1 pseudogene	Adrenal	3
LOC103219050	uncharacterized LOC103219050	Adrenal	3
LOC103219409	uncharacterized LOC103219409	Adrenal	3
LOC103219451	ubiquitin-40S ribosomal protein S27a pseudogene	Adrenal	3
LOC103219985	regenerating islet-derived protein 3-alpha	Adrenal	3



**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103219988	lithostathine-1-alpha-like	Adrenal	3
LOC103219990	regenerating islet-derived protein 3-gamma	Adrenal	3
LOC103220053	60S ribosomal protein L3 pseudogene	Adrenal	3
LOC103221597	heterogeneous nuclear ribonucleoprotein H-like	Adrenal	3
LOC103221683	major histocompatibility complex, class II, DP alpha 1	Adrenal	3
LOC103221786	class I histocompatibility antigen, Gogo-B*0101 alpha chain-like	Adrenal	3
LOC103221843	HLA class I histocompatibility antigen, alpha chain G-like	Adrenal	3
LOC103222059	60S ribosomal protein L3 pseudogene	Adrenal	3
LOC103222213	peptidyl-prolyl cis-trans isomerase A pseudogene	Adrenal	3
LOC103222346	uncharacterized LOC103222346	Adrenal	3
LOC103222361	HLA class I histocompatibility antigen, B-14 alpha chain-like	Adrenal	3
LOC103222374	uncharacterized LOC103222374	Adrenal	3
LOC103222418	26S protease regulatory subunit 6A pseudogene	Adrenal	3
LOC103223519	uncharacterized LOC103223519	Adrenal	3
LOC103224452	60S ribosomal protein L5 pseudogene	Adrenal	3
LOC103224596	60S ribosomal protein L29-like	Adrenal	3
LOC103224767	uncharacterized LOC103224767	Adrenal	3
LOC103225055	non-histone chromosomal protein HMG-17 pseudogene	Adrenal	3
LOC103225263	uncharacterized LOC103225263	Adrenal	3
LOC103225291	hemoglobin subunit alpha	Adrenal	3
LOC103225416	BRCA2 and CDKN1A-interacting protein pseudogene	Adrenal	3
LOC103226462	60S ribosomal protein L7a pseudogene	Adrenal	3
LOC103226590	uncharacterized LOC103226590	Adrenal	3
LOC103226832	elongation factor 1-gamma-like	Adrenal	3
LOC103226903	uncharacterized LOC103226903	Adrenal	3
LOC103227063	trypsin-2-like	Adrenal	3
LOC103227729	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform pseudogene	Adrenal	3
LOC103228110	uncharacterized LOC103228110	Adrenal	3
LOC103228978	uncharacterized LOC103228978	Adrenal	3
LOC103229364	calmodulin-A pseudogene	Adrenal	3
LOC103229828	putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8	Adrenal	3
LOC103229860	homer protein homolog 2 pseudogene	Adrenal	3
LOC103229939	putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8	Adrenal	3
LOC103229961	uncharacterized LOC103229961	Adrenal	3
LOC103230389	putative elongation factor 1-alpha-like 3	Adrenal	3
LOC103230559	putative 60S ribosomal protein L37a	Adrenal	3
LOC103230632	uncharacterized LOC103230632	Adrenal	3
LOC103230925	heat shock cognate 71 kDa protein-like	Adrenal	3
LOC103231044	elongation factor 1-alpha 1 pseudogene	Adrenal	3
LOC103231559	trifunctional enzyme subunit beta, mitochondrial-like	Adrenal	3
LOC103231823	chloride intracellular channel protein 4 pseudogene	Adrenal	3
LOC103231930	uncharacterized LOC103231930	Adrenal	3
LOC103232041	ATP synthase subunit beta, mitochondrial pseudogene	Adrenal	3
LOC103232191	uncharacterized LOC103232191	Adrenal	3
LOC103232291	stress-induced-phosphoprotein 1 pseudogene	Adrenal	3
LOC103232315	AP-2 complex subunit beta pseudogene	Adrenal	3
LOC103232474	non-histone chromosomal protein HMG-14 pseudogene	Adrenal	3
LOC103232530	cytochrome c oxidase subunit 6A1, mitochondrial pseudogene	Adrenal	3
LOC103232772	synaptonemal complex protein 3-like	Adrenal	3
LOC103232774	melanoma-associated antigen 4-like	Adrenal	3
LOC103233496	tubulin beta-3 chain	Adrenal	3
LOC103233816	C-type lectin domain family 4 member G-like	Adrenal	3
LOC103234510	elongation factor 1-alpha 1 pseudogene	Adrenal	3
LOC103235197	14-3-3 protein epsilon pseudogene	Adrenal	3
LOC103235251	ATP-dependent zinc metalloprotease YME1L1 pseudogene	Adrenal	3
LOC103235253	trifunctional enzyme subunit beta, mitochondrial-like	Adrenal	3
LOC103235262	leukocyte-associated immunoglobulin-like receptor 2	Adrenal	3
LOC103236223	very-long-chain enoyl-CoA reductase pseudogene	Adrenal	3
LOC103236661	uncharacterized LOC103236661	Adrenal	3
LOC103237018	40S ribosomal protein S5 pseudogene	Adrenal	3
LOC103237180	40S ribosomal protein S18 pseudogene	Adrenal	3
LOC103237550	uncharacterized LOC103237550	Adrenal	3
LOC103238179	uncharacterized LOC103238179	Adrenal	3
LOC103238951	10 kDa heat shock protein, mitochondrial pseudogene	Adrenal	3
LOC103239044	40S ribosomal protein SA-like	Adrenal	3
LOC103239517	nascent polypeptide-associated complex subunit alpha pseudogene	Adrenal	3
LOC103239891	transcription factor BTF3 pseudogene	Adrenal	3
LOC103240885	putative transcriptional regulator encoded by LINC00473	Adrenal	3

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103241006	elongation factor 1-delta-like	Adrenal	3
LOC103242126	transcription initiation factor TFIID subunit 4-like	Adrenal	3
LOC103242380	ubiquitin-40S ribosomal protein S27a-like	Adrenal	3
LOC103242477	uncharacterized LOC103242477	Adrenal	3
LOC103242499	CMT1A duplicated region transcript 15 protein-like protein	Adrenal	3
LOC103243156	60S ribosomal protein L17 pseudogene	Adrenal	3
LOC103243211	somatotropin	Adrenal	3
LOC103244762	ovomuroid-like	Adrenal	3
LOC103245358	40S ribosomal protein S17 pseudogene	Adrenal	3
LOC103245711	uncharacterized LOC103245711	Adrenal	3
LOC103246092	U3 small nucleolar ribonucleoprotein protein MPP10-like	Adrenal	3
LOC103246666	farnesyl pyrophosphate synthase pseudogene	Adrenal	3
LOC103246967	40S ribosomal protein S4, Y isoform 1	Adrenal	3
LOC103246978	uncharacterized LOC103246978	Adrenal	3
LOC103246986	gamma-taxilin-like	Adrenal	3
LOC103246988	eukaryotic translation initiation factor 1A, Y-chromosomal	Adrenal	3
LOC103246990	uncharacterized LOC103246990	Adrenal	3
LOC103246991	uncharacterized LOC103246991	Adrenal	3
LOC103246992	40S ribosomal protein S4, Y isoform 1	Adrenal	3
LOC103248959	thymosin beta-4 pseudogene	Adrenal	3
LRR8E	leucine rich repeat containing 8 family member E	Adrenal	3
LRR8M3	leucine rich repeat transmembrane neuronal 3	Adrenal	3
MCCD1	mitochondrial coiled-coil domain 1	Adrenal	3
MX1	MX dynamin like GTPase 1	Adrenal	3
NEFL	neurofilament light	Adrenal	3
NELL2	neural EGFL like 2	Adrenal	3
NLRP2	NLR family pyrin domain containing 2	Adrenal	3
NPY	neuropeptide Y	Adrenal	3
NRSN1	neurensin 1	Adrenal	3
NRSN2	neurensin 2	Adrenal	3
NTRK1	neurotrophic receptor tyrosine kinase 1	Adrenal	3
NXPH1	neurexophilin 1	Adrenal	3
P2RX2	purinergic receptor P2X 2	Adrenal	3
PLAC1	placenta specific 1	Adrenal	3
PNMA3	paraneoplastic Ma antigen 3	Adrenal	3
POU3F1	POU class 3 homeobox 1	Adrenal	3
PRL	prolactin	Adrenal	3
PRLR	prolactin receptor	Adrenal	3
PRPH	peripherin	Adrenal	3
PRSS2	protease, serine 2	Adrenal	3
PVALB	parvalbumin	Adrenal	3
RELT	RELT, TNF receptor	Adrenal	3
RLN3	relaxin 3	Adrenal	3
SALL4	spalt like transcription factor 4	Adrenal	3
SERPINE1	serpin family E member 1	Adrenal	3
SHISA2	shisa family member 2	Adrenal	3
SLC18A3	solute carrier family 18 member A3	Adrenal	3
SLC24A2	solute carrier family 24 member 2	Adrenal	3
SLC8A3	solute carrier family 8 member A3	Adrenal	3
SOX30	SRY-box 30	Adrenal	3
SPINK13	serine peptidase inhibitor, Kazal type 13 (putative)	Adrenal	3
STMN2	stathmin 2	Adrenal	3
SULT2A1	sulfotransferase family 2A member 1	Adrenal	3
SYT1	synaptotagmin 1	Adrenal	3
TBX20	T-box 20	Adrenal	3
TECRL	trans-2,3-enoyl-CoA reductase like	Adrenal	3
TFAP2B	transcription factor AP-2 beta	Adrenal	3
TMEM72	transmembrane protein 72	Adrenal	3
TRIM71	tripartite motif containing 71	Adrenal	3
TSHB	thyroid stimulating hormone beta	Adrenal	3
USP9Y	ubiquitin specific peptidase 9, Y-linked	Adrenal	3
UTY	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	Adrenal	3
ZFY	zinc finger protein, Y-linked	Adrenal	3
ZNF331	zinc finger protein 331	Adrenal	3
ANKRD62	ankyrin repeat domain 62	BA46	2
APOL6	apolipoprotein L6	BA46	2
ATF3	activating transcription factor 3	BA46	2
C1QTNF9	C1q and TNF related 9	BA46	2

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
<i>C20H1orf87</i>	chromosome 20 open reading frame, human C1orf87	BA46	2
<i>C26H15orf43</i>	telomere repeat binding bouquet formation protein 2	BA46	2
<i>C6</i>	complement C6	BA46	2
<i>C7</i>	complement C7	BA46	2
<i>CATSPERB</i>	cation channel sperm associated auxiliary subunit beta	BA46	2
<i>CD74</i>	CD74 molecule	BA46	2
<i>CETP</i>	cholesteryl ester transfer protein	BA46	2
<i>CHRNA3</i>	cholinergic receptor nicotinic alpha 3 subunit	BA46	2
<i>CHRNA9</i>	cholinergic receptor nicotinic alpha 9 subunit	BA46	2
<i>CILP2</i>	cartilage intermediate layer protein 2	BA46	2
<i>CLRN2</i>	clarin 2	BA46	2
<i>CNDP1</i>	carnosine dipeptidase 1	BA46	2
<i>CNN1</i>	calponin 1	BA46	2
<i>CPB1</i>	carboxypeptidase B1	BA46	2
<i>CRISP2</i>	cysteine rich secretory protein 2	BA46	2
<i>CRISPLD1</i>	cysteine rich secretory protein LCCL domain containing 1	BA46	2
<i>CTAG2</i>	cancer/testis antigen 2	BA46	2
<i>CXCL10</i>	C-X-C motif chemokine ligand 10	BA46	2
<i>DDX3Y</i>	DEAD-box helicase 3, Y-linked	BA46	2
<i>DDX60</i>	DEAD/H-box helicase 60	BA46	2
<i>DNAJB3</i>	DnaJ heat shock protein family (Hsp40) member B3	BA46	2
<i>DPPA5</i>	developmental pluripotency associated 5	BA46	2
<i>ELF5</i>	E74 like ETS transcription factor 5	BA46	2
<i>FBXO39</i>	F-box protein 39	BA46	2
<i>FMO3</i>	flavin containing monooxygenase 3	BA46	2
<i>GIN5A</i>	GIN5 complex subunit 4	BA46	2
<i>GJB4</i>	gap junction protein beta 4	BA46	2
<i>GPC3</i>	glypican 3	BA46	2
<i>GPR143</i>	G protein-coupled receptor 143	BA46	2
<i>GPR6</i>	G protein-coupled receptor 6	BA46	2
<i>IFI44</i>	interferon induced protein 44	BA46	2
<i>IFI44L</i>	interferon induced protein 44 like	BA46	2
<i>KDM5D</i>	lysine demethylase 5D	BA46	2
<i>KERA</i>	keratocan	BA46	2
<i>KLK1</i>	kallikrein 1	BA46	2
<i>KLK15</i>	kallikrein related peptidase 15	BA46	2
<i>KLKB1</i>	kallikrein B1	BA46	2
<i>KRBOX1</i>	KRAB box domain containing 1	BA46	2
<i>KRT7</i>	keratin 7	BA46	2
<i>LOC103214547</i>	beta-citrylglutamate synthase B pseudogene	BA46	2
<i>LOC103214954</i>	uncharacterized LOC103214954	BA46	2
<i>LOC103215442</i>	POTE ankyrin domain family member B2-like	BA46	2
<i>LOC103215612</i>	putative UPF0607 protein ENSP00000382826	BA46	2
<i>LOC103215615</i>	uncharacterized LOC103215615	BA46	2
<i>LOC103215729</i>	uncharacterized LOC103215729	BA46	2
<i>LOC103216766</i>	putative vomeronasal receptor-like protein 4	BA46	2
<i>LOC103216854</i>	uncharacterized LOC103216854	BA46	2
<i>LOC103217617</i>	aldehyde oxidase 4-like	BA46	2
<i>LOC103217729</i>	gamma-crystallin D	BA46	2
<i>LOC103218379</i>	unconventional myosin-Vb pseudogene	BA46	2
<i>LOC103218546</i>	pregnancy zone protein	BA46	2
<i>LOC103219098</i>	uncharacterized LOC103219098	BA46	2
<i>LOC103219099</i>	uncharacterized LOC103219099	BA46	2
<i>LOC103220153</i>	protein IQ-DOMAIN 14-like	BA46	2
<i>LOC103220854</i>	ARF GTPase-activating protein GIT1 pseudogene	BA46	2
<i>LOC103220953</i>	uncharacterized LOC103220953	BA46	2
<i>LOC103221671</i>	uncharacterized LOC103221671	BA46	2
<i>LOC103221684</i>	major histocompatibility complex, class II, DO alpha	BA46	2
<i>LOC103221700</i>	HLA class II histocompatibility antigen, DRB1-4 beta chain-like	BA46	2
<i>LOC103221702</i>	HLA class II histocompatibility antigen, DRB1-4 beta chain	BA46	2
<i>LOC103221704</i>	major histocompatibility complex, class II, DR alpha	BA46	2
<i>LOC103221720</i>	tenascin XA (pseudogene)	BA46	2
<i>LOC103221773</i>	class I histocompatibility antigen, Gogo-B*0102 alpha chain-like	BA46	2
<i>LOC103221779</i>	HLA class I histocompatibility antigen, B-46 alpha chain-like	BA46	2
<i>LOC103221781</i>	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like	BA46	2
<i>LOC103221783</i>	HLA class I histocompatibility antigen, B-15 alpha chain-like	BA46	2
<i>LOC103221786</i>	class I histocompatibility antigen, Gogo-B*0101 alpha chain-like	BA46	2
<i>LOC103221790</i>	uncharacterized LOC103221790	BA46	2

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103221792	saoe class I histocompatibility antigen, A alpha chain-like	BA46	2
LOC103221843	HLA class I histocompatibility antigen, alpha chain G-like	BA46	2
LOC103221863	mamu class I histocompatibility antigen, alpha chain F-like	BA46	2
LOC103221867	HLA class I histocompatibility antigen, B-38 alpha chain-like	BA46	2
LOC103221925	olfactory receptor 2B6-like	BA46	2
LOC103222083	uncharacterized LOC103222083	BA46	2
LOC103222361	HLA class I histocompatibility antigen, B-14 alpha chain-like	BA46	2
LOC103222365	putative olfactory receptor 211	BA46	2
LOC103223461	uncharacterized LOC103223461	BA46	2
LOC103223596	uncharacterized LOC103223596	BA46	2
LOC103223757	olfactory receptor 10J1-like	BA46	2
LOC103223762	olfactory receptor 10J1-like	BA46	2
LOC103224012	uncharacterized LOC103224012	BA46	2
LOC103224103	glyceraldehyde-3-phosphate dehydrogenase pseudogene	BA46	2
LOC103224105	glyceraldehyde-3-phosphate dehydrogenase pseudogene	BA46	2
LOC103224107	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1-like	BA46	2
LOC103224108	putative RNA polymerase II subunit A C-terminal domain phosphatase SSU72-like protein 2	BA46	2
LOC103224327	neuroblastoma breakpoint family member 4-like	BA46	2
LOC103224379	high mobility group protein B3 pseudogene	BA46	2
LOC103225878	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1 pseudogene	BA46	2
LOC103225919	phosphate carrier protein, mitochondrial pseudogene	BA46	2
LOC103226029	ribonuclease T2 pseudogene	BA46	2
LOC103226088	uncharacterized LOC103226088	BA46	2
LOC103226590	uncharacterized LOC103226590	BA46	2
LOC103226929	aldo-keto reductase family 1 member B10-like	BA46	2
LOC103226936	uncharacterized LOC103226936	BA46	2
LOC103227997	uncharacterized LOC103227997	BA46	2
LOC103228754	uncharacterized LOC103228754	BA46	2
LOC103231504	putative golgin subfamily A member 6-like protein 8	BA46	2
LOC103231552	uncharacterized LOC103231552	BA46	2
LOC103231553	uncharacterized LOC103231553	BA46	2
LOC103231554	60S ribosomal protein L24-like	BA46	2
LOC103231593	zinc finger protein 729-like	BA46	2
LOC103231790	uncharacterized LOC103231790	BA46	2
LOC103231837	uncharacterized LOC103231837	BA46	2
LOC103231952	angiogenic factor with G patch and FHA domains 1 pseudogene	BA46	2
LOC103232191	uncharacterized LOC103232191	BA46	2
LOC103233035	metallothionein-1E-like	BA46	2
LOC103234401	zinc finger protein 85-like	BA46	2
LOC103234406	uncharacterized LOC103234406	BA46	2
LOC103234986	galactoside 2-alpha-L-fucosyltransferase 2	BA46	2
LOC103235388	uncharacterized LOC103235388	BA46	2
LOC103235584	UDP-glucuronosyltransferase 2B4-like	BA46	2
LOC103235585	UDP-glucuronosyltransferase 2B23	BA46	2
LOC103236661	uncharacterized LOC103236661	BA46	2
LOC103236959	transient receptor potential cation channel subfamily A member 1-like	BA46	2
LOC103237729	uncharacterized protein FLJ40521-like	BA46	2
LOC103237869	uncharacterized LOC103237869	BA46	2
LOC103238179	uncharacterized LOC103238179	BA46	2
LOC103239373	uncharacterized LOC103239373	BA46	2
LOC103240473	uncharacterized LOC103240473	BA46	2
LOC103240493	40S ribosomal protein S24 pseudogene	BA46	2
LOC103240941	uncharacterized LOC103240941	BA46	2
LOC103242499	CMT1A duplicated region transcript 15 protein-like protein	BA46	2
LOC103242671	uncharacterized LOC103242671	BA46	2
LOC103242716	uncharacterized LOC103242716	BA46	2
LOC103243248	leucine-rich repeat-containing protein 37A-like	BA46	2
LOC103243770	uncharacterized LOC103243770	BA46	2
LOC103244037	uncharacterized LOC103244037	BA46	2
LOC103244121	uncharacterized LOC103244121	BA46	2
LOC103244746	uncharacterized LOC103244746	BA46	2
LOC103244873	uncharacterized LOC103244873	BA46	2
LOC103245207	golgin subfamily A member 2-like	BA46	2
LOC103245980	shadow of prion protein-like	BA46	2
LOC103246187	uncharacterized LOC103246187	BA46	2
LOC103246188	uncharacterized LOC103246188	BA46	2
LOC103246200	WD repeat-containing protein 5 pseudogene	BA46	2
LOC103246313	40S ribosomal protein S7 pseudogene	BA46	2

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>LOC103246510</i>	uncharacterized LOC103246510	BA46	2
<i>LOC103246852</i>	uncharacterized LOC103246852	BA46	2
<i>LOC103246967</i>	40S ribosomal protein S4, Y isoform 1	BA46	2
<i>LOC103246968</i>	heat shock transcription factor, Y-linked-like	BA46	2
<i>LOC103246974</i>	developmental pluripotency-associated protein 2 pseudogene	BA46	2
<i>LOC103246975</i>	uncharacterized LOC103246975	BA46	2
<i>LOC103246978</i>	uncharacterized LOC103246978	BA46	2
<i>LOC103246979</i>	ribose-phosphate pyrophosphokinase 2 pseudogene	BA46	2
<i>LOC103246980</i>	uncharacterized LOC103246980	BA46	2
<i>LOC103246982</i>	acylglycerol kinase, mitochondrial pseudogene	BA46	2
<i>LOC103246983</i>	neuroligin-4, X-linked-like	BA46	2
<i>LOC103246986</i>	gamma-taxilin-like	BA46	2
<i>LOC103246988</i>	eukaryotic translation initiation factor 1A, Y-chromosomal	BA46	2
<i>LOC103246990</i>	uncharacterized LOC103246990	BA46	2
<i>LOC103246991</i>	uncharacterized LOC103246991	BA46	2
<i>LOC103246992</i>	40S ribosomal protein S4, Y isoform 1	BA46	2
<i>LOC103246998</i>	ankyrin repeat domain-containing protein 37 pseudogene	BA46	2
<i>LOC103247901</i>	hemoglobin subunit beta	BA46	2
<i>LTF</i>	lactotransferrin	BA46	2
<i>LY6K</i>	lymphocyte antigen 6 family member K	BA46	2
<i>MALRD1</i>	MAM and LDL receptor class A domain containing 1	BA46	2
<i>MB21D1</i>	Mab-21 domain containing 1	BA46	2
<i>MDFI</i>	MyoD family inhibitor	BA46	2
<i>MEOX1</i>	mesenchyme homeobox 1	BA46	2
<i>MGP</i>	matrix Gla protein	BA46	2
<i>MS4A6A</i>	membrane spanning 4-domains A6A	BA46	2
<i>MSH5</i>	mutS homolog 5	BA46	2
<i>MUSK</i>	muscle associated receptor tyrosine kinase	BA46	2
<i>MX2</i>	MX dynamin like GTPase 2	BA46	2
<i>MYOC</i>	myocilin	BA46	2
<i>NHLH2</i>	nescient helix-loop-helix 2	BA46	2
<i>NR5A2</i>	nuclear receptor subfamily 5 group A member 2	BA46	2
<i>OAS2</i>	2'-5'-oligoadenylate synthetase 2	BA46	2
<i>PAX7</i>	paired box 7	BA46	2
<i>PKP1</i>	plakophilin 1	BA46	2
<i>PRSS45</i>	protease, serine 45	BA46	2
<i>PTPN20B</i>	protein tyrosine phosphatase, non-receptor type 20	BA46	2
<i>RGS21</i>	regulator of G-protein signaling 21	BA46	2
<i>SERPINB13</i>	serpin family B member 13	BA46	2
<i>SLC16A12</i>	solute carrier family 16 member 12	BA46	2
<i>SPDYE4</i>	speedy/RINGO cell cycle regulator family member E4	BA46	2
<i>STC2</i>	stanniocalcin 2	BA46	2
<i>SYCE1</i>	synaptonemal complex central element protein 1	BA46	2
<i>SYTL1</i>	synaptotagmin like 1	BA46	2
<i>TDRD5</i>	tudor domain containing 5	BA46	2
<i>TDRD9</i>	tudor domain containing 9	BA46	2
<i>THEMIS</i>	thymocyte selection associated	BA46	2
<i>TICRR</i>	TOPBP1 interacting checkpoint and replication regulator	BA46	2
<i>TMEM125</i>	transmembrane protein 125	BA46	2
<i>TPO</i>	thyroid peroxidase	BA46	2
<i>TRNAP-AGG</i>	transfer RNA proline (anticodon AGG)	BA46	2
<i>UGT3A1</i>	UDP glycosyltransferase family 3 member A1	BA46	2
<i>USP9Y</i>	ubiquitin specific peptidase 9, Y-linked	BA46	2
<i>UTY</i>	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	BA46	2
<i>VGLL2</i>	vestigial like family member 2	BA46	2
<i>XAF1</i>	XIAP associated factor 1	BA46	2
<i>XIRP2</i>	xin actin binding repeat containing 2	BA46	2
<i>XPNPEP2</i>	X-prolyl aminopeptidase 2	BA46	2
<i>ZFP57</i>	ZFP57 zinc finger protein	BA46	2
<i>ZFY</i>	zinc finger protein, Y-linked	BA46	2
<i>ADCYAP1</i>	adenylate cyclase activating polypeptide 1	Caudate	2
<i>AGPAT9</i>	glycerol-3-phosphate acyltransferase 3	Caudate	2
<i>AGT</i>	angiotensinogen	Caudate	2
<i>ANKRD30A</i>	ankyrin repeat domain 30A	Caudate	2
<i>ANKRD62</i>	ankyrin repeat domain 62	Caudate	2
<i>ARHGEF38</i>	Rho guanine nucleotide exchange factor 38	Caudate	2
<i>ASPM</i>	abnormal spindle microtubule assembly	Caudate	2
<i>BUB1</i>	BUB1 mitotic checkpoint serine/threonine kinase	Caudate	2

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
<i>C17H6orf10</i>	chromosome 17 open reading frame, human C6orf10	Caudate	2
<i>CILP2</i>	cartilage intermediate layer protein 2	Caudate	2
<i>CNDP1</i>	carnosine dipeptidase 1	Caudate	2
<i>COL6A5</i>	collagen type VI alpha 5 chain	Caudate	2
<i>CPB1</i>	carboxypeptidase B1	Caudate	2
<i>CPS1</i>	carbamoyl-phosphate synthase 1	Caudate	2
<i>CXCL11</i>	C-X-C motif chemokine ligand 11	Caudate	2
<i>DDX3Y</i>	DEAD-box helicase 3, Y-linked	Caudate	2
<i>DMP1</i>	dentin matrix acidic phosphoprotein 1	Caudate	2
<i>DNAJB3</i>	DnaJ heat shock protein family (Hsp40) member B3	Caudate	2
<i>DPEP3</i>	dipeptidase 3	Caudate	2
<i>DPPA5</i>	developmental pluripotency associated 5	Caudate	2
<i>DSP</i>	desmoplakin	Caudate	2
<i>ERVMER34-1</i>	endogenous retrovirus group MER34 member 1, envelope	Caudate	2
<i>FAM163B</i>	family with sequence similarity 163 member B	Caudate	2
<i>FAT2</i>	FAT atypical cadherin 2	Caudate	2
<i>FCAR</i>	Fc fragment of IgA receptor	Caudate	2
<i>GABRA6</i>	gamma-aminobutyric acid type A receptor alpha6 subunit	Caudate	2
<i>GADL1</i>	glutamate decarboxylase like 1	Caudate	2
<i>GJD2</i>	gap junction protein delta 2	Caudate	2
<i>GPR143</i>	G protein-coupled receptor 143	Caudate	2
<i>HAPLN4</i>	hyaluronan and proteoglycan link protein 4	Caudate	2
<i>HOXD3</i>	homeobox D3	Caudate	2
<i>HSF4</i>	heat shock transcription factor 4	Caudate	2
<i>HTRA3</i>	HtrA serine peptidase 3	Caudate	2
<i>IL23R</i>	interleukin 23 receptor	Caudate	2
<i>IRX3</i>	iroquois homeobox 3	Caudate	2
<i>ISLR</i>	immunoglobulin superfamily containing leucine rich repeat	Caudate	2
<i>ITK</i>	IL2 inducible T-cell kinase	Caudate	2
<i>KDM5D</i>	lysine demethylase 5D	Caudate	2
<i>KLHL4</i>	kelch like family member 4	Caudate	2
<i>KLK1</i>	kallikrein 1	Caudate	2
<i>KLK15</i>	kallikrein related peptidase 15	Caudate	2
<i>KRBOX1</i>	KRAB box domain containing 1	Caudate	2
<i>LOC103214240</i>	uncharacterized LOC103214240	Caudate	2
<i>LOC103214954</i>	uncharacterized LOC103214954	Caudate	2
<i>LOC103215075</i>	succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial-like	Caudate	2
<i>LOC103215493</i>	uncharacterized LOC103215493	Caudate	2
<i>LOC103215615</i>	uncharacterized LOC103215615	Caudate	2
<i>LOC103216172</i>	uncharacterized LOC103216172	Caudate	2
<i>LOC103216766</i>	putative vomeronasal receptor-like protein 4	Caudate	2
<i>LOC103216848</i>	uncharacterized LOC103216848	Caudate	2
<i>LOC103216882</i>	cytochrome P450 family 27 subfamily C member 1	Caudate	2
<i>LOC103217040</i>	uncharacterized LOC103217040	Caudate	2
<i>LOC103218057</i>	uncharacterized LOC103218057	Caudate	2
<i>LOC103218206</i>	olfactory receptor 6B3	Caudate	2
<i>LOC103218379</i>	unconventional myosin-Vb pseudogene	Caudate	2
<i>LOC103218511</i>	C-type lectin domain family 4 member C-like	Caudate	2
<i>LOC103218545</i>	alpha-2-macroglobulin-like	Caudate	2
<i>LOC103218697</i>	uncharacterized LOC103218697	Caudate	2
<i>LOC103218793</i>	uncharacterized LOC103218793	Caudate	2
<i>LOC103218849</i>	C-type lectin domain family 4 member C pseudogene	Caudate	2
<i>LOC103218865</i>	C-type lectin domain family 4 member C-like	Caudate	2
<i>LOC103219098</i>	uncharacterized LOC103219098	Caudate	2
<i>LOC103219657</i>	uncharacterized LOC103219657	Caudate	2
<i>LOC103220361</i>	uncharacterized LOC103220361	Caudate	2
<i>LOC103220719</i>	aryl hydrocarbon receptor-like	Caudate	2
<i>LOC103220953</i>	uncharacterized LOC103220953	Caudate	2
<i>LOC103220966</i>	uncharacterized LOC103220966	Caudate	2
<i>LOC103221007</i>	uncharacterized LOC103221007	Caudate	2
<i>LOC103221295</i>	uncharacterized LOC103221295	Caudate	2
<i>LOC103221683</i>	major histocompatibility complex, class II, DP alpha 1	Caudate	2
<i>LOC103221696</i>	major histocompatibility complex, class II, DQ beta 1	Caudate	2
<i>LOC103221700</i>	HLA class II histocompatibility antigen, DRB1-4 beta chain-like	Caudate	2
<i>LOC103221702</i>	HLA class II histocompatibility antigen, DRB1-4 beta chain	Caudate	2
<i>LOC103221703</i>	DLA class II histocompatibility antigen, DR-1 beta chain-like	Caudate	2
<i>LOC103221705</i>	heterogeneous nuclear ribonucleoprotein A1-like	Caudate	2
<i>LOC103221720</i>	tenascin XA (pseudogene)	Caudate	2

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103221724	cytochrome P450 family 21 subfamily A member 2	Caudate	2
LOC103221773	class I histocompatibility antigen, Gogo-B*0102 alpha chain-like	Caudate	2
LOC103221779	HLA class I histocompatibility antigen, B-46 alpha chain-like	Caudate	2
LOC103221781	class I histocompatibility antigen, Gogo-B*0103 alpha chain-like	Caudate	2
LOC103221783	HLA class I histocompatibility antigen, B-15 alpha chain-like	Caudate	2
LOC103221786	class I histocompatibility antigen, Gogo-B*0101 alpha chain-like	Caudate	2
LOC103221792	saoe class I histocompatibility antigen, A alpha chain-like	Caudate	2
LOC103221843	HLA class I histocompatibility antigen, alpha chain G-like	Caudate	2
LOC103221863	mamu class I histocompatibility antigen, alpha chain F-like	Caudate	2
LOC103221864	keratin, type II cytoskeletal 8 pseudogene	Caudate	2
LOC103221867	HLA class I histocompatibility antigen, B-38 alpha chain-like	Caudate	2
LOC103221876	olfactory receptor 2H2-like	Caudate	2
LOC103221924	putative olfactory receptor 2W6	Caudate	2
LOC103221925	olfactory receptor 2B6-like	Caudate	2
LOC103221927	olfactory receptor 2B2-like	Caudate	2
LOC103221933	histone cluster 1, H2bo	Caudate	2
LOC103221937	histone H2B type 1-M	Caudate	2
LOC103221944	histone cluster 1, H1b	Caudate	2
LOC103222079	uncharacterized LOC103222079	Caudate	2
LOC103222083	uncharacterized LOC103222083	Caudate	2
LOC103222279	uncharacterized LOC103222279	Caudate	2
LOC103222361	HLA class I histocompatibility antigen, B-14 alpha chain-like	Caudate	2
LOC103223315	uncharacterized LOC103223315	Caudate	2
LOC103224012	uncharacterized LOC103224012	Caudate	2
LOC103224456	uncharacterized LOC103224456	Caudate	2
LOC103224846	putative selection and upkeep of intraepithelial T-cells protein 1 homolog	Caudate	2
LOC103225919	phosphate carrier protein, mitochondrial pseudogene	Caudate	2
LOC103226029	ribonuclease T2 pseudogene	Caudate	2
LOC103226041	uncharacterized LOC103226041	Caudate	2
LOC103227848	uncharacterized LOC103227848	Caudate	2
LOC103227916	uncharacterized LOC103227916	Caudate	2
LOC103227997	uncharacterized LOC103227997	Caudate	2
LOC103228240	uncharacterized LOC103228240	Caudate	2
LOC103228374	uncharacterized LOC103228374	Caudate	2
LOC103229265	disintegrin and metalloproteinase domain-containing protein 20-like	Caudate	2
LOC103229673	uncharacterized LOC103229673	Caudate	2
LOC103231241	uncharacterized LOC103231241	Caudate	2
LOC103231552	uncharacterized LOC103231552	Caudate	2
LOC103231553	uncharacterized LOC103231553	Caudate	2
LOC103231554	60S ribosomal protein L24-like	Caudate	2
LOC103231593	zinc finger protein 729-like	Caudate	2
LOC103232191	uncharacterized LOC103232191	Caudate	2
LOC103233032	metallothionein-2-like	Caudate	2
LOC103233547	uncharacterized LOC103233547	Caudate	2
LOC103234252	zinc finger protein 676-like	Caudate	2
LOC103235585	UDP-glucuronosyltransferase 2B23	Caudate	2
LOC103235936	uncharacterized LOC103235936	Caudate	2
LOC103235937	uncharacterized LOC103235937	Caudate	2
LOC103236042	uncharacterized LOC103236042	Caudate	2
LOC103236044	uncharacterized LOC103236044	Caudate	2
LOC103236253	uncharacterized LOC103236253	Caudate	2
LOC103236371	ankyrin repeat domain-containing protein 30A-like	Caudate	2
LOC103236499	keratin, type II cytoskeletal 8-like	Caudate	2
LOC103236661	uncharacterized LOC103236661	Caudate	2
LOC103236959	transient receptor potential cation channel subfamily A member 1-like	Caudate	2
LOC103237663	olfactory receptor 2V1	Caudate	2
LOC103239373	uncharacterized LOC103239373	Caudate	2
LOC103239374	uncharacterized LOC103239374	Caudate	2
LOC103239458	NHP2-like protein 1 pseudogene	Caudate	2
LOC103239535	uncharacterized LOC103239535	Caudate	2
LOC103240343	uncharacterized LOC103240343	Caudate	2
LOC103241392	uncharacterized LOC103241392	Caudate	2
LOC103241524	uncharacterized LOC103241524	Caudate	2
LOC103241538	uncharacterized LOC103241538	Caudate	2
LOC103242499	CMT1A duplicated region transcript 15 protein-like protein	Caudate	2
LOC103242547	olfactory receptor 3A1	Caudate	2
LOC103242588	uncharacterized LOC103242588	Caudate	2
LOC103242716	uncharacterized LOC103242716	Caudate	2

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103243101	uncharacterized LOC103243101	Caudate	2
LOC103243247	endophilin-A2 pseudogene	Caudate	2
LOC103243248	leucine-rich repeat-containing protein 37A-like	Caudate	2
LOC103244770	uncharacterized LOC103244770	Caudate	2
LOC103246347	uncharacterized protein C9orf78 pseudogene	Caudate	2
LOC103246967	40S ribosomal protein S4, Y isoform 1	Caudate	2
LOC103246968	heat shock transcription factor, Y-linked-like	Caudate	2
LOC103246974	developmental pluripotency-associated protein 2 pseudogene	Caudate	2
LOC103246975	uncharacterized LOC103246975	Caudate	2
LOC103246978	uncharacterized LOC103246978	Caudate	2
LOC103246979	ribose-phosphate pyrophosphokinase 2 pseudogene	Caudate	2
LOC103246980	uncharacterized LOC103246980	Caudate	2
LOC103246982	acylglycerol kinase, mitochondrial pseudogene	Caudate	2
LOC103246983	neuroligin-4, X-linked-like	Caudate	2
LOC103246986	gamma-taxilin-like	Caudate	2
LOC103246988	eukaryotic translation initiation factor 1A, Y-chromosomal	Caudate	2
LOC103246990	uncharacterized LOC103246990	Caudate	2
LOC103246991	uncharacterized LOC103246991	Caudate	2
LOC103246992	40S ribosomal protein S4, Y isoform 1	Caudate	2
LOC103246998	ankyrin repeat domain-containing protein 37 pseudogene	Caudate	2
LOC103247901	hemoglobin subunit beta	Caudate	2
LOC103248295	uncharacterized LOC103248295	Caudate	2
LOC103248363	caspase-1-like	Caudate	2
LOC103248486	uncharacterized LOC103248486	Caudate	2
MBL2	mannose binding lectin 2	Caudate	2
MLPH	melanophilin	Caudate	2
MUC22	mucin 22	Caudate	2
MYBL2	MYB proto-oncogene like 2	Caudate	2
NEUROD1	neuronal differentiation 1	Caudate	2
NKX3-1	NK3 homeobox 1	Caudate	2
OXTR	oxytocin receptor	Caudate	2
P2RX1	purinergic receptor P2X 1	Caudate	2
PLA2G2F	phospholipase A2 group IIF	Caudate	2
PPAP2C	phospholipid phosphatase 2	Caudate	2
PRL	prolactin	Caudate	2
PTPN20B	protein tyrosine phosphatase, non-receptor type 20	Caudate	2
SECTM1	secreted and transmembrane 1	Caudate	2
SHCBP1	SHC binding and spindle associated 1	Caudate	2
SLC17A3	solute carrier family 17 member 3	Caudate	2
SLC17A6	solute carrier family 17 member 6	Caudate	2
SLC6A5	solute carrier family 6 member 5	Caudate	2
SP8	Sp8 transcription factor	Caudate	2
STYK1	serine/threonine/tyrosine kinase 1	Caudate	2
TESPA1	thymocyte expressed, positive selection associated 1	Caudate	2
THEG	theg spermatid protein	Caudate	2
TMEM235	transmembrane protein 235	Caudate	2
TPO	thyroid peroxidase	Caudate	2
TRHR	thyrotropin releasing hormone receptor	Caudate	2
TRPC5	transient receptor potential cation channel subfamily C member 5	Caudate	2
TSPAN2	tetraspanin 2	Caudate	2
TSPEAR	thrombospondin type laminin G domain and EAR repeats	Caudate	2
USP9Y	ubiquitin specific peptidase 9, Y-linked	Caudate	2
UTY	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	Caudate	2
WNT9B	Wnt family member 9B	Caudate	2
ZFP57	ZFP57 zinc finger protein	Caudate	2
ZFY	zinc finger protein, Y-linked	Caudate	2
ABCA13	ATP binding cassette subfamily A member 13	Hippocampus	1
ALOX15	arachidonate 15-lipoxygenase	Hippocampus	1
ANKRD30A	ankyrin repeat domain 30A	Hippocampus	1
ARHGEF38	Rho guanine nucleotide exchange factor 38	Hippocampus	1
ATP6V0D2	ATPase H <sup>+</sup> transporting V0 subunit d2	Hippocampus	1
AVPR1A	arginine vasopressin receptor 1A	Hippocampus	1
C12H9orf135	chromosome 12 open reading frame, human C9orf135	Hippocampus	1
C20H1orf141	chromosome 20 open reading frame, human C1orf141	Hippocampus	1
CAPSL	calcyphosine like	Hippocampus	1
CCR6	C-C motif chemokine receptor 6	Hippocampus	1
CHRNA9	cholinergic receptor nicotinic alpha 9 subunit	Hippocampus	1
CLCA2	chloride channel accessory 2	Hippocampus	1



**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>CLRN2</i>	clarin 2	Hippocampus	1
<i>CNDP1</i>	carnosine dipeptidase 1	Hippocampus	1
<i>CNGB3</i>	cyclic nucleotide gated channel beta 3	Hippocampus	1
<i>CNN1</i>	calponin 1	Hippocampus	1
<i>COL1A1</i>	collagen type I alpha 1 chain	Hippocampus	1
<i>COMP</i>	cartilage oligomeric matrix protein	Hippocampus	1
<i>CPAMD8</i>	C3 and PZP like, alpha-2-macroglobulin domain containing 8	Hippocampus	1
<i>CPZ</i>	carboxypeptidase Z	Hippocampus	1
<i>CTAG2</i>	cancer/testis antigen 2	Hippocampus	1
<i>DDX3Y</i>	DEAD-box helicase 3, Y-linked	Hippocampus	1
<i>DMP1</i>	dentin matrix acidic phosphoprotein 1	Hippocampus	1
<i>DNAJB3</i>	DnaJ heat shock protein family (Hsp40) member B3	Hippocampus	1
<i>DRAXIN</i>	dorsal inhibitory axon guidance protein	Hippocampus	1
<i>EBF3</i>	early B-cell factor 3	Hippocampus	1
<i>FERD3L</i>	Fer3 like bHLH transcription factor	Hippocampus	1
<i>FFAR2</i>	free fatty acid receptor 2	Hippocampus	1
<i>FMO2</i>	flavin containing monooxygenase 2	Hippocampus	1
<i>FREM3</i>	FRAS1 related extracellular matrix 3	Hippocampus	1
<i>GPR101</i>	G protein-coupled receptor 101	Hippocampus	1
<i>GPR111</i>	adhesion G protein-coupled receptor F2	Hippocampus	1
<i>GPR142</i>	G protein-coupled receptor 142	Hippocampus	1
<i>HTATIP2</i>	HIV-1 Tat interactive protein 2	Hippocampus	1
<i>IFI44</i>	interferon induced protein 44	Hippocampus	1
<i>IL23R</i>	interleukin 23 receptor	Hippocampus	1
<i>ISG15</i>	ISG15 ubiquitin-like modifier	Hippocampus	1
<i>ISLR</i>	immunoglobulin superfamily containing leucine rich repeat	Hippocampus	1
<i>KDM5D</i>	lysine demethylase 5D	Hippocampus	1
<i>KLK1</i>	kallikrein 1	Hippocampus	1
<i>KLK15</i>	kallikrein related peptidase 15	Hippocampus	1
<i>KRBOX1</i>	KRAB box domain containing 1	Hippocampus	1
<i>LCK</i>	LCK proto-oncogene, Src family tyrosine kinase	Hippocampus	1
<i>LOC103214649</i>	uncharacterized LOC103214649	Hippocampus	1
<i>LOC103214759</i>	uncharacterized LOC103214759	Hippocampus	1
<i>LOC103214761</i>	uncharacterized LOC103214761	Hippocampus	1
<i>LOC103214881</i>	asparagine synthetase [glutamine-hydrolyzing] pseudogene	Hippocampus	1
<i>LOC103214916</i>	uncharacterized LOC103214916	Hippocampus	1
<i>LOC103214934</i>	uncharacterized LOC103214934	Hippocampus	1
<i>LOC103214935</i>	uncharacterized LOC103214935	Hippocampus	1
<i>LOC103215125</i>	uncharacterized LOC103215125	Hippocampus	1
<i>LOC103215127</i>	uncharacterized LOC103215127	Hippocampus	1
<i>LOC103215284</i>	uncharacterized LOC103215284	Hippocampus	1
<i>LOC103215442</i>	POTE ankyrin domain family member B2-like	Hippocampus	1
<i>LOC103215729</i>	uncharacterized LOC103215729	Hippocampus	1
<i>LOC103215730</i>	putative ankyrin repeat domain-containing protein ENSP00000330211	Hippocampus	1
<i>LOC103215870</i>	putative BMS1-like protein	Hippocampus	1
<i>LOC103217614</i>	uncharacterized LOC103217614	Hippocampus	1
<i>LOC103217729</i>	gamma-crystallin D	Hippocampus	1
<i>LOC103217805</i>	uncharacterized LOC103217805	Hippocampus	1
<i>LOC103218206</i>	olfactory receptor 6B3	Hippocampus	1
<i>LOC103218320</i>	ATP-binding cassette transporter 13	Hippocampus	1
<i>LOC103218379</i>	unconventional myosin-Vb pseudogene	Hippocampus	1
<i>LOC103218399</i>	uncharacterized LOC103218399	Hippocampus	1
<i>LOC103218597</i>	taste 2 receptor member 8	Hippocampus	1
<i>LOC103218793</i>	uncharacterized LOC103218793	Hippocampus	1
<i>LOC103219091</i>	uncharacterized LOC103219091	Hippocampus	1
<i>LOC103219652</i>	uncharacterized protein FLJ46757-like	Hippocampus	1
<i>LOC103219692</i>	uncharacterized LOC103219692	Hippocampus	1
<i>LOC103220953</i>	uncharacterized LOC103220953	Hippocampus	1
<i>LOC103221225</i>	uncharacterized LOC103221225	Hippocampus	1
<i>LOC103221683</i>	major histocompatibility complex, class II, DP alpha 1	Hippocampus	1
<i>LOC103221700</i>	HLA class II histocompatibility antigen, DRB1-4 beta chain-like	Hippocampus	1
<i>LOC103221720</i>	tenascin XA (pseudogene)	Hippocampus	1
<i>LOC103221773</i>	class I histocompatibility antigen, Gogo-B*0102 alpha chain-like	Hippocampus	1
<i>LOC103221779</i>	HLA class I histocompatibility antigen, B-46 alpha chain-like	Hippocampus	1
<i>LOC103221786</i>	class I histocompatibility antigen, Gogo-B*0101 alpha chain-like	Hippocampus	1
<i>LOC103221843</i>	HLA class I histocompatibility antigen, alpha chain G-like	Hippocampus	1
<i>LOC103221867</i>	HLA class I histocompatibility antigen, B-38 alpha chain-like	Hippocampus	1
<i>LOC103222066</i>	uncharacterized LOC103222066	Hippocampus	1

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103222086	60S ribosomal protein L29 pseudogene	Hippocampus	1
LOC103222279	uncharacterized LOC103222279	Hippocampus	1
LOC103222322	uncharacterized LOC103222322	Hippocampus	1
LOC103222465	RNA polymerase II transcription factor SIII subunit A3-like	Hippocampus	1
LOC103222493	inhibitor of Bruton tyrosine kinase pseudogene	Hippocampus	1
LOC103222914	immunoglobulin omega chain-like	Hippocampus	1
LOC103223611	atrophin-1 pseudogene	Hippocampus	1
LOC103224012	uncharacterized LOC103224012	Hippocampus	1
LOC103224097	glyceraldehyde-3-phosphate dehydrogenase pseudogene	Hippocampus	1
LOC103224107	3 beta-hydroxysteroid dehydrogenase/Delta 5-->4-isomerase type 1-like	Hippocampus	1
LOC103224108	putative RNA polymerase II subunit A C-terminal domain phosphatase SSU72-like protein 2	Hippocampus	1
LOC103224355	uncharacterized LOC103224355	Hippocampus	1
LOC103224886	vitamin D3 hydroxylase-associated protein-like	Hippocampus	1
LOC103225263	uncharacterized LOC103225263	Hippocampus	1
LOC103225907	omega-amidase NIT2 pseudogene	Hippocampus	1
LOC103225919	phosphate carrier protein, mitochondrial pseudogene	Hippocampus	1
LOC103226041	uncharacterized LOC103226041	Hippocampus	1
LOC103226088	uncharacterized LOC103226088	Hippocampus	1
LOC103226903	uncharacterized LOC103226903	Hippocampus	1
LOC103226931	aldo-keto reductase family 1 member B10	Hippocampus	1
LOC103227329	protein-L-isoaspartate O-methyltransferase domain-containing protein 1 pseudogene	Hippocampus	1
LOC103228545	uncharacterized LOC103228545	Hippocampus	1
LOC103228547	uncharacterized LOC103228547	Hippocampus	1
LOC103228548	uncharacterized LOC103228548	Hippocampus	1
LOC103228982	cofilin-2 pseudogene	Hippocampus	1
LOC103229122	uncharacterized LOC103229122	Hippocampus	1
LOC103229662	uncharacterized LOC103229662	Hippocampus	1
LOC103229673	uncharacterized LOC103229673	Hippocampus	1
LOC103230925	heat shock cognate 71 kDa protein-like	Hippocampus	1
LOC103231011	glutamyl-tRNA(Gln) amidotransferase subunit A, mitochondrial pseudogene	Hippocampus	1
LOC103231099	ubiquitin-conjugating enzyme E2 Q2-like	Hippocampus	1
LOC103231241	uncharacterized LOC103231241	Hippocampus	1
LOC103231244	uncharacterized LOC103231244	Hippocampus	1
LOC103231512	double homeobox protein 4C-like	Hippocampus	1
LOC103231553	uncharacterized LOC103231553	Hippocampus	1
LOC103231593	zinc finger protein 729-like	Hippocampus	1
LOC103231952	angiogenic factor with G patch and FHA domains 1 pseudogene	Hippocampus	1
LOC103232191	uncharacterized LOC103232191	Hippocampus	1
LOC103232192	uncharacterized LOC103232192	Hippocampus	1
LOC103232524	actin-related protein T1-like	Hippocampus	1
LOC103233776	tubulin beta-4A chain-like	Hippocampus	1
LOC103234223	PHD finger-like domain-containing protein 5A pseudogene	Hippocampus	1
LOC103234401	zinc finger protein 85-like	Hippocampus	1
LOC103234406	uncharacterized LOC103234406	Hippocampus	1
LOC103235014	choriogonadotropin subunit beta	Hippocampus	1
LOC103235584	UDP-glucuronosyltransferase 2B4-like	Hippocampus	1
LOC103235585	UDP-glucuronosyltransferase 2B23	Hippocampus	1
LOC103236371	ankyrin repeat domain-containing protein 30A-like	Hippocampus	1
LOC103236500	uncharacterized LOC103236500	Hippocampus	1
LOC103236604	uncharacterized LOC103236604	Hippocampus	1
LOC103236661	uncharacterized LOC103236661	Hippocampus	1
LOC103236694	proliferating cell nuclear antigen pseudogene	Hippocampus	1
LOC103237370	uncharacterized LOC103237370	Hippocampus	1
LOC103237371	uncharacterized LOC103237371	Hippocampus	1
LOC103237524	uncharacterized LOC103237524	Hippocampus	1
LOC103239390	uncharacterized LOC103239390	Hippocampus	1
LOC103239520	elongation factor 1-alpha 1 pseudogene	Hippocampus	1
LOC103239649	beta-lactoglobulin-1-like	Hippocampus	1
LOC103241059	glycerol-3-phosphate acyltransferase 2, mitochondrial	Hippocampus	1
LOC103241171	uncharacterized LOC103241171	Hippocampus	1
LOC103241834	putative uncharacterized protein UNQ6490/PRO21339	Hippocampus	1
LOC103242256	uncharacterized LOC103242256	Hippocampus	1
LOC103242499	CMT1A duplicated region transcript 15 protein-like protein	Hippocampus	1
LOC103242588	uncharacterized LOC103242588	Hippocampus	1
LOC103242716	uncharacterized LOC103242716	Hippocampus	1
LOC103243948	solute carrier family 25 member 51-like	Hippocampus	1
LOC103244016	uncharacterized LOC103244016	Hippocampus	1
LOC103244018	vegetative cell wall protein gp1-like	Hippocampus	1

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103245914	uncharacterized LOC103245914	Hippocampus	1
LOC103246085	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 pseudogene	Hippocampus	1
LOC103246296	uncharacterized LOC103246296	Hippocampus	1
LOC103246967	40S ribosomal protein S4, Y isoform 1	Hippocampus	1
LOC103246968	heat shock transcription factor, Y-linked-like	Hippocampus	1
LOC103246974	developmental pluripotency-associated protein 2 pseudogene	Hippocampus	1
LOC103246975	uncharacterized LOC103246975	Hippocampus	1
LOC103246978	uncharacterized LOC103246978	Hippocampus	1
LOC103246979	ribose-phosphate pyrophosphokinase 2 pseudogene	Hippocampus	1
LOC103246980	uncharacterized LOC103246980	Hippocampus	1
LOC103246981	anosmin-1-like	Hippocampus	1
LOC103246982	acylglycerol kinase, mitochondrial pseudogene	Hippocampus	1
LOC103246983	neuroligin-4, X-linked-like	Hippocampus	1
LOC103246984	uncharacterized LOC103246984	Hippocampus	1
LOC103246986	gamma-taxilin-like	Hippocampus	1
LOC103246988	eukaryotic translation initiation factor 1A, Y-chromosomal	Hippocampus	1
LOC103246990	uncharacterized LOC103246990	Hippocampus	1
LOC103246991	uncharacterized LOC103246991	Hippocampus	1
LOC103246992	40S ribosomal protein S4, Y isoform 1	Hippocampus	1
LOC103246998	ankyrin repeat domain-containing protein 37 pseudogene	Hippocampus	1
LOC103248933	caspase-1-like	Hippocampus	1
LY6K	lymphocyte antigen 6 family member K	Hippocampus	1
MKI67	marker of proliferation Ki-67	Hippocampus	1
MORC1	MORC family CW-type zinc finger 1	Hippocampus	1
MSH5	mutS homolog 5	Hippocampus	1
NEUROG3	neurogenin 3	Hippocampus	1
NPBWR1	neuropeptides B and W receptor 1	Hippocampus	1
NTSR1	neurotensin receptor 1	Hippocampus	1
OAS1	2'-5'-oligoadenylate synthetase 1	Hippocampus	1
OPN4	opsin 4	Hippocampus	1
PDYN	prodynorphin	Hippocampus	1
PIWIL2	piwi like RNA-mediated gene silencing 2	Hippocampus	1
PRDM7	PR/SET domain 7	Hippocampus	1
PTPN20B	protein tyrosine phosphatase, non-receptor type 20	Hippocampus	1
SHCBP1	SHC binding and spindle associated 1	Hippocampus	1
SIX3	SIX homeobox 3	Hippocampus	1
SLC22A12	solute carrier family 22 member 12	Hippocampus	1
SLC5A7	solute carrier family 5 member 7	Hippocampus	1
SPATA22	spermatogenesis associated 22	Hippocampus	1
SYNDIG1L	synapse differentiation inducing 1 like	Hippocampus	1
T	T brachyury transcription factor	Hippocampus	1
TDRD1	tudor domain containing 1	Hippocampus	1
THEG	theg spermatid protein	Hippocampus	1
TNIP3	TNFAIP3 interacting protein 3	Hippocampus	1
TPO	thyroid peroxidase	Hippocampus	1
UGT3A1	UDP glycosyltransferase family 3 member A1	Hippocampus	1
ULBP1	UL16 binding protein 1	Hippocampus	1
USP9Y	ubiquitin specific peptidase 9, Y-linked	Hippocampus	1
UTY	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	Hippocampus	1
WDR72	WD repeat domain 72	Hippocampus	1
WFDC1	WAP four-disulfide core domain 1	Hippocampus	1
ZFY	zinc finger protein, Y-linked	Hippocampus	1
A2ML1	alpha-2-macroglobulin like 1	Pituitary	1
ACTG2	actin, gamma 2, smooth muscle, enteric	Pituitary	1
ADAMTS20	ADAM metallopeptidase with thrombospondin type 1 motif 20	Pituitary	1
AGXT	alanine-glyoxylate aminotransferase	Pituitary	1
APOA2	apolipoprotein A2	Pituitary	1
ATF3	activating transcription factor 3	Pituitary	1
AZU1	azurocidin 1	Pituitary	1
BPI	bactericidal/permeability-increasing protein	Pituitary	1
BPIFB4	BPI fold containing family B member 4	Pituitary	1
C1H11orf86	chromosome 1 open reading frame, human C11orf86	Pituitary	1
CA1	carbonic anhydrase 1	Pituitary	1
CAMP	cathelicidin antimicrobial peptide	Pituitary	1
CARTPT	CART prepropeptide	Pituitary	1
CCDC68	coiled-coil domain containing 68	Pituitary	1
CDH9	cadherin 9	Pituitary	1
CDHR1	cadherin related family member 1	Pituitary	1

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
CHP2	calcineurin like EF-hand protein 2	Pituitary	1
CNN1	calponin 1	Pituitary	1
COL19A1	collagen type XIX alpha 1 chain	Pituitary	1
CRISP3	cysteine rich secretory protein 3	Pituitary	1
CST5	cystatin D	Pituitary	1
CTSG	cathepsin G	Pituitary	1
DDX3Y	DEAD-box helicase 3, Y-linked	Pituitary	1
DEFA1	defensin alpha 1	Pituitary	1
DHH	desert hedgehog	Pituitary	1
DMKN	dermokine	Pituitary	1
DNAJB3	DnaJ heat shock protein family (Hsp40) member B3	Pituitary	1
ELANE	elastase, neutrophil expressed	Pituitary	1
ESPNL	espin-like	Pituitary	1
FGF19	fibroblast growth factor 19	Pituitary	1
FLG2	filaggrin family member 2	Pituitary	1
FMO3	flavin containing monooxygenase 3	Pituitary	1
FOSB	FosB proto-oncogene, AP-1 transcription factor subunit	Pituitary	1
FSHB	follicle stimulating hormone beta subunit	Pituitary	1
FTHL17	ferritin heavy chain like 17	Pituitary	1
GFY	golgi associated olfactory signaling regulator	Pituitary	1
GIPR	gastric inhibitory polypeptide receptor	Pituitary	1
HAND2	heart and neural crest derivatives expressed 2	Pituitary	1
HAVCR1	hepatitis A virus cellular receptor 1	Pituitary	1
HEMGN	hemogen	Pituitary	1
IAPP	islet amyloid polypeptide	Pituitary	1
ISM2	isthmin 2	Pituitary	1
ITGAX	integrin subunit alpha X	Pituitary	1
KDM5D	lysine demethylase 5D	Pituitary	1
KLHL1	kelch like family member 1	Pituitary	1
KLK3	kallikrein related peptidase 3	Pituitary	1
KRBOX1	KRAB box domain containing 1	Pituitary	1
LOC103215303	theta defensin subunit A	Pituitary	1
LOC103215747	serine/threonine-protein kinase tousled-like 2	Pituitary	1
LOC103216175	fer-1-like 4 (C. elegans)	Pituitary	1
LOC103216821	mitochondrial import receptor subunit TOM22 homolog pseudogene	Pituitary	1
LOC103217729	gamma-crystallin D	Pituitary	1
LOC103218057	uncharacterized LOC103218057	Pituitary	1
LOC103218363	uncharacterized LOC103218363	Pituitary	1
LOC103218379	unconventional myosin-Vb pseudogene	Pituitary	1
LOC103218546	pregnancy zone protein	Pituitary	1
LOC103218625	basic salivary proline-rich protein 1-like	Pituitary	1
LOC103218626	basic salivary proline-rich protein 1-like	Pituitary	1
LOC103218629	basic salivary proline-rich protein 1-like	Pituitary	1
LOC103218630	basic salivary proline-rich protein 1-like	Pituitary	1
LOC103218706	elongation factor 1-alpha 1 pseudogene	Pituitary	1
LOC103219103	uncharacterized LOC103219103	Pituitary	1
LOC103219314	ADP/ATP translocase 3-like	Pituitary	1
LOC103219987	lithostathine-1-alpha	Pituitary	1
LOC103220320	ubiquitin-40S ribosomal protein S27a pseudogene	Pituitary	1
LOC103220426	uncharacterized LOC103220426	Pituitary	1
LOC103220845	extensin-like	Pituitary	1
LOC103220953	uncharacterized LOC103220953	Pituitary	1
LOC103221597	heterogeneous nuclear ribonucleoprotein H-like	Pituitary	1
LOC103221683	major histocompatibility complex, class II, DP alpha 1	Pituitary	1
LOC103221773	class I histocompatibility antigen, Gogo-B*0102 alpha chain-like	Pituitary	1
LOC103221779	HLA class I histocompatibility antigen, B-46 alpha chain-like	Pituitary	1
LOC103221786	class I histocompatibility antigen, Gogo-B*0101 alpha chain-like	Pituitary	1
LOC103221791	uncharacterized LOC103221791	Pituitary	1
LOC103221843	HLA class I histocompatibility antigen, alpha chain G-like	Pituitary	1
LOC103221863	mamu class I histocompatibility antigen, alpha chain F-like	Pituitary	1
LOC103221867	HLA class I histocompatibility antigen, B-38 alpha chain-like	Pituitary	1
LOC103222059	60S ribosomal protein L3 pseudogene	Pituitary	1
LOC103222242	uncharacterized LOC103222242	Pituitary	1
LOC103222803	phosphomannomutase 2-like	Pituitary	1
LOC103223466	uncharacterized LOC103223466	Pituitary	1
LOC103225055	non-histone chromosomal protein HMG-17 pseudogene	Pituitary	1
LOC103225263	uncharacterized LOC103225263	Pituitary	1
LOC103225291	hemoglobin subunit alpha	Pituitary	1

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

VervetGeneSymbol	Description	Tissue	PC Dimension
LOC103225416	BRCA2 and CDKN1A-interacting protein pseudogene	Pituitary	1
LOC103225474	40S ribosomal protein S14 pseudogene	Pituitary	1
LOC103225656	60S ribosomal protein L7-like	Pituitary	1
LOC103225919	phosphate carrier protein, mitochondrial pseudogene	Pituitary	1
LOC103226375	ATP-binding cassette sub-family E member 1 pseudogene	Pituitary	1
LOC103226579	Golgi apparatus membrane protein TVP23 homolog B pseudogene	Pituitary	1
LOC103226903	uncharacterized LOC103226903	Pituitary	1
LOC103227729	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform pseudogene	Pituitary	1
LOC103229447	uncharacterized LOC103229447	Pituitary	1
LOC103229828	putative V-set and immunoglobulin domain-containing-like protein IGHV4OR15-8	Pituitary	1
LOC103229848	Ig heavy chain V-III region VH26-like	Pituitary	1
LOC103230114	uncharacterized LOC103230114	Pituitary	1
LOC103230143	extensin-1	Pituitary	1
LOC103230442	tRNA (uracil(54)-C(5))-methyltransferase homolog pseudogene	Pituitary	1
LOC103231553	uncharacterized LOC103231553	Pituitary	1
LOC103231559	trifunctional enzyme subunit beta, mitochondrial-like	Pituitary	1
LOC103232041	ATP synthase subunit beta, mitochondrial pseudogene	Pituitary	1
LOC103232191	uncharacterized LOC103232191	Pituitary	1
LOC103232315	AP-2 complex subunit beta pseudogene	Pituitary	1
LOC103233555	uncharacterized LOC103233555	Pituitary	1
LOC103233753	ran-binding protein 3-like	Pituitary	1
LOC103234078	cytochrome P450 4F8	Pituitary	1
LOC103234079	leukotriene-B(4) omega-hydroxylase 2	Pituitary	1
LOC103235251	ATP-dependent zinc metalloprotease YME1L1 pseudogene	Pituitary	1
LOC103235270	leukocyte-associated immunoglobulin-like receptor 2	Pituitary	1
LOC103235584	UDP-glucuronosyltransferase 2B4-like	Pituitary	1
LOC103235585	UDP-glucuronosyltransferase 2B23	Pituitary	1
LOC103236661	uncharacterized LOC103236661	Pituitary	1
LOC103236796	mitogen-activated protein kinase 6 pseudogene	Pituitary	1
LOC103237018	40S ribosomal protein S5 pseudogene	Pituitary	1
LOC103238014	uncharacterized LOC103238014	Pituitary	1
LOC103238626	glyceraldehyde-3-phosphate dehydrogenase pseudogene	Pituitary	1
LOC103239662	ficolin-2	Pituitary	1
LOC103240185	uncharacterized LOC103240185	Pituitary	1
LOC103241059	glycerol-3-phosphate acyltransferase 2, mitochondrial	Pituitary	1
LOC103241700	collagen alpha-4(VI) chain-like	Pituitary	1
LOC103242499	CMT1A duplicated region transcript 15 protein-like protein	Pituitary	1
LOC103242716	uncharacterized LOC103242716	Pituitary	1
LOC103243233	angiotensin-converting enzyme-like	Pituitary	1
LOC103243247	endophilin-A2 pseudogene	Pituitary	1
LOC103243248	leucine-rich repeat-containing protein 37A-like	Pituitary	1
LOC103246105	splicing factor 45 pseudogene	Pituitary	1
LOC103246281	uncharacterized LOC103246281	Pituitary	1
LOC103246424	uncharacterized LOC103246424	Pituitary	1
LOC103246666	farnesyl pyrophosphate synthase pseudogene	Pituitary	1
LOC103246884	homeobox protein unc-4 homolog	Pituitary	1
LOC103246964	homeobox protein unc-4 homolog	Pituitary	1
LOC103246967	40S ribosomal protein S4, Y isoform 1	Pituitary	1
LOC103246968	heat shock transcription factor, Y-linked-like	Pituitary	1
LOC103246975	uncharacterized LOC103246975	Pituitary	1
LOC103246978	uncharacterized LOC103246978	Pituitary	1
LOC103246979	ribose-phosphate pyrophosphokinase 2 pseudogene	Pituitary	1
LOC103246980	uncharacterized LOC103246980	Pituitary	1
LOC103246983	neuroligin-4, X-linked-like	Pituitary	1
LOC103246986	gamma-taxilin-like	Pituitary	1
LOC103246988	eukaryotic translation initiation factor 1A, Y-chromosomal	Pituitary	1
LOC103246990	uncharacterized LOC103246990	Pituitary	1
LOC103246991	uncharacterized LOC103246991	Pituitary	1
LOC103246992	40S ribosomal protein S4, Y isoform 1	Pituitary	1
LOC103247001	heat shock transcription factor, Y-linked-like	Pituitary	1
LOC103247901	hemoglobin subunit beta	Pituitary	1
LOC103247968	voltage-dependent anion-selective channel protein 1 pseudogene	Pituitary	1
LOC103247990	folate receptor gamma	Pituitary	1
LOC103249008	uncharacterized LOC103249008	Pituitary	1
MMP8	matrix metalloproteinase 8	Pituitary	1
MSLN	mesothelin	Pituitary	1
MUC6	mucin 6, oligomeric mucus/gel-forming	Pituitary	1
MYOC	myocilin	Pituitary	1

**Supplementary Table 7. Genes in the top or bottom 10% of loadings on PC 1, PC 2, or PC 3, for tissues where that dimension in PCA showed a clear pattern with sex as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>NPTX2</i>	neuronal pentraxin 2	Pituitary	1
<i>NR1H4</i>	nuclear receptor subfamily 1 group H member 4	Pituitary	1
<i>NR1I3</i>	nuclear receptor subfamily 1 group I member 3	Pituitary	1
<i>ORM1</i>	orosomucoid 1	Pituitary	1
<i>OTOL1</i>	otolin 1	Pituitary	1
<i>PADI4</i>	peptidyl arginine deiminase 4	Pituitary	1
<i>PCP4L1</i>	Purkinje cell protein 4 like 1	Pituitary	1
<i>PLSCR5</i>	phospholipid scramblase family member 5	Pituitary	1
<i>PRB4</i>	proline rich protein BstNI subfamily 4	Pituitary	1
<i>PRDM6</i>	PR/SET domain 6	Pituitary	1
<i>PRG2</i>	proteoglycan 2, pro eosinophil major basic protein	Pituitary	1
<i>PRTN3</i>	proteinase 3	Pituitary	1
<i>PTGER2</i>	prostaglandin E receptor 2	Pituitary	1
<i>PTPN20B</i>	protein tyrosine phosphatase, non-receptor type 20	Pituitary	1
<i>PTPRH</i>	protein tyrosine phosphatase, receptor type H	Pituitary	1
<i>QRFP</i>	pyroglutamylated RFamide peptide receptor	Pituitary	1
<i>RASGRP3</i>	RAS guanyl releasing protein 3	Pituitary	1
<i>S100A8</i>	S100 calcium binding protein A8	Pituitary	1
<i>S100A9</i>	S100 calcium binding protein A9	Pituitary	1
<i>SCGB1D4</i>	secretoglobin family 1D member 4	Pituitary	1
<i>SERPINA5</i>	serpin family A member 5	Pituitary	1
<i>SERPINA6</i>	serpin family A member 6	Pituitary	1
<i>SERPINF2</i>	serpin family F member 2	Pituitary	1
<i>SHCBP1</i>	SHC binding and spindle associated 1	Pituitary	1
<i>SLC1A6</i>	solute carrier family 1 member 6	Pituitary	1
<i>SLC22A6</i>	solute carrier family 22 member 6	Pituitary	1
<i>SLC22A8</i>	solute carrier family 22 member 8	Pituitary	1
<i>SLC34A3</i>	solute carrier family 34 member 3	Pituitary	1
<i>SLC4A1</i>	solute carrier family 4 member 1 (Diego blood group)	Pituitary	1
<i>SLC5A8</i>	solute carrier family 5 member 8	Pituitary	1
<i>SLC6A20</i>	solute carrier family 6 member 20	Pituitary	1
<i>SPATA22</i>	spermatogenesis associated 22	Pituitary	1
<i>SPC25</i>	SPC25, NDC80 kinetochore complex component	Pituitary	1
<i>SPTA1</i>	spectrin alpha, erythrocytic 1	Pituitary	1
<i>TAC1</i>	tachykinin precursor 1	Pituitary	1
<i>THEG</i>	theg spermatid protein	Pituitary	1
<i>TMPRSS12</i>	transmembrane protease, serine 12	Pituitary	1
<i>TPH2</i>	tryptophan hydroxylase 2	Pituitary	1
<i>TYRP1</i>	tyrosinase related protein 1	Pituitary	1
<i>USP26</i>	ubiquitin specific peptidase 26	Pituitary	1
<i>USP9Y</i>	ubiquitin specific peptidase 9, Y-linked	Pituitary	1
<i>UTY</i>	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	Pituitary	1
<i>VASH2</i>	vasohibin 2	Pituitary	1
<i>VGLL2</i>	vestigial like family member 2	Pituitary	1
<i>ZFY</i>	zinc finger protein, Y-linked	Pituitary	1
<i>ZIC1</i>	Zic family member 1	Pituitary	1
<i>ZIC2</i>	Zic family member 2	Pituitary	1
<i>ZIC4</i>	Zic family member 4	Pituitary	1

**Supplementary Table 8. Genes in the top or bottom 10% of loadings on PC 1 for Caudate and BA46, where that dimension in PCA showed a clear pattern with age as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>ADAMTS14</i>	ADAM metallopeptidase with thrombospondin type 1 motif, 14	BA46	1
<i>AGPAT9</i>	1-acylglycerol-3-phosphate O-acyltransferase 9	BA46	1
<i>AGT</i>	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	BA46	1
<i>AIRE</i>	autoimmune regulator	BA46	1
<i>ANKRD63</i>	ankyrin repeat domain 63	BA46	1
<i>ANLN</i>	anillin, actin binding protein	BA46	1
<i>APOC2</i>	apolipoprotein C-II	BA46	1
<i>ASB2</i>	ankyrin repeat and SOCS box containing 2	BA46	1
<i>ATP4A</i>	ATPase, H+/K+ exchanging, alpha polypeptide	BA46	1
<i>BARX2</i>	BARX homeobox 2	BA46	1
<i>BDKRB1</i>	bradykinin receptor B1	BA46	1
<i>BDKRB2</i>	bradykinin receptor B2	BA46	1
<i>BHMT</i>	betaine--homocysteine S-methyltransferase	BA46	1
<i>BHMT2</i>	betaine--homocysteine S-methyltransferase 2	BA46	1
<i>BMP5</i>	bone morphogenetic protein 5	BA46	1
<i>C14H2orf91</i>	chromosome 14 open reading frame, human C2orf91	BA46	1
<i>C22H3orf56</i>	chromosome 22 open reading frame, human C3orf56	BA46	1
<i>C26H15orf54</i>	chromosome 26 open reading frame, human C15orf54	BA46	1
<i>C2H20orf195</i>	chromosome 2 open reading frame, human C20orf195	BA46	1
<i>C7</i>	complement component 7	BA46	1
<i>CACNA1S</i>	calcium channel, voltage-dependent, L type, alpha 1S subunit	BA46	1
<i>CARTPT</i>	CART prepropeptide	BA46	1
<i>CCDC179</i>	coiled-coil domain containing 179	BA46	1
<i>CCR3</i>	chemokine (C-C motif) receptor 3	BA46	1
<i>CD24</i>	CD24 molecule	BA46	1
<i>CD96</i>	CD96 molecule	BA46	1
<i>CHI3L1</i>	chitinase 3-like 1 (cartilage glycoprotein-39)	BA46	1
<i>CHRNA3</i>	cholinergic receptor, nicotinic, alpha 3 (neuronal)	BA46	1
<i>CLIC6</i>	chloride intracellular channel 6	BA46	1
<i>CNDP1</i>	carnosine dipeptidase 1 (metallopeptidase M20 family)	BA46	1
<i>COL1A1</i>	collagen, type I, alpha 1	BA46	1
<i>COL1A2</i>	collagen, type I, alpha 2	BA46	1
<i>COL3A1</i>	collagen, type III, alpha 1	BA46	1
<i>COL4A6</i>	collagen, type IV, alpha 6	BA46	1
<i>COL6A3</i>	collagen, type VI, alpha 3	BA46	1
<i>CPB1</i>	carboxypeptidase B1 (tissue)	BA46	1
<i>CPZ</i>	carboxypeptidase Z	BA46	1
<i>CRISPLD1</i>	cysteine-rich secretory protein LCCL domain containing 1	BA46	1
<i>DACT2</i>	dishevelled-binding antagonist of beta-catenin 2	BA46	1
<i>DCDC2C</i>	doublecortin domain containing 2C	BA46	1
<i>DPYSL3</i>	dihydropyrimidinase-like 3	BA46	1
<i>DPYSL5</i>	dihydropyrimidinase-like 5	BA46	1
<i>DRAXIN</i>	dorsal inhibitory axon guidance protein	BA46	1
<i>DSP</i>	desmoplakin	BA46	1
<i>DTL</i>	denticleless E3 ubiquitin protein ligase homolog (Drosophila)	BA46	1
<i>EMILIN3</i>	elastin microfibril interfacier 3	BA46	1
<i>ERMN</i>	ermin, ERM-like protein	BA46	1
<i>ETNPPL</i>	ethanolamine-phosphate phospho-lyase	BA46	1
<i>FAM132A</i>	family with sequence similarity 132, member A	BA46	1
<i>FAM159B</i>	family with sequence similarity 159, member B	BA46	1
<i>FCN3</i>	ficolin (collagen/fibrinogen domain containing) 3	BA46	1
<i>FERD3L</i>	Fer3-like bHLH transcription factor	BA46	1
<i>FNDC1</i>	fibronectin type III domain containing 1	BA46	1
<i>FOXI3</i>	forkhead box I3	BA46	1
<i>FREM3</i>	FRAS1 related extracellular matrix 3	BA46	1
<i>FST</i>	follistatin	BA46	1

**Supplementary Table 8. Genes in the top or bottom 10% of loadings on PC 1 for Caudate and BA46, where that dimension in PCA showed a clear pattern with age as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>GALNT5</i>	polypeptide N-acetylgalactosaminyltransferase 5	BA46	1
<i>GDF10</i>	growth differentiation factor 10	BA46	1
<i>GJB1</i>	gap junction protein, beta 1, 32kDa	BA46	1
<i>GJB5</i>	gap junction protein, beta 5, 31.1kDa	BA46	1
<i>GNA14</i>	guanine nucleotide binding protein (G protein), alpha 14	BA46	1
<i>GRP</i>	gastrin-releasing peptide	BA46	1
<i>HAPLN4</i>	hyaluronan and proteoglycan link protein 4	BA46	1
<i>HSPB8</i>	heat shock 22kDa protein 8	BA46	1
<i>HTR3A</i>	5-hydroxytryptamine (serotonin) receptor 3A, ionotropic	BA46	1
<i>IGF2BP2</i>	insulin-like growth factor 2 mRNA binding protein 2	BA46	1
<i>ISM2</i>	isthmin 2	BA46	1
<i>KCNS1</i>	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1	BA46	1
<i>KERA</i>	keratocan	BA46	1
<i>KLK6</i>	kallikrein-related peptidase 6	BA46	1
<i>KRT19</i>	keratin 19	BA46	1
<i>KRT7</i>	keratin 7	BA46	1
<i>KRT80</i>	keratin 80	BA46	1
<i>LGR6</i>	leucine-rich repeat containing G protein-coupled receptor 6	BA46	1
<i>LOC103214977</i>	uncharacterized LOC103214977	BA46	1
<i>LOC103216325</i>	uncharacterized LOC103216325	BA46	1
<i>LOC103216876</i>	uncharacterized LOC103216876	BA46	1
<i>LOC103217402</i>	uncharacterized LOC103217402	BA46	1
<i>LOC103218887</i>	olfactory receptor 1J2	BA46	1
<i>LOC103218889</i>	olfactory receptor 1J4-like	BA46	1
<i>LOC103219658</i>	uncharacterized LOC103219658	BA46	1
<i>LOC103219850</i>	proteasome subunit beta type-1 pseudogene	BA46	1
<i>LOC103220411</i>	40S ribosomal protein S12 pseudogene	BA46	1
<i>LOC103221116</i>	putative uncharacterized protein C21orf125	BA46	1
<i>LOC103221863</i>	mamu class I histocompatibility antigen, alpha chain F-like	BA46	1
<i>LOC103221894</i>	olfactory receptor 10C1-like	BA46	1
<i>LOC103221933</i>	histone H2B type 1-O	BA46	1
<i>LOC103221935</i>	histone H2A type 1	BA46	1
<i>LOC103221943</i>	histone H2A type 1	BA46	1
<i>LOC103221944</i>	histone H1.5	BA46	1
<i>LOC103221945</i>	histone H3.1-like	BA46	1
<i>LOC103221996</i>	histone H2B type 1-F/J/L-like	BA46	1
<i>LOC103222083</i>	uncharacterized LOC103222083	BA46	1
<i>LOC103222154</i>	uncharacterized LOC103222154	BA46	1
<i>LOC103222155</i>	uncharacterized LOC103222155	BA46	1
<i>LOC103222369</i>	uncharacterized LOC103222369	BA46	1
<i>LOC103222593</i>	uncharacterized LOC103222593	BA46	1
<i>LOC103222965</i>	P2X purinoceptor 6-like	BA46	1
<i>LOC103223518</i>	uncharacterized LOC103223518	BA46	1
<i>LOC103223762</i>	olfactory receptor 10J1-like	BA46	1
<i>LOC103224231</i>	uncharacterized LOC103224231	BA46	1
<i>LOC103224977</i>	uncharacterized LOC103224977	BA46	1
<i>LOC103225645</i>	uncharacterized LOC103225645	BA46	1
<i>LOC103226929</i>	aldo-keto reductase family 1 member B10-like	BA46	1
<i>LOC103226931</i>	aldo-keto reductase family 1 member B10	BA46	1
<i>LOC103226932</i>	aldo-keto reductase family 1 member B10-like	BA46	1
<i>LOC103228345</i>	putative uncharacterized protein	BA46	1
<i>LOC103230633</i>	uncharacterized LOC103230633	BA46	1
<i>LOC103230880</i>	uncharacterized LOC103230880	BA46	1
<i>LOC103231593</i>	zinc finger protein 729-like	BA46	1
<i>LOC103231996</i>	centromere protein V-like	BA46	1
<i>LOC103233113</i>	uncharacterized LOC103233113	BA46	1



**Supplementary Table 8. Genes in the top or bottom 10% of loadings on PC 1 for Caudate and BA46, where that dimension in PCA showed a clear pattern with age as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>LOC103233444</i>	bile salt-activated lipase-like	BA46	1
<i>LOC103233832</i>	fibrillin-3-like	BA46	1
<i>LOC103234284</i>	zinc finger protein 98-like	BA46	1
<i>LOC103234347</i>	fibrillin-3-like	BA46	1
<i>LOC103234986</i>	galactoside 2-alpha-L-fucosyltransferase 2	BA46	1
<i>LOC103234988</i>	galactoside 2-alpha-L-fucosyltransferase 2-like	BA46	1
<i>LOC103236784</i>	uncharacterized LOC103236784	BA46	1
<i>LOC103237464</i>	uncharacterized LOC103237464	BA46	1
<i>LOC103237465</i>	uncharacterized LOC103237465	BA46	1
<i>LOC103237714</i>	lymphocyte-specific protein 1	BA46	1
<i>LOC103239382</i>	uncharacterized LOC103239382	BA46	1
<i>LOC103240941</i>	uncharacterized LOC103240941	BA46	1
<i>LOC103241172</i>	adenosylhomocysteinase pseudogene	BA46	1
<i>LOC103241685</i>	uncharacterized LOC103241685	BA46	1
<i>LOC103241849</i>	spidroin-1	BA46	1
<i>LOC103242716</i>	uncharacterized LOC103242716	BA46	1
<i>LOC103242774</i>	TBC1 domain family member 3G-like	BA46	1
<i>LOC103243079</i>	ras-related protein Rab-37	BA46	1
<i>LOC103244091</i>	uncharacterized LOC103244091	BA46	1
<i>LOC103244197</i>	uncharacterized LOC103244197	BA46	1
<i>LOC103244931</i>	uncharacterized LOC103244931	BA46	1
<i>LOC103245855</i>	uncharacterized LOC103245855	BA46	1
<i>LOC103247904</i>	hemoglobin subunit gamma-1	BA46	1
<i>LOC103248295</i>	uncharacterized LOC103248295	BA46	1
<i>LYVE1</i>	lymphatic vessel endothelial hyaluronan receptor 1	BA46	1
<i>MAG</i>	myelin associated glycoprotein	BA46	1
<i>MBP</i>	myelin basic protein	BA46	1
<i>MDFI</i>	MyoD family inhibitor	BA46	1
<i>MEOX1</i>	mesenchyme homeobox 1	BA46	1
<i>MKI67</i>	marker of proliferation Ki-67	BA46	1
<i>MOG</i>	myelin oligodendrocyte glycoprotein	BA46	1
<i>MUC4</i>	mucin 4, cell surface associated	BA46	1
<i>MYH13</i>	myosin, heavy chain 13, skeletal muscle	BA46	1
<i>MYL10</i>	myosin, light chain 10, regulatory	BA46	1
<i>NKX6-2</i>	NK6 homeobox 2	BA46	1
<i>NMRK2</i>	nicotinamide riboside kinase 2	BA46	1
<i>NPBWR1</i>	neuropeptides B/W receptor 1	BA46	1
<i>NTSR1</i>	neurotensin receptor 1 (high affinity)	BA46	1
<i>OAS1</i>	2'-5'-oligoadenylate synthetase 1, 40/46kDa	BA46	1
<i>OAS2</i>	2'-5'-oligoadenylate synthetase 2, 69/71kDa	BA46	1
<i>OPALIN</i>	oligodendrocytic myelin paranodal and inner loop protein	BA46	1
<i>OSR1</i>	odd-skipped related transcription factor 1	BA46	1
<i>OSTN</i>	osteocrin	BA46	1
<i>PLAC8</i>	placenta-specific 8	BA46	1
<i>PRSS35</i>	protease, serine, 35	BA46	1
<i>PRSS45</i>	protease, serine, 45	BA46	1
<i>PTF1A</i>	pancreas specific transcription factor, 1a	BA46	1
<i>PTGS1</i>	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	BA46	1
<i>PTX3</i>	pentraxin 3, long	BA46	1
<i>RASD1</i>	RAS, dexamethasone-induced 1	BA46	1
<i>RASEF</i>	RAS and EF-hand domain containing	BA46	1
<i>RASSF10</i>	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	BA46	1
<i>RORC</i>	RAR-related orphan receptor C	BA46	1
<i>RPRM</i>	reprimin, TP53 dependent G2 arrest mediator candidate	BA46	1
<i>S1PR5</i>	sphingosine-1-phosphate receptor 5	BA46	1
<i>SEC14L5</i>	SEC14-like 5 ( <i>S. cerevisiae</i> )	BA46	1

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<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>SECTM1</i>	secreted and transmembrane 1	BA46	1
<i>SERINC2</i>	serine incorporator 2	BA46	1
<i>SH2D5</i>	SH2 domain containing 5	BA46	1
<i>SHCBP1</i>	SHC SH2-domain binding protein 1	BA46	1
<i>SLA</i>	Src-like-adaptor	BA46	1
<i>SLC22A2</i>	solute carrier family 22 (organic cation transporter), member 2	BA46	1
<i>SLC22A8</i>	solute carrier family 22 (organic anion transporter), member 8	BA46	1
<i>SLC25A45</i>	solute carrier family 25, member 45	BA46	1
<i>SLC6A20</i>	solute carrier family 6 (proline IMINO transporter), member 20	BA46	1
<i>SLITRK6</i>	SLIT and NTRK-like family, member 6	BA46	1
<i>SOHLH1</i>	spermatogenesis and oogenesis specific basic helix-loop-helix 1	BA46	1
<i>SOX11</i>	SRY (sex determining region Y)-box 11	BA46	1
<i>SPINK2</i>	serine peptidase inhibitor, Kazal type 2 (acrosin-trypsin inhibitor)	BA46	1
<i>SPINT1</i>	serine peptidase inhibitor, Kunitz type 1	BA46	1
<i>STRA6</i>	stimulated by retinoic acid 6	BA46	1
<i>SULT1E1</i>	sulfotransferase family 1E, estrogen-preferring, member 1	BA46	1
<i>SYTL1</i>	synaptotagmin-like 1	BA46	1
<i>TACR3</i>	tachykinin receptor 3	BA46	1
<i>TEX37</i>	testis expressed 37	BA46	1
<i>TG</i>	thyroglobulin	BA46	1
<i>THBS1</i>	thrombospondin 1	BA46	1
<i>THBS2</i>	thrombospondin 2	BA46	1
<i>THBS4</i>	thrombospondin 4	BA46	1
<i>THSD4</i>	thrombospondin, type I, domain containing 4	BA46	1
<i>TICRR</i>	TOPBP1-interacting checkpoint and replication regulator	BA46	1
<i>TIMD4</i>	T-cell immunoglobulin and mucin domain containing 4	BA46	1
<i>TMEM125</i>	transmembrane protein 125	BA46	1
<i>TNNT2</i>	troponin T type 2 (cardiac)	BA46	1
<i>UHRF1</i>	ubiquitin-like with PHD and ring finger domains 1	BA46	1
<i>VEPH1</i>	ventricular zone expressed PH domain-containing 1	BA46	1
<i>WFIKN2</i>	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain containing 2	BA46	1
<i>ZNF469</i>	zinc finger protein 469	BA46	1
<i>SEPT4</i>	septin 4	Caudate	1
<i>ABCA8</i>	ATP-binding cassette, sub-family A (ABC1), member 8	Caudate	1
<i>AGPAT9</i>	1-acylglycerol-3-phosphate O-acyltransferase 9	Caudate	1
<i>AGT</i>	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	Caudate	1
<i>AIPL1</i>	aryl hydrocarbon receptor interacting protein-like 1	Caudate	1
<i>ALAS2</i>	aminolevulinate, delta-, synthase 2	Caudate	1
<i>ALOX15</i>	arachidonate 15-lipoxygenase	Caudate	1
<i>ANLN</i>	anillin, actin binding protein	Caudate	1
<i>APOB</i>	apolipoprotein B	Caudate	1
<i>APOC2</i>	apolipoprotein C-II	Caudate	1
<i>ASAH2</i>	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	Caudate	1
<i>ASPM</i>	asp (abnormal spindle) homolog, microcephaly associated ( <i>Drosophila</i> )	Caudate	1
<i>BUB1</i>	BUB1 mitotic checkpoint serine/threonine kinase	Caudate	1
<i>C17H6orf10</i>	chromosome 17 open reading frame, human C6orf10	Caudate	1
<i>C20H1orf177</i>	chromosome 20 open reading frame, human C1orf177	Caudate	1
<i>CACNA1S</i>	calcium channel, voltage-dependent, L type, alpha 1S subunit	Caudate	1
<i>CD177</i>	CD177 molecule	Caudate	1
<i>CDK1</i>	cyclin-dependent kinase 1	Caudate	1
<i>CLCA2</i>	chloride channel accessory 2	Caudate	1
<i>CLRN2</i>	clarin 2	Caudate	1
<i>CNDP1</i>	carnosine dipeptidase 1 (metallopeptidase M20 family)	Caudate	1
<i>CNTN6</i>	contactin 6	Caudate	1
<i>COL1A1</i>	collagen, type I, alpha 1	Caudate	1
<i>COL3A1</i>	collagen, type III, alpha 1	Caudate	1

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<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>COL6A5</i>	collagen, type VI, alpha 5	Caudate	1
<i>CPB1</i>	carboxypeptidase B1 (tissue)	Caudate	1
<i>CRYAB</i>	crystallin, alpha B	Caudate	1
<i>CRYBB1</i>	crystallin, beta B1	Caudate	1
<i>DLGAP5</i>	discs, large (Drosophila) homolog-associated protein 5	Caudate	1
<i>DMKN</i>	dermokine	Caudate	1
<i>DMP1</i>	dentin matrix acidic phosphoprotein 1	Caudate	1
<i>DOCK5</i>	dedicator of cytokinesis 5	Caudate	1
<i>DSP</i>	desmoplakin	Caudate	1
<i>E2F2</i>	E2F transcription factor 2	Caudate	1
<i>ERMN</i>	ermin, ERM-like protein	Caudate	1
<i>ERVMER34-1</i>	endogenous retrovirus group MER34, member 1	Caudate	1
<i>FAM159A</i>	family with sequence similarity 159, member A	Caudate	1
<i>FAM163B</i>	family with sequence similarity 163, member B	Caudate	1
<i>FAM19A1</i>	family with sequence similarity 19 (chemokine (C-C motif)-like), member A1	Caudate	1
<i>FAM19A2</i>	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	Caudate	1
<i>FAT2</i>	FAT atypical cadherin 2	Caudate	1
<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	Caudate	1
<i>FOXI3</i>	forkhead box I3	Caudate	1
<i>FST</i>	follistatin	Caudate	1
<i>GADL1</i>	glutamate decarboxylase-like 1	Caudate	1
<i>GALNT5</i>	polypeptide N-acetylgalactosaminyltransferase 5	Caudate	1
<i>GCNT1</i>	glucosaminyl (N-acetyl) transferase 1, core 2	Caudate	1
<i>GDF2</i>	growth differentiation factor 2	Caudate	1
<i>GJB1</i>	gap junction protein, beta 1, 32kDa	Caudate	1
<i>GJD2</i>	gap junction protein, delta 2, 36kDa	Caudate	1
<i>GLRA2</i>	glycine receptor, alpha 2	Caudate	1
<i>GPNMB</i>	glycoprotein (transmembrane) nmb	Caudate	1
<i>GPX2</i>	glutathione peroxidase 2 (gastrointestinal)	Caudate	1
<i>HAPLN2</i>	hyaluronan and proteoglycan link protein 2	Caudate	1
<i>HAPLN4</i>	hyaluronan and proteoglycan link protein 4	Caudate	1
<i>HOXD1</i>	homeobox D1	Caudate	1
<i>HOXD3</i>	homeobox D3	Caudate	1
<i>HSF4</i>	heat shock transcription factor 4	Caudate	1
<i>HSPB8</i>	heat shock 22kDa protein 8	Caudate	1
<i>IGFBP3</i>	insulin-like growth factor binding protein 3	Caudate	1
<i>IGFBP6</i>	insulin-like growth factor binding protein 6	Caudate	1
<i>IRX3</i>	iroquois homeobox 3	Caudate	1
<i>ISX</i>	intestine-specific homeobox	Caudate	1
<i>KANK4</i>	KN motif and ankyrin repeat domains 4	Caudate	1
<i>KDM5D</i>	lysine (K)-specific demethylase 5D	Caudate	1
<i>KLHL4</i>	kelch-like family member 4	Caudate	1
<i>KLK6</i>	kallikrein-related peptidase 6	Caudate	1
<i>LOC103214240</i>	uncharacterized LOC103214240	Caudate	1
<i>LOC103214520</i>	uncharacterized LOC103214520	Caudate	1
<i>LOC103214814</i>	uncharacterized LOC103214814	Caudate	1
<i>LOC103215490</i>	uncharacterized LOC103215490	Caudate	1
<i>LOC103215493</i>	uncharacterized LOC103215493	Caudate	1
<i>LOC103215864</i>	neuropeptide Y receptor type 4	Caudate	1
<i>LOC103216365</i>	uncharacterized LOC103216365	Caudate	1
<i>LOC103216366</i>	uncharacterized LOC103216366	Caudate	1
<i>LOC103216558</i>	uncharacterized LOC103216558	Caudate	1
<i>LOC103216690</i>	uncharacterized LOC103216690	Caudate	1
<i>LOC103217039</i>	uncharacterized LOC103217039	Caudate	1
<i>LOC103217040</i>	uncharacterized LOC103217040	Caudate	1
<i>LOC103217195</i>	uncharacterized LOC103217195	Caudate	1

**Supplementary Table 8. Genes in the top or bottom 10% of loadings on PC 1 for Caudate and BA46, where that dimension in PCA showed a clear pattern with age as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>LOC103217614</i>	uncharacterized LOC103217614	Caudate	1
<i>LOC103217927</i>	uncharacterized LOC103217927	Caudate	1
<i>LOC103218545</i>	alpha-2-macroglobulin-like	Caudate	1
<i>LOC103218697</i>	uncharacterized LOC103218697	Caudate	1
<i>LOC103218698</i>	uncharacterized LOC103218698	Caudate	1
<i>LOC103218845</i>	hsc70-interacting protein pseudogene	Caudate	1
<i>LOC103219103</i>	uncharacterized LOC103219103	Caudate	1
<i>LOC103219657</i>	uncharacterized LOC103219657	Caudate	1
<i>LOC103219832</i>	uncharacterized LOC103219832	Caudate	1
<i>LOC103219872</i>	keratin-associated protein 10-11-like	Caudate	1
<i>LOC103221007</i>	uncharacterized LOC103221007	Caudate	1
<i>LOC103221705</i>	heterogeneous nuclear ribonucleoprotein A1-like	Caudate	1
<i>LOC103221863</i>	mamu class I histocompatibility antigen, alpha chain F-like	Caudate	1
<i>LOC103221933</i>	histone H2B type 1-O	Caudate	1
<i>LOC103221935</i>	histone H2A type 1	Caudate	1
<i>LOC103221936</i>	histone H2A type 1-J	Caudate	1
<i>LOC103221937</i>	histone H2B type 1-M	Caudate	1
<i>LOC103221943</i>	histone H2A type 1	Caudate	1
<i>LOC103221944</i>	histone H1.5	Caudate	1
<i>LOC103221945</i>	histone H3.1-like	Caudate	1
<i>LOC103221968</i>	histone H2A type 1-H	Caudate	1
<i>LOC103221996</i>	histone H2B type 1-F/J/L-like	Caudate	1
<i>LOC103222004</i>	histone H3.1	Caudate	1
<i>LOC103222079</i>	uncharacterized LOC103222079	Caudate	1
<i>LOC103222083</i>	uncharacterized LOC103222083	Caudate	1
<i>LOC103222087</i>	uncharacterized LOC103222087	Caudate	1
<i>LOC103222429</i>	uncharacterized LOC103222429	Caudate	1
<i>LOC103222617</i>	uncharacterized LOC103222617	Caudate	1
<i>LOC103224231</i>	uncharacterized LOC103224231	Caudate	1
<i>LOC103224548</i>	uncharacterized LOC103224548	Caudate	1
<i>LOC103224550</i>	uncharacterized LOC103224550	Caudate	1
<i>LOC103224553</i>	hsc70-interacting protein-like	Caudate	1
<i>LOC103225907</i>	omega-amidase NIT2 pseudogene	Caudate	1
<i>LOC103226631</i>	elongation factor 1-delta-like	Caudate	1
<i>LOC103226870</i>	brain-specific serine protease 4	Caudate	1
<i>LOC103228374</i>	uncharacterized LOC103228374	Caudate	1
<i>LOC103231548</i>	neuronal regeneration-related protein pseudogene	Caudate	1
<i>LOC103232191</i>	uncharacterized LOC103232191	Caudate	1
<i>LOC103233113</i>	uncharacterized LOC103233113	Caudate	1
<i>LOC103233444</i>	bile salt-activated lipase-like	Caudate	1
<i>LOC103233527</i>	uncharacterized LOC103233527	Caudate	1
<i>LOC103234347</i>	fibrillin-3-like	Caudate	1
<i>LOC103234988</i>	galactoside 2-alpha-L-fucosyltransferase 2-like	Caudate	1
<i>LOC103236664</i>	uncharacterized LOC103236664	Caudate	1
<i>LOC103236776</i>	uncharacterized LOC103236776	Caudate	1
<i>LOC103236784</i>	uncharacterized LOC103236784	Caudate	1
<i>LOC103237807</i>	aldo-keto reductase family 1 member C1 homolog	Caudate	1
<i>LOC103238617</i>	40S ribosomal protein S3 pseudogene	Caudate	1
<i>LOC103239962</i>	uncharacterized LOC103239962	Caudate	1
<i>LOC103240326</i>	uncharacterized LOC103240326	Caudate	1
<i>LOC103240468</i>	uncharacterized LOC103240468	Caudate	1
<i>LOC103240469</i>	uncharacterized LOC103240469	Caudate	1
<i>LOC103240470</i>	uncharacterized LOC103240470	Caudate	1
<i>LOC103240471</i>	uncharacterized LOC103240471	Caudate	1
<i>LOC103240472</i>	uncharacterized LOC103240472	Caudate	1
<i>LOC103240473</i>	uncharacterized LOC103240473	Caudate	1

**Supplementary Table 8. Genes in the top or bottom 10% of loadings on PC 1 for Caudate and BA46, where that dimension in PCA showed a clear pattern with age as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>LOC103240474</i>	uncharacterized LOC103240474	Caudate	1
<i>LOC103240475</i>	uncharacterized LOC103240475	Caudate	1
<i>LOC103240939</i>	putative uncharacterized protein FLJ45177	Caudate	1
<i>LOC103240941</i>	uncharacterized LOC103240941	Caudate	1
<i>LOC103241538</i>	uncharacterized LOC103241538	Caudate	1
<i>LOC103241700</i>	collagen alpha-4(VI) chain-like	Caudate	1
<i>LOC103242716</i>	uncharacterized LOC103242716	Caudate	1
<i>LOC103243101</i>	uncharacterized LOC103243101	Caudate	1
<i>LOC103243139</i>	uncharacterized LOC103243139	Caudate	1
<i>LOC103243458</i>	keratin, type I cuticular Ha7-like	Caudate	1
<i>LOC103244383</i>	uncharacterized LOC103244383	Caudate	1
<i>LOC103244770</i>	uncharacterized LOC103244770	Caudate	1
<i>LOC103244868</i>	uncharacterized LOC103244868	Caudate	1
<i>LOC103246345</i>	uncharacterized LOC103246345	Caudate	1
<i>LOC103246967</i>	40S ribosomal protein S4, Y isoform 1	Caudate	1
<i>LOC103246998</i>	ankyrin repeat domain-containing protein 37 pseudogene	Caudate	1
<i>LOC103247901</i>	hemoglobin subunit beta	Caudate	1
<i>LOC103247904</i>	hemoglobin subunit gamma-1	Caudate	1
<i>LRRC55</i>	leucine rich repeat containing 55	Caudate	1
<i>MKI67</i>	marker of proliferation Ki-67	Caudate	1
<i>MYC</i>	v-myc avian myelocytomatosis viral oncogene homolog	Caudate	1
<i>MYO5B</i>	myosin VB	Caudate	1
<i>NDC80</i>	NDC80 kinetochore complex component	Caudate	1
<i>NDRG1</i>	N-myc downstream regulated 1	Caudate	1
<i>NGFR</i>	nerve growth factor receptor	Caudate	1
<i>NKX3-1</i>	NK3 homeobox 1	Caudate	1
<i>NPBWR1</i>	neuropeptides B/W receptor 1	Caudate	1
<i>NTS</i>	neurotensin	Caudate	1
<i>OTOG</i>	otogelin	Caudate	1
<i>PMEL</i>	premelanosome protein	Caudate	1
<i>POPDC3</i>	popeye domain containing 3	Caudate	1
<i>PPAP2C</i>	phosphatidic acid phosphatase type 2C	Caudate	1
<i>PTF1A</i>	pancreas specific transcription factor, 1a	Caudate	1
<i>RAB7B</i>	RAB7B, member RAS oncogene family	Caudate	1
<i>RBP3</i>	retinol binding protein 3, interstitial	Caudate	1
<i>RNF152</i>	ring finger protein 152	Caudate	1
<i>S1PR5</i>	sphingosine-1-phosphate receptor 5	Caudate	1
<i>SGOL1</i>	shugoshin-like 1 (S. pombe)	Caudate	1
<i>SHCBP1</i>	SHC SH2-domain binding protein 1	Caudate	1
<i>SLC16A11</i>	solute carrier family 16, member 11	Caudate	1
<i>SLC17A2</i>	solute carrier family 17, member 2	Caudate	1
<i>SLC17A3</i>	solute carrier family 17 (organic anion transporter), member 3	Caudate	1
<i>SLC5A11</i>	solute carrier family 5 (sodium/inositol cotransporter), member 11	Caudate	1
<i>SLC6A7</i>	solute carrier family 6 (neurotransmitter transporter), member 7	Caudate	1
<i>SP8</i>	Sp8 transcription factor	Caudate	1
<i>SPTA1</i>	spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	Caudate	1
<i>ST8SIA2</i>	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	Caudate	1
<i>STRA6</i>	stimulated by retinoic acid 6	Caudate	1
<i>STYK1</i>	serine/threonine/tyrosine kinase 1	Caudate	1
<i>SULT1E1</i>	sulfotransferase family 1E, estrogen-preferring, member 1	Caudate	1
<i>SYT10</i>	synaptotagmin X	Caudate	1
<i>SYTL1</i>	synaptotagmin-like 1	Caudate	1
<i>TESPA1</i>	thymocyte expressed, positive selection associated 1	Caudate	1
<i>TFCP2L1</i>	transcription factor CP2-like 1	Caudate	1
<i>TIMD4</i>	T-cell immunoglobulin and mucin domain containing 4	Caudate	1
<i>TMEM235</i>	transmembrane protein 235	Caudate	1

**Supplementary Table 8. Genes in the top or bottom 10% of loadings on PC 1 for Caudate and BA46, where that dimension in PCA showed a clear pattern with age as illustrated in Figure 1.**

<b>VervetGeneSymbol</b>	<b>Description</b>	<b>Tissue</b>	<b>PC Dimension</b>
<i>TRHR</i>	thyrotropin-releasing hormone receptor	Caudate	1
<i>TRPC5</i>	transient receptor potential cation channel, subfamily C, member 5	Caudate	1
<i>TRPC5OS</i>	TRPC5 opposite strand	Caudate	1
<i>TSPAN2</i>	tetraspanin 2	Caudate	1
<i>TSPEAR</i>	thrombospondin-type laminin G domain and EAR repeats	Caudate	1
<i>USP9Y</i>	ubiquitin specific peptidase 9, Y-linked	Caudate	1
<i>UTY</i>	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked	Caudate	1
<i>WNT6</i>	wingless-type MMTV integration site family, member 6	Caudate	1

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>AASS</i>	Adrenal	5.42E-14	0.000812	2.06E-10	increasing	0
<i>ABCA3</i>	Adrenal	5.51E-12	0.000792	4.79E-10	increasing	0
<i>ABCA5</i>	Adrenal	4.39E-09	0.000653	1.42E-06	increasing	0
<i>ABCB4</i>	Adrenal	3.09E-10	-0.00077	1.99E-09	decreasing	0
<i>ABCF1</i>	Adrenal	1.10E-08	-0.00077	6.20E-09	decreasing	0
<i>ABHD17C</i>	Adrenal	1.90E-08	-0.00058	3.29E-05	decreasing	0
<i>ABT1</i>	Adrenal	9.14E-08	-0.00058	3.15E-05	decreasing	0
<i>ACAA2</i>	Adrenal	3.03E-08	-0.00077	1.07E-08	decreasing	0
<i>ACAT2</i>	Adrenal	2.73E-08	0.000454	0.001966	other	0
<i>ACP2</i>	Adrenal	3.78E-11	-0.00071	5.12E-08	decreasing	0
<i>ACSF3</i>	Adrenal	1.67E-09	-0.00074	1.50E-08	decreasing	0
<i>ADAM22</i>	Adrenal	3.84E-09	0.000687	3.70E-07	increasing	0
<i>ADAMTSL5</i>	Adrenal	3.52E-08	-0.00068	2.02E-07	decreasing	0
<i>ADARB2</i>	Adrenal	1.67E-08	0.000716	2.51E-08	increasing	0
<i>ADCY9</i>	Adrenal	3.25E-09	0.000637	1.74E-06	increasing	0
<i>ADORA3</i>	Adrenal	9.48E-07	-0.00073	9.53E-08	decreasing	0
<i>AFG3L2</i>	Adrenal	4.78E-11	-0.00079	7.57E-10	decreasing	0
<i>AGXT2</i>	Adrenal	6.66E-09	0.000674	2.89E-07	increasing	0
<i>AHCY</i>	Adrenal	6.37E-09	-0.00071	1.07E-07	decreasing	0
<i>AHNAK</i>	Adrenal	1.23E-07	0.00066	1.02E-06	increasing	0
<i>AHNAK2</i>	Adrenal	2.30E-07	0.000674	6.84E-07	increasing	0
<i>AIMP1</i>	Adrenal	1.68E-08	-0.0005	0.000483	other	0
<i>ALDH6A1</i>	Adrenal	2.58E-07	0.000379	0.010287	other	0
<i>ALG3</i>	Adrenal	5.87E-09	-0.00069	2.91E-07	decreasing	0
<i>ALOX12</i>	Adrenal	1.92E-07	0.000608	9.73E-06	increasing	0
<i>ALPP</i>	Adrenal	3.41E-11	0.000615	4.60E-06	increasing	0
<i>AMIGO3</i>	Adrenal	9.16E-08	0.000326	0.02716	other	0
<i>ANGPTL1</i>	Adrenal	2.26E-09	-0.00067	5.19E-07	decreasing	0
<i>ANGPTL4</i>	Adrenal	7.09E-08	-0.00066	1.99E-06	decreasing	0
<i>ANKH</i>	Adrenal	5.20E-08	0.000527	0.000198	other	0
<i>ANKRD6</i>	Adrenal	1.00E-11	0.000795	7.94E-10	increasing	0
<i>ANLN</i>	Adrenal	3.66E-10	-0.0008	2.67E-10	decreasing	0
<i>ANO8</i>	Adrenal	2.19E-11	0.000323	0.024605	other	0
<i>AP1S3</i>	Adrenal	8.35E-08	0.000606	1.73E-05	increasing	0
<i>AP2A1</i>	Adrenal	6.88E-08	-0.0007	2.78E-07	decreasing	0
<i>AP2S1</i>	Adrenal	4.17E-10	-0.00059	3.53E-05	decreasing	0
<i>AP3B2</i>	Adrenal	1.28E-10	0.000699	1.15E-07	increasing	0
<i>APBB1</i>	Adrenal	5.20E-09	0.000594	1.71E-05	increasing	0
<i>APBB3</i>	Adrenal	2.71E-08	0.000318	0.02892	other	0
<i>APCDD1</i>	Adrenal	1.20E-09	-8.64E-05	0.563137	other	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>APEX2</i>	Adrenal	3.06E-08	-0.00076	1.34E-08	decreasing	0
<i>APPL2</i>	Adrenal	7.66E-10	0.000203	0.167808	other	0
<i>ARF6</i>	Adrenal	2.89E-10	-0.00034	0.019937	other	0
<i>ARHGAP11A</i>	Adrenal	6.54E-13	-0.00083	1.38E-11	decreasing	0
<i>ARHGAP33</i>	Adrenal	2.11E-08	0.000232	0.115129	other	0
<i>ARHGDIB</i>	Adrenal	2.22E-09	-0.00062	1.14E-05	decreasing	0
<i>ARHGEF10L</i>	Adrenal	1.17E-07	0.000274	0.058003	other	0
<i>ARHGEF28</i>	Adrenal	6.23E-09	0.000491	0.000414	other	0
<i>ARHGEF37</i>	Adrenal	2.52E-07	6.47E-05	0.66333	other	0
<i>ARHGEF5</i>	Adrenal	2.23E-08	0.000104	0.491124	other	0
<i>ARHGEF9</i>	Adrenal	1.10E-08	0.000698	1.89E-07	increasing	0
<i>ARL2</i>	Adrenal	2.79E-06	-0.00071	2.24E-07	decreasing	0
<i>ASPM</i>	Adrenal	3.71E-10	-0.00079	5.35E-10	decreasing	0
<i>ASPN</i>	Adrenal	1.67E-07	-0.00075	1.79E-08	decreasing	0
<i>ATG7</i>	Adrenal	2.56E-08	-0.00069	4.62E-07	decreasing	0
<i>ATP4A</i>	Adrenal	7.11E-09	-0.00061	8.74E-06	decreasing	1
<i>ATP5A1</i>	Adrenal	1.60E-07	-0.00071	1.88E-07	decreasing	0
<i>ATP7B</i>	Adrenal	1.29E-11	0.000727	6.41E-08	increasing	0
<i>AURKA</i>	Adrenal	1.76E-11	-0.00077	3.27E-09	decreasing	0
<i>AVP</i>	Adrenal	6.02E-09	0.000476	0.001157	other	0
<i>B4GALT5</i>	Adrenal	5.26E-09	-0.00065	1.68E-06	decreasing	0
<i>BAHCC1</i>	Adrenal	1.26E-16	0.000747	2.20E-08	increasing	0
<i>BAK1</i>	Adrenal	1.15E-08	-0.00067	1.15E-06	decreasing	1
<i>BCKDK</i>	Adrenal	1.46E-15	-0.00086	3.45E-12	decreasing	0
<i>BCL6</i>	Adrenal	4.48E-12	0.000714	8.17E-08	increasing	0
<i>BCL7A</i>	Adrenal	1.51E-06	-0.00075	2.11E-08	decreasing	0
<i>BCL7C</i>	Adrenal	1.91E-07	-0.00022	0.141291	other	0
<i>BEND7</i>	Adrenal	5.05E-12	0.000802	3.69E-10	increasing	0
<i>BHLHB9</i>	Adrenal	1.08E-08	0.000666	1.22E-06	increasing	0
<i>BIRC5</i>	Adrenal	2.11E-13	-0.00076	7.25E-09	decreasing	0
<i>BLMH</i>	Adrenal	3.40E-10	-0.00069	2.45E-07	decreasing	0
<i>BMP3</i>	Adrenal	3.49E-08	-0.00071	1.29E-07	decreasing	0
<i>BRD2</i>	Adrenal	3.47E-09	0.000316	0.032069	other	0
<i>BRSK1</i>	Adrenal	7.21E-09	-1.45E-05	0.923278	other	0
<i>BUB1</i>	Adrenal	8.94E-12	-0.00079	5.34E-10	decreasing	0
<i>BUB1B</i>	Adrenal	2.99E-11	-0.00078	2.43E-09	decreasing	0
<i>BZRAP1</i>	Adrenal	2.07E-08	0.000398	0.007218	other	0
<i>C11H12orf75</i>	Adrenal	7.75E-08	0.000135	0.361226	other	0
<i>C12H9orf173</i>	Adrenal	3.70E-08	0.000109	0.466527	other	0
<i>C13H6orf203</i>	Adrenal	1.24E-08	-0.00059	1.69E-05	decreasing	0



**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>C19H22orf39</i>	Adrenal	9.10E-09	0.000381	0.009846	other	0
<i>C1H11orf57</i>	Adrenal	7.89E-08	-0.00043	0.002859	other	0
<i>C20H1orf50</i>	Adrenal	1.19E-07	-0.00044	0.002092	other	0
<i>C21H7orf73</i>	Adrenal	2.50E-11	-0.0008	1.84E-10	decreasing	0
<i>C23H5orf46</i>	Adrenal	1.88E-07	-0.00028	0.020073	other	0
<i>C25H1orf101</i>	Adrenal	8.21E-08	0.000651	2.65E-06	increasing	1
<i>C2CD2L</i>	Adrenal	2.33E-07	0.000286	0.047375	other	0
<i>C3AR1</i>	Adrenal	2.47E-07	-0.00055	0.000118	other	0
<i>C5H16orf62</i>	Adrenal	2.29E-09	-0.00015	0.33484	other	0
<i>C7H4orf45</i>	Adrenal	1.00E-07	0.000294	0.036891	other	0
<i>C8H8orf88</i>	Adrenal	2.03E-07	0.000669	3.73E-07	increasing	0
<i>CAMK2B</i>	Adrenal	2.10E-07	0.000597	1.96E-05	increasing	0
<i>CAMK2D</i>	Adrenal	7.82E-10	0.000705	1.65E-07	increasing	0
<i>CAMSAP3</i>	Adrenal	9.60E-09	0.000625	4.99E-06	increasing	0
<i>CANT1</i>	Adrenal	3.35E-09	-0.00067	1.01E-06	decreasing	0
<i>CAP2</i>	Adrenal	2.54E-08	0.000551	7.12E-05	increasing	0
<i>CAPN6</i>	Adrenal	4.50E-08	-0.00071	1.93E-07	decreasing	0
<i>CAV1</i>	Adrenal	2.09E-11	-0.00053	0.000233	other	0
<i>CBX7</i>	Adrenal	4.59E-12	0.000696	1.72E-07	increasing	0
<i>CCDC136</i>	Adrenal	2.25E-07	0.000648	2.25E-06	increasing	0
<i>CCDC78</i>	Adrenal	2.42E-12	0.000241	0.109926	other	1
<i>CCNB1</i>	Adrenal	6.16E-09	-0.00078	2.42E-09	decreasing	0
<i>CCNB2</i>	Adrenal	1.23E-12	-0.00084	1.83E-11	decreasing	0
<i>CCND2</i>	Adrenal	7.60E-10	0.000711	1.27E-07	increasing	0
<i>CD177</i>	Adrenal	1.63E-07	0.000466	0.001209	other	0
<i>CD248</i>	Adrenal	1.33E-07	-0.00063	8.80E-06	decreasing	0
<i>CD276</i>	Adrenal	3.71E-08	-0.00058	2.98E-05	decreasing	0
<i>CD300A</i>	Adrenal	3.73E-05	-0.00071	2.61E-07	decreasing	0
<i>CD79B</i>	Adrenal	3.53E-06	-0.00078	5.96E-09	decreasing	0
<i>CDC25C</i>	Adrenal	8.10E-09	-0.00075	1.32E-08	decreasing	0
<i>CDC34</i>	Adrenal	5.28E-08	-0.00059	2.58E-05	decreasing	0
<i>CDC6</i>	Adrenal	1.48E-08	-0.00076	6.51E-09	decreasing	0
<i>CDCA2</i>	Adrenal	3.33E-09	-0.00073	2.44E-08	decreasing	0
<i>CDCA3</i>	Adrenal	1.59E-07	-0.00075	1.52E-08	decreasing	0
<i>CDCA5</i>	Adrenal	1.59E-07	-0.00077	9.97E-09	decreasing	0
<i>CDCA8</i>	Adrenal	4.68E-13	-0.00087	6.73E-12	decreasing	0
<i>CDH20</i>	Adrenal	2.30E-07	-0.00065	3.30E-06	decreasing	0
<i>CDK1</i>	Adrenal	6.80E-10	-0.00079	1.17E-09	decreasing	0
<i>CDS1</i>	Adrenal	8.01E-08	0.000217	0.145706	other	1
<i>CELF6</i>	Adrenal	4.34E-08	0.000585	4.05E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CENPA</i>	Adrenal	1.35E-10	-0.00069	4.40E-07	decreasing	0
<i>CENPE</i>	Adrenal	4.33E-10	-0.0007	1.05E-07	decreasing	0
<i>CENPF</i>	Adrenal	2.36E-14	-0.00085	3.48E-12	decreasing	0
<i>CEP170B</i>	Adrenal	1.44E-07	0.000472	0.000732	other	0
<i>CEP250</i>	Adrenal	2.80E-10	0.000566	6.18E-05	increasing	0
<i>CEP55</i>	Adrenal	2.11E-10	-0.00076	1.38E-08	decreasing	0
<i>CEP83</i>	Adrenal	7.66E-12	0.000752	5.20E-09	increasing	0
<i>CHMP1A</i>	Adrenal	3.57E-05	-0.00071	1.67E-07	decreasing	0
<i>CKAP2</i>	Adrenal	9.24E-10	-0.0008	7.81E-10	decreasing	0
<i>CKAP2L</i>	Adrenal	1.85E-08	-0.00051	0.000319	other	0
<i>CKAP4</i>	Adrenal	7.32E-08	-0.00041	0.004858	other	0
<i>CKS2</i>	Adrenal	1.70E-07	-0.00077	8.89E-09	decreasing	0
<i>CLASP2</i>	Adrenal	1.23E-07	0.000711	2.14E-07	increasing	0
<i>CLDN11</i>	Adrenal	1.68E-08	-0.00054	0.000133	other	0
<i>CLEC1A</i>	Adrenal	2.73E-08	-0.00031	0.031339	other	0
<i>CLIC1</i>	Adrenal	4.57E-07	-0.00071	1.39E-07	decreasing	1
<i>CLK1</i>	Adrenal	6.49E-09	0.000542	0.000141	other	0
<i>CLP1</i>	Adrenal	7.93E-09	-0.0006	1.78E-05	decreasing	0
<i>CNDP2</i>	Adrenal	4.56E-10	-0.00055	9.28E-05	decreasing	0
<i>CNR1</i>	Adrenal	8.35E-08	0.000641	2.45E-06	increasing	0
<i>COASY</i>	Adrenal	3.39E-06	-0.00073	9.09E-09	decreasing	0
<i>COL1A1</i>	Adrenal	5.35E-13	-0.0008	4.12E-10	decreasing	0
<i>COL1A2</i>	Adrenal	4.00E-13	-0.00081	1.98E-10	decreasing	0
<i>COL3A1</i>	Adrenal	1.33E-12	-0.00079	1.03E-09	decreasing	0
<i>COL4A1</i>	Adrenal	3.67E-08	-0.00059	3.18E-05	decreasing	0
<i>COL5A2</i>	Adrenal	2.57E-07	-0.00043	0.003368	other	0
<i>COL8A2</i>	Adrenal	5.96E-07	-0.00075	2.36E-08	decreasing	0
<i>COLEC12</i>	Adrenal	4.01E-08	-0.00051	0.000363	other	0
<i>COPS5</i>	Adrenal	3.86E-09	-0.00066	2.67E-06	decreasing	0
<i>COQ5</i>	Adrenal	2.54E-09	-0.00071	1.07E-07	decreasing	0
<i>COQ9</i>	Adrenal	9.13E-13	-0.00075	9.58E-09	decreasing	0
<i>COTL1</i>	Adrenal	5.57E-08	-0.0007	2.87E-07	decreasing	0
<i>CPNE2</i>	Adrenal	1.58E-06	-0.00071	2.31E-07	decreasing	0
<i>CPNE8</i>	Adrenal	3.43E-08	0.000652	1.24E-06	increasing	0
<i>CPT1A</i>	Adrenal	2.70E-08	-0.00076	1.09E-08	decreasing	0
<i>CPT1B</i>	Adrenal	4.99E-08	-0.00064	2.86E-06	decreasing	0
<i>CPT2</i>	Adrenal	1.53E-13	-0.00081	1.68E-10	decreasing	0
<i>CPVL</i>	Adrenal	2.85E-09	-0.00075	2.98E-09	decreasing	0
<i>CPXM1</i>	Adrenal	5.60E-10	-0.00067	1.02E-06	decreasing	0
<i>CPXM2</i>	Adrenal	7.92E-08	-0.00023	0.114092	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CPZ</i>	Adrenal	7.24E-08	-0.00059	2.82E-05	decreasing	0
<i>CRABP2</i>	Adrenal	2.04E-07	-0.00069	4.00E-07	decreasing	0
<i>CRAMP1L</i>	Adrenal	1.67E-11	0.000361	0.01422	other	0
<i>CRHR1</i>	Adrenal	4.39E-08	0.000632	2.16E-06	increasing	0
<i>CS</i>	Adrenal	1.83E-09	-0.00067	7.53E-07	decreasing	0
<i>CTC1</i>	Adrenal	1.68E-11	0.000413	0.004215	other	0
<i>CTH</i>	Adrenal	2.37E-07	0.000535	0.000177	other	0
<i>CTIF</i>	Adrenal	2.54E-08	-0.00012	0.415788	other	0
<i>CTSA</i>	Adrenal	9.15E-08	-0.0006	1.13E-05	decreasing	1
<i>CUL9</i>	Adrenal	5.76E-09	0.000283	0.057442	other	0
<i>DAP3</i>	Adrenal	1.76E-08	-0.00069	5.63E-07	decreasing	0
<i>DCLK3</i>	Adrenal	7.03E-08	-0.00042	0.00473	other	0
<i>DDX19A</i>	Adrenal	3.49E-08	-0.00063	6.39E-06	decreasing	0
<i>DDX47</i>	Adrenal	2.29E-08	-0.00068	2.78E-07	decreasing	0
<i>DDX5</i>	Adrenal	2.50E-09	0.000298	0.038929	other	0
<i>DGKQ</i>	Adrenal	1.14E-10	0.000267	0.064755	other	0
<i>DHCR7</i>	Adrenal	1.58E-07	0.000534	0.000231	other	0
<i>DLD</i>	Adrenal	4.52E-09	-0.00074	2.29E-08	decreasing	0
<i>DLG4</i>	Adrenal	1.25E-07	0.000165	0.267995	other	0
<i>DLGAP5</i>	Adrenal	6.38E-11	-0.00074	1.94E-08	decreasing	0
<i>DMKN</i>	Adrenal	5.42E-08	-0.00069	3.86E-07	decreasing	0
<i>DMTF1</i>	Adrenal	2.42E-07	0.000587	3.31E-05	increasing	0
<i>DNAH11</i>	Adrenal	9.05E-08	-0.00059	2.63E-05	decreasing	0
<i>DNAJA3</i>	Adrenal	1.20E-05	-0.00071	2.52E-07	decreasing	0
<i>DNAJC3</i>	Adrenal	7.98E-08	0.000473	0.001024	other	0
<i>DNAJC6</i>	Adrenal	5.57E-11	0.000785	2.15E-09	increasing	0
<i>DND1</i>	Adrenal	6.95E-07	-0.0007	2.17E-07	decreasing	0
<i>DNMT3B</i>	Adrenal	2.16E-07	0.000606	1.91E-05	increasing	0
<i>DOCK3</i>	Adrenal	4.43E-08	0.000506	0.000371	other	0
<i>DOT1L</i>	Adrenal	1.37E-07	-0.0002	0.167192	other	0
<i>DPH2</i>	Adrenal	3.37E-07	-0.00074	2.87E-08	decreasing	0
<i>DPM2</i>	Adrenal	9.92E-11	-0.00076	5.57E-09	decreasing	0
<i>DPP4</i>	Adrenal	2.94E-07	0.000758	1.65E-08	increasing	0
<i>DTL</i>	Adrenal	7.29E-08	-0.00067	7.07E-07	decreasing	0
<i>DTWD1</i>	Adrenal	1.23E-08	0.000291	0.050058	other	0
<i>DUSP3</i>	Adrenal	4.52E-08	3.22E-05	0.831681	other	0
<i>E2F1</i>	Adrenal	2.07E-09	-0.00075	1.65E-08	decreasing	0
<i>E2F2</i>	Adrenal	2.97E-09	-0.00074	3.58E-08	decreasing	0
<i>E2F8</i>	Adrenal	2.54E-09	-0.00067	5.34E-07	decreasing	0
<i>ECHS1</i>	Adrenal	3.41E-07	-0.00073	8.36E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ECI2</i>	Adrenal	8.42E-08	-0.00068	7.09E-07	decreasing	0
<i>ECSIT</i>	Adrenal	2.49E-06	-0.00073	8.47E-08	decreasing	0
<i>EDIL3</i>	Adrenal	9.85E-08	0.00068	3.09E-07	increasing	0
<i>EDNRB</i>	Adrenal	7.92E-10	-0.00071	6.03E-08	decreasing	0
<i>EFHD1</i>	Adrenal	1.77E-07	-0.0005	0.000464	other	0
<i>EHD3</i>	Adrenal	1.05E-06	-0.00072	1.42E-07	decreasing	0
<i>EIF2S2</i>	Adrenal	7.08E-08	-0.00044	0.002847	other	0
<i>EIF4E2</i>	Adrenal	6.28E-10	-0.00064	3.98E-06	decreasing	0
<i>ELF4</i>	Adrenal	2.59E-10	-0.00064	2.34E-06	decreasing	0
<i>ELFN2</i>	Adrenal	7.04E-08	0.000538	0.000155	other	0
<i>ELN</i>	Adrenal	4.08E-08	-0.00054	0.00017	other	0
<i>EML2</i>	Adrenal	4.04E-08	0.000508	0.000386	other	0
<i>ENO2</i>	Adrenal	6.00E-08	0.000513	0.000256	other	1
<i>ENPP4</i>	Adrenal	1.43E-08	0.000744	1.65E-08	increasing	0
<i>ENPP5</i>	Adrenal	6.22E-09	0.000762	5.73E-09	increasing	0
<i>EPB41</i>	Adrenal	1.23E-08	0.000745	2.15E-08	increasing	0
<i>EPB41L5</i>	Adrenal	9.06E-09	0.000792	1.68E-09	increasing	0
<i>ERAL1</i>	Adrenal	3.64E-07	-0.00075	2.12E-08	decreasing	0
<i>ERBB4</i>	Adrenal	4.51E-09	0.000751	1.70E-08	increasing	0
<i>ERO1LB</i>	Adrenal	2.27E-09	0.000643	4.61E-06	increasing	0
<i>ESPL1</i>	Adrenal	2.63E-06	-0.00073	4.20E-08	decreasing	0
<i>ESYT1</i>	Adrenal	4.26E-12	0.000655	7.25E-07	increasing	0
<i>ETFA</i>	Adrenal	2.14E-08	-0.00072	1.02E-07	decreasing	0
<i>ETFDH</i>	Adrenal	1.65E-08	-0.00068	3.72E-07	decreasing	0
<i>ETNK1</i>	Adrenal	2.95E-08	0.000471	0.000758	other	0
<i>ETS2</i>	Adrenal	1.74E-08	-0.00067	1.47E-06	decreasing	0
<i>EVA1B</i>	Adrenal	2.72E-10	-0.00067	1.00E-06	decreasing	0
<i>EXO1</i>	Adrenal	1.63E-09	-0.00072	4.33E-08	decreasing	0
<i>FAM101A</i>	Adrenal	1.73E-07	-0.00067	1.37E-06	decreasing	0
<i>FAM103A1</i>	Adrenal	9.77E-08	-0.00046	0.001282	other	0
<i>FAM13B</i>	Adrenal	4.70E-08	0.000616	6.03E-06	increasing	0
<i>FAM155A</i>	Adrenal	1.61E-09	0.000619	7.78E-06	increasing	0
<i>FAM155B</i>	Adrenal	2.07E-07	0.000152	0.298289	other	0
<i>FAM160A1</i>	Adrenal	8.96E-07	0.000722	7.15E-08	increasing	0
<i>FAM198A</i>	Adrenal	6.79E-08	0.000405	0.004259	other	0
<i>FAM221A</i>	Adrenal	4.50E-09	0.000659	1.07E-06	increasing	0
<i>FAM43B</i>	Adrenal	4.66E-08	-0.00018	0.231492	other	0
<i>FAM53C</i>	Adrenal	1.12E-08	7.02E-05	0.640182	other	0
<i>FARS2</i>	Adrenal	4.95E-09	-0.00079	3.10E-09	decreasing	0
<i>FBLIM1</i>	Adrenal	7.34E-13	-0.00085	2.38E-11	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FBN2</i>	Adrenal	2.38E-14	-0.00083	5.89E-11	decreasing	0
<i>FGF14</i>	Adrenal	6.46E-09	0.000687	3.32E-07	increasing	0
<i>FGFR1OP2</i>	Adrenal	1.23E-09	0.000581	3.39E-05	increasing	0
<i>FKBP1A</i>	Adrenal	5.63E-08	-0.00056	8.36E-05	decreasing	0
<i>FNDC1</i>	Adrenal	5.20E-08	-0.00066	5.18E-07	decreasing	0
<i>FOXD1</i>	Adrenal	2.72E-09	-0.00037	0.014712	other	0
<i>FOXP1</i>	Adrenal	5.64E-08	2.12E-05	0.885449	other	0
<i>FSCN1</i>	Adrenal	1.54E-06	-0.00073	6.91E-08	decreasing	0
<i>GABBR1</i>	Adrenal	1.99E-09	0.000594	1.09E-05	increasing	0
<i>GALK1</i>	Adrenal	5.38E-10	-0.00062	5.17E-06	decreasing	0
<i>GALNT12</i>	Adrenal	1.54E-10	0.000455	0.00176	other	0
<i>GAPDH</i>	Adrenal	5.39E-08	-0.0007	2.48E-07	decreasing	0
<i>GCFC2</i>	Adrenal	5.56E-09	0.000195	0.199128	other	0
<i>GDAP1</i>	Adrenal	4.12E-08	0.000645	3.07E-06	increasing	0
<i>GDI2</i>	Adrenal	9.03E-08	-0.00018	0.219284	other	0
<i>GK5</i>	Adrenal	9.61E-13	0.000811	2.61E-10	increasing	0
<i>GLCC1</i>	Adrenal	1.40E-07	0.000731	5.22E-08	increasing	0
<i>GLIS2</i>	Adrenal	1.10E-07	-0.00064	2.18E-06	decreasing	0
<i>GMNN</i>	Adrenal	1.89E-08	-0.00067	6.45E-07	decreasing	0
<i>GNB1</i>	Adrenal	1.53E-07	-0.00049	0.000371	other	0
<i>GNB5</i>	Adrenal	1.82E-07	0.000403	0.005693	other	0
<i>GNG12</i>	Adrenal	1.67E-09	0.000748	2.16E-08	increasing	0
<i>GNG7</i>	Adrenal	1.39E-07	0.000615	9.06E-06	increasing	0
<i>GOLGA7</i>	Adrenal	4.22E-09	-0.00079	2.31E-09	decreasing	0
<i>GOT2</i>	Adrenal	7.12E-13	-0.00072	5.10E-08	decreasing	0
<i>GPC4</i>	Adrenal	1.02E-09	-0.00072	1.97E-08	decreasing	0
<i>GPC6</i>	Adrenal	5.10E-08	0.000102	0.485496	other	0
<i>GPM6A</i>	Adrenal	2.28E-08	0.000647	3.88E-06	increasing	0
<i>GPR1</i>	Adrenal	2.81E-08	0.000547	0.000121	other	0
<i>GPR137B</i>	Adrenal	2.60E-08	-0.00036	0.013195	other	0
<i>GPR155</i>	Adrenal	9.03E-07	0.000686	1.48E-07	increasing	0
<i>GPR17</i>	Adrenal	1.72E-07	0.000278	0.06549	other	0
<i>GPX7</i>	Adrenal	7.76E-13	-0.0007	8.71E-08	decreasing	0
<i>GRB10</i>	Adrenal	6.77E-14	0.000799	1.30E-09	increasing	0
<i>GRB14</i>	Adrenal	7.06E-11	0.000213	0.142766	other	0
<i>GREB1</i>	Adrenal	4.18E-08	0.000143	0.33783	other	0
<i>GRIN3B</i>	Adrenal	2.01E-07	0.000183	0.218782	other	0
<i>GRIPAP1</i>	Adrenal	3.26E-09	0.00034	0.019181	other	0
<i>GRSF1</i>	Adrenal	2.37E-07	-0.00039	0.006396	other	0
<i>GSTM5</i>	Adrenal	7.62E-08	0.000607	1.02E-05	increasing	1

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GTF3C2</i>	Adrenal	2.27E-07	-0.00075	1.45E-08	decreasing	0
<i>GTSE1</i>	Adrenal	1.76E-08	-0.0007	1.47E-07	decreasing	0
<i>HDAC6</i>	Adrenal	1.47E-09	0.000213	0.142772	other	0
<i>HERC3</i>	Adrenal	4.80E-09	0.00063	3.95E-06	increasing	0
<i>HHEX</i>	Adrenal	3.46E-08	-0.00045	0.001571	other	0
<i>HJURP</i>	Adrenal	2.01E-14	-0.00086	1.26E-11	decreasing	0
<i>HMGA2</i>	Adrenal	8.55E-08	-0.00044	0.001045	other	0
<i>HMMR</i>	Adrenal	5.12E-07	-0.00072	4.71E-08	decreasing	0
<i>HN1</i>	Adrenal	9.30E-09	-0.00065	3.19E-06	decreasing	0
<i>HNRNPA2B1</i>	Adrenal	2.49E-07	0.000207	0.169268	other	0
<i>HOPX</i>	Adrenal	2.66E-12	-0.00079	4.47E-10	decreasing	0
<i>HOXB5</i>	Adrenal	1.79E-07	0.000439	0.002259	other	0
<i>HOXB6</i>	Adrenal	2.23E-07	0.000503	0.000285	other	0
<i>HOXB7</i>	Adrenal	5.29E-08	0.000569	4.31E-05	increasing	0
<i>HOXB8</i>	Adrenal	7.21E-11	0.00073	3.82E-08	increasing	0
<i>HS3ST3A1</i>	Adrenal	4.81E-13	-0.00086	3.71E-12	decreasing	0
<i>HSPA9</i>	Adrenal	8.40E-09	-0.00072	9.89E-08	decreasing	0
<i>HTRA3</i>	Adrenal	7.52E-09	-0.00076	1.33E-08	decreasing	0
<i>HYOU1</i>	Adrenal	1.91E-07	0.000502	0.000447	other	0
<i>IDH2</i>	Adrenal	2.21E-10	-0.00073	2.39E-08	decreasing	0
<i>IFITM1</i>	Adrenal	4.01E-10	-0.0004	0.006062	other	0
<i>IFITM10</i>	Adrenal	1.00E-07	-0.0007	3.29E-07	decreasing	0
<i>IFT172</i>	Adrenal	3.18E-12	0.000732	5.02E-08	increasing	0
<i>IGF2</i>	Adrenal	6.20E-10	-0.0006	1.33E-05	decreasing	0
<i>IGF2BP2</i>	Adrenal	3.14E-14	-0.00066	5.49E-07	decreasing	0
<i>IGF2BP3</i>	Adrenal	1.73E-13	-0.00073	1.16E-08	decreasing	0
<i>IGFBP2</i>	Adrenal	5.63E-09	-0.00068	4.28E-07	decreasing	0
<i>IGLON5</i>	Adrenal	1.49E-07	0.000353	0.016156	other	1
<i>IGSF9B</i>	Adrenal	7.03E-09	0.000703	2.82E-07	increasing	0
<i>IL1RAPL1</i>	Adrenal	3.76E-09	-0.00075	1.44E-08	decreasing	0
<i>ING4</i>	Adrenal	3.28E-08	-0.00065	1.99E-06	decreasing	0
<i>ING5</i>	Adrenal	7.16E-11	0.000568	6.27E-05	increasing	1
<i>INHA</i>	Adrenal	2.56E-10	-0.00053	0.000135	other	0
<i>INPP4B</i>	Adrenal	1.18E-07	-0.00065	1.41E-06	decreasing	0
<i>INPP5F</i>	Adrenal	3.80E-07	0.000765	9.82E-09	increasing	0
<i>INTS5</i>	Adrenal	8.05E-07	-0.00071	2.06E-07	decreasing	0
<i>INTS7</i>	Adrenal	3.41E-09	-0.00018	0.238827	other	0
<i>IQGAP3</i>	Adrenal	1.50E-07	-0.00079	1.79E-09	decreasing	0
<i>IQSEC2</i>	Adrenal	5.62E-08	0.000386	0.007381	other	0
<i>IRF6</i>	Adrenal	3.20E-08	0.000616	1.12E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ITGAX</i>	Adrenal	2.28E-08	-0.00068	2.37E-07	decreasing	0
<i>ITGB5</i>	Adrenal	5.07E-11	-0.0008	4.39E-10	decreasing	0
<i>ITGBL1</i>	Adrenal	1.83E-07	0.000507	0.000257	other	0
<i>JPH1</i>	Adrenal	1.79E-07	0.000509	0.000445	other	0
<i>KCNA2</i>	Adrenal	5.62E-10	0.000674	8.93E-07	increasing	0
<i>KCNF1</i>	Adrenal	3.91E-07	-0.00068	1.71E-07	decreasing	0
<i>KCNK1</i>	Adrenal	2.93E-08	-0.00065	1.44E-06	decreasing	0
<i>KCNQ1</i>	Adrenal	4.34E-11	-0.00075	1.47E-08	decreasing	0
<i>KCTD18</i>	Adrenal	1.71E-07	0.000279	0.062374	other	0
<i>KCTD5</i>	Adrenal	1.60E-06	-0.0007	1.74E-07	decreasing	0
<i>KDELC1</i>	Adrenal	3.92E-08	-0.00064	1.19E-06	decreasing	0
<i>KIAA0101</i>	Adrenal	2.40E-09	-0.00075	1.95E-08	decreasing	0
<i>KIAA0391</i>	Adrenal	1.67E-07	-0.00062	4.13E-06	decreasing	0
<i>KIAA0895L</i>	Adrenal	4.06E-10	0.000412	0.004561	other	0
<i>KIAA1467</i>	Adrenal	9.54E-08	0.000609	1.39E-05	increasing	0
<i>KIAA1715</i>	Adrenal	9.14E-08	0.000606	1.09E-05	increasing	0
<i>KIDINS220</i>	Adrenal	5.11E-06	0.000714	1.86E-07	increasing	0
<i>KIF11</i>	Adrenal	6.32E-11	-0.00075	2.95E-09	decreasing	0
<i>KIF15</i>	Adrenal	1.41E-08	-0.00071	1.43E-07	decreasing	0
<i>KIF18A</i>	Adrenal	1.96E-09	-0.00071	1.02E-07	decreasing	0
<i>KIF18B</i>	Adrenal	2.85E-07	-0.00073	2.26E-08	decreasing	0
<i>KIF20A</i>	Adrenal	1.11E-10	-0.00079	1.08E-09	decreasing	0
<i>KIF23</i>	Adrenal	4.80E-08	-0.00062	9.14E-06	decreasing	0
<i>KIF2C</i>	Adrenal	4.14E-11	-0.00073	3.75E-08	decreasing	0
<i>KIF4A</i>	Adrenal	1.09E-09	-0.00074	1.13E-08	decreasing	0
<i>KIFC1</i>	Adrenal	3.56E-09	-0.0008	1.53E-09	decreasing	0
<i>KIFC2</i>	Adrenal	2.09E-07	0.000286	0.050159	other	0
<i>KLF15</i>	Adrenal	1.04E-08	0.000541	0.000116	other	0
<i>KLHL2</i>	Adrenal	7.99E-10	0.000524	0.000203	other	0
<i>KLHL3</i>	Adrenal	1.31E-11	0.000777	1.78E-09	increasing	0
<i>KLHL32</i>	Adrenal	9.74E-09	0.000669	1.40E-06	increasing	0
<i>KLK3</i>	Adrenal	9.48E-09	0.000633	4.68E-06	increasing	0
<i>KNSTRN</i>	Adrenal	7.74E-10	-0.00075	2.51E-08	decreasing	0
<i>KRI1</i>	Adrenal	4.48E-09	0.0003	0.037185	other	0
<i>LAMB2</i>	Adrenal	1.27E-09	0.000416	0.003669	other	0
<i>LBH</i>	Adrenal	7.75E-10	-0.0005	0.000537	other	0
<i>LEAP2</i>	Adrenal	2.45E-07	0.000514	0.000296	other	0
<i>LENG8</i>	Adrenal	6.42E-08	0.000385	0.009207	other	0
<i>LIMD2</i>	Adrenal	1.58E-08	-0.00068	2.79E-07	decreasing	0
<i>LMTK3</i>	Adrenal	2.04E-12	0.000381	0.009005	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103214525</i>	Adrenal	1.91E-08	-0.00012	0.437459	other	0
<i>LOC103214682</i>	Adrenal	6.35E-09	-2.58E-05	0.863128	other	0
<i>LOC103215073</i>	Adrenal	1.35E-07	-0.00024	0.112893	other	0
<i>LOC103215169</i>	Adrenal	7.26E-10	-0.00034	0.022378	other	0
<i>LOC103215206</i>	Adrenal	1.21E-11	0.000746	4.38E-09	increasing	0
<i>LOC103215596</i>	Adrenal	1.38E-11	-0.00084	3.23E-11	decreasing	0
<i>LOC103215799</i>	Adrenal	1.72E-08	-0.00047	0.00113	other	0
<i>LOC103215811</i>	Adrenal	3.26E-08	-0.0002	0.19586	other	0
<i>LOC103215822</i>	Adrenal	1.08E-08	-0.00064	3.81E-06	decreasing	0
<i>LOC103216057</i>	Adrenal	2.11E-07	-0.00072	1.24E-07	decreasing	0
<i>LOC103216143</i>	Adrenal	2.93E-14	-0.00026	0.003633	other	0
<i>LOC103216302</i>	Adrenal	5.68E-08	-0.00019	0.219776	other	0
<i>LOC103216605</i>	Adrenal	2.09E-08	0.000627	4.54E-06	increasing	0
<i>LOC103216629</i>	Adrenal	1.01E-10	7.02E-05	0.568142	other	0
<i>LOC103216770</i>	Adrenal	3.22E-08	-0.00052	0.000302	other	0
<i>LOC103217048</i>	Adrenal	3.93E-09	-0.00028	0.054182	other	0
<i>LOC103217611</i>	Adrenal	1.20E-11	0.000707	4.66E-08	increasing	0
<i>LOC103217681</i>	Adrenal	2.82E-09	0.00075	2.12E-08	increasing	0
<i>LOC103217954</i>	Adrenal	2.56E-07	0.00062	9.85E-06	increasing	0
<i>LOC103218075</i>	Adrenal	2.09E-08	0.000487	0.000684	other	0
<i>LOC103218076</i>	Adrenal	1.34E-10	0.000501	0.000332	other	0
<i>LOC103218078</i>	Adrenal	2.04E-10	0.000491	0.000456	other	0
<i>LOC103218120</i>	Adrenal	4.16E-09	-0.00058	3.56E-05	decreasing	0
<i>LOC103218277</i>	Adrenal	8.17E-09	0.000521	0.000181	other	0
<i>LOC103218335</i>	Adrenal	1.37E-10	0.000488	0.000547	other	0
<i>LOC103218342</i>	Adrenal	2.41E-07	0.000469	0.001334	other	0
<i>LOC103218500</i>	Adrenal	5.58E-10	0.00031	0.036423	other	0
<i>LOC103218561</i>	Adrenal	1.92E-11	0.000738	2.37E-08	increasing	0
<i>LOC103218873</i>	Adrenal	1.07E-07	0.000386	0.008864	other	1
<i>LOC103219292</i>	Adrenal	4.67E-08	0.000496	0.000558	other	0
<i>LOC103219460</i>	Adrenal	3.08E-08	-0.0005	0.000391	other	0
<i>LOC103219487</i>	Adrenal	7.57E-09	0.000386	0.0066	other	0
<i>LOC103219495</i>	Adrenal	2.02E-07	0.000529	0.000151	other	0
<i>LOC103219590</i>	Adrenal	5.07E-10	-0.00019	0.05761	other	0
<i>LOC103219699</i>	Adrenal	5.69E-08	0.000293	0.052731	other	1
<i>LOC103219720</i>	Adrenal	8.78E-09	4.92E-06	0.973258	other	0
<i>LOC103219727</i>	Adrenal	6.19E-08	0.00016	0.27311	other	0
<i>LOC103219791</i>	Adrenal	2.38E-07	0.000411	0.003687	other	1
<i>LOC103219806</i>	Adrenal	1.32E-10	0.000429	0.003211	other	0
<i>LOC103219855</i>	Adrenal	2.15E-06	-0.00072	1.26E-07	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103219913</i>	Adrenal	1.69E-07	0.000504	0.000375	other	0
<i>LOC103219980</i>	Adrenal	1.85E-07	-0.00023	0.127786	other	0
<i>LOC103220002</i>	Adrenal	1.56E-09	-0.00055	7.53E-05	decreasing	0
<i>LOC103220015</i>	Adrenal	9.10E-08	-0.00038	0.009522	other	0
<i>LOC103220052</i>	Adrenal	6.44E-08	-0.00032	0.033481	other	0
<i>LOC103220535</i>	Adrenal	6.61E-09	0.000515	0.000355	other	0
<i>LOC103220998</i>	Adrenal	1.70E-07	-2.93E-05	0.848492	other	0
<i>LOC103221080</i>	Adrenal	1.54E-07	-0.0002	0.178369	other	0
<i>LOC103221325</i>	Adrenal	1.28E-07	-0.00012	0.41872	other	0
<i>LOC103221711</i>	Adrenal	5.43E-09	0.000367	0.013593	other	0
<i>LOC103221955</i>	Adrenal	2.64E-08	-0.00058	3.44E-05	decreasing	0
<i>LOC103222389</i>	Adrenal	1.75E-07	-9.68E-05	0.525306	other	0
<i>LOC103222782</i>	Adrenal	5.77E-09	-0.00068	6.63E-07	decreasing	0
<i>LOC103222898</i>	Adrenal	1.54E-11	-0.00083	4.72E-11	decreasing	0
<i>LOC103222969</i>	Adrenal	9.72E-08	0.000499	0.000507	other	0
<i>LOC103223027</i>	Adrenal	5.95E-08	-4.12E-05	0.777056	other	0
<i>LOC103223217</i>	Adrenal	2.85E-11	0.000631	3.13E-06	increasing	0
<i>LOC103223219</i>	Adrenal	1.27E-08	0.000557	8.46E-05	increasing	0
<i>LOC103223276</i>	Adrenal	2.11E-07	0.000521	0.00025	other	0
<i>LOC103223412</i>	Adrenal	1.26E-07	0.000411	0.005248	other	0
<i>LOC103223413</i>	Adrenal	1.70E-07	0.000284	0.060438	other	0
<i>LOC103223421</i>	Adrenal	9.00E-09	-0.00048	0.000892	other	0
<i>LOC103223422</i>	Adrenal	7.11E-08	-0.00071	6.46E-08	decreasing	0
<i>LOC103223583</i>	Adrenal	2.21E-08	0.000545	0.00012	other	0
<i>LOC103224177</i>	Adrenal	1.21E-08	0.000696	1.13E-08	increasing	0
<i>LOC103224222</i>	Adrenal	9.15E-09	-0.00047	0.001398	other	0
<i>LOC103224274</i>	Adrenal	8.26E-08	0.000719	7.54E-08	increasing	0
<i>LOC103224310</i>	Adrenal	5.02E-09	-2.36E-05	0.875471	other	0
<i>LOC103224428</i>	Adrenal	1.67E-08	-0.00057	4.68E-05	decreasing	0
<i>LOC103224472</i>	Adrenal	7.63E-08	-0.00013	0.377428	other	0
<i>LOC103224513</i>	Adrenal	9.40E-10	-0.00063	7.81E-06	decreasing	0
<i>LOC103225645</i>	Adrenal	7.33E-11	0.000739	1.89E-08	increasing	1
<i>LOC103225803</i>	Adrenal	2.62E-08	0.000452	0.002181	other	0
<i>LOC103225929</i>	Adrenal	8.02E-08	0.000365	0.014468	other	0
<i>LOC103226015</i>	Adrenal	1.13E-08	-0.00014	0.338574	other	0
<i>LOC103226801</i>	Adrenal	2.55E-10	0.000798	8.00E-10	increasing	0
<i>LOC103226836</i>	Adrenal	7.64E-08	0.000268	0.075088	other	0
<i>LOC103226908</i>	Adrenal	2.23E-08	0.000629	4.66E-06	increasing	0
<i>LOC103227374</i>	Adrenal	4.06E-08	-6.19E-05	0.685668	other	0
<i>LOC103227921</i>	Adrenal	6.21E-09	4.93E-05	0.691378	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103227965</i>	Adrenal	1.87E-09	0.000588	3.50E-05	increasing	0
<i>LOC103228469</i>	Adrenal	1.52E-07	-0.00011	0.326262	other	0
<i>LOC103228547</i>	Adrenal	1.03E-08	0.000648	2.73E-06	increasing	0
<i>LOC103228610</i>	Adrenal	6.80E-08	9.92E-05	0.458497	other	0
<i>LOC103229081</i>	Adrenal	9.37E-09	-0.00047	0.001353	other	0
<i>LOC103229468</i>	Adrenal	2.28E-08	-0.00069	2.43E-07	decreasing	0
<i>LOC103229581</i>	Adrenal	1.93E-09	0.000366	0.008097	other	0
<i>LOC103229682</i>	Adrenal	3.82E-08	0.000534	0.000104	other	0
<i>LOC103229888</i>	Adrenal	4.15E-08	0.000563	7.52E-05	increasing	0
<i>LOC103230072</i>	Adrenal	3.11E-08	-0.0001	0.503064	other	0
<i>LOC103230870</i>	Adrenal	4.87E-09	0.000455	0.001837	other	0
<i>LOC103231021</i>	Adrenal	5.12E-11	0.000538	0.00017	other	0
<i>LOC103231181</i>	Adrenal	1.39E-08	0.000365	0.014334	other	0
<i>LOC103231233</i>	Adrenal	2.12E-08	-0.00041	0.004654	other	0
<i>LOC103231443</i>	Adrenal	1.10E-08	-0.00061	1.22E-05	decreasing	0
<i>LOC103231470</i>	Adrenal	2.41E-07	0.000301	0.042665	other	0
<i>LOC103231503</i>	Adrenal	3.07E-08	0.000372	0.012468	other	0
<i>LOC103231759</i>	Adrenal	1.29E-07	-0.00031	0.014843	other	0
<i>LOC103232029</i>	Adrenal	1.30E-10	-0.00078	7.98E-10	decreasing	0
<i>LOC103232075</i>	Adrenal	2.44E-07	0.000183	0.220664	other	0
<i>LOC103232220</i>	Adrenal	7.24E-08	0.000706	1.75E-07	increasing	0
<i>LOC103232225</i>	Adrenal	1.11E-08	0.000636	1.77E-06	increasing	0
<i>LOC103232248</i>	Adrenal	1.72E-07	-0.00012	0.437187	other	0
<i>LOC103232258</i>	Adrenal	8.66E-08	-0.00064	5.32E-06	decreasing	0
<i>LOC103232371</i>	Adrenal	1.24E-07	1.29E-05	0.921494	other	0
<i>LOC103232495</i>	Adrenal	1.18E-08	0.000666	1.11E-06	increasing	0
<i>LOC103232675</i>	Adrenal	1.42E-09	-0.00022	0.044683	other	0
<i>LOC103232783</i>	Adrenal	2.37E-08	0.00048	0.000675	other	0
<i>LOC103232839</i>	Adrenal	1.20E-05	0.000624	1.15E-07	increasing	0
<i>LOC103232846</i>	Adrenal	5.76E-11	0.000819	9.44E-11	increasing	0
<i>LOC103232870</i>	Adrenal	3.25E-11	-0.0008	7.29E-10	decreasing	0
<i>LOC103232983</i>	Adrenal	4.63E-08	-0.00074	2.37E-08	decreasing	0
<i>LOC103233446</i>	Adrenal	8.35E-10	0.000615	1.42E-05	increasing	0
<i>LOC103233666</i>	Adrenal	1.79E-07	0.000173	0.245623	other	0
<i>LOC103234319</i>	Adrenal	5.71E-11	0.000486	0.00063	other	0
<i>LOC103234347</i>	Adrenal	1.70E-08	-0.00049	0.00056	other	0
<i>LOC103234417</i>	Adrenal	5.71E-09	-0.00067	1.11E-06	decreasing	0
<i>LOC103234458</i>	Adrenal	2.57E-07	1.02E-05	0.94683	other	0
<i>LOC103234540</i>	Adrenal	1.59E-08	0.000307	0.033182	other	0
<i>LOC103234987</i>	Adrenal	2.66E-09	0.000393	0.005958	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103234988</i>	Adrenal	1.79E-07	0.000293	0.043853	other	0
<i>LOC103235510</i>	Adrenal	8.25E-08	0.000402	0.005453	other	0
<i>LOC103235529</i>	Adrenal	2.20E-09	0.000209	0.159281	other	0
<i>LOC103235723</i>	Adrenal	3.03E-08	0.000166	0.272671	other	0
<i>LOC103236385</i>	Adrenal	1.44E-08	-0.00049	0.000611	other	0
<i>LOC103236489</i>	Adrenal	6.69E-09	-0.0003	0.043299	other	0
<i>LOC103236588</i>	Adrenal	2.35E-07	-0.00019	0.046746	other	0
<i>LOC103237601</i>	Adrenal	1.06E-07	0.000219	0.136794	other	0
<i>LOC103237606</i>	Adrenal	4.05E-08	0.000379	0.010183	other	0
<i>LOC103237612</i>	Adrenal	1.41E-09	0.000452	0.002014	other	0
<i>LOC103237685</i>	Adrenal	9.26E-08	-0.00012	0.448578	other	0
<i>LOC103237714</i>	Adrenal	1.19E-07	-6.45E-05	0.660355	other	0
<i>LOC103237731</i>	Adrenal	7.27E-09	0.00032	0.030562	other	0
<i>LOC103237932</i>	Adrenal	3.10E-09	0.000343	0.021707	other	0
<i>LOC103238047</i>	Adrenal	1.18E-09	-0.00026	0.091345	other	0
<i>LOC103238059</i>	Adrenal	7.98E-08	-1.49E-05	0.922617	other	0
<i>LOC103238179</i>	Adrenal	3.84E-10	0.000505	0.000267	other	0
<i>LOC103238689</i>	Adrenal	9.25E-08	-0.00018	0.210861	other	0
<i>LOC103238749</i>	Adrenal	1.29E-08	-0.00073	5.27E-08	decreasing	0
<i>LOC103238863</i>	Adrenal	1.92E-11	-0.00064	3.23E-06	decreasing	0
<i>LOC103239186</i>	Adrenal	3.26E-09	0.000433	0.002957	other	0
<i>LOC103239433</i>	Adrenal	3.58E-09	0.000368	0.011538	other	1
<i>LOC103239713</i>	Adrenal	1.57E-07	-2.52E-05	0.869467	other	0
<i>LOC103240394</i>	Adrenal	5.68E-08	-0.00014	0.350845	other	0
<i>LOC103240550</i>	Adrenal	8.54E-08	-0.00016	0.283054	other	0
<i>LOC103240700</i>	Adrenal	1.14E-06	-0.00069	1.15E-07	decreasing	0
<i>LOC103241261</i>	Adrenal	2.66E-08	-0.00017	0.268181	other	0
<i>LOC103241750</i>	Adrenal	4.00E-10	-0.00055	0.000145	other	0
<i>LOC103241820</i>	Adrenal	5.64E-09	0.000478	0.000793	other	0
<i>LOC103241849</i>	Adrenal	1.09E-15	-0.00082	4.92E-11	decreasing	0
<i>LOC103241860</i>	Adrenal	8.69E-08	-0.00029	0.042873	other	0
<i>LOC103242266</i>	Adrenal	4.49E-14	0.000861	2.33E-12	increasing	0
<i>LOC103242316</i>	Adrenal	1.53E-08	0.00025	0.096251	other	0
<i>LOC103242374</i>	Adrenal	2.56E-08	0.000446	0.002195	other	0
<i>LOC103242416</i>	Adrenal	1.54E-14	-0.00081	2.05E-10	decreasing	0
<i>LOC103242623</i>	Adrenal	3.49E-08	0.000503	0.000438	other	0
<i>LOC103242644</i>	Adrenal	3.22E-13	0.000466	0.001278	other	0
<i>LOC103243150</i>	Adrenal	2.17E-09	0.000324	0.025655	other	0
<i>LOC103243227</i>	Adrenal	1.43E-10	-0.00071	1.26E-07	decreasing	0
<i>LOC103243406</i>	Adrenal	2.68E-08	1.05E-05	0.945565	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103243565</i>	Adrenal	1.25E-07	0.000448	0.002256	other	0
<i>LOC103243610</i>	Adrenal	4.56E-11	0.000704	1.54E-07	increasing	0
<i>LOC103243718</i>	Adrenal	6.31E-09	0.000405	0.005331	other	0
<i>LOC103243762</i>	Adrenal	7.91E-09	0.000328	0.0281	other	0
<i>LOC103244088</i>	Adrenal	5.77E-10	0.000511	0.000385	other	0
<i>LOC103244129</i>	Adrenal	3.54E-10	1.06E-06	0.994458	other	0
<i>LOC103244719</i>	Adrenal	9.37E-08	-0.00071	2.29E-07	decreasing	0
<i>LOC103245136</i>	Adrenal	8.89E-08	0.00072	1.18E-07	increasing	0
<i>LOC103245138</i>	Adrenal	1.16E-09	0.000666	1.28E-06	increasing	0
<i>LOC103245177</i>	Adrenal	9.10E-10	0.000732	4.41E-08	increasing	0
<i>LOC103245178</i>	Adrenal	2.44E-06	0.000708	2.35E-07	increasing	0
<i>LOC103245181</i>	Adrenal	9.35E-09	0.000691	4.39E-07	increasing	0
<i>LOC103245320</i>	Adrenal	1.72E-09	-0.0005	0.000438	other	0
<i>LOC103245358</i>	Adrenal	8.98E-08	7.95E-06	0.958186	other	0
<i>LOC103246025</i>	Adrenal	2.84E-08	0.000618	1.00E-05	increasing	0
<i>LOC103246038</i>	Adrenal	3.91E-08	0.000641	3.07E-06	increasing	0
<i>LOC103246419</i>	Adrenal	6.05E-08	0.000162	0.282691	other	0
<i>LOC103246433</i>	Adrenal	2.26E-07	-0.0003	0.045604	other	0
<i>LOC103246486</i>	Adrenal	3.95E-08	0.000555	0.000115	other	1
<i>LOC103246522</i>	Adrenal	2.25E-07	0.000611	1.39E-05	increasing	0
<i>LOC103246602</i>	Adrenal	4.14E-08	-0.00028	0.063012	other	0
<i>LOC103246666</i>	Adrenal	2.47E-08	0.000112	0.459475	other	0
<i>LOC103246766</i>	Adrenal	2.09E-07	0.000469	0.001175	other	0
<i>LOC103246879</i>	Adrenal	1.67E-07	0.000442	0.002593	other	0
<i>LOC103247904</i>	Adrenal	2.24E-08	-0.00011	0.3142	other	0
<i>LOC103248224</i>	Adrenal	1.69E-10	0.000578	3.78E-05	increasing	0
<i>LOC103248994</i>	Adrenal	1.89E-07	-0.00034	0.019796	other	0
<i>LOC103249008</i>	Adrenal	2.26E-07	-6.07E-05	0.68702	other	0
<i>LOX</i>	Adrenal	4.04E-08	-0.00068	5.22E-07	decreasing	0
<i>LOXL2</i>	Adrenal	1.32E-09	-0.00076	4.61E-09	decreasing	0
<i>LOXL4</i>	Adrenal	1.03E-08	0.000635	1.88E-06	increasing	0
<i>LRP1</i>	Adrenal	1.19E-08	0.000578	2.74E-05	increasing	0
<i>LRRC23</i>	Adrenal	5.59E-09	0.000443	0.002322	other	0
<i>LRRC39</i>	Adrenal	9.62E-08	-0.00015	0.290741	other	0
<i>LRRC8E</i>	Adrenal	1.17E-07	0.000512	0.000215	other	0
<i>LRRFIP1</i>	Adrenal	4.39E-06	0.000701	2.20E-07	increasing	0
<i>LRWD1</i>	Adrenal	2.31E-08	-0.00055	8.19E-05	decreasing	0
<i>LSR</i>	Adrenal	9.40E-08	-0.00066	7.97E-07	decreasing	0
<i>LSS</i>	Adrenal	3.74E-08	0.000552	0.000128	other	0
<i>MAD2L1</i>	Adrenal	8.36E-06	-0.00072	1.55E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MALSU1</i>	Adrenal	5.64E-08	-0.00068	6.77E-07	decreasing	0
<i>MAMDC2</i>	Adrenal	1.02E-09	0.000783	2.20E-09	increasing	0
<i>MAN2A2</i>	Adrenal	4.96E-08	0.00022	0.144659	other	0
<i>MAN2C1</i>	Adrenal	5.68E-09	0.000439	0.002063	other	0
<i>MAOB</i>	Adrenal	7.07E-08	0.00071	6.45E-08	increasing	0
<i>MAP7</i>	Adrenal	3.92E-09	0.000678	5.11E-07	increasing	0
<i>MAPKBP1</i>	Adrenal	1.06E-09	0.00031	0.040034	other	0
<i>MARCH3</i>	Adrenal	1.92E-07	-0.00054	9.86E-05	decreasing	0
<i>MARCKS</i>	Adrenal	9.68E-08	-0.00011	0.472105	other	0
<i>MARK1</i>	Adrenal	5.55E-11	0.000781	1.32E-09	increasing	0
<i>MAVS</i>	Adrenal	6.81E-10	0.000779	4.43E-09	increasing	0
<i>MAZ</i>	Adrenal	2.02E-07	-0.00068	8.45E-07	decreasing	0
<i>MBOAT7</i>	Adrenal	4.99E-10	-0.00077	3.63E-09	decreasing	0
<i>MCCD1</i>	Adrenal	2.39E-07	-0.00032	0.028937	other	0
<i>MCF2L2</i>	Adrenal	1.43E-08	0.000594	1.71E-05	increasing	0
<i>MDK</i>	Adrenal	1.44E-08	-0.00063	2.37E-06	decreasing	0
<i>ME1</i>	Adrenal	1.61E-09	0.000456	0.001828	other	0
<i>MECOM</i>	Adrenal	5.63E-08	-0.00017	0.242053	other	0
<i>MED6</i>	Adrenal	2.25E-07	-0.00063	5.26E-06	decreasing	0
<i>MEGF8</i>	Adrenal	7.46E-09	0.000324	0.030151	other	0
<i>MELK</i>	Adrenal	4.69E-10	-0.00069	3.60E-07	decreasing	0
<i>MFAP2</i>	Adrenal	1.05E-12	-0.00082	8.74E-11	decreasing	0
<i>MFAP5</i>	Adrenal	1.49E-07	-0.00064	4.67E-06	decreasing	0
<i>MGAT4B</i>	Adrenal	2.45E-07	-0.0007	1.84E-07	decreasing	0
<i>MGLL</i>	Adrenal	5.91E-07	-0.00076	1.11E-08	decreasing	0
<i>MGRN1</i>	Adrenal	1.21E-08	-0.00058	3.43E-05	decreasing	0
<i>MICAL2</i>	Adrenal	1.38E-07	-4.05E-05	0.782671	other	0
<i>MKI67</i>	Adrenal	1.99E-11	-0.00073	3.46E-08	decreasing	0
<i>MLLT6</i>	Adrenal	4.24E-10	0.000313	0.031654	other	0
<i>MLYCD</i>	Adrenal	6.69E-09	-0.00073	3.39E-08	decreasing	0
<i>MMP10</i>	Adrenal	9.81E-08	-0.00023	0.057503	other	0
<i>MMP2</i>	Adrenal	7.69E-08	-0.00073	9.25E-08	decreasing	0
<i>MMP24</i>	Adrenal	5.29E-08	0.000507	0.000344	other	0
<i>MPP3</i>	Adrenal	2.91E-08	0.000386	0.008755	other	0
<i>MPP6</i>	Adrenal	5.43E-08	0.000152	0.308788	other	0
<i>MROH1</i>	Adrenal	2.31E-07	0.000326	0.025848	other	0
<i>MRPL1</i>	Adrenal	4.80E-08	-0.00058	2.53E-05	decreasing	0
<i>MRPL10</i>	Adrenal	4.91E-08	-0.00069	3.99E-07	decreasing	0
<i>MRPL16</i>	Adrenal	9.60E-10	-0.00075	7.59E-09	decreasing	0
<i>MRPL22</i>	Adrenal	4.73E-08	-0.00066	2.17E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MRPL30</i>	Adrenal	2.17E-07	-0.00022	0.145258	other	0
<i>MRPL37</i>	Adrenal	2.71E-10	-0.00074	2.78E-08	decreasing	0
<i>MRPS18A</i>	Adrenal	4.10E-08	-0.00074	5.71E-08	decreasing	0
<i>MRPS2</i>	Adrenal	2.95E-08	-0.00076	1.10E-08	decreasing	0
<i>MRPS22</i>	Adrenal	9.35E-11	-0.00077	2.74E-09	decreasing	0
<i>MRPS7</i>	Adrenal	1.14E-11	-0.00081	4.36E-10	decreasing	0
<i>MRRF</i>	Adrenal	1.15E-09	-0.00073	8.41E-08	decreasing	0
<i>MTCH2</i>	Adrenal	1.89E-09	-0.00066	2.10E-06	decreasing	0
<i>MTPAP</i>	Adrenal	6.24E-11	-0.00055	0.000119	other	1
<i>MYB</i>	Adrenal	9.97E-08	-0.00063	3.50E-06	decreasing	0
<i>MYBL2</i>	Adrenal	4.00E-10	-0.00076	5.85E-09	decreasing	0
<i>MYO16</i>	Adrenal	1.39E-07	-0.00067	6.28E-07	decreasing	0
<i>MYO18A</i>	Adrenal	2.03E-10	0.000395	0.006459	other	0
<i>MYO6</i>	Adrenal	9.93E-08	0.000679	7.42E-07	increasing	0
<i>MYRIP</i>	Adrenal	6.03E-08	0.000679	8.75E-07	increasing	1
<i>NALCN</i>	Adrenal	5.03E-09	0.000592	1.18E-05	increasing	0
<i>NAP1L2</i>	Adrenal	2.59E-09	0.000704	1.56E-07	increasing	0
<i>NCAPG</i>	Adrenal	1.21E-07	-0.00069	4.44E-07	decreasing	0
<i>NCAPH</i>	Adrenal	7.73E-11	-0.00078	1.66E-09	decreasing	0
<i>NCK2</i>	Adrenal	5.36E-08	-0.00047	0.000955	other	0
<i>NCMAP</i>	Adrenal	1.45E-07	-0.00054	9.33E-05	decreasing	0
<i>NDC80</i>	Adrenal	4.40E-09	-0.00068	6.50E-07	decreasing	0
<i>NDUFA10</i>	Adrenal	7.97E-12	-0.0008	5.78E-10	decreasing	0
<i>NDUFA9</i>	Adrenal	1.01E-09	-0.00065	3.11E-06	decreasing	0
<i>NDUFS2</i>	Adrenal	6.81E-08	-0.00068	7.41E-07	decreasing	0
<i>NDUFS3</i>	Adrenal	5.42E-07	-0.00072	1.56E-07	decreasing	0
<i>NEFH</i>	Adrenal	1.35E-07	-2.37E-05	0.873135	other	0
<i>NEK1</i>	Adrenal	2.05E-07	0.000621	4.86E-06	increasing	0
<i>NEK2</i>	Adrenal	8.90E-12	-0.00081	1.61E-10	decreasing	0
<i>NEO1</i>	Adrenal	1.39E-08	0.000599	1.57E-05	increasing	0
<i>NEU3</i>	Adrenal	1.91E-07	0.000718	1.45E-07	increasing	0
<i>NEURL3</i>	Adrenal	6.39E-08	-0.0004	0.001492	other	0
<i>NFS1</i>	Adrenal	5.12E-12	-0.00073	3.76E-08	decreasing	0
<i>NID1</i>	Adrenal	8.48E-08	-0.00062	4.00E-06	decreasing	0
<i>NIPSNAP1</i>	Adrenal	4.34E-08	-0.00077	5.78E-09	decreasing	0
<i>NLRX1</i>	Adrenal	9.66E-10	-0.00069	3.04E-07	decreasing	0
<i>NOP16</i>	Adrenal	2.73E-09	-0.00074	3.22E-08	decreasing	0
<i>NOP9</i>	Adrenal	6.13E-08	0.00025	0.084069	other	0
<i>NOTCH3</i>	Adrenal	2.46E-08	0.000123	0.420028	other	0
<i>NPAP1</i>	Adrenal	2.99E-08	0.000739	3.63E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>NPC1L1</i>	Adrenal	2.29E-07	0.000501	0.000373	other	0
<i>NPFFR2</i>	Adrenal	2.34E-05	0.000705	1.10E-07	increasing	1
<i>NPNT</i>	Adrenal	1.36E-08	-0.00029	0.054288	other	0
<i>NPR2</i>	Adrenal	1.92E-07	5.04E-05	0.731286	other	0
<i>NR2E3</i>	Adrenal	9.89E-08	-0.00074	4.17E-08	decreasing	0
<i>NR3C2</i>	Adrenal	1.43E-13	0.000781	1.08E-09	increasing	0
<i>NRAS</i>	Adrenal	9.19E-08	-0.00014	0.340664	other	0
<i>NRBP1</i>	Adrenal	8.91E-10	-0.00077	3.03E-09	decreasing	0
<i>NRBP2</i>	Adrenal	1.56E-08	0.000614	4.84E-06	increasing	1
<i>NRCAM</i>	Adrenal	1.13E-08	0.000715	9.34E-08	increasing	0
<i>NREP</i>	Adrenal	2.08E-07	-0.00013	0.366821	other	0
<i>NRM</i>	Adrenal	5.20E-08	-0.00068	1.11E-06	decreasing	0
<i>NRP1</i>	Adrenal	1.22E-07	-0.00045	0.001453	other	0
<i>NRTN</i>	Adrenal	1.60E-07	-0.00056	4.66E-05	decreasing	0
<i>NT5C3A</i>	Adrenal	9.06E-09	-1.42E-05	0.92495	other	0
<i>NUCB2</i>	Adrenal	8.18E-08	0.000678	6.54E-07	increasing	0
<i>NUP85</i>	Adrenal	6.56E-08	-0.00071	2.51E-07	decreasing	0
<i>NUSAP1</i>	Adrenal	2.59E-10	-0.00074	1.79E-08	decreasing	0
<i>NUTF2</i>	Adrenal	1.55E-07	-0.00043	0.003174	other	0
<i>NXN</i>	Adrenal	2.77E-09	-0.00078	4.17E-09	decreasing	1
<i>NXPH1</i>	Adrenal	1.68E-07	0.000509	0.000316	other	0
<i>OGDHL</i>	Adrenal	4.53E-08	0.000433	0.002721	other	0
<i>OPLAH</i>	Adrenal	2.92E-09	0.000398	0.005631	other	0
<i>OPN15W</i>	Adrenal	1.05E-07	-0.00022	0.138939	other	0
<i>OSBPL10</i>	Adrenal	4.34E-08	-0.0005	0.00049	other	0
<i>OSBPL2</i>	Adrenal	3.72E-09	0.000412	0.005109	other	0
<i>OSTF1</i>	Adrenal	2.32E-09	-0.00073	4.99E-08	decreasing	0
<i>OTOL1</i>	Adrenal	4.12E-11	-0.00014	0.128125	other	0
<i>OTUD3</i>	Adrenal	2.13E-07	0.000584	2.77E-05	increasing	0
<i>PABPC3</i>	Adrenal	6.45E-08	-8.96E-05	0.548788	other	0
<i>PAN2</i>	Adrenal	3.51E-08	0.000428	0.003664	other	0
<i>PAPSS2</i>	Adrenal	9.44E-09	0.00047	0.000987	other	0
<i>PAQR4</i>	Adrenal	2.64E-10	-0.00078	2.26E-09	decreasing	0
<i>PBK</i>	Adrenal	1.18E-08	-0.00074	2.24E-08	decreasing	0
<i>PBX3</i>	Adrenal	1.58E-09	0.000645	2.31E-06	increasing	0
<i>PCDHB7</i>	Adrenal	1.19E-08	0.000706	1.04E-07	increasing	0
<i>PDE2A</i>	Adrenal	2.08E-07	-0.00014	0.340239	other	0
<i>PDGFRL</i>	Adrenal	1.87E-09	-0.00067	1.72E-06	decreasing	0
<i>PDHB</i>	Adrenal	1.52E-11	-0.00079	1.07E-09	decreasing	0
<i>PDHX</i>	Adrenal	1.55E-08	-0.0007	1.30E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PDIA2</i>	Adrenal	2.44E-09	0.000527	0.000196	other	0
<i>PEX13</i>	Adrenal	1.04E-08	-0.00039	0.008211	other	0
<i>PFDN1</i>	Adrenal	2.20E-07	-0.00055	0.000126	other	0
<i>PHB2</i>	Adrenal	3.29E-06	-0.00073	6.39E-08	decreasing	0
<i>PHF2</i>	Adrenal	1.55E-07	0.000268	0.068718	other	0
<i>PI15</i>	Adrenal	4.54E-10	-0.00068	7.08E-07	decreasing	0
<i>PI16</i>	Adrenal	5.51E-09	-0.00077	9.17E-09	decreasing	0
<i>PIGU</i>	Adrenal	1.48E-08	-0.00072	2.79E-08	decreasing	0
<i>PIP4K2B</i>	Adrenal	2.01E-08	-9.33E-05	0.536545	other	0
<i>PITPNC1</i>	Adrenal	1.11E-07	-0.00058	2.18E-05	decreasing	0
<i>PKIB</i>	Adrenal	1.09E-12	-0.00073	5.93E-08	decreasing	0
<i>PKMYT1</i>	Adrenal	7.65E-08	-0.00075	1.50E-08	decreasing	0
<i>PKP2</i>	Adrenal	2.59E-09	0.000678	5.60E-07	increasing	0
<i>PLBD2</i>	Adrenal	2.35E-07	0.000508	0.000434	other	1
<i>PLCL2</i>	Adrenal	2.07E-09	-0.00042	0.003181	other	0
<i>PLEKHH1</i>	Adrenal	3.26E-08	0.000342	0.018263	other	0
<i>PLP2</i>	Adrenal	2.55E-13	-0.00078	1.51E-09	decreasing	0
<i>PNMA1</i>	Adrenal	5.99E-09	7.61E-05	0.603795	other	0
<i>POC1B</i>	Adrenal	1.88E-08	-0.00046	0.001944	other	1
<i>POGLUT1</i>	Adrenal	6.57E-08	0.000168	0.261756	other	0
<i>POLG</i>	Adrenal	1.47E-07	-0.00069	5.41E-07	decreasing	0
<i>POMGNT2</i>	Adrenal	3.20E-08	-9.72E-05	0.512312	other	0
<i>POSTN</i>	Adrenal	3.50E-08	-0.00057	4.39E-05	decreasing	0
<i>POU6F1</i>	Adrenal	2.72E-09	0.000469	0.001152	other	0
<i>PPAP2A</i>	Adrenal	6.20E-10	-0.00071	2.61E-07	decreasing	0
<i>PPIP5K2</i>	Adrenal	2.04E-08	0.000311	0.030512	other	0
<i>PPM1B</i>	Adrenal	9.12E-12	0.000845	4.84E-11	increasing	0
<i>PPP1R14B</i>	Adrenal	7.37E-08	-0.0007	2.59E-07	decreasing	0
<i>PPP2R5E</i>	Adrenal	5.62E-09	0.000648	2.07E-06	increasing	0
<i>PPP4C</i>	Adrenal	1.44E-08	-0.00077	3.46E-09	decreasing	0
<i>PRC1</i>	Adrenal	2.18E-09	-0.00071	5.64E-08	decreasing	0
<i>PRKAA2</i>	Adrenal	5.64E-09	0.000629	4.74E-06	increasing	0
<i>PRKCA</i>	Adrenal	9.39E-08	0.000639	3.65E-06	increasing	0
<i>PRLR</i>	Adrenal	2.40E-13	0.000832	2.14E-11	increasing	0
<i>PRPS2</i>	Adrenal	4.47E-08	0.000442	0.001697	other	0
<i>PRPSAP1</i>	Adrenal	6.35E-06	-0.00071	2.56E-07	decreasing	0
<i>PRR16</i>	Adrenal	3.78E-07	0.000703	1.40E-07	increasing	0
<i>PRSS23</i>	Adrenal	7.19E-08	-0.00061	9.17E-06	decreasing	0
<i>PRUNE2</i>	Adrenal	5.18E-07	0.000742	2.85E-08	increasing	0
<i>PSKH1</i>	Adrenal	1.88E-06	-0.0007	2.35E-07	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PSMA2</i>	Adrenal	1.24E-07	-0.0004	0.006226	other	0
<i>PXDN</i>	Adrenal	2.61E-09	-0.00076	3.71E-09	decreasing	0
<i>PYROXD2</i>	Adrenal	1.83E-07	0.000415	0.004497	other	0
<i>QPCT</i>	Adrenal	7.32E-08	-0.00065	1.91E-06	decreasing	0
<i>RAC1</i>	Adrenal	1.11E-08	-0.00031	0.036275	other	0
<i>RACGAP1</i>	Adrenal	3.27E-09	-0.00073	4.05E-08	decreasing	1
<i>RANBP1</i>	Adrenal	2.56E-07	-0.00064	3.05E-06	decreasing	0
<i>RASL10B</i>	Adrenal	2.39E-11	-0.00078	1.93E-09	decreasing	0
<i>RBM19</i>	Adrenal	1.83E-13	-0.00079	7.24E-10	decreasing	1
<i>RBM38</i>	Adrenal	1.98E-09	-0.0007	1.81E-07	decreasing	0
<i>RBPM52</i>	Adrenal	4.66E-10	-0.00075	2.15E-08	decreasing	0
<i>REXO2</i>	Adrenal	8.45E-11	-0.00072	2.04E-08	decreasing	0
<i>RGMA</i>	Adrenal	3.30E-08	-0.00055	0.000126	other	0
<i>RGP1</i>	Adrenal	4.48E-14	0.000446	0.00204	other	0
<i>RHBG</i>	Adrenal	3.45E-08	0.000163	0.251851	other	0
<i>RHOA</i>	Adrenal	8.43E-08	-0.00045	0.001859	other	0
<i>RIMS4</i>	Adrenal	2.25E-09	0.000629	5.15E-06	increasing	0
<i>RMI2</i>	Adrenal	2.82E-09	-0.0005	0.00053	other	0
<i>RNF130</i>	Adrenal	4.12E-07	-0.00073	1.02E-07	decreasing	0
<i>ROBO2</i>	Adrenal	4.51E-09	-0.00072	6.08E-08	decreasing	0
<i>RORC</i>	Adrenal	2.42E-08	0.000668	1.34E-06	increasing	0
<i>RPF1</i>	Adrenal	7.69E-09	-0.00036	0.016546	other	0
<i>RPL22L1</i>	Adrenal	2.17E-10	-0.00075	1.19E-08	decreasing	0
<i>RPS6KA1</i>	Adrenal	2.17E-05	-0.00072	1.28E-07	decreasing	0
<i>RQCD1</i>	Adrenal	2.45E-08	-0.00047	0.001244	other	0
<i>RRM2</i>	Adrenal	5.58E-08	-0.00076	9.15E-09	decreasing	0
<i>RSPO3</i>	Adrenal	8.72E-09	-0.00035	0.015917	other	0
<i>RSRP1</i>	Adrenal	3.59E-09	0.000514	0.000314	other	0
<i>RTN1</i>	Adrenal	1.37E-09	0.000652	8.48E-07	increasing	0
<i>RUSC2</i>	Adrenal	2.50E-07	0.000358	0.012267	other	0
<i>SAFB2</i>	Adrenal	8.62E-09	0.000368	0.010793	other	0
<i>SAMD12</i>	Adrenal	9.83E-10	0.000748	8.96E-09	increasing	0
<i>SARM1</i>	Adrenal	5.56E-08	0.000216	0.136639	other	0
<i>SASH1</i>	Adrenal	4.43E-08	0.000778	2.83E-09	increasing	0
<i>SATB1</i>	Adrenal	1.52E-08	0.000715	6.24E-08	increasing	0
<i>SC5D</i>	Adrenal	1.06E-09	0.000588	3.74E-05	increasing	0
<i>SCAMP5</i>	Adrenal	7.19E-09	0.000582	2.38E-05	increasing	0
<i>SCML1</i>	Adrenal	2.56E-07	0.000273	0.062503	other	0
<i>SCN8A</i>	Adrenal	1.41E-09	0.000261	0.078061	other	0
<i>SDC2</i>	Adrenal	2.80E-11	0.000384	0.006936	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SDHAF2</i>	Adrenal	4.56E-08	-0.00065	3.40E-06	decreasing	0
<i>SEC31B</i>	Adrenal	4.45E-11	0.00029	0.050911	other	0
<i>SERBP1</i>	Adrenal	1.62E-07	-0.00057	2.95E-05	decreasing	0
<i>SERPIND1</i>	Adrenal	9.87E-08	9.01E-05	0.543592	other	0
<i>SET</i>	Adrenal	2.66E-08	-0.00032	0.034432	other	0
<i>SFRP4</i>	Adrenal	8.20E-08	0.000474	0.000817	other	0
<i>SGOL1</i>	Adrenal	5.32E-07	-0.00071	1.91E-07	decreasing	0
<i>SGSM1</i>	Adrenal	8.22E-10	0.000664	1.48E-06	increasing	1
<i>SHANK1</i>	Adrenal	1.84E-10	0.000634	4.15E-06	increasing	0
<i>SHC2</i>	Adrenal	5.87E-09	0.000252	0.09309	other	0
<i>SHC3</i>	Adrenal	4.99E-08	0.000162	0.271969	other	0
<i>SHISA8</i>	Adrenal	2.66E-09	-0.00075	1.50E-08	decreasing	0
<i>SIAE</i>	Adrenal	1.47E-07	0.000518	0.000244	other	0
<i>SIDT1</i>	Adrenal	7.95E-09	0.000612	9.39E-06	increasing	0
<i>SLAMF9</i>	Adrenal	2.90E-09	-0.00081	3.83E-10	decreasing	0
<i>SLC12A5</i>	Adrenal	1.30E-07	0.000461	0.00152	other	0
<i>SLC22A15</i>	Adrenal	1.28E-07	0.000683	7.55E-07	increasing	0
<i>SLC24A3</i>	Adrenal	4.95E-08	-0.00071	2.13E-07	decreasing	0
<i>SLC25A20</i>	Adrenal	8.87E-12	-0.00082	1.82E-10	decreasing	0
<i>SLC25A29</i>	Adrenal	3.90E-10	0.000656	1.43E-06	increasing	0
<i>SLC2A4</i>	Adrenal	1.71E-05	-0.00071	2.16E-07	decreasing	0
<i>SLC4A1</i>	Adrenal	1.67E-07	-0.00065	2.07E-06	decreasing	0
<i>SLC4A11</i>	Adrenal	1.38E-07	0.000281	0.051586	other	0
<i>SLC6A16</i>	Adrenal	2.22E-08	0.000242	0.099632	other	1
<i>SMARCAL1</i>	Adrenal	1.25E-08	-0.00073	1.60E-08	decreasing	0
<i>SMARCC2</i>	Adrenal	4.49E-10	0.00061	1.36E-05	increasing	0
<i>SMARCD3</i>	Adrenal	1.13E-06	-0.00075	1.60E-08	decreasing	0
<i>SMIM14</i>	Adrenal	6.95E-08	0.000571	6.01E-05	increasing	0
<i>SMTNL2</i>	Adrenal	4.48E-10	-0.00071	1.30E-07	decreasing	0
<i>SMUG1</i>	Adrenal	7.63E-08	-0.00062	6.54E-06	decreasing	0
<i>SNRPC</i>	Adrenal	3.02E-09	-0.00068	6.94E-07	decreasing	0
<i>SNRPD3</i>	Adrenal	3.17E-08	-0.00065	3.05E-06	decreasing	0
<i>SNX32</i>	Adrenal	9.61E-08	9.09E-05	0.542958	other	0
<i>SOWAHB</i>	Adrenal	1.19E-07	-0.00075	7.85E-09	decreasing	0
<i>SOX11</i>	Adrenal	6.88E-11	-0.00074	1.80E-08	decreasing	0
<i>SOX21</i>	Adrenal	1.74E-10	0.000785	4.02E-10	increasing	0
<i>SP4</i>	Adrenal	2.46E-08	0.000705	1.98E-07	increasing	0
<i>SPAG7</i>	Adrenal	4.42E-09	-0.0007	2.15E-07	decreasing	0
<i>SPARC</i>	Adrenal	8.98E-17	-0.00088	3.97E-13	decreasing	0
<i>SPATA1</i>	Adrenal	6.39E-08	-0.00065	2.20E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SPEF2</i>	Adrenal	2.61E-08	0.000781	3.68E-09	increasing	0
<i>SPRED3</i>	Adrenal	2.61E-07	0.000604	1.78E-05	increasing	0
<i>SPTBN2</i>	Adrenal	3.37E-12	0.000556	6.94E-05	increasing	0
<i>SPTBN4</i>	Adrenal	1.96E-10	0.000647	2.17E-06	increasing	0
<i>SRCIN1</i>	Adrenal	3.59E-09	0.00011	0.451438	other	0
<i>SRPK2</i>	Adrenal	2.66E-06	0.000713	1.93E-07	increasing	0
<i>SRRM2</i>	Adrenal	1.53E-10	0.00039	0.008541	other	0
<i>SRSF5</i>	Adrenal	2.29E-08	0.000286	0.051657	other	0
<i>ST8SIA5</i>	Adrenal	1.68E-09	-0.00068	6.79E-07	decreasing	0
<i>STARD4</i>	Adrenal	8.76E-09	0.000478	0.000995	other	0
<i>STAT5B</i>	Adrenal	7.27E-08	0.00038	0.009514	other	0
<i>STK24</i>	Adrenal	2.28E-11	-0.00045	0.001372	other	0
<i>STK31</i>	Adrenal	4.14E-09	0.000652	1.52E-06	increasing	1
<i>STRADA</i>	Adrenal	1.28E-07	-0.00068	5.57E-07	decreasing	0
<i>STX1B</i>	Adrenal	1.08E-11	0.000691	3.97E-07	increasing	0
<i>SUCLA2</i>	Adrenal	1.01E-07	-0.00064	3.90E-06	decreasing	0
<i>SUGP2</i>	Adrenal	1.90E-09	0.000179	0.234527	other	0
<i>SUN1</i>	Adrenal	1.77E-08	0.000373	0.011964	other	0
<i>SUPV3L1</i>	Adrenal	4.75E-09	-0.00061	1.25E-05	decreasing	0
<i>SYN2</i>	Adrenal	5.88E-09	0.000549	6.07E-05	increasing	0
<i>SYN3</i>	Adrenal	3.10E-08	0.000499	0.00056	other	0
<i>SYT9</i>	Adrenal	1.31E-08	0.000562	6.15E-05	increasing	0
<i>SZT2</i>	Adrenal	9.08E-09	0.000321	0.030608	other	0
<i>TACC2</i>	Adrenal	1.33E-07	0.000353	0.014889	other	0
<i>TACC3</i>	Adrenal	5.92E-12	-0.00085	2.66E-11	decreasing	0
<i>TAF9B</i>	Adrenal	1.19E-07	0.000706	1.56E-07	increasing	0
<i>TBC1D22A</i>	Adrenal	3.21E-07	-0.00073	3.86E-08	decreasing	0
<i>TECRL</i>	Adrenal	1.68E-19	-0.00034	0.000808	other	0
<i>TEFM</i>	Adrenal	7.09E-10	-0.00067	9.70E-07	decreasing	0
<i>TEP1</i>	Adrenal	1.42E-11	0.000425	0.003349	other	0
<i>TFG</i>	Adrenal	9.34E-08	-0.00038	0.010134	other	0
<i>TGM3</i>	Adrenal	4.03E-07	-0.00071	1.58E-07	decreasing	1
<i>TIAF1</i>	Adrenal	2.00E-12	0.000413	0.003523	other	0
<i>TICRR</i>	Adrenal	1.35E-07	-0.00057	5.50E-05	decreasing	0
<i>TIFA</i>	Adrenal	4.43E-08	-0.00065	9.89E-07	decreasing	0
<i>TIMM17B</i>	Adrenal	1.33E-07	-0.00072	5.60E-08	decreasing	0
<i>TIMM50</i>	Adrenal	2.93E-06	-0.00075	2.22E-08	decreasing	0
<i>TIMM8B</i>	Adrenal	7.49E-09	-0.00061	9.33E-06	decreasing	0
<i>TK1</i>	Adrenal	4.58E-10	-0.00074	2.99E-08	decreasing	0
<i>TKT</i>	Adrenal	7.18E-09	-0.00064	5.70E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TMEM117</i>	Adrenal	1.12E-07	-0.00055	6.89E-05	decreasing	0
<i>TMEM132E</i>	Adrenal	2.82E-10	-0.00077	5.57E-09	decreasing	0
<i>TMEM179</i>	Adrenal	7.69E-09	0.000582	3.55E-05	increasing	0
<i>TMEM189</i>	Adrenal	4.77E-10	-0.00072	1.00E-07	decreasing	0
<i>TMEM246</i>	Adrenal	4.68E-09	0.000666	8.84E-07	increasing	0
<i>TMEM51</i>	Adrenal	1.72E-07	-0.00064	3.41E-06	decreasing	1
<i>TMEM86B</i>	Adrenal	2.50E-08	0.000368	0.013536	other	0
<i>TMOD1</i>	Adrenal	8.76E-12	0.000734	2.09E-08	increasing	0
<i>TNFRSF10B</i>	Adrenal	1.70E-07	0.000519	0.00025	other	0
<i>TNFSF10</i>	Adrenal	7.40E-08	7.00E-05	0.639389	other	0
<i>TNK2</i>	Adrenal	1.97E-09	0.000488	0.000457	other	0
<i>TNNI1</i>	Adrenal	2.76E-06	-0.00071	1.95E-07	decreasing	1
<i>TNRC6C</i>	Adrenal	5.79E-10	0.000751	1.68E-08	increasing	0
<i>TOP2A</i>	Adrenal	7.55E-12	-0.00081	2.14E-10	decreasing	0
<i>TPM2</i>	Adrenal	4.59E-06	-0.00074	3.76E-08	decreasing	1
<i>TPX2</i>	Adrenal	1.37E-15	-0.00085	9.19E-12	decreasing	0
<i>TRIM3</i>	Adrenal	2.20E-07	0.000612	5.15E-06	increasing	0
<i>TRIM72</i>	Adrenal	2.77E-08	0.000174	0.24335	other	0
<i>TROAP</i>	Adrenal	2.97E-08	-0.00074	3.46E-08	decreasing	0
<i>TRPC1</i>	Adrenal	6.82E-09	0.000727	6.80E-08	increasing	0
<i>TRPC4</i>	Adrenal	6.14E-08	-0.00019	0.196869	other	0
<i>TRUB2</i>	Adrenal	1.92E-08	-0.00072	7.77E-08	decreasing	0
<i>TSNARE1</i>	Adrenal	2.18E-10	0.000351	0.016891	other	0
<i>TSPAN13</i>	Adrenal	3.56E-08	-0.00061	4.84E-06	decreasing	0
<i>TSPAN9</i>	Adrenal	7.21E-07	-0.00069	2.53E-07	decreasing	0
<i>TSPYL2</i>	Adrenal	5.80E-08	0.000443	0.00188	other	0
<i>TSPYL4</i>	Adrenal	2.43E-07	0.000528	0.000268	other	0
<i>TSTA3</i>	Adrenal	1.91E-08	-0.00075	1.03E-08	decreasing	0
<i>TTC21A</i>	Adrenal	1.24E-07	0.000426	0.003982	other	0
<i>TTC22</i>	Adrenal	1.21E-09	0.000761	6.13E-09	increasing	0
<i>TTK</i>	Adrenal	1.97E-10	-0.00078	1.28E-09	decreasing	0
<i>TTPAL</i>	Adrenal	2.26E-07	0.000632	6.19E-06	increasing	0
<i>TUFT1</i>	Adrenal	1.11E-07	0.000514	0.000271	other	0
<i>TXNL1</i>	Adrenal	1.98E-08	-0.00046	0.001404	other	0
<i>TYMS</i>	Adrenal	4.87E-10	-0.00068	5.51E-07	decreasing	0
<i>UBE2C</i>	Adrenal	1.47E-08	-0.00074	4.18E-08	decreasing	0
<i>UBE2G1</i>	Adrenal	1.49E-07	-0.00038	0.008516	other	0
<i>UBE2L3</i>	Adrenal	2.96E-08	-0.00052	0.000313	other	0
<i>UBE2M</i>	Adrenal	1.12E-07	-0.0005	0.000616	other	0
<i>UBE2R2</i>	Adrenal	9.78E-08	1.41E-05	0.924404	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>UBE2T</i>	Adrenal	2.78E-11	-0.00086	1.14E-11	decreasing	0
<i>UBE2V1</i>	Adrenal	3.23E-11	-0.00051	0.000489	other	0
<i>UBFD1</i>	Adrenal	2.16E-08	-0.00048	0.00062	other	0
<i>UCMA</i>	Adrenal	1.04E-06	-0.00071	1.84E-07	decreasing	0
<i>URI1</i>	Adrenal	7.59E-08	-0.00028	0.054907	other	0
<i>USP15</i>	Adrenal	3.27E-08	0.000417	0.004392	other	0
<i>USP4</i>	Adrenal	2.46E-08	-0.00047	0.001087	other	0
<i>USP44</i>	Adrenal	2.61E-09	0.000711	1.09E-07	increasing	0
<i>USP54</i>	Adrenal	1.93E-07	0.000483	0.000849	other	0
<i>VAMP2</i>	Adrenal	2.19E-08	0.000415	0.004077	other	0
<i>VPS25</i>	Adrenal	4.12E-08	-0.00074	2.84E-08	decreasing	0
<i>VSIG8</i>	Adrenal	3.09E-08	0.000304	0.044251	other	0
<i>VWA9</i>	Adrenal	9.73E-08	-0.0005	0.000426	other	0
<i>WBSCR16</i>	Adrenal	1.13E-06	-0.00073	4.66E-08	decreasing	0
<i>WDR41</i>	Adrenal	4.06E-08	-0.00039	0.008987	other	0
<i>WDR55</i>	Adrenal	1.48E-07	-0.00051	0.000423	other	0
<i>WDR91</i>	Adrenal	3.89E-10	0.000281	0.055101	other	0
<i>WDR96</i>	Adrenal	8.55E-09	0.000678	6.57E-07	increasing	0
<i>WFIKKN1</i>	Adrenal	2.19E-07	0.000536	0.000164	other	0
<i>WISP2</i>	Adrenal	2.35E-08	0.000514	0.000244	other	0
<i>WNK2</i>	Adrenal	6.84E-12	0.000356	0.014466	other	0
<i>XPO6</i>	Adrenal	1.73E-07	-0.00057	5.24E-05	decreasing	0
<i>YBX3</i>	Adrenal	1.76E-07	-0.0003	0.038707	other	0
<i>ZBTB4</i>	Adrenal	5.58E-08	0.000379	0.009604	other	0
<i>ZBTB7C</i>	Adrenal	6.42E-10	-1.02E-05	0.946014	other	0
<i>ZC2HC1A</i>	Adrenal	5.01E-06	0.000745	3.06E-08	increasing	0
<i>ZDHC15</i>	Adrenal	1.09E-09	0.000727	4.40E-08	increasing	0
<i>ZMAT1</i>	Adrenal	4.10E-08	0.000674	8.42E-07	increasing	0
<i>ZMYM6NB</i>	Adrenal	3.92E-08	-0.00068	5.11E-07	decreasing	0
<i>ZNF483</i>	Adrenal	1.47E-07	0.000689	4.77E-07	increasing	0
<i>ZNF536</i>	Adrenal	9.64E-08	-0.00052	0.000151	other	0
<i>ZNF540</i>	Adrenal	2.47E-10	0.000781	1.09E-09	increasing	0
<i>ZSCAN18</i>	Adrenal	3.67E-08	-9.67E-06	0.948116	other	0
<i>ZSWIM8</i>	Adrenal	3.11E-08	0.000172	0.25077	other	0
<i>ZWINT</i>	Adrenal	3.36E-10	-0.00081	2.31E-10	decreasing	0
<i>AAAS</i>	BA46	2.17E-08	0.000673	4.21E-07	increasing	0
<i>AATK</i>	BA46	3.93E-08	0.000766	6.18E-09	increasing	0
<i>ABCA8</i>	BA46	1.04E-11	0.000821	4.41E-11	increasing	0
<i>ABCC3</i>	BA46	1.92E-10	-0.00061	1.18E-05	decreasing	0
<i>ABCC8</i>	BA46	1.08E-16	0.000883	5.22E-13	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ABCC9</i>	BA46	2.28E-08	-0.0007	2.81E-07	decreasing	0
<i>ABCG1</i>	BA46	5.59E-09	0.000801	1.38E-10	increasing	0
<i>ABHD17C</i>	BA46	2.16E-07	-0.00066	1.70E-06	decreasing	0
<i>ABHD2</i>	BA46	1.65E-07	-0.00066	1.90E-06	decreasing	0
<i>ABHD5</i>	BA46	4.00E-10	-0.00077	4.69E-09	decreasing	0
<i>ABI3BP</i>	BA46	5.16E-09	-0.00049	0.000746	other	0
<i>ABLIM2</i>	BA46	2.69E-12	0.000798	3.59E-10	increasing	0
<i>ABTB1</i>	BA46	7.53E-08	0.00074	2.92E-08	increasing	1
<i>ACAD10</i>	BA46	2.33E-07	0.000714	4.76E-08	increasing	0
<i>ACHE</i>	BA46	1.29E-06	0.000749	2.01E-08	increasing	0
<i>ACOT11</i>	BA46	2.71E-08	0.000536	0.000145	other	1
<i>ACSL6</i>	BA46	1.53E-07	-0.00039	0.006589	other	0
<i>ACTN1</i>	BA46	3.00E-08	0.000142	0.341383	other	0
<i>ACVR1</i>	BA46	1.40E-05	-0.00073	7.41E-08	decreasing	0
<i>ACVR2A</i>	BA46	1.13E-10	-0.00075	7.37E-09	decreasing	0
<i>ADAM19</i>	BA46	6.18E-11	-0.00083	3.74E-11	decreasing	0
<i>ADAM32</i>	BA46	2.62E-13	0.000822	9.26E-11	increasing	0
<i>ADAM33</i>	BA46	9.12E-09	0.000643	3.29E-06	increasing	0
<i>ADAMTS15</i>	BA46	1.06E-11	-0.00084	1.72E-11	decreasing	0
<i>ADAMTS17</i>	BA46	3.82E-06	-0.00072	1.12E-07	decreasing	0
<i>ADAMTS18</i>	BA46	6.93E-06	-0.00073	6.38E-08	decreasing	0
<i>ADAMTS9</i>	BA46	1.72E-13	-0.00083	2.55E-11	decreasing	0
<i>ADAMTSL2</i>	BA46	3.62E-11	-0.00076	2.23E-09	decreasing	0
<i>ADARB1</i>	BA46	2.42E-07	-0.00014	0.356524	other	0
<i>ADCK3</i>	BA46	6.73E-10	0.000799	7.70E-11	increasing	0
<i>ADCY2</i>	BA46	1.15E-07	-0.00013	0.397717	other	0
<i>ADCY7</i>	BA46	2.35E-07	-0.00069	3.52E-07	decreasing	0
<i>ADCY9</i>	BA46	3.33E-09	0.00066	8.06E-07	increasing	0
<i>ADD1</i>	BA46	6.94E-08	0.000465	0.001199	other	0
<i>ADORA1</i>	BA46	3.37E-10	0.000592	2.63E-05	increasing	1
<i>ADPRHL1</i>	BA46	1.96E-10	0.00017	0.242943	other	0
<i>ADRA1B</i>	BA46	7.46E-11	0.000104	0.484593	other	0
<i>ADRA1D</i>	BA46	1.55E-09	-0.00015	0.296781	other	0
<i>AEBP2</i>	BA46	1.38E-08	0.000678	2.06E-07	increasing	0
<i>AFF2</i>	BA46	1.33E-09	-0.0008	4.56E-10	decreasing	0
<i>AGA</i>	BA46	2.40E-08	0.000159	0.290492	other	0
<i>AGPAT9</i>	BA46	1.71E-09	0.000624	4.14E-06	increasing	0
<i>AGRN</i>	BA46	1.29E-10	-0.00082	4.15E-11	decreasing	0
<i>AGTPBP1</i>	BA46	6.99E-08	-0.00062	6.31E-06	decreasing	0
<i>AHCYL1</i>	BA46	1.03E-07	0.000648	1.70E-06	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>AHI1</i>	BA46	1.60E-08	0.000704	1.05E-07	increasing	0
<i>AIRE</i>	BA46	6.36E-16	0.000864	4.89E-13	increasing	0
<i>AK5</i>	BA46	9.54E-11	0.000597	1.24E-05	increasing	0
<i>AKAP12</i>	BA46	2.35E-17	0.000829	1.43E-11	increasing	0
<i>AKAP7</i>	BA46	1.90E-08	-0.0005	0.000387	other	0
<i>AKTIP</i>	BA46	1.08E-07	0.000392	0.00633	other	0
<i>ALCAM</i>	BA46	2.33E-09	-0.00066	1.19E-06	decreasing	0
<i>ALDH1A1</i>	BA46	3.66E-09	-0.00053	0.000171	other	0
<i>ALDOA</i>	BA46	2.31E-11	0.000779	7.33E-10	increasing	0
<i>ALDOC</i>	BA46	1.79E-07	0.000662	7.14E-07	increasing	0
<i>ALKBH5</i>	BA46	1.18E-07	0.000685	2.86E-07	increasing	0
<i>ALOX15B</i>	BA46	5.96E-10	-0.00023	0.017473	other	0
<i>ANGEL1</i>	BA46	3.85E-10	0.000843	4.20E-11	increasing	0
<i>ANKH</i>	BA46	3.42E-09	0.000734	1.45E-08	increasing	0
<i>ANKMY2</i>	BA46	5.07E-07	0.000728	8.27E-08	increasing	0
<i>ANKRD12</i>	BA46	7.49E-08	0.000392	0.006366	other	0
<i>ANKRD2</i>	BA46	8.25E-07	0.000676	2.35E-07	increasing	0
<i>ANKRD32</i>	BA46	6.32E-06	0.000696	1.91E-07	increasing	0
<i>ANKRD35</i>	BA46	1.77E-09	0.000765	5.73E-09	increasing	1
<i>ANKRD42</i>	BA46	7.10E-12	0.000789	5.02E-10	increasing	1
<i>ANKRD50</i>	BA46	2.12E-08	-0.0006	8.37E-06	decreasing	0
<i>ANKRD63</i>	BA46	1.60E-15	0.000652	7.81E-07	increasing	0
<i>ANKZF1</i>	BA46	4.06E-05	0.000717	1.09E-07	increasing	0
<i>ANLN</i>	BA46	3.69E-12	0.000801	4.51E-10	increasing	0
<i>ANTXR1</i>	BA46	1.27E-07	-0.00067	6.49E-07	decreasing	0
<i>ANXA11</i>	BA46	3.72E-11	0.000713	2.96E-08	increasing	1
<i>ANXA4</i>	BA46	2.57E-05	0.000707	2.47E-07	increasing	0
<i>ANXA7</i>	BA46	9.83E-07	0.000746	9.09E-09	increasing	0
<i>AP4B1</i>	BA46	9.96E-06	0.000711	1.90E-07	increasing	1
<i>APC</i>	BA46	2.30E-20	-0.00092	1.11E-14	decreasing	0
<i>APLN</i>	BA46	4.37E-07	-0.00074	4.59E-08	decreasing	0
<i>AQP11</i>	BA46	1.51E-09	0.000668	5.38E-07	increasing	0
<i>ARC</i>	BA46	5.44E-11	-0.00076	6.91E-09	decreasing	0
<i>ARFGAP2</i>	BA46	5.31E-08	0.000137	0.349208	other	0
<i>ARHGAP10</i>	BA46	4.73E-09	-0.00063	6.10E-06	decreasing	0
<i>ARHGAP15</i>	BA46	5.82E-08	-0.00051	0.00038	other	0
<i>ARHGAP18</i>	BA46	9.85E-09	-0.00048	0.000696	other	0
<i>ARHGAP20</i>	BA46	2.69E-08	-0.00079	2.49E-09	decreasing	0
<i>ARHGAP26</i>	BA46	3.46E-09	0.000657	1.44E-06	increasing	0
<i>ARHGAP4</i>	BA46	2.40E-07	7.36E-05	0.625121	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ARHGAP9</i>	BA46	2.76E-08	0.000745	1.20E-08	increasing	0
<i>ARHGEF17</i>	BA46	2.40E-12	0.000841	2.54E-11	increasing	0
<i>ARHGEF18</i>	BA46	1.12E-07	-0.00069	2.68E-07	decreasing	1
<i>ARHGEF2</i>	BA46	9.55E-11	-0.00077	1.61E-09	decreasing	0
<i>ARHGEF25</i>	BA46	1.66E-07	0.000717	5.30E-08	increasing	0
<i>ARHGEF37</i>	BA46	2.09E-07	0.00072	1.11E-07	increasing	0
<i>ARID5B</i>	BA46	8.90E-07	0.000701	1.99E-07	increasing	0
<i>ARL2</i>	BA46	3.93E-09	0.000629	7.55E-06	increasing	0
<i>ARL4D</i>	BA46	4.81E-09	-0.00065	1.98E-06	decreasing	0
<i>ARMC5</i>	BA46	8.02E-08	0.000669	1.47E-06	increasing	0
<i>ARMC6</i>	BA46	8.16E-08	-0.00043	0.002807	other	0
<i>ARPP21</i>	BA46	1.15E-15	-0.00087	3.44E-13	decreasing	0
<i>ARRDC3</i>	BA46	1.13E-07	0.000239	0.106983	other	0
<i>ARRDC4</i>	BA46	4.77E-10	-0.00071	4.02E-08	decreasing	0
<i>ASAP1</i>	BA46	6.46E-12	-0.00076	1.25E-08	decreasing	0
<i>ASAP2</i>	BA46	3.71E-11	-0.00084	2.89E-11	decreasing	0
<i>ASB2</i>	BA46	7.66E-13	0.000813	5.17E-11	increasing	0
<i>ASIC2</i>	BA46	3.08E-12	-0.00083	7.94E-12	decreasing	0
<i>ASTN1</i>	BA46	7.48E-09	-0.0007	1.12E-07	decreasing	0
<i>ASTN2</i>	BA46	1.93E-06	-0.00071	1.20E-07	decreasing	0
<i>ASXL3</i>	BA46	3.47E-09	-0.00072	4.22E-08	decreasing	0
<i>ATF7IP</i>	BA46	6.45E-12	-0.00068	5.24E-07	decreasing	0
<i>ATG13</i>	BA46	1.10E-13	0.00081	1.02E-10	increasing	0
<i>ATG9B</i>	BA46	2.08E-10	0.000838	6.78E-11	increasing	0
<i>ATP11C</i>	BA46	4.49E-10	-0.00058	1.71E-05	decreasing	0
<i>ATP1A4</i>	BA46	5.35E-08	0.000691	2.07E-07	increasing	0
<i>ATP2B2</i>	BA46	2.32E-07	-0.00061	1.62E-05	decreasing	0
<i>ATP2B3</i>	BA46	9.20E-16	0.000869	5.58E-13	increasing	0
<i>ATP4A</i>	BA46	3.24E-10	0.000326	0.025758	other	1
<i>ATP6V0B</i>	BA46	1.67E-08	-0.00055	9.62E-05	decreasing	0
<i>ATP6V1B2</i>	BA46	2.92E-08	0.000768	3.77E-09	increasing	0
<i>ATP8A1</i>	BA46	5.33E-09	0.000758	1.42E-08	increasing	0
<i>ATP9B</i>	BA46	1.81E-08	0.000627	3.58E-06	increasing	0
<i>ATPAF1</i>	BA46	1.82E-08	0.000737	1.61E-08	increasing	0
<i>ATRNL1</i>	BA46	1.06E-09	0.000512	0.000258	other	0
<i>B3GAT1</i>	BA46	3.72E-08	-0.00069	6.01E-07	decreasing	0
<i>B4GALNT3</i>	BA46	2.78E-08	0.00061	1.36E-05	increasing	0
<i>B4GALT2</i>	BA46	1.15E-16	-0.00089	3.79E-13	decreasing	0
<i>BACE2</i>	BA46	7.44E-10	-0.00077	7.41E-09	decreasing	0
<i>BAG5</i>	BA46	3.62E-06	0.000686	2.10E-07	increasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>BAIAP3</i>	BA46	1.37E-13	0.000836	2.86E-12	increasing	0
<i>BAMBI</i>	BA46	2.03E-07	-0.00055	8.52E-05	decreasing	0
<i>BAZ1B</i>	BA46	1.15E-07	0.000679	1.98E-07	increasing	0
<i>BBX</i>	BA46	3.28E-10	0.000813	8.20E-11	increasing	0
<i>BCAN</i>	BA46	3.97E-12	-0.00083	1.86E-11	decreasing	0
<i>BCAP31</i>	BA46	4.30E-09	0.000746	3.70E-09	increasing	0
<i>BDKRB1</i>	BA46	2.62E-13	0.000815	2.25E-10	increasing	0
<i>BDKRB2</i>	BA46	5.02E-11	0.000752	4.44E-09	increasing	0
<i>BEGAIN</i>	BA46	1.28E-07	-0.00055	0.000128	other	0
<i>BHLHE22</i>	BA46	5.06E-09	-0.00065	1.02E-06	decreasing	0
<i>BHLHE41</i>	BA46	7.03E-11	0.000696	8.02E-08	increasing	0
<i>BHMT2</i>	BA46	2.51E-08	0.000207	0.16288	other	1
<i>BICD1</i>	BA46	8.61E-11	-0.00075	2.18E-08	decreasing	0
<i>BIN2</i>	BA46	1.15E-06	-0.00072	8.83E-08	decreasing	0
<i>BLCAP</i>	BA46	7.27E-08	0.000516	0.000377	other	0
<i>BLVRA</i>	BA46	3.85E-15	0.000832	4.08E-12	increasing	0
<i>BMP2K</i>	BA46	1.44E-07	-0.00047	0.000981	other	0
<i>BMP4</i>	BA46	9.45E-06	0.000716	1.50E-07	increasing	0
<i>BRD8</i>	BA46	7.41E-08	0.000738	4.18E-08	increasing	0
<i>BRINP1</i>	BA46	4.35E-08	-0.0007	2.97E-07	decreasing	0
<i>BRINP2</i>	BA46	4.06E-13	-0.00081	1.64E-10	decreasing	1
<i>BRINP3</i>	BA46	1.02E-15	-0.00087	1.40E-12	decreasing	0
<i>BTBD17</i>	BA46	1.17E-10	-0.00083	5.70E-11	decreasing	0
<i>BTBD3</i>	BA46	2.40E-08	0.000605	9.23E-06	increasing	0
<i>BTG3</i>	BA46	4.57E-11	-0.00071	8.62E-08	decreasing	0
<i>BTNL8</i>	BA46	1.38E-07	0.000668	1.01E-06	increasing	0
<i>C11H12orf29</i>	BA46	8.23E-07	0.000741	5.25E-09	increasing	0
<i>C11H12orf49</i>	BA46	2.30E-07	-0.00073	4.81E-08	decreasing	0
<i>C11H12orf5</i>	BA46	2.94E-08	-0.00024	0.110995	other	0
<i>C12H9orf16</i>	BA46	3.46E-08	-0.0007	2.25E-07	decreasing	0
<i>C12H9orf41</i>	BA46	1.79E-06	-0.00073	7.40E-08	decreasing	0
<i>C12H9orf91</i>	BA46	6.41E-09	0.000812	4.65E-10	increasing	0
<i>C14H2orf91</i>	BA46	3.47E-08	-5.25E-05	0.728454	other	1
<i>C15H3orf70</i>	BA46	6.48E-07	-0.00072	9.52E-08	decreasing	0
<i>C15H3orf80</i>	BA46	2.48E-07	0.00063	3.19E-06	increasing	0
<i>C16H17orf58</i>	BA46	1.42E-08	-0.0007	1.34E-07	decreasing	0
<i>C17H6orf106</i>	BA46	6.32E-08	-0.00012	0.432127	other	0
<i>C17H6orf141</i>	BA46	1.64E-08	-0.00019	0.210495	other	0
<i>C18H18orf54</i>	BA46	1.64E-08	-0.0006	1.08E-05	decreasing	0
<i>C19H22orf24</i>	BA46	4.29E-07	0.000709	1.47E-07	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>C1H11orf24</i>	BA46	1.97E-11	-0.00085	1.02E-11	decreasing	0
<i>C1QTNF1</i>	BA46	8.16E-16	-0.0009	1.54E-13	decreasing	0
<i>C22H3orf56</i>	BA46	2.24E-12	-0.00081	2.36E-11	decreasing	0
<i>C25H1orf106</i>	BA46	1.65E-11	-0.00076	9.59E-09	decreasing	0
<i>C25H1orf21</i>	BA46	6.25E-08	-0.00061	1.01E-05	decreasing	0
<i>C25H1orf95</i>	BA46	8.04E-07	-0.00073	5.97E-08	decreasing	0
<i>C27H4orf19</i>	BA46	6.64E-06	-0.00076	1.50E-08	decreasing	0
<i>C2CD2</i>	BA46	4.83E-10	0.000764	1.04E-09	increasing	0
<i>C2CD4C</i>	BA46	2.69E-08	0.000802	8.39E-10	increasing	0
<i>C8H8orf34</i>	BA46	2.13E-21	-0.00089	5.37E-15	decreasing	0
<i>C8H8orf88</i>	BA46	2.44E-07	0.000763	1.03E-08	increasing	0
<i>C9H10orf11</i>	BA46	1.20E-10	0.00065	1.24E-06	increasing	0
<i>C9H10orf90</i>	BA46	2.82E-10	0.000824	1.16E-10	increasing	0
<i>CA11</i>	BA46	2.03E-08	-0.00022	0.134082	other	0
<i>CABP1</i>	BA46	2.36E-15	0.000861	7.03E-13	increasing	0
<i>CACNA1G</i>	BA46	1.92E-06	-0.00076	4.73E-09	decreasing	0
<i>CACNA1S</i>	BA46	1.31E-12	-0.00079	2.47E-10	decreasing	0
<i>CACNG4</i>	BA46	4.46E-13	-0.00085	2.48E-12	decreasing	0
<i>CADM1</i>	BA46	1.41E-10	-0.00077	2.13E-09	decreasing	0
<i>CALCOCO1</i>	BA46	3.76E-14	0.00085	1.97E-12	increasing	0
<i>CALM1</i>	BA46	3.76E-06	-0.00071	1.68E-07	decreasing	0
<i>CALN1</i>	BA46	3.65E-08	-0.0006	1.18E-05	decreasing	0
<i>CALU</i>	BA46	4.19E-06	-0.00073	6.78E-08	decreasing	0
<i>CAMK2B</i>	BA46	4.30E-08	-0.00064	1.99E-06	decreasing	0
<i>CAMK2G</i>	BA46	1.27E-11	0.0008	1.45E-10	increasing	0
<i>CAMK2N1</i>	BA46	1.03E-12	-0.00054	0.000155	other	0
<i>CAMKK1</i>	BA46	1.70E-21	0.000914	3.65E-15	increasing	0
<i>CAMSAP1</i>	BA46	9.36E-08	-0.00064	2.38E-06	decreasing	0
<i>CAP1</i>	BA46	1.22E-09	-0.00074	4.95E-08	decreasing	0
<i>CAPN14</i>	BA46	1.59E-05	-0.0007	2.16E-07	decreasing	1
<i>CAPS2</i>	BA46	4.62E-15	0.000859	1.43E-12	increasing	0
<i>CARNS1</i>	BA46	2.65E-12	0.000817	7.93E-11	increasing	0
<i>CARTPT</i>	BA46	1.71E-07	-0.0002	0.173192	other	0
<i>CASC3</i>	BA46	3.93E-07	0.000767	8.05E-09	increasing	0
<i>CASK</i>	BA46	1.46E-13	-0.00083	3.57E-11	decreasing	0
<i>CAST</i>	BA46	1.35E-07	0.000744	7.60E-09	increasing	0
<i>CBLN1</i>	BA46	2.02E-08	-0.00077	4.36E-09	decreasing	0
<i>CBR1</i>	BA46	3.55E-08	0.000726	1.35E-08	increasing	0
<i>CBX7</i>	BA46	2.93E-17	0.000873	2.07E-13	increasing	0
<i>CBX8</i>	BA46	4.56E-16	-0.00089	1.08E-13	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CCDC136</i>	BA46	5.57E-09	0.000693	3.20E-07	increasing	0
<i>CCDC147</i>	BA46	1.30E-07	0.000417	0.003524	other	0
<i>CCDC15</i>	BA46	2.94E-07	-0.00074	2.01E-08	decreasing	0
<i>CCDC181</i>	BA46	1.04E-07	0.000772	4.78E-09	increasing	1
<i>CCDC28A</i>	BA46	1.97E-13	0.000865	4.19E-12	increasing	0
<i>CCDC37</i>	BA46	1.51E-09	-0.00056	4.38E-05	decreasing	0
<i>CCDC47</i>	BA46	4.56E-09	0.000725	5.11E-08	increasing	0
<i>CCDC50</i>	BA46	3.64E-12	-0.00074	1.20E-08	decreasing	0
<i>CCDC64</i>	BA46	1.87E-09	-0.00079	3.20E-10	decreasing	0
<i>CCDC69</i>	BA46	1.42E-07	0.000588	2.07E-05	increasing	0
<i>CCDC71L</i>	BA46	2.49E-08	1.92E-05	0.898181	other	0
<i>CCDC80</i>	BA46	7.30E-06	-0.00071	1.93E-07	decreasing	0
<i>CCDC81</i>	BA46	9.82E-12	-0.00074	9.91E-09	decreasing	0
<i>CCDC85A</i>	BA46	1.93E-08	-0.0007	1.26E-07	decreasing	0
<i>CCDC85C</i>	BA46	1.06E-08	-0.00079	1.71E-09	decreasing	0
<i>CCDC88B</i>	BA46	3.44E-09	0.000506	0.000256	other	0
<i>CCDC92</i>	BA46	7.64E-11	0.000794	5.91E-10	increasing	0
<i>CCHCR1</i>	BA46	4.23E-07	0.000744	2.69E-08	increasing	0
<i>CCK</i>	BA46	1.69E-09	0.000568	5.92E-05	increasing	0
<i>CCND2</i>	BA46	1.23E-09	-0.0002	0.168824	other	0
<i>CD24</i>	BA46	3.02E-12	-0.00076	2.30E-09	decreasing	0
<i>CD276</i>	BA46	2.73E-05	-0.0007	5.32E-08	decreasing	0
<i>CD36</i>	BA46	5.00E-09	-0.00067	7.19E-07	decreasing	0
<i>CD53</i>	BA46	3.44E-13	0.000588	1.35E-05	increasing	0
<i>CD96</i>	BA46	1.54E-10	-0.00077	8.64E-10	decreasing	0
<i>CDC14B</i>	BA46	8.74E-08	0.000553	8.61E-05	increasing	0
<i>CDC42</i>	BA46	5.49E-08	-0.00054	0.000156	other	0
<i>CDC42BPB</i>	BA46	5.93E-09	-0.0008	5.06E-10	decreasing	0
<i>CDCA7L</i>	BA46	9.76E-08	-0.00047	0.000891	other	0
<i>CDH10</i>	BA46	3.13E-09	-0.00073	2.28E-08	decreasing	0
<i>CDH11</i>	BA46	4.28E-17	-0.00086	1.89E-13	decreasing	0
<i>CDH13</i>	BA46	4.29E-11	-0.00075	7.85E-09	decreasing	0
<i>CDH26</i>	BA46	5.99E-08	0.000551	5.57E-05	increasing	1
<i>CDH3</i>	BA46	4.52E-09	-0.00079	1.50E-09	decreasing	0
<i>CDH6</i>	BA46	1.74E-13	-0.00081	1.26E-10	decreasing	0
<i>CDIP1</i>	BA46	1.34E-11	0.000744	1.28E-08	increasing	0
<i>CDK14</i>	BA46	4.22E-15	0.000818	3.57E-11	increasing	0
<i>CDK18</i>	BA46	2.76E-11	0.000768	4.35E-09	increasing	0
<i>CDK5R1</i>	BA46	1.90E-07	-0.00059	1.79E-05	decreasing	0
<i>CDK5R2</i>	BA46	2.38E-09	-0.00081	2.01E-10	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CDK6</i>	BA46	2.23E-08	0.000698	1.95E-07	increasing	0
<i>CDKL2</i>	BA46	4.10E-08	-0.00067	7.59E-07	decreasing	0
<i>CDKN1C</i>	BA46	7.11E-09	0.000659	1.94E-06	increasing	0
<i>CDR1</i>	BA46	1.29E-10	0.000787	1.46E-09	increasing	0
<i>CDYL</i>	BA46	2.81E-13	0.000782	5.78E-10	increasing	0
<i>CECR6</i>	BA46	1.25E-10	-0.00082	1.21E-10	decreasing	0
<i>CELF2</i>	BA46	5.14E-07	-0.00076	5.65E-09	decreasing	0
<i>CEND1</i>	BA46	2.36E-10	0.000799	4.74E-10	increasing	0
<i>CENPB</i>	BA46	1.98E-07	-0.00074	3.19E-08	decreasing	0
<i>CEP112</i>	BA46	8.59E-08	0.000572	5.70E-05	increasing	0
<i>CEP290</i>	BA46	6.29E-06	0.000732	6.21E-08	increasing	0
<i>CEP72</i>	BA46	6.41E-14	-0.00083	1.81E-11	decreasing	0
<i>CETP</i>	BA46	2.24E-11	-0.00084	3.32E-11	decreasing	0
<i>CHAF1B</i>	BA46	2.25E-07	0.000696	3.43E-07	increasing	0
<i>CHCHD7</i>	BA46	5.32E-06	0.00069	1.07E-07	increasing	0
<i>CHD3</i>	BA46	2.43E-13	-0.00085	3.02E-12	decreasing	0
<i>CHD6</i>	BA46	1.13E-15	0.000867	3.68E-13	increasing	0
<i>CHI3L1</i>	BA46	3.32E-11	0.000704	1.26E-07	increasing	0
<i>CHN2</i>	BA46	5.21E-08	-0.00045	0.001806	other	0
<i>CHRM2</i>	BA46	3.50E-08	-0.00054	0.000104	other	0
<i>CHRNA2</i>	BA46	3.84E-06	-0.00075	2.15E-08	decreasing	0
<i>CHRNA7</i>	BA46	3.11E-08	0.0003	0.042543	other	0
<i>CIRBP</i>	BA46	1.30E-07	0.000103	0.495659	other	0
<i>CISD3</i>	BA46	1.97E-07	0.000425	0.003135	other	0
<i>CIT</i>	BA46	1.58E-08	0.00069	2.24E-07	increasing	0
<i>CLASP2</i>	BA46	2.74E-08	-0.00062	5.02E-06	decreasing	0
<i>CLCN5</i>	BA46	1.13E-06	0.000712	6.81E-08	increasing	0
<i>CLDND1</i>	BA46	2.82E-10	0.000833	3.39E-11	increasing	0
<i>CLIC6</i>	BA46	6.15E-08	3.43E-05	0.818838	other	0
<i>CLK4</i>	BA46	2.00E-07	-0.00065	2.82E-06	decreasing	0
<i>CLMP</i>	BA46	9.83E-08	-0.00015	0.322998	other	0
<i>CLN6</i>	BA46	9.61E-09	0.00077	1.35E-09	increasing	0
<i>CLOCK</i>	BA46	7.90E-08	-0.00079	2.35E-09	decreasing	0
<i>CMYA5</i>	BA46	2.40E-14	0.000812	2.61E-11	increasing	1
<i>CNDP1</i>	BA46	1.08E-15	0.00087	1.47E-12	increasing	0
<i>CNP</i>	BA46	6.28E-08	0.000697	1.21E-07	increasing	0
<i>CNTN2</i>	BA46	2.37E-15	0.00087	1.76E-12	increasing	0
<i>CNTN3</i>	BA46	1.45E-08	-0.00069	2.57E-07	decreasing	0
<i>CNTNAP1</i>	BA46	1.99E-07	0.00042	0.003574	other	0
<i>CNTNAP5</i>	BA46	1.55E-07	-0.00068	5.16E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>COBLL1</i>	BA46	1.49E-07	-0.00069	5.52E-07	decreasing	0
<i>COCH</i>	BA46	1.61E-13	-0.00083	3.53E-11	decreasing	0
<i>COG2</i>	BA46	2.78E-08	0.000713	6.50E-08	increasing	0
<i>COG5</i>	BA46	6.67E-07	0.000747	8.97E-09	increasing	0
<i>COL19A1</i>	BA46	1.24E-08	-0.00032	0.031876	other	0
<i>COL22A1</i>	BA46	6.96E-06	-0.00071	1.15E-07	decreasing	0
<i>COL23A1</i>	BA46	1.06E-10	-0.00012	0.418085	other	0
<i>COL26A1</i>	BA46	2.14E-15	-0.00088	1.29E-13	decreasing	0
<i>COL4A1</i>	BA46	1.83E-15	-0.00084	4.36E-12	decreasing	0
<i>COL4A2</i>	BA46	1.98E-15	-0.00085	9.22E-13	decreasing	0
<i>COL5A2</i>	BA46	1.45E-12	-0.00085	2.06E-11	decreasing	0
<i>COL5A3</i>	BA46	2.57E-08	-0.00056	7.99E-05	decreasing	0
<i>COL8A1</i>	BA46	1.15E-07	0.000801	6.20E-10	increasing	0
<i>COLQ</i>	BA46	2.02E-11	0.000821	1.29E-10	increasing	1
<i>COMMD2</i>	BA46	1.89E-07	-0.0005	0.000455	other	0
<i>COQ10A</i>	BA46	7.08E-08	-0.00059	2.66E-05	decreasing	0
<i>CPB1</i>	BA46	2.17E-15	0.000841	1.21E-13	increasing	0
<i>CPEB1</i>	BA46	1.08E-17	0.000882	7.48E-14	increasing	0
<i>CPEB3</i>	BA46	3.52E-06	0.000713	1.53E-07	increasing	0
<i>CPLX1</i>	BA46	1.51E-09	0.000698	1.44E-07	increasing	0
<i>CPNE6</i>	BA46	2.32E-08	-0.00072	7.06E-08	decreasing	0
<i>CREBRF</i>	BA46	8.32E-18	0.000896	3.06E-14	increasing	0
<i>CRH</i>	BA46	3.25E-10	-0.00079	9.93E-10	decreasing	0
<i>CRHBP</i>	BA46	2.51E-07	-0.00062	7.47E-06	decreasing	0
<i>CRISPLD1</i>	BA46	1.99E-11	-0.00072	1.64E-08	decreasing	0
<i>CRKL</i>	BA46	2.39E-12	0.000821	2.85E-11	increasing	0
<i>CRMP1</i>	BA46	1.36E-12	-0.00078	5.52E-10	decreasing	0
<i>CRTAC1</i>	BA46	2.62E-09	-0.00077	3.97E-09	decreasing	0
<i>CRYAB</i>	BA46	1.58E-11	0.000775	9.40E-10	increasing	0
<i>CRYL1</i>	BA46	5.90E-08	0.000578	3.07E-05	increasing	0
<i>CSDC2</i>	BA46	3.64E-12	-0.00081	2.49E-10	decreasing	0
<i>CSF1R</i>	BA46	3.18E-07	-0.00074	3.74E-08	decreasing	0
<i>CSMD2</i>	BA46	9.91E-18	-0.00086	3.84E-13	decreasing	0
<i>CSPG5</i>	BA46	6.29E-10	-0.00079	6.53E-10	decreasing	0
<i>CSRNP3</i>	BA46	1.86E-08	1.11E-05	0.941096	other	0
<i>CSRP2</i>	BA46	8.39E-09	-0.00066	8.16E-07	decreasing	0
<i>CST6</i>	BA46	4.67E-08	0.000765	9.91E-10	increasing	0
<i>CTDSPL2</i>	BA46	3.50E-08	3.40E-05	0.822225	other	0
<i>CTIF</i>	BA46	5.31E-08	0.000675	6.29E-07	increasing	0
<i>CTNNA2</i>	BA46	1.74E-10	-0.00076	6.35E-09	decreasing	0

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<i>CTNNA3</i>	BA46	9.41E-12	0.000815	1.95E-11	increasing	0
<i>CTNNBIP1</i>	BA46	2.39E-11	-0.00083	4.33E-11	decreasing	0
<i>CTSB</i>	BA46	1.21E-07	-0.00064	3.92E-06	decreasing	0
<i>CTSV</i>	BA46	7.07E-06	-0.00068	2.54E-07	decreasing	0
<i>CTXN2</i>	BA46	4.72E-09	0.000744	7.65E-09	increasing	0
<i>CTXN3</i>	BA46	2.94E-09	0.00046	0.001537	other	0
<i>CUX2</i>	BA46	6.41E-06	-0.00071	1.19E-07	decreasing	0
<i>CWF19L2</i>	BA46	5.28E-14	0.000874	6.79E-13	increasing	0
<i>CX3CL1</i>	BA46	3.13E-12	-0.00084	4.75E-11	decreasing	0
<i>CX3CR1</i>	BA46	1.38E-06	-0.00073	7.85E-08	decreasing	0
<i>CXADR</i>	BA46	1.03E-12	-0.00079	6.17E-10	decreasing	0
<i>CXCL12</i>	BA46	8.86E-14	-0.00085	2.07E-11	decreasing	0
<i>CXCL14</i>	BA46	1.57E-07	-0.00071	9.01E-08	decreasing	0
<i>CYFIP1</i>	BA46	8.04E-13	-0.0008	8.79E-11	decreasing	1
<i>CYGB</i>	BA46	7.57E-10	0.000752	1.05E-08	increasing	0
<i>CYTH3</i>	BA46	7.09E-11	-0.00069	2.43E-07	decreasing	0
<i>CYTH4</i>	BA46	9.42E-08	-0.00075	1.39E-08	decreasing	0
<i>DAAM1</i>	BA46	1.22E-07	-0.00057	3.55E-05	decreasing	0
<i>DAB1</i>	BA46	7.02E-10	-0.00082	9.15E-11	decreasing	0
<i>DAB2IP</i>	BA46	7.57E-08	-0.00076	1.05E-08	decreasing	0
<i>DACT2</i>	BA46	8.18E-12	0.000751	8.17E-09	increasing	1
<i>DACT3</i>	BA46	1.91E-07	-0.00072	8.56E-08	decreasing	0
<i>DAGLB</i>	BA46	7.37E-12	0.000839	9.55E-12	increasing	0
<i>DCAF7</i>	BA46	8.27E-08	-0.00079	1.88E-09	decreasing	0
<i>DCAF8</i>	BA46	7.52E-09	0.000779	1.02E-09	increasing	0
<i>DCLK1</i>	BA46	1.96E-10	-0.00072	7.03E-08	decreasing	0
<i>DCLK3</i>	BA46	7.26E-12	-0.00077	2.92E-09	decreasing	0
<i>DCUN1D5</i>	BA46	3.36E-08	-0.00063	5.57E-06	decreasing	0
<i>DCX</i>	BA46	6.97E-08	-0.00051	0.000235	other	0
<i>DDN</i>	BA46	2.69E-09	-0.00046	0.001313	other	0
<i>DDOST</i>	BA46	9.54E-08	-0.0001	0.493878	other	0
<i>DDRKG1</i>	BA46	9.18E-10	0.000249	0.093878	other	0
<i>DDX21</i>	BA46	3.38E-08	-0.00066	9.87E-07	decreasing	0
<i>DDX24</i>	BA46	3.31E-09	0.000786	1.19E-09	increasing	0
<i>DEPDC5</i>	BA46	1.33E-10	0.000804	4.74E-10	increasing	0
<i>DESI1</i>	BA46	2.31E-07	-0.00073	5.75E-08	decreasing	0
<i>DFNA5</i>	BA46	2.61E-06	-0.00069	8.92E-08	decreasing	0
<i>DGCR2</i>	BA46	2.07E-06	0.000713	1.26E-07	increasing	0
<i>DGKA</i>	BA46	2.76E-13	0.000849	7.42E-12	increasing	0
<i>DGKB</i>	BA46	1.19E-12	0.000259	0.076945	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>DGKD</i>	BA46	4.07E-19	-0.00084	1.56E-12	decreasing	0
<i>DGKI</i>	BA46	8.64E-09	-8.47E-06	0.955536	other	0
<i>DGKZ</i>	BA46	1.66E-08	-0.00032	0.026718	other	0
<i>DHDH</i>	BA46	2.84E-08	0.00075	2.75E-09	increasing	0
<i>DHRS7C</i>	BA46	3.11E-06	0.000761	1.25E-08	increasing	0
<i>DIO2</i>	BA46	2.48E-16	-0.00091	8.68E-14	decreasing	0
<i>DKK3</i>	BA46	1.54E-09	0.000812	4.75E-10	increasing	0
<i>DLG2</i>	BA46	1.47E-12	-0.00086	6.66E-12	decreasing	0
<i>DMD</i>	BA46	3.46E-08	-9.26E-05	0.535304	other	0
<i>DMKN</i>	BA46	4.10E-09	0.000737	5.77E-09	increasing	0
<i>DNAH11</i>	BA46	2.23E-08	-0.00065	1.13E-06	decreasing	0
<i>DNAJA4</i>	BA46	1.89E-10	0.000837	7.39E-11	increasing	0
<i>DNAJB5</i>	BA46	1.29E-13	-0.00086	6.33E-13	decreasing	0
<i>DNAJC21</i>	BA46	3.54E-09	0.000662	1.04E-06	increasing	0
<i>DNAL1</i>	BA46	4.71E-12	-0.00085	1.05E-11	decreasing	0
<i>DNER</i>	BA46	6.91E-10	-0.00057	4.49E-05	decreasing	0
<i>DNM1</i>	BA46	9.77E-09	0.00068	4.30E-07	increasing	0
<i>DNM3</i>	BA46	1.22E-06	0.000729	3.15E-08	increasing	0
<i>DNMBP</i>	BA46	1.03E-07	0.00056	4.01E-05	increasing	0
<i>DOC2A</i>	BA46	1.20E-08	0.000764	9.27E-09	increasing	0
<i>DOCK5</i>	BA46	3.34E-10	0.000776	8.67E-10	increasing	0
<i>DOCK9</i>	BA46	3.31E-17	-0.00086	2.69E-13	decreasing	0
<i>DOK4</i>	BA46	1.47E-09	-0.00067	3.87E-07	decreasing	0
<i>DOK5</i>	BA46	4.31E-12	-0.00077	1.17E-09	decreasing	0
<i>DPF2</i>	BA46	3.72E-06	0.000725	9.51E-08	increasing	0
<i>DPYS</i>	BA46	5.72E-10	0.000744	1.47E-08	increasing	0
<i>DPYSL3</i>	BA46	7.08E-19	-0.00089	3.74E-14	decreasing	0
<i>DPYSL5</i>	BA46	9.44E-16	-0.00087	4.52E-13	decreasing	0
<i>DRAXIN</i>	BA46	1.49E-07	-0.00051	0.000287	other	0
<i>DRD2</i>	BA46	3.12E-06	-0.00072	8.53E-08	decreasing	0
<i>DSG3</i>	BA46	5.81E-08	-0.00063	4.32E-06	decreasing	1
<i>DSTYK</i>	BA46	4.14E-07	0.000737	3.49E-08	increasing	0
<i>DTNA</i>	BA46	7.49E-08	-0.00045	0.001532	other	0
<i>DTX4</i>	BA46	1.86E-14	-0.00085	2.36E-12	decreasing	0
<i>DUSP16</i>	BA46	1.03E-09	0.000518	0.000175	other	0
<i>DUSP18</i>	BA46	3.44E-06	-0.00072	5.25E-08	decreasing	1
<i>DUSP7</i>	BA46	2.71E-06	-0.00074	3.31E-08	decreasing	0
<i>DYRK2</i>	BA46	8.61E-15	-0.00085	5.06E-12	decreasing	0
<i>DYRK3</i>	BA46	7.48E-13	-0.00082	5.04E-11	decreasing	0
<i>EEF2</i>	BA46	3.08E-07	-0.00078	3.26E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>EFHD2</i>	BA46	2.53E-19	0.000901	1.72E-14	increasing	0
<i>EFNA5</i>	BA46	7.70E-06	-0.00072	1.22E-07	decreasing	0
<i>EHD3</i>	BA46	5.02E-10	0.000694	2.08E-07	increasing	0
<i>EIF4A1</i>	BA46	1.80E-07	-0.00035	0.015972	other	0
<i>EIF4B</i>	BA46	1.45E-08	0.000673	1.22E-06	increasing	0
<i>ELK1</i>	BA46	1.97E-08	0.000655	1.26E-06	increasing	0
<i>ELMO1</i>	BA46	9.13E-09	0.000493	0.00046	other	0
<i>EMCN</i>	BA46	1.12E-08	-0.00076	1.75E-08	decreasing	0
<i>EMILIN3</i>	BA46	8.54E-17	0.000875	3.03E-13	increasing	0
<i>EML2</i>	BA46	1.62E-07	0.000785	1.42E-09	increasing	0
<i>EML4</i>	BA46	1.87E-07	-0.00011	0.458111	other	0
<i>EML6</i>	BA46	1.19E-07	0.000217	0.139402	other	0
<i>ENAH</i>	BA46	5.04E-12	-0.00083	1.13E-10	decreasing	0
<i>ENDOD1</i>	BA46	1.13E-09	0.000806	2.43E-10	increasing	0
<i>ENOX1</i>	BA46	1.32E-12	-0.00077	1.68E-09	decreasing	0
<i>ENPP2</i>	BA46	5.88E-11	0.000804	1.10E-10	increasing	0
<i>ENTPD3</i>	BA46	6.62E-07	0.000757	1.43E-08	increasing	0
<i>EPAS1</i>	BA46	6.15E-09	-0.00055	6.82E-05	decreasing	0
<i>EPB41</i>	BA46	2.35E-13	0.00083	1.26E-11	increasing	0
<i>EPB41L2</i>	BA46	1.15E-10	-1.54E-05	0.917516	other	0
<i>EPB41L4B</i>	BA46	1.68E-07	0.000121	0.40714	other	0
<i>EPDR1</i>	BA46	1.51E-10	0.000675	3.74E-07	increasing	0
<i>EPHA5</i>	BA46	1.31E-13	-0.00085	7.28E-12	decreasing	0
<i>EPHA6</i>	BA46	1.43E-06	-0.00072	6.52E-08	decreasing	0
<i>EPHB1</i>	BA46	5.73E-06	-0.00071	1.82E-07	decreasing	0
<i>EPHB2</i>	BA46	2.46E-12	-0.00082	7.38E-11	decreasing	0
<i>EPHB3</i>	BA46	2.41E-07	-0.00076	1.40E-08	decreasing	0
<i>EPHB6</i>	BA46	1.41E-09	0.000738	2.45E-08	increasing	0
<i>EPHX4</i>	BA46	2.00E-07	0.000706	7.23E-08	increasing	0
<i>EPM2A</i>	BA46	6.41E-06	0.000735	2.91E-08	increasing	0
<i>EPN2</i>	BA46	1.69E-08	-0.00077	6.97E-09	decreasing	0
<i>EPN3</i>	BA46	1.10E-15	0.00088	5.64E-13	increasing	0
<i>EPX</i>	BA46	1.50E-07	0.000457	0.001925	other	0
<i>ERGIC1</i>	BA46	7.95E-13	-0.00087	2.36E-12	decreasing	0
<i>ERMN</i>	BA46	1.32E-13	0.00083	7.13E-12	increasing	0
<i>ERMP1</i>	BA46	5.59E-06	0.000686	2.19E-07	increasing	0
<i>ESYT3</i>	BA46	1.32E-12	0.0008	3.69E-10	increasing	0
<i>ETNK2</i>	BA46	5.07E-06	-0.00076	9.04E-09	decreasing	0
<i>ETNPPL</i>	BA46	2.98E-08	0.000531	0.00014	other	0
<i>ETS1</i>	BA46	2.21E-10	-0.00075	1.77E-08	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ETS2</i>	BA46	6.77E-15	0.000858	1.70E-12	increasing	0
<i>ETV4</i>	BA46	7.60E-09	-0.00079	2.14E-09	decreasing	0
<i>EVL</i>	BA46	6.54E-11	-0.00083	1.56E-11	decreasing	0
<i>EXPH5</i>	BA46	1.75E-09	-0.00043	0.00285	other	0
<i>EXT1</i>	BA46	1.23E-10	-0.00076	4.58E-09	decreasing	0
<i>EXTL2</i>	BA46	2.00E-07	0.00039	0.008039	other	0
<i>EZH1</i>	BA46	3.11E-17	0.000883	6.84E-14	increasing	0
<i>EZR</i>	BA46	5.23E-08	-0.00074	2.67E-08	decreasing	0
<i>FABP3</i>	BA46	3.72E-08	-0.00048	0.000793	other	0
<i>FAIM3</i>	BA46	6.81E-05	-0.00071	2.19E-07	decreasing	0
<i>FAM102B</i>	BA46	3.01E-13	-0.00083	2.63E-11	decreasing	0
<i>FAM110B</i>	BA46	5.01E-09	-0.00032	0.027889	other	0
<i>FAM110C</i>	BA46	2.32E-08	0.000651	1.74E-06	increasing	0
<i>FAM115A</i>	BA46	1.17E-08	0.000765	8.75E-09	increasing	0
<i>FAM117A</i>	BA46	2.35E-07	0.000591	2.39E-05	increasing	0
<i>FAM131B</i>	BA46	3.92E-09	0.000761	1.02E-08	increasing	0
<i>FAM132A</i>	BA46	2.10E-08	0.00058	3.99E-05	increasing	0
<i>FAM133B</i>	BA46	5.59E-06	0.000701	2.46E-07	increasing	0
<i>FAM13A</i>	BA46	6.60E-07	0.000735	3.61E-08	increasing	0
<i>FAM155B</i>	BA46	2.77E-08	-0.0008	6.56E-10	decreasing	0
<i>FAM159B</i>	BA46	2.24E-08	-0.00058	2.99E-05	decreasing	0
<i>FAM171A1</i>	BA46	3.30E-11	0.000847	3.16E-11	increasing	0
<i>FAM172A</i>	BA46	1.43E-07	-0.00064	4.75E-06	decreasing	0
<i>FAM177A1</i>	BA46	2.31E-07	-0.00065	3.25E-06	decreasing	0
<i>FAM184A</i>	BA46	2.89E-09	-0.0007	1.27E-07	decreasing	0
<i>FAM189B</i>	BA46	9.60E-06	0.000698	1.73E-07	increasing	0
<i>FAM195B</i>	BA46	2.46E-07	-0.00072	6.43E-08	decreasing	0
<i>FAM196A</i>	BA46	7.60E-08	-0.00028	0.055028	other	1
<i>FAM19A1</i>	BA46	7.42E-13	-0.0008	4.12E-10	decreasing	0
<i>FAM207A</i>	BA46	5.04E-08	0.000448	0.001777	other	0
<i>FAM210B</i>	BA46	2.36E-07	5.79E-05	0.692882	other	0
<i>FAM212B</i>	BA46	1.61E-07	-0.00064	5.74E-06	decreasing	0
<i>FAM213A</i>	BA46	1.07E-12	0.000789	6.62E-10	increasing	0
<i>FAM53B</i>	BA46	1.53E-08	0.00068	4.76E-07	increasing	0
<i>FAM57B</i>	BA46	2.32E-07	-0.00075	1.21E-08	decreasing	0
<i>FAM65B</i>	BA46	1.68E-14	-0.0008	1.39E-10	decreasing	0
<i>FAM78A</i>	BA46	7.03E-08	0.000296	0.045238	other	0
<i>FAM81A</i>	BA46	4.26E-10	0.000318	0.026962	other	0
<i>FAM84B</i>	BA46	3.29E-08	-0.00069	2.52E-07	decreasing	0
<i>FARP1</i>	BA46	1.94E-09	-0.00067	5.83E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FARP2</i>	BA46	1.51E-10	-2.44E-05	0.869422	other	0
<i>FAT4</i>	BA46	9.61E-08	-0.00025	0.087362	other	0
<i>FBLIM1</i>	BA46	9.79E-08	-0.00065	1.50E-06	decreasing	1
<i>FBXO10</i>	BA46	2.50E-12	-0.00079	1.35E-09	decreasing	0
<i>FBXO2</i>	BA46	5.17E-09	0.000573	4.06E-05	increasing	1
<i>FBXO21</i>	BA46	3.00E-08	0.000689	5.81E-07	increasing	0
<i>FBXO33</i>	BA46	2.69E-09	0.000816	4.10E-11	increasing	0
<i>FCN3</i>	BA46	2.59E-10	0.000138	0.346092	other	0
<i>FEM1C</i>	BA46	3.61E-13	0.000797	3.77E-10	increasing	1
<i>FERD3L</i>	BA46	1.91E-13	0.000829	8.38E-11	increasing	0
<i>FGD3</i>	BA46	8.54E-14	-0.00081	6.69E-11	decreasing	0
<i>FGD4</i>	BA46	1.11E-08	-0.00067	6.34E-07	decreasing	0
<i>FGF1</i>	BA46	6.58E-09	0.000632	2.84E-06	increasing	0
<i>FGF11</i>	BA46	1.48E-13	-0.00086	3.32E-12	decreasing	0
<i>FGF13</i>	BA46	2.38E-10	-0.00084	6.88E-11	decreasing	0
<i>FHL1</i>	BA46	1.83E-08	0.000177	0.229503	other	0
<i>FIBCD1</i>	BA46	2.71E-08	-0.00033	0.02136	other	0
<i>FJX1</i>	BA46	4.09E-08	-0.00067	6.25E-07	decreasing	0
<i>FKBP1B</i>	BA46	1.38E-07	-0.00064	2.53E-06	decreasing	0
<i>FLYWCH1</i>	BA46	1.45E-08	0.00076	3.91E-09	increasing	0
<i>FMNL1</i>	BA46	1.40E-09	-0.00071	1.59E-07	decreasing	0
<i>FNBP1L</i>	BA46	8.47E-11	-0.00075	2.25E-09	decreasing	0
<i>FNDC4</i>	BA46	1.45E-11	0.000724	4.26E-08	increasing	0
<i>FOSB</i>	BA46	1.52E-09	0.000589	2.70E-05	increasing	0
<i>FOXI3</i>	BA46	4.17E-10	-0.00077	3.27E-10	decreasing	0
<i>FOXO3</i>	BA46	1.85E-08	0.000717	6.16E-08	increasing	0
<i>FOXO6</i>	BA46	1.15E-09	-0.00075	4.01E-09	decreasing	0
<i>FOXP1</i>	BA46	2.39E-07	-0.00046	0.001458	other	0
<i>FREM3</i>	BA46	2.98E-10	0.000147	0.31413	other	0
<i>FRMD3</i>	BA46	4.11E-11	-0.00061	8.91E-06	decreasing	0
<i>FRMD4A</i>	BA46	3.46E-10	-0.00079	4.10E-10	decreasing	0
<i>FSTL5</i>	BA46	1.01E-09	-0.0007	1.58E-07	decreasing	0
<i>FUT8</i>	BA46	7.33E-13	-0.00083	1.18E-11	decreasing	0
<i>FZD7</i>	BA46	5.52E-06	0.000696	1.27E-07	increasing	0
<i>GAB1</i>	BA46	1.48E-09	0.000786	6.63E-10	increasing	0
<i>GABPB2</i>	BA46	9.18E-08	0.000775	2.17E-09	increasing	0
<i>GABRA2</i>	BA46	9.19E-08	-0.00068	8.62E-07	decreasing	0
<i>GABRA5</i>	BA46	9.82E-13	-0.00079	7.95E-10	decreasing	0
<i>GABRB1</i>	BA46	1.05E-07	-0.0005	0.000456	other	0
<i>GABRG2</i>	BA46	3.76E-08	0.000749	2.04E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GAL3ST2</i>	BA46	5.84E-07	0.000754	1.02E-08	increasing	0
<i>GALNS</i>	BA46	2.92E-08	0.000116	0.442777	other	0
<i>GALNT13</i>	BA46	5.22E-08	-0.00014	0.359876	other	0
<i>GALNT14</i>	BA46	6.58E-08	-0.00079	1.26E-09	decreasing	0
<i>GALNT5</i>	BA46	6.63E-10	0.000809	1.68E-10	increasing	0
<i>GALNT9</i>	BA46	1.07E-07	-0.00027	0.064127	other	0
<i>GALT</i>	BA46	1.42E-07	-0.0006	7.99E-06	decreasing	0
<i>GAS2L3</i>	BA46	6.42E-08	-0.00063	5.80E-06	decreasing	0
<i>GATA4</i>	BA46	1.15E-08	-0.00012	0.418909	other	0
<i>GBGT1</i>	BA46	2.34E-08	0.000663	1.10E-06	increasing	0
<i>GCNT4</i>	BA46	1.53E-08	0.000492	0.000389	other	0
<i>GDAP2</i>	BA46	4.46E-10	0.000688	2.97E-07	increasing	0
<i>GDF10</i>	BA46	5.47E-09	-0.0003	0.042336	other	0
<i>GFOD1</i>	BA46	4.33E-10	0.000788	5.51E-10	increasing	0
<i>GFPT1</i>	BA46	2.90E-08	-0.00062	7.38E-06	decreasing	0
<i>GGNBP2</i>	BA46	1.92E-07	0.000766	4.45E-09	increasing	0
<i>GIGYF1</i>	BA46	4.30E-06	0.000717	9.91E-08	increasing	0
<i>GJA3</i>	BA46	9.92E-09	-0.00041	0.004678	other	0
<i>GJB1</i>	BA46	1.33E-10	0.00075	5.08E-09	increasing	0
<i>GJB5</i>	BA46	1.45E-09	-4.80E-05	0.748395	other	0
<i>GJC1</i>	BA46	1.57E-09	-0.00067	3.68E-07	decreasing	0
<i>GLCC1</i>	BA46	5.06E-06	0.000698	2.40E-07	increasing	0
<i>GLDC</i>	BA46	7.67E-08	-0.00047	0.0011	other	0
<i>GLP2R</i>	BA46	1.04E-18	0.00085	6.31E-12	increasing	0
<i>GLS</i>	BA46	2.23E-07	0.000611	8.41E-06	increasing	0
<i>GLYR1</i>	BA46	5.20E-08	-0.0005	0.000389	other	0
<i>GMIP</i>	BA46	1.45E-13	0.000861	5.22E-12	increasing	0
<i>GNA14</i>	BA46	4.03E-12	0.000699	1.07E-07	increasing	0
<i>GNAQ</i>	BA46	6.83E-09	-0.00072	3.33E-08	decreasing	0
<i>GNAZ</i>	BA46	3.37E-12	-0.00084	9.61E-12	decreasing	0
<i>GNB4</i>	BA46	2.17E-16	-0.00088	8.82E-14	decreasing	0
<i>GNL1</i>	BA46	5.46E-06	0.000705	1.68E-07	increasing	0
<i>GNPTAB</i>	BA46	4.17E-18	-0.0009	4.81E-14	decreasing	0
<i>GOT1</i>	BA46	2.13E-08	0.000755	9.00E-09	increasing	0
<i>GP1BB</i>	BA46	6.42E-09	-0.00082	1.70E-10	decreasing	0
<i>GPC6</i>	BA46	1.72E-07	-0.00038	0.008613	other	0
<i>GPD1</i>	BA46	3.14E-11	-0.00078	7.88E-10	decreasing	0
<i>GPD2</i>	BA46	2.83E-09	-0.00075	2.29E-08	decreasing	1
<i>GPNMB</i>	BA46	1.02E-07	0.000178	0.233707	other	0
<i>GPR116</i>	BA46	2.15E-08	-0.00077	8.40E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GPR12</i>	BA46	2.14E-09	0.000222	0.125701	other	0
<i>GPR155</i>	BA46	1.74E-07	0.000738	1.55E-08	increasing	0
<i>GPR161</i>	BA46	3.95E-08	-0.00034	0.021873	other	0
<i>GPR17</i>	BA46	4.57E-07	-0.00075	2.28E-08	decreasing	0
<i>GPR21</i>	BA46	1.48E-12	-0.00075	7.03E-09	decreasing	0
<i>GPR26</i>	BA46	5.81E-13	-0.00085	2.16E-11	decreasing	0
<i>GPR37</i>	BA46	1.98E-07	0.000553	6.63E-05	increasing	0
<i>GPR83</i>	BA46	5.93E-14	0.000768	2.31E-09	increasing	0
<i>GPR88</i>	BA46	3.24E-09	0.000171	0.253034	other	0
<i>GPRASP1</i>	BA46	1.06E-10	0.000847	3.13E-11	increasing	0
<i>GPRASP2</i>	BA46	1.61E-07	0.000674	1.17E-06	increasing	0
<i>GPRIN1</i>	BA46	1.30E-07	-0.00057	3.77E-05	decreasing	0
<i>GPX1</i>	BA46	1.65E-06	0.000704	1.55E-07	increasing	0
<i>GRAMD4</i>	BA46	3.63E-11	-0.00079	1.30E-09	decreasing	0
<i>GRAP2</i>	BA46	5.09E-08	-0.00079	9.84E-10	decreasing	0
<i>GREB1</i>	BA46	4.48E-08	0.00013	0.378179	other	0
<i>GREB1L</i>	BA46	6.68E-07	0.00073	2.47E-08	increasing	0
<i>GRIA4</i>	BA46	4.35E-08	-0.00066	1.46E-06	decreasing	0
<i>GRID2</i>	BA46	7.52E-09	-0.00076	1.22E-08	decreasing	0
<i>GRIK1</i>	BA46	5.73E-08	-0.00074	3.37E-08	decreasing	0
<i>GRIK3</i>	BA46	1.65E-09	-0.00062	5.31E-06	decreasing	0
<i>GRIK4</i>	BA46	3.36E-08	-0.00054	0.000205	other	0
<i>GRIN2A</i>	BA46	7.13E-08	-0.00072	1.46E-07	decreasing	0
<i>GRIN2B</i>	BA46	5.46E-11	-0.00078	1.29E-09	decreasing	0
<i>GRIN3A</i>	BA46	4.69E-12	-0.00078	8.31E-10	decreasing	0
<i>GRIP1</i>	BA46	2.34E-07	-0.00032	0.031353	other	0
<i>GRM1</i>	BA46	1.67E-07	0.000701	2.36E-07	increasing	1
<i>GRM2</i>	BA46	7.31E-08	-0.00038	0.010364	other	0
<i>GRM3</i>	BA46	2.60E-07	-0.0008	1.21E-09	decreasing	0
<i>GRM5</i>	BA46	2.05E-07	-0.00049	0.000581	other	0
<i>GRM7</i>	BA46	1.41E-13	-0.00085	4.94E-13	decreasing	0
<i>GRP</i>	BA46	2.18E-14	-0.00086	1.52E-12	decreasing	1
<i>GSE1</i>	BA46	2.82E-09	-0.00027	0.064563	other	0
<i>GSG1L</i>	BA46	2.30E-08	-0.00059	3.11E-05	decreasing	0
<i>GSKIP</i>	BA46	1.31E-09	0.000582	1.69E-05	increasing	0
<i>GSTO1</i>	BA46	4.12E-10	0.000784	5.01E-10	increasing	0
<i>GULP1</i>	BA46	1.10E-11	-0.00074	1.59E-08	decreasing	0
<i>GYG1</i>	BA46	5.99E-06	0.000723	9.71E-08	increasing	0
<i>HABP4</i>	BA46	1.78E-07	0.000335	0.021802	other	0
<i>HACL1</i>	BA46	1.57E-07	0.000666	3.85E-07	increasing	1

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>HAMP</i>	BA46	2.24E-07	0.000641	1.32E-06	increasing	0
<i>HAPLN1</i>	BA46	3.92E-20	-0.0009	3.71E-14	decreasing	0
<i>HAPLN2</i>	BA46	5.52E-13	0.000811	2.21E-10	increasing	0
<i>HAPLN4</i>	BA46	8.03E-17	0.000883	1.96E-13	increasing	0
<i>HAS2</i>	BA46	1.66E-10	-0.00074	4.66E-09	decreasing	0
<i>HAUS5</i>	BA46	9.81E-08	0.000764	8.79E-09	increasing	0
<i>HBP1</i>	BA46	7.10E-05	0.000693	1.48E-07	increasing	0
<i>HCRTR1</i>	BA46	1.65E-08	-0.00074	3.87E-08	decreasing	0
<i>HDAC9</i>	BA46	2.69E-10	-0.0008	3.46E-10	decreasing	0
<i>HECTD2</i>	BA46	3.94E-12	-0.00079	1.77E-10	decreasing	0
<i>HECW2</i>	BA46	1.04E-08	-0.00073	2.99E-08	decreasing	0
<i>HES4</i>	BA46	2.25E-08	-0.00071	6.03E-08	decreasing	0
<i>HHIP</i>	BA46	9.55E-14	0.000849	1.65E-11	increasing	0
<i>HIP1</i>	BA46	4.06E-21	-0.00092	2.65E-15	decreasing	0
<i>HIPK4</i>	BA46	1.19E-10	0.000758	7.18E-09	increasing	0
<i>HIVEP2</i>	BA46	4.42E-12	-0.00085	1.03E-11	decreasing	0
<i>HIVEP3</i>	BA46	1.19E-06	-0.00075	1.31E-08	decreasing	0
<i>HLF</i>	BA46	4.68E-08	0.000533	0.000128	other	0
<i>HMCN1</i>	BA46	1.09E-07	-0.00074	2.17E-08	decreasing	0
<i>HMGA2</i>	BA46	6.80E-07	-0.0007	1.85E-07	decreasing	0
<i>HMGB2</i>	BA46	2.15E-06	0.000722	6.91E-08	increasing	0
<i>HMGR</i>	BA46	8.22E-10	-0.00072	5.59E-08	decreasing	0
<i>HN1</i>	BA46	1.75E-07	-0.00055	7.38E-05	decreasing	0
<i>HNRNPUL2</i>	BA46	1.02E-07	0.000587	2.39E-05	increasing	0
<i>HOMER1</i>	BA46	1.04E-08	-0.00054	0.000127	other	0
<i>HOMER2</i>	BA46	4.72E-09	-0.00078	2.59E-10	decreasing	1
<i>HOPX</i>	BA46	1.09E-07	0.000697	1.85E-07	increasing	0
<i>HPCAL1</i>	BA46	8.56E-08	0.000315	0.032199	other	0
<i>HPCAL4</i>	BA46	7.91E-09	0.000185	0.20871	other	0
<i>HRH2</i>	BA46	5.81E-08	-0.0001	0.490604	other	0
<i>HS2ST1</i>	BA46	1.97E-08	-0.0008	8.67E-10	decreasing	0
<i>HSBP1</i>	BA46	1.13E-08	-0.00067	6.48E-07	decreasing	0
<i>HSD11B1</i>	BA46	1.26E-06	0.000752	6.25E-09	increasing	0
<i>HSDL1</i>	BA46	4.37E-08	0.000596	2.28E-05	increasing	0
<i>HSF4</i>	BA46	6.10E-12	0.000824	2.11E-11	increasing	0
<i>HSPA1A</i>	BA46	4.15E-08	0.000653	7.51E-07	increasing	0
<i>HSPA1B</i>	BA46	4.80E-08	0.000679	3.86E-07	increasing	0
<i>HSPB8</i>	BA46	2.40E-18	0.000883	3.61E-13	increasing	0
<i>HTR1A</i>	BA46	1.10E-12	0.000749	2.13E-08	increasing	0
<i>HTR1E</i>	BA46	3.18E-13	0.000791	4.62E-10	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>HTR3A</i>	BA46	1.18E-09	0.000735	2.21E-08	increasing	0
<i>HTRA1</i>	BA46	2.32E-06	-0.00073	8.23E-08	decreasing	0
<i>HTRA3</i>	BA46	2.28E-07	-0.00045	0.001565	other	0
<i>HTRA4</i>	BA46	8.71E-08	0.000757	7.66E-09	increasing	0
<i>IDH2</i>	BA46	1.66E-07	-0.00077	3.30E-09	decreasing	0
<i>IFFO1</i>	BA46	9.31E-10	0.000763	2.21E-09	increasing	0
<i>IGF1</i>	BA46	1.38E-10	-0.00076	4.24E-09	decreasing	0
<i>IGF2BP2</i>	BA46	2.45E-08	-0.00056	6.61E-05	decreasing	0
<i>IGF2R</i>	BA46	5.68E-09	-0.00017	0.248159	other	0
<i>IGFBP3</i>	BA46	4.13E-08	-0.0006	1.92E-05	decreasing	0
<i>IGFBPL1</i>	BA46	1.41E-07	-0.00061	8.35E-06	decreasing	0
<i>IGSF3</i>	BA46	7.79E-08	0.000135	0.360788	other	0
<i>IGSF8</i>	BA46	3.89E-08	0.000709	6.03E-08	increasing	0
<i>IGSF9B</i>	BA46	6.35E-08	0.000193	0.197559	other	0
<i>IL12RB2</i>	BA46	4.45E-08	4.56E-05	0.755999	other	0
<i>IL17D</i>	BA46	1.77E-07	0.000402	0.005867	other	0
<i>IL17RD</i>	BA46	2.61E-12	-0.00083	1.37E-11	decreasing	0
<i>IL1RAP</i>	BA46	8.35E-07	-0.00071	8.54E-08	decreasing	0
<i>IL34</i>	BA46	9.22E-10	-0.00077	2.99E-09	decreasing	0
<i>ILDR2</i>	BA46	6.78E-20	-0.00089	1.17E-14	decreasing	0
<i>INPP5A</i>	BA46	7.27E-18	0.000869	9.35E-14	increasing	0
<i>INPP5B</i>	BA46	8.87E-12	0.000807	3.27E-10	increasing	0
<i>INPP5D</i>	BA46	1.02E-08	-0.00062	8.57E-06	decreasing	0
<i>INSM1</i>	BA46	3.51E-08	-0.00072	3.84E-08	decreasing	0
<i>IP6K2</i>	BA46	2.49E-07	0.000104	0.476668	other	0
<i>IPMK</i>	BA46	2.11E-08	-0.00081	4.86E-10	decreasing	0
<i>IPO11</i>	BA46	2.25E-07	0.000635	2.49E-06	increasing	0
<i>IQGAP2</i>	BA46	1.46E-08	-0.00066	1.18E-06	decreasing	0
<i>IRF2</i>	BA46	7.04E-12	0.000827	2.69E-11	increasing	0
<i>IRF5</i>	BA46	6.70E-11	0.000833	5.10E-11	increasing	0
<i>IRF8</i>	BA46	7.24E-08	-0.00071	1.88E-07	decreasing	0
<i>IRS2</i>	BA46	1.90E-07	0.000677	3.41E-07	increasing	0
<i>ISCU</i>	BA46	1.83E-15	0.000852	1.75E-12	increasing	0
<i>ITGA1</i>	BA46	6.52E-08	-0.00073	8.44E-08	decreasing	0
<i>ITGA2B</i>	BA46	8.10E-11	-0.00063	6.12E-06	decreasing	0
<i>ITGA3</i>	BA46	1.81E-16	0.000886	2.11E-13	increasing	0
<i>ITGA4</i>	BA46	1.62E-07	0.000435	0.001976	other	0
<i>ITGA9</i>	BA46	1.76E-12	-0.0008	1.76E-10	decreasing	0
<i>ITGAM</i>	BA46	3.96E-06	-0.00073	8.81E-08	decreasing	0
<i>ITPKB</i>	BA46	1.19E-07	0.000625	4.74E-06	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ITPR1</i>	BA46	1.39E-16	0.000694	1.44E-07	increasing	0
<i>IVNS1ABP</i>	BA46	5.16E-16	-0.00087	3.93E-13	decreasing	0
<i>JADE1</i>	BA46	8.14E-07	0.000747	2.93E-08	increasing	0
<i>JADE2</i>	BA46	1.26E-13	0.000769	2.58E-09	increasing	0
<i>JAKMIP2</i>	BA46	6.03E-10	-0.00075	1.57E-08	decreasing	0
<i>JAM2</i>	BA46	5.66E-05	-0.0007	2.54E-07	decreasing	0
<i>JAZF1</i>	BA46	9.94E-09	-0.00064	1.56E-06	decreasing	0
<i>JMY</i>	BA46	9.25E-10	-0.00021	0.150884	other	0
<i>JPH1</i>	BA46	9.55E-09	0.00044	0.002257	other	0
<i>KBTBD11</i>	BA46	5.18E-10	0.000751	6.99E-09	increasing	0
<i>KBTBD7</i>	BA46	7.13E-08	-3.42E-05	0.82017	other	0
<i>KCNA2</i>	BA46	1.85E-12	0.000826	7.12E-12	increasing	0
<i>KCNA6</i>	BA46	3.50E-08	-0.00072	2.80E-08	decreasing	0
<i>KCNAB2</i>	BA46	3.09E-10	0.000671	5.75E-07	increasing	0
<i>KCNC1</i>	BA46	1.62E-15	0.00084	5.25E-12	increasing	0
<i>KCND3</i>	BA46	2.91E-13	0.000832	1.75E-11	increasing	0
<i>KCNF1</i>	BA46	1.75E-08	-0.00076	3.67E-09	decreasing	0
<i>KCNG1</i>	BA46	7.90E-12	-0.00084	1.07E-11	decreasing	0
<i>KCNH1</i>	BA46	1.29E-07	0.000237	0.10712	other	0
<i>KCNH2</i>	BA46	2.50E-07	8.49E-05	0.571634	other	0
<i>KCNH3</i>	BA46	6.41E-08	-0.00065	3.66E-06	decreasing	0
<i>KCNIP2</i>	BA46	2.28E-10	0.000641	3.58E-06	increasing	0
<i>KCNIP3</i>	BA46	4.43E-11	-0.00069	5.68E-07	decreasing	0
<i>KCNIP4</i>	BA46	9.07E-08	0.000664	1.04E-06	increasing	0
<i>KCNJ11</i>	BA46	4.38E-08	0.000658	1.09E-06	increasing	0
<i>KCNK1</i>	BA46	2.55E-07	0.000575	2.98E-05	increasing	0
<i>KCNN2</i>	BA46	2.81E-08	0.000376	0.010363	other	0
<i>KCNQ2</i>	BA46	3.55E-08	-0.0004	0.00669	other	0
<i>KCNQ3</i>	BA46	1.87E-16	-0.0009	7.39E-14	decreasing	0
<i>KCNQ5</i>	BA46	7.17E-08	0.000279	0.056004	other	0
<i>KCNS1</i>	BA46	1.53E-23	0.000921	6.09E-16	increasing	0
<i>KCNT1</i>	BA46	3.33E-10	0.000694	2.08E-07	increasing	0
<i>KCNT2</i>	BA46	1.10E-17	-0.00088	1.82E-13	decreasing	0
<i>KCTD1</i>	BA46	1.11E-09	0.000154	0.291483	other	0
<i>KCTD16</i>	BA46	8.71E-08	-0.00063	6.68E-06	decreasing	0
<i>KCTD2</i>	BA46	9.52E-10	0.000831	7.24E-11	increasing	0
<i>KCTD9</i>	BA46	7.90E-08	0.000752	8.13E-09	increasing	0
<i>KDM2B</i>	BA46	3.77E-11	-0.0008	2.02E-10	decreasing	0
<i>KDM7A</i>	BA46	1.86E-07	-0.00077	5.80E-09	decreasing	0
<i>KEL</i>	BA46	2.11E-06	0.000728	6.09E-08	increasing	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>KIAA0100</i>	BA46	2.43E-06	-0.00073	8.06E-08	decreasing	0
<i>KIAA0430</i>	BA46	1.26E-08	0.000536	0.000118	other	0
<i>KIAA0513</i>	BA46	3.45E-17	0.000871	1.42E-12	increasing	0
<i>KIAA1045</i>	BA46	3.19E-12	-0.00085	6.37E-12	decreasing	0
<i>KIAA1211</i>	BA46	2.47E-07	-0.00045	0.001736	other	0
<i>KIAA1211L</i>	BA46	8.46E-11	0.00064	2.45E-06	increasing	0
<i>KIAA1549</i>	BA46	1.14E-08	-0.00031	0.035606	other	1
<i>KIAA1598</i>	BA46	1.98E-07	0.000442	0.002454	other	1
<i>KIAA1644</i>	BA46	2.21E-08	-0.0002	0.17551	other	0
<i>KIF21B</i>	BA46	5.65E-19	-0.0009	1.15E-14	decreasing	0
<i>KIF2A</i>	BA46	1.19E-12	-0.00077	1.63E-09	decreasing	0
<i>KIF3C</i>	BA46	3.10E-07	-0.00074	2.06E-08	decreasing	0
<i>KIF5C</i>	BA46	1.84E-12	-0.00086	1.07E-11	decreasing	0
<i>KIRREL</i>	BA46	1.58E-07	-0.00048	0.000633	other	0
<i>KIRREL3</i>	BA46	2.96E-10	-0.00082	5.98E-11	decreasing	0
<i>KISS1R</i>	BA46	3.93E-13	0.000844	1.26E-12	increasing	0
<i>KIZ</i>	BA46	7.69E-09	0.000417	0.003606	other	0
<i>KLF13</i>	BA46	1.41E-10	-0.00085	9.76E-12	decreasing	0
<i>KLF6</i>	BA46	2.59E-07	-0.00069	2.34E-07	decreasing	0
<i>KLF7</i>	BA46	3.36E-11	-0.00076	4.58E-09	decreasing	0
<i>KLF9</i>	BA46	1.02E-10	-0.00077	4.00E-09	decreasing	0
<i>KLHDC9</i>	BA46	1.01E-07	0.000762	4.96E-09	increasing	0
<i>KLHL11</i>	BA46	6.59E-07	0.00075	2.26E-08	increasing	0
<i>KLHL18</i>	BA46	2.33E-07	-0.00055	6.33E-05	decreasing	0
<i>KLHL21</i>	BA46	4.87E-11	0.00083	4.98E-11	increasing	0
<i>KLHL23</i>	BA46	1.50E-09	-0.00068	2.71E-07	decreasing	0
<i>KLHL24</i>	BA46	5.84E-11	0.00068	3.64E-07	increasing	0
<i>KLHL25</i>	BA46	1.82E-09	-0.00077	5.35E-09	decreasing	0
<i>KLHL29</i>	BA46	3.14E-07	-0.00072	4.12E-08	decreasing	0
<i>KLHL32</i>	BA46	4.19E-12	0.000692	2.71E-07	increasing	0
<i>KLHL9</i>	BA46	1.67E-07	1.56E-05	0.917069	other	1
<i>KLK6</i>	BA46	1.88E-10	0.000812	5.71E-11	increasing	0
<i>KMT2A</i>	BA46	1.97E-06	0.000703	1.94E-07	increasing	0
<i>KNCN</i>	BA46	4.57E-05	0.000695	2.53E-07	increasing	0
<i>KPNA3</i>	BA46	3.36E-09	-0.00059	1.99E-05	decreasing	0
<i>KRBOX4</i>	BA46	2.93E-05	0.000725	8.43E-08	increasing	0
<i>KRT7</i>	BA46	9.20E-10	-0.0001	0.500892	other	0
<i>KRT80</i>	BA46	1.10E-07	-1.42E-05	0.92546	other	1
<i>KY</i>	BA46	6.67E-07	0.000712	5.27E-08	increasing	0
<i>L3MBTL1</i>	BA46	1.22E-09	-0.00078	9.33E-10	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LAMA4	BA46	7.39E-08	-0.00054	0.000143	other	0
LAMC1	BA46	1.06E-09	-0.00068	3.39E-07	decreasing	0
LANCL2	BA46	1.87E-09	-0.00074	1.44E-08	decreasing	0
LASP1	BA46	1.30E-07	-0.00078	3.30E-09	decreasing	0
LCORL	BA46	7.25E-16	-0.00084	1.29E-12	decreasing	0
LCP2	BA46	2.88E-06	-0.00076	1.60E-08	decreasing	0
LDB3	BA46	3.94E-15	0.000836	2.26E-11	increasing	0
LDOC1L	BA46	1.14E-07	-0.00043	0.002659	other	0
LGALS8	BA46	2.32E-07	0.000696	4.06E-07	increasing	0
LGI3	BA46	7.04E-17	0.000852	1.64E-12	increasing	0
LGR6	BA46	7.12E-09	-0.00074	2.14E-08	decreasing	0
LHFPL3	BA46	3.07E-14	-0.00087	1.56E-12	decreasing	0
LHFPL5	BA46	8.73E-08	0.000651	2.70E-06	increasing	0
LIMD2	BA46	1.18E-06	-0.00073	1.91E-08	decreasing	0
LINGO4	BA46	6.75E-08	0.000658	1.46E-06	increasing	0
LOC103214744	BA46	8.28E-09	0.000667	1.00E-06	increasing	0
LOC103214965	BA46	2.38E-08	-0.00026	0.073126	other	1
LOC103215127	BA46	3.48E-06	0.00055	9.48E-08	increasing	0
LOC103215262	BA46	2.03E-07	-0.00029	0.053851	other	0
LOC103215364	BA46	4.00E-08	-5.90E-05	0.690935	other	0
LOC103215829	BA46	1.16E-06	-0.00072	5.55E-08	decreasing	0
LOC103215843	BA46	4.64E-09	-0.00068	7.51E-07	decreasing	0
LOC103215951	BA46	1.18E-05	0.000704	1.61E-07	increasing	0
LOC103216062	BA46	1.66E-07	-7.11E-05	0.627942	other	0
LOC103216066	BA46	2.62E-11	0.000759	6.12E-09	increasing	0
LOC103216135	BA46	1.59E-08	0.000498	0.000398	other	0
LOC103216175	BA46	4.82E-09	0.000767	1.68E-09	increasing	1
LOC103216270	BA46	7.83E-08	-0.00052	0.000231	other	0
LOC103216325	BA46	1.34E-08	0.000706	8.52E-08	increasing	0
LOC103216550	BA46	2.47E-07	-0.00072	7.26E-08	decreasing	0
LOC103217195	BA46	2.03E-07	-0.00064	1.50E-06	decreasing	0
LOC103217197	BA46	1.70E-06	-0.00073	1.06E-08	decreasing	0
LOC103217236	BA46	6.08E-08	0.000357	0.016041	other	0
LOC103217966	BA46	1.00E-07	0.000278	0.058185	other	1
LOC103218099	BA46	3.97E-08	-0.00066	2.28E-06	decreasing	0
LOC103218165	BA46	2.66E-09	0.000723	8.73E-08	increasing	0
LOC103218261	BA46	2.53E-08	0.000624	5.49E-06	increasing	1
LOC103218710	BA46	3.67E-09	-0.00071	1.15E-07	decreasing	0
LOC103218716	BA46	2.39E-07	-0.00038	0.0111	other	0
LOC103218887	BA46	7.51E-08	0.000444	0.00166	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103219120	BA46	1.79E-15	-0.00085	1.35E-12	decreasing	0
LOC103219428	BA46	2.41E-07	0.000712	8.01E-08	increasing	0
LOC103219982	BA46	5.47E-10	-0.00072	2.45E-08	decreasing	0
LOC103220245	BA46	2.40E-07	0.000117	0.434963	other	0
LOC103221116	BA46	2.05E-10	0.000717	2.30E-08	increasing	0
LOC103221138	BA46	1.39E-08	0.000777	2.11E-09	increasing	0
LOC103221197	BA46	5.81E-09	0.000178	0.224468	other	0
LOC103221287	BA46	3.83E-11	-0.00079	5.25E-10	decreasing	0
LOC103221291	BA46	1.61E-12	-0.0008	7.55E-10	decreasing	0
LOC103221412	BA46	3.23E-09	0.000795	1.04E-10	increasing	0
LOC103221449	BA46	1.96E-07	-0.00059	1.50E-05	decreasing	0
LOC103221689	BA46	1.47E-05	-0.00071	2.45E-07	decreasing	0
LOC103221863	BA46	2.49E-07	0.000667	6.88E-07	increasing	1
LOC103221933	BA46	2.00E-08	-0.00061	4.81E-06	decreasing	0
LOC103221935	BA46	1.34E-08	-0.00061	4.94E-06	decreasing	0
LOC103221944	BA46	8.34E-09	-0.00057	3.96E-05	decreasing	0
LOC103221945	BA46	1.01E-10	-0.00076	5.28E-09	decreasing	0
LOC103221971	BA46	1.96E-09	0.000192	0.205255	other	0
LOC103221972	BA46	5.49E-08	7.82E-05	0.60266	other	0
LOC103221997	BA46	7.12E-08	-0.0006	1.61E-05	decreasing	0
LOC103221998	BA46	1.77E-07	-0.00049	0.00059	other	0
LOC103222001	BA46	1.90E-07	-0.00049	0.000683	other	0
LOC103222004	BA46	9.51E-10	-0.00064	1.74E-06	decreasing	0
LOC103222006	BA46	1.08E-10	-0.00065	2.38E-06	decreasing	0
LOC103222008	BA46	2.12E-09	-4.53E-05	0.762793	other	0
LOC103222017	BA46	3.67E-09	0.000319	0.033366	other	0
LOC103222020	BA46	3.79E-08	0.000521	0.000286	other	0
LOC103222057	BA46	6.40E-09	-0.00013	0.387705	other	0
LOC103222075	BA46	1.36E-09	-0.00076	1.13E-08	decreasing	0
LOC103222083	BA46	2.53E-11	0.000789	7.09E-11	increasing	0
LOC103222154	BA46	5.09E-08	0.000104	0.490053	other	0
LOC103222274	BA46	6.30E-09	-0.00055	0.000113	other	0
LOC103222280	BA46	5.19E-11	-0.00074	7.48E-09	decreasing	0
LOC103222373	BA46	1.59E-08	-0.00065	1.88E-06	decreasing	0
LOC103222510	BA46	1.26E-11	-0.0008	3.87E-10	decreasing	0
LOC103222548	BA46	1.34E-07	0.000662	1.94E-06	increasing	0
LOC103222563	BA46	4.61E-09	-0.00079	5.45E-10	decreasing	0
LOC103222608	BA46	2.22E-08	0.000514	0.00024	other	0
LOC103222721	BA46	1.43E-08	-0.0007	3.55E-07	decreasing	1
LOC103222800	BA46	2.82E-08	-0.00054	0.000119	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103222940	BA46	3.52E-08	-0.00069	2.88E-07	decreasing	1
LOC103222965	BA46	2.24E-09	0.000691	1.67E-07	increasing	0
LOC103223027	BA46	4.50E-06	0.00068	3.97E-09	increasing	0
LOC103223096	BA46	4.74E-12	-0.00084	7.59E-12	decreasing	0
LOC103223099	BA46	4.50E-13	-0.00083	3.43E-12	decreasing	0
LOC103223177	BA46	8.66E-09	-0.00069	2.13E-07	decreasing	0
LOC103223219	BA46	1.40E-08	0.000612	1.00E-05	increasing	0
LOC103223445	BA46	6.20E-15	-0.00084	3.92E-12	decreasing	0
LOC103223518	BA46	5.31E-08	0.000401	0.005459	other	0
LOC103223600	BA46	1.10E-06	0.000732	9.09E-09	increasing	1
LOC103223617	BA46	1.15E-06	-0.00069	1.44E-07	decreasing	1
LOC103223633	BA46	1.26E-14	-0.00052	0.000208	other	0
LOC103223656	BA46	1.72E-12	-0.00053	0.000123	other	0
LOC103223660	BA46	2.84E-10	-0.00058	3.22E-05	decreasing	0
LOC103223665	BA46	2.05E-07	-0.00023	0.117863	other	0
LOC103224231	BA46	3.22E-14	0.000836	4.82E-12	increasing	0
LOC103224287	BA46	5.65E-10	-0.00077	2.64E-09	decreasing	0
LOC103224382	BA46	2.43E-12	-0.00078	2.10E-09	decreasing	0
LOC103224383	BA46	1.20E-15	-0.00086	1.50E-12	decreasing	0
LOC103224431	BA46	4.99E-13	-0.0008	1.28E-10	decreasing	0
LOC103224456	BA46	1.68E-09	0.00052	0.000162	other	0
LOC103224536	BA46	4.86E-11	-0.0008	8.65E-10	decreasing	0
LOC103224678	BA46	1.63E-07	-0.00074	4.03E-08	decreasing	0
LOC103224735	BA46	1.17E-08	-0.00071	1.22E-07	decreasing	0
LOC103225435	BA46	1.25E-07	-0.00029	0.045631	other	0
LOC103225645	BA46	3.83E-13	0.000822	4.19E-11	increasing	0
LOC103225786	BA46	5.42E-10	-0.00011	0.461591	other	0
LOC103225826	BA46	5.35E-08	-0.00075	3.24E-09	decreasing	0
LOC103225917	BA46	4.65E-06	-0.00073	5.50E-08	decreasing	0
LOC103226050	BA46	2.78E-07	-0.0007	1.46E-07	decreasing	0
LOC103226149	BA46	5.03E-11	0.000849	1.94E-11	increasing	0
LOC103226232	BA46	1.84E-07	-0.00067	8.66E-07	decreasing	1
LOC103226647	BA46	3.33E-08	-0.00067	9.59E-07	decreasing	0
LOC103226670	BA46	2.30E-06	0.000716	1.44E-07	increasing	0
LOC103226908	BA46	1.02E-11	0.000728	1.22E-08	increasing	0
LOC103226909	BA46	1.13E-07	0.000654	1.06E-06	increasing	0
LOC103226929	BA46	6.31E-08	0.000673	4.15E-07	increasing	0
LOC103227909	BA46	3.33E-08	-0.00071	9.74E-08	decreasing	0
LOC103227910	BA46	5.11E-09	-0.00073	2.85E-08	decreasing	0
LOC103227976	BA46	1.02E-07	-0.00031	0.034182	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103228058	BA46	2.86E-09	-0.00065	2.28E-06	decreasing	1
LOC103228345	BA46	6.28E-08	-0.00039	0.006832	other	1
LOC103228593	BA46	1.42E-07	-0.00062	3.88E-06	decreasing	0
LOC103228595	BA46	7.85E-13	-0.00083	1.48E-11	decreasing	0
LOC103228596	BA46	8.21E-07	-0.00075	1.77E-08	decreasing	0
LOC103228598	BA46	5.58E-08	-0.00073	2.84E-08	decreasing	0
LOC103228599	BA46	6.98E-11	-0.00084	2.19E-11	decreasing	0
LOC103228600	BA46	7.11E-08	-0.00071	6.15E-08	decreasing	0
LOC103228601	BA46	4.54E-10	-0.00078	8.49E-10	decreasing	0
LOC103228602	BA46	7.98E-12	-0.00082	4.07E-11	decreasing	0
LOC103228603	BA46	1.40E-09	-0.00079	6.78E-10	decreasing	0
LOC103228604	BA46	8.33E-13	-0.00081	9.36E-11	decreasing	0
LOC103228607	BA46	2.87E-10	-0.00075	1.20E-08	decreasing	0
LOC103228626	BA46	3.20E-10	-0.00083	1.44E-11	decreasing	0
LOC103228749	BA46	3.07E-08	-0.00023	0.118746	other	0
LOC103228897	BA46	4.83E-08	0.000729	5.21E-08	increasing	0
LOC103229137	BA46	2.32E-12	-0.00081	1.72E-10	decreasing	0
LOC103229197	BA46	8.40E-12	-0.00072	2.46E-08	decreasing	0
LOC103229569	BA46	1.87E-09	0.000693	9.14E-08	increasing	0
LOC103229610	BA46	2.12E-09	-0.00073	5.83E-08	decreasing	0
LOC103229611	BA46	1.99E-08	-0.00072	1.14E-07	decreasing	1
LOC103229921	BA46	7.87E-11	-0.00074	1.68E-08	decreasing	0
LOC103230141	BA46	2.08E-07	1.18E-05	0.937602	other	0
LOC103230209	BA46	8.14E-06	-0.00071	1.66E-07	decreasing	1
LOC103230295	BA46	2.44E-07	0.000657	1.42E-06	increasing	0
LOC103230361	BA46	1.75E-07	-0.00071	1.29E-07	decreasing	0
LOC103230633	BA46	6.14E-10	2.85E-06	0.984955	other	0
LOC103230635	BA46	8.06E-09	-4.80E-05	0.746767	other	0
LOC103230650	BA46	1.35E-08	-0.00073	1.32E-08	decreasing	1
LOC103230770	BA46	5.52E-12	0.0008	4.98E-10	increasing	0
LOC103230800	BA46	3.22E-18	-0.0009	4.33E-14	decreasing	0
LOC103231081	BA46	1.58E-09	-0.00076	9.75E-09	decreasing	0
LOC103231153	BA46	1.06E-10	-0.00078	1.96E-09	decreasing	1
LOC103231470	BA46	7.51E-09	0.000651	1.19E-06	increasing	0
LOC103231498	BA46	5.19E-08	-0.00074	2.58E-08	decreasing	0
LOC103231548	BA46	1.28E-10	-0.00077	1.79E-09	decreasing	0
LOC103231593	BA46	1.65E-07	0.000581	3.23E-05	increasing	0
LOC103231987	BA46	4.76E-08	0.000722	8.01E-08	increasing	0
LOC103232002	BA46	5.76E-08	-0.00011	0.473175	other	0
LOC103232043	BA46	4.26E-08	0.000216	0.147582	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103232203	BA46	1.32E-08	0.000742	2.29E-08	increasing	0
LOC103232311	BA46	9.73E-09	-0.00072	2.43E-08	decreasing	0
LOC103232409	BA46	5.55E-07	0.000736	3.81E-08	increasing	0
LOC103232553	BA46	5.00E-08	0.000617	7.44E-06	increasing	0
LOC103232974	BA46	9.29E-08	-0.00049	0.000655	other	0
LOC103233113	BA46	1.17E-10	-0.0008	3.26E-10	decreasing	0
LOC103233444	BA46	3.33E-08	0.000515	0.000234	other	1
LOC103233451	BA46	1.89E-07	0.000703	2.84E-07	increasing	0
LOC103233667	BA46	2.04E-08	0.000694	2.11E-07	increasing	0
LOC103233674	BA46	8.01E-06	-0.00075	1.99E-08	decreasing	0
LOC103233923	BA46	6.17E-07	-0.00078	2.39E-09	decreasing	0
LOC103233961	BA46	6.51E-08	-0.0007	5.22E-08	decreasing	0
LOC103234031	BA46	3.08E-11	0.000772	1.74E-09	increasing	0
LOC103234033	BA46	3.25E-10	-0.00081	2.11E-10	decreasing	0
LOC103234347	BA46	4.23E-11	-0.00064	2.10E-06	decreasing	0
LOC103234469	BA46	4.83E-08	0.000741	3.54E-08	increasing	0
LOC103234618	BA46	1.08E-07	-0.0007	1.18E-07	decreasing	0
LOC103234986	BA46	2.09E-09	0.000652	2.11E-06	increasing	0
LOC103235597	BA46	5.13E-09	-0.00064	2.65E-06	decreasing	0
LOC103235792	BA46	4.81E-06	0.0007	1.43E-07	increasing	0
LOC103236318	BA46	1.38E-07	0.000754	1.27E-08	increasing	0
LOC103236784	BA46	8.49E-08	0.000712	6.41E-08	increasing	0
LOC103236863	BA46	1.97E-09	0.000148	0.325265	other	0
LOC103236930	BA46	5.49E-10	-0.00081	3.32E-10	decreasing	0
LOC103237300	BA46	7.77E-08	-0.00074	6.00E-09	decreasing	0
LOC103237306	BA46	1.76E-06	-0.00071	3.47E-08	decreasing	0
LOC103237374	BA46	3.03E-05	-0.00069	2.09E-07	decreasing	0
LOC103237383	BA46	1.25E-06	-0.00074	2.67E-08	decreasing	0
LOC103237442	BA46	1.23E-05	-0.00071	2.09E-07	decreasing	0
LOC103237464	BA46	2.81E-10	-0.0007	1.40E-07	decreasing	0
LOC103237465	BA46	1.49E-11	-0.00069	3.55E-08	decreasing	0
LOC103237488	BA46	1.31E-07	-0.00047	0.001304	other	0
LOC103237511	BA46	6.90E-16	0.000815	7.32E-11	increasing	0
LOC103237714	BA46	8.07E-09	0.000606	8.81E-06	increasing	0
LOC103237778	BA46	1.83E-07	0.000531	0.000169	other	0
LOC103237807	BA46	1.73E-09	-7.08E-05	0.635606	other	0
LOC103237842	BA46	1.35E-08	-0.00028	0.05356	other	1
LOC103237870	BA46	3.57E-09	-0.00076	2.48E-09	decreasing	0
LOC103237871	BA46	2.83E-09	-0.00074	4.69E-09	decreasing	0
LOC103237872	BA46	4.53E-09	-0.0007	4.54E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103237873</i>	BA46	2.40E-09	-0.00075	2.33E-09	decreasing	0
<i>LOC103238342</i>	BA46	1.73E-13	0.000755	6.55E-09	increasing	0
<i>LOC103239234</i>	BA46	2.35E-08	0.000795	5.39E-10	increasing	0
<i>LOC103239260</i>	BA46	1.07E-09	0.000668	3.49E-07	increasing	0
<i>LOC103239367</i>	BA46	1.74E-11	-0.0008	7.15E-11	decreasing	0
<i>LOC103239368</i>	BA46	5.99E-09	-0.00073	9.61E-09	decreasing	0
<i>LOC103239374</i>	BA46	3.25E-10	-0.00075	1.21E-08	decreasing	0
<i>LOC103239382</i>	BA46	1.10E-09	-0.00011	0.448152	other	0
<i>LOC103239398</i>	BA46	3.76E-08	-0.00064	4.72E-06	decreasing	0
<i>LOC103239420</i>	BA46	7.22E-08	0.000137	0.36223	other	0
<i>LOC103239443</i>	BA46	5.66E-08	-9.13E-05	0.544187	other	0
<i>LOC103239471</i>	BA46	1.69E-08	0.000786	1.82E-09	increasing	0
<i>LOC103239535</i>	BA46	1.13E-09	-0.00082	1.89E-10	decreasing	1
<i>LOC103240196</i>	BA46	1.35E-09	0.000579	3.25E-05	increasing	0
<i>LOC103240214</i>	BA46	1.21E-08	-0.00073	2.20E-08	decreasing	0
<i>LOC103240400</i>	BA46	2.51E-09	0.000621	8.05E-06	increasing	0
<i>LOC103240653</i>	BA46	1.56E-07	-0.00053	2.36E-05	decreasing	0
<i>LOC103240698</i>	BA46	1.64E-06	-0.00072	1.01E-07	decreasing	0
<i>LOC103240889</i>	BA46	1.39E-07	-3.86E-06	0.979662	other	0
<i>LOC103240941</i>	BA46	1.85E-08	-0.00072	6.56E-08	decreasing	0
<i>LOC103241172</i>	BA46	9.70E-08	-0.00062	1.47E-06	decreasing	0
<i>LOC103241174</i>	BA46	5.10E-12	-0.00078	5.69E-10	decreasing	0
<i>LOC103241371</i>	BA46	6.82E-15	-0.00081	4.23E-11	decreasing	0
<i>LOC103241400</i>	BA46	1.03E-06	0.000724	3.71E-09	increasing	0
<i>LOC103241685</i>	BA46	1.45E-12	0.000813	1.12E-10	increasing	0
<i>LOC103241686</i>	BA46	4.12E-08	0.000713	2.92E-08	increasing	0
<i>LOC103242438</i>	BA46	2.59E-07	-0.00069	1.00E-07	decreasing	0
<i>LOC103242583</i>	BA46	5.34E-12	-0.00082	3.95E-11	decreasing	0
<i>LOC103242586</i>	BA46	1.01E-07	-0.00078	1.36E-09	decreasing	0
<i>LOC103242716</i>	BA46	4.73E-08	0.000663	1.47E-06	increasing	0
<i>LOC103242734</i>	BA46	1.56E-09	-0.00071	1.98E-07	decreasing	1
<i>LOC103242748</i>	BA46	1.42E-16	-0.00077	5.67E-09	decreasing	0
<i>LOC103242768</i>	BA46	2.04E-07	-0.00066	1.95E-06	decreasing	0
<i>LOC103242825</i>	BA46	1.87E-09	-0.00035	0.018082	other	0
<i>LOC103242925</i>	BA46	1.11E-08	0.000684	2.35E-07	increasing	0
<i>LOC103243079</i>	BA46	9.80E-16	0.000876	9.03E-13	increasing	0
<i>LOC103243159</i>	BA46	8.98E-11	-0.00077	7.00E-10	decreasing	0
<i>LOC103243177</i>	BA46	2.72E-09	-5.59E-05	0.709057	other	0
<i>LOC103243838</i>	BA46	1.04E-11	-0.00075	9.65E-09	decreasing	0
<i>LOC103243870</i>	BA46	5.30E-06	0.000613	1.41E-07	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103244047</i>	BA46	2.99E-10	0.000702	1.38E-07	increasing	0
<i>LOC103244070</i>	BA46	2.71E-09	0.000702	5.74E-08	increasing	0
<i>LOC103244091</i>	BA46	3.18E-10	0.000734	2.90E-08	increasing	0
<i>LOC103244127</i>	BA46	1.80E-07	0.000464	0.00121	other	0
<i>LOC103244197</i>	BA46	2.39E-07	-0.00035	0.014657	other	0
<i>LOC103244243</i>	BA46	4.81E-10	0.000843	3.10E-11	increasing	0
<i>LOC103244421</i>	BA46	1.17E-10	-0.00081	1.20E-10	decreasing	0
<i>LOC103244468</i>	BA46	8.00E-08	-0.00069	9.26E-08	decreasing	0
<i>LOC103244678</i>	BA46	1.83E-11	-0.00071	4.49E-08	decreasing	0
<i>LOC103244679</i>	BA46	8.36E-10	-0.0008	3.49E-10	decreasing	0
<i>LOC103244751</i>	BA46	5.54E-08	-0.00068	5.44E-07	decreasing	0
<i>LOC103245124</i>	BA46	2.90E-09	0.000661	1.22E-10	increasing	0
<i>LOC103245136</i>	BA46	2.43E-08	0.000725	7.87E-08	increasing	0
<i>LOC103245175</i>	BA46	1.29E-09	-0.00058	3.02E-05	decreasing	0
<i>LOC103245191</i>	BA46	2.53E-07	-0.00065	2.58E-06	decreasing	0
<i>LOC103245291</i>	BA46	7.66E-08	0.000762	4.90E-09	increasing	0
<i>LOC103245629</i>	BA46	2.25E-07	2.00E-05	0.893554	other	0
<i>LOC103245855</i>	BA46	2.32E-08	-0.00057	3.99E-05	decreasing	0
<i>LOC103246030</i>	BA46	7.08E-08	0.00068	8.45E-07	increasing	0
<i>LOC103246386</i>	BA46	4.61E-08	0.000292	0.045208	other	0
<i>LOC103246438</i>	BA46	2.52E-07	-0.00023	0.119512	other	0
<i>LOC103246562</i>	BA46	4.66E-07	0.000723	1.06E-07	increasing	0
<i>LOC103247226</i>	BA46	2.37E-11	0.000628	3.49E-06	increasing	0
<i>LOC103247904</i>	BA46	3.44E-14	-0.00023	0.016166	other	0
<i>LOC103248295</i>	BA46	1.95E-16	0.0008	5.46E-11	increasing	0
<i>LOC103248411</i>	BA46	6.67E-08	0.000504	0.000397	other	0
<i>LOC103248425</i>	BA46	1.46E-08	-0.00077	5.15E-09	decreasing	0
<i>LOC103248740</i>	BA46	2.00E-07	-0.00046	0.001714	other	0
<i>LOC103248801</i>	BA46	3.73E-10	-0.00057	2.28E-05	decreasing	0
<i>LOC103248867</i>	BA46	4.25E-09	-0.00067	2.65E-07	decreasing	0
<i>LOC103248870</i>	BA46	6.22E-08	-0.00067	1.17E-06	decreasing	0
<i>LOC103248873</i>	BA46	1.67E-09	-0.00073	5.70E-08	decreasing	0
<i>LOC103248904</i>	BA46	2.34E-07	-0.00056	8.38E-05	decreasing	0
<i>LONRF1</i>	BA46	1.02E-08	0.000547	6.47E-05	increasing	0
<i>LOXHD1</i>	BA46	5.32E-08	-0.00051	0.00032	other	0
<i>LPA</i>	BA46	4.90E-07	-0.0007	4.73E-08	decreasing	1
<i>LPCAT1</i>	BA46	4.09E-08	-0.00058	1.91E-05	decreasing	0
<i>LPCAT3</i>	BA46	1.68E-07	-0.0006	1.18E-05	decreasing	0
<i>LPHN1</i>	BA46	9.50E-06	-0.0007	2.44E-07	decreasing	0
<i>LPIN1</i>	BA46	1.30E-08	0.000689	3.42E-07	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LRP8</i>	BA46	3.72E-08	-0.0006	9.57E-06	decreasing	1
<i>LRRC16B</i>	BA46	1.61E-15	-0.00086	3.35E-13	decreasing	0
<i>LRRC3B</i>	BA46	1.64E-11	-0.00076	6.53E-09	decreasing	0
<i>LRRC4C</i>	BA46	1.63E-08	-0.00061	8.89E-06	decreasing	0
<i>LRRC7</i>	BA46	1.33E-20	-0.00091	1.67E-14	decreasing	0
<i>LRRK2</i>	BA46	7.01E-08	0.000572	3.34E-05	increasing	0
<i>LRRN3</i>	BA46	8.07E-08	4.25E-05	0.777377	other	0
<i>LRRTM1</i>	BA46	3.88E-10	-0.00079	6.02E-10	decreasing	0
<i>LTBP3</i>	BA46	1.14E-08	0.000794	4.63E-10	increasing	0
<i>LTBP4</i>	BA46	2.02E-07	-0.00077	1.52E-09	decreasing	0
<i>LTK</i>	BA46	1.09E-08	-1.94E-05	0.896674	other	0
<i>LURAP1</i>	BA46	2.08E-08	-0.00074	9.84E-09	decreasing	0
<i>LUZP1</i>	BA46	2.96E-13	0.000807	2.13E-10	increasing	0
<i>LUZP2</i>	BA46	1.35E-10	-0.00082	2.16E-10	decreasing	1
<i>LYN</i>	BA46	1.94E-08	-0.00076	7.86E-09	decreasing	0
<i>LYPD6</i>	BA46	4.71E-05	-0.00072	1.14E-07	decreasing	0
<i>LYPD6B</i>	BA46	1.10E-08	-0.00013	0.37541	other	0
<i>LYST</i>	BA46	6.02E-10	0.000774	1.46E-09	increasing	0
<i>MACROD1</i>	BA46	3.61E-06	0.000709	2.23E-07	increasing	0
<i>MAF</i>	BA46	6.07E-10	-0.00074	1.44E-08	decreasing	0
<i>MAG</i>	BA46	4.93E-10	0.000764	2.96E-09	increasing	0
<i>MAG11</i>	BA46	8.62E-07	-0.00072	1.25E-07	decreasing	0
<i>MAN2A2</i>	BA46	1.01E-14	0.000868	8.87E-13	increasing	0
<i>MAN2C1</i>	BA46	1.67E-12	0.00084	8.33E-12	increasing	0
<i>MAP1S</i>	BA46	1.19E-08	0.000727	4.47E-08	increasing	0
<i>MAP2K1</i>	BA46	1.21E-07	0.00075	2.02E-08	increasing	0
<i>MAP3K6</i>	BA46	7.80E-14	0.000819	7.12E-11	increasing	0
<i>MAP4K2</i>	BA46	6.83E-09	0.000711	1.51E-07	increasing	0
<i>MAP6D1</i>	BA46	4.54E-08	0.000755	1.14E-08	increasing	0
<i>MAP7</i>	BA46	4.78E-12	0.000801	2.16E-10	increasing	0
<i>MAP7D2</i>	BA46	6.15E-08	0.000735	4.99E-08	increasing	0
<i>MAPK10</i>	BA46	1.91E-07	0.000709	9.56E-08	increasing	0
<i>MAPK11</i>	BA46	3.08E-08	-0.00019	0.201367	other	0
<i>MAPK3</i>	BA46	1.84E-07	0.000579	2.88E-05	increasing	0
<i>MAPK8</i>	BA46	1.55E-11	-0.00072	3.60E-08	decreasing	0
<i>MAPK8IP3</i>	BA46	5.16E-07	0.000741	2.96E-08	increasing	0
<i>MAPK9</i>	BA46	4.03E-08	7.21E-05	0.627106	other	0
<i>MAPKAPK2</i>	BA46	1.19E-09	-0.00079	9.47E-10	decreasing	0
<i>MAPRE1</i>	BA46	1.73E-16	-0.00086	2.17E-12	decreasing	0
<i>MARCH1</i>	BA46	7.13E-09	-0.00062	5.89E-06	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MARCH4</i>	BA46	6.06E-14	-0.00087	4.27E-13	decreasing	0
<i>MARCH8</i>	BA46	2.15E-11	0.000784	4.93E-10	increasing	0
<i>MARCKS</i>	BA46	1.12E-09	-0.00069	2.34E-07	decreasing	0
<i>MARCKSL1</i>	BA46	5.62E-12	-0.00071	6.52E-08	decreasing	0
<i>MARVELD1</i>	BA46	7.72E-09	-0.00077	2.26E-09	decreasing	0
<i>MASP1</i>	BA46	1.15E-07	-0.00065	6.85E-07	decreasing	0
<i>MAST2</i>	BA46	8.39E-13	-0.00077	1.43E-09	decreasing	0
<i>MAST3</i>	BA46	5.08E-08	-0.00016	0.294123	other	0
<i>MATN3</i>	BA46	4.29E-12	-0.0008	2.42E-10	decreasing	0
<i>MATN4</i>	BA46	2.13E-07	0.000747	2.94E-08	increasing	0
<i>MAZ</i>	BA46	7.80E-11	-0.00082	6.94E-11	decreasing	0
<i>MBLAC2</i>	BA46	1.86E-07	4.87E-05	0.747402	other	0
<i>MBNL1</i>	BA46	4.62E-08	0.000604	9.56E-06	increasing	0
<i>MBNL2</i>	BA46	1.17E-18	0.000894	1.90E-14	increasing	0
<i>MBOAT2</i>	BA46	3.40E-06	-0.00074	4.72E-08	decreasing	0
<i>MBP</i>	BA46	1.63E-11	0.00078	9.56E-10	increasing	0
<i>MBTPS1</i>	BA46	9.12E-08	0.00067	1.16E-06	increasing	0
<i>MCM6</i>	BA46	9.47E-09	0.000124	0.407121	other	0
<i>MCOLN1</i>	BA46	4.14E-06	-0.00069	2.42E-07	decreasing	0
<i>MDGA1</i>	BA46	1.60E-07	-0.00061	1.59E-05	decreasing	0
<i>MDN1</i>	BA46	2.05E-07	0.000739	4.12E-08	increasing	1
<i>ME2</i>	BA46	8.34E-08	-0.00065	2.83E-06	decreasing	0
<i>MEF2C</i>	BA46	6.33E-08	-0.00051	0.000305	other	0
<i>MEIS3</i>	BA46	1.08E-11	-0.00069	3.60E-07	decreasing	0
<i>MEMO1</i>	BA46	6.39E-07	-0.00077	4.18E-09	decreasing	0
<i>MEOX1</i>	BA46	9.14E-09	-0.00052	1.26E-05	decreasing	0
<i>MET</i>	BA46	7.45E-05	-0.00071	2.31E-07	decreasing	0
<i>MEX3A</i>	BA46	1.15E-07	-0.00053	0.000142	other	0
<i>MEX3B</i>	BA46	7.65E-15	-0.00082	2.42E-11	decreasing	0
<i>MFSD2A</i>	BA46	1.56E-07	-0.00068	6.41E-07	decreasing	0
<i>MFSD4</i>	BA46	2.87E-10	0.000234	0.113219	other	0
<i>MGAT4B</i>	BA46	4.75E-07	-0.00069	2.02E-07	decreasing	0
<i>MGLL</i>	BA46	8.77E-11	-0.00064	3.02E-06	decreasing	0
<i>MICAL2</i>	BA46	3.34E-09	-0.00079	1.27E-09	decreasing	0
<i>MID1</i>	BA46	6.25E-08	-0.00069	5.04E-07	decreasing	0
<i>MID2</i>	BA46	3.27E-06	0.000711	1.80E-07	increasing	0
<i>MKI67</i>	BA46	4.45E-08	-0.0006	1.20E-05	decreasing	0
<i>MKL2</i>	BA46	2.66E-08	0.000232	0.113823	other	0
<i>MKRN3</i>	BA46	1.46E-22	-0.00091	3.58E-15	decreasing	0
<i>MKX</i>	BA46	5.21E-08	0.000365	0.012587	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MLLT4</i>	BA46	7.94E-16	-0.00085	4.22E-12	decreasing	0
<i>MLXIPL</i>	BA46	6.31E-13	-0.00066	2.01E-06	decreasing	0
<i>MMD</i>	BA46	1.16E-19	-0.0009	3.42E-14	decreasing	0
<i>MN1</i>	BA46	6.61E-07	-0.00076	1.26E-08	decreasing	0
<i>MOB1B</i>	BA46	1.94E-09	-0.00073	3.52E-08	decreasing	0
<i>MOB3B</i>	BA46	2.58E-09	-0.00043	0.002437	other	0
<i>MOG</i>	BA46	1.37E-11	0.000788	8.83E-10	increasing	0
<i>MPDZ</i>	BA46	9.57E-13	0.000783	8.17E-10	increasing	0
<i>MPHOSPH8</i>	BA46	1.11E-10	0.000755	5.19E-09	increasing	0
<i>MPP1</i>	BA46	5.19E-15	0.000865	2.06E-12	increasing	0
<i>MPP3</i>	BA46	2.31E-11	-0.00078	5.22E-10	decreasing	1
<i>MPP4</i>	BA46	1.36E-08	8.46E-06	0.954033	other	0
<i>MPP5</i>	BA46	5.29E-09	0.000722	2.87E-08	increasing	0
<i>MPP6</i>	BA46	1.97E-05	-0.00071	1.69E-07	decreasing	0
<i>MPP7</i>	BA46	2.29E-13	0.000697	7.29E-08	increasing	0
<i>MPPED1</i>	BA46	3.61E-09	-0.00073	2.44E-08	decreasing	0
<i>MPRIP</i>	BA46	2.57E-08	-0.00039	0.006455	other	0
<i>MPZL1</i>	BA46	3.10E-06	-0.00072	5.23E-08	decreasing	1
<i>MRC1</i>	BA46	6.15E-08	-0.00077	3.77E-09	decreasing	0
<i>MREG</i>	BA46	1.72E-07	-0.00035	0.014847	other	0
<i>MRPS30</i>	BA46	4.30E-07	0.000709	3.84E-08	increasing	0
<i>MSANTD3</i>	BA46	1.74E-07	-0.00049	0.000557	other	0
<i>MSRA</i>	BA46	8.06E-08	-0.00072	3.60E-08	decreasing	0
<i>MTHFD2L</i>	BA46	1.17E-09	0.000797	9.35E-10	increasing	0
<i>MTPN</i>	BA46	2.33E-09	-0.00073	4.98E-08	decreasing	0
<i>MTSS1</i>	BA46	7.95E-08	-0.00054	9.05E-05	decreasing	0
<i>MXI1</i>	BA46	2.96E-09	0.000689	2.31E-07	increasing	0
<i>MYBBP1A</i>	BA46	1.44E-08	0.000751	1.14E-08	increasing	0
<i>MYCN</i>	BA46	5.40E-09	-0.00058	2.50E-05	decreasing	0
<i>MYH13</i>	BA46	4.31E-09	0.000551	8.04E-05	increasing	0
<i>MYL10</i>	BA46	4.00E-10	0.0001	0.498227	other	0
<i>MYLIP</i>	BA46	3.86E-12	-0.00077	1.85E-09	decreasing	0
<i>MYLK</i>	BA46	2.85E-16	0.000784	2.37E-10	increasing	0
<i>MYO16</i>	BA46	1.46E-27	-0.00092	1.07E-15	decreasing	0
<i>MYO1B</i>	BA46	7.97E-06	-0.0007	2.04E-07	decreasing	0
<i>MYO5B</i>	BA46	5.17E-14	-0.00073	8.60E-09	decreasing	0
<i>MYO5C</i>	BA46	1.80E-07	0.000657	1.46E-06	increasing	0
<i>MYRF</i>	BA46	9.79E-10	0.000808	2.07E-10	increasing	0
<i>N4BP2</i>	BA46	2.24E-07	0.000178	0.227442	other	0
<i>N4BP2L1</i>	BA46	9.61E-11	0.00081	6.77E-11	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>N4BP3</i>	BA46	2.16E-07	-0.00064	1.82E-06	decreasing	0
<i>NAA60</i>	BA46	1.81E-09	-0.0008	9.19E-10	decreasing	0
<i>NAB1</i>	BA46	1.38E-05	0.000711	1.82E-07	increasing	0
<i>NADK</i>	BA46	1.90E-08	-0.00082	2.99E-10	decreasing	0
<i>NAP1L5</i>	BA46	7.29E-08	0.000265	0.072216	other	0
<i>NAPEPLD</i>	BA46	1.38E-16	0.000885	1.56E-13	increasing	0
<i>NASP</i>	BA46	1.89E-12	-0.00078	1.97E-09	decreasing	0
<i>NAV1</i>	BA46	3.09E-14	-0.00086	1.61E-12	decreasing	0
<i>NAV2</i>	BA46	2.40E-07	-0.00068	2.31E-07	decreasing	0
<i>NAV3</i>	BA46	1.19E-06	-0.00072	5.30E-08	decreasing	0
<i>NBEA</i>	BA46	1.84E-07	-0.00067	2.47E-07	decreasing	0
<i>NCAN</i>	BA46	3.29E-08	-0.00071	1.06E-07	decreasing	0
<i>NCDN</i>	BA46	7.72E-10	0.000815	2.82E-10	increasing	0
<i>NCKAP1L</i>	BA46	7.51E-08	-0.00076	1.07E-08	decreasing	0
<i>NCKIPSD</i>	BA46	1.21E-21	0.0009	2.30E-15	increasing	0
<i>NCOR1</i>	BA46	2.02E-07	-0.00074	3.63E-08	decreasing	0
<i>NDRG1</i>	BA46	1.30E-08	-0.00064	2.80E-06	decreasing	0
<i>NDRG2</i>	BA46	9.10E-08	9.12E-05	0.538782	other	0
<i>NDUFB9</i>	BA46	6.06E-09	0.000613	6.60E-06	increasing	0
<i>NECAB1</i>	BA46	6.66E-11	0.000817	5.91E-11	increasing	0
<i>NEFH</i>	BA46	1.81E-09	0.0008	5.03E-10	increasing	0
<i>NEFM</i>	BA46	2.00E-07	0.000673	8.53E-07	increasing	0
<i>NEK10</i>	BA46	2.38E-09	-0.00072	6.89E-08	decreasing	1
<i>NETO2</i>	BA46	2.57E-10	-0.00079	6.68E-10	decreasing	0
<i>NEURL1B</i>	BA46	1.79E-17	-0.00089	3.29E-14	decreasing	0
<i>NFIB</i>	BA46	3.40E-08	-0.00077	7.54E-09	decreasing	0
<i>NGB</i>	BA46	9.10E-07	0.000722	1.11E-07	increasing	0
<i>NHSL2</i>	BA46	8.14E-08	0.000637	1.62E-06	increasing	0
<i>NIN</i>	BA46	4.51E-10	-0.00042	0.003556	other	0
<i>NISCH</i>	BA46	2.32E-08	0.000772	2.20E-09	increasing	0
<i>NKAIN2</i>	BA46	6.70E-10	-0.00071	5.87E-08	decreasing	0
<i>NKD1</i>	BA46	1.94E-07	-0.00074	3.88E-08	decreasing	0
<i>NKIRAS2</i>	BA46	3.87E-16	-0.00086	2.91E-12	decreasing	0
<i>NKX3.1</i>	BA46	3.63E-08	0.000766	2.25E-09	increasing	0
<i>NKX6.2</i>	BA46	3.51E-13	0.000757	8.43E-09	increasing	0
<i>NLGN1</i>	BA46	1.31E-10	-0.00078	2.30E-09	decreasing	0
<i>NME7</i>	BA46	5.98E-08	-0.00066	1.78E-06	decreasing	0
<i>NOL4</i>	BA46	7.63E-09	-0.00077	4.75E-09	decreasing	0
<i>NPBWR1</i>	BA46	7.53E-14	-0.00082	1.14E-11	decreasing	0
<i>NPBWR2</i>	BA46	7.85E-09	0.000662	8.82E-07	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>NPHP3</i>	BA46	7.83E-08	0.000651	1.87E-06	increasing	0
<i>NPR3</i>	BA46	5.03E-08	-0.00063	4.46E-06	decreasing	0
<i>NPTX1</i>	BA46	1.26E-15	0.000855	4.13E-12	increasing	0
<i>NPY1R</i>	BA46	1.76E-07	-0.00067	6.10E-07	decreasing	0
<i>NR1H2</i>	BA46	3.80E-11	0.000787	1.11E-09	increasing	0
<i>NR2C2</i>	BA46	6.42E-08	-0.00061	1.02E-05	decreasing	0
<i>NR3C1</i>	BA46	2.32E-16	0.000783	5.33E-10	increasing	0
<i>NR3C2</i>	BA46	2.88E-19	0.000892	2.32E-14	increasing	0
<i>NRAS</i>	BA46	6.22E-12	-0.00078	1.30E-09	decreasing	0
<i>NREP</i>	BA46	1.38E-15	-0.00087	2.95E-13	decreasing	0
<i>NRG3</i>	BA46	3.11E-06	-0.00073	4.05E-08	decreasing	0
<i>NRG4</i>	BA46	1.07E-07	0.000794	1.05E-09	increasing	0
<i>NRP1</i>	BA46	8.16E-07	-0.00074	2.11E-08	decreasing	0
<i>NRXN1</i>	BA46	9.65E-11	-0.00072	3.56E-08	decreasing	0
<i>NRXN2</i>	BA46	6.63E-11	-0.00083	2.11E-11	decreasing	0
<i>NRXN3</i>	BA46	3.83E-08	-0.00057	6.08E-05	decreasing	0
<i>NSD1</i>	BA46	2.97E-08	-0.00066	9.79E-07	decreasing	0
<i>NSF</i>	BA46	1.29E-07	0.000636	2.42E-06	increasing	0
<i>NT5C1A</i>	BA46	6.77E-07	0.000759	1.25E-08	increasing	0
<i>NT5DC1</i>	BA46	1.63E-08	0.000637	3.15E-06	increasing	0
<i>NT5DC2</i>	BA46	1.14E-07	-0.00026	0.082196	other	0
<i>NTM</i>	BA46	1.46E-10	-0.00082	2.10E-10	decreasing	0
<i>NTNG1</i>	BA46	5.50E-08	-0.00079	2.02E-09	decreasing	0
<i>NTSR1</i>	BA46	8.97E-08	-0.00063	3.01E-06	decreasing	0
<i>NTSR2</i>	BA46	3.39E-11	0.000694	2.11E-07	increasing	0
<i>NUB1</i>	BA46	6.75E-07	0.00072	1.97E-08	increasing	0
<i>NUDT3</i>	BA46	5.97E-10	-0.00054	9.89E-05	decreasing	0
<i>NUMA1</i>	BA46	7.23E-11	0.000854	1.51E-11	increasing	0
<i>NUP93</i>	BA46	1.28E-07	0.00021	0.148046	other	0
<i>NWD2</i>	BA46	1.94E-15	-0.00086	1.24E-12	decreasing	0
<i>NYAP2</i>	BA46	1.66E-10	-0.0008	5.15E-10	decreasing	0
<i>OBSCN</i>	BA46	1.00E-07	0.000511	0.000296	other	1
<i>OGDHL</i>	BA46	4.41E-13	0.000812	1.54E-10	increasing	0
<i>OLFM2</i>	BA46	6.14E-08	-0.00079	1.88E-09	decreasing	0
<i>OPALIN</i>	BA46	2.14E-11	0.000773	1.58E-09	increasing	0
<i>OPRK1</i>	BA46	1.23E-09	0.000116	0.426435	other	0
<i>OSBPL6</i>	BA46	1.88E-11	-0.00044	0.002966	other	0
<i>OTUB2</i>	BA46	1.67E-07	-0.00055	7.01E-05	decreasing	0
<i>P2RX7</i>	BA46	3.20E-09	0.000738	1.87E-08	increasing	0
<i>P2RY12</i>	BA46	9.68E-09	-0.00081	3.69E-10	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>P4HTM</i>	BA46	8.03E-07	0.000757	1.57E-08	increasing	0
<i>PABPC1</i>	BA46	1.02E-09	-0.00081	1.70E-10	decreasing	0
<i>PABPC5</i>	BA46	1.09E-07	-0.00049	0.000537	other	0
<i>PAC SIN1</i>	BA46	3.08E-08	-0.00039	0.006945	other	0
<i>PAC SIN2</i>	BA46	2.17E-08	-0.00034	0.02238	other	0
<i>PAC SIN3</i>	BA46	1.53E-07	-0.00061	8.82E-06	decreasing	0
<i>PAK3</i>	BA46	6.40E-09	-0.00066	1.58E-06	decreasing	0
<i>PAK6</i>	BA46	1.21E-08	-0.00081	3.54E-10	decreasing	0
<i>PALMD</i>	BA46	1.57E-07	-0.00051	0.000327	other	0
<i>PAM</i>	BA46	1.20E-09	0.000753	4.28E-09	increasing	0
<i>PAMR1</i>	BA46	2.42E-07	8.37E-05	0.5754	other	0
<i>PANK3</i>	BA46	2.20E-08	-0.0007	1.62E-07	decreasing	0
<i>PANX1</i>	BA46	7.57E-08	0.000274	0.060886	other	0
<i>PAPPA2</i>	BA46	3.50E-08	-0.0005	0.00037	other	0
<i>PAPSS2</i>	BA46	1.51E-08	0.000639	3.40E-06	increasing	0
<i>PARP6</i>	BA46	1.21E-09	-0.00075	6.81E-09	decreasing	1
<i>PASK</i>	BA46	2.73E-11	-0.00057	6.08E-05	decreasing	0
<i>PC</i>	BA46	7.24E-11	0.000774	1.52E-09	increasing	0
<i>PCBD1</i>	BA46	1.72E-08	0.00072	1.88E-08	increasing	0
<i>PCDH10</i>	BA46	1.98E-07	-0.00061	9.49E-06	decreasing	0
<i>PCDH11X</i>	BA46	4.56E-19	-0.00089	9.76E-14	decreasing	0
<i>PCDH15</i>	BA46	1.09E-17	-0.00088	4.80E-14	decreasing	0
<i>PCDH20</i>	BA46	4.55E-11	-0.00074	4.37E-09	decreasing	0
<i>PCDH7</i>	BA46	3.38E-10	-2.14E-05	0.885408	other	0
<i>PCDHB14</i>	BA46	1.07E-11	-0.00081	1.34E-10	decreasing	0
<i>PCGF3</i>	BA46	1.23E-06	-0.00074	2.52E-08	decreasing	0
<i>PCNXL2</i>	BA46	1.39E-09	-0.00014	0.339208	other	0
<i>PCNXL4</i>	BA46	1.13E-07	-0.00067	6.77E-07	decreasing	0
<i>PCSK5</i>	BA46	9.72E-11	-0.00076	2.21E-09	decreasing	0
<i>PDCD2</i>	BA46	9.66E-06	-0.0007	2.52E-07	decreasing	0
<i>PDE1A</i>	BA46	3.16E-07	0.000709	2.20E-07	increasing	0
<i>PDE1B</i>	BA46	2.85E-10	0.000717	5.13E-08	increasing	0
<i>PDE2A</i>	BA46	1.28E-07	-0.00028	0.062611	other	0
<i>PDE3A</i>	BA46	1.63E-09	-0.00079	1.26E-09	decreasing	0
<i>PDE8B</i>	BA46	7.79E-09	5.71E-05	0.700668	other	0
<i>PDGFRA</i>	BA46	4.98E-18	-0.00087	1.23E-12	decreasing	0
<i>PDIA5</i>	BA46	4.20E-08	-0.00054	0.000123	other	0
<i>PDIA6</i>	BA46	5.11E-09	-0.00075	6.69E-09	decreasing	0
<i>PDK1</i>	BA46	1.63E-09	0.000672	2.93E-07	increasing	0
<i>PDK2</i>	BA46	8.80E-08	0.000528	0.000173	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PDK3</i>	BA46	3.17E-09	0.0002	0.175543	other	0
<i>PDLIM2</i>	BA46	8.08E-07	0.000726	4.40E-08	increasing	1
<i>PDZD2</i>	BA46	4.74E-12	0.000777	1.82E-09	increasing	0
<i>PDZD4</i>	BA46	1.71E-07	-0.00036	0.014305	other	0
<i>PDZRN3</i>	BA46	1.35E-13	-0.00083	2.58E-11	decreasing	0
<i>PEA15</i>	BA46	1.94E-08	0.000645	2.21E-06	increasing	0
<i>PEAK1</i>	BA46	5.38E-09	0.000315	0.030664	other	0
<i>PEG3</i>	BA46	1.09E-07	0.000793	1.67E-09	increasing	0
<i>PELI1</i>	BA46	1.34E-08	-0.00034	0.021767	other	0
<i>PELI3</i>	BA46	1.09E-09	0.000749	1.63E-08	increasing	0
<i>PEX5L</i>	BA46	7.25E-08	-0.00026	0.085248	other	0
<i>PFKFB3</i>	BA46	4.63E-08	-0.00012	0.422415	other	0
<i>PFKP</i>	BA46	2.01E-12	0.000826	2.78E-11	increasing	0
<i>PGBD5</i>	BA46	2.11E-09	0.000138	0.35785	other	0
<i>PHACTR1</i>	BA46	3.96E-08	-0.00057	5.41E-05	decreasing	0
<i>PHACTR3</i>	BA46	1.02E-07	-0.00062	7.73E-06	decreasing	0
<i>PHF1</i>	BA46	8.10E-08	0.000703	1.31E-07	increasing	0
<i>PHF14</i>	BA46	1.33E-11	-0.00077	2.48E-09	decreasing	0
<i>PHF20L1</i>	BA46	2.25E-07	-0.00078	2.41E-09	decreasing	0
<i>PHF21A</i>	BA46	6.38E-12	0.000774	5.32E-10	increasing	0
<i>PHKA1</i>	BA46	2.34E-06	-0.00076	1.63E-08	decreasing	0
<i>PHYHD1</i>	BA46	1.18E-07	0.000728	2.78E-08	increasing	0
<i>PHYHIP</i>	BA46	1.73E-07	0.000608	1.05E-05	increasing	0
<i>PI4KA</i>	BA46	1.62E-09	0.000607	1.10E-05	increasing	0
<i>PIEZO2</i>	BA46	1.79E-08	-0.00066	6.56E-07	decreasing	0
<i>PIK3C2B</i>	BA46	1.04E-11	-0.00075	5.80E-09	decreasing	0
<i>PIP4K2A</i>	BA46	7.07E-11	0.00082	6.66E-11	increasing	0
<i>PIP4K2C</i>	BA46	1.54E-08	0.000712	8.33E-08	increasing	0
<i>PIP5K1C</i>	BA46	1.88E-07	-0.0004	0.005822	other	0
<i>PISD</i>	BA46	6.11E-07	0.000782	2.59E-09	increasing	0
<i>PITHD1</i>	BA46	1.65E-08	0.000779	1.35E-09	increasing	0
<i>PITPNC1</i>	BA46	4.27E-15	-0.00086	1.99E-12	decreasing	0
<i>PIWIL1</i>	BA46	8.15E-11	-0.00076	1.75E-09	decreasing	0
<i>PKN1</i>	BA46	1.40E-09	-0.00054	9.27E-05	decreasing	0
<i>PKP1</i>	BA46	1.73E-05	-0.00073	5.98E-08	decreasing	0
<i>PKP4</i>	BA46	4.26E-12	-0.00084	1.10E-11	decreasing	0
<i>PLA2G15</i>	BA46	1.64E-08	-0.00071	9.99E-08	decreasing	0
<i>PLA2G16</i>	BA46	1.24E-09	0.00076	2.64E-09	increasing	0
<i>PLAG1</i>	BA46	5.79E-09	0.000714	8.34E-08	increasing	0
<i>PLCD3</i>	BA46	2.58E-09	-0.00071	2.51E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PLEK</i>	BA46	6.75E-06	0.000714	7.43E-08	increasing	0
<i>PLEKHA1</i>	BA46	1.93E-12	0.000843	6.39E-12	increasing	0
<i>PLEKHA2</i>	BA46	2.43E-10	0.000803	5.51E-11	increasing	0
<i>PLEKHA5</i>	BA46	2.66E-08	-0.00035	0.017013	other	0
<i>PLEKHB1</i>	BA46	1.03E-07	0.00056	3.95E-05	increasing	0
<i>PLEKHG3</i>	BA46	2.29E-09	0.000767	3.02E-09	increasing	0
<i>PLEKHH1</i>	BA46	2.46E-12	0.000802	1.97E-10	increasing	0
<i>PLP1</i>	BA46	2.66E-10	0.000748	1.17E-08	increasing	0
<i>PLXDC1</i>	BA46	9.50E-08	-0.0005	0.000367	other	0
<i>PLXNB3</i>	BA46	2.89E-11	0.000803	3.48E-10	increasing	0
<i>PLXND1</i>	BA46	3.04E-08	-0.00078	2.72E-09	decreasing	0
<i>PM20D2</i>	BA46	7.19E-06	0.000719	1.34E-07	increasing	0
<i>PMEL</i>	BA46	1.58E-07	0.000732	9.37E-09	increasing	0
<i>PMPCB</i>	BA46	3.53E-07	0.000743	1.09E-08	increasing	0
<i>PNCK</i>	BA46	5.27E-07	0.000722	9.22E-08	increasing	0
<i>PNKD</i>	BA46	2.83E-17	0.00088	2.63E-14	increasing	0
<i>PNMAL1</i>	BA46	1.96E-07	0.000659	1.74E-06	increasing	0
<i>PNMAL2</i>	BA46	2.23E-07	0.00075	2.41E-08	increasing	0
<i>PNPLA2</i>	BA46	1.20E-07	0.000718	6.79E-08	increasing	0
<i>PNPLA5</i>	BA46	3.76E-05	0.000702	2.11E-07	increasing	0
<i>PNRC1</i>	BA46	2.24E-16	0.000865	4.51E-13	increasing	0
<i>PODXL2</i>	BA46	1.33E-07	-0.00014	0.348717	other	0
<i>POLG</i>	BA46	3.20E-06	0.000728	5.07E-08	increasing	0
<i>POPDC3</i>	BA46	2.33E-08	0.000775	3.50E-09	increasing	0
<i>POSTN</i>	BA46	1.21E-10	-0.00073	9.23E-09	decreasing	0
<i>POU3F2</i>	BA46	3.88E-07	-0.00075	2.01E-08	decreasing	0
<i>POU3F3</i>	BA46	2.08E-08	-0.00078	2.22E-09	decreasing	0
<i>PPARD</i>	BA46	2.11E-08	-0.00021	0.153287	other	0
<i>PPARGC1A</i>	BA46	1.73E-06	0.000705	4.63E-08	increasing	0
<i>PPEF1</i>	BA46	2.19E-11	-0.0008	7.02E-11	decreasing	0
<i>PPFIA4</i>	BA46	6.37E-09	0.000689	2.75E-07	increasing	0
<i>PIIP5K1</i>	BA46	1.40E-10	0.000715	4.42E-08	increasing	0
<i>PPL</i>	BA46	8.27E-12	0.000857	4.26E-12	increasing	0
<i>PPM1E</i>	BA46	9.76E-13	-0.00082	6.27E-11	decreasing	0
<i>PPM1K</i>	BA46	5.08E-05	0.000707	2.17E-07	increasing	0
<i>PPP1R14C</i>	BA46	3.95E-13	-0.00086	3.08E-12	decreasing	0
<i>PPP1R3C</i>	BA46	1.54E-07	-0.00023	0.113592	other	0
<i>PPP1R3E</i>	BA46	2.25E-10	0.00081	2.14E-10	increasing	0
<i>PPP1R3F</i>	BA46	5.33E-10	0.000722	2.98E-08	increasing	0
<i>PPP2R1A</i>	BA46	6.92E-08	-0.00037	0.010104	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PPP2R5A</i>	BA46	8.88E-09	-0.00079	1.44E-09	decreasing	0
<i>PPP2R5B</i>	BA46	2.28E-08	-0.00075	8.25E-09	decreasing	0
<i>PPP3CA</i>	BA46	1.90E-07	0.000596	1.32E-05	increasing	0
<i>PPP3CC</i>	BA46	1.51E-09	-0.00067	5.53E-07	decreasing	0
<i>PPP4R4</i>	BA46	5.93E-08	-0.00026	0.073855	other	0
<i>PPP5C</i>	BA46	1.67E-07	-0.00045	0.001674	other	0
<i>PRCD</i>	BA46	6.35E-08	0.000593	2.16E-05	increasing	0
<i>PRDM5</i>	BA46	2.38E-09	0.000793	6.36E-10	increasing	0
<i>PRDM8</i>	BA46	1.63E-05	-0.00072	5.51E-08	decreasing	0
<i>PREPL</i>	BA46	1.52E-07	0.000731	6.98E-08	increasing	0
<i>PREX1</i>	BA46	3.63E-09	-0.00079	1.33E-09	decreasing	0
<i>PRICKLE2</i>	BA46	5.64E-14	-0.00083	1.94E-11	decreasing	0
<i>PRKAG2</i>	BA46	1.91E-07	0.000516	0.000251	other	0
<i>PRKCB</i>	BA46	2.54E-08	-0.00076	1.14E-08	decreasing	0
<i>PRKG2</i>	BA46	3.51E-11	-0.00078	3.39E-09	decreasing	0
<i>PROK2</i>	BA46	1.80E-07	-0.00061	1.37E-05	decreasing	0
<i>PROM1</i>	BA46	2.17E-08	-0.00079	8.57E-10	decreasing	0
<i>PRPF19</i>	BA46	9.75E-11	0.000824	2.11E-11	increasing	0
<i>PRR13</i>	BA46	3.07E-07	0.000714	4.68E-08	increasing	0
<i>PRR5</i>	BA46	6.56E-08	-0.0008	8.65E-10	decreasing	0
<i>PRUNE2</i>	BA46	1.15E-10	0.000752	1.14E-08	increasing	0
<i>PSMC5</i>	BA46	2.94E-11	0.000772	1.76E-09	increasing	0
<i>PTBP3</i>	BA46	2.16E-07	-0.00074	3.62E-08	decreasing	0
<i>PTEN</i>	BA46	4.88E-08	-0.00066	1.33E-06	decreasing	0
<i>PTF1A</i>	BA46	1.71E-10	0.000715	3.33E-08	increasing	0
<i>PTGS1</i>	BA46	4.89E-11	0.000736	1.70E-08	increasing	0
<i>PTK2B</i>	BA46	1.02E-23	0.000924	9.36E-16	increasing	0
<i>PTK7</i>	BA46	1.04E-07	-0.0005	0.000378	other	0
<i>PTMS</i>	BA46	1.30E-05	-0.00071	1.60E-07	decreasing	0
<i>PTN</i>	BA46	3.27E-09	-0.00078	1.44E-09	decreasing	0
<i>PTP4A1</i>	BA46	4.93E-10	-0.00067	7.61E-07	decreasing	0
<i>PTPN13</i>	BA46	2.09E-09	-0.00058	2.89E-05	decreasing	1
<i>PTPN14</i>	BA46	3.13E-12	0.000797	1.97E-10	increasing	0
<i>PTPN5</i>	BA46	4.27E-09	0.000738	2.89E-08	increasing	0
<i>PTPN9</i>	BA46	5.79E-10	-0.00066	1.18E-06	decreasing	0
<i>PTPRA</i>	BA46	1.63E-07	-0.00066	9.93E-07	decreasing	0
<i>PTPRD</i>	BA46	2.52E-13	-0.00085	6.44E-12	decreasing	0
<i>PTPRG</i>	BA46	3.25E-19	-0.00092	9.76E-15	decreasing	0
<i>PTPRJ</i>	BA46	2.46E-09	-0.00082	2.55E-10	decreasing	0
<i>PTPRR</i>	BA46	2.24E-07	-0.00073	8.78E-09	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PURA</i>	BA46	7.07E-09	0.000732	9.05E-09	increasing	0
<i>PURG</i>	BA46	1.05E-11	-0.00081	1.25E-10	decreasing	0
<i>PVRL2</i>	BA46	7.76E-09	-0.00077	2.30E-09	decreasing	0
<i>PVRL3</i>	BA46	1.38E-12	-0.00083	1.02E-10	decreasing	0
<i>PWWP2B</i>	BA46	2.61E-08	0.000599	1.85E-05	increasing	0
<i>PXYLP1</i>	BA46	3.99E-09	0.000707	2.44E-07	increasing	0
<i>PYGM</i>	BA46	8.92E-08	-0.00047	0.000795	other	0
<i>QDPR</i>	BA46	8.55E-14	0.000847	2.82E-12	increasing	0
<i>R3HCC1</i>	BA46	1.93E-10	-0.00074	1.64E-08	decreasing	0
<i>R3HDM1</i>	BA46	9.65E-11	-0.00082	1.70E-10	decreasing	0
<i>R3HDM2</i>	BA46	6.83E-06	-0.00074	5.27E-08	decreasing	0
<i>R3HDM4</i>	BA46	5.87E-10	-0.00076	8.43E-09	decreasing	0
<i>RAB11FIP4</i>	BA46	7.88E-08	-0.00074	3.25E-08	decreasing	0
<i>RAB11FIP5</i>	BA46	4.29E-10	0.000685	3.44E-07	increasing	0
<i>RAB22A</i>	BA46	2.97E-08	0.000727	2.21E-08	increasing	0
<i>RAE1</i>	BA46	6.77E-11	0.000389	0.007319	other	0
<i>RAI14</i>	BA46	2.33E-07	-0.00066	1.13E-06	decreasing	1
<i>RALA</i>	BA46	1.02E-12	-0.0008	4.70E-10	decreasing	0
<i>RALBP1</i>	BA46	8.07E-09	-9.10E-05	0.539591	other	0
<i>RALGPS2</i>	BA46	2.83E-07	-0.00072	5.47E-08	decreasing	1
<i>RALYL</i>	BA46	6.93E-08	0.000709	2.24E-07	increasing	0
<i>RAP1GAP2</i>	BA46	3.74E-15	-0.00085	1.31E-11	decreasing	0
<i>RAPGEF4</i>	BA46	3.27E-11	-0.00018	0.234045	other	0
<i>RASAL2</i>	BA46	3.31E-08	8.12E-05	0.586891	other	0
<i>RASD1</i>	BA46	1.54E-13	0.000783	2.71E-10	increasing	0
<i>RASEF</i>	BA46	1.25E-11	0.000765	3.44E-09	increasing	0
<i>RASGRF2</i>	BA46	8.06E-12	0.000576	3.63E-05	increasing	1
<i>RASL10B</i>	BA46	1.15E-11	-0.00082	3.42E-10	decreasing	0
<i>RASSF10</i>	BA46	1.79E-07	-0.00062	4.08E-06	decreasing	0
<i>RASSF3</i>	BA46	5.71E-09	-0.0007	1.29E-07	decreasing	0
<i>RASSF5</i>	BA46	1.43E-08	0.000315	0.032654	other	0
<i>RAVER2</i>	BA46	3.63E-14	-0.00077	7.76E-10	decreasing	0
<i>RBBP5</i>	BA46	3.74E-05	0.000722	1.05E-07	increasing	0
<i>RBFOX2</i>	BA46	1.11E-13	-0.00081	1.70E-10	decreasing	0
<i>RBPJL</i>	BA46	1.32E-09	0.000726	3.67E-08	increasing	0
<i>RCAN2</i>	BA46	4.34E-16	0.000867	3.60E-13	increasing	0
<i>RCAN3</i>	BA46	3.03E-08	-0.00071	4.97E-08	decreasing	0
<i>RDH10</i>	BA46	1.91E-11	-0.00077	2.51E-09	decreasing	0
<i>REEP1</i>	BA46	2.35E-07	-0.00053	0.000159	other	0
<i>RELN</i>	BA46	2.45E-07	-0.00054	0.000139	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>REPS1</i>	BA46	1.61E-08	0.000668	6.60E-07	increasing	0
<i>REPS2</i>	BA46	4.89E-13	0.000836	7.43E-12	increasing	0
<i>RFC2</i>	BA46	1.85E-07	-0.00073	2.08E-08	decreasing	0
<i>RFFL</i>	BA46	1.47E-06	0.000716	1.41E-07	increasing	0
<i>RFX3</i>	BA46	6.62E-12	-0.00074	1.04E-08	decreasing	0
<i>RGS10</i>	BA46	1.84E-06	-0.00073	6.35E-08	decreasing	0
<i>RGS20</i>	BA46	7.02E-06	-0.00074	4.43E-08	decreasing	0
<i>RGS6</i>	BA46	6.11E-08	-9.51E-05	0.53254	other	0
<i>RGS8</i>	BA46	7.49E-08	-0.00056	4.58E-05	decreasing	1
<i>RHAG</i>	BA46	6.02E-09	-0.00011	0.458954	other	1
<i>RIF1</i>	BA46	1.52E-06	0.000756	7.20E-09	increasing	0
<i>RIIAD1</i>	BA46	1.91E-07	-0.0006	1.47E-05	decreasing	0
<i>RIMBP2</i>	BA46	2.28E-07	-0.0006	2.10E-05	decreasing	0
<i>RIMKLA</i>	BA46	8.41E-07	-0.00077	5.62E-09	decreasing	0
<i>RIMS1</i>	BA46	2.49E-10	-0.00042	0.003554	other	0
<i>RIMS2</i>	BA46	4.53E-10	0.000706	1.13E-07	increasing	0
<i>RIMS3</i>	BA46	1.44E-14	0.000773	2.04E-09	increasing	0
<i>RIMS4</i>	BA46	4.52E-07	-0.00075	8.67E-09	decreasing	0
<i>RLBP1</i>	BA46	4.25E-08	-9.16E-05	0.544261	other	0
<i>RND2</i>	BA46	2.16E-09	0.00075	5.15E-09	increasing	0
<i>RNF111</i>	BA46	1.38E-10	0.000714	8.21E-08	increasing	0
<i>RNF112</i>	BA46	5.77E-08	-0.00078	2.71E-09	decreasing	0
<i>RNF152</i>	BA46	6.32E-19	-0.00088	6.59E-14	decreasing	0
<i>RNF165</i>	BA46	6.07E-14	-0.00087	1.75E-12	decreasing	0
<i>RNMT</i>	BA46	8.41E-07	0.000718	8.81E-08	increasing	0
<i>ROBO1</i>	BA46	5.19E-09	-0.00051	0.000267	other	0
<i>ROBO2</i>	BA46	1.94E-18	-0.00089	3.43E-14	decreasing	0
<i>ROBO3</i>	BA46	7.07E-08	4.92E-05	0.745444	other	0
<i>RORC</i>	BA46	9.81E-14	0.000855	3.42E-12	increasing	0
<i>RPE65</i>	BA46	5.87E-09	-0.00055	9.26E-05	decreasing	0
<i>RPH3A</i>	BA46	5.63E-09	-0.00027	0.063841	other	0
<i>RPS6KA5</i>	BA46	6.35E-08	0.00072	1.26E-07	increasing	0
<i>RPS6KC1</i>	BA46	1.06E-08	0.000737	1.63E-08	increasing	0
<i>RRAS2</i>	BA46	8.44E-15	-0.00086	3.46E-12	decreasing	0
<i>RRN3</i>	BA46	1.16E-08	0.000519	0.000335	other	0
<i>RSAD1</i>	BA46	6.57E-08	0.000805	7.30E-10	increasing	0
<i>RSBN1</i>	BA46	9.74E-08	0.000532	0.000199	other	0
<i>RSPH4A</i>	BA46	7.21E-08	-0.00074	8.91E-09	decreasing	0
<i>RTKN2</i>	BA46	1.63E-06	0.000719	1.29E-07	increasing	0
<i>RUNDC3B</i>	BA46	1.98E-07	0.000202	0.172772	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>RYR1</i>	BA46	7.50E-09	0.000719	7.68E-08	increasing	0
<i>RYR3</i>	BA46	1.95E-16	-0.00087	1.07E-13	decreasing	0
<i>S1PR5</i>	BA46	1.57E-13	0.000846	1.15E-11	increasing	0
<i>SAFB2</i>	BA46	1.84E-07	0.000695	2.95E-07	increasing	0
<i>SBK1</i>	BA46	4.87E-06	-0.00075	2.75E-08	decreasing	0
<i>SCG2</i>	BA46	6.15E-08	-0.00064	5.28E-06	decreasing	0
<i>SCG3</i>	BA46	1.30E-09	-0.00034	0.015921	other	0
<i>SCGB3A1</i>	BA46	5.84E-09	0.000644	1.89E-07	increasing	0
<i>SCN1A</i>	BA46	9.26E-11	0.000838	1.02E-11	increasing	0
<i>SCN1B</i>	BA46	5.28E-20	0.000893	5.31E-15	increasing	0
<i>SCN3A</i>	BA46	3.94E-11	-0.00073	2.71E-08	decreasing	0
<i>SCN4B</i>	BA46	2.61E-08	0.000134	0.377394	other	1
<i>SCUBE1</i>	BA46	9.88E-10	-0.00079	1.46E-09	decreasing	0
<i>SDC3</i>	BA46	2.19E-12	-0.00086	2.38E-12	decreasing	0
<i>SDK1</i>	BA46	8.68E-15	-0.00083	1.46E-11	decreasing	0
<i>SDK2</i>	BA46	3.51E-11	-0.00077	1.90E-09	decreasing	0
<i>SEC14L5</i>	BA46	1.24E-15	0.000852	1.60E-12	increasing	0
<i>SEC24C</i>	BA46	7.70E-08	0.000571	5.97E-05	increasing	0
<i>SEC31B</i>	BA46	1.54E-10	0.00078	1.30E-09	increasing	0
<i>SELPLG</i>	BA46	1.73E-09	-0.00068	6.34E-07	decreasing	0
<i>SEMA3B</i>	BA46	7.27E-07	0.000725	3.95E-08	increasing	0
<i>SEMA3G</i>	BA46	3.34E-09	-0.00067	1.11E-06	decreasing	0
<i>SEMA5B</i>	BA46	3.96E-22	-0.00091	3.11E-14	decreasing	0
<i>SEMA7A</i>	BA46	2.15E-05	0.000719	1.30E-07	increasing	0
<i>SEPT4</i>	BA46	1.04E-16	0.000857	3.38E-13	increasing	0
<i>SERBP1</i>	BA46	1.30E-07	-0.00034	0.01968	other	0
<i>SERINC5</i>	BA46	2.72E-09	-0.00071	7.65E-08	decreasing	1
<i>SERPINA1</i>	BA46	1.00E-10	-0.00077	5.19E-09	decreasing	0
<i>SESTD1</i>	BA46	3.91E-08	-0.00047	0.000959	other	0
<i>SEZ6</i>	BA46	2.39E-12	-0.00085	7.35E-12	decreasing	0
<i>SFMBT2</i>	BA46	2.44E-20	-0.0009	1.42E-15	decreasing	0
<i>SFXN5</i>	BA46	1.58E-07	-0.00038	0.008158	other	0
<i>SGCZ</i>	BA46	6.39E-12	-0.00082	3.91E-11	decreasing	0
<i>SH2B2</i>	BA46	1.99E-07	-0.00069	1.22E-07	decreasing	0
<i>SH2D5</i>	BA46	1.15E-18	0.000893	4.21E-14	increasing	0
<i>SH3BGRL2</i>	BA46	1.10E-11	0.000851	1.99E-11	increasing	0
<i>SH3GL2</i>	BA46	2.06E-08	0.000761	7.54E-09	increasing	0
<i>SH3RF2</i>	BA46	3.17E-12	0.000834	1.47E-11	increasing	0
<i>SH3RF3</i>	BA46	4.53E-20	-0.00091	7.03E-15	decreasing	0
<i>SHANK2</i>	BA46	1.24E-08	-0.00081	3.97E-10	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SHISA9</i>	BA46	5.38E-11	-0.00085	6.01E-12	decreasing	0
<i>SIK1</i>	BA46	1.61E-07	4.43E-05	0.766944	other	0
<i>SIMC1</i>	BA46	2.52E-10	-0.00072	2.86E-08	decreasing	0
<i>SIPA1L1</i>	BA46	1.59E-07	0.000171	0.249023	other	0
<i>SIPA1L2</i>	BA46	1.75E-11	-0.00077	7.76E-09	decreasing	0
<i>SIX4</i>	BA46	2.17E-11	0.000733	1.99E-08	increasing	0
<i>SLA</i>	BA46	3.09E-17	-0.00085	5.70E-13	decreasing	0
<i>SLC16A1</i>	BA46	3.81E-11	-0.00069	4.26E-07	decreasing	0
<i>SLC16A11</i>	BA46	1.88E-07	0.000665	7.59E-07	increasing	0
<i>SLC16A2</i>	BA46	1.00E-07	-0.00072	4.81E-08	decreasing	0
<i>SLC22A23</i>	BA46	8.32E-14	-0.00082	2.56E-11	decreasing	0
<i>SLC23A2</i>	BA46	3.72E-10	-0.00071	9.67E-08	decreasing	0
<i>SLC24A2</i>	BA46	4.38E-08	0.000623	4.23E-06	increasing	0
<i>SLC24A3</i>	BA46	1.25E-10	-0.00072	5.63E-08	decreasing	0
<i>SLC24A4</i>	BA46	3.65E-15	0.000817	1.57E-11	increasing	0
<i>SLC25A23</i>	BA46	2.38E-07	4.07E-05	0.78541	other	0
<i>SLC25A26</i>	BA46	1.28E-07	0.00054	0.000128	other	1
<i>SLC25A27</i>	BA46	2.23E-05	0.000711	1.57E-07	increasing	0
<i>SLC25A45</i>	BA46	4.51E-15	0.000793	6.06E-10	increasing	0
<i>SLC26A11</i>	BA46	1.98E-14	0.000888	3.92E-13	increasing	0
<i>SLC26A5</i>	BA46	8.05E-06	0.000719	5.53E-08	increasing	0
<i>SLC27A2</i>	BA46	7.20E-08	0.000786	2.55E-09	increasing	0
<i>SLC29A4</i>	BA46	1.29E-10	-0.00082	9.91E-11	decreasing	0
<i>SLC2A5</i>	BA46	2.16E-05	-0.00072	1.20E-07	decreasing	0
<i>SLC30A10</i>	BA46	4.84E-15	-0.00086	4.46E-12	decreasing	0
<i>SLC30A3</i>	BA46	2.53E-07	-0.00067	6.10E-07	decreasing	0
<i>SLC35C1</i>	BA46	3.56E-11	-0.00075	1.25E-08	decreasing	0
<i>SLC35F1</i>	BA46	1.57E-07	-0.00049	0.000565	other	0
<i>SLC35F3</i>	BA46	4.85E-08	0.000559	6.74E-05	increasing	0
<i>SLC38A3</i>	BA46	1.42E-05	-0.00072	1.09E-07	decreasing	0
<i>SLC3A1</i>	BA46	2.75E-08	0.000715	1.52E-07	increasing	0
<i>SLC40A1</i>	BA46	5.99E-08	-0.00072	4.18E-08	decreasing	0
<i>SLC44A5</i>	BA46	7.40E-08	-0.00063	1.96E-06	decreasing	0
<i>SLC4A11</i>	BA46	3.35E-08	0.000776	1.92E-09	increasing	0
<i>SLC4A3</i>	BA46	1.24E-10	-0.00083	2.65E-11	decreasing	0
<i>SLC6A7</i>	BA46	1.20E-08	0.000763	8.69E-09	increasing	0
<i>SLC7A14</i>	BA46	7.57E-11	0.000855	1.36E-11	increasing	1
<i>SLC7A8</i>	BA46	9.71E-08	0.000487	0.000651	other	0
<i>SLC8A3</i>	BA46	4.94E-08	-0.00053	0.000148	other	0
<i>SLC9A1</i>	BA46	3.84E-08	0.000535	0.000136	other	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SLC9A6</i>	BA46	5.12E-08	0.000304	0.040661	other	0
<i>SLCO1C1</i>	BA46	1.47E-08	-0.0008	1.00E-09	decreasing	0
<i>SLCO4A1</i>	BA46	3.28E-11	0.00079	1.54E-09	increasing	0
<i>SLCO5A1</i>	BA46	1.19E-07	3.58E-05	0.811887	other	0
<i>SLIT1</i>	BA46	1.72E-14	-0.00086	7.31E-13	decreasing	0
<i>SLITRK6</i>	BA46	1.80E-07	-0.00064	1.72E-06	decreasing	0
<i>SMAD2</i>	BA46	5.32E-11	-0.00072	8.85E-08	decreasing	0
<i>SMAD5</i>	BA46	1.42E-06	0.000737	1.59E-08	increasing	0
<i>SMARCA2</i>	BA46	1.04E-10	-0.00076	3.71E-09	decreasing	0
<i>SMARCD1</i>	BA46	7.12E-09	-0.00062	6.27E-06	decreasing	0
<i>SMCR8</i>	BA46	7.36E-09	0.000794	1.61E-09	increasing	0
<i>SMOC2</i>	BA46	2.24E-08	5.10E-05	0.731205	other	0
<i>SMPD3</i>	BA46	7.15E-13	-0.00083	1.93E-11	decreasing	0
<i>SMURF2</i>	BA46	1.93E-12	-0.00079	5.24E-10	decreasing	0
<i>SMYD5</i>	BA46	1.02E-11	0.000854	8.64E-12	increasing	0
<i>SNAP25</i>	BA46	1.89E-10	0.000678	3.16E-07	increasing	0
<i>SNCB</i>	BA46	2.71E-09	0.000621	5.67E-06	increasing	0
<i>SNCG</i>	BA46	3.40E-09	0.000641	1.95E-06	increasing	0
<i>SNN</i>	BA46	2.47E-09	0.000821	1.88E-10	increasing	0
<i>SNTB2</i>	BA46	1.86E-07	0.000303	0.037585	other	0
<i>SNTG1</i>	BA46	1.61E-05	-0.00071	2.44E-07	decreasing	0
<i>SNTG2</i>	BA46	1.13E-11	0.000811	9.54E-11	increasing	1
<i>SNX21</i>	BA46	9.82E-07	0.000724	5.32E-08	increasing	0
<i>SNX7</i>	BA46	2.28E-07	-0.00043	0.003162	other	0
<i>SOBP</i>	BA46	2.67E-05	-0.00072	8.05E-08	decreasing	0
<i>SOCS7</i>	BA46	5.21E-10	-0.00078	2.40E-09	decreasing	0
<i>SOHLH1</i>	BA46	1.54E-08	0.000411	0.004419	other	0
<i>SORBS2</i>	BA46	2.45E-16	-0.00091	1.47E-13	decreasing	0
<i>SORT1</i>	BA46	1.56E-10	0.000805	1.05E-10	increasing	0
<i>SOWAHB</i>	BA46	8.14E-13	0.000774	5.36E-10	increasing	0
<i>SOWAHC</i>	BA46	4.70E-10	-0.00072	1.43E-08	decreasing	1
<i>SOX11</i>	BA46	1.56E-21	-0.0009	1.77E-14	decreasing	0
<i>SOX4</i>	BA46	1.57E-16	-0.00089	4.95E-14	decreasing	0
<i>SPATA18</i>	BA46	2.09E-07	0.000754	3.89E-09	increasing	0
<i>SPATA2</i>	BA46	2.23E-06	0.0007	1.32E-07	increasing	0
<i>SPATA20</i>	BA46	1.66E-09	0.000733	8.73E-09	increasing	0
<i>SPATA2L</i>	BA46	3.79E-10	-0.00079	2.02E-10	decreasing	0
<i>SPECC1</i>	BA46	8.72E-10	3.95E-05	0.790239	other	0
<i>SPEF1</i>	BA46	1.46E-08	-0.00061	8.33E-06	decreasing	0
<i>SPG21</i>	BA46	5.03E-07	0.00072	6.91E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SPHKAP</i>	BA46	1.50E-08	-0.00071	1.67E-07	decreasing	0
<i>SPIN3</i>	BA46	5.24E-06	0.000765	7.52E-09	increasing	0
<i>SPIN4</i>	BA46	1.11E-08	-0.00041	0.004729	other	0
<i>SPINK2</i>	BA46	3.93E-11	-0.00078	1.76E-09	decreasing	0
<i>SPINK5</i>	BA46	8.70E-06	-0.00072	1.07E-07	decreasing	0
<i>SPINT1</i>	BA46	1.92E-07	-0.00023	0.121418	other	0
<i>SPNS2</i>	BA46	2.32E-07	0.000619	6.09E-06	increasing	0
<i>SPOCD1</i>	BA46	4.65E-10	0.000647	1.44E-06	increasing	0
<i>SPOCK2</i>	BA46	5.03E-08	0.000749	2.41E-08	increasing	0
<i>SPON1</i>	BA46	8.41E-09	-0.0005	0.000318	other	0
<i>SPRN</i>	BA46	1.40E-08	-0.00077	6.09E-10	decreasing	0
<i>SPSB1</i>	BA46	2.04E-09	0.000831	1.12E-10	increasing	0
<i>SPTB</i>	BA46	6.74E-14	-0.00087	3.14E-12	decreasing	0
<i>SPTBN1</i>	BA46	2.30E-07	-0.00078	1.72E-09	decreasing	0
<i>SPTBN2</i>	BA46	8.14E-10	-0.00056	7.70E-05	decreasing	0
<i>SPTBN5</i>	BA46	2.44E-10	-0.00055	0.000127	other	0
<i>SRD5A1</i>	BA46	2.86E-11	-0.00077	1.13E-09	decreasing	0
<i>SREBF1</i>	BA46	1.15E-09	0.000765	1.98E-09	increasing	0
<i>SRGAP1</i>	BA46	5.72E-09	-0.00065	1.65E-06	decreasing	0
<i>SRGAP2</i>	BA46	1.90E-08	-0.00078	8.35E-10	decreasing	0
<i>SRGAP3</i>	BA46	3.25E-08	-0.00075	5.51E-09	decreasing	0
<i>SRP68</i>	BA46	7.50E-13	0.000776	1.65E-09	increasing	0
<i>SRPX2</i>	BA46	1.46E-08	-0.00071	2.28E-07	decreasing	0
<i>SSBP2</i>	BA46	1.83E-07	-0.00049	0.000647	other	0
<i>SSH1</i>	BA46	4.02E-09	0.000691	1.69E-07	increasing	0
<i>SSH3</i>	BA46	1.02E-11	0.00081	2.41E-10	increasing	0
<i>SSTR1</i>	BA46	9.64E-12	-0.00079	1.05E-10	decreasing	0
<i>SSTR2</i>	BA46	2.04E-09	-0.00066	7.11E-07	decreasing	0
<i>SSTR3</i>	BA46	5.11E-11	0.000762	3.44E-09	increasing	0
<i>ST18</i>	BA46	1.78E-14	0.000867	9.89E-13	increasing	0
<i>ST6GAL2</i>	BA46	9.92E-10	-0.00075	8.08E-09	decreasing	0
<i>ST6GALNAC6</i>	BA46	6.12E-08	-0.00077	7.07E-09	decreasing	0
<i>ST8SIA1</i>	BA46	5.30E-12	0.000818	9.62E-11	increasing	0
<i>ST8SIA2</i>	BA46	6.90E-14	-0.00085	1.51E-12	decreasing	0
<i>ST8SIA4</i>	BA46	8.88E-11	-0.0008	5.13E-10	decreasing	0
<i>ST8SIA5</i>	BA46	3.66E-08	-2.69E-06	0.985726	other	0
<i>STAB1</i>	BA46	2.30E-09	-0.00077	3.30E-09	decreasing	0
<i>STAC2</i>	BA46	5.66E-12	0.00084	1.52E-11	increasing	0
<i>STAMBPL1</i>	BA46	2.79E-14	0.000853	5.44E-13	increasing	0
<i>STARD13</i>	BA46	9.24E-07	0.000729	3.60E-08	increasing	1

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>STARD9</i>	BA46	2.27E-07	0.00051	0.000269	other	0
<i>STAT4</i>	BA46	9.67E-06	0.000696	7.82E-08	increasing	0
<i>STAT6</i>	BA46	1.42E-07	0.000745	1.64E-08	increasing	0
<i>STAU2</i>	BA46	4.04E-09	0.000171	0.240999	other	0
<i>STEAP2</i>	BA46	2.92E-14	0.000851	1.87E-12	increasing	0
<i>STEAP3</i>	BA46	3.92E-11	0.000784	7.36E-10	increasing	0
<i>STK17A</i>	BA46	1.10E-08	-0.00077	5.94E-09	decreasing	1
<i>STMN2</i>	BA46	1.74E-07	-0.00051	0.000284	other	0
<i>STRADB</i>	BA46	5.38E-09	-0.00074	1.76E-08	decreasing	0
<i>STRIP2</i>	BA46	5.96E-06	-0.00075	2.54E-08	decreasing	1
<i>STRN4</i>	BA46	4.42E-11	-0.00085	2.18E-11	decreasing	0
<i>STX1A</i>	BA46	2.20E-07	-0.00062	1.16E-05	decreasing	0
<i>SUN2</i>	BA46	1.20E-09	0.000745	4.04E-09	increasing	0
<i>SUPT16H</i>	BA46	2.90E-09	0.000637	4.97E-06	increasing	0
<i>SUPT6H</i>	BA46	1.60E-06	0.000706	1.66E-07	increasing	0
<i>SUSD4</i>	BA46	9.10E-17	0.000872	6.54E-14	increasing	0
<i>SUSD5</i>	BA46	2.11E-09	0.000665	6.17E-07	increasing	0
<i>SV2B</i>	BA46	4.00E-08	0.000768	7.00E-09	increasing	0
<i>SYN2</i>	BA46	3.40E-08	0.000616	7.77E-06	increasing	0
<i>SYN3</i>	BA46	5.20E-09	0.000704	1.71E-07	increasing	0
<i>SYNDIG1</i>	BA46	1.51E-11	0.000697	1.20E-07	increasing	0
<i>SYNGAP1</i>	BA46	1.46E-05	-0.00073	6.09E-08	decreasing	0
<i>SYNJ2</i>	BA46	2.12E-18	0.0009	8.96E-15	increasing	0
<i>SYT14</i>	BA46	1.49E-07	0.00067	8.66E-07	increasing	0
<i>SYT17</i>	BA46	5.68E-12	-0.00081	1.27E-10	decreasing	0
<i>SYT2</i>	BA46	2.65E-13	0.000824	2.11E-11	increasing	0
<i>SYT6</i>	BA46	1.25E-06	-0.00069	9.74E-08	decreasing	0
<i>SYTL1</i>	BA46	4.98E-16	0.000869	9.12E-14	increasing	0
<i>TACR1</i>	BA46	5.47E-08	-0.00044	0.002237	other	0
<i>TACR3</i>	BA46	1.76E-09	0.000669	1.04E-06	increasing	1
<i>TADA2A</i>	BA46	1.45E-07	-0.0007	3.29E-07	decreasing	0
<i>TAF4B</i>	BA46	1.61E-16	0.000858	2.37E-12	increasing	0
<i>TAGLN2</i>	BA46	1.29E-07	-0.00075	2.78E-08	decreasing	0
<i>TAGLN3</i>	BA46	6.23E-08	0.000744	1.67E-08	increasing	0
<i>TAL1</i>	BA46	5.93E-08	-0.00073	7.41E-08	decreasing	0
<i>TAP2</i>	BA46	1.51E-06	0.000732	1.62E-08	increasing	0
<i>TAPBP</i>	BA46	2.51E-08	0.000691	1.63E-07	increasing	0
<i>TARSL2</i>	BA46	3.85E-16	0.000899	1.56E-13	increasing	0
<i>TATDN2</i>	BA46	1.11E-10	-0.00079	1.59E-10	decreasing	0
<i>TBC1D22B</i>	BA46	7.86E-09	-0.00073	4.47E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TBC1D4</i>	BA46	3.28E-08	0.000609	9.02E-06	increasing	0
<i>TBCEL</i>	BA46	1.55E-05	-0.00075	2.36E-08	decreasing	0
<i>TBR1</i>	BA46	7.67E-07	0.000745	3.16E-08	increasing	0
<i>TBX3</i>	BA46	3.29E-08	-0.00082	3.07E-10	decreasing	0
<i>TCEAL6</i>	BA46	4.70E-07	0.000707	6.97E-08	increasing	0
<i>TCF12</i>	BA46	1.03E-07	-0.00018	0.225039	other	0
<i>TCN2</i>	BA46	9.99E-07	-0.00071	1.04E-07	decreasing	0
<i>TCTN1</i>	BA46	2.52E-08	-0.00059	1.20E-05	decreasing	0
<i>TECTA</i>	BA46	1.15E-11	-0.00065	2.98E-06	decreasing	0
<i>TENM3</i>	BA46	2.66E-12	-0.0008	1.78E-10	decreasing	0
<i>TENM4</i>	BA46	2.48E-05	-0.00069	1.79E-07	decreasing	0
<i>TERF2IP</i>	BA46	1.42E-08	0.000748	2.51E-08	increasing	0
<i>TESC</i>	BA46	2.95E-08	0.000306	0.035758	other	0
<i>TESK2</i>	BA46	2.40E-07	0.000169	0.258315	other	0
<i>TESPA1</i>	BA46	8.89E-09	7.37E-05	0.621982	other	0
<i>TET1</i>	BA46	4.39E-13	-0.00082	8.64E-11	decreasing	0
<i>TET2</i>	BA46	6.67E-12	-0.0008	4.42E-10	decreasing	0
<i>TET3</i>	BA46	4.61E-17	-0.00088	1.15E-13	decreasing	0
<i>TEX29</i>	BA46	3.79E-08	0.000362	0.01457	other	0
<i>TEX37</i>	BA46	3.41E-10	-0.00075	3.24E-09	decreasing	0
<i>TF</i>	BA46	5.40E-08	0.000663	6.76E-07	increasing	0
<i>TFAP4</i>	BA46	7.71E-07	0.000767	5.44E-09	increasing	0
<i>TFDP2</i>	BA46	9.12E-11	0.000666	8.63E-07	increasing	0
<i>TFRC</i>	BA46	1.78E-07	-0.00055	9.64E-05	decreasing	0
<i>TGM3</i>	BA46	2.14E-06	-0.00071	3.51E-08	decreasing	1
<i>TGM6</i>	BA46	1.53E-09	-9.34E-05	0.542292	other	0
<i>THBS4</i>	BA46	5.91E-16	0.000778	2.82E-09	increasing	0
<i>THRB</i>	BA46	1.27E-08	0.000683	4.21E-07	increasing	0
<i>THUMPD1</i>	BA46	8.07E-09	0.000473	0.001106	other	0
<i>THYN1</i>	BA46	1.34E-06	0.000766	7.96E-09	increasing	1
<i>TICRR</i>	BA46	2.56E-07	-0.00058	2.08E-05	decreasing	0
<i>TIMD4</i>	BA46	4.02E-08	-0.00064	1.87E-06	decreasing	0
<i>TIMP2</i>	BA46	6.43E-11	-0.00074	8.12E-09	decreasing	0
<i>TLE2</i>	BA46	3.38E-16	0.000871	4.77E-13	increasing	0
<i>TLE3</i>	BA46	2.50E-12	-0.00084	5.50E-12	decreasing	0
<i>TLL1</i>	BA46	1.92E-09	-0.00044	0.002124	other	0
<i>TLR6</i>	BA46	9.24E-06	-0.00072	1.25E-07	decreasing	0
<i>TLR7</i>	BA46	1.09E-06	-0.00074	3.39E-08	decreasing	0
<i>TM9SF2</i>	BA46	1.29E-07	-0.00052	0.00034	other	0
<i>TMCC2</i>	BA46	5.89E-12	0.000823	5.00E-11	increasing	0



**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TMED10</i>	BA46	9.35E-10	-8.48E-05	0.575099	other	0
<i>TMEM125</i>	BA46	2.17E-10	0.000763	3.12E-09	increasing	0
<i>TMEM130</i>	BA46	3.06E-10	0.000618	5.25E-06	increasing	0
<i>TMEM132B</i>	BA46	2.96E-14	-0.00082	2.10E-11	decreasing	0
<i>TMEM132D</i>	BA46	2.19E-10	-0.00065	2.98E-06	decreasing	0
<i>TMEM144</i>	BA46	1.64E-09	0.000777	2.67E-09	increasing	0
<i>TMEM151B</i>	BA46	4.77E-09	-0.00081	4.77E-10	decreasing	0
<i>TMEM163</i>	BA46	3.08E-14	-0.00079	4.26E-10	decreasing	0
<i>TMEM164</i>	BA46	2.97E-07	-0.00075	1.82E-08	decreasing	0
<i>TMEM169</i>	BA46	9.10E-09	-0.00068	3.43E-07	decreasing	0
<i>TMEM178A</i>	BA46	7.09E-08	0.000107	0.480287	other	0
<i>TMEM178B</i>	BA46	1.98E-09	-0.00065	1.30E-06	decreasing	0
<i>TMEM192</i>	BA46	2.38E-09	0.000698	1.10E-07	increasing	0
<i>TMEM200B</i>	BA46	1.45E-06	0.000715	1.03E-07	increasing	0
<i>TMEM200C</i>	BA46	4.27E-08	-0.00078	1.21E-09	decreasing	0
<i>TMEM233</i>	BA46	7.41E-06	0.000701	2.48E-07	increasing	0
<i>TMEM235</i>	BA46	2.03E-09	0.000746	2.85E-08	increasing	0
<i>TMEM25</i>	BA46	2.05E-12	0.000781	2.15E-09	increasing	0
<i>TMEM26</i>	BA46	0.000114949	0.000706	2.50E-07	increasing	0
<i>TMEM35</i>	BA46	1.51E-10	0.000174	0.243402	other	0
<i>TMEM38A</i>	BA46	9.59E-10	-0.00068	2.94E-07	decreasing	0
<i>TMEM74</i>	BA46	7.76E-12	-0.00079	1.04E-09	decreasing	0
<i>TMEM86B</i>	BA46	1.28E-07	0.000633	6.03E-06	increasing	0
<i>TMEM88B</i>	BA46	5.30E-09	0.000781	2.25E-09	increasing	0
<i>TMEM8B</i>	BA46	2.30E-07	-0.0006	2.09E-05	decreasing	0
<i>TMEM91</i>	BA46	1.30E-06	0.000737	5.03E-08	increasing	0
<i>TMOD3</i>	BA46	1.14E-07	-0.00063	3.24E-06	decreasing	0
<i>TMPRSS13</i>	BA46	1.81E-09	-0.00073	4.25E-08	decreasing	0
<i>TMTC2</i>	BA46	1.32E-07	0.000687	2.55E-07	increasing	0
<i>TMX4</i>	BA46	9.34E-11	0.000724	5.76E-08	increasing	0
<i>TNC</i>	BA46	1.33E-11	-0.00078	6.24E-10	decreasing	0
<i>TNFRSF14</i>	BA46	2.92E-06	0.000707	1.25E-07	increasing	0
<i>TNFRSF18</i>	BA46	2.07E-05	0.000717	1.43E-07	increasing	0
<i>TNFSF9</i>	BA46	1.18E-10	0.000744	1.68E-08	increasing	0
<i>TNKS2</i>	BA46	2.15E-11	-0.00075	6.53E-09	decreasing	0
<i>TNNC2</i>	BA46	5.27E-11	0.000802	2.52E-10	increasing	0
<i>TNNT2</i>	BA46	4.40E-09	0.000728	2.04E-08	increasing	1
<i>TNRC6A</i>	BA46	1.94E-06	0.000749	2.63E-08	increasing	0
<i>TOLLIP</i>	BA46	6.67E-10	0.00033	0.023998	other	0
<i>TOMM34</i>	BA46	3.44E-12	0.000846	7.12E-12	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TOR1AIP1</i>	BA46	3.07E-09	0.000734	1.39E-08	increasing	0
<i>TP53INP2</i>	BA46	2.53E-07	-0.00076	9.51E-09	decreasing	0
<i>TPD52</i>	BA46	1.09E-10	0.000753	4.32E-09	increasing	0
<i>TPD52L1</i>	BA46	3.82E-14	0.00079	6.44E-10	increasing	0
<i>TPRG1L</i>	BA46	8.89E-12	0.000825	9.11E-11	increasing	0
<i>TRAF3</i>	BA46	3.30E-11	-0.00071	1.66E-07	decreasing	0
<i>TREM2</i>	BA46	5.38E-08	-0.00078	2.72E-09	decreasing	0
<i>TRHDE</i>	BA46	4.46E-08	-0.00077	6.69E-09	decreasing	0
<i>TRIB1</i>	BA46	5.22E-07	-0.00075	1.52E-08	decreasing	0
<i>TRIB2</i>	BA46	1.04E-13	-0.00087	2.08E-12	decreasing	0
<i>TRIM46</i>	BA46	1.61E-08	-0.00073	1.21E-08	decreasing	0
<i>TRIM66</i>	BA46	7.44E-11	0.000758	8.77E-09	increasing	0
<i>TRIM9</i>	BA46	3.82E-11	-0.00085	3.25E-11	decreasing	0
<i>TRIO</i>	BA46	9.68E-16	-0.00088	1.49E-13	decreasing	0
<i>TRPC3</i>	BA46	6.89E-08	-0.00073	4.59E-08	decreasing	0
<i>TRPV2</i>	BA46	4.45E-09	0.000682	3.29E-07	increasing	0
<i>TSHZ2</i>	BA46	1.78E-08	0.000661	1.09E-06	increasing	0
<i>TSPAN14</i>	BA46	4.61E-16	-0.00088	2.38E-13	decreasing	0
<i>TSPAN15</i>	BA46	2.48E-07	0.000377	0.008923	other	0
<i>TSPAN2</i>	BA46	2.39E-07	-0.00043	0.002606	other	0
<i>TSPYL2</i>	BA46	3.59E-18	0.000875	1.54E-13	increasing	0
<i>TTBK2</i>	BA46	5.77E-13	0.000822	2.57E-11	increasing	0
<i>TTC1</i>	BA46	1.63E-10	0.000668	8.51E-07	increasing	0
<i>TTC22</i>	BA46	1.18E-05	0.00072	1.23E-07	increasing	0
<i>TTC38</i>	BA46	3.00E-08	-0.00067	6.97E-07	decreasing	0
<i>TTC40</i>	BA46	4.24E-10	-0.00025	0.092192	other	0
<i>TTC9</i>	BA46	6.37E-08	-0.00054	9.42E-05	decreasing	0
<i>TTC9B</i>	BA46	4.57E-07	-0.00074	2.33E-08	decreasing	1
<i>TTL</i>	BA46	2.11E-09	-0.00079	2.02E-09	decreasing	0
<i>TUBA1A</i>	BA46	4.99E-09	-0.00055	7.66E-05	decreasing	0
<i>TUBB</i>	BA46	1.31E-07	-0.00046	0.001245	other	0
<i>TUFT1</i>	BA46	1.63E-07	0.000688	3.55E-07	increasing	0
<i>TXLNG</i>	BA46	5.03E-08	0.000689	2.32E-07	increasing	0
<i>UBP1</i>	BA46	1.97E-10	0.000583	2.56E-05	increasing	0
<i>UBTD2</i>	BA46	2.31E-09	-0.0007	1.38E-07	decreasing	0
<i>UBXN2B</i>	BA46	1.55E-11	-0.00076	6.38E-09	decreasing	0
<i>UCK2</i>	BA46	2.97E-14	-0.00083	9.17E-12	decreasing	0
<i>UGT3A1</i>	BA46	1.87E-06	0.000696	7.36E-09	increasing	0
<i>UNC13C</i>	BA46	5.46E-11	-0.00086	9.42E-12	decreasing	1
<i>UNC45B</i>	BA46	1.31E-06	0.000737	2.08E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>UNC79</i>	BA46	5.64E-08	-8.78E-05	0.559878	other	0
<i>URM1</i>	BA46	3.52E-08	-0.00075	1.48E-08	decreasing	0
<i>USH1C</i>	BA46	3.61E-11	0.000814	1.58E-10	increasing	0
<i>USP11</i>	BA46	2.10E-08	0.000765	7.48E-09	increasing	0
<i>USP12</i>	BA46	8.56E-13	-0.00086	8.99E-12	decreasing	0
<i>USP28</i>	BA46	1.19E-07	0.000623	8.46E-06	increasing	0
<i>USP45</i>	BA46	4.23E-08	0.000575	2.23E-05	increasing	0
<i>USP46</i>	BA46	5.55E-09	-0.0008	7.81E-10	decreasing	0
<i>USP54</i>	BA46	7.53E-07	0.000698	1.13E-07	increasing	0
<i>USP6NL</i>	BA46	1.16E-08	-0.00055	6.46E-05	decreasing	0
<i>UTRN</i>	BA46	2.94E-08	-0.00072	9.47E-08	decreasing	0
<i>VAMP1</i>	BA46	1.77E-12	0.000811	2.79E-11	increasing	1
<i>VASH1</i>	BA46	6.16E-06	-0.00072	3.91E-08	decreasing	0
<i>VAV2</i>	BA46	2.35E-09	-0.00081	8.16E-11	decreasing	0
<i>VEPH1</i>	BA46	1.05E-12	-0.00077	1.81E-09	decreasing	0
<i>VHL</i>	BA46	2.86E-09	-0.00073	2.27E-08	decreasing	1
<i>VLDLR</i>	BA46	1.52E-09	-0.00071	1.64E-07	decreasing	0
<i>VOPP1</i>	BA46	1.20E-14	-0.00085	6.09E-12	decreasing	0
<i>VPS13A</i>	BA46	9.03E-08	0.000574	3.53E-05	increasing	0
<i>VPS37B</i>	BA46	1.60E-05	-0.00073	5.36E-08	decreasing	0
<i>WAC</i>	BA46	2.20E-09	-6.38E-05	0.667542	other	0
<i>WASL</i>	BA46	4.71E-10	0.000691	1.03E-07	increasing	0
<i>WBP2</i>	BA46	3.62E-11	0.000747	6.24E-09	increasing	0
<i>WBP4</i>	BA46	6.64E-06	0.000691	1.65E-07	increasing	0
<i>WDR1</i>	BA46	2.05E-12	-0.00078	1.28E-09	decreasing	0
<i>WDR6</i>	BA46	1.43E-07	0.000229	0.118871	other	0
<i>WDTC1</i>	BA46	2.92E-09	0.000668	6.62E-07	increasing	0
<i>WEE1</i>	BA46	5.44E-10	-0.00058	4.20E-05	decreasing	0
<i>WFIKKN1</i>	BA46	2.25E-08	-0.00016	0.284026	other	0
<i>WFS1</i>	BA46	2.88E-11	0.000821	5.77E-11	increasing	0
<i>WIPF3</i>	BA46	2.75E-07	0.000785	1.92E-09	increasing	0
<i>WLS</i>	BA46	2.10E-11	-1.00E-05	0.946954	other	0
<i>WNT2</i>	BA46	1.23E-09	0.000655	6.66E-07	increasing	0
<i>WSB2</i>	BA46	1.75E-13	-0.00086	3.04E-12	decreasing	0
<i>WWC1</i>	BA46	8.95E-19	-0.00089	3.47E-14	decreasing	0
<i>WWC2</i>	BA46	1.71E-09	-0.00078	1.29E-09	decreasing	0
<i>XKR4</i>	BA46	6.63E-16	-0.00086	4.89E-13	decreasing	0
<i>XPR1</i>	BA46	4.73E-11	-0.00075	7.14E-09	decreasing	0
<i>XRCC5</i>	BA46	3.74E-08	0.000176	0.236581	other	0
<i>XRN2</i>	BA46	1.04E-08	-0.00064	3.17E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>XYLT1</i>	BA46	7.63E-10	-0.0008	1.65E-10	decreasing	0
<i>YBX1</i>	BA46	1.18E-15	-0.00087	3.40E-13	decreasing	0
<i>YES1</i>	BA46	8.85E-09	-0.00073	3.20E-08	decreasing	0
<i>YPEL1</i>	BA46	9.25E-16	-0.00087	1.84E-13	decreasing	0
<i>YPEL4</i>	BA46	2.00E-08	0.000775	1.38E-09	increasing	0
<i>YWHAB</i>	BA46	1.96E-07	0.000159	0.289663	other	0
<i>ZBED1</i>	BA46	4.05E-05	0.000726	7.40E-08	increasing	0
<i>ZBTB10</i>	BA46	1.08E-11	-0.00073	4.05E-08	decreasing	0
<i>ZBTB16</i>	BA46	4.39E-12	0.000827	1.67E-11	increasing	0
<i>ZBTB18</i>	BA46	5.58E-09	-0.00069	1.41E-07	decreasing	0
<i>ZBTB7C</i>	BA46	1.45E-08	-1.69E-05	0.9093	other	0
<i>ZBTB8A</i>	BA46	2.65E-08	-0.00059	1.40E-05	decreasing	0
<i>ZC4H2</i>	BA46	2.20E-08	-0.00067	5.81E-07	decreasing	0
<i>ZDHHC14</i>	BA46	3.08E-13	-0.00088	1.42E-12	decreasing	0
<i>ZDHHC2</i>	BA46	2.92E-08	-0.00033	0.02128	other	0
<i>ZEB1</i>	BA46	1.38E-07	7.00E-05	0.637483	other	0
<i>ZFAND6</i>	BA46	4.32E-07	-0.00071	1.46E-07	decreasing	0
<i>ZFYVE20</i>	BA46	1.01E-10	0.000795	3.26E-10	increasing	0
<i>ZMYND11</i>	BA46	2.64E-09	-0.0007	2.72E-07	decreasing	0
<i>ZNF106</i>	BA46	8.60E-08	0.000188	0.201732	other	0
<i>ZNF229</i>	BA46	4.98E-16	-0.00086	1.75E-13	decreasing	0
<i>ZNF248</i>	BA46	6.13E-08	0.000782	2.51E-09	increasing	0
<i>ZNF282</i>	BA46	1.99E-07	-9.25E-05	0.532992	other	0
<i>ZNF300</i>	BA46	3.23E-14	-0.0008	6.98E-11	decreasing	0
<i>ZNF331</i>	BA46	4.54E-07	0.000782	2.94E-09	increasing	0
<i>ZNF346</i>	BA46	5.75E-11	-0.0008	7.45E-11	decreasing	0
<i>ZNF395</i>	BA46	1.58E-07	0.000764	1.08E-09	increasing	0
<i>ZNF404</i>	BA46	1.93E-07	-0.00071	1.15E-07	decreasing	0
<i>ZNF436</i>	BA46	4.33E-11	-0.00078	2.20E-09	decreasing	0
<i>ZNF462</i>	BA46	2.78E-06	-0.00074	2.25E-08	decreasing	0
<i>ZNF469</i>	BA46	4.32E-08	0.00024	0.101555	other	1
<i>ZNF483</i>	BA46	1.16E-18	0.000891	7.22E-15	increasing	0
<i>ZNF528</i>	BA46	1.11E-08	-0.00072	1.49E-08	decreasing	0
<i>ZNF540</i>	BA46	3.06E-09	0.00078	1.01E-09	increasing	0
<i>ZNF557</i>	BA46	8.16E-05	0.000706	2.50E-07	increasing	0
<i>ZNF641</i>	BA46	4.16E-10	-0.00072	4.48E-08	decreasing	1
<i>ZNF704</i>	BA46	6.20E-09	-0.00076	3.82E-09	decreasing	0
<i>ZNF711</i>	BA46	5.40E-08	-0.0003	0.046192	other	0
<i>ZNF727P</i>	BA46	2.37E-10	-0.00074	5.70E-09	decreasing	0
<i>ABCA3</i>	Blood	8.08E-10	0.000624	9.72E-06	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ABCC3</i>	Blood	1.40E-07	0.00032	0.033084	other	0
<i>ACVR1C</i>	Blood	4.43E-08	0.000576	5.50E-05	increasing	0
<i>ADAMTS13</i>	Blood	9.57E-08	0.000227	0.135995	other	0
<i>AFMID</i>	Blood	1.57E-07	0.000525	0.000281	other	0
<i>AIFM3</i>	Blood	7.44E-08	0.000341	0.022849	other	1
<i>AKAP12</i>	Blood	9.11E-09	-0.00048	0.000911	other	0
<i>ALDH3B1</i>	Blood	1.54E-09	0.00016	0.296119	other	0
<i>ANGPTL1</i>	Blood	1.58E-08	-0.00054	0.000213	other	0
<i>AR</i>	Blood	2.77E-07	0.000732	7.26E-08	increasing	0
<i>ASB13</i>	Blood	1.36E-07	0.000196	0.196867	other	0
<i>BCL11A</i>	Blood	3.65E-08	-0.00061	1.61E-05	decreasing	0
<i>BEND5</i>	Blood	2.36E-08	-0.00054	0.000136	other	0
<i>BLNK</i>	Blood	3.48E-11	-0.00064	3.95E-06	decreasing	0
<i>BRCA2</i>	Blood	2.32E-07	-0.00055	0.000115	other	0
<i>C1H11orf82</i>	Blood	1.17E-07	-0.00042	0.004274	other	0
<i>CASC5</i>	Blood	1.09E-07	-0.00056	7.56E-05	decreasing	0
<i>CCDC180</i>	Blood	1.28E-07	0.000625	9.78E-06	increasing	0
<i>CD38</i>	Blood	8.43E-09	-0.00059	2.48E-05	decreasing	0
<i>CD72</i>	Blood	4.27E-08	-0.00051	0.000303	other	0
<i>CD79A</i>	Blood	2.08E-07	-0.00041	0.00447	other	0
<i>CDC42BPB</i>	Blood	1.68E-07	0.000185	0.226215	other	0
<i>CDC42BPG</i>	Blood	1.90E-09	0.000495	0.000705	other	0
<i>CDHR2</i>	Blood	2.46E-07	0.000458	0.001878	other	0
<i>CEP131</i>	Blood	7.73E-08	0.000468	0.001432	other	0
<i>CHI3L2</i>	Blood	5.72E-08	-0.00078	4.59E-09	decreasing	0
<i>CLEC17A</i>	Blood	1.32E-07	-0.0004	0.006203	other	0
<i>CLSTN3</i>	Blood	6.01E-08	0.00069	4.89E-07	increasing	0
<i>CR2</i>	Blood	1.59E-08	-0.00066	2.27E-06	decreasing	0
<i>DAPK2</i>	Blood	2.48E-07	0.000689	5.63E-07	increasing	0
<i>DDR1</i>	Blood	4.88E-08	0.000576	5.78E-05	increasing	0
<i>DLL1</i>	Blood	2.37E-10	0.000709	1.99E-07	increasing	0
<i>EBF1</i>	Blood	6.31E-09	-0.00048	0.000872	other	0
<i>EFR3B</i>	Blood	2.55E-07	-6.98E-05	0.649506	other	0
<i>ELK4</i>	Blood	1.61E-11	-0.0004	0.006549	other	0
<i>EPHB2</i>	Blood	2.91E-08	0.000108	0.479213	other	0
<i>EPHB6</i>	Blood	5.15E-08	0.000534	0.000228	other	0
<i>FAM110C</i>	Blood	4.82E-08	0.000761	1.38E-08	increasing	0
<i>FAM129C</i>	Blood	1.84E-07	-0.0005	0.000502	other	0
<i>FAM216B</i>	Blood	3.16E-08	-0.00035	0.019494	other	0
<i>FAM69A</i>	Blood	1.39E-07	-0.00059	2.52E-05	decreasing	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FCER2</i>	Blood	4.37E-08	-0.00052	0.000259	other	0
<i>FCRL1</i>	Blood	1.30E-07	-0.00045	0.00205	other	0
<i>FCRLA</i>	Blood	1.61E-07	-0.00045	0.001604	other	0
<i>GEN1</i>	Blood	7.79E-08	-0.00055	0.00011	other	0
<i>GPR160</i>	Blood	6.80E-08	-0.00027	0.075089	other	0
<i>HHIPL1</i>	Blood	1.98E-08	0.000138	0.366392	other	0
<i>HNRNPA3</i>	Blood	1.17E-07	-0.00045	0.002252	other	0
<i>HS3ST1</i>	Blood	8.89E-08	-0.00054	0.000156	other	0
<i>IFI6</i>	Blood	4.29E-09	-0.00034	0.025306	other	0
<i>IFNLR1</i>	Blood	1.21E-07	-0.00043	0.00265	other	1
<i>IGF2BP3</i>	Blood	1.48E-07	-0.00052	0.000322	other	0
<i>INADL</i>	Blood	1.99E-08	0.000678	8.67E-07	increasing	0
<i>INPP5E</i>	Blood	5.14E-09	0.000489	0.000845	other	0
<i>JUP</i>	Blood	1.29E-07	-0.0004	0.006566	other	0
<i>KCNA2</i>	Blood	1.22E-07	0.00036	0.014856	other	0
<i>KCNQ5</i>	Blood	2.71E-08	-0.00071	1.48E-07	decreasing	0
<i>KIAA0040</i>	Blood	1.11E-07	-0.00036	0.014713	other	0
<i>KIAA1524</i>	Blood	1.76E-08	-0.00068	8.28E-07	decreasing	0
<i>KIF21A</i>	Blood	1.93E-07	0.000693	3.82E-07	increasing	0
<i>KLHL14</i>	Blood	4.03E-09	-0.00066	2.00E-06	decreasing	0
<i>LATS2</i>	Blood	9.86E-08	9.23E-05	0.538339	other	0
<i>LDB2</i>	Blood	1.35E-07	-0.00057	5.17E-05	decreasing	0
<i>LEF1</i>	Blood	2.15E-07	-0.00056	9.55E-05	decreasing	0
<i>LOC103214438</i>	Blood	2.03E-08	-0.00046	0.001669	other	0
<i>LOC103214439</i>	Blood	5.46E-08	-0.00043	0.003143	other	0
<i>LOC103214991</i>	Blood	8.67E-08	-0.00073	8.55E-08	decreasing	0
<i>LOC103217853</i>	Blood	2.11E-08	-3.76E-07	0.99805	other	0
<i>LOC103218130</i>	Blood	7.38E-07	-0.00074	3.32E-08	decreasing	0
<i>LOC103220571</i>	Blood	4.18E-08	-0.00039	0.007641	other	0
<i>LOC103221838</i>	Blood	4.09E-09	-0.00066	2.03E-06	decreasing	0
<i>LOC103222076</i>	Blood	1.80E-05	-0.0007	2.59E-07	decreasing	0
<i>LOC103222418</i>	Blood	2.36E-08	4.28E-05	0.779213	other	0
<i>LOC103224147</i>	Blood	1.59E-07	0.000282	0.061705	other	0
<i>LOC103225055</i>	Blood	1.83E-09	-0.0001	0.499157	other	0
<i>LOC103225074</i>	Blood	1.17E-08	-6.31E-05	0.680106	other	0
<i>LOC103225142</i>	Blood	5.37E-08	-2.31E-05	0.87638	other	0
<i>LOC103226462</i>	Blood	1.04E-07	0.000117	0.428418	other	0
<i>LOC103229635</i>	Blood	5.26E-08	-0.00069	6.51E-07	decreasing	0
<i>LOC103230929</i>	Blood	1.25E-09	0.000192	0.205963	other	0
<i>LOC103231026</i>	Blood	3.63E-08	0.00034	0.023124	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103231767</i>	Blood	7.64E-10	-5.17E-05	0.735427	other	0
<i>LOC103232315</i>	Blood	1.77E-07	4.84E-05	0.750523	other	0
<i>LOC103232530</i>	Blood	2.47E-07	-2.24E-05	0.883424	other	0
<i>LOC103232593</i>	Blood	2.02E-07	-0.00063	6.01E-06	decreasing	0
<i>LOC103232959</i>	Blood	2.65E-08	-0.00052	0.000254	other	0
<i>LOC103234031</i>	Blood	9.64E-08	0.000746	3.32E-08	increasing	0
<i>LOC103235169</i>	Blood	9.85E-08	0.000252	0.093873	other	0
<i>LOC103237606</i>	Blood	1.22E-07	0.000478	0.000926	other	0
<i>LOC103237774</i>	Blood	2.80E-08	-0.00067	1.51E-06	decreasing	0
<i>LOC103239517</i>	Blood	5.91E-08	7.82E-06	0.959405	other	0
<i>LOC103239668</i>	Blood	1.75E-07	0.000547	0.000144	other	0
<i>LOC103240114</i>	Blood	1.97E-07	-1.31E-07	0.999321	other	0
<i>LOC103241811</i>	Blood	2.94E-08	-0.00045	0.002046	other	0
<i>LOC103242065</i>	Blood	1.42E-07	0.000188	0.203367	other	0
<i>LOC103244408</i>	Blood	9.39E-08	-0.00046	0.00157	other	0
<i>LOC103245978</i>	Blood	3.03E-08	0.000375	0.012135	other	0
<i>LOC103246317</i>	Blood	2.31E-08	-0.00059	3.66E-05	decreasing	0
<i>LOC103246543</i>	Blood	7.38E-08	-0.00049	0.000715	other	0
<i>LOC103248861</i>	Blood	5.37E-06	0.000711	2.13E-07	increasing	0
<i>LRP12</i>	Blood	6.60E-08	-0.0006	2.33E-05	decreasing	0
<i>LTBP3</i>	Blood	1.30E-09	-5.31E-05	0.729359	other	0
<i>LZTFL1</i>	Blood	1.80E-08	-0.00073	5.91E-08	decreasing	0
<i>MAPK1IP1L</i>	Blood	1.60E-07	-0.0004	0.006007	other	0
<i>MBNL3</i>	Blood	4.93E-09	-0.00025	0.087893	other	0
<i>MCF2L</i>	Blood	7.96E-08	9.53E-05	0.534342	other	0
<i>MID2</i>	Blood	1.27E-06	0.000766	1.05E-08	increasing	0
<i>MMP11</i>	Blood	4.87E-09	-0.00018	0.234224	other	0
<i>MS4A1</i>	Blood	9.30E-08	-0.00046	0.001424	other	0
<i>NBEA</i>	Blood	4.08E-08	-0.00058	3.08E-05	decreasing	0
<i>NEK2</i>	Blood	4.13E-08	-0.00039	0.008315	other	0
<i>NETO2</i>	Blood	9.15E-08	-0.00054	0.000126	other	0
<i>NMUR1</i>	Blood	7.46E-08	0.000716	1.56E-07	increasing	0
<i>NREP</i>	Blood	2.36E-09	-0.00081	6.61E-10	decreasing	0
<i>NTN3</i>	Blood	3.70E-08	0.000179	0.240786	other	0
<i>NTRK1</i>	Blood	1.06E-07	-3.08E-05	0.841051	other	0
<i>PAX5</i>	Blood	3.22E-09	-0.00053	0.000223	other	0
<i>PDZD4</i>	Blood	6.59E-07	0.000718	5.33E-08	increasing	0
<i>PGM5</i>	Blood	1.98E-07	0.000675	1.02E-06	increasing	0
<i>PHLDB3</i>	Blood	2.33E-07	0.00034	0.023705	other	0
<i>PLCD1</i>	Blood	5.23E-08	0.000468	0.001419	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PLD2</i>	Blood	9.31E-08	0.000476	0.001177	other	0
<i>PMEPA1</i>	Blood	5.88E-08	-0.00068	5.51E-07	decreasing	0
<i>PPFIA4</i>	Blood	5.41E-08	6.63E-05	0.665763	other	0
<i>PPP1CB</i>	Blood	5.06E-08	-0.00031	0.034605	other	0
<i>PRDM8</i>	Blood	2.40E-08	0.000543	0.00017	other	0
<i>PSAT1</i>	Blood	1.68E-07	-0.00066	1.20E-06	decreasing	0
<i>R3HDM1</i>	Blood	1.93E-08	-0.00046	0.001887	other	0
<i>RAB30</i>	Blood	4.21E-08	-0.00061	1.51E-05	decreasing	0
<i>RALGPS2</i>	Blood	2.16E-08	-0.00051	0.000401	other	0
<i>RAPGEF5</i>	Blood	2.54E-10	-0.00072	1.23E-07	decreasing	0
<i>RFX2</i>	Blood	4.65E-08	-5.32E-05	0.729063	other	0
<i>RIN1</i>	Blood	1.45E-07	0.000343	0.022185	other	0
<i>RIN2</i>	Blood	1.76E-07	-9.06E-05	0.548428	other	0
<i>SCAI</i>	Blood	6.10E-08	-0.00031	0.034368	other	0
<i>SCIN</i>	Blood	1.83E-07	6.63E-05	0.658968	other	0
<i>SEMA4C</i>	Blood	3.62E-08	0.000194	0.202818	other	0
<i>SEMA4F</i>	Blood	2.29E-08	0.000618	1.28E-05	increasing	0
<i>SFRP4</i>	Blood	8.23E-09	-0.00017	0.264873	other	0
<i>SFXN5</i>	Blood	1.27E-07	0.000182	0.232415	other	0
<i>SLC16A10</i>	Blood	8.51E-08	-0.00025	0.099055	other	0
<i>SLC25A10</i>	Blood	8.79E-08	5.36E-05	0.727143	other	0
<i>SLC35E4</i>	Blood	1.37E-07	0.000189	0.216585	other	0
<i>SOX4</i>	Blood	2.59E-08	-0.00075	2.01E-08	decreasing	0
<i>SPTBN5</i>	Blood	2.06E-07	-3.60E-05	0.814449	other	0
<i>ST8SIA1</i>	Blood	9.50E-08	0.000738	4.63E-08	increasing	0
<i>STAB1</i>	Blood	1.25E-09	0.000111	0.469968	other	0
<i>STOX1</i>	Blood	2.04E-07	-0.00056	8.64E-05	decreasing	0
<i>TAF4B</i>	Blood	7.37E-08	-0.00075	3.46E-08	decreasing	0
<i>TBKBP1</i>	Blood	2.39E-07	0.000534	0.000217	other	0
<i>TCF4</i>	Blood	1.78E-07	-0.00049	0.000659	other	0
<i>TCL1A</i>	Blood	6.60E-09	-0.00065	2.60E-06	decreasing	0
<i>TET1</i>	Blood	1.18E-07	-0.00057	6.60E-05	decreasing	0
<i>TIMELESS</i>	Blood	5.49E-08	-2.38E-05	0.876199	other	0
<i>TMEM44</i>	Blood	1.59E-07	0.000432	0.003481	other	0
<i>TPD52</i>	Blood	1.74E-07	-0.00051	0.000314	other	0
<i>TSPAN13</i>	Blood	6.12E-08	-0.00068	6.91E-07	decreasing	0
<i>TSPO2</i>	Blood	1.11E-07	-4.52E-05	0.768144	other	0
<i>VPREB3</i>	Blood	6.12E-10	-0.00057	3.35E-05	decreasing	0
<i>VWA2</i>	Blood	2.00E-07	-0.0004	0.00674	other	0
<i>WNT11</i>	Blood	4.32E-08	0.000717	1.60E-07	increasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>XKRX</i>	Blood	4.19E-08	-0.00037	0.011613	other	0
<i>ZDHC21</i>	Blood	2.34E-08	-0.00046	0.001692	other	0
<i>ZNF606</i>	Blood	4.09E-06	-0.00072	1.35E-07	decreasing	0
<i>ZNF709</i>	Blood	1.33E-08	-0.00071	2.70E-07	decreasing	0
<i>AACS</i>	Caudate	1.01E-10	0.000137	0.358733	other	0
<i>AAR2</i>	Caudate	1.24E-08	-0.00022	0.129388	other	0
<i>AARS2</i>	Caudate	4.46E-08	0.000353	0.016358	other	0
<i>AATK</i>	Caudate	1.42E-11	0.000786	1.43E-09	increasing	0
<i>ABCA2</i>	Caudate	2.59E-07	0.000752	9.28E-09	increasing	0
<i>ABCA3</i>	Caudate	3.62E-12	0.000549	0.000138	other	0
<i>ABCA8</i>	Caudate	5.28E-18	0.000846	2.97E-12	increasing	0
<i>ABCB9</i>	Caudate	3.08E-11	0.000686	4.61E-07	increasing	0
<i>ABCC10</i>	Caudate	9.85E-08	0.000161	0.284924	other	0
<i>ABCC8</i>	Caudate	2.27E-08	0.000763	4.02E-09	increasing	1
<i>ABCE1</i>	Caudate	7.50E-07	-0.00071	1.19E-07	decreasing	0
<i>ABCF3</i>	Caudate	6.73E-11	0.000605	1.80E-05	increasing	0
<i>ABCG1</i>	Caudate	1.44E-14	0.000824	1.71E-10	increasing	0
<i>ABCG2</i>	Caudate	7.81E-10	-0.00011	0.469516	other	0
<i>ABHD13</i>	Caudate	1.14E-06	-0.00072	1.04E-07	decreasing	0
<i>ABHD17A</i>	Caudate	8.53E-09	0.000415	0.004495	other	0
<i>ABHD5</i>	Caudate	1.71E-08	-0.00077	3.53E-09	decreasing	0
<i>ABHD8</i>	Caudate	1.75E-09	0.000648	2.37E-06	increasing	0
<i>ABLIM2</i>	Caudate	5.20E-08	0.000615	7.91E-06	increasing	1
<i>ABTB2</i>	Caudate	3.61E-12	0.000667	1.30E-06	increasing	0
<i>ACAD10</i>	Caudate	9.23E-10	0.000759	1.19E-08	increasing	0
<i>ACADS</i>	Caudate	1.19E-07	0.000676	9.41E-07	increasing	0
<i>ACAP3</i>	Caudate	5.78E-09	0.000571	6.65E-05	increasing	0
<i>ACKR1</i>	Caudate	1.94E-08	0.00016	0.274571	other	0
<i>ACO1</i>	Caudate	4.90E-08	0.000351	0.016632	other	1
<i>ACOT11</i>	Caudate	2.27E-14	0.000864	3.43E-12	increasing	0
<i>ACOT7</i>	Caudate	1.72E-07	0.000196	0.194521	other	0
<i>ACSBG1</i>	Caudate	6.88E-07	0.000706	1.30E-07	increasing	0
<i>ACSF3</i>	Caudate	3.36E-10	0.00057	5.95E-05	increasing	0
<i>ACSL4</i>	Caudate	1.90E-08	-0.00077	4.05E-09	decreasing	0
<i>ACSL6</i>	Caudate	2.37E-07	-1.45E-05	0.922416	other	0
<i>ACSM5</i>	Caudate	4.10E-15	0.000864	4.59E-12	increasing	0
<i>ACSS2</i>	Caudate	4.19E-08	0.000687	2.05E-07	increasing	0
<i>ACTA1</i>	Caudate	4.27E-08	0.000765	8.61E-09	increasing	0
<i>ACTB</i>	Caudate	2.22E-07	-0.00032	0.033575	other	0
<i>ACTC1</i>	Caudate	5.00E-09	-0.00066	1.11E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ACTL6B</i>	Caudate	1.23E-09	0.00033	0.027775	other	0
<i>ACTN1</i>	Caudate	1.28E-09	0.000675	2.50E-07	increasing	0
<i>ACTR2</i>	Caudate	2.96E-10	-0.00034	0.01633	other	0
<i>ACTR3</i>	Caudate	2.19E-05	-0.00072	1.17E-07	decreasing	0
<i>ACTR3B</i>	Caudate	2.22E-11	-0.00078	5.19E-09	decreasing	0
<i>ACTR5</i>	Caudate	3.37E-10	0.000594	3.04E-05	increasing	1
<i>ADA</i>	Caudate	4.97E-15	0.000828	5.82E-12	increasing	0
<i>ADAM15</i>	Caudate	1.37E-09	0.000705	2.70E-07	increasing	0
<i>ADAM19</i>	Caudate	1.87E-11	-0.00077	1.58E-09	decreasing	0
<i>ADAM32</i>	Caudate	1.87E-08	0.000696	2.81E-07	increasing	0
<i>ADAM33</i>	Caudate	5.45E-14	0.000863	8.05E-12	increasing	0
<i>ADAM8</i>	Caudate	1.90E-11	0.000817	2.05E-10	increasing	0
<i>ADAMTS10</i>	Caudate	7.64E-10	0.000285	0.048069	other	0
<i>ADAMTS18</i>	Caudate	1.82E-11	-0.00073	4.21E-08	decreasing	1
<i>ADAMTS19</i>	Caudate	2.84E-08	4.21E-05	0.779537	other	0
<i>ADAMTS3</i>	Caudate	2.73E-07	-0.00072	5.54E-08	decreasing	1
<i>ADAMTSL1</i>	Caudate	1.12E-07	-0.00051	0.000243	other	0
<i>ADAMTSL2</i>	Caudate	1.63E-07	-0.0002	0.181782	other	0
<i>ADAP1</i>	Caudate	1.94E-09	0.000564	7.71E-05	increasing	0
<i>ADARB2</i>	Caudate	1.23E-07	0.000135	0.36814	other	0
<i>ADAT3</i>	Caudate	3.32E-07	0.000721	1.17E-07	increasing	0
<i>ADCK3</i>	Caudate	5.73E-10	0.000638	3.81E-06	increasing	0
<i>ADCK4</i>	Caudate	8.11E-09	0.000622	7.68E-06	increasing	0
<i>ADCK5</i>	Caudate	2.56E-10	0.00024	0.110816	other	0
<i>ADCY1</i>	Caudate	2.40E-08	-0.00044	0.002229	other	0
<i>ADCY6</i>	Caudate	7.79E-08	0.000137	0.35559	other	0
<i>ADCY8</i>	Caudate	1.23E-08	-0.00033	0.024421	other	0
<i>ADIPOR2</i>	Caudate	1.94E-10	0.000771	1.81E-09	increasing	0
<i>ADIRF</i>	Caudate	1.61E-09	0.000511	0.000372	other	0
<i>ADO</i>	Caudate	1.05E-07	-0.00021	0.160211	other	0
<i>ADORA1</i>	Caudate	5.39E-12	0.000149	0.313466	other	1
<i>ADRB1</i>	Caudate	2.13E-10	0.000677	6.53E-07	increasing	0
<i>ADRBK1</i>	Caudate	1.92E-08	0.000439	0.002906	other	0
<i>ADSSL1</i>	Caudate	4.64E-13	0.000799	6.57E-10	increasing	0
<i>AES</i>	Caudate	4.26E-08	2.98E-05	0.843197	other	0
<i>AFAP1</i>	Caudate	2.41E-07	-0.00035	0.014216	other	0
<i>AFF1</i>	Caudate	1.07E-07	0.00019	0.201532	other	0
<i>AFF2</i>	Caudate	1.45E-07	-0.00039	0.00915	other	0
<i>AGAP3</i>	Caudate	3.53E-09	0.000735	4.70E-08	increasing	0
<i>AGFG1</i>	Caudate	2.31E-07	-0.0006	2.02E-05	decreasing	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>AGFG2</i>	Caudate	4.32E-09	0.000416	0.003927	other	0
<i>AGK</i>	Caudate	1.41E-07	-0.00066	9.63E-07	decreasing	1
<i>AGMO</i>	Caudate	3.31E-12	0.000727	6.21E-08	increasing	0
<i>AGO4</i>	Caudate	5.92E-11	-0.00056	8.67E-05	decreasing	0
<i>AGPAT9</i>	Caudate	2.38E-11	0.000606	6.26E-06	increasing	0
<i>AGPS</i>	Caudate	7.43E-08	-0.00076	8.28E-09	decreasing	0
<i>AGT</i>	Caudate	6.03E-13	0.000731	3.68E-08	increasing	1
<i>AHCY</i>	Caudate	2.33E-08	0.000716	2.47E-08	increasing	0
<i>AHCYL2</i>	Caudate	2.90E-08	3.49E-05	0.817967	other	0
<i>AHR</i>	Caudate	8.18E-09	-0.00072	2.36E-08	decreasing	0
<i>AIF1L</i>	Caudate	1.31E-08	0.00069	5.41E-07	increasing	0
<i>AIFM3</i>	Caudate	3.22E-08	0.000501	0.000588	other	0
<i>AIRE</i>	Caudate	2.81E-13	0.00087	2.04E-12	increasing	0
<i>AJAP1</i>	Caudate	1.66E-08	0.000148	0.325113	other	0
<i>AJUBA</i>	Caudate	1.94E-07	-0.00058	2.22E-05	decreasing	0
<i>AKAP2</i>	Caudate	1.31E-07	-0.00012	0.42402	other	0
<i>AKAP8</i>	Caudate	6.29E-12	0.000751	2.06E-08	increasing	0
<i>AKAP9</i>	Caudate	9.18E-09	-0.00076	1.04E-08	decreasing	0
<i>AKR1B1</i>	Caudate	1.39E-10	0.000726	2.30E-08	increasing	0
<i>AKT1</i>	Caudate	8.57E-11	0.000494	0.000705	other	0
<i>AKTIP</i>	Caudate	4.89E-08	5.28E-05	0.723976	other	0
<i>ALAD</i>	Caudate	7.69E-11	0.000697	7.29E-08	increasing	0
<i>ALDH16A1</i>	Caudate	4.30E-09	0.000522	0.000268	other	1
<i>ALDOA</i>	Caudate	3.50E-14	0.000837	2.73E-12	increasing	0
<i>ALDOC</i>	Caudate	2.56E-09	0.000675	4.79E-07	increasing	0
<i>ALG12</i>	Caudate	3.79E-09	0.000663	1.94E-06	increasing	0
<i>ALG3</i>	Caudate	2.59E-07	6.78E-05	0.658238	other	0
<i>ALKBH4</i>	Caudate	5.06E-11	0.00017	0.263932	other	0
<i>ALKBH5</i>	Caudate	1.56E-08	0.000637	5.58E-06	increasing	0
<i>ALKBH7</i>	Caudate	1.20E-07	0.000517	0.000378	other	0
<i>AMBRA1</i>	Caudate	1.91E-09	0.000172	0.250323	other	0
<i>AMDHD2</i>	Caudate	2.77E-13	0.000368	0.012798	other	0
<i>AMER2</i>	Caudate	4.38E-11	0.000804	1.12E-10	increasing	0
<i>AMIGO2</i>	Caudate	4.52E-14	-0.0008	2.15E-10	decreasing	0
<i>AMIGO3</i>	Caudate	2.15E-10	0.000684	6.17E-07	increasing	0
<i>AMPD2</i>	Caudate	1.85E-11	0.000658	1.26E-06	increasing	0
<i>AMT</i>	Caudate	2.42E-07	0.000794	1.14E-09	increasing	0
<i>ANGEL1</i>	Caudate	3.21E-10	0.000711	8.46E-08	increasing	1
<i>ANGPTL1</i>	Caudate	1.35E-07	-0.00072	6.83E-08	decreasing	0
<i>ANGPTL3</i>	Caudate	1.78E-07	-0.00066	2.02E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ANKRA2</i>	Caudate	3.51E-07	-0.0007	1.56E-07	decreasing	0
<i>ANKRD12</i>	Caudate	4.36E-15	-6.14E-05	0.679194	other	0
<i>ANKRD13A</i>	Caudate	7.08E-11	0.000643	3.38E-06	increasing	0
<i>ANKRD13C</i>	Caudate	7.74E-08	-0.00069	1.38E-07	decreasing	0
<i>ANKRD13D</i>	Caudate	5.24E-11	0.000556	0.000107	other	0
<i>ANKRD16</i>	Caudate	4.17E-07	0.000709	2.20E-07	increasing	0
<i>ANKRD23</i>	Caudate	1.61E-09	0.000692	3.34E-07	increasing	0
<i>ANKRD34B</i>	Caudate	1.50E-08	-0.00066	1.82E-06	decreasing	0
<i>ANKRD42</i>	Caudate	2.76E-08	0.00049	0.000688	other	0
<i>ANKRD44</i>	Caudate	1.20E-08	-0.00053	9.95E-05	decreasing	0
<i>ANKRD50</i>	Caudate	2.74E-19	-0.0009	1.83E-14	decreasing	0
<i>ANKRD54</i>	Caudate	1.74E-08	9.18E-05	0.530763	other	0
<i>ANKRD55</i>	Caudate	5.10E-11	-0.00075	1.01E-08	decreasing	0
<i>ANKRD63</i>	Caudate	1.14E-11	0.000294	0.043953	other	0
<i>ANKRD9</i>	Caudate	1.06E-08	0.00056	8.52E-05	increasing	0
<i>ANKS1B</i>	Caudate	1.03E-07	-0.00043	0.002117	other	0
<i>ANKS3</i>	Caudate	8.46E-09	0.000423	0.003277	other	0
<i>ANKZF1</i>	Caudate	1.84E-07	0.000502	0.000386	other	0
<i>ANLN</i>	Caudate	4.42E-11	0.000424	0.003345	other	0
<i>ANO2</i>	Caudate	9.08E-20	0.000896	3.11E-14	increasing	0
<i>ANO7</i>	Caudate	4.71E-08	0.00073	7.40E-08	increasing	0
<i>ANO8</i>	Caudate	9.21E-10	0.000242	0.104472	other	0
<i>ANXA11</i>	Caudate	2.51E-09	0.000558	6.35E-05	increasing	0
<i>AP1M1</i>	Caudate	5.69E-12	0.000208	0.161202	other	0
<i>AP2A2</i>	Caudate	2.93E-11	0.000489	0.00083	other	0
<i>AP2M1</i>	Caudate	5.45E-08	-0.00011	0.477277	other	0
<i>AP3D1</i>	Caudate	9.29E-08	0.000633	6.73E-06	increasing	0
<i>AP3M1</i>	Caudate	9.84E-11	-0.00043	0.003294	other	0
<i>AP3S1</i>	Caudate	3.38E-10	-0.00062	9.00E-06	decreasing	0
<i>AP4M1</i>	Caudate	5.05E-08	0.000262	0.073729	other	0
<i>AP4S1</i>	Caudate	6.05E-08	-0.00076	1.34E-08	decreasing	0
<i>AP5Z1</i>	Caudate	4.94E-10	0.000582	4.60E-05	increasing	1
<i>APAF1</i>	Caudate	4.97E-11	-0.00081	5.46E-10	decreasing	0
<i>APBA2</i>	Caudate	5.27E-12	0.000339	0.020449	other	0
<i>APBB1</i>	Caudate	1.74E-09	0.000607	1.82E-05	increasing	0
<i>APC</i>	Caudate	2.03E-07	-0.00075	3.08E-08	decreasing	0
<i>APC2</i>	Caudate	1.93E-11	0.000368	0.013061	other	0
<i>APEH</i>	Caudate	3.68E-08	0.000559	0.0001	other	0
<i>API5</i>	Caudate	4.11E-10	-0.00025	0.089051	other	0
<i>APLP1</i>	Caudate	7.80E-12	0.000544	0.000165	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>APOC2</i>	Caudate	1.29E-07	0.000343	0.021041	other	1
<i>APOE</i>	Caudate	1.58E-07	0.000569	7.09E-05	increasing	0
<i>AQP1</i>	Caudate	3.16E-17	0.000862	2.77E-12	increasing	0
<i>AR</i>	Caudate	7.70E-10	-0.00082	1.25E-10	decreasing	0
<i>AREL1</i>	Caudate	2.08E-14	-0.00081	2.19E-10	decreasing	0
<i>ARFGAP2</i>	Caudate	2.18E-08	0.000342	0.0217	other	0
<i>ARFRP1</i>	Caudate	2.02E-08	0.000259	0.085768	other	0
<i>ARHGAP10</i>	Caudate	8.02E-06	-0.00074	5.03E-08	decreasing	0
<i>ARHGAP20</i>	Caudate	5.10E-08	-0.00068	8.77E-07	decreasing	0
<i>ARHGAP22</i>	Caudate	5.90E-08	0.0007	3.45E-07	increasing	1
<i>ARHGAP23</i>	Caudate	3.11E-10	0.000826	1.23E-10	increasing	0
<i>ARHGAP27</i>	Caudate	2.23E-13	0.000793	1.20E-10	increasing	0
<i>ARHGAP29</i>	Caudate	1.80E-07	-0.00073	4.60E-08	decreasing	0
<i>ARHGAP39</i>	Caudate	2.24E-08	0.000445	0.001914	other	0
<i>ARHGAP9</i>	Caudate	5.17E-12	0.000825	3.07E-11	increasing	0
<i>ARHGDIB</i>	Caudate	1.24E-07	-0.00042	0.004418	other	0
<i>ARHGDIG</i>	Caudate	1.47E-08	0.000523	0.000318	other	0
<i>ARHGEF10</i>	Caudate	6.13E-14	0.000829	3.09E-11	increasing	0
<i>ARHGEF10L</i>	Caudate	1.05E-09	0.000273	0.069015	other	0
<i>ARHGEF12</i>	Caudate	2.34E-09	-0.00078	3.00E-09	decreasing	0
<i>ARHGEF17</i>	Caudate	4.29E-10	0.000743	3.11E-08	increasing	0
<i>ARHGEF2</i>	Caudate	1.13E-10	-0.00014	0.361579	other	0
<i>ARHGEF37</i>	Caudate	5.98E-11	0.000831	6.96E-11	increasing	0
<i>ARHGEF38</i>	Caudate	2.61E-06	0.000757	1.64E-08	increasing	0
<i>ARIH2</i>	Caudate	2.36E-10	1.29E-05	0.931755	other	0
<i>ARL10</i>	Caudate	3.24E-10	0.000367	0.011122	other	0
<i>ARL15</i>	Caudate	1.38E-07	-0.00075	2.93E-08	decreasing	0
<i>ARL2</i>	Caudate	1.52E-11	0.00071	9.04E-08	increasing	0
<i>ARL4C</i>	Caudate	1.94E-10	-0.00065	8.02E-07	decreasing	0
<i>ARL5B</i>	Caudate	1.72E-11	-0.00082	1.43E-10	decreasing	0
<i>ARL6IP4</i>	Caudate	1.35E-09	0.000583	4.22E-05	increasing	0
<i>ARL8A</i>	Caudate	3.42E-08	-0.00052	0.00023	other	0
<i>ARL8B</i>	Caudate	1.14E-14	-0.00032	0.02389	other	0
<i>ARMC1</i>	Caudate	7.83E-08	-0.0005	0.000577	other	0
<i>ARMC5</i>	Caudate	2.61E-07	0.000446	0.002459	other	0
<i>ARMC6</i>	Caudate	5.34E-11	-3.87E-05	0.791768	other	0
<i>ARMC8</i>	Caudate	5.60E-11	-0.00056	6.30E-05	decreasing	0
<i>ARMCX2</i>	Caudate	1.46E-09	0.000574	4.18E-05	increasing	0
<i>ARMCX5</i>	Caudate	2.21E-08	-0.00062	6.72E-06	decreasing	0
<i>ARPC5L</i>	Caudate	7.39E-10	0.000201	0.172308	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ARRB1</i>	Caudate	3.03E-11	0.000488	0.000852	other	0
<i>ARRDC2</i>	Caudate	5.00E-09	0.000757	9.28E-09	increasing	1
<i>ARRDC4</i>	Caudate	4.13E-08	-0.00068	1.93E-07	decreasing	0
<i>ARSB</i>	Caudate	2.32E-07	-0.00063	7.04E-06	decreasing	0
<i>ARSG</i>	Caudate	8.64E-08	0.000628	5.52E-06	increasing	0
<i>ARVCF</i>	Caudate	3.58E-10	0.000513	0.000206	other	0
<i>ASB1</i>	Caudate	1.25E-09	0.00068	7.73E-07	increasing	0
<i>ASB6</i>	Caudate	4.68E-09	0.000382	0.010553	other	0
<i>ASGR1</i>	Caudate	3.20E-09	0.000737	3.79E-08	increasing	0
<i>ASIC4</i>	Caudate	1.62E-08	1.87E-05	0.899914	other	0
<i>ASL</i>	Caudate	3.86E-15	0.000802	4.37E-10	increasing	0
<i>ASPA</i>	Caudate	7.41E-09	0.000634	3.15E-06	increasing	0
<i>ASPM</i>	Caudate	3.93E-17	-0.00087	5.78E-13	decreasing	0
<i>ASPRV1</i>	Caudate	1.21E-13	0.000824	5.90E-11	increasing	0
<i>ASPSCR1</i>	Caudate	1.04E-09	0.000652	2.94E-06	increasing	0
<i>ASTN2</i>	Caudate	1.79E-09	-0.00032	0.030768	other	0
<i>ASUN</i>	Caudate	4.31E-10	-0.00061	1.47E-05	decreasing	0
<i>ASXL3</i>	Caudate	8.34E-09	-0.00072	2.46E-08	decreasing	0
<i>ATAD1</i>	Caudate	7.70E-06	-0.00071	1.46E-07	decreasing	0
<i>ATF2</i>	Caudate	7.99E-10	-0.00067	1.41E-06	decreasing	0
<i>ATF4</i>	Caudate	5.87E-08	-0.00036	0.014969	other	0
<i>ATF5</i>	Caudate	3.84E-10	0.000155	0.300834	other	0
<i>ATF7IP</i>	Caudate	3.88E-15	-0.00073	3.89E-08	decreasing	0
<i>ATG12</i>	Caudate	6.49E-07	-0.00074	3.16E-08	decreasing	0
<i>ATG13</i>	Caudate	1.51E-08	0.000599	8.48E-06	increasing	0
<i>ATG16L1</i>	Caudate	5.94E-07	-0.0007	2.38E-07	decreasing	0
<i>ATG2A</i>	Caudate	1.21E-08	0.000576	5.58E-05	increasing	0
<i>ATG4D</i>	Caudate	1.79E-10	0.000516	0.000373	other	0
<i>ATG7</i>	Caudate	2.16E-10	0.000711	5.50E-08	increasing	0
<i>ATG9A</i>	Caudate	1.96E-09	0.000676	8.14E-07	increasing	0
<i>ATP10B</i>	Caudate	6.34E-09	0.000771	1.78E-09	increasing	0
<i>ATP10D</i>	Caudate	2.57E-08	-0.00061	6.25E-06	decreasing	0
<i>ATP11B</i>	Caudate	1.85E-07	-0.00065	3.86E-06	decreasing	0
<i>ATP11C</i>	Caudate	2.31E-06	-0.00072	5.46E-08	decreasing	0
<i>ATP13A2</i>	Caudate	5.93E-16	0.0008	1.08E-09	increasing	0
<i>ATP1B3</i>	Caudate	1.87E-07	-0.00042	0.004449	other	0
<i>ATP6VOA2</i>	Caudate	1.16E-07	-0.0005	0.000408	other	0
<i>ATP6VOE2</i>	Caudate	4.78E-08	-0.00014	0.355094	other	0
<i>ATP6V1C1</i>	Caudate	2.37E-07	-9.89E-05	0.513239	other	0
<i>ATP7A</i>	Caudate	2.04E-08	-0.00075	2.08E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ATP9A</i>	Caudate	1.51E-08	0.000444	0.002617	other	0
<i>ATPAF1</i>	Caudate	5.92E-08	0.000621	3.39E-06	increasing	0
<i>ATR</i>	Caudate	7.19E-07	-0.00071	6.85E-08	decreasing	0
<i>ATRIP</i>	Caudate	1.60E-09	0.000187	0.207419	other	0
<i>ATRNL1</i>	Caudate	1.86E-07	-0.00054	7.54E-05	decreasing	0
<i>ATRX</i>	Caudate	2.93E-09	-0.00078	5.48E-09	decreasing	0
<i>ATXN10</i>	Caudate	2.72E-11	-0.00034	0.018683	other	0
<i>ATXN2</i>	Caudate	3.94E-09	7.30E-05	0.628129	other	0
<i>ATXN7L3</i>	Caudate	1.53E-10	0.00032	0.0337	other	0
<i>ATXN7L3B</i>	Caudate	2.90E-08	-0.00065	1.52E-06	decreasing	0
<i>AURKAIP1</i>	Caudate	1.63E-07	0.000392	0.008474	other	0
<i>AVPI1</i>	Caudate	8.17E-08	0.000509	0.000283	other	0
<i>AVPR1A</i>	Caudate	3.01E-08	-0.00052	0.000249	other	0
<i>AXIN1</i>	Caudate	2.22E-10	0.00061	1.59E-05	increasing	0
<i>AZIN1</i>	Caudate	1.24E-10	-0.00077	1.48E-09	decreasing	0
<i>B3GALT2</i>	Caudate	4.83E-13	-0.00082	1.34E-10	decreasing	0
<i>B3GALT6</i>	Caudate	6.51E-11	0.000127	0.394218	other	0
<i>B3GAT1</i>	Caudate	2.51E-07	0.000575	5.74E-05	increasing	0
<i>B3GNT9</i>	Caudate	1.25E-09	0.000371	0.010042	other	0
<i>B3GNTL1</i>	Caudate	1.16E-07	0.000662	1.94E-06	increasing	0
<i>B4GALNT1</i>	Caudate	1.70E-08	0.000719	1.26E-07	increasing	0
<i>B4GALNT4</i>	Caudate	1.95E-11	0.000599	2.29E-05	increasing	0
<i>B4GALT2</i>	Caudate	1.21E-07	0.000189	0.210349	other	0
<i>B4GALT6</i>	Caudate	3.15E-12	-0.00082	1.92E-10	decreasing	0
<i>B4GALT7</i>	Caudate	6.45E-10	0.000311	0.033854	other	0
<i>B9D1</i>	Caudate	6.52E-08	0.00052	0.000338	other	0
<i>B9D2</i>	Caudate	5.82E-09	1.56E-05	0.916368	other	0
<i>BAI1</i>	Caudate	1.71E-08	0.000425	0.003779	other	0
<i>BAI2</i>	Caudate	8.33E-10	0.000342	0.022795	other	0
<i>BAI3</i>	Caudate	8.41E-07	-0.00077	5.00E-09	decreasing	0
<i>BAIAP2L2</i>	Caudate	4.55E-09	0.000804	7.84E-10	increasing	0
<i>BAIAP3</i>	Caudate	8.81E-09	0.000721	7.56E-08	increasing	0
<i>BAMBI</i>	Caudate	1.23E-09	-0.00075	8.90E-09	decreasing	0
<i>BANF1</i>	Caudate	6.56E-09	-0.00011	0.469378	other	0
<i>BANP</i>	Caudate	3.90E-07	0.000709	2.11E-07	increasing	0
<i>BASP1</i>	Caudate	2.46E-08	-0.00073	4.27E-08	decreasing	1
<i>BAZ1B</i>	Caudate	5.66E-08	0.000653	7.47E-07	increasing	0
<i>BBIP1</i>	Caudate	5.01E-07	-0.00075	8.57E-09	decreasing	0
<i>BCAP29</i>	Caudate	4.40E-10	-0.00074	4.97E-08	decreasing	0
<i>BCAR1</i>	Caudate	5.09E-11	0.000453	0.001959	other	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>BCAT2</i>	Caudate	1.16E-09	0.000771	6.01E-09	increasing	0
<i>BCKDHA</i>	Caudate	1.77E-08	0.000414	0.004954	other	0
<i>BCL11B</i>	Caudate	4.00E-10	-4.60E-05	0.764316	other	0
<i>BCL7A</i>	Caudate	6.52E-10	0.000167	0.268042	other	0
<i>BCL7C</i>	Caudate	9.62E-12	0.000641	3.77E-06	increasing	0
<i>BCLAF1</i>	Caudate	6.31E-09	-0.0006	2.02E-05	decreasing	0
<i>BDP1</i>	Caudate	4.31E-11	-0.00083	1.42E-10	decreasing	0
<i>BEND4</i>	Caudate	3.91E-14	-0.00084	1.86E-11	decreasing	0
<i>BEST1</i>	Caudate	8.18E-09	0.000692	3.37E-07	increasing	1
<i>BHLHE40</i>	Caudate	2.12E-09	0.000281	0.055947	other	0
<i>BHLHE41</i>	Caudate	2.49E-09	0.00024	0.097475	other	0
<i>BHMT</i>	Caudate	8.92E-07	0.000791	8.37E-10	increasing	0
<i>BICD2</i>	Caudate	2.67E-08	0.000515	0.000393	other	0
<i>BIN1</i>	Caudate	3.91E-12	0.000732	3.44E-08	increasing	0
<i>BIN2</i>	Caudate	1.32E-07	-0.00078	2.56E-09	decreasing	0
<i>BIRC2</i>	Caudate	7.10E-07	-0.00073	4.11E-08	decreasing	0
<i>BIRC3</i>	Caudate	1.51E-11	-0.00075	9.68E-09	decreasing	0
<i>BIVM</i>	Caudate	4.16E-09	-0.00068	2.65E-07	decreasing	0
<i>BLOC1S4</i>	Caudate	1.32E-07	-0.00016	0.286445	other	0
<i>BLVRA</i>	Caudate	3.01E-11	0.000762	7.08E-09	increasing	0
<i>BLVRB</i>	Caudate	3.29E-10	0.000752	1.17E-08	increasing	0
<i>BMP1</i>	Caudate	3.31E-08	0.000716	1.20E-07	increasing	0
<i>BMP2K</i>	Caudate	7.83E-09	-0.00056	7.36E-05	decreasing	0
<i>BMPER</i>	Caudate	1.05E-12	-0.00081	1.87E-10	decreasing	0
<i>BMPR1A</i>	Caudate	5.84E-09	-0.00076	5.18E-09	decreasing	0
<i>BOK</i>	Caudate	3.36E-12	0.000824	1.04E-10	increasing	0
<i>BRAF</i>	Caudate	2.15E-09	-0.00046	0.001284	other	0
<i>BRAT1</i>	Caudate	3.35E-10	0.00046	0.001761	other	0
<i>BRCA2</i>	Caudate	4.23E-08	-0.00042	0.003008	other	0
<i>BRD1</i>	Caudate	1.12E-12	0.000668	1.41E-06	increasing	0
<i>BRD9</i>	Caudate	1.16E-08	0.000306	0.038125	other	1
<i>BRF1</i>	Caudate	6.39E-12	0.000586	3.68E-05	increasing	0
<i>BRINP1</i>	Caudate	1.56E-13	-0.00073	4.69E-08	decreasing	0
<i>BRINP3</i>	Caudate	2.24E-08	-0.00068	6.44E-07	decreasing	0
<i>BRMS1L</i>	Caudate	3.74E-09	-0.00078	3.72E-09	decreasing	0
<i>BROX</i>	Caudate	4.29E-09	-0.00066	2.33E-06	decreasing	0
<i>BRPF1</i>	Caudate	2.42E-08	0.000359	0.016259	other	0
<i>BRSK1</i>	Caudate	2.04E-08	0.000528	0.000268	other	0
<i>BRSK2</i>	Caudate	2.01E-08	0.000515	0.000361	other	0
<i>BRWD3</i>	Caudate	1.56E-09	-0.00071	1.86E-07	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>BSG</i>	Caudate	2.73E-09	0.000746	6.78E-09	increasing	0
<i>BSPRY</i>	Caudate	1.11E-07	0.000582	2.61E-05	increasing	0
<i>BTBD1</i>	Caudate	2.86E-06	-0.00074	1.81E-08	decreasing	0
<i>BTBD2</i>	Caudate	2.34E-07	0.000315	0.036438	other	0
<i>BTBD9</i>	Caudate	7.98E-14	0.000756	1.93E-09	increasing	0
<i>BTG3</i>	Caudate	1.61E-09	-0.00059	1.78E-05	decreasing	0
<i>BTNL8</i>	Caudate	2.99E-14	0.000853	6.02E-12	increasing	0
<i>BUB1</i>	Caudate	1.93E-10	-0.00075	6.61E-09	decreasing	0
<i>BUB1B</i>	Caudate	6.32E-08	-0.0004	0.005312	other	0
<i>BVES</i>	Caudate	7.15E-09	0.000784	2.86E-09	increasing	0
<i>BZRAP1</i>	Caudate	5.78E-09	0.000649	3.56E-06	increasing	0
<i>BZW1</i>	Caudate	3.85E-06	-0.00073	3.91E-08	decreasing	0
<i>C10H2orf69</i>	Caudate	3.54E-10	-0.0004	0.0066	other	0
<i>C10H2orf72</i>	Caudate	6.06E-10	0.000607	1.62E-05	increasing	0
<i>C11H12orf10</i>	Caudate	1.83E-07	0.000148	0.328091	other	0
<i>C11H12orf5</i>	Caudate	3.96E-08	-0.00059	3.20E-05	decreasing	0
<i>C12H9orf41</i>	Caudate	2.38E-07	-0.00065	2.22E-06	decreasing	0
<i>C12H9orf69</i>	Caudate	2.32E-08	0.000312	0.038839	other	0
<i>C12H9orf72</i>	Caudate	4.37E-09	-0.00063	7.10E-06	decreasing	0
<i>C12H9orf89</i>	Caudate	1.24E-10	0.000619	9.93E-06	increasing	0
<i>C14H2orf81</i>	Caudate	1.74E-09	0.00077	5.41E-09	increasing	1
<i>C16H17orf100</i>	Caudate	4.17E-09	8.26E-06	0.956643	other	0
<i>C16H17orf59</i>	Caudate	2.87E-08	0.000329	0.026765	other	0
<i>C17H6orf141</i>	Caudate	2.67E-08	0.000119	0.423672	other	0
<i>C17H6orf62</i>	Caudate	3.92E-07	-0.00076	5.72E-09	decreasing	0
<i>C19H22orf29</i>	Caudate	3.71E-09	0.00029	0.048697	other	0
<i>C1H11orf1</i>	Caudate	9.72E-08	0.000562	4.69E-05	increasing	0
<i>C1H11orf30</i>	Caudate	3.71E-08	-0.00016	0.276219	other	0
<i>C1H11orf82</i>	Caudate	2.49E-10	-0.00064	2.07E-06	decreasing	0
<i>C1H11orf87</i>	Caudate	7.35E-12	-0.00083	1.35E-10	decreasing	0
<i>C1H11orf95</i>	Caudate	1.44E-10	0.00044	0.002877	other	0
<i>C1QB</i>	Caudate	1.99E-07	0.000325	0.030137	other	0
<i>C1QL3</i>	Caudate	6.36E-10	0.000703	2.20E-07	increasing	0
<i>C1QTNF4</i>	Caudate	9.20E-12	0.000481	0.001005	other	0
<i>C20H1orf159</i>	Caudate	8.46E-09	0.000502	0.000458	other	0
<i>C20H1orf233</i>	Caudate	5.38E-08	0.00075	2.32E-08	increasing	0
<i>C20H1orf52</i>	Caudate	4.10E-05	-0.00072	1.10E-07	decreasing	0
<i>C21H7orf60</i>	Caudate	1.44E-06	-0.00076	8.83E-09	decreasing	0
<i>C21H7orf73</i>	Caudate	4.69E-11	-0.00056	9.70E-05	decreasing	0
<i>C23H5orf15</i>	Caudate	3.94E-16	-0.00089	4.77E-13	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>C23H5orf24</i>	Caudate	6.52E-07	-0.00073	6.46E-08	decreasing	0
<i>C23H5orf45</i>	Caudate	3.49E-10	0.000439	0.002482	other	0
<i>C24H14orf169</i>	Caudate	9.41E-08	0.000369	0.012933	other	0
<i>C24H14orf80</i>	Caudate	2.76E-08	0.000134	0.376842	other	1
<i>C26H15orf27</i>	Caudate	5.49E-08	-8.97E-05	0.549846	other	0
<i>C26H15orf41</i>	Caudate	6.10E-08	-0.00073	4.23E-08	decreasing	0
<i>C26H15orf59</i>	Caudate	1.07E-07	-5.04E-05	0.742835	other	0
<i>C26H15orf62</i>	Caudate	1.61E-07	0.00057	6.17E-05	increasing	0
<i>C27H4orf48</i>	Caudate	4.86E-08	0.000504	0.000544	other	0
<i>C27H4orf50</i>	Caudate	3.78E-05	0.000697	2.29E-07	increasing	0
<i>C28H7orf26</i>	Caudate	2.35E-11	0.000346	0.018579	other	0
<i>C28H7orf50</i>	Caudate	1.37E-09	0.000553	0.000122	other	0
<i>C2CD2</i>	Caudate	4.94E-08	0.000728	3.29E-08	increasing	0
<i>C2CD4C</i>	Caudate	2.44E-07	0.000552	9.97E-05	increasing	0
<i>C2CD4D</i>	Caudate	6.00E-07	0.000728	7.60E-08	increasing	0
<i>C2H20orf27</i>	Caudate	4.79E-12	0.000719	5.67E-08	increasing	0
<i>C2H21orf2</i>	Caudate	2.54E-08	0.00038	0.010759	other	0
<i>C4H5orf51</i>	Caudate	3.36E-10	-0.00078	2.69E-09	decreasing	0
<i>C5H16orf52</i>	Caudate	1.72E-08	-0.00076	1.56E-08	decreasing	0
<i>C5H16orf86</i>	Caudate	2.55E-08	0.000229	0.131071	other	0
<i>C5H16orf89</i>	Caudate	1.81E-13	0.000705	2.00E-07	increasing	0
<i>C6H19orf10</i>	Caudate	1.27E-07	0.000198	0.187065	other	0
<i>C6H19orf12</i>	Caudate	9.58E-09	0.000616	1.24E-05	increasing	0
<i>C6H19orf60</i>	Caudate	9.02E-11	0.000583	2.50E-05	increasing	0
<i>C6H19orf66</i>	Caudate	4.54E-14	0.000764	5.13E-09	increasing	0
<i>C6H19orf68</i>	Caudate	1.89E-09	0.000688	1.97E-07	increasing	0
<i>C8H8orf34</i>	Caudate	5.55E-15	-0.00082	1.40E-11	decreasing	0
<i>C8H8orf37</i>	Caudate	4.21E-08	-0.00075	7.15E-09	decreasing	0
<i>C8H8orf82</i>	Caudate	2.15E-09	0.000604	2.08E-05	increasing	0
<i>C9H10orf11</i>	Caudate	1.26E-14	0.000848	2.50E-12	increasing	0
<i>C9H10orf118</i>	Caudate	9.95E-10	-0.00075	2.18E-08	decreasing	0
<i>C9H10orf35</i>	Caudate	3.46E-09	0.000703	2.87E-07	increasing	0
<i>C9H10orf62</i>	Caudate	7.23E-06	0.000724	2.53E-08	increasing	0
<i>C9H10orf90</i>	Caudate	3.10E-16	0.000848	1.48E-11	increasing	0
<i>CA10</i>	Caudate	8.01E-15	-0.00087	4.75E-13	decreasing	0
<i>CA12</i>	Caudate	1.78E-07	0.000588	2.05E-05	increasing	0
<i>CA7</i>	Caudate	1.99E-07	0.000667	1.58E-06	increasing	0
<i>CA8</i>	Caudate	3.69E-09	-0.00062	4.23E-06	decreasing	1
<i>CABP1</i>	Caudate	3.59E-17	0.000857	9.57E-12	increasing	0
<i>CACFD1</i>	Caudate	4.18E-10	0.000389	0.006171	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CACNA1F</i>	Caudate	2.06E-07	0.000534	0.000126	other	0
<i>CACNA1H</i>	Caudate	4.33E-09	0.00054	0.000174	other	0
<i>CACNA2D1</i>	Caudate	7.07E-08	-0.00077	6.26E-09	decreasing	0
<i>CACNA2D3</i>	Caudate	5.88E-17	-0.00085	6.24E-12	decreasing	0
<i>CACNA2D4</i>	Caudate	7.62E-12	0.000716	6.58E-08	increasing	0
<i>CACNB2</i>	Caudate	1.58E-09	-0.00011	0.441923	other	0
<i>CACNB3</i>	Caudate	2.67E-10	0.000563	9.00E-05	increasing	0
<i>CACNB4</i>	Caudate	2.89E-08	-0.00052	0.000139	other	0
<i>CACNG5</i>	Caudate	7.42E-08	-0.00055	0.000104	other	0
<i>CACTIN</i>	Caudate	5.07E-10	0.000428	0.003829	other	0
<i>CAD</i>	Caudate	2.01E-11	0.000332	0.022155	other	0
<i>CADM2</i>	Caudate	1.03E-08	-0.00073	7.69E-08	decreasing	0
<i>CADM4</i>	Caudate	8.39E-10	0.000376	0.011719	other	0
<i>CALB1</i>	Caudate	1.55E-07	-0.00023	0.12146	other	0
<i>CALCOCO2</i>	Caudate	1.36E-08	0.000493	0.000578	other	0
<i>CALCRL</i>	Caudate	4.06E-13	-0.00088	2.55E-12	decreasing	0
<i>CALU</i>	Caudate	1.48E-08	-0.00068	8.55E-07	decreasing	0
<i>CALY</i>	Caudate	2.41E-10	0.000782	3.30E-09	increasing	0
<i>CAMK2A</i>	Caudate	4.29E-11	0.000721	4.21E-08	increasing	0
<i>CAMK2D</i>	Caudate	1.04E-09	-0.00074	1.17E-08	decreasing	0
<i>CAMK2N1</i>	Caudate	6.18E-11	-0.00072	1.26E-07	decreasing	0
<i>CAMK4</i>	Caudate	3.14E-10	-0.00081	5.44E-10	decreasing	0
<i>CAMKK1</i>	Caudate	2.57E-19	0.000837	1.08E-11	increasing	0
<i>CAMKK2</i>	Caudate	1.69E-08	0.000552	8.88E-05	increasing	0
<i>CAMKV</i>	Caudate	2.27E-09	0.000478	0.001102	other	0
<i>CAMSAP1</i>	Caudate	1.07E-09	0.000268	0.070404	other	0
<i>CAMSAP3</i>	Caudate	1.58E-10	0.000532	0.000198	other	0
<i>CAND2</i>	Caudate	1.65E-10	0.00064	4.64E-06	increasing	0
<i>CANT1</i>	Caudate	1.98E-11	-0.00017	0.266772	other	0
<i>CAP2</i>	Caudate	2.10E-15	-0.00035	0.014753	other	0
<i>CAPN1</i>	Caudate	1.24E-09	0.000595	2.70E-05	increasing	0
<i>CAPN10</i>	Caudate	1.17E-09	0.000355	0.014927	other	0
<i>CAPN15</i>	Caudate	2.65E-08	0.000503	0.000565	other	0
<i>CAPN2</i>	Caudate	7.22E-08	0.000721	8.20E-08	increasing	0
<i>CAPN3</i>	Caudate	4.15E-08	0.000744	2.42E-08	increasing	1
<i>CAPZB</i>	Caudate	1.76E-09	-0.00053	0.000173	other	0
<i>CARNS1</i>	Caudate	7.40E-16	0.000855	1.21E-12	increasing	0
<i>CASK</i>	Caudate	8.38E-16	-0.00087	6.38E-13	decreasing	0
<i>CASKIN1</i>	Caudate	3.59E-10	0.000752	1.91E-08	increasing	0
<i>CASKIN2</i>	Caudate	1.72E-08	0.000764	5.64E-09	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CASP3</i>	Caudate	1.51E-13	-0.00079	1.92E-09	decreasing	0
<i>CASP6</i>	Caudate	7.68E-08	-0.00065	1.63E-06	decreasing	0
<i>CAST</i>	Caudate	2.23E-10	0.000391	0.006895	other	0
<i>CAV2</i>	Caudate	8.65E-09	-0.00074	5.17E-09	decreasing	0
<i>CBLB</i>	Caudate	9.31E-10	-0.00069	6.43E-07	decreasing	0
<i>CBLL1</i>	Caudate	4.79E-09	-0.00066	1.76E-06	decreasing	0
<i>CBR1</i>	Caudate	6.23E-13	0.000761	6.90E-09	increasing	0
<i>CBS</i>	Caudate	3.59E-09	0.000656	1.90E-06	increasing	0
<i>CBX2</i>	Caudate	2.06E-08	-0.0006	9.89E-06	decreasing	0
<i>CBX7</i>	Caudate	9.33E-17	0.000859	2.92E-13	increasing	0
<i>CBX8</i>	Caudate	1.18E-11	-0.00077	1.86E-09	decreasing	0
<i>CBY3</i>	Caudate	1.02E-08	0.000321	0.029967	other	0
<i>CC2D1A</i>	Caudate	1.41E-11	0.000756	1.68E-08	increasing	0
<i>CC2D1B</i>	Caudate	3.01E-09	0.000483	0.000864	other	0
<i>CCAR1</i>	Caudate	5.32E-08	-0.00064	4.46E-06	decreasing	0
<i>CCAR2</i>	Caudate	1.32E-08	0.000449	0.002323	other	0
<i>CCBL1</i>	Caudate	2.09E-09	0.000616	1.17E-05	increasing	1
<i>CCDC104</i>	Caudate	7.44E-08	-0.00036	0.01553	other	0
<i>CCDC106</i>	Caudate	3.53E-08	0.000193	0.204623	other	0
<i>CCDC136</i>	Caudate	1.81E-10	0.000693	3.01E-07	increasing	0
<i>CCDC14</i>	Caudate	2.66E-08	-0.00075	3.67E-09	decreasing	0
<i>CCDC148</i>	Caudate	1.92E-08	-0.00032	0.028248	other	0
<i>CCDC159</i>	Caudate	7.00E-09	0.000799	9.90E-10	increasing	0
<i>CCDC173</i>	Caudate	2.15E-07	-0.00069	1.08E-07	decreasing	0
<i>CCDC177</i>	Caudate	1.60E-08	0.00021	0.160477	other	0
<i>CCDC22</i>	Caudate	1.80E-08	0.00049	0.000812	other	0
<i>CCDC28A</i>	Caudate	1.88E-07	0.000512	0.00033	other	0
<i>CCDC47</i>	Caudate	3.69E-12	0.000629	2.28E-06	increasing	0
<i>CCDC50</i>	Caudate	1.32E-15	-0.00088	6.24E-13	decreasing	0
<i>CCDC61</i>	Caudate	1.55E-08	0.000579	4.37E-05	increasing	0
<i>CCDC69</i>	Caudate	2.59E-07	0.000551	0.000129	other	0
<i>CCDC78</i>	Caudate	2.05E-09	0.000689	5.53E-07	increasing	0
<i>CCDC85B</i>	Caudate	1.09E-09	0.000452	0.00166	other	0
<i>CCDC85C</i>	Caudate	2.26E-08	0.000311	0.037972	other	0
<i>CCDC9</i>	Caudate	4.15E-06	0.000706	2.56E-07	increasing	0
<i>CCDC90B</i>	Caudate	1.56E-07	-0.00075	1.30E-08	decreasing	0
<i>CCDC94</i>	Caudate	8.87E-08	0.000343	0.02208	other	0
<i>CCHCR1</i>	Caudate	2.40E-10	0.000788	2.35E-09	increasing	0
<i>CCM2</i>	Caudate	2.66E-09	0.000459	0.001225	other	0
<i>CCNC</i>	Caudate	1.61E-05	-0.00074	4.16E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CCND2</i>	Caudate	1.96E-07	-0.00025	0.084501	other	0
<i>CCND3</i>	Caudate	4.55E-11	0.000788	5.65E-10	increasing	0
<i>CCNG2</i>	Caudate	1.20E-10	-0.00079	1.05E-09	decreasing	0
<i>CCNJ</i>	Caudate	9.89E-09	-0.00059	2.52E-05	decreasing	0
<i>CCP110</i>	Caudate	3.32E-08	0.000473	0.000965	other	0
<i>CCPG1</i>	Caudate	1.84E-08	-0.00025	0.092692	other	0
<i>CCS</i>	Caudate	5.87E-08	0.000538	0.000167	other	0
<i>CCSER1</i>	Caudate	3.75E-10	-0.00071	3.36E-08	decreasing	0
<i>CCSER2</i>	Caudate	9.71E-09	-0.00049	0.000708	other	0
<i>CCT6B</i>	Caudate	3.95E-09	5.74E-05	0.703885	other	0
<i>CD151</i>	Caudate	7.49E-08	0.000427	0.003919	other	0
<i>CD177</i>	Caudate	1.57E-08	0.000228	0.126808	other	0
<i>CD22</i>	Caudate	1.30E-07	0.000739	1.07E-08	increasing	0
<i>CD276</i>	Caudate	1.30E-12	0.000849	1.89E-11	increasing	0
<i>CD2AP</i>	Caudate	3.85E-08	-0.0007	3.12E-07	decreasing	0
<i>CD81</i>	Caudate	1.31E-07	0.000674	1.14E-06	increasing	1
<i>CD83</i>	Caudate	4.86E-09	0.000592	2.02E-05	increasing	0
<i>CDADC1</i>	Caudate	4.48E-08	0.000156	0.299589	other	0
<i>CDAN1</i>	Caudate	2.14E-11	0.000753	1.85E-08	increasing	0
<i>CDC14A</i>	Caudate	2.03E-08	-0.00073	1.39E-08	decreasing	0
<i>CDC14B</i>	Caudate	5.05E-08	0.00037	0.011506	other	0
<i>CDC42</i>	Caudate	4.52E-13	-0.00082	2.18E-10	decreasing	0
<i>CDC42EP1</i>	Caudate	3.35E-14	0.000826	2.95E-11	increasing	0
<i>CDC42EP2</i>	Caudate	3.78E-12	0.000795	2.30E-10	increasing	0
<i>CDC73</i>	Caudate	2.01E-09	-0.00065	3.59E-06	decreasing	0
<i>CDH11</i>	Caudate	1.33E-08	-0.00069	5.68E-07	decreasing	0
<i>CDH13</i>	Caudate	1.10E-15	-0.00087	7.82E-13	decreasing	0
<i>CDH20</i>	Caudate	1.56E-11	0.000759	6.03E-09	increasing	0
<i>CDH22</i>	Caudate	4.38E-10	0.000415	0.005186	other	0
<i>CDH24</i>	Caudate	7.25E-09	0.000406	0.005321	other	0
<i>CDH4</i>	Caudate	4.54E-06	0.000729	6.91E-08	increasing	0
<i>CDHR5</i>	Caudate	2.07E-06	0.000744	3.12E-08	increasing	0
<i>CDK1</i>	Caudate	1.84E-07	-0.00054	9.96E-05	decreasing	0
<i>CDK10</i>	Caudate	7.85E-09	0.000393	0.006223	other	0
<i>CDK11B</i>	Caudate	5.50E-06	0.000708	1.60E-07	increasing	0
<i>CDK18</i>	Caudate	4.58E-07	0.000723	3.64E-08	increasing	0
<i>CDK5R1</i>	Caudate	1.00E-09	-0.00054	0.0001	other	0
<i>CDK5RAP3</i>	Caudate	1.44E-09	0.000783	3.33E-09	increasing	0
<i>CDK9</i>	Caudate	4.80E-08	0.000352	0.013596	other	0
<i>CDKN1C</i>	Caudate	4.43E-10	0.000628	6.08E-06	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CDKN2AIPNL</i>	Caudate	1.02E-07	-0.00056	6.92E-05	decreasing	0
<i>CDKN2D</i>	Caudate	7.07E-11	-6.26E-05	0.669728	other	0
<i>CDR2</i>	Caudate	6.78E-10	0.000634	3.60E-06	increasing	0
<i>CDS1</i>	Caudate	2.31E-09	-0.00029	0.05619	other	0
<i>CDT1</i>	Caudate	5.14E-08	0.000113	0.447498	other	0
<i>CDYL</i>	Caudate	1.36E-15	0.000765	2.80E-09	increasing	0
<i>CEBPA</i>	Caudate	1.39E-14	0.000735	2.58E-08	increasing	0
<i>CEBPB</i>	Caudate	9.14E-12	0.000705	2.36E-07	increasing	0
<i>CELF6</i>	Caudate	7.45E-09	0.00067	3.21E-07	increasing	0
<i>CELSR2</i>	Caudate	2.04E-08	0.000427	0.0039	other	0
<i>CELSR3</i>	Caudate	1.89E-09	0.00056	9.22E-05	increasing	0
<i>CEMP1</i>	Caudate	3.33E-11	0.00038	0.00921	other	0
<i>CENPB</i>	Caudate	3.02E-10	0.000196	0.191765	other	0
<i>CENPF</i>	Caudate	1.19E-08	-0.00053	0.00022	other	0
<i>CENPK</i>	Caudate	1.83E-09	-0.00076	3.57E-09	decreasing	0
<i>CENPV</i>	Caudate	9.38E-09	1.33E-05	0.928903	other	0
<i>CEP131</i>	Caudate	1.90E-11	0.00072	5.40E-08	increasing	0
<i>CEP135</i>	Caudate	1.59E-07	-0.00063	2.17E-06	decreasing	0
<i>CEP162</i>	Caudate	1.45E-07	-0.00062	9.81E-06	decreasing	0
<i>CEP164</i>	Caudate	2.07E-08	0.000355	0.01291	other	0
<i>CEP170</i>	Caudate	6.30E-17	-0.00079	4.79E-10	decreasing	0
<i>CEP170B</i>	Caudate	8.68E-11	0.000751	1.73E-08	increasing	0
<i>CEP250</i>	Caudate	1.54E-10	0.000621	9.23E-06	increasing	0
<i>CEP290</i>	Caudate	4.03E-09	-0.00067	4.87E-07	decreasing	0
<i>CEP85</i>	Caudate	1.23E-10	0.000836	8.02E-11	increasing	0
<i>CEP85L</i>	Caudate	6.11E-17	-0.0009	5.73E-14	decreasing	0
<i>CERCAM</i>	Caudate	4.75E-11	0.00075	2.17E-08	increasing	0
<i>CERK</i>	Caudate	2.10E-07	0.000155	0.30397	other	0
<i>CETN3</i>	Caudate	1.20E-07	-0.00044	0.002857	other	0
<i>CETP</i>	Caudate	5.12E-10	-0.00082	1.44E-10	decreasing	0
<i>CFD</i>	Caudate	2.04E-08	0.000467	0.000987	other	0
<i>CFL1</i>	Caudate	2.54E-07	-1.22E-05	0.936052	other	0
<i>CGGBP1</i>	Caudate	6.76E-11	-0.00072	1.19E-07	decreasing	0
<i>CHADL</i>	Caudate	6.26E-11	0.000501	0.00054	other	0
<i>CHCHD6</i>	Caudate	3.88E-08	0.000446	0.002383	other	0
<i>CHD1</i>	Caudate	1.65E-10	-0.00076	9.44E-09	decreasing	0
<i>CHD3</i>	Caudate	9.54E-08	-0.00021	0.165451	other	0
<i>CHD4</i>	Caudate	4.71E-10	0.000581	4.68E-05	increasing	0
<i>CHD5</i>	Caudate	1.55E-09	0.000227	0.129048	other	0
<i>CHD6</i>	Caudate	7.06E-06	0.000727	4.95E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CHD9</i>	Caudate	3.23E-10	-0.00052	0.000373	other	0
<i>CHDH</i>	Caudate	1.39E-09	0.000778	2.04E-09	increasing	0
<i>CHFR</i>	Caudate	6.20E-09	0.00049	0.000759	other	0
<i>CHGA</i>	Caudate	4.73E-10	-0.00076	2.62E-09	decreasing	0
<i>CHI3L1</i>	Caudate	3.51E-10	0.000544	0.000132	other	0
<i>CHIC1</i>	Caudate	1.50E-09	-0.00041	0.004948	other	0
<i>CHIC2</i>	Caudate	5.86E-08	-0.00074	1.55E-08	decreasing	0
<i>CHL1</i>	Caudate	1.25E-08	-0.00056	5.25E-05	decreasing	1
<i>CHML</i>	Caudate	4.61E-10	-0.00065	2.33E-06	decreasing	0
<i>CHMP1A</i>	Caudate	9.09E-08	0.000128	0.399325	other	0
<i>CHMP4B</i>	Caudate	3.51E-11	3.72E-05	0.799949	other	0
<i>CHMP7</i>	Caudate	1.67E-07	-3.11E-05	0.836213	other	0
<i>CHORDC1</i>	Caudate	5.32E-10	-0.0004	0.006499	other	0
<i>CHP1</i>	Caudate	4.29E-09	-0.00024	0.097419	other	0
<i>CHPF2</i>	Caudate	1.11E-07	0.000352	0.018233	other	0
<i>CHRD</i>	Caudate	2.06E-10	0.000816	2.64E-10	increasing	0
<i>CHRD1</i>	Caudate	3.49E-08	-0.00061	6.10E-06	decreasing	0
<i>CHRM2</i>	Caudate	2.31E-10	-0.00078	3.50E-09	decreasing	0
<i>CHST10</i>	Caudate	2.44E-08	0.000619	1.14E-05	increasing	0
<i>CHST2</i>	Caudate	1.21E-07	-5.17E-05	0.727765	other	0
<i>CHST7</i>	Caudate	6.81E-12	7.05E-05	0.637132	other	0
<i>CHTF18</i>	Caudate	1.70E-07	0.000592	2.88E-05	increasing	0
<i>CIR1</i>	Caudate	3.16E-08	-0.00032	0.029547	other	0
<i>CISD3</i>	Caudate	2.13E-11	0.000659	1.05E-06	increasing	0
<i>CIT</i>	Caudate	1.89E-08	0.000721	3.01E-08	increasing	0
<i>CKAP2</i>	Caudate	7.73E-08	-0.00073	3.87E-08	decreasing	1
<i>CKAP4</i>	Caudate	1.07E-08	-0.00048	0.000641	other	0
<i>CKB</i>	Caudate	1.67E-09	0.000487	0.000552	other	0
<i>CKMT1B</i>	Caudate	3.97E-09	0.000212	0.1568	other	0
<i>CLASRP</i>	Caudate	6.73E-08	0.000703	2.83E-07	increasing	0
<i>CLCN2</i>	Caudate	3.01E-08	0.000733	5.60E-08	increasing	0
<i>CLCN7</i>	Caudate	1.12E-11	0.000253	0.085048	other	0
<i>CLDND1</i>	Caudate	1.36E-12	0.00079	6.43E-10	increasing	0
<i>CLEC18C</i>	Caudate	8.79E-08	0.000654	2.20E-06	increasing	0
<i>CLIP2</i>	Caudate	8.74E-15	0.000784	2.93E-09	increasing	0
<i>CLMN</i>	Caudate	8.30E-08	0.000549	0.000118	other	0
<i>CLOCK</i>	Caudate	7.54E-11	-0.00078	4.45E-09	decreasing	0
<i>CLPB</i>	Caudate	4.56E-09	-3.89E-05	0.798648	other	0
<i>CLPP</i>	Caudate	1.63E-07	0.000296	0.048256	other	0
<i>CLPX</i>	Caudate	3.43E-09	-0.00077	3.34E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CLRN2</i>	Caudate	5.84E-07	0.000686	1.82E-07	increasing	1
<i>CLUH</i>	Caudate	7.66E-12	0.000493	0.000738	other	0
<i>CLVS1</i>	Caudate	6.58E-08	-0.00055	7.05E-05	decreasing	0
<i>CMPK1</i>	Caudate	1.26E-12	-0.00085	2.11E-12	decreasing	0
<i>CMTM2</i>	Caudate	9.52E-09	0.000719	7.14E-08	increasing	0
<i>CMTM7</i>	Caudate	1.15E-07	-0.00053	0.000149	other	0
<i>CMTR1</i>	Caudate	8.71E-12	0.000279	0.05605	other	0
<i>CNDP1</i>	Caudate	2.30E-19	0.000865	8.39E-13	increasing	0
<i>CNDP2</i>	Caudate	5.89E-06	0.000699	2.07E-07	increasing	1
<i>CNIH1</i>	Caudate	2.24E-07	-0.00071	1.80E-07	decreasing	0
<i>CNOT6L</i>	Caudate	5.82E-08	-0.00072	1.24E-07	decreasing	0
<i>CNPPD1</i>	Caudate	1.22E-07	0.000426	0.003844	other	0
<i>CNPY3</i>	Caudate	1.74E-07	0.000191	0.197274	other	0
<i>CNTN2</i>	Caudate	1.68E-15	0.000849	3.97E-12	increasing	0
<i>CNTN3</i>	Caudate	7.44E-11	-0.0008	1.17E-09	decreasing	0
<i>CNTN4</i>	Caudate	2.33E-10	-0.00083	1.12E-10	decreasing	0
<i>CNTN5</i>	Caudate	1.59E-12	-0.00079	1.35E-10	decreasing	0
<i>CNTN6</i>	Caudate	3.33E-15	-0.00085	6.69E-12	decreasing	0
<i>CNTROB</i>	Caudate	7.35E-08	0.000489	0.000515	other	0
<i>COBL</i>	Caudate	2.64E-08	0.000602	1.47E-05	increasing	0
<i>COCH</i>	Caudate	5.23E-10	0.000573	3.60E-05	increasing	0
<i>COG4</i>	Caudate	1.62E-08	7.89E-05	0.601369	other	0
<i>COG8</i>	Caudate	2.43E-10	0.000467	0.001475	other	0
<i>COL13A1</i>	Caudate	1.72E-09	0.00064	2.47E-06	increasing	0
<i>COL18A1</i>	Caudate	1.86E-08	-0.00019	0.215679	other	0
<i>COL1A2</i>	Caudate	7.81E-14	-0.00065	2.43E-06	decreasing	0
<i>COL3A1</i>	Caudate	4.33E-13	-0.00078	1.32E-09	decreasing	0
<i>COL4A1</i>	Caudate	4.02E-11	-0.00065	2.23E-06	decreasing	0
<i>COL4A2</i>	Caudate	6.83E-12	-8.81E-05	0.558443	other	0
<i>COL4A3BP</i>	Caudate	1.13E-07	-0.00065	3.03E-06	decreasing	0
<i>COL6A1</i>	Caudate	3.78E-11	-0.00023	0.120029	other	0
<i>COL6A2</i>	Caudate	1.43E-09	-0.00034	0.022375	other	0
<i>COL6A5</i>	Caudate	5.40E-08	-0.00064	2.42E-06	decreasing	1
<i>COMMD2</i>	Caudate	1.64E-10	-0.00079	2.24E-10	decreasing	0
<i>COMT</i>	Caudate	5.11E-11	0.000663	1.46E-06	increasing	0
<i>COMTD1</i>	Caudate	4.06E-08	0.000434	0.002886	other	0
<i>COPS2</i>	Caudate	7.80E-10	-0.00062	9.51E-06	decreasing	0
<i>COPS8</i>	Caudate	1.84E-15	-0.00064	3.98E-06	decreasing	0
<i>COQ4</i>	Caudate	1.77E-10	0.000582	2.28E-05	increasing	0
<i>CORO1B</i>	Caudate	2.55E-11	0.000423	0.004248	other	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CORO2A</i>	Caudate	1.90E-07	-0.00027	0.072758	other	0
<i>CORO2B</i>	Caudate	1.76E-07	0.000585	2.01E-05	increasing	0
<i>CORO6</i>	Caudate	5.54E-11	0.000819	2.57E-10	increasing	0
<i>CORO7</i>	Caudate	2.50E-10	0.000593	2.71E-05	increasing	0
<i>CPA3</i>	Caudate	2.46E-08	0.000795	1.37E-09	increasing	0
<i>CPB1</i>	Caudate	2.18E-23	0.000907	8.51E-15	increasing	0
<i>CPEB1</i>	Caudate	2.03E-25	0.000917	2.25E-15	increasing	0
<i>CPNE6</i>	Caudate	5.00E-08	-0.00027	0.07121	other	0
<i>CPQ</i>	Caudate	9.75E-08	0.000689	3.75E-07	increasing	0
<i>CPS1</i>	Caudate	7.40E-08	0.000742	3.41E-08	increasing	0
<i>CPSF1</i>	Caudate	2.10E-11	0.000608	1.43E-05	increasing	0
<i>CPSF3L</i>	Caudate	7.96E-10	0.000333	0.022605	other	0
<i>CPSF4</i>	Caudate	1.87E-10	0.000549	0.00013	other	0
<i>CPT1A</i>	Caudate	2.03E-07	-0.00017	0.275093	other	0
<i>CPT1C</i>	Caudate	4.30E-09	0.00045	0.002185	other	0
<i>CRAT</i>	Caudate	2.21E-09	0.000532	0.000206	other	0
<i>CRB2</i>	Caudate	1.59E-10	0.000821	1.96E-10	increasing	0
<i>CRB3</i>	Caudate	3.22E-10	0.000744	7.50E-09	increasing	0
<i>CREB1</i>	Caudate	3.29E-10	-0.00075	1.90E-08	decreasing	0
<i>CREM</i>	Caudate	5.22E-09	-0.00081	3.23E-10	decreasing	0
<i>CRIP2</i>	Caudate	1.99E-10	0.000113	0.447089	other	0
<i>CRISPLD1</i>	Caudate	4.75E-11	-0.00065	9.32E-07	decreasing	0
<i>CRTAC1</i>	Caudate	1.32E-07	5.58E-05	0.712075	other	0
<i>CRYAB</i>	Caudate	3.32E-14	0.000456	0.001414	other	0
<i>CRYBB1</i>	Caudate	2.37E-07	-0.0007	2.47E-07	decreasing	0
<i>CRYL1</i>	Caudate	2.82E-11	0.000819	1.39E-10	increasing	0
<i>CRYZL1</i>	Caudate	1.60E-11	-0.00042	0.003941	other	0
<i>CSK</i>	Caudate	1.09E-10	0.000148	0.310466	other	0
<i>CSMD3</i>	Caudate	3.96E-08	-0.00074	2.22E-08	decreasing	0
<i>CSNK1G2</i>	Caudate	4.42E-08	0.000425	0.004119	other	0
<i>CSNK1G3</i>	Caudate	5.92E-07	-0.00071	1.69E-07	decreasing	0
<i>CSNK2A1</i>	Caudate	5.26E-08	-0.00071	1.48E-07	decreasing	0
<i>CSPP1</i>	Caudate	1.06E-12	8.39E-05	0.583555	other	0
<i>CSRNP3</i>	Caudate	2.48E-10	-0.00082	1.70E-10	decreasing	0
<i>CSRP1</i>	Caudate	2.29E-10	0.000638	2.15E-06	increasing	0
<i>CST6</i>	Caudate	2.18E-08	0.000741	2.41E-08	increasing	0
<i>CSTB</i>	Caudate	1.44E-08	9.39E-05	0.532831	other	0
<i>CSTF3</i>	Caudate	6.25E-09	-0.00072	1.35E-07	decreasing	0
<i>CTBP1</i>	Caudate	2.02E-09	0.00044	0.002847	other	0
<i>CTDP1</i>	Caudate	2.67E-09	0.000571	6.44E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CTDSPL2</i>	Caudate	4.68E-08	-0.00067	7.42E-07	decreasing	0
<i>CTHRC1</i>	Caudate	2.48E-07	-0.00058	1.55E-05	decreasing	0
<i>CTNNA1</i>	Caudate	1.90E-08	0.000506	0.000426	other	0
<i>CTNNA2</i>	Caudate	5.63E-08	-0.0006	8.07E-06	decreasing	0
<i>CTNNA3</i>	Caudate	1.47E-18	0.000873	6.09E-14	increasing	0
<i>CTNNBIP1</i>	Caudate	4.56E-12	-0.00016	0.286034	other	0
<i>CTSD</i>	Caudate	1.73E-07	0.00071	1.14E-07	increasing	0
<i>CTSF</i>	Caudate	1.45E-09	0.000653	2.85E-06	increasing	0
<i>CTTN</i>	Caudate	9.67E-09	0.000657	2.01E-06	increasing	0
<i>CTTNBP2</i>	Caudate	4.78E-08	-0.00017	0.234035	other	0
<i>CTTNBP2NL</i>	Caudate	5.22E-11	-0.00066	1.80E-06	decreasing	0
<i>CTU1</i>	Caudate	4.62E-11	3.19E-05	0.829742	other	0
<i>CTXN1</i>	Caudate	8.11E-08	0.000596	1.30E-05	increasing	0
<i>CUL7</i>	Caudate	6.76E-10	0.000507	0.000447	other	0
<i>CUL9</i>	Caudate	3.50E-09	0.000809	5.57E-10	increasing	0
<i>CWC22</i>	Caudate	2.19E-09	-0.00037	0.011143	other	0
<i>CX3CL1</i>	Caudate	2.18E-07	-0.00064	5.67E-06	decreasing	0
<i>CXADR</i>	Caudate	1.07E-18	-0.00085	3.68E-12	decreasing	0
<i>CXCL14</i>	Caudate	2.17E-11	-0.0007	1.10E-07	decreasing	0
<i>CXXC4</i>	Caudate	5.66E-08	-0.00039	0.007949	other	0
<i>CYFIP2</i>	Caudate	5.90E-08	0.000609	5.52E-06	increasing	0
<i>CYLD</i>	Caudate	1.75E-08	-0.00057	5.09E-05	decreasing	0
<i>CYSLTR1</i>	Caudate	1.83E-07	-0.00077	8.13E-09	decreasing	0
<i>D2HGDH</i>	Caudate	6.79E-09	0.000505	0.000458	other	1
<i>DAAM1</i>	Caudate	1.40E-17	-0.00084	3.42E-12	decreasing	0
<i>DAAM2</i>	Caudate	5.85E-09	0.00069	2.18E-07	increasing	1
<i>DAB1</i>	Caudate	2.05E-09	-0.0008	1.50E-09	decreasing	1
<i>DAB2</i>	Caudate	1.69E-11	-0.0008	8.24E-10	decreasing	0
<i>DACH1</i>	Caudate	5.96E-15	-0.00085	1.56E-11	decreasing	0
<i>DACT1</i>	Caudate	3.39E-09	-0.00056	6.96E-05	decreasing	1
<i>DACT2</i>	Caudate	1.87E-09	0.000668	1.06E-06	increasing	0
<i>DACT3</i>	Caudate	1.73E-10	0.00031	0.036638	other	0
<i>DAGLB</i>	Caudate	3.45E-08	0.000646	4.06E-06	increasing	0
<i>DALRD3</i>	Caudate	1.11E-07	0.000397	0.005731	other	0
<i>DAPK2</i>	Caudate	3.37E-07	0.000728	3.80E-08	increasing	0
<i>DAZAP1</i>	Caudate	3.00E-10	0.000721	1.16E-07	increasing	0
<i>DAZAP2</i>	Caudate	4.75E-11	-0.00027	0.063242	other	0
<i>DBNDD1</i>	Caudate	3.01E-08	0.000668	6.71E-07	increasing	1
<i>DBNDD2</i>	Caudate	5.54E-08	0.000197	0.182302	other	0
<i>DBNL</i>	Caudate	4.61E-11	0.000469	0.001399	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>DBT</i>	Caudate	1.46E-10	-0.00078	3.55E-09	decreasing	0
<i>DCAF12</i>	Caudate	2.38E-10	-0.00055	0.00012	other	0
<i>DCAF15</i>	Caudate	5.84E-09	0.000237	0.101568	other	0
<i>DCBLD1</i>	Caudate	6.56E-09	-0.00063	2.01E-06	decreasing	0
<i>DCHS1</i>	Caudate	2.19E-10	0.00019	0.202114	other	0
<i>DCK</i>	Caudate	2.44E-08	-0.00074	4.82E-08	decreasing	0
<i>DCLK1</i>	Caudate	3.54E-23	-0.00093	8.80E-15	decreasing	0
<i>DCP1B</i>	Caudate	2.25E-10	-0.00026	0.082636	other	0
<i>DCPS</i>	Caudate	2.59E-08	0.000206	0.168905	other	1
<i>DCST1</i>	Caudate	1.55E-08	0.000703	2.21E-07	increasing	0
<i>DCUN1D1</i>	Caudate	2.90E-09	-0.00073	5.51E-08	decreasing	0
<i>DCUN1D4</i>	Caudate	2.24E-08	-0.00065	2.65E-06	decreasing	0
<i>DCX</i>	Caudate	5.16E-10	-0.00073	3.31E-08	decreasing	0
<i>DDIT4L</i>	Caudate	2.18E-10	7.41E-05	0.621838	other	0
<i>DDR1</i>	Caudate	3.88E-11	0.000412	0.003598	other	0
<i>DDRGK1</i>	Caudate	3.10E-11	0.000629	5.21E-06	increasing	0
<i>DDX1</i>	Caudate	3.48E-09	-0.00059	3.05E-05	decreasing	0
<i>DDX21</i>	Caudate	3.07E-11	-0.0008	1.83E-10	decreasing	0
<i>DDX24</i>	Caudate	2.79E-08	0.00038	0.008326	other	0
<i>DDX39A</i>	Caudate	3.28E-10	0.000169	0.257261	other	0
<i>DDX41</i>	Caudate	1.82E-09	0.000449	0.00214	other	0
<i>DDX42</i>	Caudate	1.81E-07	0.000176	0.234015	other	0
<i>DDX49</i>	Caudate	3.62E-08	-3.94E-05	0.791066	other	0
<i>DDX51</i>	Caudate	3.96E-11	0.000523	0.000256	other	0
<i>DDX53</i>	Caudate	1.08E-08	-0.00075	2.91E-08	decreasing	0
<i>DDX56</i>	Caudate	2.97E-09	0.000389	0.007948	other	0
<i>DEAF1</i>	Caudate	8.24E-09	0.000389	0.00825	other	0
<i>DECR2</i>	Caudate	8.63E-08	0.000545	0.000155	other	0
<i>DEDD2</i>	Caudate	5.85E-08	0.000676	6.31E-07	increasing	0
<i>DEF8</i>	Caudate	1.36E-08	0.000437	0.002909	other	0
<i>DEGS2</i>	Caudate	2.53E-12	0.000816	6.52E-11	increasing	0
<i>DENND1B</i>	Caudate	6.78E-08	-0.00037	0.010528	other	0
<i>DENND4A</i>	Caudate	3.68E-11	-0.00071	1.95E-07	decreasing	0
<i>DENND4B</i>	Caudate	1.25E-07	0.000757	9.89E-09	increasing	0
<i>DENND6B</i>	Caudate	6.23E-11	0.000354	0.01331	other	0
<i>DEPDC5</i>	Caudate	1.47E-10	0.000846	9.32E-12	increasing	0
<i>DERA</i>	Caudate	3.66E-09	-0.00076	1.39E-09	decreasing	0
<i>DGCR14</i>	Caudate	5.52E-09	0.00037	0.012481	other	0
<i>DGCR2</i>	Caudate	6.06E-11	0.000741	1.80E-08	increasing	0
<i>DGCR6</i>	Caudate	6.44E-13	0.000254	0.079815	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>DGKA</i>	Caudate	1.09E-15	0.000869	5.40E-13	increasing	0
<i>DGKB</i>	Caudate	1.13E-12	-0.0003	0.035119	other	0
<i>DGKQ</i>	Caudate	1.31E-10	0.000601	2.02E-05	increasing	0
<i>DHCR24</i>	Caudate	2.42E-08	0.000476	0.000828	other	0
<i>DHRS11</i>	Caudate	5.90E-10	0.000425	0.002908	other	0
<i>DHRS13</i>	Caudate	1.58E-11	0.00011	0.457912	other	0
<i>DHTKD1</i>	Caudate	2.80E-09	0.000384	0.009455	other	0
<i>DHX30</i>	Caudate	7.42E-12	0.000522	0.000315	other	0
<i>DHX34</i>	Caudate	4.92E-08	0.000317	0.027236	other	1
<i>DHX35</i>	Caudate	3.53E-08	0.000605	1.82E-05	increasing	0
<i>DHX36</i>	Caudate	1.10E-08	-0.00064	4.53E-06	decreasing	0
<i>DHX37</i>	Caudate	5.89E-11	0.000379	0.00945	other	0
<i>DHX38</i>	Caudate	1.60E-10	0.000536	0.000199	other	0
<i>DHX8</i>	Caudate	4.37E-11	-0.00014	0.350667	other	0
<i>DIAPH1</i>	Caudate	1.98E-08	0.000627	4.86E-06	increasing	0
<i>DIAPH2</i>	Caudate	1.72E-07	-0.0007	3.38E-07	decreasing	0
<i>DIAPH3</i>	Caudate	1.84E-07	-0.00073	5.70E-08	decreasing	0
<i>DIP2C</i>	Caudate	1.01E-10	0.000448	0.002295	other	0
<i>DIRAS2</i>	Caudate	3.55E-10	-0.0008	7.02E-10	decreasing	0
<i>DKK3</i>	Caudate	3.02E-13	0.000684	3.51E-07	increasing	0
<i>DLC1</i>	Caudate	2.74E-06	-0.00071	1.58E-07	decreasing	0
<i>DLD</i>	Caudate	5.06E-13	-0.00061	1.58E-05	decreasing	1
<i>DLG1</i>	Caudate	2.24E-10	-0.00036	0.011781	other	0
<i>DLG2</i>	Caudate	1.23E-11	-0.00083	1.25E-10	decreasing	0
<i>DLG3</i>	Caudate	7.53E-10	-0.00058	3.90E-05	decreasing	0
<i>DLK2</i>	Caudate	5.34E-08	2.29E-05	0.879056	other	0
<i>DLX5</i>	Caudate	1.35E-10	-0.00077	1.24E-09	decreasing	0
<i>DLX6</i>	Caudate	2.00E-07	-0.00058	5.76E-05	decreasing	0
<i>DMAP1</i>	Caudate	4.89E-08	0.000353	0.017833	other	0
<i>DMKN</i>	Caudate	9.64E-14	0.000809	5.12E-11	increasing	0
<i>DNAJA3</i>	Caudate	6.57E-09	0.000481	0.001023	other	0
<i>DNAJB4</i>	Caudate	1.97E-09	-0.00023	0.121925	other	0
<i>DNAJB5</i>	Caudate	9.89E-15	-0.00087	3.34E-12	decreasing	0
<i>DNAJC13</i>	Caudate	6.50E-08	-0.00072	1.38E-07	decreasing	0
<i>DNAJC17</i>	Caudate	1.88E-08	0.000268	0.063358	other	1
<i>DNAJC27</i>	Caudate	5.33E-08	-0.00079	1.98E-09	decreasing	0
<i>DNAJC5</i>	Caudate	1.15E-09	0.000175	0.25095	other	0
<i>DNAJC7</i>	Caudate	5.87E-11	0.000323	0.027467	other	0
<i>DNAL1</i>	Caudate	3.22E-05	-0.0007	1.13E-07	decreasing	0
<i>DNM1</i>	Caudate	1.75E-09	0.00077	3.70E-09	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>DNMBP</i>	Caudate	8.66E-11	0.000759	4.16E-09	increasing	0
<i>DNMT3A</i>	Caudate	5.30E-09	0.00024	0.107266	other	0
<i>DNPB1</i>	Caudate	5.86E-08	0.000301	0.041398	other	0
<i>DNTT</i>	Caudate	1.01E-11	0.000763	1.11E-09	increasing	0
<i>DOC2A</i>	Caudate	1.02E-05	0.000726	8.36E-08	increasing	0
<i>DOCK1</i>	Caudate	3.83E-09	0.000782	1.72E-09	increasing	0
<i>DOCK4</i>	Caudate	6.50E-11	-9.32E-05	0.524706	other	0
<i>DOCK5</i>	Caudate	9.40E-19	0.000876	4.19E-14	increasing	0
<i>DOLPP1</i>	Caudate	4.45E-09	-8.23E-05	0.584678	other	0
<i>DPH1</i>	Caudate	2.54E-08	0.000714	1.70E-07	increasing	0
<i>DPYSL2</i>	Caudate	1.28E-07	0.000554	9.29E-05	increasing	0
<i>DPYSL4</i>	Caudate	7.74E-10	7.08E-05	0.635635	other	0
<i>DRAM2</i>	Caudate	7.71E-12	-0.00081	1.82E-10	decreasing	0
<i>DSP</i>	Caudate	1.74E-17	0.000891	1.14E-13	increasing	0
<i>DSTYK</i>	Caudate	5.20E-09	2.07E-05	0.889845	other	0
<i>DTD1</i>	Caudate	8.10E-08	0.000627	4.98E-06	increasing	0
<i>DTL</i>	Caudate	4.08E-09	-0.00064	2.40E-06	decreasing	0
<i>DTNA</i>	Caudate	8.00E-09	-0.00011	0.449043	other	0
<i>DTNBP1</i>	Caudate	2.61E-12	0.000708	6.35E-08	increasing	0
<i>DTWD2</i>	Caudate	1.71E-11	-0.00079	8.65E-10	decreasing	0
<i>DTX2</i>	Caudate	1.29E-09	0.000682	8.11E-07	increasing	0
<i>DTX3</i>	Caudate	5.59E-08	4.49E-05	0.768747	other	0
<i>DUS1L</i>	Caudate	7.01E-11	0.000449	0.002335	other	0
<i>DUS3L</i>	Caudate	2.51E-11	0.000521	0.000297	other	0
<i>DUSP15</i>	Caudate	2.51E-10	0.000193	0.193311	other	0
<i>DUSP16</i>	Caudate	4.07E-09	0.000663	8.61E-07	increasing	0
<i>DUSP4</i>	Caudate	9.63E-08	-0.00073	8.71E-08	decreasing	0
<i>DUSP6</i>	Caudate	3.12E-05	-0.00072	1.19E-07	decreasing	0
<i>DUSP9</i>	Caudate	4.28E-08	0.000642	3.63E-06	increasing	0
<i>DVL1</i>	Caudate	1.47E-09	0.0006	2.28E-05	increasing	0
<i>DVL2</i>	Caudate	6.99E-10	0.000555	6.10E-05	increasing	0
<i>DVL3</i>	Caudate	5.34E-08	0.000593	2.81E-05	increasing	0
<i>DYNC1LI1</i>	Caudate	2.49E-08	-0.00075	9.62E-09	decreasing	0
<i>DYNC1LI2</i>	Caudate	1.74E-07	7.05E-05	0.636994	other	0
<i>DYNLL2</i>	Caudate	4.33E-08	0.000114	0.44415	other	0
<i>DYNLRB1</i>	Caudate	5.33E-08	0.00024	0.101855	other	1
<i>DYRK2</i>	Caudate	1.15E-14	-0.00086	9.85E-13	decreasing	0
<i>DYSF</i>	Caudate	6.57E-08	0.00041	0.005041	other	0
<i>DZIP3</i>	Caudate	1.70E-09	-0.00057	7.85E-05	decreasing	0
<i>E2F2</i>	Caudate	8.48E-08	-0.00043	0.001513	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>E2F3</i>	Caudate	2.17E-09	-0.00062	7.56E-06	decreasing	0
<i>E4F1</i>	Caudate	4.50E-10	0.000411	0.00496	other	0
<i>EBF1</i>	Caudate	9.48E-14	-0.0008	6.99E-11	decreasing	0
<i>EDEM3</i>	Caudate	4.53E-08	-0.00074	2.23E-08	decreasing	0
<i>EDNRA</i>	Caudate	3.94E-08	-0.00054	0.00017	other	0
<i>EDNRB</i>	Caudate	4.11E-09	-0.00072	4.83E-08	decreasing	0
<i>EEA1</i>	Caudate	7.09E-10	-0.00037	0.01103	other	0
<i>EEF1D</i>	Caudate	4.66E-09	0.000575	5.11E-05	increasing	0
<i>EEF2</i>	Caudate	5.91E-11	3.68E-05	0.807047	other	0
<i>EFHD1</i>	Caudate	1.86E-12	0.000733	1.53E-08	increasing	0
<i>EFNA1</i>	Caudate	2.39E-14	0.000826	3.84E-11	increasing	0
<i>EFNB1</i>	Caudate	2.08E-09	0.000157	0.288358	other	0
<i>EFR3A</i>	Caudate	7.36E-09	-0.00042	0.003355	other	0
<i>EGFL6</i>	Caudate	8.16E-09	6.22E-05	0.680417	other	0
<i>EGLN1</i>	Caudate	6.50E-08	0.000215	0.156092	other	0
<i>EGLN2</i>	Caudate	5.12E-10	0.000515	0.000369	other	0
<i>EGR3</i>	Caudate	3.54E-08	-4.41E-05	0.763624	other	0
<i>EHBP1</i>	Caudate	9.07E-08	-0.00066	2.14E-06	decreasing	0
<i>EHBP1L1</i>	Caudate	1.31E-09	0.000206	0.156443	other	0
<i>EHD1</i>	Caudate	1.14E-07	0.000693	4.86E-07	increasing	1
<i>EHMT1</i>	Caudate	2.42E-10	0.000436	0.002804	other	0
<i>EHMT2</i>	Caudate	1.28E-08	0.000488	0.000818	other	0
<i>EIF1B</i>	Caudate	2.25E-11	-9.60E-05	0.517554	other	0
<i>EIF3B</i>	Caudate	5.24E-13	0.000787	4.03E-10	increasing	0
<i>ELAC2</i>	Caudate	2.02E-12	0.000281	0.058656	other	0
<i>ELAVL4</i>	Caudate	5.47E-09	-0.00079	1.17E-09	decreasing	0
<i>ELK1</i>	Caudate	1.04E-07	0.000743	2.23E-08	increasing	0
<i>ELL</i>	Caudate	1.73E-07	0.000664	1.62E-06	increasing	0
<i>ELMO1</i>	Caudate	7.12E-08	5.69E-05	0.701363	other	0
<i>ELMO3</i>	Caudate	5.24E-10	0.000637	4.99E-06	increasing	0
<i>ELMOD2</i>	Caudate	3.73E-09	-0.00079	1.28E-09	decreasing	0
<i>ELN</i>	Caudate	2.56E-07	-0.00031	0.033923	other	0
<i>ELOVL2</i>	Caudate	2.31E-08	-0.00062	4.48E-06	decreasing	0
<i>ELTD1</i>	Caudate	5.66E-08	-0.00057	6.88E-05	decreasing	0
<i>EMB</i>	Caudate	4.27E-09	-0.00066	1.92E-06	decreasing	0
<i>EMC10</i>	Caudate	1.21E-08	0.000326	0.029887	other	0
<i>EMCN</i>	Caudate	1.60E-12	-0.0008	1.00E-09	decreasing	0
<i>EME2</i>	Caudate	2.44E-09	0.00054	0.000189	other	0
<i>EMILIN1</i>	Caudate	9.31E-10	0.000193	0.197788	other	0
<i>EML1</i>	Caudate	1.53E-08	0.000433	0.002428	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>EML2</i>	Caudate	7.27E-13	0.000795	1.03E-09	increasing	0
<i>EML3</i>	Caudate	3.72E-12	0.000645	3.80E-06	increasing	0
<i>EML5</i>	Caudate	9.07E-09	-0.00073	2.37E-08	decreasing	0
<i>ENAH</i>	Caudate	5.20E-11	-0.0008	4.81E-11	decreasing	0
<i>ENKD1</i>	Caudate	2.49E-08	0.000235	0.110411	other	0
<i>ENKUR</i>	Caudate	6.02E-09	-0.00069	1.40E-07	decreasing	0
<i>ENO2</i>	Caudate	4.20E-09	0.000618	7.06E-06	increasing	0
<i>ENOSF1</i>	Caudate	2.58E-07	0.00063	6.73E-06	increasing	0
<i>ENOX1</i>	Caudate	5.95E-10	-0.00074	2.03E-08	decreasing	0
<i>ENPP2</i>	Caudate	5.08E-14	0.00079	4.89E-10	increasing	0
<i>ENPP6</i>	Caudate	1.73E-11	-0.00076	5.40E-09	decreasing	0
<i>ENTHD1</i>	Caudate	5.99E-10	-0.00029	0.009679	other	0
<i>ENTHD2</i>	Caudate	8.62E-08	0.000578	5.36E-05	increasing	0
<i>EPB41L2</i>	Caudate	2.38E-09	-0.00048	0.000615	other	1
<i>EPDR1</i>	Caudate	4.51E-08	0.000499	0.000452	other	0
<i>EPHA10</i>	Caudate	1.50E-09	0.000565	8.29E-05	increasing	0
<i>EPHA5</i>	Caudate	1.45E-21	-0.00089	7.91E-14	decreasing	0
<i>EPHB2</i>	Caudate	1.95E-08	4.39E-05	0.771399	other	0
<i>EPHB3</i>	Caudate	1.39E-09	1.69E-05	0.909663	other	0
<i>EPHB6</i>	Caudate	4.35E-11	0.000574	5.00E-05	increasing	0
<i>EPHX1</i>	Caudate	1.38E-10	0.000722	7.99E-08	increasing	0
<i>EPN3</i>	Caudate	7.37E-08	0.000773	6.31E-09	increasing	0
<i>EPS15</i>	Caudate	1.39E-11	-0.00061	1.38E-05	decreasing	0
<i>EPS8L2</i>	Caudate	2.43E-07	0.000746	3.07E-08	increasing	0
<i>EPT1</i>	Caudate	1.17E-07	-0.00047	0.00097	other	0
<i>ERBB2IP</i>	Caudate	1.33E-08	0.000434	0.002507	other	0
<i>ERBB3</i>	Caudate	4.20E-11	0.000795	4.32E-10	increasing	0
<i>ERCC2</i>	Caudate	9.07E-08	-0.00026	0.078262	other	0
<i>ERLIN1</i>	Caudate	5.00E-08	0.000534	0.000163	other	0
<i>ERMN</i>	Caudate	2.78E-14	0.000718	4.84E-08	increasing	0
<i>ERO1LB</i>	Caudate	4.51E-08	-0.00039	0.007641	other	0
<i>ERP44</i>	Caudate	7.88E-11	-0.00045	0.001832	other	0
<i>ESRRG</i>	Caudate	4.31E-09	-0.00075	3.16E-08	decreasing	0
<i>ESYT1</i>	Caudate	6.76E-08	0.000515	0.000373	other	0
<i>ESYT3</i>	Caudate	1.43E-11	0.000749	5.45E-09	increasing	0
<i>ETNK2</i>	Caudate	1.36E-11	-0.00072	8.24E-08	decreasing	0
<i>ETNPPL</i>	Caudate	2.78E-09	0.000665	6.29E-07	increasing	0
<i>ETS1</i>	Caudate	3.19E-11	-0.00071	1.31E-07	decreasing	0
<i>ETV5</i>	Caudate	1.68E-07	-0.00045	0.001626	other	0
<i>EVA1C</i>	Caudate	3.30E-10	0.000837	6.01E-11	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>EVC</i>	Caudate	6.11E-08	0.000289	0.054378	other	0
<i>EVI2A</i>	Caudate	1.61E-07	0.000475	0.000908	other	0
<i>EVI5L</i>	Caudate	9.92E-10	0.000448	0.002329	other	0
<i>EVPL</i>	Caudate	2.52E-10	0.000771	1.30E-09	increasing	0
<i>EXD3</i>	Caudate	2.43E-08	0.000708	1.82E-07	increasing	1
<i>EXOC3</i>	Caudate	9.04E-08	0.000519	0.000347	other	0
<i>EXOC3L1</i>	Caudate	1.89E-09	0.000584	4.35E-05	increasing	0
<i>EXOC7</i>	Caudate	1.55E-09	0.000473	0.001125	other	1
<i>EXOSC6</i>	Caudate	2.27E-10	0.000348	0.017976	other	0
<i>EXT1</i>	Caudate	2.26E-10	-0.00055	5.89E-05	decreasing	0
<i>EYA1</i>	Caudate	4.04E-08	0.000296	0.046792	other	0
<i>EZH1</i>	Caudate	5.68E-14	0.000853	2.60E-12	increasing	0
<i>EZH2</i>	Caudate	5.08E-09	-0.00052	0.000264	other	0
<i>F10</i>	Caudate	1.35E-08	0.000661	1.98E-06	increasing	0
<i>F12</i>	Caudate	1.12E-10	0.000787	2.45E-09	increasing	0
<i>FA2H</i>	Caudate	1.19E-07	0.000714	4.75E-08	increasing	0
<i>FABP7</i>	Caudate	4.91E-14	-0.00083	5.89E-12	decreasing	0
<i>FADS3</i>	Caudate	1.26E-10	0.000385	0.008574	other	0
<i>FAHD1</i>	Caudate	2.40E-08	0.000633	3.30E-06	increasing	0
<i>FAM101A</i>	Caudate	5.22E-12	0.000432	0.00213	other	0
<i>FAM101B</i>	Caudate	4.56E-09	0.000701	2.32E-07	increasing	1
<i>FAM102A</i>	Caudate	6.98E-08	0.000607	1.01E-05	increasing	0
<i>FAM102B</i>	Caudate	1.38E-11	-0.00079	3.08E-10	decreasing	0
<i>FAM104B</i>	Caudate	2.52E-08	-0.00049	0.000726	other	0
<i>FAM109A</i>	Caudate	7.15E-08	0.000297	0.041395	other	0
<i>FAM109B</i>	Caudate	2.16E-07	-0.00034	0.021815	other	0
<i>FAM111A</i>	Caudate	1.86E-07	-0.00038	0.009751	other	0
<i>FAM115A</i>	Caudate	6.52E-10	0.000576	5.62E-05	increasing	0
<i>FAM117A</i>	Caudate	3.00E-11	0.000794	5.69E-10	increasing	0
<i>FAM131B</i>	Caudate	6.70E-11	0.000355	0.01654	other	0
<i>FAM132B</i>	Caudate	3.60E-07	0.000728	3.94E-08	increasing	0
<i>FAM135A</i>	Caudate	7.61E-08	-0.00067	8.36E-07	decreasing	0
<i>FAM13B</i>	Caudate	2.58E-08	-0.00069	5.26E-07	decreasing	0
<i>FAM151A</i>	Caudate	3.79E-09	0.00078	3.86E-09	increasing	0
<i>FAM151B</i>	Caudate	6.41E-09	-0.0008	1.78E-10	decreasing	0
<i>FAM155A</i>	Caudate	4.72E-12	-0.00081	1.98E-10	decreasing	0
<i>FAM160B1</i>	Caudate	1.06E-09	-0.00075	2.39E-08	decreasing	0
<i>FAM163B</i>	Caudate	1.27E-08	-0.00056	5.02E-05	decreasing	0
<i>FAM171A2</i>	Caudate	2.70E-10	0.000236	0.116802	other	0
<i>FAM173A</i>	Caudate	4.55E-08	0.000574	5.76E-05	increasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FAM181B</i>	Caudate	1.66E-08	0.000124	0.395358	other	0
<i>FAM184A</i>	Caudate	6.49E-10	-0.00072	2.59E-08	decreasing	0
<i>FAM196A</i>	Caudate	6.38E-09	-0.00047	0.000975	other	0
<i>FAM198B</i>	Caudate	1.11E-08	-0.00067	4.95E-07	decreasing	0
<i>FAM199X</i>	Caudate	1.50E-07	-0.00014	0.353048	other	0
<i>FAM19A1</i>	Caudate	6.35E-10	-0.00079	3.53E-10	decreasing	0
<i>FAM19A2</i>	Caudate	1.05E-17	-0.00086	2.62E-12	decreasing	0
<i>FAM19A5</i>	Caudate	8.95E-08	6.16E-06	0.966911	other	0
<i>FAM207A</i>	Caudate	1.16E-10	0.000789	2.23E-09	increasing	0
<i>FAM208A</i>	Caudate	1.52E-08	-0.00066	1.14E-06	decreasing	0
<i>FAM208B</i>	Caudate	6.09E-08	-0.00052	0.000299	other	0
<i>FAM20B</i>	Caudate	1.27E-08	0.000711	1.31E-07	increasing	0
<i>FAM214A</i>	Caudate	1.13E-10	-0.00072	8.54E-08	decreasing	0
<i>FAM3C</i>	Caudate	6.17E-14	-0.00084	2.94E-11	decreasing	0
<i>FAM69B</i>	Caudate	3.39E-12	0.000149	0.32212	other	0
<i>FAM71E1</i>	Caudate	1.57E-07	0.000425	0.003814	other	0
<i>FAM73A</i>	Caudate	5.50E-10	-0.00042	0.003531	other	0
<i>FAM73B</i>	Caudate	2.01E-08	0.000625	9.46E-06	increasing	0
<i>FAM76B</i>	Caudate	3.42E-07	-0.00069	2.58E-07	decreasing	0
<i>FAM78A</i>	Caudate	3.58E-08	0.000325	0.027153	other	0
<i>FAM83D</i>	Caudate	8.91E-08	0.000562	6.48E-05	increasing	0
<i>FAM84A</i>	Caudate	8.84E-12	-0.00073	3.55E-08	decreasing	0
<i>FAM84B</i>	Caudate	6.96E-11	-0.00079	8.54E-10	decreasing	0
<i>FAM89B</i>	Caudate	1.14E-08	0.000257	0.086297	other	0
<i>FAM8A1</i>	Caudate	3.60E-10	-0.00078	1.11E-09	decreasing	0
<i>FANCG</i>	Caudate	5.80E-09	0.000489	0.000438	other	0
<i>FAR1</i>	Caudate	1.45E-11	-0.0007	2.77E-07	decreasing	0
<i>FARP2</i>	Caudate	2.53E-09	0.000539	0.00012	other	0
<i>FARSB</i>	Caudate	4.43E-12	-0.00057	6.84E-05	decreasing	0
<i>FASN</i>	Caudate	1.07E-09	0.000389	0.008904	other	0
<i>FAT3</i>	Caudate	2.70E-06	-0.00072	1.51E-07	decreasing	0
<i>FBF1</i>	Caudate	7.66E-11	0.000681	7.88E-07	increasing	0
<i>FBLN2</i>	Caudate	1.67E-07	-0.00041	0.005412	other	0
<i>FBN2</i>	Caudate	1.31E-10	-0.00014	0.358907	other	0
<i>FBXL15</i>	Caudate	1.21E-07	0.000493	0.000747	other	0
<i>FBXL19</i>	Caudate	6.13E-09	0.000264	0.080956	other	0
<i>FBXL8</i>	Caudate	4.75E-11	0.000368	0.01261	other	0
<i>FBXO11</i>	Caudate	2.37E-08	-0.00073	5.05E-08	decreasing	0
<i>FBXO17</i>	Caudate	1.65E-09	0.000719	9.44E-08	increasing	0
<i>FBXO2</i>	Caudate	1.11E-17	0.000715	4.36E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FBXO31</i>	Caudate	1.53E-11	0.00083	5.87E-11	increasing	0
<i>FBXO46</i>	Caudate	2.12E-08	0.000504	0.000517	other	0
<i>FBXO9</i>	Caudate	6.29E-09	-0.00077	9.44E-09	decreasing	0
<i>FBXW4</i>	Caudate	6.64E-10	0.000702	2.36E-07	increasing	1
<i>FBXW5</i>	Caudate	2.79E-08	0.000275	0.069009	other	0
<i>FBXW7</i>	Caudate	1.18E-06	-0.00076	1.31E-08	decreasing	0
<i>FBXW9</i>	Caudate	9.48E-09	9.87E-05	0.505849	other	0
<i>FCHO2</i>	Caudate	5.36E-11	-0.0007	3.11E-07	decreasing	0
<i>FCHSD2</i>	Caudate	1.03E-07	-0.00055	9.55E-05	decreasing	0
<i>FEM1A</i>	Caudate	3.26E-12	8.53E-05	0.573795	other	0
<i>FEM1C</i>	Caudate	1.14E-07	0.000122	0.417561	other	1
<i>FEZF2</i>	Caudate	4.86E-10	0.000724	4.88E-08	increasing	0
<i>FGF12</i>	Caudate	4.08E-08	-0.00058	4.41E-05	decreasing	0
<i>FGF22</i>	Caudate	1.37E-08	0.000645	4.08E-06	increasing	0
<i>FGFR2</i>	Caudate	1.01E-09	0.000696	3.88E-07	increasing	0
<i>FGFR3</i>	Caudate	1.65E-10	0.000559	0.000102	other	0
<i>FHDC1</i>	Caudate	2.52E-07	1.07E-05	0.942132	other	0
<i>FHOD1</i>	Caudate	2.13E-07	0.000742	1.45E-08	increasing	0
<i>FHOD3</i>	Caudate	4.21E-12	-0.00073	2.54E-08	decreasing	1
<i>FIGNL2</i>	Caudate	5.42E-11	0.000337	0.022509	other	0
<i>FIZ1</i>	Caudate	1.70E-07	0.000673	8.87E-07	increasing	0
<i>FJX1</i>	Caudate	5.26E-09	0.000177	0.230826	other	0
<i>FKBP10</i>	Caudate	9.47E-09	0.000182	0.221032	other	0
<i>FKBP14</i>	Caudate	2.70E-08	-0.0007	1.21E-07	decreasing	0
<i>FKBP1A</i>	Caudate	1.05E-11	0.000106	0.468065	other	0
<i>FKBP5</i>	Caudate	2.84E-06	0.000718	1.07E-07	increasing	0
<i>FKBP8</i>	Caudate	6.61E-10	0.000519	0.000248	other	0
<i>FKTN</i>	Caudate	8.59E-10	-0.00077	6.26E-09	decreasing	0
<i>FLCN</i>	Caudate	1.59E-10	0.000713	1.67E-07	increasing	0
<i>FLII</i>	Caudate	1.47E-10	0.000703	2.91E-07	increasing	0
<i>FLNA</i>	Caudate	3.26E-09	0.000294	0.043649	other	0
<i>FLNB</i>	Caudate	1.02E-10	0.000757	1.51E-08	increasing	0
<i>FLOT1</i>	Caudate	9.66E-09	0.000525	0.00025	other	0
<i>FLOT2</i>	Caudate	1.97E-11	0.000759	4.98E-09	increasing	0
<i>FLRT2</i>	Caudate	8.26E-14	-0.00087	5.36E-13	decreasing	0
<i>FLYWCH1</i>	Caudate	5.45E-11	0.000799	7.13E-10	increasing	0
<i>FMNL2</i>	Caudate	7.28E-08	0.000155	0.297303	other	0
<i>FMR1</i>	Caudate	5.29E-11	-0.00073	5.90E-08	decreasing	0
<i>FN1</i>	Caudate	1.47E-07	-0.00053	0.000243	other	1
<i>FN3KRP</i>	Caudate	7.97E-10	0.000727	8.48E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FNBP1L</i>	Caudate	8.23E-09	-0.00076	2.99E-09	decreasing	0
<i>FNDC3B</i>	Caudate	1.96E-08	-0.00074	4.42E-08	decreasing	0
<i>FOLH1B</i>	Caudate	3.15E-13	0.000777	1.21E-09	increasing	1
<i>FOSB</i>	Caudate	9.83E-09	0.000671	3.06E-07	increasing	0
<i>FOXG1</i>	Caudate	6.36E-09	-0.00073	9.02E-08	decreasing	0
<i>FOXI3</i>	Caudate	1.68E-14	-0.00035	0.000774	other	0
<i>FOXJ3</i>	Caudate	1.31E-07	-0.00034	0.019724	other	0
<i>FOXO4</i>	Caudate	8.59E-16	0.000796	2.05E-10	increasing	0
<i>FOXP1</i>	Caudate	7.25E-16	-0.00085	2.12E-11	decreasing	0
<i>FOXP2</i>	Caudate	1.64E-20	-0.00087	5.94E-13	decreasing	0
<i>FPGS</i>	Caudate	1.62E-08	0.000608	1.48E-05	increasing	0
<i>FPR1</i>	Caudate	8.18E-08	-0.00056	7.18E-05	decreasing	0
<i>FRA10AC1</i>	Caudate	6.83E-10	-0.00052	0.000325	other	0
<i>FRAS1</i>	Caudate	4.11E-13	-0.00084	1.40E-11	decreasing	0
<i>FRMD3</i>	Caudate	9.72E-09	-0.00077	2.09E-09	decreasing	0
<i>FRMD5</i>	Caudate	2.23E-09	0.000312	0.036436	other	0
<i>FRMD8</i>	Caudate	5.35E-09	0.000789	6.56E-10	increasing	0
<i>FRMPD1</i>	Caudate	6.60E-09	-0.00054	9.77E-05	decreasing	0
<i>FSCN1</i>	Caudate	5.22E-12	0.000304	0.041522	other	0
<i>FST</i>	Caudate	1.20E-09	-0.00077	5.12E-09	decreasing	0
<i>FTL</i>	Caudate	3.00E-09	0.00069	4.75E-07	increasing	0
<i>FUK</i>	Caudate	8.16E-09	0.000607	1.89E-05	increasing	0
<i>FUOM</i>	Caudate	4.11E-09	0.000477	0.001142	other	0
<i>FUT1</i>	Caudate	1.63E-07	0.000771	6.58E-09	increasing	0
<i>FUT9</i>	Caudate	5.42E-08	-0.00067	1.27E-06	decreasing	0
<i>FUZ</i>	Caudate	2.18E-07	0.00052	0.00034	other	0
<i>FXR1</i>	Caudate	2.40E-07	-0.00012	0.434533	other	0
<i>FXYD1</i>	Caudate	1.48E-09	0.000537	0.000115	other	0
<i>FXYD6</i>	Caudate	4.29E-09	-0.00038	0.006822	other	0
<i>FYB</i>	Caudate	1.59E-07	-0.00051	0.00037	other	0
<i>FZD3</i>	Caudate	7.23E-08	-0.00075	1.23E-08	decreasing	0
<i>FZD6</i>	Caudate	8.30E-09	-0.0007	1.56E-07	decreasing	0
<i>FZD8</i>	Caudate	2.31E-07	4.88E-05	0.742616	other	0
<i>G2E3</i>	Caudate	1.25E-06	-0.00073	4.17E-08	decreasing	0
<i>G3BP1</i>	Caudate	1.22E-09	-0.00053	0.000227	other	0
<i>G6PD</i>	Caudate	3.49E-10	0.000462	0.001542	other	0
<i>GAA</i>	Caudate	7.90E-08	0.000706	1.70E-07	increasing	0
<i>GAB1</i>	Caudate	1.52E-10	0.00044	0.002185	other	0
<i>GAB2</i>	Caudate	2.94E-11	0.000738	2.71E-08	increasing	0
<i>GABBR2</i>	Caudate	1.46E-08	-0.00051	0.000396	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GABPB2</i>	Caudate	1.99E-10	0.000751	1.95E-08	increasing	0
<i>GABRA1</i>	Caudate	2.37E-07	-0.00054	0.000155	other	0
<i>GABRA2</i>	Caudate	3.10E-10	-0.0007	2.38E-07	decreasing	0
<i>GABRA3</i>	Caudate	2.16E-09	-0.00062	7.76E-06	decreasing	0
<i>GABRA4</i>	Caudate	6.04E-10	-0.00052	0.000312	other	0
<i>GADL1</i>	Caudate	4.42E-10	-0.00072	6.52E-08	decreasing	0
<i>GAK</i>	Caudate	2.62E-11	0.000324	0.029232	other	0
<i>GAL3ST2</i>	Caudate	8.74E-09	0.000363	0.013028	other	0
<i>GAL3ST3</i>	Caudate	6.38E-10	0.000171	0.259672	other	0
<i>GALK1</i>	Caudate	2.96E-08	0.000538	0.000183	other	0
<i>GALNT10</i>	Caudate	8.98E-10	-0.00044	0.001805	other	0
<i>GALNT12</i>	Caudate	7.00E-10	-0.00054	0.000104	other	0
<i>GALNT13</i>	Caudate	9.02E-10	-0.00063	1.83E-06	decreasing	1
<i>GALNT14</i>	Caudate	5.73E-10	-0.00073	1.92E-08	decreasing	0
<i>GALNT15</i>	Caudate	1.20E-07	0.000453	0.001419	other	0
<i>GALNT18</i>	Caudate	9.17E-12	0.000421	0.004394	other	0
<i>GALNT5</i>	Caudate	1.68E-09	0.000611	7.07E-06	increasing	0
<i>GALNT6</i>	Caudate	2.04E-12	0.000816	6.67E-11	increasing	0
<i>GALNT9</i>	Caudate	1.19E-09	-4.52E-05	0.765311	other	0
<i>GALR3</i>	Caudate	2.58E-08	0.00066	2.11E-06	increasing	0
<i>GALT</i>	Caudate	1.11E-08	0.000349	0.018019	other	0
<i>GAMT</i>	Caudate	3.59E-10	0.000683	6.68E-07	increasing	0
<i>GANAB</i>	Caudate	9.09E-12	0.000191	0.210117	other	0
<i>GAR1</i>	Caudate	3.84E-08	-0.00038	0.009282	other	0
<i>GARNL3</i>	Caudate	1.75E-08	0.000695	8.43E-08	increasing	0
<i>GAS1</i>	Caudate	1.96E-10	0.000274	0.057814	other	0
<i>GAS2L1</i>	Caudate	2.77E-11	0.000645	3.70E-06	increasing	0
<i>GAS6</i>	Caudate	1.00E-09	0.000363	0.015254	other	0
<i>GATAD1</i>	Caudate	2.88E-08	0.00044	0.002469	other	1
<i>GATAD2A</i>	Caudate	5.02E-10	0.000686	4.99E-07	increasing	0
<i>GCC1</i>	Caudate	1.46E-10	0.000514	0.000406	other	0
<i>GCC2</i>	Caudate	4.04E-08	-0.00064	4.56E-06	decreasing	0
<i>GCDH</i>	Caudate	1.57E-09	0.000574	6.04E-05	increasing	0
<i>GCH1</i>	Caudate	1.99E-07	0.000443	0.001985	other	0
<i>GCHFR</i>	Caudate	2.11E-10	0.00082	2.56E-10	increasing	0
<i>GCLC</i>	Caudate	8.95E-09	0.000628	3.50E-06	increasing	0
<i>GCN1L1</i>	Caudate	4.25E-09	0.000414	0.004754	other	0
<i>GCNT1</i>	Caudate	7.03E-10	0.000384	0.008344	other	0
<i>GDAP1L1</i>	Caudate	3.26E-11	0.000513	0.000345	other	0
<i>GDF2</i>	Caudate	1.66E-08	0.000725	2.00E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GDF5</i>	Caudate	2.59E-06	-0.00076	1.51E-08	decreasing	0
<i>GDF9</i>	Caudate	2.06E-06	-0.00071	1.71E-07	decreasing	0
<i>GDPD1</i>	Caudate	6.65E-11	-0.00077	9.42E-09	decreasing	0
<i>GEN1</i>	Caudate	1.98E-08	-0.00066	4.87E-07	decreasing	1
<i>GET4</i>	Caudate	1.40E-09	0.000655	2.73E-06	increasing	0
<i>GFER</i>	Caudate	4.42E-09	0.000545	0.000154	other	0
<i>GFOD1</i>	Caudate	2.08E-14	0.000733	8.37E-09	increasing	1
<i>GFOD2</i>	Caudate	6.32E-09	0.000191	0.20706	other	0
<i>GGA2</i>	Caudate	7.96E-08	0.000719	4.72E-08	increasing	0
<i>GGPS1</i>	Caudate	2.61E-07	-0.00076	1.11E-08	decreasing	0
<i>GGT7</i>	Caudate	4.47E-11	0.000435	0.003062	other	0
<i>GHDC</i>	Caudate	8.59E-08	0.000751	1.63E-08	increasing	0
<i>GIGYF1</i>	Caudate	3.31E-11	0.00071	2.04E-07	increasing	0
<i>GIPC1</i>	Caudate	1.41E-08	0.00042	0.004598	other	0
<i>GIPC2</i>	Caudate	2.37E-07	0.000383	0.008608	other	0
<i>GJB1</i>	Caudate	6.02E-14	0.000741	9.20E-09	increasing	0
<i>GJB5</i>	Caudate	3.20E-10	0.000494	0.000498	other	0
<i>GJC1</i>	Caudate	3.33E-11	-0.00058	4.07E-05	decreasing	0
<i>GJC2</i>	Caudate	4.63E-11	0.000754	1.11E-08	increasing	0
<i>GJD2</i>	Caudate	3.70E-15	-0.00084	6.62E-12	decreasing	0
<i>GKAP1</i>	Caudate	1.19E-08	-1.10E-05	0.943194	other	0
<i>GLCE</i>	Caudate	1.37E-10	-0.00077	2.38E-09	decreasing	0
<i>GLI1</i>	Caudate	4.48E-08	0.000378	0.010426	other	0
<i>GLI4</i>	Caudate	6.92E-08	0.000498	0.000433	other	0
<i>GLMN</i>	Caudate	1.34E-08	-0.00076	1.28E-08	decreasing	0
<i>GLRA2</i>	Caudate	9.67E-15	-0.00085	5.11E-12	decreasing	0
<i>GLRX</i>	Caudate	1.18E-08	-0.00049	0.00071	other	0
<i>GLTPD1</i>	Caudate	7.69E-10	0.00047	0.001244	other	0
<i>GLTSCR2</i>	Caudate	1.76E-08	0.000484	0.000856	other	0
<i>GMEB2</i>	Caudate	1.14E-11	0.000355	0.017647	other	0
<i>GMPPB</i>	Caudate	7.73E-08	0.000267	0.070652	other	0
<i>GNA11</i>	Caudate	8.51E-08	0.000446	0.002487	other	0
<i>GNAQ</i>	Caudate	4.19E-12	-0.00084	2.18E-11	decreasing	0
<i>GNAZ</i>	Caudate	2.41E-12	-1.72E-05	0.908468	other	0
<i>GNB1</i>	Caudate	1.84E-08	-0.00039	0.007257	other	0
<i>GNB1L</i>	Caudate	2.07E-09	0.000487	0.000875	other	0
<i>GNB4</i>	Caudate	9.78E-16	-0.00084	4.96E-12	decreasing	0
<i>GNG12</i>	Caudate	3.40E-06	-0.00073	3.50E-08	decreasing	1
<i>GNG2</i>	Caudate	3.83E-15	-0.00071	3.65E-08	decreasing	0
<i>GNG3</i>	Caudate	2.30E-08	-0.00057	7.07E-05	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GNL1</i>	Caudate	4.36E-14	0.000812	5.91E-11	increasing	0
<i>GNMT</i>	Caudate	5.29E-05	0.000711	1.92E-07	increasing	0
<i>GNPNAT1</i>	Caudate	5.47E-10	-0.00077	6.92E-09	decreasing	0
<i>GNPTAB</i>	Caudate	5.59E-09	-0.00078	3.36E-09	decreasing	0
<i>GNPTG</i>	Caudate	2.55E-07	0.00041	0.005642	other	0
<i>GOLGA3</i>	Caudate	7.73E-12	0.000477	0.001146	other	0
<i>GOLGA4</i>	Caudate	2.42E-08	-0.0006	1.39E-05	decreasing	0
<i>GOLT1B</i>	Caudate	7.86E-07	-0.00072	1.16E-07	decreasing	0
<i>GOPC</i>	Caudate	5.11E-10	-0.00073	3.15E-08	decreasing	0
<i>GORASP1</i>	Caudate	1.03E-07	0.000379	0.010964	other	1
<i>GPAA1</i>	Caudate	7.43E-10	0.000592	3.17E-05	increasing	0
<i>GPATCH4</i>	Caudate	2.22E-08	0.000321	0.027469	other	0
<i>GPBP1L1</i>	Caudate	6.52E-11	-0.00016	0.287258	other	0
<i>GPCPD1</i>	Caudate	1.13E-07	-0.00072	7.79E-08	decreasing	0
<i>GPHN</i>	Caudate	6.34E-11	-0.0008	1.14E-09	decreasing	0
<i>GPKOW</i>	Caudate	8.04E-08	0.000209	0.163117	other	0
<i>GPM6B</i>	Caudate	7.54E-10	-0.00066	1.74E-06	decreasing	0
<i>GPN2</i>	Caudate	2.26E-09	0.000551	0.000128	other	0
<i>GPNMB</i>	Caudate	1.94E-09	0.000592	2.16E-05	increasing	0
<i>GPR101</i>	Caudate	5.95E-15	0.000847	6.85E-12	increasing	0
<i>GPR126</i>	Caudate	3.60E-12	-0.00018	0.209986	other	0
<i>GPR133</i>	Caudate	6.35E-08	0.000391	0.005827	other	0
<i>GPR143</i>	Caudate	1.59E-09	0.000813	1.96E-10	increasing	0
<i>GPR146</i>	Caudate	3.35E-07	0.000727	6.48E-08	increasing	0
<i>GPR158</i>	Caudate	2.23E-08	-0.00055	8.50E-05	decreasing	0
<i>GPR162</i>	Caudate	2.34E-14	0.000279	0.053566	other	0
<i>GPR171</i>	Caudate	6.90E-10	-0.00072	1.19E-07	decreasing	0
<i>GPR27</i>	Caudate	2.45E-11	0.000504	0.000531	other	0
<i>GPR37</i>	Caudate	7.96E-17	0.000793	3.77E-10	increasing	0
<i>GPR52</i>	Caudate	8.89E-08	-0.00035	0.017634	other	0
<i>GPR62</i>	Caudate	2.37E-12	0.000824	1.90E-10	increasing	0
<i>GPR63</i>	Caudate	2.83E-08	-0.00077	3.91E-09	decreasing	0
<i>GPR82</i>	Caudate	6.60E-08	-0.00071	1.15E-07	decreasing	0
<i>GPR85</i>	Caudate	7.74E-07	-0.00075	1.98E-08	decreasing	0
<i>GPR88</i>	Caudate	2.20E-07	-0.00061	1.72E-05	decreasing	0
<i>GPRC5B</i>	Caudate	4.52E-15	0.000851	6.74E-13	increasing	0
<i>GPRIN3</i>	Caudate	7.13E-10	-0.00076	1.38E-08	decreasing	0
<i>GPS1</i>	Caudate	7.26E-13	0.000213	0.15245	other	0
<i>GPSM1</i>	Caudate	6.81E-11	0.00032	0.026046	other	0
<i>GPT2</i>	Caudate	1.26E-09	0.000362	0.015247	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>GPX1</i>	Caudate	4.84E-13	0.000797	7.86E-10	increasing	0
<i>GPX2</i>	Caudate	1.46E-09	0.000276	0.058944	other	0
<i>GRAMD1A</i>	Caudate	5.77E-11	0.0003	0.040983	other	0
<i>GRAMD1C</i>	Caudate	5.19E-08	-1.22E-05	0.935037	other	1
<i>GRAP</i>	Caudate	6.45E-08	-0.00027	0.068746	other	0
<i>GRB2</i>	Caudate	2.98E-08	4.12E-05	0.786185	other	0
<i>GRIA1</i>	Caudate	3.37E-12	-0.00076	3.72E-09	decreasing	0
<i>GRIK3</i>	Caudate	1.23E-07	-0.00023	0.119683	other	0
<i>GRIN2C</i>	Caudate	6.66E-13	0.00074	5.66E-09	increasing	0
<i>GRIP1</i>	Caudate	8.26E-08	-0.00065	2.68E-06	decreasing	0
<i>GRK4</i>	Caudate	3.97E-09	0.000822	6.74E-11	increasing	0
<i>GRK5</i>	Caudate	2.19E-08	0.000119	0.432594	other	0
<i>GRK6</i>	Caudate	1.03E-12	0.000317	0.033335	other	0
<i>GRM1</i>	Caudate	3.12E-08	-0.00041	0.00436	other	1
<i>GRM3</i>	Caudate	1.74E-13	-0.00084	1.40E-11	decreasing	0
<i>GRM5</i>	Caudate	1.65E-06	-0.0007	1.86E-07	decreasing	0
<i>GRM7</i>	Caudate	3.44E-09	-0.00069	1.72E-07	decreasing	0
<i>GSTA4</i>	Caudate	1.27E-07	-0.0007	7.89E-08	decreasing	0
<i>GSTM5</i>	Caudate	1.78E-07	0.000111	0.466247	other	0
<i>GSTP1</i>	Caudate	6.14E-10	0.00043	0.002778	other	0
<i>GTF2F1</i>	Caudate	1.94E-08	0.000355	0.015979	other	0
<i>GTF2I</i>	Caudate	4.39E-08	-0.00066	6.83E-07	decreasing	0
<i>GTF3C5</i>	Caudate	1.84E-07	0.000627	7.59E-06	increasing	0
<i>GTF3C6</i>	Caudate	7.42E-08	-0.00055	0.000136	other	0
<i>GTPBP1</i>	Caudate	1.79E-10	0.000319	0.029401	other	0
<i>GUCD1</i>	Caudate	1.10E-07	0.00024	0.108757	other	0
<i>GUCY1A2</i>	Caudate	6.86E-09	-0.00078	3.83E-09	decreasing	0
<i>GYPC</i>	Caudate	2.50E-09	-0.0002	0.195621	other	1
<i>H6PD</i>	Caudate	1.13E-10	0.000637	5.80E-06	increasing	0
<i>HABP4</i>	Caudate	3.68E-16	0.000692	1.53E-07	increasing	0
<i>HAGH</i>	Caudate	2.74E-18	0.000716	7.50E-08	increasing	0
<i>HAGHL</i>	Caudate	1.07E-09	0.000609	1.61E-05	increasing	0
<i>HAP1</i>	Caudate	1.13E-08	0.000754	1.78E-08	increasing	1
<i>HAPLN1</i>	Caudate	4.69E-17	-0.0009	3.27E-14	decreasing	0
<i>HAPLN2</i>	Caudate	1.72E-18	0.000873	1.92E-13	increasing	0
<i>HAPLN4</i>	Caudate	2.10E-15	0.000824	8.83E-12	increasing	0
<i>HAS2</i>	Caudate	6.28E-07	-0.0007	8.23E-08	decreasing	0
<i>HAUS5</i>	Caudate	2.92E-10	0.000771	5.33E-09	increasing	0
<i>HBM</i>	Caudate	7.46E-07	0.000705	3.36E-08	increasing	0
<i>HCFC1R1</i>	Caudate	6.01E-12	-6.76E-05	0.644692	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>HDAC10</i>	Caudate	4.78E-08	0.000744	2.39E-08	increasing	0
<i>HDAC11</i>	Caudate	3.12E-12	0.000687	3.09E-07	increasing	0
<i>HDAC2</i>	Caudate	6.18E-09	-0.00062	7.98E-06	decreasing	0
<i>HDAC6</i>	Caudate	2.64E-08	0.000269	0.062444	other	0
<i>HDAC7</i>	Caudate	2.89E-08	0.000628	7.60E-06	increasing	0
<i>HDAC9</i>	Caudate	2.16E-14	-0.00087	6.73E-13	decreasing	0
<i>HDLBP</i>	Caudate	1.19E-09	7.46E-05	0.620618	other	0
<i>HECTD2</i>	Caudate	1.57E-07	-0.00066	1.49E-06	decreasing	0
<i>HEMK1</i>	Caudate	7.67E-07	0.000709	2.05E-07	increasing	1
<i>HERC2</i>	Caudate	7.43E-10	0.000713	1.80E-07	increasing	0
<i>HES4</i>	Caudate	1.60E-08	0.000546	0.000123	other	0
<i>HES7</i>	Caudate	7.09E-06	0.000719	1.14E-07	increasing	0
<i>HEXA</i>	Caudate	7.46E-08	0.000374	0.008635	other	0
<i>HEXDC</i>	Caudate	3.93E-10	0.000633	4.08E-06	increasing	0
<i>HEYL</i>	Caudate	6.19E-08	0.00057	2.76E-05	increasing	0
<i>HGS</i>	Caudate	3.29E-10	0.000553	0.000122	other	0
<i>HGSNAT</i>	Caudate	4.92E-10	0.000739	5.72E-09	increasing	0
<i>HHAT</i>	Caudate	9.74E-10	0.000644	3.02E-06	increasing	0
<i>HHATL</i>	Caudate	4.29E-08	0.000559	8.45E-05	increasing	0
<i>HHIP</i>	Caudate	6.90E-10	0.000675	4.86E-07	increasing	0
<i>HHIPL1</i>	Caudate	2.91E-08	0.000534	0.000226	other	0
<i>HIC2</i>	Caudate	3.51E-08	0.000622	9.26E-06	increasing	0
<i>HID1</i>	Caudate	1.95E-07	0.000733	4.82E-08	increasing	0
<i>HIF1A</i>	Caudate	1.53E-07	-0.00066	2.00E-06	decreasing	0
<i>HIP1R</i>	Caudate	4.71E-09	0.000663	1.84E-06	increasing	0
<i>HIPK4</i>	Caudate	7.17E-12	0.000679	4.53E-07	increasing	0
<i>HIVEP2</i>	Caudate	1.58E-09	-0.00069	2.96E-07	decreasing	0
<i>HK1</i>	Caudate	5.48E-08	0.000417	0.004925	other	0
<i>HLF</i>	Caudate	8.28E-10	-0.00017	0.23801	other	0
<i>HMCN2</i>	Caudate	1.52E-07	0.000406	0.006211	other	0
<i>HMGCR</i>	Caudate	5.29E-07	-0.00075	2.61E-08	decreasing	0
<i>HMGCS1</i>	Caudate	4.69E-11	-0.00058	4.38E-05	decreasing	0
<i>HMGXB3</i>	Caudate	2.15E-11	0.000109	0.476876	other	0
<i>HMOX2</i>	Caudate	2.16E-08	0.00054	0.000125	other	0
<i>HN1</i>	Caudate	4.66E-11	-0.00045	0.001515	other	0
<i>HNF1A</i>	Caudate	7.93E-08	0.000422	0.004423	other	0
<i>HNRNPA0</i>	Caudate	8.54E-09	-0.00052	0.000283	other	0
<i>HNRNPA1</i>	Caudate	7.82E-09	-0.00031	0.042445	other	0
<i>HNRNPA2B1</i>	Caudate	5.40E-12	-0.00036	0.016436	other	0
<i>HNRNPH1</i>	Caudate	4.57E-08	-0.00064	2.81E-06	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>HNRNPL</i>	Caudate	3.49E-08	5.65E-05	0.70947	other	0
<i>HOGA1</i>	Caudate	2.23E-13	0.000847	1.74E-11	increasing	0
<i>HOMER1</i>	Caudate	2.41E-11	-0.00077	6.74E-09	decreasing	0
<i>HOMER3</i>	Caudate	2.54E-08	0.000411	0.005688	other	0
<i>HOXD1</i>	Caudate	2.46E-08	0.000622	2.93E-06	increasing	0
<i>HOXD3</i>	Caudate	1.78E-08	0.000596	9.53E-06	increasing	0
<i>HPCA</i>	Caudate	1.72E-12	-0.00011	0.461055	other	0
<i>HPCAL4</i>	Caudate	5.76E-11	0.00061	8.94E-06	increasing	0
<i>HPGD</i>	Caudate	1.11E-09	-0.00081	1.04E-10	decreasing	0
<i>HPN</i>	Caudate	3.83E-13	0.000782	5.72E-10	increasing	0
<i>HPRT1</i>	Caudate	2.47E-13	-0.00019	0.195952	other	0
<i>HPSE2</i>	Caudate	1.26E-08	0.000656	1.19E-06	increasing	0
<i>HRH3</i>	Caudate	8.48E-08	0.000672	1.32E-06	increasing	0
<i>HS1BP3</i>	Caudate	9.01E-11	0.000537	0.000171	other	0
<i>HS2ST1</i>	Caudate	6.43E-11	-0.00081	6.98E-10	decreasing	0
<i>HS3ST5</i>	Caudate	1.79E-10	-0.00072	6.82E-08	decreasing	0
<i>HS6ST3</i>	Caudate	7.88E-10	-0.00056	8.18E-05	decreasing	0
<i>HSBP1</i>	Caudate	1.10E-09	-0.0008	1.42E-10	decreasing	0
<i>HSD11B1L</i>	Caudate	4.74E-09	0.000419	0.003818	other	1
<i>HSD17B12</i>	Caudate	6.16E-08	-0.00072	1.36E-07	decreasing	0
<i>HSF4</i>	Caudate	2.59E-18	0.000887	4.16E-14	increasing	0
<i>HSP90B1</i>	Caudate	5.60E-11	-0.00029	0.044656	other	0
<i>HSPA12B</i>	Caudate	2.31E-09	0.000666	1.61E-06	increasing	0
<i>HSPA1B</i>	Caudate	1.07E-07	0.000579	4.25E-05	increasing	0
<i>HSPA6</i>	Caudate	9.63E-09	0.000696	3.97E-07	increasing	0
<i>HSPB8</i>	Caudate	4.61E-13	0.000811	1.00E-10	increasing	0
<i>HSPD1</i>	Caudate	7.31E-10	-0.00025	0.097709	other	0
<i>HTRA2</i>	Caudate	8.62E-08	0.000137	0.367931	other	0
<i>HTRA3</i>	Caudate	6.74E-09	-0.00067	7.87E-07	decreasing	0
<i>HTRA4</i>	Caudate	2.37E-07	0.000624	2.90E-06	increasing	0
<i>HYOU1</i>	Caudate	1.92E-07	0.000318	0.026644	other	0
<i>IBA57</i>	Caudate	2.13E-07	0.000524	0.000307	other	0
<i>ICAM5</i>	Caudate	8.49E-11	0.000498	0.000556	other	0
<i>IDE</i>	Caudate	8.63E-11	-0.00078	9.72E-10	decreasing	0
<i>IDH2</i>	Caudate	2.19E-13	0.000172	0.247847	other	0
<i>IDH3G</i>	Caudate	4.38E-08	0.000479	0.000971	other	0
<i>IFFO1</i>	Caudate	9.76E-12	0.000707	2.47E-07	increasing	0
<i>IFI16</i>	Caudate	3.25E-07	-0.00073	6.18E-08	decreasing	0
<i>IFI27L2</i>	Caudate	3.85E-09	0.000684	7.15E-07	increasing	0
<i>IFI44L</i>	Caudate	1.71E-09	-0.00066	1.24E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>IFNAR1</i>	Caudate	3.23E-10	-0.00078	2.85E-09	decreasing	0
<i>IFNAR2</i>	Caudate	1.88E-08	-0.00023	0.130845	other	0
<i>IFNGR1</i>	Caudate	5.76E-07	-0.00076	1.37E-08	decreasing	0
<i>IFT140</i>	Caudate	1.84E-09	0.00039	0.006023	other	0
<i>IFT74</i>	Caudate	3.04E-08	-0.00073	2.33E-08	decreasing	0
<i>IFT80</i>	Caudate	9.48E-10	-0.00076	6.01E-09	decreasing	0
<i>IFT81</i>	Caudate	9.71E-11	-0.00079	1.95E-10	decreasing	0
<i>IGF1</i>	Caudate	1.68E-14	-0.00081	1.23E-10	decreasing	0
<i>IGF2BP2</i>	Caudate	1.55E-10	-0.00069	4.19E-07	decreasing	0
<i>IGF2BP3</i>	Caudate	3.39E-08	-0.00052	0.000173	other	0
<i>IGF2R</i>	Caudate	1.97E-12	-0.00012	0.41894	other	0
<i>IGFALS</i>	Caudate	1.51E-08	0.00069	2.62E-07	increasing	0
<i>IGFBP2</i>	Caudate	1.28E-11	-0.0005	0.000422	other	0
<i>IGFBP3</i>	Caudate	2.44E-07	-0.00039	0.00803	other	0
<i>IGFBP6</i>	Caudate	6.45E-17	0.000693	1.89E-07	increasing	0
<i>IGFBP7</i>	Caudate	1.46E-09	-0.00046	0.001331	other	0
<i>IGSF1</i>	Caudate	3.83E-09	-0.0007	6.81E-08	decreasing	0
<i>IGSF3</i>	Caudate	1.00E-09	-4.35E-05	0.769606	other	0
<i>IKZF3</i>	Caudate	6.34E-09	0.00063	3.18E-06	increasing	0
<i>IKZF5</i>	Caudate	5.47E-09	-0.00025	0.087942	other	0
<i>IL10RB</i>	Caudate	5.25E-10	-0.00073	3.60E-08	decreasing	0
<i>IL11RA</i>	Caudate	7.48E-10	0.000621	6.75E-06	increasing	0
<i>IL15RA</i>	Caudate	9.85E-16	0.000872	6.89E-14	increasing	0
<i>IL17D</i>	Caudate	3.40E-11	0.000468	0.001155	other	0
<i>IL17RC</i>	Caudate	1.56E-08	0.000761	1.30E-08	increasing	0
<i>IL6ST</i>	Caudate	2.74E-06	-0.00075	2.29E-08	decreasing	1
<i>ILF3</i>	Caudate	4.72E-08	0.000421	0.004289	other	0
<i>ILVBL</i>	Caudate	1.83E-09	0.000649	3.16E-06	increasing	0
<i>IMP4</i>	Caudate	1.06E-09	8.84E-05	0.559176	other	0
<i>INADL</i>	Caudate	1.63E-10	0.000728	1.17E-08	increasing	0
<i>ING5</i>	Caudate	3.31E-11	0.000765	8.05E-09	increasing	1
<i>INHBA</i>	Caudate	1.61E-20	-0.00088	2.17E-13	decreasing	0
<i>INO80B</i>	Caudate	3.14E-10	0.000661	1.86E-06	increasing	0
<i>INPP5A</i>	Caudate	3.87E-10	0.000514	0.000194	other	0
<i>INPP5E</i>	Caudate	1.02E-08	0.000706	2.44E-07	increasing	0
<i>INSIG2</i>	Caudate	7.18E-15	-0.00071	1.27E-07	decreasing	0
<i>INTS1</i>	Caudate	5.03E-12	0.000577	5.43E-05	increasing	0
<i>IP6K3</i>	Caudate	1.95E-07	0.000784	2.78E-09	increasing	0
<i>IPMK</i>	Caudate	1.73E-10	-0.00071	1.67E-07	decreasing	0
<i>IPO11</i>	Caudate	4.36E-08	-0.00051	0.0005	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>IPO13</i>	Caudate	1.07E-08	0.000529	0.000209	other	0
<i>IPO9</i>	Caudate	1.61E-07	-0.00028	0.058158	other	0
<i>IREB2</i>	Caudate	1.10E-09	-0.00078	3.96E-09	decreasing	0
<i>IRF2</i>	Caudate	1.37E-14	0.000821	7.32E-11	increasing	0
<i>IRF2BP1</i>	Caudate	1.28E-10	0.000569	7.16E-05	increasing	0
<i>IRF2BPL</i>	Caudate	5.58E-09	0.000227	0.127481	other	0
<i>IRGQ</i>	Caudate	8.34E-08	0.000424	0.004109	other	0
<i>IRS1</i>	Caudate	6.24E-08	0.00016	0.296242	other	0
<i>ISCU</i>	Caudate	5.30E-08	0.000471	0.001015	other	0
<i>ISM1</i>	Caudate	3.54E-08	-0.00066	2.65E-06	decreasing	0
<i>ISYNA1</i>	Caudate	2.64E-10	0.000617	1.17E-05	increasing	0
<i>ITFG3</i>	Caudate	8.12E-09	0.000434	0.003008	other	0
<i>ITGA1</i>	Caudate	9.46E-11	-0.0008	9.04E-10	decreasing	0
<i>ITGA2B</i>	Caudate	5.04E-09	0.000694	3.44E-07	increasing	0
<i>ITGA3</i>	Caudate	2.41E-11	0.000789	2.18E-09	increasing	0
<i>ITGA9</i>	Caudate	5.41E-08	-0.00032	0.030761	other	0
<i>ITGAV</i>	Caudate	1.52E-07	-0.0008	8.16E-10	decreasing	0
<i>ITK</i>	Caudate	4.51E-08	0.000705	4.68E-08	increasing	0
<i>ITM2A</i>	Caudate	5.33E-06	-0.00072	8.87E-08	decreasing	0
<i>ITM2B</i>	Caudate	4.98E-16	-0.00035	0.018433	other	0
<i>ITPKA</i>	Caudate	4.51E-09	0.000457	0.001804	other	0
<i>ITPR1</i>	Caudate	2.21E-09	3.95E-05	0.790291	other	0
<i>ITPR3</i>	Caudate	7.96E-10	0.000821	7.25E-11	increasing	0
<i>IVNS1ABP</i>	Caudate	2.12E-08	-0.00076	1.15E-08	decreasing	0
<i>IZUMO4</i>	Caudate	2.87E-09	0.000524	0.000141	other	0
<i>JADE2</i>	Caudate	3.77E-16	0.000889	6.37E-14	increasing	0
<i>JAG2</i>	Caudate	2.41E-09	0.000511	0.000426	other	0
<i>JAK2</i>	Caudate	1.04E-07	-0.00055	0.000132	other	0
<i>JAKMIP1</i>	Caudate	1.52E-08	0.00069	5.64E-07	increasing	0
<i>JAKMIP2</i>	Caudate	7.80E-12	-0.00077	6.35E-10	decreasing	0
<i>JAKMIP3</i>	Caudate	3.34E-08	0.000742	2.81E-08	increasing	0
<i>JAM3</i>	Caudate	2.28E-15	0.000792	1.28E-10	increasing	0
<i>JAZF1</i>	Caudate	2.21E-07	-0.00073	5.33E-08	decreasing	0
<i>JMJD1C</i>	Caudate	8.85E-14	-0.00077	4.38E-09	decreasing	0
<i>JMJD4</i>	Caudate	1.68E-07	0.000327	0.026943	other	0
<i>JMJD8</i>	Caudate	5.06E-10	0.00038	0.010814	other	0
<i>JOSD2</i>	Caudate	2.46E-07	0.000582	4.07E-05	increasing	0
<i>JPH1</i>	Caudate	6.72E-12	0.000611	8.26E-06	increasing	0
<i>JRK</i>	Caudate	2.64E-12	0.000646	3.05E-06	increasing	0
<i>JUND</i>	Caudate	1.64E-08	0.000751	1.63E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>KALRN</i>	Caudate	1.84E-10	-0.00066	1.54E-06	decreasing	0
<i>KANK4</i>	Caudate	5.51E-10	0.00069	1.12E-07	increasing	1
<i>KAT6B</i>	Caudate	6.91E-08	-0.0003	0.044506	other	0
<i>KATNB1</i>	Caudate	1.49E-09	0.000503	0.000565	other	0
<i>KATNBL1</i>	Caudate	4.02E-06	-0.00072	1.37E-07	decreasing	0
<i>KBTBD11</i>	Caudate	7.28E-14	0.000763	2.24E-09	increasing	0
<i>KCNAB2</i>	Caudate	5.62E-10	0.000722	1.67E-08	increasing	0
<i>KCNB2</i>	Caudate	3.95E-15	-0.00086	2.49E-12	decreasing	0
<i>KCND3</i>	Caudate	5.34E-07	0.000771	3.45E-09	increasing	0
<i>KCNG1</i>	Caudate	1.89E-09	-0.00074	1.34E-08	decreasing	0
<i>KCNG2</i>	Caudate	3.43E-12	0.000242	0.107658	other	0
<i>KCNH2</i>	Caudate	3.10E-10	0.00067	7.17E-07	increasing	0
<i>KCNH3</i>	Caudate	5.21E-09	0.000396	0.007768	other	0
<i>KCNH5</i>	Caudate	2.31E-16	-0.00087	4.51E-13	decreasing	0
<i>KCNH8</i>	Caudate	4.55E-12	0.000839	2.99E-11	increasing	0
<i>KCNIP2</i>	Caudate	2.61E-09	0.000778	2.07E-09	increasing	0
<i>KCNJ12</i>	Caudate	2.62E-09	0.000585	4.13E-05	increasing	0
<i>KCNJ14</i>	Caudate	1.60E-09	0.00051	0.00036	other	1
<i>KCNJ2</i>	Caudate	3.80E-11	0.000735	2.64E-08	increasing	0
<i>KCNJ4</i>	Caudate	3.11E-08	0.000205	0.177213	other	0
<i>KCNJ6</i>	Caudate	3.70E-11	-0.00083	2.31E-11	decreasing	0
<i>KCNJ9</i>	Caudate	3.46E-09	0.000499	0.000633	other	0
<i>KCNK12</i>	Caudate	8.11E-11	-6.99E-05	0.63358	other	0
<i>KCNK2</i>	Caudate	1.01E-07	-0.00071	1.77E-07	decreasing	0
<i>KCNK3</i>	Caudate	7.01E-09	-0.00064	3.24E-06	decreasing	0
<i>KCNK9</i>	Caudate	1.35E-08	-0.00068	4.66E-07	decreasing	0
<i>KCNN1</i>	Caudate	2.49E-08	0.000629	4.56E-06	increasing	0
<i>KCNQ2</i>	Caudate	2.03E-08	0.000536	0.000194	other	0
<i>KCNT2</i>	Caudate	1.97E-12	-0.00077	2.62E-09	decreasing	0
<i>KCTD11</i>	Caudate	1.70E-07	0.0006	1.68E-05	increasing	0
<i>KCTD16</i>	Caudate	3.02E-11	-0.0008	7.08E-10	decreasing	0
<i>KCTD2</i>	Caudate	9.22E-11	0.000761	1.25E-08	increasing	0
<i>KCTD3</i>	Caudate	2.55E-09	-0.00076	4.07E-09	decreasing	0
<i>KDELR2</i>	Caudate	1.17E-10	-0.00078	7.00E-10	decreasing	0
<i>KDM1A</i>	Caudate	2.38E-08	-0.00055	7.53E-05	decreasing	0
<i>KDM7A</i>	Caudate	3.41E-08	-0.00037	0.010591	other	0
<i>KDR</i>	Caudate	6.48E-11	-0.00079	1.09E-09	decreasing	0
<i>KDSR</i>	Caudate	4.25E-09	0.000758	1.58E-09	increasing	0
<i>KEAP1</i>	Caudate	1.37E-10	0.000462	0.001382	other	0
<i>KHK</i>	Caudate	5.41E-08	0.000573	6.39E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>KHNYN</i>	Caudate	4.14E-09	0.00074	3.59E-08	increasing	0
<i>KIAA0195</i>	Caudate	2.85E-12	0.000765	8.73E-09	increasing	0
<i>KIAA0196</i>	Caudate	1.85E-07	-0.00069	5.61E-07	decreasing	0
<i>KIAA0232</i>	Caudate	2.05E-07	-0.00072	1.09E-07	decreasing	0
<i>KIAA0368</i>	Caudate	2.19E-08	-0.00032	0.026735	other	0
<i>KIAA0513</i>	Caudate	6.68E-12	0.000826	6.06E-11	increasing	0
<i>KIAA0895L</i>	Caudate	4.53E-09	0.00021	0.154349	other	0
<i>KIAA0930</i>	Caudate	1.24E-08	0.000588	3.32E-05	increasing	0
<i>KIAA1024</i>	Caudate	2.49E-07	-0.00049	0.000525	other	0
<i>KIAA1211L</i>	Caudate	4.55E-10	0.000509	0.000452	other	0
<i>KIAA1217</i>	Caudate	4.73E-09	0.000236	0.112597	other	0
<i>KIAA1377</i>	Caudate	8.67E-08	-0.00065	2.72E-06	decreasing	0
<i>KIAA1586</i>	Caudate	2.05E-06	-0.00076	9.70E-09	decreasing	0
<i>KIAA1598</i>	Caudate	5.11E-13	0.000751	6.63E-09	increasing	0
<i>KIAA2013</i>	Caudate	1.83E-07	0.000422	0.004385	other	0
<i>KIAA2022</i>	Caudate	4.83E-09	-0.00064	4.59E-06	decreasing	0
<i>KIAA2026</i>	Caudate	2.85E-08	-0.00013	0.389792	other	0
<i>KIDINS220</i>	Caudate	8.42E-12	-0.00079	8.37E-10	decreasing	1
<i>KIF13B</i>	Caudate	2.51E-13	0.000829	1.36E-11	increasing	0
<i>KIF15</i>	Caudate	8.56E-08	-0.00048	0.000823	other	0
<i>KIF18A</i>	Caudate	8.84E-08	-0.00059	1.58E-05	decreasing	0
<i>KIF1A</i>	Caudate	1.53E-07	0.00062	1.11E-05	increasing	0
<i>KIF21A</i>	Caudate	1.89E-08	-0.00055	9.37E-05	decreasing	0
<i>KIF22</i>	Caudate	1.56E-11	-0.0003	0.040422	other	0
<i>KIF23</i>	Caudate	1.97E-07	-0.00043	0.002853	other	0
<i>KIF26A</i>	Caudate	5.71E-09	-2.27E-05	0.878586	other	0
<i>KIF3A</i>	Caudate	6.42E-11	-0.00064	4.26E-06	decreasing	0
<i>KIF3B</i>	Caudate	1.77E-08	-0.00023	0.119108	other	0
<i>KIF5A</i>	Caudate	4.83E-10	0.000779	3.57E-10	increasing	0
<i>KIF7</i>	Caudate	6.76E-09	0.000659	2.10E-06	increasing	0
<i>KIFC2</i>	Caudate	6.19E-09	0.000482	0.001005	other	1
<i>KIFC3</i>	Caudate	2.59E-10	0.000397	0.005669	other	0
<i>KIRREL</i>	Caudate	7.88E-09	-0.00045	0.001905	other	0
<i>KITLG</i>	Caudate	9.17E-15	-0.00087	7.15E-13	decreasing	0
<i>KIZ</i>	Caudate	2.92E-13	0.000703	1.52E-07	increasing	0
<i>KLC2</i>	Caudate	4.18E-09	0.000763	6.33E-09	increasing	0
<i>KLF10</i>	Caudate	1.19E-11	-0.00077	2.81E-09	decreasing	0
<i>KLF12</i>	Caudate	1.00E-11	-0.00078	1.13E-09	decreasing	0
<i>KLF13</i>	Caudate	8.73E-09	0.00012	0.432892	other	0
<i>KLF9</i>	Caudate	1.96E-13	-0.00084	3.89E-11	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>KLHDC10</i>	Caudate	2.93E-08	-0.00068	3.84E-07	decreasing	0
<i>KLHDC4</i>	Caudate	1.97E-08	0.00048	0.001052	other	1
<i>KLHDC8B</i>	Caudate	4.56E-09	0.000462	0.000954	other	0
<i>KLHL17</i>	Caudate	3.74E-08	0.000536	0.00021	other	0
<i>KLHL21</i>	Caudate	7.75E-12	0.000662	1.14E-06	increasing	0
<i>KLHL22</i>	Caudate	1.16E-09	0.000516	0.00037	other	0
<i>KLHL26</i>	Caudate	2.27E-11	0.00051	0.000384	other	0
<i>KLHL28</i>	Caudate	4.70E-07	-0.00072	7.85E-08	decreasing	0
<i>KLHL32</i>	Caudate	5.04E-09	0.000599	2.33E-05	increasing	0
<i>KLHL35</i>	Caudate	2.25E-12	0.000256	0.076628	other	0
<i>KLHL36</i>	Caudate	3.94E-09	0.000304	0.044314	other	1
<i>KLHL4</i>	Caudate	1.78E-16	0.000788	3.71E-10	increasing	0
<i>KLHL40</i>	Caudate	8.92E-08	0.000778	2.41E-09	increasing	0
<i>KLHL7</i>	Caudate	2.41E-08	-0.00068	4.38E-07	decreasing	0
<i>KLK6</i>	Caudate	1.05E-15	0.000849	2.23E-12	increasing	0
<i>KPNA2</i>	Caudate	1.87E-09	-0.0007	3.17E-07	decreasing	0
<i>KPNA3</i>	Caudate	9.93E-08	-0.00068	7.75E-07	decreasing	0
<i>KPNA4</i>	Caudate	1.43E-09	-0.00028	0.066223	other	0
<i>KPNA5</i>	Caudate	1.37E-06	-0.00074	1.64E-08	decreasing	0
<i>KRAS</i>	Caudate	1.23E-10	-0.00076	1.12E-08	decreasing	0
<i>KRBA1</i>	Caudate	9.83E-11	0.000708	2.26E-07	increasing	0
<i>KRBA2</i>	Caudate	9.13E-08	0.000453	0.001863	other	0
<i>KRBOX4</i>	Caudate	2.70E-05	0.000701	1.27E-07	increasing	0
<i>KTN1</i>	Caudate	2.66E-11	-0.0003	0.043752	other	0
<i>KY</i>	Caudate	3.81E-14	0.000871	4.29E-12	increasing	0
<i>L3MBTL2</i>	Caudate	7.79E-08	0.000709	2.26E-07	increasing	0
<i>LACE1</i>	Caudate	3.15E-07	-0.00074	2.53E-08	decreasing	0
<i>LAMA2</i>	Caudate	8.49E-12	-0.00079	1.50E-09	decreasing	0
<i>LAMA4</i>	Caudate	2.25E-11	-0.00075	9.57E-09	decreasing	0
<i>LAMB3</i>	Caudate	1.75E-10	0.000413	0.00389	other	0
<i>LAMC1</i>	Caudate	1.05E-10	-0.00074	1.88E-08	decreasing	0
<i>LARP4</i>	Caudate	2.14E-08	-0.00062	1.02E-05	decreasing	0
<i>LARP6</i>	Caudate	3.81E-09	0.000576	4.81E-05	increasing	1
<i>LARS</i>	Caudate	1.18E-07	-0.00068	3.66E-07	decreasing	0
<i>LASP1</i>	Caudate	4.14E-09	-0.00058	3.32E-05	decreasing	0
<i>LAT</i>	Caudate	3.96E-07	0.000743	2.53E-08	increasing	0
<i>LBH</i>	Caudate	6.98E-13	-0.00086	1.33E-12	decreasing	0
<i>LBR</i>	Caudate	1.55E-07	-0.00064	2.13E-06	decreasing	0
<i>LCLAT1</i>	Caudate	1.20E-12	-0.00072	4.38E-08	decreasing	0
<i>LCORL</i>	Caudate	2.68E-13	-0.00085	2.65E-12	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LDB1</i>	Caudate	9.80E-12	0.000525	0.000285	other	0
<i>LDHD</i>	Caudate	9.37E-08	0.000674	1.15E-06	increasing	0
<i>LEMD2</i>	Caudate	3.18E-08	0.000219	0.14886	other	0
<i>LEPREL1</i>	Caudate	4.33E-08	0.000656	6.47E-07	increasing	1
<i>LEPREL2</i>	Caudate	4.20E-10	0.000501	0.000359	other	0
<i>LEPREL4</i>	Caudate	3.01E-10	0.000492	0.000392	other	0
<i>LEPROTL1</i>	Caudate	1.63E-07	-0.00051	0.000406	other	0
<i>LETM1</i>	Caudate	3.36E-10	0.000463	0.00156	other	0
<i>LGALS2</i>	Caudate	1.03E-07	0.000686	4.25E-07	increasing	0
<i>LGALSL</i>	Caudate	4.27E-12	-0.00081	1.25E-10	decreasing	0
<i>LGI2</i>	Caudate	2.27E-08	-0.00053	0.000158	other	0
<i>LGI3</i>	Caudate	3.29E-16	0.000884	5.78E-14	increasing	0
<i>LHFPL3</i>	Caudate	8.88E-11	-0.00085	2.82E-11	decreasing	0
<i>LHFPL4</i>	Caudate	1.20E-10	-5.13E-05	0.732965	other	0
<i>LIG1</i>	Caudate	1.81E-09	0.000345	0.015886	other	0
<i>LIMA1</i>	Caudate	7.64E-09	-0.00079	1.76E-09	decreasing	0
<i>LIMCH1</i>	Caudate	6.46E-09	0.00056	6.79E-05	increasing	0
<i>LIMD2</i>	Caudate	2.45E-07	0.000149	0.322898	other	0
<i>LIME1</i>	Caudate	3.69E-11	0.000635	5.88E-06	increasing	0
<i>LIMK2</i>	Caudate	1.38E-08	0.000664	1.20E-06	increasing	0
<i>LIN7C</i>	Caudate	1.91E-12	-0.00077	1.04E-09	decreasing	0
<i>LINGO2</i>	Caudate	1.28E-07	-0.00066	1.72E-06	decreasing	0
<i>LIPE</i>	Caudate	1.14E-09	0.000784	2.47E-09	increasing	0
<i>LIPH</i>	Caudate	6.51E-08	0.000762	9.49E-09	increasing	0
<i>LIX1L</i>	Caudate	1.95E-07	0.000551	0.000126	other	0
<i>LLGL1</i>	Caudate	1.19E-10	0.000653	2.42E-06	increasing	0
<i>LMBRD1</i>	Caudate	3.80E-09	-0.00036	0.013569	other	0
<i>LMNA</i>	Caudate	1.75E-08	0.000404	0.00571	other	0
<i>LMNB2</i>	Caudate	1.68E-10	0.000217	0.140311	other	0
<i>LMO3</i>	Caudate	1.63E-07	-0.00075	2.13E-08	decreasing	0
<i>LOC103214240</i>	Caudate	7.06E-08	-0.00035	0.017221	other	1
<i>LOC103214253</i>	Caudate	3.37E-15	0.000852	7.65E-12	increasing	0
<i>LOC103214288</i>	Caudate	3.24E-11	-7.53E-05	0.611734	other	0
<i>LOC103214300</i>	Caudate	2.34E-07	-0.0005	0.000397	other	0
<i>LOC103214446</i>	Caudate	2.17E-16	0.000873	3.84E-13	increasing	0
<i>LOC103214510</i>	Caudate	3.12E-09	0.000601	2.35E-05	increasing	0
<i>LOC103214520</i>	Caudate	1.17E-11	-0.00042	0.000134	other	0
<i>LOC103214531</i>	Caudate	7.99E-10	9.60E-05	0.52977	other	0
<i>LOC103214546</i>	Caudate	9.38E-09	-0.00066	2.35E-06	decreasing	0
<i>LOC103214562</i>	Caudate	5.34E-08	-0.00027	0.059325	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103214618</i>	Caudate	6.41E-08	-7.55E-05	0.617849	other	0
<i>LOC103214728</i>	Caudate	5.07E-08	0.000251	0.097158	other	0
<i>LOC103214744</i>	Caudate	2.06E-07	0.000574	4.45E-05	increasing	0
<i>LOC103214747</i>	Caudate	1.34E-07	0.000658	1.07E-06	increasing	0
<i>LOC103214772</i>	Caudate	1.56E-09	-0.0008	1.01E-09	decreasing	0
<i>LOC103214785</i>	Caudate	1.88E-07	-0.00065	2.22E-06	decreasing	0
<i>LOC103214822</i>	Caudate	1.34E-08	0.000546	0.00014	other	0
<i>LOC103214824</i>	Caudate	1.27E-07	-0.00073	8.17E-08	decreasing	0
<i>LOC103214847</i>	Caudate	1.25E-09	0.000689	3.36E-07	increasing	0
<i>LOC103214904</i>	Caudate	2.97E-05	0.000721	9.44E-08	increasing	0
<i>LOC103215235</i>	Caudate	4.38E-09	0.000541	0.000178	other	0
<i>LOC103215277</i>	Caudate	3.71E-16	0.000697	1.17E-07	increasing	0
<i>LOC103215364</i>	Caudate	1.33E-06	0.000698	2.59E-07	increasing	0
<i>LOC103215370</i>	Caudate	6.13E-09	0.000332	0.026308	other	1
<i>LOC103215486</i>	Caudate	8.68E-06	0.000683	1.98E-07	increasing	0
<i>LOC103215493</i>	Caudate	6.67E-08	-0.00014	0.336265	other	0
<i>LOC103215517</i>	Caudate	2.89E-08	0.000675	7.26E-07	increasing	0
<i>LOC103215726</i>	Caudate	4.08E-09	0.000263	0.07497	other	0
<i>LOC103215734</i>	Caudate	1.20E-07	-0.00037	0.011655	other	0
<i>LOC103215758</i>	Caudate	7.18E-09	-0.00017	0.268398	other	0
<i>LOC103215811</i>	Caudate	1.98E-07	-0.00019	0.217671	other	0
<i>LOC103215843</i>	Caudate	6.79E-11	-0.00077	2.77E-09	decreasing	0
<i>LOC103215864</i>	Caudate	5.39E-12	0.000791	7.10E-10	increasing	0
<i>LOC103215883</i>	Caudate	1.09E-08	-0.00072	1.78E-08	decreasing	0
<i>LOC103215907</i>	Caudate	1.37E-08	0.000425	0.00401	other	0
<i>LOC103215957</i>	Caudate	3.31E-08	0.000698	2.48E-07	increasing	0
<i>LOC103215963</i>	Caudate	3.01E-10	0.000275	0.068678	other	0
<i>LOC103216023</i>	Caudate	3.66E-08	0.000152	0.315903	other	0
<i>LOC103216066</i>	Caudate	1.93E-09	0.000675	6.05E-07	increasing	0
<i>LOC103216108</i>	Caudate	1.41E-07	0.000683	5.00E-07	increasing	0
<i>LOC103216190</i>	Caudate	2.64E-12	-0.00035	0.018056	other	0
<i>LOC103216365</i>	Caudate	1.15E-09	0.000643	1.24E-06	increasing	0
<i>LOC103216544</i>	Caudate	1.54E-10	0.000706	1.46E-07	increasing	0
<i>LOC103216563</i>	Caudate	2.46E-07	-0.00027	0.064914	other	0
<i>LOC103216688</i>	Caudate	4.67E-09	0.000718	1.03E-07	increasing	0
<i>LOC103216690</i>	Caudate	2.19E-07	-0.00069	2.22E-07	decreasing	0
<i>LOC103216740</i>	Caudate	5.16E-08	0.000683	4.57E-07	increasing	0
<i>LOC103216760</i>	Caudate	8.34E-08	0.00033	0.025547	other	0
<i>LOC103216779</i>	Caudate	1.21E-07	0.000339	0.024094	other	0
<i>LOC103216788</i>	Caudate	6.06E-08	0.000297	0.047174	other	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103216985	Caudate	8.05E-09	-0.00028	0.054531	other	0
LOC103217039	Caudate	2.65E-17	0.00083	1.65E-13	increasing	0
LOC103217040	Caudate	3.70E-12	0.000785	7.53E-11	increasing	0
LOC103217121	Caudate	9.26E-10	0.000208	0.171888	other	0
LOC103217195	Caudate	1.83E-07	-0.00048	0.000917	other	0
LOC103217276	Caudate	7.44E-05	-0.00069	1.91E-07	decreasing	1
LOC103217305	Caudate	7.34E-08	2.99E-06	0.9842	other	0
LOC103217633	Caudate	7.25E-08	0.000587	2.36E-05	increasing	1
LOC103217745	Caudate	4.79E-08	-0.00058	4.69E-05	decreasing	0
LOC103217768	Caudate	1.35E-07	-0.00058	4.76E-05	decreasing	0
LOC103217882	Caudate	1.65E-12	0.000682	5.20E-07	increasing	0
LOC103217924	Caudate	1.67E-07	-0.00059	7.28E-06	decreasing	0
LOC103217926	Caudate	1.86E-08	-0.00027	0.023123	other	0
LOC103217978	Caudate	4.27E-09	-0.00076	1.31E-08	decreasing	0
LOC103218258	Caudate	3.33E-06	0.000759	1.12E-08	increasing	0
LOC103218260	Caudate	4.30E-06	0.000718	1.38E-07	increasing	0
LOC103218261	Caudate	1.09E-09	0.000793	1.52E-09	increasing	1
LOC103218284	Caudate	2.44E-09	0.000384	0.010031	other	0
LOC103218293	Caudate	1.92E-07	-0.00068	9.57E-07	decreasing	0
LOC103218319	Caudate	2.59E-09	-0.00053	0.000197	other	0
LOC103218335	Caudate	3.70E-08	0.000458	0.001633	other	0
LOC103218545	Caudate	1.70E-07	0.000633	1.95E-06	increasing	1
LOC103218621	Caudate	5.31E-08	-0.00072	6.86E-08	decreasing	0
LOC103218697	Caudate	3.80E-13	-0.00072	5.07E-08	decreasing	0
LOC103218711	Caudate	1.11E-09	-0.00029	0.050496	other	0
LOC103218764	Caudate	1.15E-07	-0.00058	3.67E-05	decreasing	0
LOC103218854	Caudate	3.04E-08	-0.00015	0.3107	other	0
LOC103218873	Caudate	1.09E-09	0.000332	0.025619	other	0
LOC103218934	Caudate	1.71E-09	0.000129	0.387994	other	0
LOC103218980	Caudate	4.75E-06	0.000742	3.63E-08	increasing	0
LOC103219243	Caudate	7.89E-08	-7.27E-05	0.631314	other	0
LOC103219257	Caudate	8.37E-10	0.00041	0.00473	other	0
LOC103219292	Caudate	1.70E-09	0.000728	6.87E-08	increasing	0
LOC103219355	Caudate	8.81E-09	0.000449	0.001803	other	0
LOC103219361	Caudate	9.04E-09	0.000697	2.10E-07	increasing	0
LOC103219369	Caudate	2.42E-06	0.000681	2.32E-07	increasing	0
LOC103219454	Caudate	2.31E-07	-0.00067	1.59E-06	decreasing	0
LOC103219603	Caudate	3.42E-05	0.000723	6.59E-08	increasing	0
LOC103219622	Caudate	9.18E-12	0.000401	0.005519	other	0
LOC103219642	Caudate	1.50E-06	0.000697	1.53E-07	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103219657</i>	Caudate	1.60E-07	-0.00057	5.25E-05	decreasing	0
<i>LOC103219726</i>	Caudate	1.19E-05	0.000712	1.87E-07	increasing	0
<i>LOC103219832</i>	Caudate	2.28E-16	0.000859	2.86E-13	increasing	0
<i>LOC103219838</i>	Caudate	5.15E-06	0.000694	9.76E-08	increasing	0
<i>LOC103219854</i>	Caudate	5.05E-11	0.000767	5.72E-09	increasing	0
<i>LOC103219872</i>	Caudate	6.89E-08	0.000712	2.42E-08	increasing	0
<i>LOC103219893</i>	Caudate	1.94E-10	0.000787	7.07E-10	increasing	0
<i>LOC103219911</i>	Caudate	6.85E-06	0.00072	1.19E-07	increasing	0
<i>LOC103219917</i>	Caudate	2.25E-08	-0.00041	0.004614	other	0
<i>LOC103219923</i>	Caudate	1.43E-08	0.000476	0.000819	other	0
<i>LOC103220009</i>	Caudate	9.59E-08	0.000254	0.094332	other	0
<i>LOC103220039</i>	Caudate	1.40E-07	7.90E-05	0.601662	other	0
<i>LOC103220051</i>	Caudate	2.29E-09	-0.00077	3.81E-09	decreasing	0
<i>LOC103220055</i>	Caudate	4.12E-13	-0.00076	5.50E-09	decreasing	0
<i>LOC103220064</i>	Caudate	5.44E-11	0.00071	3.63E-08	increasing	0
<i>LOC103220067</i>	Caudate	1.50E-12	0.000753	7.58E-09	increasing	0
<i>LOC103220168</i>	Caudate	4.78E-08	-6.89E-05	0.647456	other	0
<i>LOC103220250</i>	Caudate	8.54E-09	-0.0005	0.000534	other	1
<i>LOC103220254</i>	Caudate	5.24E-08	0.000444	0.002626	other	0
<i>LOC103220286</i>	Caudate	5.15E-07	-0.00071	1.91E-07	decreasing	0
<i>LOC103220291</i>	Caudate	1.62E-09	-0.00076	4.93E-09	decreasing	0
<i>LOC103220292</i>	Caudate	1.91E-08	-0.00073	1.73E-08	decreasing	0
<i>LOC103220293</i>	Caudate	9.27E-08	-0.00068	2.69E-07	decreasing	0
<i>LOC103220295</i>	Caudate	1.73E-09	-0.0007	1.12E-07	decreasing	0
<i>LOC103220316</i>	Caudate	4.61E-06	-0.00074	4.71E-08	decreasing	0
<i>LOC103220360</i>	Caudate	2.41E-10	0.000684	7.52E-09	increasing	0
<i>LOC103220361</i>	Caudate	2.43E-13	0.000828	1.08E-12	increasing	0
<i>LOC103220457</i>	Caudate	9.17E-09	0.000622	4.50E-06	increasing	0
<i>LOC103220496</i>	Caudate	1.43E-07	-0.00072	1.32E-07	decreasing	0
<i>LOC103220516</i>	Caudate	2.30E-07	0.000633	2.77E-06	increasing	0
<i>LOC103221007</i>	Caudate	3.49E-22	0.000907	1.91E-14	increasing	0
<i>LOC103221019</i>	Caudate	3.46E-08	-0.00023	0.125455	other	0
<i>LOC103221138</i>	Caudate	6.84E-10	0.000834	4.45E-11	increasing	1
<i>LOC103221185</i>	Caudate	4.45E-09	-0.00055	9.06E-05	decreasing	0
<i>LOC103221248</i>	Caudate	4.53E-09	-0.0004	0.007863	other	0
<i>LOC103221263</i>	Caudate	1.59E-06	0.000706	7.39E-08	increasing	0
<i>LOC103221272</i>	Caudate	5.69E-09	6.24E-05	0.67629	other	0
<i>LOC103221287</i>	Caudate	3.45E-12	-0.0008	2.63E-10	decreasing	0
<i>LOC103221288</i>	Caudate	4.49E-08	-0.00066	1.33E-06	decreasing	0
<i>LOC103221289</i>	Caudate	1.13E-07	-0.0007	3.63E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103221290	Caudate	5.72E-11	-0.00073	2.27E-08	decreasing	0
LOC103221330	Caudate	2.06E-08	-0.00056	8.68E-05	decreasing	0
LOC103221414	Caudate	1.82E-07	0.000338	0.021972	other	0
LOC103221628	Caudate	1.32E-07	-0.00055	0.00011	other	0
LOC103221735	Caudate	1.03E-08	0.000812	3.90E-10	increasing	0
LOC103221855	Caudate	5.54E-06	0.000696	1.65E-07	increasing	0
LOC103221863	Caudate	1.39E-07	0.000634	3.23E-06	increasing	1
LOC103221933	Caudate	4.11E-12	-0.00071	4.68E-08	decreasing	0
LOC103221935	Caudate	8.06E-09	-0.00061	6.89E-06	decreasing	0
LOC103221937	Caudate	3.24E-08	-0.00051	0.000406	other	1
LOC103221943	Caudate	1.33E-09	-0.00067	5.69E-07	decreasing	0
LOC103221944	Caudate	1.20E-13	-0.00078	7.69E-10	decreasing	0
LOC103221945	Caudate	7.75E-09	-0.00066	1.13E-06	decreasing	0
LOC103221946	Caudate	1.86E-07	-0.0005	0.00034	other	1
LOC103221996	Caudate	2.65E-10	-0.00071	6.84E-08	decreasing	1
LOC103221997	Caudate	4.84E-11	-0.00077	2.71E-09	decreasing	0
LOC103221998	Caudate	1.88E-12	-0.0008	2.58E-10	decreasing	0
LOC103222001	Caudate	3.20E-14	-0.00087	5.08E-13	decreasing	0
LOC103222003	Caudate	6.77E-13	-0.00081	1.11E-10	decreasing	0
LOC103222004	Caudate	4.98E-09	-0.0007	1.31E-07	decreasing	0
LOC103222006	Caudate	8.38E-14	-0.00083	2.69E-11	decreasing	0
LOC103222008	Caudate	9.86E-08	-0.00042	0.003396	other	0
LOC103222018	Caudate	1.39E-11	-0.00068	4.00E-07	decreasing	0
LOC103222019	Caudate	9.81E-08	-0.00057	4.68E-05	decreasing	0
LOC103222069	Caudate	1.48E-07	0.000649	2.89E-06	increasing	0
LOC103222075	Caudate	1.36E-17	-0.00085	2.31E-12	decreasing	0
LOC103222076	Caudate	6.03E-09	-0.00071	9.29E-08	decreasing	0
LOC103222080	Caudate	1.15E-13	-0.00083	5.79E-11	decreasing	0
LOC103222083	Caudate	1.18E-15	0.000809	1.50E-10	increasing	0
LOC103222091	Caudate	3.49E-08	0.000648	3.26E-06	increasing	1
LOC103222183	Caudate	1.23E-11	-0.0008	2.95E-10	decreasing	0
LOC103222354	Caudate	2.38E-07	0.000626	5.49E-06	increasing	0
LOC103222369	Caudate	1.49E-11	-0.00062	5.77E-06	decreasing	0
LOC103222373	Caudate	2.01E-11	-0.00075	4.78E-09	decreasing	0
LOC103222375	Caudate	4.46E-10	0.0007	9.11E-09	increasing	0
LOC103222429	Caudate	1.61E-08	-0.00045	0.001477	other	1
LOC103222460	Caudate	8.49E-07	0.000613	1.83E-07	increasing	0
LOC103222548	Caudate	6.77E-11	0.000793	7.39E-10	increasing	0
LOC103222593	Caudate	2.05E-09	0.000696	1.88E-07	increasing	0
LOC103222617	Caudate	1.01E-07	-0.00057	3.05E-05	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103222895	Caudate	1.02E-08	0.000718	1.42E-07	increasing	0
LOC103222898	Caudate	2.74E-11	0.000771	6.48E-10	increasing	0
LOC103223006	Caudate	5.56E-10	0.000163	0.277883	other	0
LOC103223027	Caudate	2.73E-09	1.10E-05	0.93661	other	0
LOC103223065	Caudate	1.21E-11	0.000327	0.027338	other	0
LOC103223096	Caudate	5.48E-10	0.000762	9.22E-09	increasing	0
LOC103223099	Caudate	3.04E-13	0.000804	7.78E-10	increasing	0
LOC103223109	Caudate	9.06E-14	-0.00088	1.05E-12	decreasing	0
LOC103223177	Caudate	4.56E-08	-0.00061	1.86E-05	decreasing	0
LOC103223180	Caudate	2.29E-11	0.000653	1.13E-06	increasing	0
LOC103223222	Caudate	9.00E-11	0.000496	0.000634	other	0
LOC103223292	Caudate	3.36E-08	-0.00048	0.000765	other	0
LOC103223382	Caudate	1.41E-07	0.000508	0.000483	other	0
LOC103223422	Caudate	4.82E-10	0.000154	0.311184	other	0
LOC103223510	Caudate	9.44E-09	0.000739	4.54E-08	increasing	0
LOC103223548	Caudate	5.61E-12	0.000664	1.78E-06	increasing	0
LOC103223549	Caudate	1.17E-08	0.000143	0.335261	other	0
LOC103223605	Caudate	1.00E-10	0.000699	3.55E-07	increasing	0
LOC103223633	Caudate	3.56E-14	-0.00074	1.87E-08	decreasing	0
LOC103223640	Caudate	1.07E-08	0.000562	9.15E-05	increasing	0
LOC103223656	Caudate	1.47E-12	-0.00072	7.37E-08	decreasing	0
LOC103223660	Caudate	2.07E-09	-0.00072	8.86E-08	decreasing	0
LOC103223735	Caudate	1.09E-07	-0.00061	1.76E-05	decreasing	0
LOC103224173	Caudate	1.94E-10	0.00034	0.020409	other	0
LOC103224231	Caudate	3.16E-15	0.000786	4.29E-10	increasing	0
LOC103224274	Caudate	1.93E-09	0.000374	0.011269	other	0
LOC103224340	Caudate	1.94E-07	-1.99E-06	0.989643	other	0
LOC103224381	Caudate	1.58E-09	-0.00059	2.88E-05	decreasing	0
LOC103224382	Caudate	2.87E-06	-0.00073	7.20E-08	decreasing	0
LOC103224383	Caudate	8.28E-14	-0.00082	1.14E-10	decreasing	0
LOC103224393	Caudate	3.46E-08	8.16E-05	0.564841	other	0
LOC103224431	Caudate	5.41E-10	-0.00073	2.14E-08	decreasing	0
LOC103224490	Caudate	1.12E-08	-0.00017	0.23691	other	0
LOC103224548	Caudate	3.58E-12	-0.00076	1.08E-09	decreasing	0
LOC103224550	Caudate	1.98E-20	-0.00088	1.54E-14	decreasing	0
LOC103224552	Caudate	7.30E-08	-0.00055	7.62E-05	decreasing	0
LOC103224719	Caudate	1.60E-07	0.000591	1.87E-05	increasing	0
LOC103224734	Caudate	1.55E-07	-0.00068	9.22E-07	decreasing	0
LOC103224735	Caudate	2.91E-08	-0.0007	2.82E-07	decreasing	0
LOC103224769	Caudate	2.18E-08	-0.00012	0.402754	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103224848	Caudate	2.10E-10	-0.00013	0.383788	other	0
LOC103224870	Caudate	9.02E-09	-0.00019	0.206668	other	0
LOC103224888	Caudate	4.28E-11	6.92E-05	0.643359	other	0
LOC103225003	Caudate	1.04E-07	-0.00064	3.84E-06	decreasing	0
LOC103225074	Caudate	3.05E-10	0.000516	0.00039	other	0
LOC103225095	Caudate	3.68E-08	0.000379	0.009794	other	0
LOC103225256	Caudate	2.51E-07	0.000127	0.4072	other	0
LOC103225445	Caudate	2.16E-07	-0.0004	0.007124	other	1
LOC103225645	Caudate	6.57E-10	0.000755	1.78E-08	increasing	0
LOC103225699	Caudate	2.60E-08	0.00079	2.07E-09	increasing	0
LOC103225785	Caudate	6.68E-10	0.000439	0.002787	other	0
LOC103225786	Caudate	1.16E-19	0.000897	1.14E-13	increasing	0
LOC103225793	Caudate	5.75E-11	0.000799	1.07E-09	increasing	0
LOC103225801	Caudate	1.03E-08	0.000585	3.86E-05	increasing	0
LOC103225812	Caudate	2.27E-07	0.000324	0.030715	other	0
LOC103225882	Caudate	1.75E-07	0.000682	8.05E-07	increasing	0
LOC103225898	Caudate	5.27E-09	0.00074	9.55E-09	increasing	0
LOC103225917	Caudate	6.09E-09	-0.00076	1.44E-08	decreasing	0
LOC103225923	Caudate	5.30E-10	0.000457	0.001861	other	0
LOC103225931	Caudate	4.20E-08	0.000782	2.55E-09	increasing	0
LOC103225940	Caudate	4.28E-10	0.000743	2.28E-08	increasing	0
LOC103225953	Caudate	3.47E-13	0.000625	9.26E-06	increasing	0
LOC103225995	Caudate	1.14E-09	0.000486	0.000802	other	0
LOC103226072	Caudate	3.33E-09	0.000664	1.37E-06	increasing	0
LOC103226149	Caudate	2.20E-10	0.000745	3.24E-08	increasing	0
LOC103226304	Caudate	7.75E-09	0.000583	4.13E-05	increasing	0
LOC103226393	Caudate	1.21E-08	0.000217	0.151093	other	0
LOC103226462	Caudate	1.69E-10	0.000202	0.15216	other	0
LOC103226606	Caudate	8.92E-08	-0.0005	0.00066	other	0
LOC103226616	Caudate	3.52E-08	-0.00072	1.41E-07	decreasing	0
LOC103226617	Caudate	2.57E-08	-0.00076	1.16E-08	decreasing	0
LOC103226835	Caudate	9.04E-10	-0.0004	0.007321	other	0
LOC103226870	Caudate	2.73E-13	0.000758	6.35E-09	increasing	0
LOC103226908	Caudate	2.95E-15	0.000856	1.12E-12	increasing	0
LOC103226909	Caudate	2.06E-07	0.000643	2.39E-06	increasing	0
LOC103226929	Caudate	6.20E-07	0.00069	1.71E-07	increasing	1
LOC103226962	Caudate	7.40E-08	0.000676	7.80E-07	increasing	0
LOC103227009	Caudate	6.58E-11	-0.00052	0.000254	other	0
LOC103227062	Caudate	2.38E-06	0.000696	2.19E-07	increasing	0
LOC103227066	Caudate	4.39E-08	0.000735	1.33E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103227172	Caudate	6.96E-09	-0.0008	9.20E-10	decreasing	0
LOC103227190	Caudate	2.75E-11	0.000401	0.005494	other	0
LOC103227191	Caudate	3.37E-12	0.000399	0.005807	other	0
LOC103227289	Caudate	7.08E-08	0.000577	4.93E-05	increasing	0
LOC103227297	Caudate	1.18E-12	-0.00055	0.000144	other	0
LOC103227322	Caudate	1.11E-09	0.00082	2.51E-10	increasing	1
LOC103227371	Caudate	4.20E-08	0.00072	6.18E-08	increasing	0
LOC103227383	Caudate	2.33E-10	0.000304	0.043909	other	0
LOC103227384	Caudate	1.43E-07	-0.0006	1.12E-05	decreasing	0
LOC103227395	Caudate	6.34E-07	-0.00076	9.68E-09	decreasing	0
LOC103227411	Caudate	4.48E-10	0.000626	7.49E-06	increasing	0
LOC103227597	Caudate	7.76E-08	0.000249	0.099012	other	0
LOC103227720	Caudate	1.76E-07	0.000293	0.051403	other	0
LOC103227757	Caudate	1.12E-07	-0.00059	2.49E-05	decreasing	0
LOC103227769	Caudate	1.63E-09	-0.00059	3.30E-05	decreasing	0
LOC103227802	Caudate	7.67E-08	0.000561	3.85E-05	increasing	0
LOC103227848	Caudate	1.51E-08	0.000767	3.54E-09	increasing	0
LOC103227928	Caudate	4.28E-10	-0.0008	6.70E-10	decreasing	0
LOC103227940	Caudate	7.75E-08	-0.00026	0.069618	other	0
LOC103227957	Caudate	2.73E-06	0.000705	2.46E-07	increasing	0
LOC103228076	Caudate	4.26E-08	0.000325	0.025375	other	0
LOC103228084	Caudate	2.06E-08	0.000158	0.302488	other	0
LOC103228153	Caudate	2.89E-11	-0.00082	2.30E-10	decreasing	0
LOC103228253	Caudate	7.59E-07	-0.0007	2.22E-07	decreasing	0
LOC103228260	Caudate	2.05E-07	-0.00072	9.89E-08	decreasing	0
LOC103228264	Caudate	1.59E-08	-0.00075	2.82E-08	decreasing	0
LOC103228267	Caudate	4.39E-10	-0.00075	2.85E-08	decreasing	0
LOC103228268	Caudate	3.62E-08	-0.00065	3.32E-06	decreasing	0
LOC103228271	Caudate	1.96E-07	-0.00067	1.24E-06	decreasing	0
LOC103228278	Caudate	1.25E-07	-0.00068	6.53E-07	decreasing	0
LOC103228401	Caudate	2.79E-08	-0.00071	2.24E-07	decreasing	0
LOC103228405	Caudate	3.11E-09	-0.00076	1.35E-08	decreasing	0
LOC103228553	Caudate	8.09E-10	-0.00068	8.89E-07	decreasing	0
LOC103228595	Caudate	1.15E-07	-0.00076	1.55E-08	decreasing	0
LOC103228599	Caudate	2.06E-07	-0.00074	4.87E-08	decreasing	0
LOC103228601	Caudate	3.05E-08	-0.00076	1.80E-08	decreasing	0
LOC103228603	Caudate	2.17E-07	-0.00071	2.47E-07	decreasing	1
LOC103228604	Caudate	6.77E-08	-0.00076	1.28E-08	decreasing	0
LOC103228606	Caudate	5.03E-08	-0.00073	5.67E-08	decreasing	1
LOC103228607	Caudate	2.33E-13	-0.00084	1.82E-11	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103228608	Caudate	1.10E-09	-0.00081	2.94E-10	decreasing	0
LOC103228609	Caudate	5.05E-10	-0.00078	1.80E-09	decreasing	0
LOC103228627	Caudate	1.14E-08	0.000153	0.316032	other	0
LOC103228672	Caudate	2.29E-08	0.000203	0.16235	other	0
LOC103228761	Caudate	1.95E-05	-0.00072	1.18E-07	decreasing	0
LOC103228824	Caudate	5.59E-11	-0.00025	0.096298	other	0
LOC103228952	Caudate	6.30E-11	0.000604	1.89E-05	increasing	0
LOC103228978	Caudate	2.10E-10	-6.20E-05	0.676121	other	0
LOC103229131	Caudate	1.51E-07	0.000658	1.21E-06	increasing	0
LOC103229137	Caudate	9.07E-15	-0.00085	2.67E-12	decreasing	0
LOC103229191	Caudate	2.64E-06	-0.00071	9.50E-08	decreasing	0
LOC103229306	Caudate	1.86E-10	-8.39E-05	0.57461	other	0
LOC103229364	Caudate	3.77E-08	2.94E-05	0.848308	other	0
LOC103229412	Caudate	4.65E-08	-0.00073	8.15E-08	decreasing	0
LOC103229417	Caudate	5.60E-08	-0.00076	6.88E-09	decreasing	0
LOC103229418	Caudate	1.29E-09	-0.00081	4.46E-10	decreasing	0
LOC103229420	Caudate	1.16E-06	-0.00072	1.58E-07	decreasing	0
LOC103229423	Caudate	5.37E-07	-0.0007	2.15E-07	decreasing	0
LOC103229426	Caudate	1.48E-07	-0.00058	5.81E-05	decreasing	0
LOC103229468	Caudate	2.84E-10	-0.00076	5.58E-09	decreasing	0
LOC103229472	Caudate	3.07E-09	-0.0008	3.19E-10	decreasing	0
LOC103229682	Caudate	5.82E-08	0.000568	2.94E-05	increasing	0
LOC103229733	Caudate	1.13E-09	0.000704	1.87E-07	increasing	0
LOC103229888	Caudate	2.25E-08	0.000406	0.005783	other	0
LOC103229956	Caudate	7.14E-09	0.00073	2.40E-08	increasing	0
LOC103229957	Caudate	8.22E-08	0.000669	6.29E-07	increasing	0
LOC103229961	Caudate	5.17E-08	0.000784	2.58E-09	increasing	0
LOC103229978	Caudate	7.27E-09	-0.00068	3.63E-07	decreasing	0
LOC103230040	Caudate	2.90E-09	-0.00029	0.056865	other	0
LOC103230295	Caudate	1.18E-10	0.000522	0.000228	other	0
LOC103230307	Caudate	2.83E-08	0.00057	3.59E-05	increasing	1
LOC103230353	Caudate	5.70E-08	0.000631	4.80E-06	increasing	1
LOC103230361	Caudate	1.17E-06	-0.00071	1.27E-07	decreasing	0
LOC103230378	Caudate	1.47E-10	0.0002	0.184948	other	0
LOC103230493	Caudate	1.23E-10	0.000449	0.002064	other	0
LOC103230509	Caudate	1.22E-08	0.000192	0.20852	other	0
LOC103230659	Caudate	3.52E-08	-0.00038	0.009592	other	0
LOC103230736	Caudate	1.20E-08	0.000637	3.22E-06	increasing	0
LOC103230770	Caudate	5.29E-08	0.00052	0.000255	other	0
LOC103230800	Caudate	4.40E-11	-0.00073	3.87E-08	decreasing	1

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103230894	Caudate	2.44E-07	-0.00057	5.38E-05	decreasing	0
LOC103230939	Caudate	2.31E-07	8.58E-05	0.565749	other	0
LOC103230993	Caudate	1.99E-07	0.000653	7.42E-07	increasing	1
LOC103231026	Caudate	2.62E-10	0.000538	0.000143	other	0
LOC103231051	Caudate	2.38E-10	-6.99E-05	0.643787	other	0
LOC103231081	Caudate	1.01E-05	-0.00074	2.89E-08	decreasing	0
LOC103231084	Caudate	4.03E-08	-0.00046	0.001609	other	0
LOC103231096	Caudate	4.05E-19	0.00091	3.81E-14	increasing	0
LOC103231101	Caudate	7.08E-08	0.000741	5.26E-09	increasing	0
LOC103231220	Caudate	6.87E-10	0.000366	0.011203	other	0
LOC103231470	Caudate	1.82E-08	0.000567	4.03E-05	increasing	0
LOC103231548	Caudate	8.97E-20	-0.0009	3.37E-14	decreasing	0
LOC103231594	Caudate	2.72E-11	-0.00082	1.43E-10	decreasing	0
LOC103231695	Caudate	9.96E-09	0.000509	0.000462	other	0
LOC103231767	Caudate	2.54E-09	0.000569	7.33E-05	increasing	0
LOC103231791	Caudate	2.62E-08	-0.00065	1.34E-06	decreasing	0
LOC103231911	Caudate	8.50E-08	0.000556	0.000105	other	0
LOC103231930	Caudate	8.03E-09	0.000726	8.13E-08	increasing	0
LOC103231962	Caudate	5.25E-09	0.000589	3.16E-05	increasing	0
LOC103232041	Caudate	3.74E-10	7.43E-05	0.628175	other	0
LOC103232058	Caudate	2.85E-08	-0.00054	0.00017	other	0
LOC103232061	Caudate	2.84E-10	-0.00078	7.40E-10	decreasing	0
LOC103232102	Caudate	1.79E-07	-0.00011	0.444075	other	0
LOC103232103	Caudate	1.53E-11	-0.00038	0.010422	other	0
LOC103232182	Caudate	2.79E-08	-0.00013	0.408963	other	0
LOC103232225	Caudate	9.43E-09	0.000477	0.000804	other	0
LOC103232226	Caudate	3.44E-09	-0.00012	0.408521	other	0
LOC103232235	Caudate	1.10E-07	-0.00036	0.016422	other	0
LOC103232291	Caudate	3.15E-09	0.000333	0.025601	other	0
LOC103232311	Caudate	1.38E-08	-0.00066	1.31E-06	decreasing	0
LOC103232315	Caudate	7.78E-08	-5.13E-05	0.735779	other	0
LOC103232394	Caudate	7.16E-16	0.000881	8.20E-13	increasing	0
LOC103232411	Caudate	1.01E-11	0.00013	0.375566	other	0
LOC103232479	Caudate	4.29E-08	0.000176	0.250353	other	0
LOC103232497	Caudate	2.76E-09	-0.00036	0.017485	other	0
LOC103232526	Caudate	3.74E-10	0.000761	5.16E-09	increasing	0
LOC103232528	Caudate	1.91E-11	0.000388	0.009207	other	0
LOC103232553	Caudate	2.18E-07	0.000581	3.78E-05	increasing	0
LOC103232574	Caudate	4.20E-10	-2.65E-05	0.859458	other	0
LOC103232592	Caudate	1.12E-10	-0.00076	4.44E-09	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103232593	Caudate	4.93E-10	-0.00076	8.13E-09	decreasing	0
LOC103232616	Caudate	5.15E-13	0.000463	0.001263	other	0
LOC103232654	Caudate	3.26E-09	0.000322	0.032239	other	0
LOC103232789	Caudate	7.44E-08	0.00049	0.00079	other	0
LOC103232897	Caudate	2.46E-08	0.000151	0.321459	other	0
LOC103232907	Caudate	9.13E-09	0.000489	0.000605	other	0
LOC103232958	Caudate	1.32E-07	8.17E-05	0.582482	other	0
LOC103232974	Caudate	1.10E-09	-0.00074	3.05E-08	decreasing	0
LOC103233030	Caudate	1.43E-10	0.000797	1.07E-09	increasing	0
LOC103233032	Caudate	1.64E-09	0.000725	1.74E-08	increasing	0
LOC103233100	Caudate	1.62E-07	-0.00011	0.46937	other	0
LOC103233139	Caudate	7.33E-13	0.000287	0.053255	other	0
LOC103233150	Caudate	2.06E-07	0.000319	0.032834	other	0
LOC103233400	Caudate	1.25E-13	-7.82E-05	0.600637	other	0
LOC103233443	Caudate	1.68E-06	0.000631	5.92E-08	increasing	0
LOC103233444	Caudate	5.22E-15	0.000885	3.01E-13	increasing	0
LOC103233451	Caudate	2.02E-10	0.000626	8.92E-06	increasing	0
LOC103233496	Caudate	1.32E-10	-0.00029	0.049291	other	0
LOC103233501	Caudate	8.92E-09	0.000626	4.56E-06	increasing	0
LOC103233511	Caudate	2.01E-07	0.000653	1.59E-06	increasing	0
LOC103233547	Caudate	1.21E-09	0.000812	9.32E-11	increasing	0
LOC103233554	Caudate	1.27E-09	0.000795	4.58E-10	increasing	0
LOC103233575	Caudate	1.54E-10	0.000222	0.138875	other	0
LOC103233604	Caudate	4.07E-11	0.000372	0.0105	other	0
LOC103233701	Caudate	1.25E-08	0.000419	0.004088	other	0
LOC103233755	Caudate	2.53E-07	0.000519	0.000315	other	0
LOC103233841	Caudate	7.43E-08	0.000696	1.91E-07	increasing	0
LOC103234031	Caudate	2.26E-10	0.000578	2.00E-05	increasing	0
LOC103234124	Caudate	6.77E-10	0.000518	0.000332	other	0
LOC103234134	Caudate	1.71E-07	0.000481	0.001032	other	0
LOC103234241	Caudate	1.15E-08	-0.00059	2.25E-05	decreasing	0
LOC103234252	Caudate	5.21E-07	0.000747	3.56E-09	increasing	0
LOC103234255	Caudate	9.26E-11	-0.00075	1.12E-08	decreasing	0
LOC103234265	Caudate	3.22E-09	-0.00075	1.40E-08	decreasing	0
LOC103234282	Caudate	1.22E-05	0.000693	3.33E-08	increasing	0
LOC103234302	Caudate	7.13E-08	-0.00055	8.10E-05	decreasing	0
LOC103234347	Caudate	5.69E-08	-1.73E-05	0.908159	other	0
LOC103234348	Caudate	6.87E-11	0.000664	6.47E-07	increasing	0
LOC103234372	Caudate	2.62E-07	0.000722	7.95E-08	increasing	0
LOC103234380	Caudate	2.71E-08	1.87E-05	0.901698	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103234406</i>	Caudate	1.21E-08	-0.00035	0.016367	other	0
<i>LOC103234416</i>	Caudate	1.11E-12	0.000819	3.35E-11	increasing	0
<i>LOC103234419</i>	Caudate	1.51E-16	0.000841	8.11E-12	increasing	0
<i>LOC103234469</i>	Caudate	1.62E-07	0.000746	1.33E-08	increasing	0
<i>LOC103234470</i>	Caudate	8.68E-10	0.00065	2.99E-06	increasing	0
<i>LOC103234473</i>	Caudate	2.32E-07	-0.00071	9.61E-08	decreasing	0
<i>LOC103234475</i>	Caudate	2.23E-07	-0.00074	1.10E-08	decreasing	0
<i>LOC103234505</i>	Caudate	6.29E-08	0.000633	4.10E-06	increasing	0
<i>LOC103234618</i>	Caudate	3.27E-13	-0.00083	2.57E-11	decreasing	0
<i>LOC103234653</i>	Caudate	5.11E-08	0.000189	0.208134	other	0
<i>LOC103234898</i>	Caudate	2.65E-08	-5.81E-05	0.692228	other	0
<i>LOC103234934</i>	Caudate	1.26E-10	1.21E-05	0.936815	other	0
<i>LOC103234950</i>	Caudate	1.82E-06	0.000741	3.95E-08	increasing	0
<i>LOC103234986</i>	Caudate	1.22E-09	0.000716	4.13E-08	increasing	0
<i>LOC103234988</i>	Caudate	4.56E-12	0.000782	1.09E-09	increasing	0
<i>LOC103235079</i>	Caudate	2.61E-09	0.00035	0.016533	other	0
<i>LOC103235442</i>	Caudate	2.25E-07	0.000228	0.126106	other	0
<i>LOC103235452</i>	Caudate	6.45E-11	0.000514	0.000404	other	0
<i>LOC103235514</i>	Caudate	2.50E-07	-0.0006	1.42E-05	decreasing	0
<i>LOC103235525</i>	Caudate	5.03E-06	0.000741	4.00E-08	increasing	0
<i>LOC103235590</i>	Caudate	5.48E-08	-0.00028	0.043795	other	0
<i>LOC103235597</i>	Caudate	1.58E-09	-0.00055	9.05E-05	decreasing	0
<i>LOC103235629</i>	Caudate	2.20E-07	-0.00023	0.129523	other	0
<i>LOC103235723</i>	Caudate	3.10E-09	0.000181	0.232403	other	0
<i>LOC103235802</i>	Caudate	4.72E-05	-0.0007	1.60E-07	decreasing	0
<i>LOC103235911</i>	Caudate	3.99E-08	0.000563	8.47E-05	increasing	0
<i>LOC103235940</i>	Caudate	4.59E-08	0.000562	4.80E-05	increasing	0
<i>LOC103236025</i>	Caudate	5.46E-08	0.000524	0.000141	other	0
<i>LOC103236032</i>	Caudate	3.65E-08	-0.00038	0.008936	other	0
<i>LOC103236037</i>	Caudate	4.26E-08	-0.00056	9.40E-05	decreasing	0
<i>LOC103236164</i>	Caudate	3.11E-10	-0.00021	0.161073	other	0
<i>LOC103236167</i>	Caudate	3.37E-09	0.000677	6.61E-07	increasing	0
<i>LOC103236536</i>	Caudate	1.53E-07	0.000609	1.09E-05	increasing	0
<i>LOC103236776</i>	Caudate	7.71E-10	0.000753	1.07E-08	increasing	0
<i>LOC103236781</i>	Caudate	1.22E-09	-0.00053	0.000188	other	0
<i>LOC103236784</i>	Caudate	2.31E-12	0.0008	2.28E-10	increasing	0
<i>LOC103236856</i>	Caudate	2.13E-08	0.000501	0.000578	other	0
<i>LOC103236915</i>	Caudate	5.69E-08	0.000524	0.000198	other	1
<i>LOC103236916</i>	Caudate	2.26E-08	0.000137	0.355118	other	1
<i>LOC103236962</i>	Caudate	9.84E-10	-0.00073	3.80E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103236980</i>	Caudate	1.42E-07	-1.65E-05	0.911363	other	0
<i>LOC103237093</i>	Caudate	8.40E-12	-0.00074	1.94E-08	decreasing	0
<i>LOC103237228</i>	Caudate	1.66E-07	0.00017	0.263	other	0
<i>LOC103237276</i>	Caudate	5.54E-10	-7.58E-05	0.617955	other	0
<i>LOC103237309</i>	Caudate	1.71E-07	-0.00073	9.09E-08	decreasing	0
<i>LOC103237319</i>	Caudate	1.52E-07	-0.00063	6.53E-06	decreasing	0
<i>LOC103237355</i>	Caudate	4.78E-09	-0.00063	6.41E-06	decreasing	0
<i>LOC103237383</i>	Caudate	6.33E-11	-0.00081	6.54E-10	decreasing	0
<i>LOC103237511</i>	Caudate	1.06E-16	0.000758	5.54E-09	increasing	0
<i>LOC103237514</i>	Caudate	6.25E-08	0.000134	0.374881	other	0
<i>LOC103237527</i>	Caudate	8.39E-09	0.000771	6.83E-09	increasing	0
<i>LOC103237606</i>	Caudate	2.16E-07	0.000661	2.04E-06	increasing	0
<i>LOC103237688</i>	Caudate	4.75E-08	-0.00024	0.114889	other	0
<i>LOC103237726</i>	Caudate	1.40E-07	-0.00034	0.019062	other	0
<i>LOC103237731</i>	Caudate	1.17E-07	0.000715	1.34E-07	increasing	0
<i>LOC103237740</i>	Caudate	6.21E-09	0.000553	0.000109	other	0
<i>LOC103237777</i>	Caudate	9.64E-11	0.000829	1.17E-10	increasing	0
<i>LOC103237779</i>	Caudate	2.31E-13	0.000187	0.212985	other	0
<i>LOC103237807</i>	Caudate	4.02E-09	0.000159	0.284175	other	0
<i>LOC103237843</i>	Caudate	2.23E-09	0.000603	1.23E-05	increasing	0
<i>LOC103237998</i>	Caudate	1.54E-09	0.000676	3.66E-07	increasing	0
<i>LOC103237999</i>	Caudate	9.48E-10	0.000766	3.16E-09	increasing	1
<i>LOC103238059</i>	Caudate	2.95E-08	0.000158	0.30101	other	0
<i>LOC103238143</i>	Caudate	1.78E-10	0.000424	0.002641	other	0
<i>LOC103238230</i>	Caudate	5.41E-08	9.24E-05	0.535992	other	0
<i>LOC103238275</i>	Caudate	2.34E-10	0.000526	0.000277	other	0
<i>LOC103238352</i>	Caudate	4.81E-13	0.000751	1.20E-13	increasing	0
<i>LOC103238411</i>	Caudate	1.11E-09	-0.00081	6.60E-10	decreasing	0
<i>LOC103238427</i>	Caudate	9.01E-07	0.000756	1.18E-08	increasing	0
<i>LOC103238480</i>	Caudate	8.27E-08	0.00062	1.16E-05	increasing	0
<i>LOC103238484</i>	Caudate	2.32E-08	0.000672	1.09E-06	increasing	0
<i>LOC103238601</i>	Caudate	8.52E-08	0.000119	0.435243	other	0
<i>LOC103238617</i>	Caudate	5.03E-12	-0.00077	1.83E-09	decreasing	0
<i>LOC103238689</i>	Caudate	2.81E-11	-0.00078	1.26E-09	decreasing	0
<i>LOC103238753</i>	Caudate	9.47E-08	-4.72E-05	0.747475	other	0
<i>LOC103238760</i>	Caudate	5.04E-08	-0.00034	0.023235	other	0
<i>LOC103238816</i>	Caudate	2.91E-10	-0.0007	1.12E-07	decreasing	0
<i>LOC103238828</i>	Caudate	6.44E-09	-0.00038	0.011218	other	0
<i>LOC103238839</i>	Caudate	5.18E-09	-0.00079	2.45E-09	decreasing	0
<i>LOC103238840</i>	Caudate	5.93E-08	-0.00073	5.90E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103239108</i>	Caudate	2.58E-11	-3.13E-05	0.837142	other	0
<i>LOC103239234</i>	Caudate	2.58E-05	0.00068	1.88E-07	increasing	1
<i>LOC103239292</i>	Caudate	6.69E-10	0.000282	0.055136	other	0
<i>LOC103239363</i>	Caudate	8.28E-10	0.000338	0.023917	other	0
<i>LOC103239473</i>	Caudate	2.88E-10	-0.00061	1.46E-05	decreasing	0
<i>LOC103239626</i>	Caudate	1.30E-07	-0.00069	1.97E-07	decreasing	0
<i>LOC103239649</i>	Caudate	5.99E-08	0.000703	8.13E-08	increasing	0
<i>LOC103239704</i>	Caudate	2.38E-10	0.000752	1.80E-08	increasing	0
<i>LOC103239792</i>	Caudate	1.01E-07	-6.34E-05	0.67471	other	0
<i>LOC103239802</i>	Caudate	5.07E-08	0.000668	1.30E-06	increasing	0
<i>LOC103239864</i>	Caudate	2.29E-10	-0.00079	2.60E-09	decreasing	0
<i>LOC103239908</i>	Caudate	1.20E-08	0.000661	7.61E-07	increasing	0
<i>LOC103239946</i>	Caudate	4.96E-08	-0.00014	0.34375	other	0
<i>LOC103239962</i>	Caudate	7.47E-11	0.000796	5.06E-10	increasing	0
<i>LOC103239981</i>	Caudate	9.96E-08	0.000696	1.97E-07	increasing	0
<i>LOC103240081</i>	Caudate	4.91E-09	0.000591	3.05E-05	increasing	0
<i>LOC103240085</i>	Caudate	1.12E-08	0.000289	0.053407	other	0
<i>LOC103240099</i>	Caudate	1.04E-07	1.72E-05	0.902767	other	0
<i>LOC103240143</i>	Caudate	7.34E-09	-0.00015	0.315084	other	0
<i>LOC103240270</i>	Caudate	1.72E-07	-0.00033	0.024373	other	1
<i>LOC103240400</i>	Caudate	9.66E-13	0.000781	1.65E-09	increasing	0
<i>LOC103240479</i>	Caudate	9.20E-09	-0.00073	3.21E-08	decreasing	0
<i>LOC103240517</i>	Caudate	2.41E-09	-0.00016	0.285561	other	0
<i>LOC103240632</i>	Caudate	2.35E-07	-0.00062	1.17E-05	decreasing	0
<i>LOC103240698</i>	Caudate	2.96E-05	-0.00073	8.02E-08	decreasing	0
<i>LOC103240739</i>	Caudate	1.24E-07	-0.00021	0.162877	other	0
<i>LOC103240747</i>	Caudate	3.99E-08	-0.00067	9.42E-07	decreasing	1
<i>LOC103240867</i>	Caudate	3.88E-10	-0.00058	4.89E-05	decreasing	0
<i>LOC103240892</i>	Caudate	6.52E-07	-0.00077	8.00E-09	decreasing	0
<i>LOC103240893</i>	Caudate	6.71E-08	-0.00076	1.55E-08	decreasing	0
<i>LOC103240894</i>	Caudate	4.07E-09	-0.0008	1.41E-09	decreasing	0
<i>LOC103240895</i>	Caudate	3.34E-07	-0.00074	3.27E-08	decreasing	0
<i>LOC103240939</i>	Caudate	1.64E-07	-0.00046	0.001712	other	1
<i>LOC103240941</i>	Caudate	1.80E-07	-0.00042	0.003507	other	0
<i>LOC103240952</i>	Caudate	1.73E-07	0.00061	1.37E-05	increasing	1
<i>LOC103240993</i>	Caudate	3.81E-05	0.000722	1.05E-07	increasing	0
<i>LOC103241014</i>	Caudate	1.41E-07	-0.00019	0.218396	other	0
<i>LOC103241031</i>	Caudate	1.04E-07	0.000435	0.00302	other	0
<i>LOC103241038</i>	Caudate	1.16E-10	0.000679	1.96E-07	increasing	0
<i>LOC103241174</i>	Caudate	1.16E-07	-0.00063	3.91E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103241683</i>	Caudate	1.13E-10	0.000786	1.43E-09	increasing	0
<i>LOC103241714</i>	Caudate	9.07E-08	0.000139	0.36305	other	0
<i>LOC103241820</i>	Caudate	6.40E-09	0.000596	2.65E-05	increasing	0
<i>LOC103241899</i>	Caudate	9.18E-09	0.000336	0.021319	other	0
<i>LOC103241967</i>	Caudate	2.03E-08	0.000763	4.67E-09	increasing	1
<i>LOC103242002</i>	Caudate	3.90E-09	0.000373	0.012708	other	0
<i>LOC103242062</i>	Caudate	1.25E-07	0.000417	0.004484	other	0
<i>LOC103242120</i>	Caudate	3.54E-11	-0.00019	0.187827	other	0
<i>LOC103242178</i>	Caudate	6.40E-08	0.000285	0.053025	other	0
<i>LOC103242238</i>	Caudate	8.08E-11	0.000676	8.75E-07	increasing	0
<i>LOC103242416</i>	Caudate	1.87E-09	-0.00069	4.40E-07	decreasing	0
<i>LOC103242421</i>	Caudate	2.13E-07	0.000731	6.98E-08	increasing	0
<i>LOC103242629</i>	Caudate	1.16E-08	0.000685	3.73E-07	increasing	0
<i>LOC103242643</i>	Caudate	5.39E-14	0.000833	1.59E-11	increasing	0
<i>LOC103242699</i>	Caudate	2.24E-10	0.000474	0.000977	other	0
<i>LOC103242716</i>	Caudate	3.90E-05	0.000701	1.47E-07	increasing	1
<i>LOC103242839</i>	Caudate	1.01E-07	0.000485	0.000917	other	0
<i>LOC103242925</i>	Caudate	9.37E-12	0.000603	7.38E-06	increasing	0
<i>LOC103242949</i>	Caudate	4.76E-09	0.000103	0.492218	other	0
<i>LOC103243100</i>	Caudate	3.02E-12	0.000858	1.27E-11	increasing	0
<i>LOC103243139</i>	Caudate	5.65E-09	0.000598	1.59E-05	increasing	0
<i>LOC103243152</i>	Caudate	3.72E-08	0.000139	0.358307	other	0
<i>LOC103243159</i>	Caudate	3.50E-11	-0.00061	6.04E-06	decreasing	0
<i>LOC103243190</i>	Caudate	3.50E-09	0.000675	1.11E-06	increasing	0
<i>LOC103243191</i>	Caudate	4.99E-08	0.000117	0.442514	other	0
<i>LOC103243230</i>	Caudate	1.28E-08	0.000677	7.84E-07	increasing	0
<i>LOC103243234</i>	Caudate	7.92E-12	0.000575	4.76E-05	increasing	0
<i>LOC103243287</i>	Caudate	1.25E-09	0.000723	4.39E-08	increasing	0
<i>LOC103243335</i>	Caudate	7.91E-08	0.000599	2.25E-05	increasing	0
<i>LOC103243427</i>	Caudate	1.58E-07	0.000621	1.02E-05	increasing	0
<i>LOC103243440</i>	Caudate	1.41E-07	0.000739	4.64E-08	increasing	1
<i>LOC103243446</i>	Caudate	2.96E-08	0.0007	3.01E-07	increasing	0
<i>LOC103243458</i>	Caudate	3.33E-12	0.000822	9.47E-11	increasing	0
<i>LOC103243459</i>	Caudate	7.02E-09	0.000781	1.68E-11	increasing	0
<i>LOC103243667</i>	Caudate	1.07E-05	0.000728	8.09E-08	increasing	0
<i>LOC103243675</i>	Caudate	1.99E-06	0.00075	2.34E-08	increasing	0
<i>LOC103243707</i>	Caudate	2.13E-07	0.000702	3.00E-07	increasing	0
<i>LOC103243721</i>	Caudate	1.16E-07	0.000158	0.285267	other	0
<i>LOC103243722</i>	Caudate	2.57E-10	0.000295	0.043098	other	0
<i>LOC103243880</i>	Caudate	4.93E-08	0.000427	0.002426	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103243906	Caudate	1.79E-08	-0.00063	4.89E-06	decreasing	0
LOC103243907	Caudate	5.00E-12	-0.00023	0.116092	other	0
LOC103243909	Caudate	3.82E-09	-0.00036	0.014949	other	0
LOC103243940	Caudate	2.12E-07	-0.00057	4.56E-05	decreasing	1
LOC103244047	Caudate	5.05E-10	0.000778	1.13E-09	increasing	0
LOC103244172	Caudate	8.67E-08	2.88E-05	0.851313	other	0
LOC103244243	Caudate	4.21E-12	0.000821	2.32E-10	increasing	0
LOC103244257	Caudate	1.68E-09	-0.00013	0.386066	other	0
LOC103244355	Caudate	2.29E-08	0.000384	0.009881	other	0
LOC103244555	Caudate	1.57E-08	-0.00073	6.35E-08	decreasing	0
LOC103244672	Caudate	4.08E-09	0.000112	0.463269	other	0
LOC103244676	Caudate	9.01E-08	-0.00029	0.045042	other	0
LOC103244678	Caudate	3.61E-08	-0.00057	4.17E-05	decreasing	0
LOC103244679	Caudate	3.14E-09	-0.00059	3.63E-05	decreasing	0
LOC103244683	Caudate	1.19E-07	-0.00056	6.38E-05	decreasing	0
LOC103244731	Caudate	2.40E-07	-6.71E-05	0.662239	other	0
LOC103244868	Caudate	1.10E-15	0.000852	4.01E-12	increasing	0
LOC103244941	Caudate	3.86E-09	0.000312	0.036787	other	0
LOC103245038	Caudate	1.02E-07	0.000687	2.07E-07	increasing	0
LOC103245076	Caudate	3.76E-09	0.000287	0.049491	other	0
LOC103245173	Caudate	6.17E-09	-0.00074	5.83E-09	decreasing	0
LOC103245175	Caudate	4.01E-13	-0.0008	1.22E-10	decreasing	0
LOC103245180	Caudate	3.41E-10	-0.0006	1.22E-05	decreasing	0
LOC103245191	Caudate	1.77E-12	-0.00082	2.75E-10	decreasing	0
LOC103245262	Caudate	6.08E-10	0.000651	2.89E-06	increasing	0
LOC103245291	Caudate	2.38E-10	0.000774	5.51E-09	increasing	0
LOC103245361	Caudate	1.70E-08	0.00069	9.89E-08	increasing	0
LOC103245389	Caudate	1.39E-07	0.000667	5.68E-07	increasing	0
LOC103245450	Caudate	3.36E-13	0.000518	0.000368	other	0
LOC103245600	Caudate	7.88E-09	0.000185	0.220568	other	0
LOC103245736	Caudate	8.91E-08	0.000662	1.16E-06	increasing	1
LOC103245737	Caudate	1.73E-18	0.000882	5.39E-13	increasing	0
LOC103245897	Caudate	4.77E-10	-0.0008	3.14E-10	decreasing	0
LOC103245947	Caudate	1.27E-08	0.000477	0.000805	other	0
LOC103246021	Caudate	2.81E-09	0.000713	1.75E-07	increasing	0
LOC103246023	Caudate	4.71E-11	0.000747	2.81E-08	increasing	0
LOC103246025	Caudate	3.09E-09	0.000716	7.43E-08	increasing	0
LOC103246030	Caudate	7.61E-13	0.000718	9.04E-08	increasing	0
LOC103246043	Caudate	1.51E-08	-0.0002	0.184473	other	0
LOC103246114	Caudate	3.45E-10	0.000226	0.133048	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103246153</i>	Caudate	4.77E-09	-0.00044	0.002964	other	0
<i>LOC103246220</i>	Caudate	1.34E-06	0.000727	3.56E-08	increasing	0
<i>LOC103246334</i>	Caudate	3.44E-10	-0.00075	3.16E-09	decreasing	0
<i>LOC103246345</i>	Caudate	5.73E-08	0.000717	2.34E-08	increasing	0
<i>LOC103246347</i>	Caudate	1.20E-06	0.000679	2.01E-07	increasing	0
<i>LOC103246417</i>	Caudate	1.20E-09	0.000453	0.001951	other	0
<i>LOC103246495</i>	Caudate	1.84E-08	0.000529	0.000223	other	0
<i>LOC103246522</i>	Caudate	1.33E-09	-0.00074	1.88E-08	decreasing	0
<i>LOC103246533</i>	Caudate	2.41E-08	-0.0001	0.497134	other	0
<i>LOC103246546</i>	Caudate	2.30E-08	0.000404	0.006294	other	0
<i>LOC103246562</i>	Caudate	2.54E-06	0.000704	2.55E-07	increasing	1
<i>LOC103246613</i>	Caudate	1.27E-07	0.000297	0.039043	other	0
<i>LOC103246651</i>	Caudate	2.68E-12	-0.00087	3.57E-12	decreasing	0
<i>LOC103246661</i>	Caudate	4.74E-08	0.000407	0.005735	other	0
<i>LOC103246814</i>	Caudate	6.71E-09	-0.00014	0.361264	other	0
<i>LOC103246838</i>	Caudate	7.31E-11	0.000388	0.007452	other	0
<i>LOC103246839</i>	Caudate	1.10E-08	0.000766	9.64E-09	increasing	0
<i>LOC103246928</i>	Caudate	1.38E-13	0.000792	1.22E-09	increasing	0
<i>LOC103246945</i>	Caudate	5.95E-11	0.000702	3.14E-07	increasing	0
<i>LOC103246970</i>	Caudate	1.79E-10	9.97E-06	0.94772	other	0
<i>LOC103247226</i>	Caudate	5.72E-14	0.00063	2.27E-06	increasing	0
<i>LOC103247904</i>	Caudate	5.71E-11	-0.00024	0.044942	other	0
<i>LOC103248139</i>	Caudate	6.39E-10	-0.00083	4.57E-11	decreasing	0
<i>LOC103248140</i>	Caudate	6.49E-13	-0.00086	4.50E-12	decreasing	0
<i>LOC103248141</i>	Caudate	2.24E-11	-0.00083	7.19E-11	decreasing	0
<i>LOC103248297</i>	Caudate	1.31E-11	-0.00077	3.02E-09	decreasing	0
<i>LOC103248300</i>	Caudate	1.72E-09	-0.00069	1.55E-07	decreasing	0
<i>LOC103248301</i>	Caudate	2.07E-08	-0.00074	1.28E-08	decreasing	0
<i>LOC103248302</i>	Caudate	7.61E-13	-0.00083	6.46E-11	decreasing	0
<i>LOC103248307</i>	Caudate	4.10E-08	-0.00077	3.02E-09	decreasing	0
<i>LOC103248308</i>	Caudate	6.24E-09	-0.00073	3.05E-08	decreasing	0
<i>LOC103248381</i>	Caudate	1.55E-08	-0.0008	1.17E-09	decreasing	0
<i>LOC103248471</i>	Caudate	6.27E-08	-0.00047	0.001247	other	0
<i>LOC103248619</i>	Caudate	3.58E-08	0.000482	0.000934	other	0
<i>LOC103248736</i>	Caudate	6.23E-10	8.58E-05	0.57002	other	0
<i>LOC103248816</i>	Caudate	9.97E-07	0.000674	2.60E-07	increasing	0
<i>LOC103248823</i>	Caudate	4.99E-10	-0.00036	0.012733	other	0
<i>LOC103248872</i>	Caudate	2.81E-08	-0.00074	3.32E-08	decreasing	0
<i>LOC103248873</i>	Caudate	6.69E-09	-0.00072	7.33E-08	decreasing	0
<i>LOC103248881</i>	Caudate	4.28E-08	-0.00071	2.46E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103248888</i>	Caudate	5.10E-08	0.000749	2.51E-08	increasing	0
<i>LOC103248909</i>	Caudate	1.98E-07	0.000572	5.38E-05	increasing	0
<i>LOC103248985</i>	Caudate	5.86E-09	0.000711	8.81E-08	increasing	0
<i>LOH12CR1</i>	Caudate	1.58E-07	0.000691	3.13E-07	increasing	0
<i>LONP1</i>	Caudate	2.08E-10	0.000541	0.000183	other	0
<i>LONRF2</i>	Caudate	7.69E-12	0.000804	1.11E-10	increasing	0
<i>LOXHD1</i>	Caudate	1.27E-07	-0.00062	7.37E-06	decreasing	1
<i>LPAR1</i>	Caudate	1.60E-11	0.000767	2.43E-09	increasing	0
<i>LPCAT4</i>	Caudate	5.68E-08	0.000585	2.35E-05	increasing	0
<i>LPHN2</i>	Caudate	5.92E-11	-0.00074	1.63E-08	decreasing	0
<i>LRCH2</i>	Caudate	1.74E-09	-0.00076	1.42E-08	decreasing	0
<i>LRCH4</i>	Caudate	3.04E-10	0.000818	2.12E-10	increasing	0
<i>LRFN1</i>	Caudate	2.60E-07	0.000685	6.46E-07	increasing	0
<i>LRFN4</i>	Caudate	2.63E-10	-0.0001	0.479848	other	0
<i>LRP3</i>	Caudate	1.24E-10	0.000482	0.000991	other	0
<i>LRP4</i>	Caudate	1.21E-08	0.000725	5.11E-08	increasing	0
<i>LRP8</i>	Caudate	4.30E-09	-0.00071	7.08E-08	decreasing	0
<i>LRRC10B</i>	Caudate	9.64E-09	0.000383	0.007743	other	0
<i>LRRC14</i>	Caudate	7.96E-12	0.000432	0.003485	other	0
<i>LRRC20</i>	Caudate	8.19E-08	0.000436	0.003169	other	0
<i>LRRC24</i>	Caudate	2.76E-09	0.000537	0.000204	other	0
<i>LRRC3</i>	Caudate	9.58E-14	0.000879	1.27E-12	increasing	0
<i>LRRC3B</i>	Caudate	3.81E-10	-0.00078	1.31E-09	decreasing	0
<i>LRRC40</i>	Caudate	2.41E-08	-0.00079	1.22E-09	decreasing	0
<i>LRRC41</i>	Caudate	2.01E-08	0.000391	0.008165	other	0
<i>LRRC47</i>	Caudate	8.53E-12	0.000652	3.03E-06	increasing	0
<i>LRRC49</i>	Caudate	9.43E-07	-0.00074	2.07E-08	decreasing	0
<i>LRRC4C</i>	Caudate	5.28E-08	-0.00077	8.05E-09	decreasing	0
<i>LRRC55</i>	Caudate	1.17E-07	-0.00043	0.002699	other	0
<i>LRRC56</i>	Caudate	2.39E-08	0.000241	0.103778	other	0
<i>LRRC7</i>	Caudate	1.33E-09	-0.00071	1.98E-07	decreasing	0
<i>LRRC75A</i>	Caudate	9.37E-09	0.000769	7.62E-09	increasing	0
<i>LRRC8B</i>	Caudate	8.62E-09	-0.00059	2.43E-05	decreasing	0
<i>LRRC8C</i>	Caudate	1.03E-08	-0.00063	6.39E-06	decreasing	0
<i>LRN1</i>	Caudate	2.54E-14	-0.00082	2.19E-10	decreasing	0
<i>LRRTM3</i>	Caudate	3.11E-09	-0.00074	3.48E-08	decreasing	0
<i>LRSAM1</i>	Caudate	6.00E-10	0.000737	4.85E-08	increasing	0
<i>LRTM2</i>	Caudate	9.39E-09	0.000327	0.022523	other	0
<i>LRWD1</i>	Caudate	6.89E-08	0.000193	0.18574	other	0
<i>LSM12</i>	Caudate	1.34E-08	-0.00065	3.23E-06	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LSM4</i>	Caudate	7.42E-08	0.000169	0.265558	other	0
<i>LSS</i>	Caudate	1.06E-10	0.00045	0.002136	other	0
<i>LTBP1</i>	Caudate	4.63E-08	-0.00062	5.88E-06	decreasing	0
<i>LTBP4</i>	Caudate	1.06E-07	0.000733	5.46E-08	increasing	1
<i>LY6E</i>	Caudate	2.35E-07	0.000611	1.53E-05	increasing	1
<i>LYNX1</i>	Caudate	1.24E-09	0.00044	0.002156	other	0
<i>LYPD1</i>	Caudate	1.39E-07	-0.0006	1.35E-05	decreasing	0
<i>LYPLA1</i>	Caudate	2.80E-06	-0.00073	5.41E-08	decreasing	0
<i>LYVE1</i>	Caudate	8.49E-08	-0.00056	8.25E-05	decreasing	0
<i>LZTR1</i>	Caudate	3.00E-09	0.000739	4.03E-08	increasing	0
<i>LZTS2</i>	Caudate	7.70E-15	0.000839	5.97E-11	increasing	0
<i>MACROD1</i>	Caudate	2.03E-12	0.000748	2.20E-08	increasing	0
<i>MAD1L1</i>	Caudate	4.70E-11	0.000245	0.097504	other	0
<i>MAGI3</i>	Caudate	4.02E-08	-0.00071	1.62E-07	decreasing	0
<i>MAL</i>	Caudate	1.96E-07	0.000636	2.98E-06	increasing	0
<i>MAN1B1</i>	Caudate	2.33E-09	0.000366	0.014208	other	0
<i>MAN2A1</i>	Caudate	8.35E-08	0.000106	0.47769	other	0
<i>MAN2A2</i>	Caudate	4.65E-10	0.000818	1.16E-10	increasing	0
<i>MAN2B2</i>	Caudate	3.72E-07	0.000714	1.43E-07	increasing	1
<i>MAN2C1</i>	Caudate	5.38E-14	0.000845	8.04E-12	increasing	0
<i>MANEA</i>	Caudate	2.67E-05	-0.0007	1.50E-07	decreasing	0
<i>MAP1LC3A</i>	Caudate	2.50E-07	1.19E-05	0.9371	other	0
<i>MAP1S</i>	Caudate	2.82E-09	0.000793	7.37E-10	increasing	0
<i>MAP2K2</i>	Caudate	3.01E-11	0.000495	0.000687	other	0
<i>MAP2K3</i>	Caudate	7.45E-11	0.000819	1.40E-10	increasing	0
<i>MAP2K7</i>	Caudate	1.00E-10	0.000561	9.41E-05	increasing	0
<i>MAP3K1</i>	Caudate	1.11E-10	-0.00075	1.32E-08	decreasing	0
<i>MAP3K10</i>	Caudate	1.68E-08	0.000541	0.000165	other	0
<i>MAP3K11</i>	Caudate	2.81E-10	0.000682	7.41E-07	increasing	0
<i>MAP3K12</i>	Caudate	2.27E-09	0.00026	0.081972	other	0
<i>MAP3K2</i>	Caudate	4.44E-09	-0.00073	6.55E-08	decreasing	0
<i>MAP3K3</i>	Caudate	1.07E-08	0.000606	1.92E-05	increasing	0
<i>MAP3K6</i>	Caudate	2.40E-13	0.000872	1.53E-12	increasing	0
<i>MAP3K7</i>	Caudate	6.42E-09	-0.0006	2.55E-05	decreasing	0
<i>MAP4K2</i>	Caudate	2.95E-10	0.000699	3.11E-07	increasing	0
<i>MAP4K3</i>	Caudate	1.61E-08	-0.00074	4.30E-08	decreasing	0
<i>MAP6D1</i>	Caudate	2.31E-11	0.000811	2.88E-10	increasing	0
<i>MAP7</i>	Caudate	1.91E-08	0.00059	1.93E-05	increasing	0
<i>MAP7D1</i>	Caudate	7.31E-14	0.000844	2.88E-11	increasing	0
<i>MAPK11</i>	Caudate	1.16E-10	0.000551	0.000123	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MAPK12</i>	Caudate	1.22E-07	0.00058	4.98E-05	increasing	0
<i>MAPK13</i>	Caudate	2.56E-08	0.0008	7.15E-10	increasing	0
<i>MAPK1IP1L</i>	Caudate	4.16E-10	-0.00041	0.005561	other	0
<i>MAPK3</i>	Caudate	1.20E-10	0.000683	3.11E-07	increasing	0
<i>MAPK8</i>	Caudate	8.57E-19	-0.0009	5.02E-14	decreasing	0
<i>MAPK8IP1</i>	Caudate	1.63E-11	0.000526	0.000277	other	0
<i>MAPK8IP2</i>	Caudate	7.65E-12	0.000711	2.00E-07	increasing	0
<i>MAPK8IP3</i>	Caudate	1.62E-12	0.00068	8.61E-07	increasing	0
<i>MAPRE1</i>	Caudate	2.38E-13	-0.00083	7.07E-11	decreasing	0
<i>MARCH5</i>	Caudate	1.51E-07	-0.00071	1.92E-07	decreasing	0
<i>MARCH8</i>	Caudate	1.59E-14	0.000865	4.68E-13	increasing	0
<i>MARCH9</i>	Caudate	1.65E-10	4.66E-05	0.755236	other	0
<i>MARCKS</i>	Caudate	5.65E-14	-0.0008	9.01E-11	decreasing	0
<i>MARCKSL1</i>	Caudate	4.43E-09	-0.00041	0.003844	other	0
<i>MARK1</i>	Caudate	1.74E-13	-0.00085	2.07E-11	decreasing	0
<i>MARK3</i>	Caudate	2.14E-08	-0.00058	3.89E-05	decreasing	0
<i>MARS</i>	Caudate	8.33E-08	0.000226	0.137564	other	0
<i>MAT2A</i>	Caudate	4.73E-08	-0.00024	0.113347	other	0
<i>MATN3</i>	Caudate	1.14E-07	-0.00068	4.16E-07	decreasing	1
<i>MAU2</i>	Caudate	8.45E-12	0.000468	0.001097	other	0
<i>MAZ</i>	Caudate	3.36E-10	-0.00043	0.002747	other	0
<i>MB21D2</i>	Caudate	3.16E-08	-0.00053	0.000164	other	0
<i>MBD1</i>	Caudate	1.93E-09	0.000371	0.01269	other	0
<i>MBD3</i>	Caudate	5.62E-08	0.000468	0.001419	other	0
<i>MBIP</i>	Caudate	8.07E-09	-0.00027	0.07755	other	1
<i>MBLAC1</i>	Caudate	3.53E-09	0.000585	3.69E-05	increasing	0
<i>MBNL1</i>	Caudate	1.23E-08	-0.00056	6.39E-05	decreasing	0
<i>MBNL2</i>	Caudate	5.06E-12	-6.63E-05	0.659027	other	0
<i>MBOAT7</i>	Caudate	6.11E-12	0.000783	8.08E-10	increasing	0
<i>MBP</i>	Caudate	1.51E-12	0.000764	2.84E-09	increasing	0
<i>MCC</i>	Caudate	5.94E-12	0.00027	0.069593	other	0
<i>MCF2L</i>	Caudate	1.69E-09	0.000693	4.83E-07	increasing	0
<i>MCF2L2</i>	Caudate	2.37E-12	0.000801	1.45E-10	increasing	1
<i>MCM2</i>	Caudate	1.94E-11	0.000166	0.271787	other	0
<i>MCM3AP</i>	Caudate	4.17E-09	0.000443	0.002687	other	0
<i>MCM7</i>	Caudate	1.44E-10	0.000248	0.087318	other	0
<i>MCTP1</i>	Caudate	3.12E-11	-0.00027	0.065714	other	0
<i>MCU</i>	Caudate	4.47E-08	-0.00073	3.06E-08	decreasing	0
<i>MEAF6</i>	Caudate	6.12E-09	-0.00021	0.16029	other	0
<i>MECR</i>	Caudate	6.88E-11	0.000161	0.277886	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MED13</i>	Caudate	5.86E-09	-0.0006	2.71E-05	decreasing	0
<i>MED16</i>	Caudate	3.39E-10	0.000577	5.19E-05	increasing	0
<i>MED22</i>	Caudate	3.36E-09	0.000405	0.005576	other	0
<i>MED25</i>	Caudate	2.25E-09	0.000489	0.000438	other	0
<i>MEF2C</i>	Caudate	2.93E-18	-0.00084	6.25E-12	decreasing	0
<i>MEGF10</i>	Caudate	2.41E-09	0.000688	2.88E-07	increasing	0
<i>MEGF6</i>	Caudate	9.26E-09	0.000662	2.03E-06	increasing	0
<i>MEGF8</i>	Caudate	2.42E-11	0.00062	1.15E-05	increasing	0
<i>MEIS2</i>	Caudate	4.04E-09	-0.00072	3.18E-08	decreasing	0
<i>MEPCE</i>	Caudate	2.76E-10	0.000773	5.72E-09	increasing	0
<i>MEST</i>	Caudate	1.71E-11	-0.00047	0.000803	other	0
<i>METRN</i>	Caudate	1.02E-08	0.000286	0.056348	other	0
<i>METTL12</i>	Caudate	2.67E-09	0.000281	0.057356	other	0
<i>METTL16</i>	Caudate	2.97E-10	0.000833	9.65E-11	increasing	0
<i>METTL7B</i>	Caudate	2.28E-07	0.000676	6.99E-07	increasing	0
<i>MEX3A</i>	Caudate	6.74E-09	-0.00064	2.86E-06	decreasing	0
<i>MEX3B</i>	Caudate	2.03E-08	-0.00054	7.69E-05	decreasing	0
<i>MEX3C</i>	Caudate	2.15E-09	-0.00067	5.53E-07	decreasing	0
<i>MEX3D</i>	Caudate	3.94E-10	0.00017	0.252501	other	0
<i>MFAP3</i>	Caudate	6.21E-18	-0.00087	1.79E-12	decreasing	0
<i>MFHAS1</i>	Caudate	6.56E-08	0.000269	0.076163	other	0
<i>MFSD10</i>	Caudate	8.87E-08	0.000314	0.032919	other	0
<i>MFSD3</i>	Caudate	3.53E-08	0.000413	0.005424	other	0
<i>MFSD8</i>	Caudate	1.23E-07	-0.00069	5.38E-07	decreasing	0
<i>MGAT1</i>	Caudate	2.51E-08	0.000555	0.000114	other	0
<i>MGAT3</i>	Caudate	1.54E-07	0.000683	7.85E-07	increasing	0
<i>MGAT4A</i>	Caudate	6.81E-08	-0.00075	2.59E-08	decreasing	0
<i>MGAT4B</i>	Caudate	1.09E-11	0.000225	0.128527	other	0
<i>MGAT4C</i>	Caudate	4.56E-13	-0.00078	1.44E-09	decreasing	0
<i>MGAT5</i>	Caudate	1.01E-07	-0.00074	3.74E-08	decreasing	0
<i>MGST1</i>	Caudate	8.66E-19	-0.00081	3.00E-10	decreasing	0
<i>MIB2</i>	Caudate	1.63E-11	0.000581	4.59E-05	increasing	0
<i>MICAL2</i>	Caudate	7.51E-14	0.00083	2.10E-11	increasing	0
<i>MID1</i>	Caudate	1.06E-07	-0.00044	0.003022	other	0
<i>MID1IP1</i>	Caudate	1.45E-20	0.000882	3.18E-13	increasing	0
<i>MIEF2</i>	Caudate	3.27E-08	0.000423	0.003706	other	0
<i>MIER1</i>	Caudate	2.61E-11	-0.00033	0.024346	other	0
<i>MIIP</i>	Caudate	6.99E-08	0.000596	2.77E-05	increasing	0
<i>MINK1</i>	Caudate	2.02E-09	0.000708	1.14E-07	increasing	0
<i>MKI67</i>	Caudate	2.72E-09	-0.00069	2.97E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MKLN1</i>	Caudate	3.87E-08	0.00014	0.344382	other	0
<i>MKRN3</i>	Caudate	7.18E-13	-0.00078	1.55E-09	decreasing	0
<i>MLC1</i>	Caudate	1.96E-07	0.000349	0.016717	other	0
<i>MLLT11</i>	Caudate	1.14E-10	-0.00053	0.000144	other	0
<i>MLLT4</i>	Caudate	3.27E-11	-0.0007	1.37E-07	decreasing	0
<i>MLLT6</i>	Caudate	7.07E-06	0.000712	1.45E-07	increasing	0
<i>MLPH</i>	Caudate	2.34E-07	0.000756	7.94E-09	increasing	0
<i>MLST8</i>	Caudate	1.13E-09	0.000343	0.022406	other	0
<i>MLYCD</i>	Caudate	4.50E-12	0.000226	0.135142	other	0
<i>MMD</i>	Caudate	7.99E-13	-0.00085	1.04E-11	decreasing	0
<i>MMGT1</i>	Caudate	5.28E-10	-0.00048	0.000968	other	0
<i>MMP16</i>	Caudate	1.51E-19	-0.00088	2.76E-13	decreasing	0
<i>MMP2</i>	Caudate	1.21E-08	-0.0007	1.96E-07	decreasing	0
<i>MMP23B</i>	Caudate	1.80E-07	0.000773	6.07E-09	increasing	0
<i>MMP24</i>	Caudate	7.25E-10	-0.00016	0.291543	other	0
<i>MMRN2</i>	Caudate	1.31E-09	0.000552	6.89E-05	increasing	0
<i>MMS19</i>	Caudate	4.28E-07	0.000706	2.27E-07	increasing	0
<i>MOB1A</i>	Caudate	1.01E-10	-0.00082	3.49E-10	decreasing	0
<i>MOB1B</i>	Caudate	1.08E-09	-0.00074	4.54E-08	decreasing	0
<i>MOB3B</i>	Caudate	6.72E-08	2.25E-05	0.878382	other	0
<i>MOG</i>	Caudate	1.22E-07	0.000614	6.20E-06	increasing	0
<i>MOGS</i>	Caudate	1.24E-09	0.000196	0.192469	other	0
<i>MOSPD2</i>	Caudate	4.43E-11	-0.00022	0.152436	other	0
<i>MOXD1</i>	Caudate	1.71E-09	0.000648	2.86E-06	increasing	0
<i>MPHOSPH8</i>	Caudate	9.41E-08	0.000313	0.033557	other	0
<i>MPP2</i>	Caudate	1.64E-08	0.00069	1.10E-07	increasing	0
<i>MPP3</i>	Caudate	7.31E-11	0.000179	0.220786	other	0
<i>MPP6</i>	Caudate	2.24E-08	-0.00022	0.146728	other	0
<i>MPPED2</i>	Caudate	1.21E-07	-0.00065	3.03E-06	decreasing	0
<i>MRC1</i>	Caudate	7.10E-07	-0.00076	1.07E-08	decreasing	0
<i>MRGPRG</i>	Caudate	1.63E-09	-0.00032	0.00657	other	0
<i>MRI1</i>	Caudate	1.70E-10	0.00061	1.66E-05	increasing	1
<i>MRM1</i>	Caudate	3.69E-08	0.000618	9.74E-06	increasing	0
<i>MROH1</i>	Caudate	4.13E-10	0.000642	4.39E-06	increasing	0
<i>MROH7</i>	Caudate	5.51E-07	0.000751	1.82E-08	increasing	1
<i>MRPL23</i>	Caudate	6.76E-08	0.000531	0.000191	other	0
<i>MRPL28</i>	Caudate	1.96E-07	0.000429	0.002827	other	0
<i>MRPL42</i>	Caudate	7.32E-10	-0.00079	2.28E-09	decreasing	1
<i>MRPS26</i>	Caudate	7.75E-09	0.000459	0.001765	other	0
<i>MRPS34</i>	Caudate	1.67E-09	0.000542	0.000173	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MRPS6</i>	Caudate	5.14E-08	0.000323	0.030947	other	0
<i>MSANTD1</i>	Caudate	2.38E-07	7.74E-05	0.610773	other	0
<i>MSH6</i>	Caudate	1.86E-07	-0.00044	0.00165	other	0
<i>MSL3</i>	Caudate	4.59E-09	-0.00073	2.24E-08	decreasing	0
<i>MSLN</i>	Caudate	6.44E-07	0.000704	2.50E-07	increasing	0
<i>MST1</i>	Caudate	1.94E-07	0.000705	2.31E-07	increasing	0
<i>MT1X</i>	Caudate	2.17E-11	0.000756	3.44E-09	increasing	0
<i>MTA2</i>	Caudate	4.35E-08	9.14E-05	0.540523	other	0
<i>MTCH1</i>	Caudate	5.51E-09	0.000611	8.57E-06	increasing	0
<i>MTG1</i>	Caudate	3.12E-11	8.87E-05	0.552736	other	0
<i>MTMR3</i>	Caudate	1.41E-15	0.000337	0.020072	other	0
<i>MTMR4</i>	Caudate	2.20E-07	0.000373	0.011525	other	0
<i>MTPAP</i>	Caudate	1.50E-07	-0.00073	5.82E-08	decreasing	1
<i>MTPN</i>	Caudate	4.98E-08	-0.00072	8.24E-08	decreasing	0
<i>MTRF1L</i>	Caudate	3.74E-11	-0.0008	1.07E-09	decreasing	1
<i>MTRR</i>	Caudate	4.88E-08	-0.00034	0.023428	other	0
<i>MTSS1</i>	Caudate	2.56E-10	-0.0005	0.000431	other	0
<i>MTURN</i>	Caudate	3.52E-08	0.000638	2.73E-06	increasing	0
<i>MTX3</i>	Caudate	7.13E-08	-0.00075	2.07E-08	decreasing	0
<i>MUSK</i>	Caudate	1.35E-11	0.000762	8.97E-09	increasing	0
<i>MUT</i>	Caudate	2.50E-07	-0.00022	0.1257	other	0
<i>MUTYH</i>	Caudate	8.09E-10	0.000425	0.002897	other	0
<i>MVB12A</i>	Caudate	1.39E-08	0.00019	0.192605	other	0
<i>MXD4</i>	Caudate	6.13E-09	0.000544	0.000166	other	0
<i>MXRA7</i>	Caudate	1.89E-08	0.000285	0.051362	other	0
<i>MXRA8</i>	Caudate	3.85E-08	0.000293	0.045911	other	0
<i>MYADML2</i>	Caudate	7.14E-10	4.90E-05	0.744558	other	0
<i>MYBBP1A</i>	Caudate	1.89E-10	0.000545	0.000153	other	0
<i>MYBPC2</i>	Caudate	5.89E-09	0.000368	0.012829	other	0
<i>MYBPH</i>	Caudate	1.62E-07	0.000542	7.72E-05	increasing	1
<i>MYCL</i>	Caudate	6.49E-09	-0.0007	1.58E-07	decreasing	0
<i>MYCN</i>	Caudate	1.31E-07	-0.00052	0.000142	other	0
<i>MYCT1</i>	Caudate	1.81E-07	-0.00067	1.58E-06	decreasing	0
<i>MYEF2</i>	Caudate	4.15E-10	-0.00065	2.58E-06	decreasing	0
<i>MYH14</i>	Caudate	5.00E-09	0.000713	1.00E-07	increasing	0
<i>MYH3</i>	Caudate	3.84E-10	-0.00069	1.97E-07	decreasing	1
<i>MYH7B</i>	Caudate	2.49E-12	0.000857	7.94E-12	increasing	0
<i>MYH9</i>	Caudate	2.06E-10	0.000692	2.89E-07	increasing	0
<i>MYO15A</i>	Caudate	6.28E-06	0.000708	1.81E-07	increasing	1
<i>MYO16</i>	Caudate	3.44E-15	-0.00074	8.08E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MYO18A</i>	Caudate	4.98E-12	0.000723	1.04E-07	increasing	0
<i>MYO1B</i>	Caudate	1.13E-13	-0.00079	7.76E-10	decreasing	1
<i>MYO5B</i>	Caudate	5.79E-18	-0.0008	6.35E-11	decreasing	0
<i>MYO5C</i>	Caudate	1.05E-11	0.000771	1.83E-09	increasing	0
<i>MYO6</i>	Caudate	7.62E-09	-0.00019	0.196571	other	1
<i>MYRF</i>	Caudate	6.65E-12	0.000815	4.48E-11	increasing	0
<i>MYT1L</i>	Caudate	6.93E-13	-0.00079	1.41E-09	decreasing	0
<i>MZF1</i>	Caudate	7.46E-10	0.00055	0.000109	other	0
<i>MZT2B</i>	Caudate	1.95E-08	0.000465	0.0015	other	0
<i>N4BP2</i>	Caudate	8.24E-09	3.71E-05	0.800181	other	0
<i>N4BP3</i>	Caudate	1.90E-08	5.90E-05	0.687375	other	0
<i>N6AMT2</i>	Caudate	2.20E-08	-7.89E-05	0.594799	other	0
<i>NAA10</i>	Caudate	1.75E-08	0.000634	6.51E-06	increasing	0
<i>NAA15</i>	Caudate	3.06E-09	-0.00069	6.39E-07	decreasing	0
<i>NAA40</i>	Caudate	2.18E-10	0.00026	0.071833	other	0
<i>NAA50</i>	Caudate	6.51E-11	-0.00054	0.000169	other	0
<i>NAALAD2</i>	Caudate	1.45E-07	0.000765	9.79E-09	increasing	1
<i>NACC2</i>	Caudate	5.89E-09	0.000681	6.19E-07	increasing	0
<i>NADK</i>	Caudate	7.05E-09	-0.00035	0.018135	other	0
<i>NAGLU</i>	Caudate	1.80E-09	0.000167	0.263147	other	0
<i>NAGPA</i>	Caudate	2.35E-08	0.000254	0.094568	other	0
<i>NAP1L1</i>	Caudate	5.28E-12	-0.00014	0.321804	other	0
<i>NARFL</i>	Caudate	5.30E-10	0.000485	0.000935	other	0
<i>NARG2</i>	Caudate	2.03E-10	-0.00054	0.000216	other	0
<i>NASP</i>	Caudate	5.30E-13	-0.00076	2.87E-09	decreasing	0
<i>NAT8L</i>	Caudate	3.98E-08	0.000516	0.000381	other	0
<i>NAT9</i>	Caudate	1.15E-07	0.000261	0.077694	other	0
<i>NAV3</i>	Caudate	8.82E-10	-0.00055	8.59E-05	decreasing	0
<i>NBAS</i>	Caudate	2.05E-07	-0.00026	0.075157	other	1
<i>NBL1</i>	Caudate	1.35E-09	-0.00046	0.001516	other	0
<i>NCAPD2</i>	Caudate	1.09E-08	0.00043	0.003118	other	0
<i>NCAPG</i>	Caudate	2.76E-12	-0.00079	8.75E-10	decreasing	0
<i>NCAPH2</i>	Caudate	1.13E-09	0.000483	0.000817	other	0
<i>NCDN</i>	Caudate	4.16E-14	0.000643	2.16E-06	increasing	0
<i>NCKIPSD</i>	Caudate	2.09E-12	0.000853	2.61E-12	increasing	0
<i>NCLN</i>	Caudate	4.94E-09	0.000455	0.002028	other	0
<i>NCOA3</i>	Caudate	1.90E-14	-0.00078	1.95E-09	decreasing	0
<i>NCR3LG1</i>	Caudate	5.72E-09	0.000826	8.64E-11	increasing	1
<i>NDE1</i>	Caudate	6.60E-10	0.000837	7.57E-11	increasing	0
<i>NDFIP1</i>	Caudate	1.21E-09	-0.00059	3.26E-05	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>NDRG1</i>	Caudate	4.75E-18	0.000839	5.69E-12	increasing	0
<i>NDRG2</i>	Caudate	6.68E-08	0.000608	1.16E-05	increasing	0
<i>NDRG4</i>	Caudate	2.37E-08	0.000601	1.39E-05	increasing	0
<i>NDST3</i>	Caudate	6.65E-09	-4.08E-05	0.786579	other	0
<i>NDUFC1</i>	Caudate	2.14E-07	-0.0003	0.042095	other	0
<i>NDUFS7</i>	Caudate	6.67E-08	0.000436	0.003201	other	0
<i>NDUFV1</i>	Caudate	2.65E-09	0.000295	0.050647	other	0
<i>NEBL</i>	Caudate	3.65E-10	-0.0003	0.042565	other	0
<i>NEFH</i>	Caudate	1.23E-09	0.000788	2.19E-09	increasing	0
<i>NEGR1</i>	Caudate	3.95E-07	-0.0007	2.21E-07	decreasing	0
<i>NEIL1</i>	Caudate	1.77E-08	0.000498	0.000433	other	0
<i>NEK10</i>	Caudate	3.87E-10	-0.00065	2.82E-06	decreasing	0
<i>NEK8</i>	Caudate	1.75E-09	0.00045	0.001333	other	0
<i>NELL2</i>	Caudate	4.32E-10	-0.00079	9.38E-10	decreasing	0
<i>NEMF</i>	Caudate	1.51E-10	-0.00044	0.002818	other	0
<i>NEURL1B</i>	Caudate	5.46E-14	-0.00031	0.033185	other	0
<i>NEURL4</i>	Caudate	3.32E-11	0.000538	0.000194	other	0
<i>NEXN</i>	Caudate	1.17E-08	-0.00058	4.92E-05	decreasing	0
<i>NF2</i>	Caudate	1.04E-11	0.000642	4.67E-06	increasing	0
<i>NFATC3</i>	Caudate	3.37E-14	0.000221	0.135524	other	0
<i>NFE2L1</i>	Caudate	9.41E-09	0.000156	0.286583	other	0
<i>NFE2L2</i>	Caudate	1.53E-09	0.000169	0.265513	other	0
<i>NFYB</i>	Caudate	1.77E-07	-0.00065	2.42E-06	decreasing	0
<i>NFYC</i>	Caudate	5.98E-09	-1.18E-05	0.937501	other	0
<i>NGEF</i>	Caudate	8.34E-08	-3.41E-05	0.823098	other	0
<i>NHS</i>	Caudate	6.40E-12	-0.00076	1.42E-09	decreasing	0
<i>NIN</i>	Caudate	1.65E-08	-0.0004	0.006271	other	0
<i>NIPAL4</i>	Caudate	6.39E-09	0.000707	1.21E-07	increasing	0
<i>NKAPL</i>	Caudate	2.56E-07	9.08E-05	0.546338	other	0
<i>NKIRAS2</i>	Caudate	8.56E-08	-0.00057	5.33E-05	decreasing	0
<i>NKPD1</i>	Caudate	2.05E-11	0.000546	0.000132	other	0
<i>NKX2.6</i>	Caudate	8.78E-07	0.000675	5.84E-10	increasing	0
<i>NKX3.1</i>	Caudate	6.75E-20	0.00088	7.76E-13	increasing	0
<i>NKX6.2</i>	Caudate	1.95E-11	0.000771	1.82E-09	increasing	0
<i>NLRX1</i>	Caudate	4.48E-10	0.000333	0.023201	other	0
<i>NMNAT3</i>	Caudate	1.30E-05	0.000742	3.52E-08	increasing	1
<i>NMRAL1</i>	Caudate	7.98E-08	0.000512	0.000426	other	0
<i>NMUR2</i>	Caudate	1.75E-08	-0.00076	7.84E-09	decreasing	0
<i>NNT</i>	Caudate	1.53E-06	-0.00076	1.41E-08	decreasing	0
<i>NOB1</i>	Caudate	9.04E-08	0.000713	1.75E-07	increasing	1

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>NOC4L</i>	Caudate	3.46E-08	0.000589	3.03E-05	increasing	0
<i>NOL11</i>	Caudate	2.24E-10	-0.00082	7.06E-11	decreasing	0
<i>NOL3</i>	Caudate	1.03E-07	0.000715	1.58E-07	increasing	0
<i>NOL6</i>	Caudate	1.35E-11	0.000435	0.002995	other	0
<i>NONO</i>	Caudate	5.33E-09	-0.00016	0.272764	other	0
<i>NOP14</i>	Caudate	2.89E-10	0.00055	8.31E-05	increasing	0
<i>NOTCH1</i>	Caudate	1.71E-08	0.000369	0.009613	other	0
<i>NPC1L1</i>	Caudate	2.88E-08	0.000702	1.44E-07	increasing	0
<i>NPFFR1</i>	Caudate	4.84E-08	0.00061	1.37E-05	increasing	1
<i>NPHP1</i>	Caudate	1.96E-08	-0.00057	7.34E-05	decreasing	0
<i>NPHP4</i>	Caudate	2.43E-08	0.00072	8.10E-08	increasing	0
<i>NPHS1</i>	Caudate	7.58E-10	0.000708	1.16E-07	increasing	0
<i>NPLOC4</i>	Caudate	1.31E-08	0.000637	5.70E-06	increasing	0
<i>NPM3</i>	Caudate	1.63E-08	0.000684	5.98E-07	increasing	0
<i>NPTX1</i>	Caudate	2.66E-09	0.000767	8.41E-10	increasing	1
<i>NPTX2</i>	Caudate	3.91E-11	-0.00082	1.31E-10	decreasing	0
<i>NQO1</i>	Caudate	2.35E-10	0.000628	5.18E-06	increasing	0
<i>NR1H2</i>	Caudate	1.81E-11	0.000672	9.40E-07	increasing	0
<i>NR2C2AP</i>	Caudate	1.32E-08	-0.00019	0.20828	other	0
<i>NR2F6</i>	Caudate	7.87E-10	0.000463	0.001567	other	0
<i>NR3C2</i>	Caudate	4.42E-13	-9.09E-05	0.534826	other	0
<i>NRAS</i>	Caudate	4.61E-11	-0.00074	8.58E-09	decreasing	0
<i>NRCAM</i>	Caudate	1.46E-07	-0.00069	3.94E-07	decreasing	0
<i>NRD1</i>	Caudate	1.48E-09	-0.00073	5.49E-08	decreasing	0
<i>NREP</i>	Caudate	1.04E-22	-0.00092	2.39E-15	decreasing	0
<i>NRG2</i>	Caudate	2.23E-11	0.000657	2.50E-06	increasing	0
<i>NRGN</i>	Caudate	7.04E-09	-5.89E-05	0.687797	other	0
<i>NRIP1</i>	Caudate	8.95E-11	-0.00082	1.87E-10	decreasing	0
<i>NRP1</i>	Caudate	2.14E-11	-0.00079	1.35E-09	decreasing	0
<i>NRXN1</i>	Caudate	3.96E-16	-0.00085	4.88E-12	decreasing	0
<i>NRXN2</i>	Caudate	6.61E-10	4.76E-05	0.754153	other	0
<i>NSF</i>	Caudate	1.09E-10	-4.24E-05	0.776762	other	0
<i>NSRP1</i>	Caudate	7.63E-08	-0.00034	0.024064	other	0
<i>NT5C</i>	Caudate	4.47E-08	0.000328	0.024804	other	0
<i>NT5DC2</i>	Caudate	4.73E-10	0.000257	0.083241	other	0
<i>NT5DC3</i>	Caudate	5.54E-10	0.000727	2.99E-08	increasing	0
<i>NT5M</i>	Caudate	3.89E-13	0.000338	0.019893	other	0
<i>NTHL1</i>	Caudate	2.80E-09	8.06E-05	0.597597	other	0
<i>NTN4</i>	Caudate	1.15E-07	0.000738	3.31E-08	increasing	1
<i>NTSR2</i>	Caudate	9.07E-14	0.000776	2.03E-09	increasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>NUBP2</i>	Caudate	2.64E-10	0.000137	0.368745	other	0
<i>NUCB1</i>	Caudate	1.18E-10	0.000307	0.041504	other	0
<i>NUDC</i>	Caudate	3.55E-08	0.000207	0.169471	other	0
<i>NUDCD1</i>	Caudate	4.12E-07	-0.00074	3.32E-08	decreasing	0
<i>NUDCD3</i>	Caudate	1.93E-14	0.000702	1.40E-07	increasing	0
<i>NUDT19</i>	Caudate	3.96E-08	-6.36E-05	0.668204	other	0
<i>NUDT4</i>	Caudate	3.43E-13	-0.0008	6.80E-10	decreasing	0
<i>NUDT9</i>	Caudate	1.62E-09	-0.00032	0.02921	other	0
<i>NUFIP1</i>	Caudate	1.03E-08	-0.0002	0.178459	other	0
<i>NUFIP2</i>	Caudate	2.43E-08	-0.00071	1.41E-07	decreasing	0
<i>NUMA1</i>	Caudate	1.21E-15	0.000798	1.02E-09	increasing	0
<i>NUMB</i>	Caudate	1.54E-12	-0.00034	0.019295	other	0
<i>NUP153</i>	Caudate	1.26E-07	-0.00062	3.68E-06	decreasing	0
<i>NUP62</i>	Caudate	2.28E-09	0.000425	0.004003	other	0
<i>NUS1</i>	Caudate	1.97E-07	-0.00058	4.28E-05	decreasing	0
<i>NXPH1</i>	Caudate	8.42E-09	-0.00066	1.31E-06	decreasing	0
<i>NYAP2</i>	Caudate	5.16E-21	-0.00087	9.37E-13	decreasing	0
<i>OAF</i>	Caudate	2.89E-11	0.000161	0.276002	other	0
<i>OARD1</i>	Caudate	3.22E-09	0.000103	0.496082	other	1
<i>OBSCN</i>	Caudate	1.33E-14	0.000845	1.22E-11	increasing	1
<i>OBSL1</i>	Caudate	7.99E-11	0.000424	0.002644	other	0
<i>ODF2L</i>	Caudate	1.41E-07	-0.00071	7.56E-08	decreasing	1
<i>ODF3</i>	Caudate	3.06E-08	0.000774	3.56E-09	increasing	0
<i>OGDH</i>	Caudate	2.79E-10	0.000671	4.69E-07	increasing	0
<i>OGDHL</i>	Caudate	6.22E-12	0.000814	1.81E-10	increasing	0
<i>OGFOD2</i>	Caudate	1.36E-07	0.000601	2.09E-05	increasing	0
<i>OGFR</i>	Caudate	3.44E-09	0.000428	0.003808	other	0
<i>OGFRL1</i>	Caudate	1.30E-08	-0.00068	5.50E-07	decreasing	0
<i>OPALIN</i>	Caudate	4.84E-08	0.000635	2.49E-06	increasing	0
<i>OPCML</i>	Caudate	6.49E-12	-0.00077	4.14E-09	decreasing	0
<i>OPLAH</i>	Caudate	3.66E-12	0.00076	1.32E-08	increasing	0
<i>OPRL1</i>	Caudate	6.08E-10	0.000755	1.14E-08	increasing	0
<i>ORAI2</i>	Caudate	1.66E-09	0.00014	0.345192	other	0
<i>ORAOV1</i>	Caudate	1.95E-05	0.000722	1.03E-07	increasing	0
<i>OSBPL2</i>	Caudate	2.25E-08	0.000398	0.0072	other	0
<i>OSBPL3</i>	Caudate	2.86E-07	-0.00076	1.66E-08	decreasing	0
<i>OSBPL6</i>	Caudate	3.07E-08	-0.00054	0.000143	other	0
<i>OSBPL7</i>	Caudate	1.37E-08	0.000604	1.68E-05	increasing	0
<i>OSBPL8</i>	Caudate	1.13E-09	-0.00043	0.002652	other	0
<i>OSGIN1</i>	Caudate	6.65E-08	0.000625	3.89E-06	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>OTOG</i>	Caudate	7.08E-13	0.000841	3.57E-11	increasing	0
<i>OTUD3</i>	Caudate	1.17E-14	-0.00082	2.32E-10	decreasing	0
<i>OTUD4</i>	Caudate	2.92E-08	-0.00066	1.71E-06	decreasing	0
<i>OTUD6B</i>	Caudate	6.70E-08	-0.00064	5.31E-06	decreasing	0
<i>OTUD7A</i>	Caudate	5.82E-12	0.00047	0.001318	other	0
<i>OXCT1</i>	Caudate	3.31E-09	-0.0007	4.94E-08	decreasing	0
<i>OXR1</i>	Caudate	3.70E-06	-0.00071	2.05E-07	decreasing	0
<i>OXSR1</i>	Caudate	7.97E-05	-0.00071	1.90E-07	decreasing	0
<i>P2RY1</i>	Caudate	2.31E-10	-0.00071	1.07E-07	decreasing	0
<i>P2RY12</i>	Caudate	5.19E-12	-0.00085	3.28E-12	decreasing	0
<i>P2RY13</i>	Caudate	7.88E-07	-0.00071	2.38E-07	decreasing	0
<i>P4HTM</i>	Caudate	1.52E-09	0.000557	1.00E-04	increasing	0
<i>PAFAH1B3</i>	Caudate	3.67E-10	0.000369	0.011764	other	0
<i>PAK3</i>	Caudate	2.57E-07	-0.00042	0.003074	other	0
<i>PALM</i>	Caudate	1.24E-07	0.000641	3.62E-06	increasing	0
<i>PAN2</i>	Caudate	1.39E-08	0.000454	0.001197	other	0
<i>PANK1</i>	Caudate	6.58E-12	-0.00085	6.18E-12	decreasing	0
<i>PANK3</i>	Caudate	1.06E-13	-0.00086	6.88E-12	decreasing	0
<i>PANK4</i>	Caudate	4.95E-09	0.000429	0.003191	other	0
<i>PAOX</i>	Caudate	5.83E-10	0.000771	4.54E-09	increasing	0
<i>PAPD4</i>	Caudate	1.02E-08	-0.00049	0.000774	other	0
<i>PAPLN</i>	Caudate	1.68E-09	0.000734	5.44E-08	increasing	0
<i>PAPOLA</i>	Caudate	3.02E-10	-0.00061	1.88E-05	decreasing	0
<i>PAPOLG</i>	Caudate	7.69E-10	-0.00057	6.41E-05	decreasing	0
<i>PAPSS1</i>	Caudate	1.17E-06	-0.0007	1.41E-07	decreasing	0
<i>PAQR3</i>	Caudate	2.60E-10	-0.00077	8.01E-09	decreasing	0
<i>PAQR6</i>	Caudate	1.60E-15	0.000832	1.07E-11	increasing	0
<i>PARP3</i>	Caudate	5.26E-08	0.000762	1.00E-08	increasing	0
<i>PARP6</i>	Caudate	3.50E-09	-0.00059	1.95E-05	decreasing	0
<i>PARP8</i>	Caudate	4.62E-17	-0.00083	6.52E-12	decreasing	0
<i>PARS2</i>	Caudate	2.11E-08	0.000133	0.370092	other	1
<i>PASK</i>	Caudate	5.59E-14	0.000638	2.64E-06	increasing	0
<i>PATZ1</i>	Caudate	7.10E-08	0.000275	0.060447	other	0
<i>PAXBP1</i>	Caudate	8.11E-09	-0.00068	2.09E-07	decreasing	0
<i>PBRM1</i>	Caudate	6.82E-11	-0.00059	1.40E-05	decreasing	0
<i>PBX3</i>	Caudate	5.35E-08	-0.00078	4.72E-09	decreasing	1
<i>PC</i>	Caudate	6.44E-18	0.00085	3.37E-12	increasing	0
<i>PCBD1</i>	Caudate	1.34E-09	0.000673	1.18E-06	increasing	0
<i>PCBP4</i>	Caudate	1.03E-11	0.000763	9.53E-09	increasing	0
<i>PCDH11X</i>	Caudate	1.13E-15	-0.00084	3.21E-11	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PCDH15</i>	Caudate	2.38E-11	-0.0008	4.04E-10	decreasing	0
<i>PCDH18</i>	Caudate	1.34E-09	-0.00073	1.63E-08	decreasing	1
<i>PCDH8</i>	Caudate	2.58E-08	0.000656	2.58E-06	increasing	0
<i>PCDHB13</i>	Caudate	5.55E-09	-0.00056	6.22E-05	decreasing	1
<i>PCDHB14</i>	Caudate	6.43E-14	-0.00072	5.74E-08	decreasing	0
<i>PCED1A</i>	Caudate	1.75E-07	0.000378	0.008667	other	0
<i>PCGF3</i>	Caudate	9.14E-08	-0.00068	2.80E-07	decreasing	0
<i>PCGF5</i>	Caudate	3.40E-12	-0.00037	0.01387	other	0
<i>PCK1</i>	Caudate	1.47E-11	0.000818	2.59E-10	increasing	0
<i>PCMTD1</i>	Caudate	6.90E-12	-0.00083	7.25E-11	decreasing	0
<i>PCNP</i>	Caudate	5.44E-11	-0.00049	0.000636	other	0
<i>PCNT</i>	Caudate	2.03E-12	0.000855	1.14E-11	increasing	0
<i>PCP4</i>	Caudate	3.26E-08	-0.00043	0.002282	other	0
<i>PCP4L1</i>	Caudate	1.54E-07	-0.00049	0.000565	other	0
<i>PCSK6</i>	Caudate	5.23E-10	0.000759	1.14E-08	increasing	0
<i>PCSK7</i>	Caudate	2.57E-11	0.000282	0.062089	other	0
<i>PCYT2</i>	Caudate	5.22E-10	0.000707	2.41E-07	increasing	0
<i>PDCD11</i>	Caudate	5.76E-11	1.69E-05	0.910338	other	0
<i>PDCD6IP</i>	Caudate	2.21E-09	-0.00048	0.000648	other	0
<i>PDDC1</i>	Caudate	5.54E-10	0.00027	0.069996	other	0
<i>PDE10A</i>	Caudate	2.65E-08	-0.00076	1.05E-08	decreasing	0
<i>PDE12</i>	Caudate	8.37E-07	-0.00074	3.24E-08	decreasing	0
<i>PDE2A</i>	Caudate	1.22E-08	-0.0003	0.04641	other	0
<i>PDE3A</i>	Caudate	4.12E-09	-0.00076	6.64E-09	decreasing	1
<i>PDE3B</i>	Caudate	2.16E-08	-0.00068	4.91E-07	decreasing	0
<i>PDE4B</i>	Caudate	2.53E-08	-0.00011	0.449119	other	0
<i>PDE8A</i>	Caudate	5.12E-14	0.000803	1.79E-10	increasing	0
<i>PDF</i>	Caudate	2.00E-10	0.000498	0.000499	other	0
<i>PDGFA</i>	Caudate	1.55E-07	8.70E-06	0.953305	other	0
<i>PDGFRA</i>	Caudate	2.37E-14	-0.00083	1.81E-11	decreasing	0
<i>PDHX</i>	Caudate	8.37E-07	-0.00073	3.90E-08	decreasing	0
<i>PDIA2</i>	Caudate	8.50E-09	0.000563	3.57E-05	increasing	0
<i>PDK1</i>	Caudate	2.52E-08	0.000711	1.73E-07	increasing	0
<i>PDK2</i>	Caudate	1.28E-08	0.000616	4.14E-06	increasing	0
<i>PDXK</i>	Caudate	6.52E-10	0.000802	2.54E-10	increasing	0
<i>PDYN</i>	Caudate	8.19E-08	-0.00026	0.084733	other	0
<i>PDZD11</i>	Caudate	5.18E-10	-0.0001	0.498739	other	0
<i>PDZD4</i>	Caudate	1.31E-07	0.000321	0.033339	other	0
<i>PDZD8</i>	Caudate	1.07E-09	-0.00056	0.000112	other	0
<i>PEBP1</i>	Caudate	3.55E-08	0.000577	3.91E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PELI1</i>	Caudate	1.81E-09	-0.00033	0.023285	other	0
<i>PELI3</i>	Caudate	1.01E-11	0.000572	3.76E-05	increasing	0
<i>PELP1</i>	Caudate	9.60E-08	0.000767	4.53E-09	increasing	0
<i>PEMT</i>	Caudate	3.49E-11	1.92E-05	0.89872	other	0
<i>PEX13</i>	Caudate	4.70E-07	-0.0007	1.07E-07	decreasing	0
<i>PEX16</i>	Caudate	1.06E-09	0.000386	0.00884	other	0
<i>PEX26</i>	Caudate	5.04E-11	0.000761	1.04E-08	increasing	0
<i>PEX6</i>	Caudate	1.01E-07	0.000528	0.000124	other	0
<i>PFAS</i>	Caudate	6.57E-09	0.000516	0.000328	other	0
<i>PFKFB4</i>	Caudate	2.61E-11	0.000586	3.51E-05	increasing	0
<i>PFKL</i>	Caudate	1.63E-09	0.00059	3.43E-05	increasing	0
<i>PFKM</i>	Caudate	1.15E-08	0.000471	0.000862	other	1
<i>PFKP</i>	Caudate	1.11E-13	0.000745	3.20E-08	increasing	0
<i>PFN2</i>	Caudate	1.13E-12	-0.00071	1.79E-07	decreasing	0
<i>PGAM5</i>	Caudate	5.14E-10	0.000343	0.020804	other	0
<i>PGAP1</i>	Caudate	2.53E-07	-0.00062	8.90E-06	decreasing	0
<i>PGAP3</i>	Caudate	1.38E-07	0.000491	0.000599	other	0
<i>PGBD5</i>	Caudate	3.25E-14	0.000509	0.000234	other	0
<i>PGGT1B</i>	Caudate	3.62E-09	-0.00067	8.66E-07	decreasing	0
<i>PGP</i>	Caudate	6.80E-09	0.000546	0.000136	other	0
<i>PGPEP1</i>	Caudate	2.40E-13	0.000762	3.41E-09	increasing	0
<i>PGR</i>	Caudate	6.45E-08	-0.00061	1.75E-05	decreasing	0
<i>PGS1</i>	Caudate	6.97E-11	0.000561	9.40E-05	increasing	0
<i>PHC2</i>	Caudate	2.08E-10	0.000204	0.179136	other	0
<i>PHEX</i>	Caudate	1.45E-08	-0.00072	1.14E-07	decreasing	0
<i>PHF1</i>	Caudate	1.09E-10	0.000712	9.38E-08	increasing	0
<i>PHF14</i>	Caudate	2.62E-13	-0.00083	2.39E-11	decreasing	0
<i>PHF19</i>	Caudate	6.14E-09	0.000813	4.22E-10	increasing	0
<i>PHF20L1</i>	Caudate	1.76E-07	-0.00034	0.022596	other	0
<i>PHF21A</i>	Caudate	6.65E-13	0.000181	0.221285	other	0
<i>PHF3</i>	Caudate	1.06E-07	-0.0006	1.91E-05	decreasing	0
<i>PHF6</i>	Caudate	1.58E-07	-0.00075	1.79E-08	decreasing	0
<i>PHGDH</i>	Caudate	1.15E-08	0.000645	3.87E-06	increasing	0
<i>PHKG2</i>	Caudate	3.62E-08	0.000378	0.010308	other	0
<i>PHLDA3</i>	Caudate	5.09E-08	2.34E-05	0.877164	other	0
<i>PHLDB1</i>	Caudate	4.55E-11	0.000828	8.08E-11	increasing	0
<i>PHLPP1</i>	Caudate	3.26E-09	0.000771	1.27E-09	increasing	0
<i>PHRF1</i>	Caudate	4.48E-11	0.000667	1.55E-06	increasing	0
<i>PHTF2</i>	Caudate	1.31E-07	-0.00073	7.66E-08	decreasing	0
<i>PHYHD1</i>	Caudate	6.06E-07	0.000773	5.26E-09	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PHYHIP</i>	Caudate	1.04E-14	0.00081	1.06E-10	increasing	0
<i>PHYHIPL</i>	Caudate	7.36E-11	-0.00064	2.82E-06	decreasing	0
<i>PHYKPL</i>	Caudate	1.77E-07	0.000685	6.85E-07	increasing	0
<i>PI4KA</i>	Caudate	3.83E-06	0.000705	1.18E-07	increasing	0
<i>PIAS1</i>	Caudate	1.07E-09	-0.00023	0.118768	other	0
<i>PIAS2</i>	Caudate	1.67E-10	-0.0006	2.09E-05	decreasing	0
<i>PIAS4</i>	Caudate	6.26E-08	0.000264	0.075767	other	0
<i>PICK1</i>	Caudate	2.64E-08	0.000368	0.012666	other	0
<i>PIDD1</i>	Caudate	1.14E-07	0.000531	0.000111	other	1
<i>PIK3C3</i>	Caudate	4.70E-09	-0.00015	0.306723	other	0
<i>PIK3CA</i>	Caudate	9.55E-11	-0.00081	4.45E-10	decreasing	0
<i>PIKFYVE</i>	Caudate	6.37E-12	-0.00077	7.04E-09	decreasing	0
<i>PINK1</i>	Caudate	4.48E-08	0.000516	0.000364	other	0
<i>PIP4K2A</i>	Caudate	1.61E-20	0.000877	1.23E-13	increasing	0
<i>PIP4K2B</i>	Caudate	2.61E-13	0.000779	1.08E-09	increasing	0
<i>PIP4K2C</i>	Caudate	1.65E-08	0.000637	4.07E-06	increasing	0
<i>PIR</i>	Caudate	5.34E-08	0.00067	9.55E-07	increasing	0
<i>PITPNC1</i>	Caudate	2.24E-08	-0.00068	1.12E-06	decreasing	0
<i>PITPNM1</i>	Caudate	2.14E-11	0.000706	2.32E-07	increasing	0
<i>PITPNM3</i>	Caudate	1.21E-09	0.000703	2.22E-07	increasing	0
<i>PJA2</i>	Caudate	1.33E-09	-0.00037	0.008725	other	0
<i>PKD1</i>	Caudate	6.32E-12	0.000698	3.76E-07	increasing	0
<i>PKD1L2</i>	Caudate	6.77E-08	0.000376	0.010741	other	0
<i>PKN1</i>	Caudate	8.28E-12	0.00028	0.058816	other	0
<i>PKN2</i>	Caudate	1.69E-09	-0.00064	3.90E-06	decreasing	0
<i>PLA2G16</i>	Caudate	5.31E-14	0.000792	7.88E-10	increasing	0
<i>PLA2G4B</i>	Caudate	1.89E-08	0.000595	2.48E-05	increasing	0
<i>PLA2G6</i>	Caudate	6.84E-11	0.000807	5.39E-10	increasing	0
<i>PLAC9</i>	Caudate	2.01E-09	0.000127	0.38556	other	0
<i>PLB1</i>	Caudate	1.62E-08	0.000663	9.62E-07	increasing	0
<i>PLCB1</i>	Caudate	8.57E-09	-0.00047	0.001139	other	0
<i>PLCB4</i>	Caudate	1.02E-09	-0.00077	5.83E-09	decreasing	0
<i>PLCG1</i>	Caudate	1.60E-12	0.000479	0.00059	other	0
<i>PLCXD3</i>	Caudate	4.79E-10	-0.00069	3.05E-07	decreasing	0
<i>PLD1</i>	Caudate	5.92E-06	0.000703	1.69E-07	increasing	0
<i>PLD2</i>	Caudate	4.45E-08	0.00071	1.02E-07	increasing	0
<i>PLD3</i>	Caudate	3.63E-10	0.000498	0.000467	other	0
<i>PLD5</i>	Caudate	5.79E-14	-0.00071	1.14E-07	decreasing	0
<i>PLD6</i>	Caudate	6.18E-07	0.00077	6.66E-09	increasing	0
<i>PLEC</i>	Caudate	2.72E-11	0.000659	2.18E-06	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PLEK</i>	Caudate	2.12E-07	0.000755	8.58E-09	increasing	0
<i>PLEKHA2</i>	Caudate	1.58E-09	0.000771	6.49E-10	increasing	0
<i>PLEKHA3</i>	Caudate	4.87E-15	-0.0002	0.176571	other	0
<i>PLEKHA5</i>	Caudate	9.20E-10	-0.00059	2.97E-05	decreasing	0
<i>PLEKHB1</i>	Caudate	1.21E-14	0.00075	2.82E-09	increasing	0
<i>PLEKHF1</i>	Caudate	7.47E-09	0.000723	5.84E-08	increasing	0
<i>PLEKHF2</i>	Caudate	1.08E-06	-0.00068	2.29E-07	decreasing	0
<i>PLEKHG3</i>	Caudate	3.38E-14	0.000866	3.89E-12	increasing	0
<i>PLEKHG4</i>	Caudate	2.69E-11	0.000814	2.12E-10	increasing	0
<i>PLEKHH1</i>	Caudate	2.26E-16	0.000871	2.38E-13	increasing	0
<i>PLEKHJ1</i>	Caudate	9.53E-09	0.000123	0.417047	other	0
<i>PLEKHM2</i>	Caudate	1.31E-09	0.000814	2.46E-10	increasing	0
<i>PLEKHO2</i>	Caudate	9.30E-08	0.000568	4.44E-05	increasing	0
<i>PLGRKT</i>	Caudate	1.12E-08	-0.0007	1.43E-07	decreasing	0
<i>PLIN3</i>	Caudate	9.69E-12	0.000531	0.000155	other	0
<i>PLIN4</i>	Caudate	6.86E-06	0.000727	7.31E-08	increasing	0
<i>PLK2</i>	Caudate	3.89E-08	-0.00067	6.09E-07	decreasing	0
<i>PLL P</i>	Caudate	1.62E-08	0.000682	3.36E-07	increasing	0
<i>PLN</i>	Caudate	8.80E-10	-0.00077	8.18E-09	decreasing	0
<i>PLXNB1</i>	Caudate	1.08E-08	0.00073	6.12E-08	increasing	0
<i>PLXNB3</i>	Caudate	7.53E-08	0.00073	7.42E-08	increasing	0
<i>PMEL</i>	Caudate	5.31E-16	0.000886	1.52E-13	increasing	0
<i>PMEPA1</i>	Caudate	5.60E-08	-0.00074	3.48E-08	decreasing	0
<i>PMF1</i>	Caudate	3.16E-08	0.000307	0.039825	other	0
<i>PMP22</i>	Caudate	2.11E-10	0.000599	1.73E-05	increasing	0
<i>PMPCA</i>	Caudate	3.06E-08	0.000439	0.002537	other	0
<i>PMVK</i>	Caudate	2.39E-07	0.000707	2.36E-07	increasing	0
<i>PNCK</i>	Caudate	1.09E-09	0.000782	2.79E-09	increasing	0
<i>PNISR</i>	Caudate	9.86E-08	-0.00065	2.38E-06	decreasing	0
<i>PNKD</i>	Caudate	3.25E-14	0.000688	1.22E-07	increasing	0
<i>PNKP</i>	Caudate	2.15E-07	0.000632	5.35E-06	increasing	0
<i>PNMA2</i>	Caudate	1.23E-07	0.000674	7.99E-07	increasing	1
<i>PNMA3</i>	Caudate	3.35E-09	0.000359	0.011863	other	0
<i>PNMAL1</i>	Caudate	2.63E-12	0.000402	0.006463	other	0
<i>PNMAL2</i>	Caudate	1.33E-10	0.000623	9.82E-06	increasing	0
<i>PNPLA2</i>	Caudate	9.71E-11	0.000779	2.17E-09	increasing	0
<i>PNPLA6</i>	Caudate	1.28E-10	0.000673	1.25E-06	increasing	0
<i>PNRC1</i>	Caudate	8.82E-09	0.000431	0.002724	other	0
<i>PNRC2</i>	Caudate	2.08E-07	-0.00055	0.000122	other	0
<i>PODXL2</i>	Caudate	1.45E-12	-0.0001	0.497241	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>POLA1</i>	Caudate	7.00E-08	-0.00065	1.70E-06	decreasing	0
<i>POLD2</i>	Caudate	1.63E-07	-4.81E-06	0.974607	other	0
<i>POLG</i>	Caudate	7.40E-11	0.000497	0.000626	other	0
<i>POLG2</i>	Caudate	2.15E-08	-0.00027	0.072643	other	0
<i>POLK</i>	Caudate	4.78E-09	-0.00035	0.020041	other	0
<i>POLR3E</i>	Caudate	1.17E-11	0.000379	0.009079	other	0
<i>POLR3H</i>	Caudate	1.23E-13	-6.69E-05	0.652366	other	0
<i>POLRMT</i>	Caudate	1.33E-11	0.000504	0.000535	other	0
<i>POMT2</i>	Caudate	7.02E-08	0.000495	0.000695	other	0
<i>POPDC3</i>	Caudate	1.63E-15	0.000873	9.50E-13	increasing	0
<i>POU3F1</i>	Caudate	6.50E-08	3.15E-05	0.837424	other	0
<i>POU3F3</i>	Caudate	2.41E-11	0.000248	0.091503	other	0
<i>POU3F4</i>	Caudate	4.82E-08	0.000508	0.000454	other	0
<i>PPAP2C</i>	Caudate	1.33E-11	0.000794	3.59E-10	increasing	0
<i>PPAPDC3</i>	Caudate	3.21E-11	0.000223	0.142317	other	0
<i>PPEF1</i>	Caudate	1.28E-07	-0.00062	3.91E-06	decreasing	0
<i>PPFIA2</i>	Caudate	1.09E-11	-0.00079	4.45E-10	decreasing	0
<i>PPFIA3</i>	Caudate	4.99E-12	5.39E-05	0.719843	other	0
<i>PPFIA4</i>	Caudate	1.69E-14	0.000808	1.22E-10	increasing	0
<i>PPFIBP2</i>	Caudate	9.16E-10	0.000739	1.44E-08	increasing	0
<i>PPIP5K1</i>	Caudate	1.02E-09	0.000728	1.16E-08	increasing	0
<i>PPL</i>	Caudate	2.31E-07	0.000741	3.31E-08	increasing	0
<i>PPM1A</i>	Caudate	3.14E-11	-0.00056	5.86E-05	decreasing	0
<i>PPM1B</i>	Caudate	1.70E-13	-0.00075	1.72E-08	decreasing	0
<i>PPM1E</i>	Caudate	2.47E-08	-0.00047	0.00094	other	0
<i>PPM1F</i>	Caudate	4.64E-10	0.000772	6.76E-09	increasing	0
<i>PPM1K</i>	Caudate	2.45E-07	0.000593	2.30E-05	increasing	0
<i>PPM1M</i>	Caudate	6.37E-13	0.000723	4.36E-08	increasing	0
<i>PPOX</i>	Caudate	1.34E-07	0.000226	0.129306	other	0
<i>PPP1R12C</i>	Caudate	5.69E-11	0.000637	3.44E-06	increasing	0
<i>PPP1R14A</i>	Caudate	4.88E-10	0.000753	1.82E-08	increasing	0
<i>PPP1R14B</i>	Caudate	4.14E-09	7.28E-05	0.619755	other	0
<i>PPP1R16A</i>	Caudate	1.10E-08	0.000296	0.048907	other	1
<i>PPP1R1B</i>	Caudate	1.52E-08	-0.0001	0.501057	other	0
<i>PPP1R26</i>	Caudate	1.18E-07	0.000451	0.002055	other	0
<i>PPP1R37</i>	Caudate	1.26E-10	0.000535	0.0002	other	0
<i>PPP1R3C</i>	Caudate	7.87E-08	-8.56E-05	0.568674	other	0
<i>PPP1R3E</i>	Caudate	2.69E-08	0.000775	5.31E-09	increasing	0
<i>PPP1R3F</i>	Caudate	3.32E-08	0.000495	0.000687	other	0
<i>PPP2CA</i>	Caudate	1.59E-05	-0.00071	1.30E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PPP2R1A</i>	Caudate	2.19E-09	-3.95E-05	0.794753	other	0
<i>PPP2R4</i>	Caudate	1.06E-08	-1.16E-05	0.939845	other	0
<i>PPP2R5B</i>	Caudate	2.65E-09	0.000532	0.000214	other	0
<i>PPP2R5E</i>	Caudate	5.35E-09	-0.00074	3.37E-08	decreasing	0
<i>PPP3R1</i>	Caudate	1.58E-12	-0.00016	0.283824	other	0
<i>PPP4C</i>	Caudate	4.84E-08	8.50E-05	0.575878	other	0
<i>PPP5C</i>	Caudate	5.33E-11	-3.58E-05	0.811541	other	0
<i>PPP6C</i>	Caudate	1.53E-09	-0.00028	0.058545	other	0
<i>PPP6R2</i>	Caudate	1.58E-08	9.41E-05	0.536701	other	0
<i>PQLC2</i>	Caudate	8.07E-09	0.000172	0.248958	other	0
<i>PREX1</i>	Caudate	1.75E-07	0.000258	0.08908	other	0
<i>PREX2</i>	Caudate	6.34E-08	-0.00032	0.025378	other	0
<i>PRICKLE1</i>	Caudate	2.45E-12	-0.00069	3.53E-07	decreasing	0
<i>PRICKLE2</i>	Caudate	8.14E-14	-0.00075	1.11E-08	decreasing	0
<i>PRKAA2</i>	Caudate	6.59E-11	-0.00083	1.77E-11	decreasing	0
<i>PRKACB</i>	Caudate	6.50E-08	-0.00064	4.57E-06	decreasing	0
<i>PRKAG2</i>	Caudate	2.66E-12	-0.00031	0.030552	other	0
<i>PRKAR1B</i>	Caudate	6.35E-08	0.000182	0.230575	other	1
<i>PRKAR2B</i>	Caudate	4.37E-09	-0.00073	2.57E-08	decreasing	0
<i>PRKCB</i>	Caudate	2.36E-07	-0.00049	0.000573	other	0
<i>PRKCDBP</i>	Caudate	7.37E-10	0.000576	3.28E-05	increasing	0
<i>PRKCE</i>	Caudate	1.60E-13	-0.00081	2.86E-10	decreasing	0
<i>PRKCQ</i>	Caudate	2.95E-20	0.000886	9.73E-14	increasing	0
<i>PRKCSH</i>	Caudate	1.33E-08	0.000527	0.000278	other	0
<i>PRMT7</i>	Caudate	2.38E-09	0.000169	0.270138	other	0
<i>PRPF19</i>	Caudate	4.28E-12	0.000841	1.83E-12	increasing	0
<i>PRPF38B</i>	Caudate	2.02E-08	-0.00017	0.264548	other	0
<i>PRPF40B</i>	Caudate	2.29E-08	0.000245	0.095599	other	0
<i>PRPF4B</i>	Caudate	4.69E-08	-0.00071	1.56E-07	decreasing	0
<i>PRPF6</i>	Caudate	6.39E-11	0.000711	1.94E-07	increasing	0
<i>PRPS1</i>	Caudate	1.47E-09	-1.56E-05	0.916863	other	0
<i>PRR13</i>	Caudate	6.47E-11	0.000248	0.087338	other	0
<i>PRR18</i>	Caudate	1.04E-08	0.000739	2.47E-08	increasing	0
<i>PRR24</i>	Caudate	1.13E-09	0.000327	0.024594	other	0
<i>PRR5</i>	Caudate	9.89E-08	0.000176	0.243871	other	0
<i>PRR5L</i>	Caudate	8.43E-14	0.000874	2.90E-12	increasing	0
<i>PRRG3</i>	Caudate	4.27E-06	0.00071	2.06E-07	increasing	0
<i>PRRT2</i>	Caudate	6.17E-09	0.000339	0.020827	other	0
<i>PRSS2</i>	Caudate	1.95E-08	0.000724	4.77E-08	increasing	0
<i>PRSS21</i>	Caudate	5.77E-11	0.00081	3.02E-10	increasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PRSS41</i>	Caudate	2.27E-09	0.000776	4.45E-09	increasing	0
<i>PRUNE2</i>	Caudate	2.74E-15	0.000871	2.58E-13	increasing	0
<i>PSD</i>	Caudate	6.49E-08	0.000594	2.80E-05	increasing	0
<i>PSMC5</i>	Caudate	1.90E-10	0.000132	0.373468	other	0
<i>PSMD12</i>	Caudate	5.80E-09	-0.00063	4.99E-06	decreasing	0
<i>PSME4</i>	Caudate	2.37E-09	-0.00077	4.28E-09	decreasing	0
<i>PSRC1</i>	Caudate	1.28E-07	0.000753	1.84E-08	increasing	0
<i>PTAR1</i>	Caudate	1.51E-07	-0.00072	5.78E-08	decreasing	0
<i>PTBP3</i>	Caudate	2.39E-07	-0.00066	1.77E-06	decreasing	0
<i>PTCD1</i>	Caudate	3.76E-08	0.000333	0.026589	other	0
<i>PTCHD1</i>	Caudate	1.07E-05	-0.0007	1.13E-07	decreasing	0
<i>PTCHD2</i>	Caudate	3.38E-12	0.000717	1.10E-07	increasing	0
<i>PTDSS2</i>	Caudate	1.99E-08	0.000323	0.024195	other	0
<i>PTEN</i>	Caudate	2.54E-13	-0.00085	4.17E-12	decreasing	0
<i>PTF1A</i>	Caudate	6.08E-13	0.000749	1.24E-08	increasing	0
<i>PTGDS</i>	Caudate	7.06E-10	0.000509	0.000311	other	0
<i>PTGER3</i>	Caudate	8.67E-08	-0.00057	4.32E-05	decreasing	0
<i>PTGES2</i>	Caudate	5.28E-09	0.000281	0.063666	other	0
<i>PTGES3</i>	Caudate	2.51E-13	-0.00011	0.470677	other	0
<i>PTGFRN</i>	Caudate	1.94E-09	-0.00033	0.02406	other	0
<i>PTN</i>	Caudate	1.17E-11	-0.00086	1.70E-12	decreasing	0
<i>PTOV1</i>	Caudate	1.13E-13	0.000691	4.66E-07	increasing	0
<i>PTP4A1</i>	Caudate	6.26E-08	-0.00068	8.42E-07	decreasing	0
<i>PTP4A3</i>	Caudate	6.24E-08	8.37E-05	0.577278	other	0
<i>PTPDC1</i>	Caudate	5.32E-13	0.000845	3.30E-12	increasing	0
<i>PTPN14</i>	Caudate	2.03E-05	0.000704	1.73E-07	increasing	0
<i>PTPN4</i>	Caudate	2.06E-08	-0.0008	1.08E-09	decreasing	0
<i>PTPN5</i>	Caudate	1.87E-14	0.000618	5.29E-06	increasing	0
<i>PTPN7</i>	Caudate	1.73E-11	0.000494	0.00049	other	0
<i>PTPRB</i>	Caudate	1.80E-08	0.000481	0.000544	other	0
<i>PTPRC</i>	Caudate	3.23E-07	-0.0007	2.29E-07	decreasing	0
<i>PTPRD</i>	Caudate	7.60E-08	-0.00063	7.02E-06	decreasing	0
<i>PTPRQ</i>	Caudate	3.80E-09	-0.00062	1.37E-05	decreasing	0
<i>PTPRT</i>	Caudate	1.06E-07	-0.00059	3.02E-05	decreasing	0
<i>PTPRU</i>	Caudate	1.34E-11	0.000518	0.000322	other	1
<i>PTPRZ1</i>	Caudate	1.51E-08	-0.00056	5.65E-05	decreasing	0
<i>PTRF</i>	Caudate	3.75E-08	0.000652	1.17E-06	increasing	0
<i>PUF60</i>	Caudate	1.07E-08	0.000356	0.015735	other	0
<i>PURB</i>	Caudate	9.49E-09	-0.00067	1.30E-06	decreasing	0
<i>PURG</i>	Caudate	2.44E-10	-0.00079	1.36E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PUSL1</i>	Caudate	3.21E-10	0.000385	0.007492	other	0
<i>PVRL3</i>	Caudate	4.70E-15	-0.00079	3.91E-10	decreasing	0
<i>PWP2</i>	Caudate	3.48E-09	0.000673	1.22E-06	increasing	1
<i>PWWP2A</i>	Caudate	4.45E-07	-0.00072	1.02E-07	decreasing	0
<i>PWWP2B</i>	Caudate	1.32E-09	0.000446	0.002402	other	0
<i>PXK</i>	Caudate	1.95E-13	0.000726	4.22E-08	increasing	0
<i>PYCR1</i>	Caudate	1.15E-09	3.97E-05	0.795843	other	0
<i>PYGO1</i>	Caudate	2.94E-09	-0.00071	7.46E-08	decreasing	0
<i>QARS</i>	Caudate	2.05E-08	0.000249	0.091316	other	0
<i>QDPR</i>	Caudate	1.77E-14	0.000701	5.92E-08	increasing	1
<i>QSOX1</i>	Caudate	4.98E-12	0.000532	0.000203	other	1
<i>QSOX2</i>	Caudate	1.48E-10	4.42E-05	0.770481	other	0
<i>RAB11FIP2</i>	Caudate	2.41E-09	-0.00071	1.61E-07	decreasing	0
<i>RAB11FIP3</i>	Caudate	1.41E-08	0.000679	7.10E-07	increasing	0
<i>RAB11FIP4</i>	Caudate	2.16E-07	0.000426	0.003951	other	0
<i>RAB11FIP5</i>	Caudate	3.51E-10	0.000754	6.88E-09	increasing	0
<i>RAB18</i>	Caudate	8.82E-10	-0.00071	2.39E-07	decreasing	0
<i>RAB26</i>	Caudate	5.21E-09	0.000605	8.97E-06	increasing	0
<i>RAB27B</i>	Caudate	4.65E-08	-0.00079	1.35E-09	decreasing	0
<i>RAB35</i>	Caudate	4.05E-09	0.000152	0.313355	other	0
<i>RAB3C</i>	Caudate	4.09E-11	-0.00078	2.82E-09	decreasing	0
<i>RAB40C</i>	Caudate	8.68E-14	0.000246	0.102007	other	0
<i>RAB43</i>	Caudate	2.41E-09	0.000711	2.03E-07	increasing	0
<i>RAB5A</i>	Caudate	1.99E-06	-0.00074	3.21E-08	decreasing	0
<i>RAB5C</i>	Caudate	1.42E-07	0.000124	0.418782	other	0
<i>RAB6A</i>	Caudate	1.38E-10	-0.00032	0.026521	other	0
<i>RABAC1</i>	Caudate	3.50E-08	0.000378	0.011323	other	0
<i>RABEP2</i>	Caudate	3.39E-09	0.00039	0.008605	other	0
<i>RABGGTA</i>	Caudate	2.03E-11	0.000756	9.35E-09	increasing	0
<i>RABL6</i>	Caudate	1.16E-09	0.000715	9.03E-08	increasing	0
<i>RAD17</i>	Caudate	1.24E-08	-0.00062	1.17E-05	decreasing	1
<i>RAD21</i>	Caudate	1.90E-07	-0.00038	0.008302	other	0
<i>RAD23B</i>	Caudate	3.16E-11	-0.00062	1.20E-05	decreasing	0
<i>RAD51D</i>	Caudate	5.04E-08	0.000641	4.82E-06	increasing	0
<i>RAD54L2</i>	Caudate	8.37E-08	0.00062	1.03E-05	increasing	0
<i>RALA</i>	Caudate	4.94E-11	-0.00076	1.15E-08	decreasing	0
<i>RALGDS</i>	Caudate	1.58E-07	0.000707	2.22E-07	increasing	0
<i>RALGPS2</i>	Caudate	4.88E-11	-0.0008	5.88E-10	decreasing	0
<i>RANGAP1</i>	Caudate	3.80E-10	0.00066	1.11E-06	increasing	0
<i>RAP1A</i>	Caudate	2.12E-10	-0.00069	3.85E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>RAP2C</i>	Caudate	5.56E-14	-0.00045	0.00144	other	0
<i>RAPGEF5</i>	Caudate	5.21E-10	0.000689	2.70E-07	increasing	0
<i>RARRES2</i>	Caudate	1.18E-12	0.000734	1.87E-08	increasing	0
<i>RASA2</i>	Caudate	6.31E-09	-0.00065	3.42E-06	decreasing	0
<i>RASA3</i>	Caudate	4.05E-09	0.000227	0.125579	other	0
<i>RASD1</i>	Caudate	5.00E-09	0.000809	1.59E-10	increasing	0
<i>RASEF</i>	Caudate	9.62E-10	0.000727	8.19E-08	increasing	1
<i>RASGRF1</i>	Caudate	2.00E-10	-0.00068	7.47E-07	decreasing	0
<i>RASGRF2</i>	Caudate	7.22E-17	0.000851	5.91E-12	increasing	0
<i>RASGRP2</i>	Caudate	2.59E-07	0.000162	0.286995	other	0
<i>RASSF10</i>	Caudate	2.81E-09	-0.00058	1.64E-05	decreasing	0
<i>RASSF2</i>	Caudate	1.89E-09	0.000779	1.84E-09	increasing	0
<i>RASSF4</i>	Caudate	1.78E-08	0.000195	0.186097	other	0
<i>RB1</i>	Caudate	2.81E-09	-0.00071	2.36E-07	decreasing	0
<i>RB1CC1</i>	Caudate	1.80E-09	-0.00062	8.80E-06	decreasing	0
<i>RBBP8</i>	Caudate	1.89E-07	-0.00036	0.0139	other	0
<i>RBCK1</i>	Caudate	7.11E-09	0.000743	3.22E-08	increasing	0
<i>RBFOX3</i>	Caudate	1.74E-07	0.000686	3.95E-07	increasing	0
<i>RBM15</i>	Caudate	8.79E-08	-0.00018	0.234717	other	0
<i>RBM15B</i>	Caudate	1.53E-09	0.000123	0.4179	other	0
<i>RBM18</i>	Caudate	1.00E-05	-0.00073	7.49E-08	decreasing	0
<i>RBM20</i>	Caudate	7.82E-08	0.000762	1.15E-08	increasing	0
<i>RBM24</i>	Caudate	1.41E-07	-0.00068	7.46E-07	decreasing	0
<i>RBM25</i>	Caudate	1.22E-08	-0.00056	8.64E-05	decreasing	0
<i>RBM26</i>	Caudate	3.97E-14	-0.00061	1.46E-05	decreasing	0
<i>RBM27</i>	Caudate	1.16E-06	-0.00071	1.93E-07	decreasing	0
<i>RBM41</i>	Caudate	1.27E-07	-0.00075	2.10E-08	decreasing	0
<i>RBM42</i>	Caudate	1.77E-08	0.0004	0.007084	other	0
<i>RBM7</i>	Caudate	1.68E-07	-0.00064	4.39E-06	decreasing	0
<i>RBMS1</i>	Caudate	1.55E-07	-0.00073	5.52E-08	decreasing	0
<i>RBMS3</i>	Caudate	7.77E-06	-0.00071	1.21E-07	decreasing	0
<i>RBP3</i>	Caudate	7.97E-15	0.000801	1.42E-10	increasing	0
<i>RC3H2</i>	Caudate	9.52E-09	-0.00066	1.48E-06	decreasing	0
<i>RCAN2</i>	Caudate	1.74E-10	0.000415	0.003703	other	0
<i>RCBTB2</i>	Caudate	6.08E-05	-0.0007	2.19E-07	decreasing	0
<i>RCCD1</i>	Caudate	1.92E-08	0.000677	1.02E-06	increasing	0
<i>RCOR2</i>	Caudate	1.43E-08	0.00076	1.31E-08	increasing	0
<i>RDH13</i>	Caudate	2.58E-09	9.23E-05	0.543192	other	1
<i>RECQL5</i>	Caudate	2.50E-07	0.000609	1.72E-05	increasing	0
<i>REEP5</i>	Caudate	9.82E-06	-0.00071	1.80E-07	decreasing	1

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<i>RELL1</i>	Caudate	7.48E-08	-0.00055	0.000128	other	0
<i>RELT</i>	Caudate	1.81E-08	0.000495	0.000513	other	0
<i>REPIN1</i>	Caudate	4.09E-09	0.0005	0.000508	other	0
<i>REPS1</i>	Caudate	9.48E-08	0.000605	1.45E-05	increasing	0
<i>REV3L</i>	Caudate	1.77E-10	-0.00054	0.000108	other	0
<i>RFFL</i>	Caudate	1.63E-09	0.000481	0.000545	other	0
<i>RFNG</i>	Caudate	4.11E-09	0.000643	4.21E-06	increasing	0
<i>RFPL1</i>	Caudate	1.88E-07	0.000237	0.119142	other	0
<i>RFX3</i>	Caudate	5.11E-11	-0.00072	9.68E-08	decreasing	0
<i>RGR</i>	Caudate	1.41E-07	-0.0002	0.178259	other	0
<i>RGS11</i>	Caudate	2.27E-08	0.000737	3.34E-08	increasing	0
<i>RGS14</i>	Caudate	7.19E-12	0.000357	0.013616	other	0
<i>RGS17</i>	Caudate	1.71E-17	-0.00088	1.94E-13	decreasing	0
<i>RGS19</i>	Caudate	1.50E-07	0.000617	1.21E-05	increasing	0
<i>RGS7BP</i>	Caudate	1.89E-09	-0.00064	3.21E-06	decreasing	0
<i>RGS9</i>	Caudate	1.62E-08	-0.00063	7.68E-06	decreasing	1
<i>RHBDD2</i>	Caudate	5.94E-08	0.000211	0.146883	other	0
<i>RHBDD3</i>	Caudate	1.95E-09	0.000381	0.008929	other	0
<i>RHBDF1</i>	Caudate	1.73E-08	0.000741	3.98E-08	increasing	0
<i>RHBDL1</i>	Caudate	2.17E-10	0.000676	9.74E-07	increasing	0
<i>RHOA</i>	Caudate	2.88E-10	-0.00048	0.001113	other	0
<i>RHOG</i>	Caudate	1.57E-10	0.000654	1.76E-06	increasing	0
<i>RHOT2</i>	Caudate	2.16E-09	0.000604	2.09E-05	increasing	0
<i>RILP</i>	Caudate	1.02E-07	0.000691	3.97E-07	increasing	0
<i>RILPL1</i>	Caudate	1.83E-07	0.00065	1.56E-06	increasing	1
<i>RIMKLA</i>	Caudate	2.26E-12	-0.00082	3.28E-10	decreasing	0
<i>RIMKLB</i>	Caudate	7.17E-11	-0.00074	4.72E-09	decreasing	0
<i>RIMS3</i>	Caudate	5.54E-06	0.000741	4.09E-08	increasing	0
<i>RIMS4</i>	Caudate	1.65E-10	0.000107	0.481263	other	0
<i>RIN1</i>	Caudate	2.62E-09	0.000707	1.74E-07	increasing	0
<i>RLTPR</i>	Caudate	3.40E-09	0.000824	1.11E-10	increasing	0
<i>RMND5B</i>	Caudate	4.26E-09	0.000329	0.027899	other	0
<i>RNASE6</i>	Caudate	3.37E-06	-0.00072	1.08E-07	decreasing	0
<i>RND2</i>	Caudate	4.57E-08	0.000734	3.07E-08	increasing	0
<i>RNF112</i>	Caudate	1.39E-08	0.000488	0.000581	other	0
<i>RNF125</i>	Caudate	6.65E-09	0.000723	2.77E-08	increasing	0
<i>RNF130</i>	Caudate	1.63E-11	0.000689	5.74E-07	increasing	0
<i>RNF138</i>	Caudate	8.07E-11	-0.00077	7.50E-10	decreasing	0
<i>RNF152</i>	Caudate	4.94E-13	-0.00076	5.12E-09	decreasing	0
<i>RNF165</i>	Caudate	2.79E-12	-0.00081	1.09E-10	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>RNF2</i>	Caudate	5.01E-07	-0.00073	3.76E-08	decreasing	0
<i>RNF215</i>	Caudate	3.67E-08	0.000403	0.006395	other	0
<i>RNF26</i>	Caudate	1.78E-07	0.000439	0.001766	other	0
<i>RNF31</i>	Caudate	8.09E-09	0.000388	0.008868	other	0
<i>RNF6</i>	Caudate	3.36E-10	-0.00049	0.000611	other	0
<i>RNH1</i>	Caudate	1.22E-07	0.000592	3.20E-05	increasing	0
<i>RNPC3</i>	Caudate	3.85E-10	-0.00022	0.14825	other	0
<i>RNPS1</i>	Caudate	2.05E-08	0.00012	0.43467	other	0
<i>ROBO1</i>	Caudate	1.01E-13	-0.00076	3.14E-09	decreasing	0
<i>ROBO2</i>	Caudate	3.23E-18	-0.00088	4.59E-13	decreasing	0
<i>ROCK1</i>	Caudate	1.60E-09	-0.00036	0.01432	other	0
<i>ROCK2</i>	Caudate	7.54E-09	-0.00043	0.002754	other	0
<i>ROGDI</i>	Caudate	1.81E-11	0.000668	5.32E-07	increasing	0
<i>RORA</i>	Caudate	2.54E-09	-0.00076	1.10E-08	decreasing	0
<i>RP2</i>	Caudate	3.38E-09	-0.0007	2.97E-07	decreasing	0
<i>RPAP3</i>	Caudate	1.95E-07	-0.00073	3.56E-08	decreasing	0
<i>RPGRIP1L</i>	Caudate	1.58E-07	-0.0007	3.75E-07	decreasing	0
<i>RPL13A</i>	Caudate	1.31E-07	0.000247	0.09774	other	0
<i>RPL36</i>	Caudate	9.05E-11	0.000107	0.482017	other	0
<i>RPP25</i>	Caudate	2.34E-13	0.00028	0.058144	other	0
<i>RPS15</i>	Caudate	4.24E-08	0.000369	0.013202	other	0
<i>RPS19</i>	Caudate	2.70E-08	0.000341	0.022315	other	0
<i>RPS6KA1</i>	Caudate	4.80E-12	0.000748	1.01E-08	increasing	0
<i>RPS6KA2</i>	Caudate	3.25E-09	0.000528	0.000261	other	0
<i>RPS6KA4</i>	Caudate	1.34E-14	0.000702	9.15E-08	increasing	0
<i>RPS6KB2</i>	Caudate	8.51E-08	0.000183	0.229462	other	0
<i>RPUSD1</i>	Caudate	4.39E-08	0.000483	0.000871	other	0
<i>RRAS2</i>	Caudate	7.04E-18	-0.00088	4.27E-13	decreasing	0
<i>RRBP1</i>	Caudate	4.14E-08	0.0003	0.0458	other	0
<i>RRP1</i>	Caudate	1.06E-08	0.000683	7.73E-07	increasing	0
<i>RRP8</i>	Caudate	9.38E-10	0.000793	1.22E-09	increasing	0
<i>RSAD1</i>	Caudate	5.55E-17	0.000879	9.82E-13	increasing	0
<i>RSBN1</i>	Caudate	2.20E-08	-0.00071	1.37E-07	decreasing	0
<i>RTEL1</i>	Caudate	1.14E-09	0.000563	7.62E-05	increasing	0
<i>RTKN</i>	Caudate	1.18E-12	0.000815	2.58E-10	increasing	0
<i>RTKN2</i>	Caudate	2.63E-09	-0.00073	3.29E-08	decreasing	0
<i>RTN3</i>	Caudate	2.19E-08	-0.00044	0.002315	other	0
<i>RUNDC3A</i>	Caudate	6.17E-09	0.000493	0.000508	other	0
<i>RUNDC3B</i>	Caudate	1.07E-09	-0.00064	3.38E-06	decreasing	0
<i>RWDD4</i>	Caudate	5.88E-06	-0.00071	1.56E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>RXRA</i>	Caudate	3.22E-08	0.000607	1.37E-05	increasing	0
<i>RXRG</i>	Caudate	1.63E-11	-0.00075	1.15E-08	decreasing	0
<i>RYBP</i>	Caudate	1.22E-14	-0.00088	5.44E-13	decreasing	0
<i>RYR1</i>	Caudate	1.27E-16	0.000834	4.06E-11	increasing	0
<i>S100A1</i>	Caudate	7.88E-09	0.000118	0.420861	other	0
<i>S1PR3</i>	Caudate	1.20E-07	-0.00048	0.000807	other	1
<i>S1PR5</i>	Caudate	1.56E-20	0.000869	5.61E-13	increasing	0
<i>SAC3D1</i>	Caudate	2.19E-09	0.000419	0.002979	other	0
<i>SAFB2</i>	Caudate	3.93E-08	0.0005	0.000554	other	0
<i>SAP25</i>	Caudate	1.06E-09	0.000828	5.02E-11	increasing	0
<i>SART1</i>	Caudate	7.57E-11	0.000535	0.000207	other	0
<i>SAV1</i>	Caudate	2.43E-07	-0.00073	8.98E-08	decreasing	0
<i>SBF1</i>	Caudate	5.03E-11	0.000535	0.000211	other	0
<i>SBNO1</i>	Caudate	1.08E-09	-0.00052	0.000309	other	0
<i>SC5D</i>	Caudate	3.42E-12	-0.00074	4.34E-08	decreasing	0
<i>SCAF1</i>	Caudate	9.60E-09	0.000744	2.56E-08	increasing	0
<i>SCAI</i>	Caudate	5.48E-07	-0.00075	1.99E-08	decreasing	0
<i>SCAND1</i>	Caudate	1.84E-09	0.000316	0.035732	other	0
<i>SCAP</i>	Caudate	2.59E-11	8.10E-05	0.587587	other	0
<i>SCARB1</i>	Caudate	5.10E-08	0.00064	1.37E-06	increasing	0
<i>SCARF1</i>	Caudate	2.20E-09	0.000698	3.68E-07	increasing	0
<i>SCARF2</i>	Caudate	7.55E-12	0.000655	2.38E-06	increasing	0
<i>SCD</i>	Caudate	1.52E-09	0.000605	9.06E-06	increasing	0
<i>SCFD1</i>	Caudate	4.54E-06	-0.00073	5.59E-08	decreasing	0
<i>SCG3</i>	Caudate	4.70E-09	-0.00037	0.009566	other	0
<i>SCGB1C1</i>	Caudate	1.09E-08	0.000782	1.67E-09	increasing	0
<i>SCGB3A1</i>	Caudate	3.05E-07	0.000758	2.05E-09	increasing	0
<i>SCN1B</i>	Caudate	3.56E-20	0.000838	6.19E-12	increasing	0
<i>SCN3A</i>	Caudate	3.86E-10	-0.00079	6.82E-10	decreasing	0
<i>SCN4B</i>	Caudate	2.42E-07	0.000282	0.053929	other	1
<i>SCP2</i>	Caudate	2.64E-08	-0.00069	6.19E-07	decreasing	0
<i>SCRIB</i>	Caudate	1.61E-12	0.000728	6.51E-08	increasing	0
<i>SCRN3</i>	Caudate	1.87E-07	-0.00073	6.10E-08	decreasing	0
<i>SCXB</i>	Caudate	1.08E-06	0.000712	1.47E-07	increasing	0
<i>SCYL2</i>	Caudate	1.05E-10	-0.00078	2.41E-09	decreasing	0
<i>SDCBP2</i>	Caudate	4.17E-08	0.000702	3.01E-07	increasing	0
<i>SDF2L1</i>	Caudate	1.45E-08	0.000678	6.24E-07	increasing	0
<i>SDHC</i>	Caudate	3.21E-09	-0.00039	0.007885	other	1
<i>SDK2</i>	Caudate	1.62E-07	0.000197	0.188669	other	0
<i>SEC14L1</i>	Caudate	5.61E-08	0.000725	2.45E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SEC14L5</i>	Caudate	2.27E-09	0.000764	2.10E-09	increasing	0
<i>SEC24C</i>	Caudate	1.33E-07	0.0004	0.006934	other	0
<i>SEC31B</i>	Caudate	5.14E-08	0.000791	1.40E-09	increasing	0
<i>SEC61A1</i>	Caudate	1.64E-12	-0.0002	0.181692	other	0
<i>SEC62</i>	Caudate	7.04E-08	-0.00047	0.001131	other	0
<i>SEMA3F</i>	Caudate	1.31E-10	8.08E-05	0.586304	other	0
<i>SEMA4C</i>	Caudate	2.33E-07	0.000607	1.81E-05	increasing	0
<i>SEMA4F</i>	Caudate	2.63E-08	0.000617	9.04E-06	increasing	0
<i>SEMA5B</i>	Caudate	9.63E-08	-0.00052	0.000192	other	0
<i>SEMA6B</i>	Caudate	8.19E-08	0.000404	0.00603	other	0
<i>SENP7</i>	Caudate	3.96E-09	-0.00079	3.45E-10	decreasing	0
<i>SEPHS1</i>	Caudate	6.30E-08	-0.0005	0.000275	other	0
<i>SEPP1</i>	Caudate	4.65E-09	0.000622	6.64E-06	increasing	0
<i>SEPT4</i>	Caudate	3.69E-21	0.000869	3.14E-13	increasing	0
<i>SEPT8</i>	Caudate	1.42E-14	0.000779	1.61E-09	increasing	0
<i>SERBP1</i>	Caudate	6.03E-11	-0.00078	1.14E-09	decreasing	0
<i>SERHL2</i>	Caudate	1.10E-07	0.000174	0.242972	other	0
<i>SERINC3</i>	Caudate	5.34E-08	-0.00048	0.00099	other	0
<i>SERPIND1</i>	Caudate	2.32E-09	0.000788	6.97E-10	increasing	0
<i>SERPINE2</i>	Caudate	1.37E-11	-0.00087	5.58E-12	decreasing	0
<i>SERPING1</i>	Caudate	8.26E-08	0.000525	0.000192	other	0
<i>SF3A2</i>	Caudate	1.28E-07	0.000526	0.000267	other	0
<i>SFMBT1</i>	Caudate	1.12E-10	-0.00078	2.81E-10	decreasing	0
<i>SFT2D3</i>	Caudate	1.02E-07	9.71E-05	0.515638	other	0
<i>SFXN3</i>	Caudate	2.29E-07	0.000593	2.92E-05	increasing	1
<i>SFXN4</i>	Caudate	1.55E-09	0.000666	1.47E-06	increasing	0
<i>SGCB</i>	Caudate	3.03E-09	-0.00076	8.19E-09	decreasing	0
<i>SGCD</i>	Caudate	5.33E-16	-0.00081	2.13E-10	decreasing	0
<i>SGCZ</i>	Caudate	5.92E-08	-0.00066	2.61E-06	decreasing	0
<i>SGOL2</i>	Caudate	4.19E-08	-0.00061	1.17E-05	decreasing	0
<i>SGPL1</i>	Caudate	3.12E-08	-0.00031	0.035173	other	0
<i>SGSM1</i>	Caudate	8.65E-11	0.00083	1.03E-10	increasing	0
<i>SGSM2</i>	Caudate	4.64E-09	0.000633	5.83E-06	increasing	0
<i>SGTB</i>	Caudate	1.83E-07	-0.00027	0.073581	other	0
<i>SH2B2</i>	Caudate	2.76E-08	4.47E-05	0.76479	other	0
<i>SH2D5</i>	Caudate	5.21E-16	0.000762	2.33E-09	increasing	0
<i>SH3BGRL3</i>	Caudate	1.37E-07	-0.00029	0.052025	other	0
<i>SH3BP2</i>	Caudate	1.58E-08	0.000171	0.250352	other	0
<i>SH3GLB2</i>	Caudate	1.96E-07	0.000532	0.000238	other	0
<i>SH3TC1</i>	Caudate	2.03E-08	0.000341	0.022091	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SH3TC2</i>	Caudate	4.97E-10	0.000793	3.91E-10	increasing	0
<i>SHARPIN</i>	Caudate	8.15E-09	0.000741	3.57E-08	increasing	1
<i>SHF</i>	Caudate	4.85E-09	0.000171	0.255302	other	0
<i>SHH</i>	Caudate	2.35E-07	0.000406	0.006194	other	0
<i>SHPRH</i>	Caudate	3.57E-13	-0.00083	1.38E-11	decreasing	0
<i>SHROOM1</i>	Caudate	2.62E-08	0.000792	9.65E-10	increasing	0
<i>SHROOM2</i>	Caudate	2.50E-07	-9.21E-06	0.950605	other	0
<i>SIGIRR</i>	Caudate	1.34E-09	0.000798	1.15E-09	increasing	1
<i>SIGLEC1</i>	Caudate	2.11E-06	0.000711	8.53E-08	increasing	0
<i>SIPA1L2</i>	Caudate	2.52E-15	-0.00082	6.52E-11	decreasing	0
<i>SIRT2</i>	Caudate	1.09E-08	-2.43E-05	0.872054	other	0
<i>SIRT3</i>	Caudate	3.17E-09	0.000647	2.93E-06	increasing	0
<i>SIRT7</i>	Caudate	9.39E-08	0.000488	0.000859	other	0
<i>SKAP1</i>	Caudate	7.13E-15	-0.00085	8.87E-12	decreasing	0
<i>SKIL</i>	Caudate	3.28E-13	-0.00086	6.06E-12	decreasing	0
<i>SLA</i>	Caudate	2.60E-09	-0.00066	7.93E-07	decreasing	0
<i>SLAIN1</i>	Caudate	4.02E-08	0.000608	1.18E-05	increasing	0
<i>SLAIN2</i>	Caudate	3.38E-12	-0.00061	1.42E-05	decreasing	0
<i>SLC10A3</i>	Caudate	2.06E-08	0.000578	3.97E-05	increasing	0
<i>SLC12A2</i>	Caudate	3.35E-09	0.000386	0.007776	other	0
<i>SLC12A3</i>	Caudate	4.42E-09	0.00053	0.000164	other	0
<i>SLC12A5</i>	Caudate	5.94E-10	0.000462	0.001691	other	0
<i>SLC12A8</i>	Caudate	2.38E-08	-0.00025	0.089704	other	0
<i>SLC12A9</i>	Caudate	1.32E-08	0.000374	0.011695	other	0
<i>SLC16A1</i>	Caudate	1.40E-13	-0.00082	6.01E-11	decreasing	0
<i>SLC16A11</i>	Caudate	7.30E-17	0.000863	1.95E-12	increasing	0
<i>SLC16A14</i>	Caudate	3.22E-10	-0.00075	1.04E-08	decreasing	0
<i>SLC16A4</i>	Caudate	8.48E-08	-0.00063	3.56E-06	decreasing	0
<i>SLC16A7</i>	Caudate	2.02E-10	-0.00079	1.66E-09	decreasing	0
<i>SLC17A2</i>	Caudate	1.10E-13	0.000822	1.01E-11	increasing	0
<i>SLC17A3</i>	Caudate	1.33E-11	0.000796	3.63E-10	increasing	0
<i>SLC17A5</i>	Caudate	8.00E-08	0.000569	5.37E-05	increasing	0
<i>SLC18A2</i>	Caudate	1.07E-07	-0.00075	1.45E-08	decreasing	0
<i>SLC1A6</i>	Caudate	2.76E-09	-0.0001	0.50221	other	0
<i>SLC20A2</i>	Caudate	3.24E-14	0.000814	4.74E-11	increasing	0
<i>SLC22A17</i>	Caudate	1.47E-09	0.000751	2.05E-08	increasing	0
<i>SLC24A3</i>	Caudate	2.48E-07	-0.00061	1.21E-05	decreasing	0
<i>SLC24A5</i>	Caudate	1.48E-08	-0.00077	7.47E-09	decreasing	0
<i>SLC25A1</i>	Caudate	4.29E-08	0.000577	5.40E-05	increasing	0
<i>SLC25A10</i>	Caudate	1.60E-10	0.000493	0.000707	other	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SLC25A13</i>	Caudate	6.55E-08	0.000734	3.35E-08	increasing	0
<i>SLC25A28</i>	Caudate	6.03E-08	0.000761	3.65E-09	increasing	0
<i>SLC25A34</i>	Caudate	1.95E-07	0.000652	3.05E-06	increasing	0
<i>SLC25A39</i>	Caudate	3.76E-10	0.000277	0.060228	other	0
<i>SLC25A40</i>	Caudate	7.34E-12	-0.00043	0.003443	other	0
<i>SLC25A42</i>	Caudate	5.60E-08	0.000743	3.61E-08	increasing	0
<i>SLC25A45</i>	Caudate	2.02E-12	0.000784	5.16E-10	increasing	0
<i>SLC26A1</i>	Caudate	3.99E-09	0.000735	5.57E-08	increasing	0
<i>SLC26A11</i>	Caudate	1.13E-11	0.000819	2.78E-10	increasing	0
<i>SLC26A5</i>	Caudate	2.72E-13	0.000847	9.92E-13	increasing	0
<i>SLC26A6</i>	Caudate	2.19E-07	0.000403	0.005897	other	0
<i>SLC27A1</i>	Caudate	1.92E-07	0.000603	1.96E-05	increasing	0
<i>SLC27A4</i>	Caudate	4.44E-09	0.00061	1.15E-05	increasing	0
<i>SLC29A2</i>	Caudate	3.75E-11	0.000415	0.004863	other	0
<i>SLC29A4</i>	Caudate	5.08E-08	0.000466	0.000863	other	0
<i>SLC2A12</i>	Caudate	1.91E-07	0.000532	0.000135	other	0
<i>SLC2A6</i>	Caudate	2.05E-11	0.000461	0.001657	other	0
<i>SLC2A8</i>	Caudate	5.61E-12	0.000474	0.000803	other	0
<i>SLC30A10</i>	Caudate	1.81E-08	-0.00073	1.92E-08	decreasing	0
<i>SLC30A4</i>	Caudate	2.91E-08	-0.00061	1.45E-05	decreasing	0
<i>SLC30A6</i>	Caudate	1.90E-07	-0.00073	5.74E-08	decreasing	0
<i>SLC30A7</i>	Caudate	2.95E-05	-0.00071	2.23E-07	decreasing	0
<i>SLC35A1</i>	Caudate	2.06E-06	-0.00071	1.32E-07	decreasing	0
<i>SLC35B2</i>	Caudate	2.61E-09	0.00033	0.02788	other	0
<i>SLC35B3</i>	Caudate	1.96E-10	-0.00084	3.39E-11	decreasing	0
<i>SLC35C2</i>	Caudate	6.51E-10	0.00016	0.288595	other	0
<i>SLC35D2</i>	Caudate	4.69E-06	0.000711	1.65E-07	increasing	0
<i>SLC35E1</i>	Caudate	1.75E-13	0.000465	0.001548	other	0
<i>SLC35F1</i>	Caudate	8.63E-16	-0.00086	3.20E-12	decreasing	1
<i>SLC35F3</i>	Caudate	1.50E-08	0.000496	0.000351	other	1
<i>SLC36A1</i>	Caudate	1.59E-09	-0.00069	3.10E-07	decreasing	0
<i>SLC38A1</i>	Caudate	4.70E-10	-0.00079	1.34E-09	decreasing	0
<i>SLC38A10</i>	Caudate	1.60E-07	0.000265	0.078611	other	0
<i>SLC39A11</i>	Caudate	4.45E-06	0.000724	1.02E-07	increasing	0
<i>SLC39A6</i>	Caudate	1.28E-08	-0.00062	1.12E-05	decreasing	0
<i>SLC40A1</i>	Caudate	1.05E-10	-0.00075	9.95E-09	decreasing	0
<i>SLC43A2</i>	Caudate	9.13E-09	9.68E-05	0.524475	other	0
<i>SLC44A1</i>	Caudate	9.92E-10	0.000726	2.35E-08	increasing	0
<i>SLC4A11</i>	Caudate	2.12E-15	0.000879	1.14E-12	increasing	0
<i>SLC4A3</i>	Caudate	7.15E-10	0.000601	1.68E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SLC4A4</i>	Caudate	1.73E-07	-0.00076	9.40E-09	decreasing	0
<i>SLC52A2</i>	Caudate	1.64E-07	1.50E-05	0.9208	other	0
<i>SLC5A11</i>	Caudate	3.14E-17	0.000848	9.29E-13	increasing	0
<i>SLC5A3</i>	Caudate	9.89E-09	0.000516	0.000325	other	0
<i>SLC6A1</i>	Caudate	9.83E-13	0.000181	0.229462	other	0
<i>SLC6A11</i>	Caudate	1.26E-09	0.000113	0.451416	other	0
<i>SLC6A6</i>	Caudate	1.46E-08	-0.0002	0.198838	other	0
<i>SLC6A8</i>	Caudate	4.34E-06	0.000721	9.35E-08	increasing	0
<i>SLC8A2</i>	Caudate	1.23E-08	2.82E-05	0.852191	other	0
<i>SLC8A3</i>	Caudate	4.33E-11	-0.00073	5.22E-08	decreasing	0
<i>SLC9A3</i>	Caudate	9.46E-11	0.000566	7.87E-05	increasing	0
<i>SLC9A5</i>	Caudate	1.23E-08	0.000721	5.73E-08	increasing	0
<i>SLC9A7</i>	Caudate	5.76E-16	0.000827	6.59E-12	increasing	0
<i>SLC9A8</i>	Caudate	1.28E-07	0.000287	0.049113	other	0
<i>SLCO1A2</i>	Caudate	8.37E-08	0.000507	0.000374	other	0
<i>SLCO1C1</i>	Caudate	4.18E-06	-0.00072	9.05E-08	decreasing	0
<i>SLCO5A1</i>	Caudate	1.67E-08	4.62E-05	0.759119	other	0
<i>SLITRK4</i>	Caudate	3.79E-11	-0.00076	1.04E-08	decreasing	0
<i>SMAD3</i>	Caudate	2.21E-08	4.52E-05	0.762465	other	0
<i>SMAD7</i>	Caudate	1.27E-07	-0.00046	0.001602	other	0
<i>SMARCA1</i>	Caudate	9.79E-08	-0.00076	3.13E-09	decreasing	0
<i>SMARCA4</i>	Caudate	5.76E-10	0.00038	0.009113	other	0
<i>SMARCA5</i>	Caudate	1.86E-08	-0.00024	0.111881	other	0
<i>SMARCE1</i>	Caudate	3.08E-08	-0.00065	2.92E-06	decreasing	0
<i>SMC4</i>	Caudate	1.91E-08	-0.00064	6.03E-06	decreasing	0
<i>SMC6</i>	Caudate	7.16E-11	-0.00074	2.17E-08	decreasing	0
<i>SMCR8</i>	Caudate	8.33E-07	0.000715	4.31E-08	increasing	0
<i>SMEK2</i>	Caudate	1.46E-11	-0.00082	5.32E-11	decreasing	0
<i>SMG5</i>	Caudate	1.74E-09	0.000451	0.002188	other	0
<i>SMG6</i>	Caudate	1.39E-08	0.000709	1.92E-07	increasing	0
<i>SMIM13</i>	Caudate	6.10E-06	-0.00071	2.45E-07	decreasing	0
<i>SMIM15</i>	Caudate	7.79E-07	-0.00071	2.39E-07	decreasing	0
<i>SMIM17</i>	Caudate	7.19E-09	-0.00079	3.62E-10	decreasing	0
<i>SMIM2</i>	Caudate	1.24E-09	0.000764	4.92E-09	increasing	0
<i>SMIM5</i>	Caudate	1.05E-09	0.000765	1.01E-08	increasing	0
<i>SMOC2</i>	Caudate	2.15E-07	-0.00044	0.002977	other	0
<i>SMPD3</i>	Caudate	2.57E-07	-0.00041	0.005719	other	0
<i>SMPD4</i>	Caudate	5.77E-08	0.000623	9.91E-06	increasing	0
<i>SMPDL3A</i>	Caudate	7.90E-10	-0.00073	9.82E-09	decreasing	0
<i>SMS</i>	Caudate	7.14E-07	-0.0007	1.57E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SMYD2</i>	Caudate	3.68E-08	9.43E-05	0.519741	other	0
<i>SNAP25</i>	Caudate	3.10E-14	9.23E-05	0.528526	other	0
<i>SNAP47</i>	Caudate	4.91E-08	0.000181	0.228318	other	0
<i>SNAPC4</i>	Caudate	2.16E-08	0.000663	1.48E-06	increasing	0
<i>SNED1</i>	Caudate	6.07E-12	0.00081	3.13E-10	increasing	0
<i>SNN</i>	Caudate	7.37E-10	0.00053	0.000176	other	0
<i>SNPH</i>	Caudate	5.25E-09	0.000743	8.37E-09	increasing	0
<i>SNRK</i>	Caudate	5.23E-07	-0.00073	3.09E-08	decreasing	0
<i>SNRNP70</i>	Caudate	8.30E-09	0.000376	0.009908	other	0
<i>SNTA1</i>	Caudate	3.63E-10	0.000677	8.53E-07	increasing	0
<i>SNTG2</i>	Caudate	2.98E-07	0.00076	1.37E-08	increasing	1
<i>SNX10</i>	Caudate	9.73E-08	-0.00076	1.43E-08	decreasing	0
<i>SNX13</i>	Caudate	6.18E-11	-0.00081	5.05E-10	decreasing	0
<i>SNX14</i>	Caudate	6.34E-11	-0.00059	3.28E-05	decreasing	0
<i>SNX2</i>	Caudate	4.10E-08	-0.00066	1.92E-06	decreasing	0
<i>SNX21</i>	Caudate	9.11E-12	0.000773	5.79E-09	increasing	0
<i>SNX30</i>	Caudate	4.98E-08	0.000771	6.61E-10	increasing	0
<i>SOCS2</i>	Caudate	8.01E-14	-0.00082	6.01E-11	decreasing	0
<i>SOCS4</i>	Caudate	9.43E-08	-0.00074	2.11E-08	decreasing	0
<i>SOCS5</i>	Caudate	4.85E-08	-0.00071	2.01E-07	decreasing	0
<i>SOGA1</i>	Caudate	1.09E-09	0.000269	0.070719	other	0
<i>SOGA3</i>	Caudate	4.51E-13	0.000456	0.001906	other	0
<i>SORT1</i>	Caudate	2.95E-09	0.000719	3.56E-08	increasing	0
<i>SOS2</i>	Caudate	3.24E-09	-0.00058	5.60E-05	decreasing	0
<i>SOWAHA</i>	Caudate	5.86E-15	0.000765	6.12E-09	increasing	0
<i>SOX10</i>	Caudate	2.30E-07	0.000644	4.33E-06	increasing	0
<i>SOX11</i>	Caudate	1.54E-13	-0.00078	8.98E-10	decreasing	0
<i>SOX4</i>	Caudate	8.80E-16	-0.00086	2.20E-13	decreasing	0
<i>SOX6</i>	Caudate	4.44E-11	-0.00071	8.39E-08	decreasing	0
<i>SOX8</i>	Caudate	1.04E-08	0.000509	0.0004	other	0
<i>SP4</i>	Caudate	3.73E-08	-0.00072	9.13E-08	decreasing	0
<i>SPAST</i>	Caudate	1.76E-08	-0.00067	6.22E-07	decreasing	0
<i>SPATA13</i>	Caudate	2.79E-10	0.000621	7.62E-06	increasing	1
<i>SPATA20</i>	Caudate	6.86E-09	0.000466	0.001449	other	0
<i>SPATA2L</i>	Caudate	4.48E-09	-0.00032	0.031834	other	0
<i>SPATA7</i>	Caudate	3.64E-08	-0.00052	0.000306	other	0
<i>SPCS2</i>	Caudate	7.12E-12	-0.0002	0.175045	other	0
<i>SPCS3</i>	Caudate	2.92E-09	-0.00079	1.84E-09	decreasing	0
<i>SPDEF</i>	Caudate	5.61E-08	0.000588	2.66E-05	increasing	0
<i>SPDYC</i>	Caudate	3.70E-07	0.000729	7.54E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SPECC1</i>	Caudate	2.07E-07	0.000551	7.10E-05	increasing	0
<i>SPICE1</i>	Caudate	4.15E-08	-0.00071	4.93E-08	decreasing	0
<i>SPIN1</i>	Caudate	8.71E-08	-0.00043	0.003458	other	0
<i>SPIN4</i>	Caudate	4.08E-09	-0.00053	0.000106	other	0
<i>SPIRE1</i>	Caudate	1.38E-07	0.000566	7.07E-05	increasing	0
<i>SPIRE2</i>	Caudate	2.83E-10	0.000307	0.03306	other	0
<i>SPNS1</i>	Caudate	4.22E-11	6.13E-05	0.682986	other	0
<i>SPNS2</i>	Caudate	9.41E-08	0.000489	0.00083	other	0
<i>SPOCK2</i>	Caudate	1.49E-09	0.000671	4.50E-07	increasing	0
<i>SPON1</i>	Caudate	1.60E-09	-0.00027	0.071856	other	0
<i>SPOPL</i>	Caudate	1.21E-10	-0.00023	0.125978	other	0
<i>SPP1</i>	Caudate	2.18E-12	0.000752	7.74E-09	increasing	0
<i>SPPL2B</i>	Caudate	1.38E-08	0.00048	0.000938	other	0
<i>SPRY3</i>	Caudate	9.32E-11	-7.98E-05	0.59352	other	0
<i>SPRYD3</i>	Caudate	3.75E-11	0.00071	3.54E-08	increasing	0
<i>SPSB1</i>	Caudate	2.67E-13	0.000843	9.34E-12	increasing	0
<i>SPSB3</i>	Caudate	6.48E-09	0.000433	0.002949	other	0
<i>SPTAN1</i>	Caudate	5.67E-10	0.000408	0.00598	other	0
<i>SPTB</i>	Caudate	1.31E-12	6.66E-05	0.657246	other	0
<i>SPTBN2</i>	Caudate	5.70E-12	0.000591	2.35E-05	increasing	0
<i>SPTBN4</i>	Caudate	1.60E-11	0.000586	3.73E-05	increasing	0
<i>SPTSSB</i>	Caudate	6.63E-06	-0.00072	1.30E-07	decreasing	0
<i>SQSTM1</i>	Caudate	1.07E-09	0.000703	2.82E-07	increasing	0
<i>SRA1</i>	Caudate	4.19E-09	0.000168	0.269608	other	0
<i>SRCIN1</i>	Caudate	6.20E-10	0.00063	7.68E-06	increasing	0
<i>SREBF1</i>	Caudate	7.25E-12	0.000836	5.30E-11	increasing	0
<i>SREK1</i>	Caudate	3.71E-11	-0.00079	6.92E-10	decreasing	0
<i>SREK1IP1</i>	Caudate	1.38E-09	-0.00076	1.50E-08	decreasing	0
<i>SRP72</i>	Caudate	5.10E-08	-0.0003	0.042149	other	0
<i>SRPK3</i>	Caudate	1.66E-09	0.000784	3.15E-09	increasing	0
<i>SRRM3</i>	Caudate	2.32E-07	0.000636	5.11E-06	increasing	0
<i>SRSF10</i>	Caudate	1.03E-08	-0.00065	3.27E-06	decreasing	0
<i>SS18L1</i>	Caudate	9.84E-12	0.0004	0.006628	other	0
<i>SSBP2</i>	Caudate	3.32E-15	-0.00083	1.63E-11	decreasing	0
<i>SSBP4</i>	Caudate	1.43E-09	0.000647	3.82E-06	increasing	0
<i>SSH3</i>	Caudate	2.91E-08	0.000661	1.96E-06	increasing	0
<i>SSR1</i>	Caudate	9.81E-10	-0.00061	1.24E-05	decreasing	0
<i>SSX2IP</i>	Caudate	1.84E-08	-0.00067	1.58E-06	decreasing	0
<i>ST18</i>	Caudate	4.70E-08	0.000733	2.06E-08	increasing	0
<i>ST3GAL2</i>	Caudate	1.08E-10	0.000196	0.19994	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ST8SIA2</i>	Caudate	7.89E-12	-0.00075	9.70E-09	decreasing	0
<i>STAB1</i>	Caudate	1.91E-07	-0.00057	4.32E-05	decreasing	0
<i>STAM</i>	Caudate	2.74E-09	-0.00041	0.005476	other	0
<i>STAM2</i>	Caudate	7.52E-08	-0.00059	3.00E-05	decreasing	0
<i>STAMBPL1</i>	Caudate	5.97E-08	0.00048	0.00079	other	0
<i>STARD10</i>	Caudate	3.80E-13	0.000641	1.93E-06	increasing	0
<i>STARD3</i>	Caudate	5.48E-10	0.000751	1.74E-08	increasing	0
<i>STAT2</i>	Caudate	1.82E-07	0.000276	0.066385	other	0
<i>STAT3</i>	Caudate	8.02E-10	0.000203	0.168726	other	0
<i>STAT4</i>	Caudate	7.26E-08	-0.0001	0.488534	other	0
<i>STAT5A</i>	Caudate	9.55E-10	0.000709	6.13E-08	increasing	0
<i>STAT6</i>	Caudate	4.08E-13	0.00074	1.34E-08	increasing	0
<i>STC1</i>	Caudate	1.86E-09	-0.00079	1.13E-09	decreasing	0
<i>STK11</i>	Caudate	7.76E-12	0.000538	0.000194	other	0
<i>STK11IP</i>	Caudate	1.48E-08	0.000598	2.17E-05	increasing	0
<i>STK39</i>	Caudate	1.63E-07	0.000354	0.015994	other	0
<i>STMN2</i>	Caudate	1.29E-12	-0.00083	1.16E-11	decreasing	0
<i>STMN3</i>	Caudate	1.60E-07	0.000322	0.032265	other	1
<i>STOML1</i>	Caudate	3.72E-08	8.09E-05	0.595345	other	0
<i>STRADB</i>	Caudate	3.68E-12	-0.0008	1.89E-10	decreasing	0
<i>STRBP</i>	Caudate	2.83E-10	-0.00076	8.10E-09	decreasing	1
<i>STRC</i>	Caudate	3.76E-13	0.000833	2.26E-11	increasing	0
<i>STRIP2</i>	Caudate	7.39E-10	-0.00074	2.92E-08	decreasing	1
<i>STRN</i>	Caudate	6.05E-10	-0.00084	2.45E-11	decreasing	0
<i>STRN4</i>	Caudate	4.07E-09	-6.39E-05	0.672532	other	0
<i>STT3B</i>	Caudate	1.95E-08	-0.00077	7.34E-09	decreasing	0
<i>STUB1</i>	Caudate	5.44E-08	0.000481	0.000956	other	0
<i>STX7</i>	Caudate	2.61E-06	-0.00071	2.18E-07	decreasing	0
<i>STXBP3</i>	Caudate	1.24E-08	9.60E-05	0.523504	other	0
<i>STXBP5</i>	Caudate	5.78E-07	-0.00071	1.71E-07	decreasing	0
<i>STXBP5L</i>	Caudate	2.40E-08	-0.00023	0.112936	other	0
<i>STXBP6</i>	Caudate	1.64E-11	-0.00084	5.94E-11	decreasing	0
<i>STYX</i>	Caudate	1.44E-09	-0.00075	3.04E-08	decreasing	0
<i>SUCO</i>	Caudate	2.32E-07	-0.00032	0.032096	other	0
<i>SUGP2</i>	Caudate	5.11E-10	0.000248	0.098183	other	0
<i>SUGT1</i>	Caudate	8.52E-10	-0.00051	0.000471	other	0
<i>SULT1E1</i>	Caudate	8.35E-11	-0.00073	3.18E-08	decreasing	0
<i>SUN2</i>	Caudate	1.92E-16	0.000847	9.82E-13	increasing	0
<i>SUPT20H</i>	Caudate	4.73E-10	-0.00026	0.085278	other	0
<i>SUPT5H</i>	Caudate	3.78E-08	0.000291	0.049936	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SURF4</i>	Caudate	4.75E-08	0.000559	0.000103	other	0
<i>SUV420H1</i>	Caudate	6.49E-10	-0.00065	1.88E-06	decreasing	0
<i>SUV420H2</i>	Caudate	2.39E-07	0.000263	0.076033	other	0
<i>SUZ12</i>	Caudate	6.87E-08	-0.0006	2.12E-05	decreasing	0
<i>SVEP1</i>	Caudate	1.02E-11	0.000834	5.15E-11	increasing	0
<i>SVIP</i>	Caudate	2.20E-07	3.57E-05	0.81245	other	0
<i>SWT1</i>	Caudate	9.92E-08	-8.87E-05	0.560996	other	0
<i>SYMPK</i>	Caudate	5.05E-09	0.000719	9.07E-08	increasing	0
<i>SYN2</i>	Caudate	4.55E-08	0.000772	6.64E-09	increasing	0
<i>SYNCRIP</i>	Caudate	1.18E-14	-0.00083	3.24E-11	decreasing	0
<i>SYNDIG1</i>	Caudate	8.16E-08	-0.00061	1.58E-05	decreasing	0
<i>SYNDIG1L</i>	Caudate	2.97E-10	-0.00073	7.44E-08	decreasing	0
<i>SYNE2</i>	Caudate	4.52E-09	-0.00062	6.19E-06	decreasing	0
<i>SYNGR3</i>	Caudate	1.20E-07	0.000491	0.000697	other	0
<i>SYNJ1</i>	Caudate	4.53E-08	-0.00012	0.401754	other	0
<i>SYNJ2</i>	Caudate	1.12E-08	0.000805	3.76E-10	increasing	0
<i>SYNJ2BP</i>	Caudate	1.45E-07	-0.00065	2.81E-06	decreasing	0
<i>SYNM</i>	Caudate	3.84E-12	0.000622	9.90E-06	increasing	1
<i>SYNPO</i>	Caudate	1.12E-09	0.000198	0.173118	other	0
<i>SYP</i>	Caudate	5.90E-08	-0.00058	3.86E-05	decreasing	0
<i>SYPL1</i>	Caudate	1.68E-10	-0.00056	8.73E-05	decreasing	0
<i>SYT10</i>	Caudate	1.03E-10	-0.00062	5.24E-06	decreasing	0
<i>SYT12</i>	Caudate	2.24E-10	0.00054	8.28E-05	increasing	0
<i>SYT17</i>	Caudate	8.48E-13	-0.00073	3.63E-08	decreasing	0
<i>SYT2</i>	Caudate	4.15E-11	0.000622	5.25E-06	increasing	1
<i>SYTL1</i>	Caudate	3.76E-20	0.000881	2.40E-13	increasing	0
<i>TAB1</i>	Caudate	2.16E-14	0.000261	0.0791	other	0
<i>TACC3</i>	Caudate	2.46E-09	-1.90E-05	0.899561	other	0
<i>TADA2B</i>	Caudate	1.48E-11	0.000362	0.014444	other	0
<i>TAF1B</i>	Caudate	1.18E-08	-0.00074	1.48E-08	decreasing	0
<i>TAF2</i>	Caudate	5.68E-09	-0.00075	1.20E-08	decreasing	0
<i>TAF3</i>	Caudate	2.55E-07	-1.11E-05	0.940878	other	0
<i>TAF6L</i>	Caudate	9.32E-11	0.000529	0.000222	other	0
<i>TAF9B</i>	Caudate	4.88E-08	-0.00052	0.000365	other	0
<i>TANGO2</i>	Caudate	6.87E-09	0.000745	3.02E-08	increasing	0
<i>TANGO6</i>	Caudate	1.82E-12	0.000448	0.001987	other	0
<i>TANK</i>	Caudate	8.49E-07	-0.00072	5.33E-08	decreasing	0
<i>TAOK2</i>	Caudate	8.26E-12	1.14E-05	0.939271	other	0
<i>TAP2</i>	Caudate	4.69E-10	0.000773	5.71E-09	increasing	0
<i>TARSL2</i>	Caudate	2.93E-13	0.000709	1.11E-07	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TATDN2</i>	Caudate	3.80E-08	-4.21E-05	0.77818	other	0
<i>TAX1BP1</i>	Caudate	7.75E-11	-0.00026	0.06882	other	0
<i>TBC1D1</i>	Caudate	7.29E-16	0.000874	6.81E-13	increasing	0
<i>TBC1D10B</i>	Caudate	9.04E-12	0.000459	0.001795	other	0
<i>TBC1D13</i>	Caudate	6.85E-09	0.000788	2.23E-09	increasing	0
<i>TBC1D14</i>	Caudate	5.77E-10	-2.96E-05	0.843063	other	0
<i>TBC1D15</i>	Caudate	8.91E-09	-0.00023	0.131269	other	0
<i>TBC1D16</i>	Caudate	1.55E-08	0.000329	0.027346	other	0
<i>TBC1D17</i>	Caudate	9.03E-11	0.000804	4.56E-10	increasing	0
<i>TBC1D22A</i>	Caudate	7.61E-10	0.000708	2.22E-07	increasing	0
<i>TBC1D2B</i>	Caudate	2.70E-07	0.000774	5.63E-09	increasing	0
<i>TBC1D4</i>	Caudate	1.72E-17	0.000808	2.10E-10	increasing	0
<i>TBC1D8B</i>	Caudate	3.90E-08	-0.00037	0.011168	other	0
<i>TBC1D9</i>	Caudate	3.66E-09	-0.00061	1.05E-05	decreasing	0
<i>TBC1D9B</i>	Caudate	7.17E-11	0.000614	1.41E-05	increasing	0
<i>TBCB</i>	Caudate	3.78E-09	0.000219	0.146353	other	0
<i>TBCEL</i>	Caudate	4.87E-07	-0.00079	1.14E-09	decreasing	0
<i>TBL1XR1</i>	Caudate	1.79E-10	-0.00082	1.95E-10	decreasing	0
<i>TBL2</i>	Caudate	1.17E-08	0.000135	0.369664	other	0
<i>TBL3</i>	Caudate	4.95E-09	0.000584	4.28E-05	increasing	0
<i>TBRG4</i>	Caudate	4.25E-08	0.000214	0.158576	other	0
<i>TCAP</i>	Caudate	7.71E-07	0.000726	8.99E-08	increasing	0
<i>TCEAL6</i>	Caudate	1.46E-07	0.000171	0.251493	other	0
<i>TCEB1</i>	Caudate	2.62E-10	-0.00058	3.30E-05	decreasing	0
<i>TCERG1</i>	Caudate	2.49E-09	-0.00077	8.17E-09	decreasing	0
<i>TCF25</i>	Caudate	4.74E-10	0.000467	0.001454	other	0
<i>TCF3</i>	Caudate	1.98E-09	0.000234	0.117356	other	0
<i>TCF4</i>	Caudate	2.42E-08	-0.0007	1.19E-07	decreasing	0
<i>TCHP</i>	Caudate	3.79E-09	0.000794	1.45E-09	increasing	0
<i>TDG</i>	Caudate	7.76E-13	-0.00079	6.82E-10	decreasing	0
<i>TECPR1</i>	Caudate	2.03E-08	0.000501	0.000589	other	0
<i>TECR</i>	Caudate	1.85E-12	0.000756	7.23E-09	increasing	0
<i>TELO2</i>	Caudate	4.73E-11	0.000461	0.00116	other	0
<i>TENC1</i>	Caudate	3.50E-07	0.00074	2.11E-08	increasing	0
<i>TENM3</i>	Caudate	9.53E-11	-0.00058	2.50E-05	decreasing	0
<i>TEP1</i>	Caudate	4.48E-09	0.000695	4.36E-07	increasing	0
<i>TEPP</i>	Caudate	9.72E-08	0.000713	1.54E-07	increasing	0
<i>TERF1</i>	Caudate	1.43E-09	-0.00053	0.000274	other	0
<i>TERF2</i>	Caudate	1.04E-12	0.000122	0.402905	other	0
<i>TERT</i>	Caudate	1.36E-12	0.000752	1.08E-08	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TESK1</i>	Caudate	2.56E-09	0.000617	1.14E-05	increasing	0
<i>TESK2</i>	Caudate	1.06E-16	0.000838	6.14E-12	increasing	0
<i>TET1</i>	Caudate	7.59E-13	-0.00072	3.33E-08	decreasing	0
<i>TET2</i>	Caudate	1.14E-11	-0.00059	2.72E-05	decreasing	0
<i>TET3</i>	Caudate	8.26E-08	-0.00074	5.10E-08	decreasing	0
<i>TEX2</i>	Caudate	7.84E-09	0.00062	4.81E-06	increasing	0
<i>TEX264</i>	Caudate	5.74E-08	0.000645	3.92E-06	increasing	0
<i>TEX37</i>	Caudate	5.62E-13	-0.00026	0.010805	other	0
<i>TFAP4</i>	Caudate	4.26E-13	0.000829	1.34E-10	increasing	0
<i>TFDP1</i>	Caudate	2.66E-08	-0.0007	1.39E-07	decreasing	0
<i>TFE3</i>	Caudate	7.90E-10	0.000719	6.33E-08	increasing	0
<i>TFG</i>	Caudate	5.72E-10	-0.00058	5.26E-05	decreasing	0
<i>TFRC</i>	Caudate	3.83E-09	-0.00072	1.48E-07	decreasing	0
<i>TGFA</i>	Caudate	1.66E-07	-0.00067	5.17E-07	decreasing	1
<i>TGFBR1</i>	Caudate	1.31E-08	-0.00074	2.53E-08	decreasing	1
<i>TGFBRAP1</i>	Caudate	6.17E-12	9.02E-05	0.550366	other	0
<i>THAP4</i>	Caudate	1.39E-08	0.000674	9.02E-07	increasing	0
<i>THEM6</i>	Caudate	2.07E-08	0.000498	0.000604	other	1
<i>THOC5</i>	Caudate	4.13E-09	0.00016	0.282662	other	0
<i>THOP1</i>	Caudate	1.37E-11	0.00058	4.80E-05	increasing	0
<i>THPO</i>	Caudate	1.79E-07	0.00073	5.67E-08	increasing	0
<i>THRA</i>	Caudate	1.69E-13	0.000759	1.34E-08	increasing	0
<i>THSD7A</i>	Caudate	5.24E-06	-0.00072	4.66E-08	decreasing	0
<i>THY1</i>	Caudate	1.02E-08	-9.07E-05	0.543841	other	0
<i>TIAM2</i>	Caudate	3.52E-08	-0.0006	1.97E-05	decreasing	0
<i>TIGD5</i>	Caudate	3.70E-10	0.000429	0.003295	other	0
<i>TIMM13</i>	Caudate	1.64E-09	1.16E-05	0.939074	other	0
<i>TIMM17B</i>	Caudate	5.78E-08	0.000262	0.083578	other	0
<i>TIMP2</i>	Caudate	4.65E-09	0.000369	0.01057	other	0
<i>TJAP1</i>	Caudate	3.42E-14	0.000857	9.00E-12	increasing	0
<i>TJP1</i>	Caudate	5.85E-12	0.000417	0.003845	other	0
<i>TJP2</i>	Caudate	4.79E-09	0.000667	1.12E-06	increasing	0
<i>TK2</i>	Caudate	1.77E-07	0.000483	0.000892	other	0
<i>TKT</i>	Caudate	6.31E-09	0.000456	0.001874	other	0
<i>TLK1</i>	Caudate	1.74E-10	-0.00037	0.010627	other	0
<i>TLN2</i>	Caudate	4.01E-11	-0.00051	0.000403	other	0
<i>TLR1</i>	Caudate	5.19E-07	-0.00074	2.89E-08	decreasing	0
<i>TM6SF2</i>	Caudate	9.77E-07	0.000779	3.78E-09	increasing	0
<i>TM7SF2</i>	Caudate	4.94E-08	-0.00022	0.141244	other	0
<i>TM9SF2</i>	Caudate	4.60E-08	-0.00077	9.13E-09	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TM9SF3</i>	Caudate	7.41E-08	-0.00076	1.76E-08	decreasing	0
<i>TMBIM1</i>	Caudate	3.67E-13	0.000777	1.23E-09	increasing	0
<i>TMC6</i>	Caudate	9.46E-15	0.000841	7.70E-12	increasing	0
<i>TMC7</i>	Caudate	5.43E-07	0.000735	1.37E-08	increasing	0
<i>TMCC2</i>	Caudate	2.92E-10	0.000799	7.37E-11	increasing	0
<i>TMED7</i>	Caudate	1.68E-09	-0.00058	4.96E-05	decreasing	0
<i>TMEM106B</i>	Caudate	4.63E-08	-0.00066	2.68E-06	decreasing	0
<i>TMEM108</i>	Caudate	3.18E-08	-0.00056	6.47E-05	decreasing	0
<i>TMEM109</i>	Caudate	1.04E-12	0.000818	3.62E-11	increasing	0
<i>TMEM115</i>	Caudate	1.51E-07	0.000163	0.280032	other	0
<i>TMEM117</i>	Caudate	6.49E-06	-0.00072	1.23E-07	decreasing	0
<i>TMEM120A</i>	Caudate	5.69E-08	0.000309	0.034927	other	0
<i>TMEM121</i>	Caudate	4.56E-10	0.000271	0.068836	other	0
<i>TMEM125</i>	Caudate	1.95E-15	0.000821	4.47E-11	increasing	0
<i>TMEM132A</i>	Caudate	2.59E-10	0.000243	0.104598	other	0
<i>TMEM132C</i>	Caudate	2.60E-07	0.000723	5.67E-08	increasing	0
<i>TMEM132D</i>	Caudate	1.39E-07	0.000569	2.83E-05	increasing	0
<i>TMEM134</i>	Caudate	4.88E-08	0.000563	8.91E-05	increasing	0
<i>TMEM135</i>	Caudate	5.18E-08	-0.00072	1.55E-07	decreasing	0
<i>TMEM144</i>	Caudate	3.21E-09	0.000622	6.60E-06	increasing	0
<i>TMEM145</i>	Caudate	9.56E-08	0.000324	0.029793	other	0
<i>TMEM150C</i>	Caudate	5.49E-11	-0.0008	4.93E-10	decreasing	1
<i>TMEM151B</i>	Caudate	1.03E-09	-0.00018	0.232428	other	0
<i>TMEM161A</i>	Caudate	2.46E-07	0.000421	0.003616	other	0
<i>TMEM161B</i>	Caudate	1.54E-06	-0.00072	3.31E-08	decreasing	0
<i>TMEM163</i>	Caudate	7.45E-18	-0.0009	8.79E-14	decreasing	0
<i>TMEM168</i>	Caudate	2.83E-10	-0.00076	1.21E-09	decreasing	1
<i>TMEM169</i>	Caudate	1.26E-08	-0.00052	0.000194	other	0
<i>TMEM170B</i>	Caudate	3.56E-08	-0.00068	6.86E-07	decreasing	0
<i>TMEM175</i>	Caudate	1.28E-08	0.000355	0.016117	other	0
<i>TMEM178B</i>	Caudate	1.79E-07	-0.00044	0.002242	other	0
<i>TMEM185B</i>	Caudate	9.46E-08	8.94E-05	0.551494	other	0
<i>TMEM191C</i>	Caudate	1.47E-12	0.000642	2.57E-06	increasing	0
<i>TMEM196</i>	Caudate	1.29E-09	-0.00077	6.70E-09	decreasing	1
<i>TMEM203</i>	Caudate	2.40E-07	-4.44E-05	0.770925	other	0
<i>TMEM235</i>	Caudate	3.48E-18	0.000857	3.44E-12	increasing	0
<i>TMEM240</i>	Caudate	1.66E-09	0.000134	0.378994	other	0
<i>TMEM246</i>	Caudate	2.69E-06	0.000759	2.85E-09	increasing	0
<i>TMEM257</i>	Caudate	2.38E-07	-0.00069	4.70E-07	decreasing	0
<i>TMEM259</i>	Caudate	4.84E-11	0.000378	0.0096	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TMEM263</i>	Caudate	1.98E-08	-0.00061	1.59E-05	decreasing	0
<i>TMEM30B</i>	Caudate	1.92E-09	0.000786	2.46E-09	increasing	0
<i>TMEM33</i>	Caudate	3.17E-09	-0.00067	1.63E-06	decreasing	0
<i>TMEM43</i>	Caudate	7.68E-08	0.000536	0.00016	other	0
<i>TMEM45A</i>	Caudate	4.96E-08	3.85E-05	0.798565	other	0
<i>TMEM55A</i>	Caudate	1.23E-07	-0.00017	0.264308	other	0
<i>TMEM63C</i>	Caudate	1.89E-07	0.000716	5.53E-08	increasing	0
<i>TMEM65</i>	Caudate	9.21E-12	-0.00081	2.98E-10	decreasing	0
<i>TMEM68</i>	Caudate	1.58E-05	-0.00072	4.60E-08	decreasing	0
<i>TMEM74B</i>	Caudate	7.32E-16	0.00083	5.08E-11	increasing	0
<i>TMEM87B</i>	Caudate	2.69E-08	-0.00034	0.022503	other	0
<i>TMEM88B</i>	Caudate	4.87E-14	0.000791	9.57E-10	increasing	0
<i>TMEM91</i>	Caudate	4.83E-10	0.000664	1.48E-06	increasing	0
<i>TMF1</i>	Caudate	1.31E-07	-0.0006	2.25E-05	decreasing	0
<i>TMOD1</i>	Caudate	2.02E-07	0.000469	0.00078	other	0
<i>TMPRSS5</i>	Caudate	5.45E-10	0.000807	5.75E-10	increasing	0
<i>TNFAIP2</i>	Caudate	8.52E-10	0.000565	5.37E-05	increasing	0
<i>TNFAIP6</i>	Caudate	1.62E-09	0.000686	3.15E-07	increasing	0
<i>TNFRSF14</i>	Caudate	4.21E-08	0.000735	4.98E-08	increasing	0
<i>TNFRSF21</i>	Caudate	1.50E-12	-0.00082	9.54E-11	decreasing	0
<i>TNFSF9</i>	Caudate	3.06E-11	0.000729	4.00E-08	increasing	1
<i>TNIP1</i>	Caudate	4.71E-13	0.00078	6.66E-10	increasing	0
<i>TNK2</i>	Caudate	2.34E-10	0.000759	1.28E-08	increasing	0
<i>TNKS1BP1</i>	Caudate	8.88E-11	0.000553	0.000113	other	0
<i>TNKS2</i>	Caudate	9.07E-08	-0.00042	0.004208	other	1
<i>TNNC2</i>	Caudate	2.48E-10	0.000763	6.10E-09	increasing	0
<i>TNXB</i>	Caudate	5.52E-11	0.000808	5.04E-10	increasing	0
<i>TOB1</i>	Caudate	4.72E-09	0.000141	0.356477	other	0
<i>TOLLIP</i>	Caudate	8.90E-09	0.000653	2.20E-06	increasing	0
<i>TOM1</i>	Caudate	8.14E-08	0.00029	0.05541	other	0
<i>TOMM34</i>	Caudate	1.03E-09	0.000473	0.000828	other	0
<i>TOMM40</i>	Caudate	1.83E-07	3.11E-05	0.838812	other	0
<i>TOP1</i>	Caudate	1.54E-07	-0.00067	1.26E-06	decreasing	0
<i>TOP2B</i>	Caudate	8.58E-15	-0.00086	7.53E-12	decreasing	0
<i>TOP3B</i>	Caudate	1.98E-08	0.000405	0.006347	other	0
<i>TOPBP1</i>	Caudate	2.51E-09	-0.00065	2.70E-06	decreasing	0
<i>TOX</i>	Caudate	6.59E-09	-0.00046	0.001126	other	0
<i>TOX3</i>	Caudate	9.94E-11	-0.00051	0.000427	other	0
<i>TP53BP2</i>	Caudate	5.78E-08	0.000103	0.498628	other	0
<i>TPCN1</i>	Caudate	3.99E-09	0.000798	7.74E-10	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TPD52L1</i>	Caudate	1.56E-07	0.000216	0.143107	other	0
<i>TPD52L2</i>	Caudate	1.11E-13	0.000723	7.84E-08	increasing	0
<i>TPGS1</i>	Caudate	5.66E-10	0.000151	0.322672	other	0
<i>TPP2</i>	Caudate	1.89E-06	-0.00076	8.75E-09	decreasing	0
<i>TPPP</i>	Caudate	4.12E-09	0.000801	3.44E-10	increasing	0
<i>TPRA1</i>	Caudate	3.10E-09	0.000443	0.002559	other	0
<i>TPRG1L</i>	Caudate	5.64E-15	0.000718	4.79E-08	increasing	0
<i>TPRN</i>	Caudate	1.21E-12	0.000817	1.36E-10	increasing	0
<i>TRADD</i>	Caudate	6.43E-09	0.000547	0.000149	other	0
<i>TRAF3</i>	Caudate	8.93E-10	-0.00054	0.000114	other	0
<i>TRAF7</i>	Caudate	1.10E-07	0.000378	0.010897	other	0
<i>TRAM1</i>	Caudate	1.18E-07	-0.00074	4.52E-09	decreasing	0
<i>TRANK1</i>	Caudate	1.41E-09	0.00024	0.107177	other	0
<i>TRAP1</i>	Caudate	5.35E-09	0.000452	0.002154	other	0
<i>TRAPPC10</i>	Caudate	3.22E-11	0.000696	1.64E-07	increasing	1
<i>TRAPPC12</i>	Caudate	1.56E-12	0.000778	4.64E-09	increasing	0
<i>TRAPPC5</i>	Caudate	3.79E-10	0.000468	0.001426	other	0
<i>TRDMT1</i>	Caudate	9.16E-09	-0.00069	3.06E-07	decreasing	0
<i>TRIB1</i>	Caudate	4.91E-08	-0.00033	0.025982	other	0
<i>TRIB2</i>	Caudate	2.44E-19	-0.0009	1.57E-14	decreasing	0
<i>TRIM24</i>	Caudate	1.20E-11	-0.00078	3.15E-09	decreasing	0
<i>TRIM26</i>	Caudate	1.01E-05	0.000724	9.71E-08	increasing	0
<i>TRIM27</i>	Caudate	4.13E-10	5.13E-05	0.729583	other	0
<i>TRIM28</i>	Caudate	8.17E-12	0.000313	0.031577	other	0
<i>TRIM3</i>	Caudate	6.67E-10	0.000796	1.44E-09	increasing	0
<i>TRIM35</i>	Caudate	1.84E-11	0.000576	5.25E-05	increasing	0
<i>TRIM54</i>	Caudate	3.40E-08	-0.00035	0.018128	other	0
<i>TRIM65</i>	Caudate	1.07E-05	0.000739	4.53E-08	increasing	1
<i>TRIO</i>	Caudate	1.80E-10	-0.00025	0.091196	other	0
<i>TRIP11</i>	Caudate	3.45E-08	-0.00036	0.015864	other	0
<i>TRIP12</i>	Caudate	1.23E-08	-0.00023	0.107592	other	0
<i>TRMT1</i>	Caudate	1.20E-09	0.000339	0.022202	other	0
<i>TRMT10A</i>	Caudate	7.53E-08	-0.00024	0.108597	other	0
<i>TRMT13</i>	Caudate	3.18E-08	-0.00049	0.000742	other	0
<i>TRMT2A</i>	Caudate	9.09E-09	0.00026	0.078431	other	0
<i>TRMT61A</i>	Caudate	5.31E-09	0.000358	0.01571	other	0
<i>TRNT1</i>	Caudate	2.33E-12	-0.00087	2.30E-12	decreasing	0
<i>TROVE2</i>	Caudate	2.42E-11	-0.00078	3.18E-09	decreasing	0
<i>TRPC1</i>	Caudate	1.46E-07	-0.00071	3.33E-08	decreasing	0
<i>TRPC4</i>	Caudate	1.36E-10	-0.00077	6.55E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TRPC4AP</i>	Caudate	8.46E-08	0.000322	0.031064	other	0
<i>TRPC5</i>	Caudate	2.47E-17	-0.0008	3.70E-10	decreasing	0
<i>TRPC5OS</i>	Caudate	2.00E-11	-0.00057	4.27E-05	decreasing	0
<i>TRPM1</i>	Caudate	7.60E-08	0.000797	1.17E-09	increasing	0
<i>TRPT1</i>	Caudate	1.50E-07	0.000557	0.000107	other	0
<i>TRUB1</i>	Caudate	6.90E-07	-0.00073	3.49E-08	decreasing	0
<i>TSC2</i>	Caudate	1.31E-11	0.000535	0.000208	other	0
<i>TSC22D4</i>	Caudate	4.14E-09	0.000719	8.32E-08	increasing	0
<i>TSG101</i>	Caudate	6.38E-09	-0.0003	0.041779	other	0
<i>TSNARE1</i>	Caudate	1.62E-07	0.000673	1.17E-06	increasing	0
<i>TSPAN12</i>	Caudate	5.16E-11	-0.00081	4.40E-11	decreasing	0
<i>TSPAN13</i>	Caudate	9.81E-11	-0.00072	1.40E-07	decreasing	0
<i>TSPAN15</i>	Caudate	2.32E-11	0.00077	3.49E-09	increasing	0
<i>TSPAN17</i>	Caudate	2.62E-08	0.000694	4.66E-07	increasing	0
<i>TSPAN2</i>	Caudate	5.84E-10	-0.00068	5.38E-07	decreasing	0
<i>TSPAN7</i>	Caudate	8.06E-11	-0.0004	0.006013	other	0
<i>TSPAN9</i>	Caudate	8.59E-09	-0.00056	8.55E-05	decreasing	0
<i>TSPEAR</i>	Caudate	2.30E-10	0.000806	9.15E-11	increasing	0
<i>TSPYL1</i>	Caudate	1.13E-08	0.000618	6.26E-06	increasing	0
<i>TSPYL2</i>	Caudate	5.16E-09	0.000691	2.14E-07	increasing	0
<i>TSR1</i>	Caudate	3.36E-09	-4.03E-05	0.789205	other	1
<i>TSR3</i>	Caudate	1.11E-09	0.000422	0.00439	other	0
<i>TTBK2</i>	Caudate	8.60E-09	0.000171	0.247467	other	0
<i>TTC1</i>	Caudate	2.85E-08	-2.33E-05	0.877108	other	0
<i>TTC3</i>	Caudate	2.16E-08	-0.00055	0.000108	other	0
<i>TTC37</i>	Caudate	6.21E-07	-0.00073	3.70E-08	decreasing	0
<i>TTC38</i>	Caudate	2.29E-13	0.000216	0.142027	other	0
<i>TPPAL</i>	Caudate	6.69E-09	-0.00066	1.12E-06	decreasing	0
<i>TTYH2</i>	Caudate	1.57E-14	0.000846	2.98E-12	increasing	0
<i>TUB</i>	Caudate	6.98E-10	0.000639	3.92E-06	increasing	0
<i>TUBA1A</i>	Caudate	1.20E-07	-0.00068	3.19E-07	decreasing	0
<i>TUBG1</i>	Caudate	2.55E-07	-0.00055	0.00012	other	0
<i>TUBGCP2</i>	Caudate	4.06E-10	0.000516	0.000356	other	0
<i>TUBGCP6</i>	Caudate	3.20E-11	0.000742	3.51E-08	increasing	0
<i>TUFT1</i>	Caudate	1.17E-07	0.000766	4.40E-09	increasing	1
<i>TULP4</i>	Caudate	8.01E-08	0.000371	0.010751	other	0
<i>TUSC1</i>	Caudate	2.95E-09	7.30E-05	0.623042	other	0
<i>TXLNA</i>	Caudate	1.76E-08	-0.00016	0.265698	other	0
<i>TXNDC5</i>	Caudate	3.44E-10	0.000804	7.66E-10	increasing	0
<i>TXNL1</i>	Caudate	1.78E-08	-0.00044	0.002568	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TYRO3</i>	Caudate	1.07E-13	0.000808	8.24E-11	increasing	0
<i>TYSND1</i>	Caudate	1.84E-11	0.00068	8.61E-07	increasing	0
<i>U2AF1</i>	Caudate	2.40E-08	0.000165	0.279351	other	0
<i>U2AF1L4</i>	Caudate	1.30E-08	-0.00044	0.002377	other	0
<i>U2AF2</i>	Caudate	1.20E-08	0.000221	0.138907	other	0
<i>U2SURP</i>	Caudate	3.62E-09	-0.00058	5.03E-05	decreasing	0
<i>UAP1L1</i>	Caudate	1.22E-06	0.000723	1.06E-07	increasing	0
<i>UBAC1</i>	Caudate	2.54E-07	0.000515	0.000383	other	0
<i>UBASH3B</i>	Caudate	1.81E-08	-0.00069	4.36E-07	decreasing	0
<i>UBE2B</i>	Caudate	8.89E-11	-0.00046	0.001513	other	0
<i>UBE2E1</i>	Caudate	6.62E-11	-0.0006	2.40E-05	decreasing	0
<i>UBE2E2</i>	Caudate	1.51E-11	-0.00062	1.21E-05	decreasing	0
<i>UBE2E3</i>	Caudate	1.36E-07	-0.00066	1.42E-06	decreasing	0
<i>UBE2G1</i>	Caudate	4.46E-10	-0.00067	1.26E-06	decreasing	0
<i>UBE2K</i>	Caudate	4.70E-10	-0.00075	2.23E-08	decreasing	0
<i>UBE2O</i>	Caudate	2.62E-12	0.000191	0.208784	other	0
<i>UBE2V1</i>	Caudate	4.75E-09	-0.00032	0.034389	other	0
<i>UBE2V2</i>	Caudate	1.21E-09	-0.00063	7.66E-06	decreasing	0
<i>UBE2W</i>	Caudate	3.64E-06	-0.00073	7.61E-08	decreasing	0
<i>UBE3A</i>	Caudate	1.59E-08	-0.00066	2.18E-06	decreasing	0
<i>UBFD1</i>	Caudate	5.80E-10	-0.00061	8.99E-06	decreasing	0
<i>UBL4A</i>	Caudate	1.88E-07	-1.74E-05	0.906648	other	0
<i>UBLCP1</i>	Caudate	5.82E-12	-0.00067	1.49E-06	decreasing	0
<i>UBN1</i>	Caudate	1.07E-07	0.000417	0.004796	other	0
<i>UBOX5</i>	Caudate	1.89E-07	0.000736	2.14E-08	increasing	0
<i>UBP1</i>	Caudate	9.75E-08	0.000247	0.087859	other	0
<i>UBR3</i>	Caudate	1.70E-08	-0.00069	5.98E-07	decreasing	0
<i>UBR7</i>	Caudate	1.11E-09	-0.00023	0.127767	other	0
<i>UBTD2</i>	Caudate	4.33E-10	-0.0007	8.48E-08	decreasing	0
<i>UBXN2B</i>	Caudate	2.89E-17	-0.00086	5.99E-12	decreasing	0
<i>UBXN6</i>	Caudate	1.25E-10	0.000643	2.90E-06	increasing	0
<i>UCK1</i>	Caudate	1.38E-08	0.000484	0.000916	other	0
<i>UCK2</i>	Caudate	5.45E-09	-0.00045	0.00197	other	0
<i>UCKL1</i>	Caudate	7.42E-12	0.00059	3.19E-05	increasing	0
<i>UFM1</i>	Caudate	1.98E-07	-0.00077	8.94E-09	decreasing	0
<i>UGDH</i>	Caudate	1.43E-07	-0.00061	1.39E-05	decreasing	0
<i>UGGT2</i>	Caudate	1.01E-09	-0.00072	6.21E-08	decreasing	0
<i>UHMK1</i>	Caudate	2.15E-07	-0.0006	1.81E-05	decreasing	0
<i>UHRF1BP1L</i>	Caudate	2.20E-10	-0.00081	4.08E-10	decreasing	0
<i>UNC13B</i>	Caudate	7.17E-09	0.000489	0.000515	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>UNC13D</i>	Caudate	8.42E-08	0.000785	2.59E-09	increasing	0
<i>UNC45A</i>	Caudate	2.57E-11	0.000363	0.012531	other	0
<i>UNC5D</i>	Caudate	2.06E-08	0.000588	3.08E-05	increasing	1
<i>UNC80</i>	Caudate	1.03E-09	0.000711	5.55E-08	increasing	0
<i>UPF1</i>	Caudate	1.58E-13	0.000713	1.74E-07	increasing	0
<i>URI1</i>	Caudate	4.69E-08	-0.00041	0.005277	other	0
<i>URM1</i>	Caudate	4.38E-08	-0.00031	0.034515	other	0
<i>UROD</i>	Caudate	8.10E-09	0.000632	4.03E-06	increasing	0
<i>USF1</i>	Caudate	1.30E-08	-0.00017	0.257732	other	0
<i>USH1C</i>	Caudate	8.26E-07	0.000749	2.53E-08	increasing	1
<i>USP11</i>	Caudate	2.06E-10	0.00081	1.07E-10	increasing	0
<i>USP12</i>	Caudate	1.81E-08	-0.00039	0.005532	other	0
<i>USP15</i>	Caudate	2.12E-10	-0.00083	3.32E-11	decreasing	0
<i>USP19</i>	Caudate	1.09E-08	0.000251	0.094058	other	0
<i>USP20</i>	Caudate	2.21E-11	0.000806	6.47E-10	increasing	0
<i>USP22</i>	Caudate	2.12E-11	0.000333	0.02523	other	0
<i>USP24</i>	Caudate	7.03E-08	-0.00072	1.04E-07	decreasing	0
<i>USP35</i>	Caudate	5.20E-10	0.000667	8.91E-07	increasing	0
<i>USP38</i>	Caudate	1.37E-10	-0.00076	2.91E-09	decreasing	0
<i>USP46</i>	Caudate	5.13E-11	-0.00071	1.76E-07	decreasing	0
<i>USP5</i>	Caudate	1.71E-08	0.000314	0.036974	other	0
<i>USP53</i>	Caudate	2.57E-10	-0.00055	8.64E-05	decreasing	0
<i>USP54</i>	Caudate	5.40E-12	0.000839	2.79E-11	increasing	0
<i>USP8</i>	Caudate	1.72E-07	-0.00043	0.003282	other	0
<i>VAMP1</i>	Caudate	2.60E-07	0.000526	0.000197	other	1
<i>VAMP4</i>	Caudate	1.58E-07	-0.0006	1.59E-05	decreasing	0
<i>VAPB</i>	Caudate	2.52E-08	-0.0005	0.000582	other	0
<i>VAR5</i>	Caudate	3.54E-13	0.000289	0.052095	other	0
<i>VAR52</i>	Caudate	4.64E-09	0.000268	0.068718	other	0
<i>VAT1</i>	Caudate	3.10E-11	0.000309	0.035819	other	0
<i>VAT1L</i>	Caudate	2.21E-09	0.000113	0.44563	other	0
<i>VCAN</i>	Caudate	8.07E-11	-0.0006	1.76E-05	decreasing	0
<i>VCPIP1</i>	Caudate	2.09E-07	-0.00032	0.024837	other	0
<i>VDAC1</i>	Caudate	1.11E-10	-0.00071	1.25E-07	decreasing	0
<i>VEGFB</i>	Caudate	8.08E-10	0.000379	0.008573	other	0
<i>VEPH1</i>	Caudate	2.07E-08	-0.00079	3.22E-10	decreasing	0
<i>VEZT</i>	Caudate	1.62E-08	-0.00076	5.17E-09	decreasing	0
<i>VIPR2</i>	Caudate	2.73E-07	0.000768	8.58E-09	increasing	1
<i>VPS13A</i>	Caudate	3.83E-08	-0.00037	0.013161	other	0
<i>VPS16</i>	Caudate	7.95E-11	0.000227	0.12262	other	0

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<i>VPS18</i>	Caudate	2.03E-08	0.000481	0.001015	other	0
<i>VPS26A</i>	Caudate	4.04E-08	-0.00047	0.001331	other	1
<i>VPS26B</i>	Caudate	3.47E-11	0.000332	0.026986	other	0
<i>VPS28</i>	Caudate	2.83E-08	0.000424	0.003888	other	0
<i>VPS37A</i>	Caudate	1.63E-08	-0.00073	6.30E-08	decreasing	0
<i>VPS37D</i>	Caudate	2.29E-07	0.000487	0.000753	other	0
<i>VPS4A</i>	Caudate	1.05E-11	0.000344	0.021142	other	0
<i>VPS51</i>	Caudate	1.01E-10	0.000362	0.013911	other	0
<i>VPS9D1</i>	Caudate	2.91E-09	0.000579	4.55E-05	increasing	0
<i>VSNL1</i>	Caudate	1.81E-10	-0.00066	9.65E-07	decreasing	1
<i>VSTM2A</i>	Caudate	3.41E-14	-0.00077	1.87E-09	decreasing	0
<i>VSTM2B</i>	Caudate	1.50E-19	0.0009	1.06E-13	increasing	0
<i>VWA1</i>	Caudate	1.50E-11	0.000594	2.95E-05	increasing	0
<i>VWF</i>	Caudate	1.36E-09	0.000728	1.16E-08	increasing	0
<i>WAC</i>	Caudate	3.20E-12	-0.00034	0.019778	other	0
<i>WASH1</i>	Caudate	1.37E-07	0.000415	0.005152	other	0
<i>WASL</i>	Caudate	1.36E-08	-0.00032	0.028838	other	0
<i>WBP2</i>	Caudate	2.06E-10	0.000498	0.000333	other	0
<i>WBP5</i>	Caudate	5.13E-09	-0.00052	0.000325	other	0
<i>WBSCR16</i>	Caudate	1.47E-07	0.000429	0.003672	other	0
<i>WDR1</i>	Caudate	1.17E-08	-0.00022	0.136223	other	0
<i>WDR12</i>	Caudate	1.87E-07	-0.00073	5.06E-08	decreasing	0
<i>WDR13</i>	Caudate	4.65E-10	0.000443	0.002683	other	0
<i>WDR18</i>	Caudate	8.35E-09	0.000102	0.50389	other	0
<i>WDR24</i>	Caudate	3.58E-11	0.000442	0.002558	other	0
<i>WDR34</i>	Caudate	2.41E-11	0.000294	0.041247	other	0
<i>WDR4</i>	Caudate	7.35E-06	0.000695	2.04E-07	increasing	0
<i>WDR6</i>	Caudate	2.35E-12	0.000228	0.121278	other	0
<i>WDR74</i>	Caudate	1.41E-07	0.000157	0.290081	other	0
<i>WDR81</i>	Caudate	7.36E-12	0.000442	0.002678	other	0
<i>WDR91</i>	Caudate	9.06E-09	0.000742	3.63E-08	increasing	0
<i>WDSUB1</i>	Caudate	2.02E-07	0.000556	8.30E-05	increasing	0
<i>WDTC1</i>	Caudate	1.79E-07	0.000733	8.62E-09	increasing	0
<i>WFS1</i>	Caudate	3.73E-12	0.000833	4.00E-11	increasing	0
<i>WIF1</i>	Caudate	8.74E-09	-0.00023	0.128637	other	0
<i>WNK3</i>	Caudate	4.82E-08	-0.00039	0.007341	other	0
<i>WNT1</i>	Caudate	1.36E-08	0.000641	4.87E-06	increasing	0
<i>WNT10B</i>	Caudate	8.56E-09	0.000668	1.57E-06	increasing	0
<i>WNT11</i>	Caudate	2.46E-06	0.000741	4.01E-08	increasing	0
<i>WNT16</i>	Caudate	2.06E-11	-0.00078	3.30E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>WNT5B</i>	Caudate	6.80E-13	-0.00071	7.35E-08	decreasing	0
<i>WNT6</i>	Caudate	1.09E-10	0.000573	2.46E-05	increasing	0
<i>WRN</i>	Caudate	3.39E-07	-0.00071	1.28E-07	decreasing	1
<i>WRNIP1</i>	Caudate	3.92E-08	0.000273	0.068821	other	0
<i>WSB2</i>	Caudate	2.39E-10	-0.00075	1.04E-08	decreasing	0
<i>WWP1</i>	Caudate	9.08E-09	-0.00054	0.000128	other	0
<i>WWP2</i>	Caudate	5.02E-09	0.000787	9.61E-10	increasing	0
<i>XAB2</i>	Caudate	2.43E-08	0.000658	2.42E-06	increasing	0
<i>XKR4</i>	Caudate	6.05E-13	-0.0001	0.500679	other	0
<i>XPC</i>	Caudate	3.66E-08	0.000699	3.19E-07	increasing	0
<i>XPNPEP1</i>	Caudate	1.37E-07	-0.00042	0.004316	other	0
<i>XPO6</i>	Caudate	1.25E-10	0.000494	0.000522	other	0
<i>XPOT</i>	Caudate	5.30E-08	-0.00072	5.92E-08	decreasing	0
<i>XPR1</i>	Caudate	4.70E-18	-0.0009	3.84E-14	decreasing	0
<i>XRN2</i>	Caudate	2.01E-08	-0.00072	4.31E-08	decreasing	0
<i>XXYLT1</i>	Caudate	1.24E-08	0.000156	0.290839	other	1
<i>XYLT2</i>	Caudate	1.85E-11	0.000721	1.17E-07	increasing	0
<i>YBX1</i>	Caudate	4.44E-08	-0.00042	0.003875	other	0
<i>YDJC</i>	Caudate	9.61E-09	0.000482	0.000985	other	0
<i>YES1</i>	Caudate	5.93E-10	-0.00081	2.17E-10	decreasing	0
<i>YIF1B</i>	Caudate	1.28E-08	-0.00028	0.055403	other	0
<i>YIPF4</i>	Caudate	4.45E-10	-0.00075	2.89E-08	decreasing	0
<i>YPEL1</i>	Caudate	3.66E-09	0.000102	0.497153	other	0
<i>YPEL3</i>	Caudate	1.14E-14	0.000862	2.25E-12	increasing	0
<i>YTHDC2</i>	Caudate	6.32E-09	-0.00056	6.94E-05	decreasing	0
<i>YTHDF3</i>	Caudate	2.09E-10	-0.00066	1.59E-06	decreasing	0
<i>YWHAE</i>	Caudate	1.51E-08	-0.00046	0.00192	other	0
<i>YWHAG</i>	Caudate	2.55E-07	-0.00019	0.182491	other	0
<i>YWHAZ</i>	Caudate	6.70E-08	-0.00071	1.67E-07	decreasing	0
<i>ZBTB12</i>	Caudate	5.39E-08	0.000697	2.92E-07	increasing	0
<i>ZBTB16</i>	Caudate	8.53E-07	0.000732	4.59E-08	increasing	0
<i>ZBTB17</i>	Caudate	2.63E-09	0.000295	0.049886	other	0
<i>ZBTB21</i>	Caudate	7.42E-12	-0.00058	4.95E-05	decreasing	0
<i>ZBTB41</i>	Caudate	4.88E-09	-0.00076	3.55E-09	decreasing	0
<i>ZBTB44</i>	Caudate	2.68E-08	0.000763	2.26E-09	increasing	0
<i>ZBTB46</i>	Caudate	1.85E-15	0.000768	1.58E-09	increasing	0
<i>ZBTB47</i>	Caudate	8.21E-10	0.000682	7.34E-07	increasing	0
<i>ZBTB8A</i>	Caudate	2.37E-09	-0.00035	0.014468	other	0
<i>ZC2HC1A</i>	Caudate	4.30E-12	-0.00044	0.002911	other	0
<i>ZC3H11A</i>	Caudate	1.41E-07	-0.00036	0.016449	other	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
ZC3H12C	Caudate	8.03E-07	-0.00077	6.94E-09	decreasing	0
ZC3H14	Caudate	1.26E-07	-0.00053	0.000264	other	0
ZC4H2	Caudate	1.09E-08	-0.00057	5.70E-05	decreasing	0
ZCCHC10	Caudate	1.88E-11	-0.00057	6.43E-05	decreasing	0
ZCCHC16	Caudate	9.06E-08	-0.00047	0.001079	other	0
ZCCHC24	Caudate	2.17E-08	0.000705	2.41E-07	increasing	0
ZCCHC7	Caudate	7.91E-08	-8.19E-05	0.589128	other	0
ZCWPW1	Caudate	3.94E-08	0.000747	1.23E-08	increasing	0
ZDHHC1	Caudate	2.01E-07	0.000656	1.81E-06	increasing	0
ZDHHC2	Caudate	3.87E-16	-0.0009	6.39E-14	decreasing	0
ZDHHC24	Caudate	1.08E-09	0.000538	0.000199	other	0
ZEB1	Caudate	1.01E-11	-0.00075	2.62E-08	decreasing	0
ZEB2	Caudate	1.28E-08	0.000618	5.34E-06	increasing	0
ZFP37	Caudate	4.14E-15	-0.0008	5.68E-10	decreasing	0
ZFP62	Caudate	1.16E-10	0.000762	1.23E-08	increasing	0
ZFPL1	Caudate	8.72E-08	0.000512	0.000374	other	0
ZFPM1	Caudate	6.45E-10	0.000662	1.47E-06	increasing	0
ZFYVE20	Caudate	1.64E-08	0.000743	3.63E-08	increasing	0
ZFYVE26	Caudate	7.36E-07	0.000727	7.23E-08	increasing	0
ZFYVE28	Caudate	6.35E-08	0.000654	1.90E-06	increasing	0
ZG16B	Caudate	1.47E-12	0.000808	2.50E-10	increasing	0
ZGPAT	Caudate	1.03E-10	0.00061	1.64E-05	increasing	0
ZIC3	Caudate	8.65E-09	-0.00073	5.73E-08	decreasing	0
ZKSCAN7	Caudate	4.08E-09	-0.00038	0.007918	other	0
ZMAT3	Caudate	2.07E-09	-0.00029	0.043773	other	0
ZMYM2	Caudate	5.16E-08	-0.00076	1.18E-08	decreasing	0
ZMYM4	Caudate	6.23E-09	-0.00064	4.54E-06	decreasing	0
ZMYND11	Caudate	5.12E-05	-0.0007	2.26E-07	decreasing	0
ZNF12	Caudate	3.42E-08	-0.00068	9.49E-07	decreasing	0
ZNF140	Caudate	3.51E-10	-0.00077	4.68E-09	decreasing	0
ZNF177	Caudate	1.12E-08	-0.00066	6.05E-07	decreasing	0
ZNF205	Caudate	2.56E-07	0.00033	0.02824	other	0
ZNF213	Caudate	4.11E-09	0.000479	0.001033	other	0
ZNF263	Caudate	2.60E-07	0.000274	0.068658	other	0
ZNF266	Caudate	4.00E-08	-0.0004	0.00607	other	0
ZNF276	Caudate	2.23E-10	0.000514	0.000304	other	0
ZNF282	Caudate	1.75E-13	0.000294	0.045726	other	0
ZNF283	Caudate	1.68E-09	-0.00073	4.54E-08	decreasing	1
ZNF292	Caudate	2.06E-08	-0.00062	8.51E-06	decreasing	0
ZNF300	Caudate	2.57E-09	-0.00069	2.20E-07	decreasing	1

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
ZNF316	Caudate	2.61E-09	0.00059	3.35E-05	increasing	0
ZNF317	Caudate	1.73E-08	0.000127	0.396911	other	0
ZNF326	Caudate	4.08E-10	-0.00042	0.005011	other	0
ZNF335	Caudate	3.68E-08	0.0005	0.000304	other	0
ZNF385B	Caudate	5.18E-08	-8.68E-05	0.553685	other	0
ZNF395	Caudate	4.72E-07	0.000762	8.16E-09	increasing	0
ZNF41	Caudate	3.63E-07	-0.00073	6.09E-08	decreasing	0
ZNF428	Caudate	2.40E-09	5.32E-05	0.725117	other	0
ZNF446	Caudate	3.32E-09	0.000491	0.000739	other	0
ZNF48	Caudate	3.17E-09	7.86E-05	0.603474	other	0
ZNF483	Caudate	5.23E-10	0.000605	1.19E-05	increasing	0
ZNF496	Caudate	1.36E-09	0.000253	0.084763	other	0
ZNF497	Caudate	6.38E-10	0.000221	0.132978	other	0
ZNF500	Caudate	5.00E-10	0.000503	0.000471	other	0
ZNF512B	Caudate	2.16E-12	0.000195	0.194344	other	0
ZNF517	Caudate	9.31E-09	0.000331	0.023506	other	1
ZNF518A	Caudate	1.24E-08	-0.00073	2.95E-08	decreasing	0
ZNF521	Caudate	6.10E-13	-0.00077	3.52E-09	decreasing	0
ZNF526	Caudate	3.82E-06	0.000718	1.43E-07	increasing	0
ZNF528	Caudate	5.07E-09	-0.00076	1.45E-09	decreasing	0
ZNF536	Caudate	9.37E-14	0.000819	1.36E-11	increasing	0
ZNF558	Caudate	2.69E-11	-0.00057	3.99E-05	decreasing	0
ZNF565	Caudate	1.86E-08	0.000796	1.32E-09	increasing	0
ZNF566	Caudate	2.91E-08	-0.00042	0.004156	other	0
ZNF569	Caudate	1.27E-09	-0.00075	9.53E-09	decreasing	0
ZNF570	Caudate	1.97E-08	-0.00055	6.79E-05	decreasing	0
ZNF598	Caudate	6.43E-12	0.000748	2.75E-08	increasing	0
ZNF623	Caudate	1.55E-07	0.000222	0.142286	other	0
ZNF627	Caudate	1.18E-07	-0.00044	0.002273	other	0
ZNF629	Caudate	2.06E-08	4.55E-06	0.975974	other	0
ZNF641	Caudate	2.12E-07	-0.00056	7.55E-05	decreasing	0
ZNF644	Caudate	5.24E-09	-0.00078	1.59E-09	decreasing	0
ZNF646	Caudate	2.57E-08	0.000538	0.000142	other	0
ZNF668	Caudate	1.51E-08	0.000378	0.010817	other	0
ZNF672	Caudate	8.38E-08	0.000312	0.036138	other	0
ZNF680	Caudate	2.77E-08	-0.00075	1.11E-08	decreasing	0
ZNF682	Caudate	1.25E-08	-0.00073	2.16E-08	decreasing	0
ZNF687	Caudate	6.38E-07	0.000726	8.35E-08	increasing	0
ZNF691	Caudate	2.22E-07	0.000442	0.002647	other	0
ZNF696	Caudate	9.14E-09	0.000621	1.04E-05	increasing	1

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
ZNF706	Caudate	4.52E-11	-0.00034	0.021384	other	0
ZNF709	Caudate	3.55E-08	-0.00062	3.95E-06	decreasing	0
ZNF710	Caudate	3.60E-09	0.000297	0.047961	other	0
ZNF711	Caudate	2.28E-08	-0.00073	3.04E-08	decreasing	0
ZNF721	Caudate	2.26E-10	-0.00072	6.89E-08	decreasing	0
ZNF74	Caudate	1.19E-08	0.000184	0.212765	other	0
ZNF740	Caudate	2.16E-10	0.000206	0.162823	other	0
ZNF746	Caudate	3.01E-10	0.000583	4.29E-05	increasing	0
ZNF76	Caudate	3.92E-08	0.000476	0.001187	other	0
ZNF771	Caudate	2.49E-09	0.000462	0.001646	other	0
ZNF775	Caudate	2.01E-10	0.000643	4.28E-06	increasing	0
ZNF787	Caudate	1.66E-10	0.000521	0.000329	other	0
ZNF79	Caudate	1.71E-07	0.000684	7.42E-07	increasing	0
ZNF800	Caudate	1.35E-09	-0.00026	0.074338	other	0
ZNF804B	Caudate	3.07E-14	-0.00081	3.41E-10	decreasing	0
ZNF821	Caudate	1.13E-08	0.000115	0.442449	other	0
ZNF835	Caudate	5.07E-08	0.000507	0.000394	other	0
ZNF853	Caudate	3.04E-11	0.000252	0.09201	other	0
ZNF883	Caudate	3.68E-10	-0.00079	5.55E-10	decreasing	0
ZNF888	Caudate	2.55E-07	-0.00033	0.023208	other	0
ZNHIT1	Caudate	3.62E-08	0.000355	0.017715	other	0
ZNHIT2	Caudate	8.18E-10	0.000221	0.139168	other	0
ZPLD1	Caudate	5.75E-09	-0.00073	2.95E-08	decreasing	0
ZSCAN25	Caudate	1.49E-07	0.000296	0.048143	other	0
ZSWIM6	Caudate	1.50E-15	-0.00082	1.76E-10	decreasing	0
ZSWIM8	Caudate	5.71E-11	0.000649	2.97E-06	increasing	0
ZXDC	Caudate	6.47E-08	0.000439	0.002245	other	0
ZYG11B	Caudate	3.70E-09	-0.00072	7.86E-08	decreasing	0
ZYX	Caudate	5.24E-09	0.000622	7.91E-06	increasing	0
ALAS2	Fibroblast	3.19E-08	0.000355	0.005256	other	0
ARID3A	Fibroblast	9.27E-09	-0.00026	0.083927	other	0
C6H19orf52	Fibroblast	1.68E-07	0.000217	0.15343	other	0
CDH10	Fibroblast	1.08E-07	-0.00049	0.000505	other	0
CDK19	Fibroblast	3.68E-09	-0.00022	0.136052	other	0
CPNE3	Fibroblast	6.72E-08	-5.81E-05	0.697382	other	0
EBF3	Fibroblast	1.47E-09	-0.00059	2.58E-05	decreasing	0
ELAC1	Fibroblast	1.85E-07	0.000219	0.143263	other	0
FAM173A	Fibroblast	2.72E-08	0.000351	0.019149	other	0
FER	Fibroblast	1.90E-07	-0.00024	0.101076	other	0
GPC6	Fibroblast	2.22E-07	-0.00049	0.000773	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>KRT10</i>	Fibroblast	2.44E-07	0.000304	0.042895	other	0
<i>LOC103214331</i>	Fibroblast	3.90E-08	-0.0002	0.186877	other	0
<i>LOC103214661</i>	Fibroblast	1.51E-08	-5.01E-05	0.744469	other	0
<i>LOC103214700</i>	Fibroblast	2.48E-08	-4.68E-05	0.722357	other	0
<i>LOC103218257</i>	Fibroblast	1.47E-07	-0.00031	0.04008	other	0
<i>LOC103220999</i>	Fibroblast	3.37E-08	0.000164	0.180218	other	0
<i>LOC103221358</i>	Fibroblast	1.47E-07	-0.00016	0.234354	other	0
<i>LOC103221731</i>	Fibroblast	1.69E-07	-3.61E-05	0.81165	other	0
<i>LOC103222287</i>	Fibroblast	1.93E-08	0.000441	0.002225	other	0
<i>LOC103222891</i>	Fibroblast	1.45E-07	-0.00025	0.09634	other	0
<i>LOC103224472</i>	Fibroblast	2.23E-08	-0.00019	0.203822	other	0
<i>LOC103224638</i>	Fibroblast	1.86E-07	-0.00023	0.135438	other	0
<i>LOC103225092</i>	Fibroblast	2.36E-07	4.05E-05	0.790973	other	0
<i>LOC103225256</i>	Fibroblast	1.03E-07	5.39E-05	0.723859	other	0
<i>LOC103225416</i>	Fibroblast	1.18E-07	-0.00012	0.448523	other	0
<i>LOC103225891</i>	Fibroblast	6.03E-08	-4.17E-06	0.978324	other	0
<i>LOC103226410</i>	Fibroblast	3.36E-08	0.000166	0.278539	other	0
<i>LOC103227129</i>	Fibroblast	5.68E-08	-5.58E-05	0.713055	other	0
<i>LOC103227227</i>	Fibroblast	4.17E-08	-0.00011	0.480189	other	0
<i>LOC103227336</i>	Fibroblast	7.84E-08	-0.00035	0.018757	other	0
<i>LOC103229008</i>	Fibroblast	7.17E-08	-0.00026	0.083738	other	0
<i>LOC103230997</i>	Fibroblast	2.53E-07	-0.00012	0.420695	other	0
<i>LOC103231822</i>	Fibroblast	6.15E-08	-0.00035	0.018266	other	0
<i>LOC103231835</i>	Fibroblast	7.84E-09	-0.00036	0.015657	other	0
<i>LOC103231865</i>	Fibroblast	1.03E-07	6.93E-05	0.600669	other	0
<i>LOC103232066</i>	Fibroblast	1.07E-07	-0.00011	0.466253	other	0
<i>LOC103232079</i>	Fibroblast	9.82E-08	-7.35E-05	0.632111	other	0
<i>LOC103232122</i>	Fibroblast	6.10E-09	-0.00027	0.074128	other	0
<i>LOC103232333</i>	Fibroblast	1.09E-07	-0.00022	0.156932	other	0
<i>LOC103232529</i>	Fibroblast	1.91E-07	-9.15E-05	0.550591	other	0
<i>LOC103232530</i>	Fibroblast	1.63E-07	-8.41E-05	0.573586	other	0
<i>LOC103232946</i>	Fibroblast	2.08E-07	-0.00015	0.328686	other	0
<i>LOC103232961</i>	Fibroblast	1.38E-07	-0.00023	0.136092	other	0
<i>LOC103234293</i>	Fibroblast	8.94E-08	-0.00022	0.145375	other	0
<i>LOC103234898</i>	Fibroblast	1.50E-07	-0.0004	0.00664	other	0
<i>LOC103236406</i>	Fibroblast	2.52E-08	-0.00016	0.286022	other	0
<i>LOC103236458</i>	Fibroblast	1.94E-07	-0.00015	0.332044	other	0
<i>LOC103236696</i>	Fibroblast	1.82E-07	-0.00016	0.304473	other	0
<i>LOC103237688</i>	Fibroblast	1.62E-08	-0.00029	0.053866	other	0
<i>LOC103238094</i>	Fibroblast	2.26E-07	-8.34E-05	0.58654	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103238464</i>	Fibroblast	1.85E-09	1.17E-06	0.993617	other	0
<i>LOC103239503</i>	Fibroblast	3.96E-08	-6.94E-05	0.643512	other	0
<i>LOC103239517</i>	Fibroblast	2.14E-07	-0.00014	0.34388	other	0
<i>LOC103240032</i>	Fibroblast	1.23E-07	0.000151	0.278815	other	0
<i>LOC103240114</i>	Fibroblast	6.60E-08	-0.00012	0.410395	other	0
<i>LOC103240394</i>	Fibroblast	1.34E-07	0.000104	0.477606	other	0
<i>LOC103241006</i>	Fibroblast	1.24E-07	-6.68E-05	0.65288	other	0
<i>LOC103241328</i>	Fibroblast	2.14E-08	-7.96E-05	0.594518	other	0
<i>LOC103241507</i>	Fibroblast	2.13E-08	-0.00022	0.146026	other	0
<i>LOC103241784</i>	Fibroblast	2.59E-08	-0.00016	0.305373	other	0
<i>LOC103242353</i>	Fibroblast	6.45E-09	0.000179	0.237463	other	0
<i>LOC103243126</i>	Fibroblast	4.13E-08	-0.0001	0.499007	other	0
<i>LOC103244321</i>	Fibroblast	1.86E-07	-0.00017	0.276751	other	0
<i>LOC103247904</i>	Fibroblast	5.97E-10	-7.86E-05	0.520463	other	0
<i>LOC103248166</i>	Fibroblast	6.52E-08	-0.00011	0.467286	other	0
<i>LOC103249061</i>	Fibroblast	1.81E-07	-0.0002	0.18101	other	0
<i>MAP2K2</i>	Fibroblast	1.54E-07	0.000293	0.049596	other	0
<i>MYPOP</i>	Fibroblast	7.41E-09	-0.00017	0.239244	other	0
<i>PXDN</i>	Fibroblast	1.03E-07	-0.00068	9.29E-07	decreasing	0
<i>REPS2</i>	Fibroblast	1.49E-09	-0.00044	0.002237	other	0
<i>S100A9</i>	Fibroblast	1.22E-08	-0.00022	0.036347	other	0
<i>SLC25A28</i>	Fibroblast	7.89E-08	0.00035	0.019567	other	0
<i>STUB1</i>	Fibroblast	1.68E-07	0.000473	0.001208	other	0
<i>TRHDE</i>	Fibroblast	8.93E-08	-0.00048	0.000752	other	0
<i>ZNF280B</i>	Fibroblast	6.12E-08	-0.00059	2.47E-05	decreasing	0
<i>AASS</i>	Hippocampus	1.02E-07	-0.00028	0.06595	other	0
<i>ABCA8</i>	Hippocampus	5.49E-10	0.000697	3.17E-07	increasing	0
<i>ACOT11</i>	Hippocampus	4.85E-08	0.000565	7.19E-05	increasing	0
<i>ACSM5</i>	Hippocampus	1.74E-07	0.000609	1.46E-05	increasing	0
<i>ADAMTS18</i>	Hippocampus	1.72E-11	-0.00076	1.29E-08	decreasing	0
<i>ADIPOR2</i>	Hippocampus	3.95E-08	0.000532	0.000211	other	0
<i>AIDA</i>	Hippocampus	1.23E-07	-0.00049	0.000771	other	0
<i>ALDH1A3</i>	Hippocampus	5.52E-07	0.000745	2.41E-08	increasing	0
<i>ALPL</i>	Hippocampus	7.21E-08	-0.00061	1.59E-05	decreasing	0
<i>AMER1</i>	Hippocampus	1.24E-07	-0.00046	0.001752	other	0
<i>AMER2</i>	Hippocampus	1.53E-07	0.000653	2.44E-06	increasing	0
<i>ANGEL1</i>	Hippocampus	8.78E-09	0.000632	5.84E-06	increasing	0
<i>ANKRD13C</i>	Hippocampus	1.67E-08	0.000118	0.435334	other	0
<i>ANKRD50</i>	Hippocampus	3.81E-09	-0.00064	4.39E-06	decreasing	0
<i>APC</i>	Hippocampus	2.82E-08	-0.0007	2.32E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ARHGEF37</i>	Hippocampus	8.28E-08	0.00065	2.73E-06	increasing	1
<i>ARHGEF38</i>	Hippocampus	2.14E-08	0.00076	9.84E-09	increasing	0
<i>ARL4C</i>	Hippocampus	8.94E-08	-0.00045	0.002089	other	0
<i>ASIC2</i>	Hippocampus	5.06E-08	-0.00061	1.51E-05	decreasing	0
<i>ASPM</i>	Hippocampus	4.99E-08	-0.00055	0.00012	other	0
<i>ATF7IP</i>	Hippocampus	1.29E-07	-0.00042	0.004621	other	0
<i>ATG4C</i>	Hippocampus	3.99E-08	0.000635	5.10E-06	increasing	0
<i>ATPAF1</i>	Hippocampus	1.39E-08	0.000649	2.87E-06	increasing	0
<i>B3GNT7</i>	Hippocampus	8.86E-08	-0.00057	6.14E-05	decreasing	0
<i>BAMBI</i>	Hippocampus	4.59E-10	-0.00063	6.34E-06	decreasing	0
<i>BBX</i>	Hippocampus	2.23E-08	0.000727	6.76E-08	increasing	0
<i>BCAN</i>	Hippocampus	2.28E-08	-0.00061	1.40E-05	decreasing	0
<i>BHLHE41</i>	Hippocampus	1.31E-08	0.000668	1.24E-06	increasing	0
<i>BZW2</i>	Hippocampus	1.35E-07	-0.00045	0.00226	other	0
<i>C1QTNF1</i>	Hippocampus	8.61E-10	-0.00065	3.25E-06	decreasing	0
<i>C9H10orf11</i>	Hippocampus	5.12E-07	0.000719	9.92E-08	increasing	0
<i>CALCOCO2</i>	Hippocampus	9.04E-09	0.000685	5.62E-07	increasing	0
<i>CAMKK1</i>	Hippocampus	6.45E-09	0.000573	5.42E-05	increasing	0
<i>CBX7</i>	Hippocampus	7.38E-09	0.000618	1.01E-05	increasing	0
<i>CENPE</i>	Hippocampus	1.77E-07	-0.00014	0.366224	other	0
<i>CEP170</i>	Hippocampus	9.12E-09	-0.00036	0.01438	other	0
<i>CETP</i>	Hippocampus	1.13E-12	-0.00082	1.67E-10	decreasing	0
<i>CHL1</i>	Hippocampus	2.61E-07	-0.00018	0.229705	other	0
<i>CLDN11</i>	Hippocampus	1.91E-07	-0.00048	0.000864	other	0
<i>CLDND1</i>	Hippocampus	1.83E-10	0.000816	2.41E-10	increasing	0
<i>CLIP4</i>	Hippocampus	5.68E-07	0.000708	1.81E-07	increasing	0
<i>CNDP1</i>	Hippocampus	4.35E-12	0.000778	3.26E-09	increasing	0
<i>COL15A1</i>	Hippocampus	9.30E-10	-0.00077	4.29E-09	decreasing	1
<i>COL4A1</i>	Hippocampus	3.47E-10	-0.00073	6.97E-08	decreasing	0
<i>COL8A1</i>	Hippocampus	3.60E-06	0.00072	9.71E-08	increasing	0
<i>CPB1</i>	Hippocampus	1.69E-20	0.000894	2.50E-13	increasing	0
<i>CREBRF</i>	Hippocampus	1.15E-14	0.000857	9.04E-12	increasing	0
<i>CRISPLD1</i>	Hippocampus	1.85E-09	-0.00063	7.46E-06	decreasing	0
<i>CRYBG3</i>	Hippocampus	6.34E-09	0.000714	1.35E-07	increasing	0
<i>CTNNA3</i>	Hippocampus	3.27E-08	0.00068	7.06E-07	increasing	0
<i>CWF19L2</i>	Hippocampus	3.44E-09	0.000752	1.58E-08	increasing	0
<i>CX3CL1</i>	Hippocampus	7.69E-06	-0.00073	6.28E-08	decreasing	0
<i>CXADR</i>	Hippocampus	4.86E-10	-0.00073	5.67E-08	decreasing	0
<i>DAB2</i>	Hippocampus	8.41E-08	-0.0005	0.000478	other	0
<i>DAG1</i>	Hippocampus	6.24E-09	-0.00072	7.66E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>DCX</i>	Hippocampus	1.06E-10	-0.0007	2.71E-07	decreasing	0
<i>DLGAP5</i>	Hippocampus	3.03E-08	-0.00058	2.44E-05	decreasing	0
<i>DMRTA2</i>	Hippocampus	2.51E-07	-0.00058	4.54E-05	decreasing	0
<i>DNAJB5</i>	Hippocampus	1.12E-10	-0.00078	3.15E-09	decreasing	0
<i>DNER</i>	Hippocampus	7.67E-08	-0.00067	1.20E-06	decreasing	0
<i>DOCK5</i>	Hippocampus	3.88E-13	0.000834	6.05E-11	increasing	0
<i>DPYSL3</i>	Hippocampus	1.76E-15	-0.00087	2.47E-12	decreasing	0
<i>DRAXIN</i>	Hippocampus	1.17E-09	-0.0005	0.000541	other	0
<i>EBF4</i>	Hippocampus	4.20E-08	-0.00054	0.00018	other	0
<i>EDIL3</i>	Hippocampus	2.47E-07	0.000598	2.16E-05	increasing	0
<i>EGFR</i>	Hippocampus	1.91E-07	-0.00062	1.01E-05	decreasing	0
<i>EMCN</i>	Hippocampus	5.03E-09	-0.00055	0.000115	other	0
<i>ENO4</i>	Hippocampus	1.26E-07	0.00052	0.000305	other	0
<i>ENOX1</i>	Hippocampus	6.26E-09	-0.00066	1.61E-06	decreasing	0
<i>ENPP6</i>	Hippocampus	9.77E-08	-0.00054	0.000149	other	0
<i>ERGIC1</i>	Hippocampus	4.12E-08	-0.00063	5.78E-06	decreasing	0
<i>ETS1</i>	Hippocampus	9.95E-09	-0.00064	3.58E-06	decreasing	0
<i>EVI2A</i>	Hippocampus	1.79E-08	0.000604	1.75E-05	increasing	0
<i>EZH1</i>	Hippocampus	1.61E-10	0.000739	3.44E-08	increasing	0
<i>FABP7</i>	Hippocampus	1.04E-07	-0.0005	0.000524	other	0
<i>FAM110B</i>	Hippocampus	6.56E-08	-0.00062	1.02E-05	decreasing	0
<i>FAM188A</i>	Hippocampus	1.15E-07	0.000638	4.47E-06	increasing	0
<i>FAM81A</i>	Hippocampus	1.53E-08	-0.00038	0.00989	other	0
<i>FBXL13</i>	Hippocampus	1.17E-06	0.000746	2.31E-08	increasing	0
<i>FERD3L</i>	Hippocampus	3.19E-13	0.000813	6.35E-11	increasing	0
<i>FGF1</i>	Hippocampus	4.35E-08	0.000712	1.48E-07	increasing	0
<i>FRMD3</i>	Hippocampus	2.10E-08	-0.0006	2.00E-05	decreasing	1
<i>FXYP1</i>	Hippocampus	6.93E-08	0.000369	0.012817	other	0
<i>FYN</i>	Hippocampus	9.82E-11	-0.00076	1.03E-08	decreasing	0
<i>GALNTL6</i>	Hippocampus	7.59E-12	-0.00081	5.22E-10	decreasing	0
<i>GAP43</i>	Hippocampus	1.75E-07	-0.00059	2.96E-05	decreasing	0
<i>GPC2</i>	Hippocampus	2.53E-07	-0.00061	1.48E-05	decreasing	0
<i>GPC5</i>	Hippocampus	6.90E-10	0.000671	1.07E-06	increasing	1
<i>GPNMB</i>	Hippocampus	8.77E-09	0.00066	1.80E-06	increasing	0
<i>GPR143</i>	Hippocampus	9.85E-06	0.000739	2.75E-08	increasing	0
<i>GPR17</i>	Hippocampus	7.60E-13	-0.00076	1.16E-08	decreasing	0
<i>GPRASP1</i>	Hippocampus	1.41E-07	0.000393	0.007802	other	0
<i>GPRC5B</i>	Hippocampus	4.06E-08	0.00057	6.11E-05	increasing	0
<i>GUCY1A3</i>	Hippocampus	1.14E-07	0.000586	3.43E-05	increasing	0
<i>HAPLN1</i>	Hippocampus	3.44E-11	-0.00068	6.88E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>HAPLN2</i>	Hippocampus	1.82E-09	0.000649	2.86E-06	increasing	0
<i>HERPUD2</i>	Hippocampus	3.81E-05	0.000708	1.81E-07	increasing	0
<i>HIPK3</i>	Hippocampus	8.49E-08	0.00071	1.58E-07	increasing	0
<i>HSF2</i>	Hippocampus	7.84E-08	1.88E-05	0.901619	other	0
<i>HSPA1A</i>	Hippocampus	2.22E-07	0.000571	5.71E-05	increasing	0
<i>IFI44L</i>	Hippocampus	1.80E-08	-0.00051	0.00043	other	0
<i>IGF2BP2</i>	Hippocampus	1.88E-12	-0.0008	9.96E-10	decreasing	0
<i>IGFBPL1</i>	Hippocampus	5.21E-09	-0.00057	6.49E-05	decreasing	0
<i>IGSF11</i>	Hippocampus	6.99E-08	0.000547	0.000129	other	0
<i>IGSF9</i>	Hippocampus	3.56E-09	-0.00064	4.45E-06	decreasing	0
<i>INF2</i>	Hippocampus	8.17E-08	8.85E-05	0.560793	other	0
<i>ITGA1</i>	Hippocampus	1.81E-08	-0.00052	0.000318	other	0
<i>JADE2</i>	Hippocampus	4.00E-11	0.000755	1.35E-08	increasing	0
<i>JARID2</i>	Hippocampus	5.93E-07	-0.00071	1.33E-07	decreasing	0
<i>KCNA6</i>	Hippocampus	1.99E-07	-0.00073	4.27E-08	decreasing	0
<i>KCNJ2</i>	Hippocampus	1.67E-08	0.000647	3.11E-06	increasing	0
<i>KIZ</i>	Hippocampus	2.10E-07	0.000479	0.000977	other	0
<i>KLF12</i>	Hippocampus	4.88E-08	-0.00073	5.27E-08	decreasing	0
<i>KLK6</i>	Hippocampus	1.09E-07	0.000656	2.14E-06	increasing	0
<i>LAMA2</i>	Hippocampus	1.32E-07	-0.00052	0.000285	other	0
<i>LAMA4</i>	Hippocampus	9.29E-08	-0.00053	0.000247	other	0
<i>LAMC1</i>	Hippocampus	1.76E-11	-0.00076	7.37E-09	decreasing	0
<i>LGALS1</i>	Hippocampus	3.41E-08	-0.00041	0.005281	other	0
<i>LHFPL3</i>	Hippocampus	3.64E-08	-0.00053	0.000212	other	0
<i>LIMA1</i>	Hippocampus	1.30E-07	-0.00056	9.72E-05	decreasing	0
<i>LOC103216135</i>	Hippocampus	8.34E-08	0.000645	3.44E-06	increasing	0
<i>LOC103217882</i>	Hippocampus	1.67E-08	0.000605	1.69E-05	increasing	0
<i>LOC103218181</i>	Hippocampus	2.50E-07	-0.00041	0.005911	other	0
<i>LOC103219120</i>	Hippocampus	1.60E-09	-0.00066	1.62E-06	decreasing	0
<i>LOC103221933</i>	Hippocampus	7.26E-11	-0.00069	3.26E-07	decreasing	0
<i>LOC103221935</i>	Hippocampus	7.68E-10	-0.00071	1.49E-07	decreasing	0
<i>LOC103221936</i>	Hippocampus	5.25E-08	-0.00054	0.000188	other	0
<i>LOC103221937</i>	Hippocampus	9.30E-08	-0.00053	0.000205	other	0
<i>LOC103221943</i>	Hippocampus	2.28E-10	-0.0007	1.88E-07	decreasing	0
<i>LOC103221944</i>	Hippocampus	1.26E-17	-0.00085	1.16E-11	decreasing	0
<i>LOC103221945</i>	Hippocampus	2.19E-09	-0.00065	2.72E-06	decreasing	0
<i>LOC103221970</i>	Hippocampus	1.69E-08	-0.00066	2.10E-06	decreasing	0
<i>LOC103221996</i>	Hippocampus	1.42E-07	-0.00054	0.000179	other	0
<i>LOC103222001</i>	Hippocampus	1.35E-07	-0.00067	1.18E-06	decreasing	0
<i>LOC103222003</i>	Hippocampus	1.08E-08	-0.00065	2.25E-06	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103222004</i>	Hippocampus	2.38E-07	-0.00069	5.52E-07	decreasing	0
<i>LOC103222006</i>	Hippocampus	7.32E-11	-0.0007	2.63E-07	decreasing	0
<i>LOC103222080</i>	Hippocampus	4.53E-08	-0.00041	0.004938	other	0
<i>LOC103222083</i>	Hippocampus	9.93E-12	0.000782	2.59E-09	increasing	0
<i>LOC103222369</i>	Hippocampus	2.09E-08	-0.00047	0.001217	other	0
<i>LOC103222373</i>	Hippocampus	1.54E-07	-0.00064	3.84E-06	decreasing	0
<i>LOC103222375</i>	Hippocampus	6.37E-11	0.000784	1.77E-11	increasing	0
<i>LOC103224456</i>	Hippocampus	5.75E-11	0.000746	2.28E-08	increasing	0
<i>LOC103226908</i>	Hippocampus	6.58E-13	0.000818	2.10E-10	increasing	0
<i>LOC103229779</i>	Hippocampus	7.79E-08	0.000713	1.39E-07	increasing	0
<i>LOC103230353</i>	Hippocampus	2.90E-08	0.000641	3.99E-06	increasing	0
<i>LOC103230650</i>	Hippocampus	5.79E-08	-0.00052	0.000331	other	0
<i>LOC103230800</i>	Hippocampus	1.24E-07	-0.00053	0.000257	other	0
<i>LOC103231153</i>	Hippocampus	1.98E-08	-0.00061	1.46E-05	decreasing	0
<i>LOC103231593</i>	Hippocampus	5.25E-09	0.000739	3.44E-08	increasing	0
<i>LOC103232525</i>	Hippocampus	1.25E-08	0.000654	2.30E-06	increasing	0
<i>LOC103232526</i>	Hippocampus	7.55E-09	0.000674	9.56E-07	increasing	0
<i>LOC103232983</i>	Hippocampus	7.84E-08	-0.00037	0.012755	other	0
<i>LOC103233496</i>	Hippocampus	1.18E-08	-0.00052	0.000271	other	0
<i>LOC103233517</i>	Hippocampus	8.67E-07	0.000633	2.41E-07	increasing	0
<i>LOC103234252</i>	Hippocampus	8.16E-11	0.000759	1.03E-08	increasing	0
<i>LOC103234282</i>	Hippocampus	3.96E-11	0.000692	2.63E-07	increasing	0
<i>LOC103234347</i>	Hippocampus	1.29E-07	-0.00062	1.01E-05	decreasing	0
<i>LOC103235597</i>	Hippocampus	5.51E-09	-0.00055	0.000106	other	0
<i>LOC103236607</i>	Hippocampus	8.18E-09	-0.00073	5.26E-08	decreasing	0
<i>LOC103236784</i>	Hippocampus	1.38E-07	0.000567	6.75E-05	increasing	0
<i>LOC103237777</i>	Hippocampus	3.26E-07	0.000758	1.09E-08	increasing	0
<i>LOC103237807</i>	Hippocampus	2.06E-08	0.000668	1.22E-06	increasing	0
<i>LOC103239962</i>	Hippocampus	4.22E-11	0.000741	1.86E-08	increasing	0
<i>LOC103240459</i>	Hippocampus	4.66E-06	0.000707	3.13E-09	increasing	0
<i>LOC103241513</i>	Hippocampus	5.23E-06	0.000619	1.26E-07	increasing	0
<i>LOC103243139</i>	Hippocampus	6.56E-09	0.000646	3.20E-06	increasing	0
<i>LONP2</i>	Hippocampus	7.30E-08	0.000636	5.03E-06	increasing	0
<i>LPCAT1</i>	Hippocampus	1.28E-09	-0.00077	4.38E-09	decreasing	0
<i>LRRK2</i>	Hippocampus	2.80E-09	0.00074	3.16E-08	increasing	0
<i>LTBP1</i>	Hippocampus	4.99E-11	-0.00076	1.10E-08	decreasing	0
<i>LY86</i>	Hippocampus	2.22E-07	0.000572	5.57E-05	increasing	0
<i>MARVELD1</i>	Hippocampus	3.68E-09	-0.00067	1.37E-06	decreasing	0
<i>MATN3</i>	Hippocampus	1.37E-08	-0.00063	5.63E-06	decreasing	0
<i>MAZ</i>	Hippocampus	3.27E-08	-0.00075	1.80E-08	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MBL2</i>	Hippocampus	8.29E-07	0.000638	6.83E-08	increasing	0
<i>MBNL2</i>	Hippocampus	2.22E-09	0.000736	4.05E-08	increasing	0
<i>MEX3A</i>	Hippocampus	2.38E-10	-0.00062	7.95E-06	decreasing	0
<i>MEX3B</i>	Hippocampus	1.18E-09	-0.0007	2.09E-07	decreasing	0
<i>MID1IP1</i>	Hippocampus	2.62E-08	0.000673	9.89E-07	increasing	0
<i>MKI67</i>	Hippocampus	2.90E-08	-0.00055	0.000106	other	0
<i>MKRN3</i>	Hippocampus	8.80E-13	-0.00063	5.22E-06	decreasing	0
<i>MPZL2</i>	Hippocampus	9.19E-08	0.000655	2.19E-06	increasing	0
<i>MRC2</i>	Hippocampus	1.51E-07	-0.00072	7.55E-08	decreasing	0
<i>MYC</i>	Hippocampus	3.22E-09	-0.00063	5.92E-06	decreasing	0
<i>MYO16</i>	Hippocampus	2.22E-09	-0.00068	5.86E-07	decreasing	0
<i>NAPEPLD</i>	Hippocampus	1.34E-10	0.000697	3.10E-07	increasing	0
<i>NASP</i>	Hippocampus	9.45E-09	-0.00056	8.84E-05	decreasing	0
<i>NAV1</i>	Hippocampus	1.26E-07	-0.00069	4.42E-07	decreasing	0
<i>NCAPG</i>	Hippocampus	1.91E-07	-0.00049	0.000764	other	0
<i>NCKIPSD</i>	Hippocampus	1.69E-08	0.000457	0.00175	other	0
<i>NCS1</i>	Hippocampus	2.61E-07	0.000518	0.000324	other	0
<i>NDC80</i>	Hippocampus	7.59E-09	-0.00056	4.60E-05	decreasing	0
<i>NDRG1</i>	Hippocampus	7.70E-10	0.000665	1.42E-06	increasing	0
<i>NDRG2</i>	Hippocampus	2.53E-07	0.000505	0.000475	other	0
<i>NETO2</i>	Hippocampus	2.17E-09	-0.00066	1.59E-06	decreasing	0
<i>NFATC3</i>	Hippocampus	5.82E-09	0.000674	9.47E-07	increasing	0
<i>NID1</i>	Hippocampus	1.34E-08	-0.00063	5.57E-06	decreasing	0
<i>NID2</i>	Hippocampus	7.49E-09	-0.00046	0.001514	other	0
<i>NKIRAS2</i>	Hippocampus	4.91E-08	-0.00071	1.38E-07	decreasing	0
<i>NQO1</i>	Hippocampus	2.49E-12	0.000848	2.01E-11	increasing	0
<i>NRAS</i>	Hippocampus	8.02E-08	-0.00043	0.003334	other	0
<i>NREP</i>	Hippocampus	9.57E-08	-0.00068	7.63E-07	decreasing	0
<i>NRXN1</i>	Hippocampus	9.60E-09	-0.00044	0.002442	other	0
<i>NT5DC2</i>	Hippocampus	1.07E-08	-0.00019	0.208959	other	0
<i>NTS</i>	Hippocampus	1.42E-07	-0.00013	0.374183	other	0
<i>NTSR2</i>	Hippocampus	6.48E-11	0.000748	2.08E-08	increasing	0
<i>NWD2</i>	Hippocampus	9.50E-09	-0.00073	5.79E-08	decreasing	0
<i>OTOG</i>	Hippocampus	1.84E-05	0.000721	9.01E-08	increasing	0
<i>PAMR1</i>	Hippocampus	8.79E-08	0.000577	4.68E-05	increasing	0
<i>PCDH15</i>	Hippocampus	3.27E-12	-0.00079	1.34E-09	decreasing	0
<i>PCGF5</i>	Hippocampus	1.13E-08	0.000674	9.48E-07	increasing	0
<i>PDE8A</i>	Hippocampus	2.47E-08	0.000646	3.28E-06	increasing	0
<i>PDGFRA</i>	Hippocampus	3.03E-09	-0.00064	3.85E-06	decreasing	0
<i>PFKP</i>	Hippocampus	5.17E-11	0.000731	5.29E-08	increasing	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PIP4K2A</i>	Hippocampus	1.60E-07	0.000659	1.84E-06	increasing	0
<i>PIR</i>	Hippocampus	9.48E-08	0.000634	5.30E-06	increasing	0
<i>PKP1</i>	Hippocampus	3.38E-08	-0.00076	1.15E-08	decreasing	0
<i>PLEKHB1</i>	Hippocampus	1.87E-09	0.000679	7.38E-07	increasing	0
<i>PMP22</i>	Hippocampus	4.47E-10	0.000731	5.41E-08	increasing	0
<i>PNRC1</i>	Hippocampus	1.47E-10	0.000759	1.08E-08	increasing	0
<i>PPL</i>	Hippocampus	5.47E-09	0.00072	9.42E-08	increasing	0
<i>PTK7</i>	Hippocampus	5.88E-08	-0.00056	7.46E-05	decreasing	0
<i>PTN</i>	Hippocampus	4.48E-09	-0.00065	2.63E-06	decreasing	0
<i>PTPRO</i>	Hippocampus	9.62E-08	-0.00047	0.001213	other	0
<i>PTX3</i>	Hippocampus	9.93E-08	-0.00066	2.18E-06	decreasing	0
<i>PXK</i>	Hippocampus	2.12E-08	0.000681	6.76E-07	increasing	0
<i>RAB7B</i>	Hippocampus	1.59E-11	-0.0007	2.18E-07	decreasing	0
<i>RASEF</i>	Hippocampus	1.06E-07	0.000661	1.71E-06	increasing	0
<i>RASGRF2</i>	Hippocampus	2.12E-07	0.000424	0.003889	other	0
<i>RASSF10</i>	Hippocampus	1.86E-07	-0.00054	0.000156	other	0
<i>RBP1</i>	Hippocampus	6.40E-08	-0.00061	1.37E-05	decreasing	0
<i>RHOQ</i>	Hippocampus	6.45E-07	0.000758	1.11E-08	increasing	0
<i>RIF1</i>	Hippocampus	7.88E-11	0.000794	1.14E-09	increasing	0
<i>RNF152</i>	Hippocampus	1.82E-07	-0.00066	1.78E-06	decreasing	0
<i>RPE65</i>	Hippocampus	1.67E-09	0.00064	4.21E-06	increasing	0
<i>RPRM</i>	Hippocampus	1.27E-07	-0.00065	3.26E-06	decreasing	0
<i>RRAS2</i>	Hippocampus	6.76E-10	-0.00058	4.24E-05	decreasing	0
<i>SCRG1</i>	Hippocampus	1.59E-07	-0.00053	0.000196	other	0
<i>SEL1L3</i>	Hippocampus	6.99E-08	-0.00057	5.17E-05	decreasing	0
<i>SEMA3C</i>	Hippocampus	6.12E-12	-0.00083	1.06E-10	decreasing	0
<i>SH2D5</i>	Hippocampus	6.72E-11	0.000665	1.40E-06	increasing	0
<i>SH3RF3</i>	Hippocampus	1.38E-08	-0.00075	1.91E-08	decreasing	0
<i>SIRT2</i>	Hippocampus	6.94E-08	-0.00046	0.001623	other	0
<i>SLC16A1</i>	Hippocampus	8.91E-08	-0.00039	0.00896	other	0
<i>SLC16A14</i>	Hippocampus	7.41E-08	-0.0004	0.006644	other	0
<i>SLC17A2</i>	Hippocampus	1.19E-10	0.000804	2.29E-10	increasing	0
<i>SLC17A3</i>	Hippocampus	7.36E-10	0.000817	1.69E-10	increasing	0
<i>SLC26A11</i>	Hippocampus	9.08E-08	0.000584	3.63E-05	increasing	0
<i>SLC36A1</i>	Hippocampus	8.61E-08	-0.00067	1.14E-06	decreasing	0
<i>SLC38A1</i>	Hippocampus	7.05E-08	-0.0005	0.000511	other	0
<i>SLC4A11</i>	Hippocampus	1.58E-08	0.000658	1.90E-06	increasing	0
<i>SLC5A11</i>	Hippocampus	5.60E-08	0.000564	7.28E-05	increasing	0
<i>SLCO1A2</i>	Hippocampus	5.35E-10	0.000728	6.19E-08	increasing	0
<i>SNCAIP</i>	Hippocampus	1.13E-09	-0.00067	1.29E-06	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SNED1</i>	Hippocampus	2.56E-07	0.000335	0.024616	other	0
<i>SOX11</i>	Hippocampus	1.40E-08	-0.00049	0.000762	other	0
<i>SOX4</i>	Hippocampus	3.22E-16	-0.00086	8.29E-12	decreasing	0
<i>SPOCK3</i>	Hippocampus	1.01E-06	0.000713	1.40E-07	increasing	0
<i>SPP1</i>	Hippocampus	1.06E-09	0.000753	1.54E-08	increasing	0
<i>SRD5A1</i>	Hippocampus	9.66E-09	-0.00066	1.68E-06	decreasing	0
<i>SSTR1</i>	Hippocampus	2.14E-09	-0.00065	2.64E-06	decreasing	0
<i>SULT1E1</i>	Hippocampus	2.46E-07	-0.00045	0.001943	other	0
<i>SVEP1</i>	Hippocampus	1.98E-08	0.000615	1.15E-05	increasing	0
<i>SYNE2</i>	Hippocampus	6.06E-08	-0.00052	0.000319	other	0
<i>TAGLN2</i>	Hippocampus	1.20E-07	-0.00042	0.004141	other	0
<i>TBX3</i>	Hippocampus	1.56E-07	-0.00061	1.22E-05	decreasing	0
<i>TCF4</i>	Hippocampus	1.50E-07	-0.00062	9.01E-06	decreasing	0
<i>TET3</i>	Hippocampus	1.43E-08	-0.0007	3.08E-07	decreasing	0
<i>THBS1</i>	Hippocampus	2.64E-08	-0.00061	1.17E-05	decreasing	0
<i>TMEM144</i>	Hippocampus	2.44E-07	0.000611	1.35E-05	increasing	0
<i>TMEM169</i>	Hippocampus	4.30E-10	-0.00076	9.08E-09	decreasing	0
<i>TMEM235</i>	Hippocampus	1.31E-08	0.000606	1.63E-05	increasing	0
<i>TNC</i>	Hippocampus	4.13E-09	-0.00071	1.55E-07	decreasing	0
<i>TNFAIP6</i>	Hippocampus	4.80E-09	0.000715	1.27E-07	increasing	0
<i>TNFSF13</i>	Hippocampus	5.01E-08	0.000682	6.30E-07	increasing	0
<i>TPD52L1</i>	Hippocampus	3.74E-06	0.000733	4.72E-08	increasing	0
<i>TRAF3</i>	Hippocampus	3.32E-08	-0.00068	8.86E-07	decreasing	0
<i>TRIB2</i>	Hippocampus	3.67E-09	-0.00072	1.08E-07	decreasing	0
<i>TRIO</i>	Hippocampus	3.29E-08	-0.00072	1.01E-07	decreasing	0
<i>TSPAN11</i>	Hippocampus	9.49E-08	-0.00063	5.45E-06	decreasing	0
<i>TSPAN2</i>	Hippocampus	2.55E-09	-0.00054	0.000189	other	0
<i>TUBB</i>	Hippocampus	6.15E-11	-0.0007	3.02E-07	decreasing	0
<i>UHRF1</i>	Hippocampus	4.69E-08	-0.00037	0.011886	other	0
<i>VAV2</i>	Hippocampus	7.64E-08	-0.0006	2.42E-05	decreasing	0
<i>YBX1</i>	Hippocampus	2.68E-11	-0.00073	4.31E-08	decreasing	0
<i>ZDHHC2</i>	Hippocampus	1.74E-07	-0.00049	0.000811	other	0
<i>ZDHHC20</i>	Hippocampus	6.05E-10	0.000737	3.81E-08	increasing	0
<i>ZNF483</i>	Hippocampus	1.19E-12	0.000705	2.07E-07	increasing	0
<i>AARD</i>	Pituitary	2.16E-08	-0.00059	1.12E-05	decreasing	0
<i>ABCA6</i>	Pituitary	2.68E-10	-0.00038	0.007225	other	0
<i>ABCA8</i>	Pituitary	1.66E-07	-0.00038	0.008439	other	0
<i>ACO1</i>	Pituitary	2.72E-10	0.000714	4.99E-08	increasing	1
<i>ADAM10</i>	Pituitary	8.13E-08	-0.00019	0.193038	other	0
<i>ADAM32</i>	Pituitary	1.14E-08	0.000447	0.002044	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ADAMTS9</i>	Pituitary	1.28E-08	-0.0007	2.06E-07	decreasing	0
<i>ADD2</i>	Pituitary	8.29E-07	0.000745	4.55E-09	increasing	0
<i>ADSSL1</i>	Pituitary	1.16E-07	0.000562	9.24E-05	increasing	0
<i>AGAP3</i>	Pituitary	3.38E-08	0.000494	0.000381	other	1
<i>AGFG2</i>	Pituitary	2.47E-08	0.00066	1.34E-06	increasing	0
<i>ALAD</i>	Pituitary	6.49E-08	0.000602	1.90E-05	increasing	0
<i>AMICA1</i>	Pituitary	7.07E-11	-0.00081	2.40E-10	decreasing	0
<i>AMMECR1</i>	Pituitary	8.61E-08	-0.00029	0.047845	other	0
<i>ANGEL1</i>	Pituitary	1.23E-11	0.00057	5.37E-05	increasing	0
<i>ANKEF1</i>	Pituitary	7.99E-08	0.000311	0.030649	other	0
<i>ANKRD34C</i>	Pituitary	1.75E-08	0.000678	2.24E-07	increasing	0
<i>ANKS1B</i>	Pituitary	5.80E-11	0.000597	2.61E-05	increasing	0
<i>ANLN</i>	Pituitary	5.19E-12	-0.0007	7.81E-08	decreasing	0
<i>ANXA11</i>	Pituitary	7.55E-08	0.000724	1.72E-08	increasing	1
<i>ANXA5</i>	Pituitary	4.91E-06	-0.00071	4.73E-08	decreasing	0
<i>APBA2</i>	Pituitary	1.33E-07	-0.00055	0.000144	other	0
<i>ARFGAP1</i>	Pituitary	1.02E-07	0.000396	0.006209	other	0
<i>ARHGAP11A</i>	Pituitary	2.07E-12	-0.00068	1.70E-07	decreasing	0
<i>ARHGEF17</i>	Pituitary	3.76E-08	0.000609	1.48E-05	increasing	0
<i>ARPP21</i>	Pituitary	5.46E-10	0.00031	0.031481	other	0
<i>ARX</i>	Pituitary	1.28E-11	0.00074	6.48E-09	increasing	0
<i>ASAP3</i>	Pituitary	9.52E-06	-0.00072	2.46E-08	decreasing	0
<i>ASPM</i>	Pituitary	8.98E-10	-0.00063	2.20E-06	decreasing	0
<i>ATP6VOA1</i>	Pituitary	2.00E-07	0.000607	6.51E-06	increasing	0
<i>AUH</i>	Pituitary	4.64E-08	0.000277	0.059605	other	0
<i>AURKB</i>	Pituitary	2.47E-09	-0.00065	2.06E-06	decreasing	0
<i>B4GALNT1</i>	Pituitary	1.26E-07	0.000566	6.26E-05	increasing	0
<i>BAHD1</i>	Pituitary	2.33E-10	0.000481	0.000736	other	0
<i>BAI1</i>	Pituitary	7.94E-08	0.000403	0.006436	other	0
<i>BARD1</i>	Pituitary	6.36E-09	-0.00062	9.99E-06	decreasing	0
<i>BBIP1</i>	Pituitary	7.78E-08	-0.00015	0.329145	other	0
<i>BHMT2</i>	Pituitary	4.78E-14	0.000789	1.39E-09	increasing	0
<i>BIRC5</i>	Pituitary	4.87E-11	-0.0007	7.82E-08	decreasing	0
<i>BIVM</i>	Pituitary	4.55E-08	-0.00058	4.15E-05	decreasing	0
<i>BMF</i>	Pituitary	7.78E-07	-0.0007	9.21E-08	decreasing	0
<i>BMP6</i>	Pituitary	4.77E-08	-0.00076	2.09E-09	decreasing	0
<i>BUB1</i>	Pituitary	1.05E-11	-0.00068	2.79E-07	decreasing	0
<i>BUB1B</i>	Pituitary	2.38E-12	-0.0007	1.40E-07	decreasing	0
<i>C18H18orf8</i>	Pituitary	2.79E-05	0.000678	2.33E-07	increasing	0
<i>C1H11orf53</i>	Pituitary	1.60E-11	-0.00083	1.17E-10	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>C23H5orf15</i>	Pituitary	3.55E-08	-0.00056	6.00E-05	decreasing	0
<i>C26H15orf27</i>	Pituitary	8.87E-08	0.000678	2.34E-07	increasing	0
<i>C5H16orf87</i>	Pituitary	7.59E-08	-0.00049	0.000836	other	0
<i>CA10</i>	Pituitary	3.12E-08	-0.00076	2.02E-09	decreasing	0
<i>CACNA1C</i>	Pituitary	3.02E-06	0.000708	7.25E-08	increasing	0
<i>CACNG4</i>	Pituitary	2.01E-07	-0.00063	3.98E-06	decreasing	0
<i>CALCR</i>	Pituitary	1.16E-08	0.000741	6.00E-09	increasing	0
<i>CAMK1G</i>	Pituitary	9.39E-11	-0.00061	1.86E-05	decreasing	0
<i>CAMKV</i>	Pituitary	7.64E-10	0.000648	1.03E-06	increasing	0
<i>CAPN6</i>	Pituitary	1.26E-07	-0.00066	2.50E-06	decreasing	0
<i>CASC5</i>	Pituitary	1.30E-07	-0.00056	4.70E-05	decreasing	0
<i>CASK</i>	Pituitary	3.70E-11	-0.00014	0.336776	other	0
<i>CAT</i>	Pituitary	4.69E-10	-0.00074	4.85E-08	decreasing	0
<i>CBFB</i>	Pituitary	1.39E-07	-0.00041	0.005438	other	0
<i>CBX2</i>	Pituitary	4.84E-08	-0.00073	9.72E-09	decreasing	0
<i>CBX7</i>	Pituitary	5.93E-10	0.000678	5.65E-07	increasing	0
<i>CCNB2</i>	Pituitary	2.69E-12	-0.00076	2.89E-09	decreasing	0
<i>CDC25C</i>	Pituitary	7.32E-10	-0.00058	2.87E-05	decreasing	0
<i>CDC42SE2</i>	Pituitary	1.12E-07	-0.00017	0.275365	other	0
<i>CDC45</i>	Pituitary	2.64E-09	-0.00068	1.76E-07	decreasing	1
<i>CDC6</i>	Pituitary	7.60E-12	-0.00061	9.20E-06	decreasing	0
<i>CDCA2</i>	Pituitary	4.54E-09	-0.00063	3.90E-06	decreasing	0
<i>CDCA3</i>	Pituitary	9.03E-08	-0.00058	3.26E-05	decreasing	0
<i>CDCA5</i>	Pituitary	1.47E-10	-0.00064	1.71E-06	decreasing	0
<i>CDCA7L</i>	Pituitary	3.65E-12	-0.00071	3.93E-08	decreasing	1
<i>CDCA8</i>	Pituitary	1.65E-12	-0.00074	1.34E-08	decreasing	0
<i>CDH13</i>	Pituitary	1.92E-08	-0.00079	3.04E-09	decreasing	0
<i>CDH26</i>	Pituitary	3.03E-10	0.000729	1.26E-08	increasing	0
<i>CDH7</i>	Pituitary	5.94E-08	-0.00056	4.44E-05	decreasing	0
<i>CDK1</i>	Pituitary	1.91E-12	-0.00064	3.48E-06	decreasing	0
<i>CDK19</i>	Pituitary	1.15E-07	-0.00024	0.091842	other	0
<i>CDT1</i>	Pituitary	5.45E-11	-0.00064	2.21E-06	decreasing	0
<i>CEACAM16</i>	Pituitary	8.15E-14	-0.00081	5.94E-11	decreasing	0
<i>CELF6</i>	Pituitary	2.55E-07	0.000551	5.79E-05	increasing	0
<i>CENPA</i>	Pituitary	3.80E-10	-0.0006	1.21E-05	decreasing	0
<i>CENPF</i>	Pituitary	1.27E-09	-0.00068	1.65E-07	decreasing	0
<i>CENPM</i>	Pituitary	6.52E-11	-0.00061	7.78E-06	decreasing	0
<i>CENPT</i>	Pituitary	5.60E-08	-0.00066	6.81E-07	decreasing	0
<i>CENPU</i>	Pituitary	2.84E-09	-0.00061	7.01E-06	decreasing	0
<i>CENPW</i>	Pituitary	1.85E-10	-0.00069	2.29E-07	decreasing	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>CEP55</i>	Pituitary	6.06E-12	-0.00064	2.10E-06	decreasing	0
<i>CHAF1B</i>	Pituitary	7.59E-08	-0.00025	0.094812	other	0
<i>CHL1</i>	Pituitary	2.20E-07	0.000434	0.003312	other	0
<i>CHPF2</i>	Pituitary	2.96E-08	0.000381	0.009382	other	0
<i>CHRNB1</i>	Pituitary	2.24E-06	-0.00069	1.54E-07	decreasing	0
<i>CKAP2</i>	Pituitary	1.43E-09	-0.00068	2.58E-07	decreasing	0
<i>CKS2</i>	Pituitary	8.49E-08	-0.00064	2.29E-06	decreasing	0
<i>CLDN1</i>	Pituitary	4.61E-07	-0.00069	1.18E-07	decreasing	0
<i>CLDN6</i>	Pituitary	1.66E-07	-0.00058	1.63E-05	decreasing	0
<i>CLIC4</i>	Pituitary	1.26E-07	-0.00063	2.23E-06	decreasing	0
<i>CLSPN</i>	Pituitary	1.50E-08	-0.00058	2.50E-05	decreasing	0
<i>CLTCL1</i>	Pituitary	8.20E-08	0.000674	2.83E-07	increasing	0
<i>CNOT2</i>	Pituitary	2.16E-07	-0.0003	0.03881	other	0
<i>COBL</i>	Pituitary	9.80E-06	0.000686	1.48E-07	increasing	0
<i>COL15A1</i>	Pituitary	8.57E-06	-0.00068	2.14E-07	decreasing	0
<i>COMMD2</i>	Pituitary	1.01E-09	-0.00058	2.86E-05	decreasing	0
<i>CPT1A</i>	Pituitary	4.62E-09	-0.00064	1.43E-06	decreasing	0
<i>CPXM1</i>	Pituitary	4.44E-10	-0.00067	3.22E-07	decreasing	0
<i>CRISPLD1</i>	Pituitary	1.06E-07	-0.00054	0.00012	other	1
<i>CST6</i>	Pituitary	1.94E-07	0.000205	0.171864	other	0
<i>CTDSPL2</i>	Pituitary	5.32E-08	-6.58E-05	0.663123	other	0
<i>CXCR4</i>	Pituitary	1.86E-07	-0.00074	5.13E-08	decreasing	0
<i>DAG1</i>	Pituitary	9.40E-08	-0.00053	0.000138	other	0
<i>DCBLD2</i>	Pituitary	7.70E-08	-0.00059	1.35E-05	decreasing	0
<i>DCTN1</i>	Pituitary	1.27E-07	0.000595	1.06E-05	increasing	0
<i>DDX24</i>	Pituitary	1.59E-07	0.000528	0.000128	other	0
<i>DDX27</i>	Pituitary	7.21E-08	0.00032	0.030538	other	0
<i>DDX6</i>	Pituitary	1.66E-07	-2.32E-05	0.879538	other	1
<i>DENND2D</i>	Pituitary	5.00E-09	0.000668	3.84E-07	increasing	0
<i>DENND3</i>	Pituitary	1.29E-09	0.000705	8.30E-08	increasing	0
<i>DENND5A</i>	Pituitary	8.42E-08	-0.00061	6.31E-06	decreasing	0
<i>DENND6A</i>	Pituitary	4.48E-10	-0.00033	0.025838	other	0
<i>DGKD</i>	Pituitary	9.80E-08	0.000646	4.04E-06	increasing	0
<i>DGKI</i>	Pituitary	2.89E-08	0.000701	6.67E-08	increasing	0
<i>DGKK</i>	Pituitary	4.96E-12	-0.00078	5.47E-10	decreasing	0
<i>DIAPH3</i>	Pituitary	2.44E-10	-0.00066	1.56E-06	decreasing	0
<i>DLGAP3</i>	Pituitary	5.65E-08	0.000729	1.23E-08	increasing	0
<i>DLGAP5</i>	Pituitary	1.57E-13	-0.00072	1.66E-08	decreasing	0
<i>DMGDH</i>	Pituitary	6.17E-13	0.000831	9.29E-11	increasing	0
<i>DNAJB13</i>	Pituitary	7.13E-08	-0.00067	4.18E-07	decreasing	0

**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>DOC2A</i>	Pituitary	1.94E-08	0.000537	0.000197	other	0
<i>DOCK3</i>	Pituitary	2.37E-09	0.000525	0.000207	other	0
<i>DOK6</i>	Pituitary	5.00E-08	-0.00062	8.53E-06	decreasing	0
<i>DSG2</i>	Pituitary	2.83E-09	-0.00068	5.66E-07	decreasing	0
<i>DTX4</i>	Pituitary	3.63E-07	-0.00073	1.27E-08	decreasing	0
<i>DUSP10</i>	Pituitary	2.73E-13	-0.0007	4.17E-07	decreasing	0
<i>E2F1</i>	Pituitary	3.04E-12	-0.00069	2.36E-07	decreasing	0
<i>E2F3</i>	Pituitary	1.80E-08	-0.00013	0.385425	other	0
<i>E2F8</i>	Pituitary	8.94E-11	-0.00071	4.07E-08	decreasing	0
<i>EBF4</i>	Pituitary	7.84E-08	-0.00062	7.67E-06	decreasing	0
<i>ELOVL2</i>	Pituitary	3.60E-09	-0.0007	7.06E-08	decreasing	0
<i>EME2</i>	Pituitary	1.24E-07	0.000414	0.003411	other	0
<i>EMP1</i>	Pituitary	7.36E-10	-0.00074	6.78E-09	decreasing	0
<i>ENPP2</i>	Pituitary	2.38E-09	-0.00077	1.40E-09	decreasing	0
<i>EPC1</i>	Pituitary	7.92E-08	-0.00037	0.014335	other	0
<i>EPDR1</i>	Pituitary	5.31E-08	0.000313	0.029777	other	0
<i>EPHA1</i>	Pituitary	1.06E-07	0.000653	7.89E-07	increasing	0
<i>ERGIC3</i>	Pituitary	2.38E-07	-0.00055	5.99E-05	decreasing	0
<i>ESPL1</i>	Pituitary	8.82E-08	-0.00056	5.53E-05	decreasing	0
<i>ESYT3</i>	Pituitary	2.14E-09	0.000511	0.000225	other	0
<i>EXO1</i>	Pituitary	1.62E-11	-0.00056	5.53E-05	decreasing	0
<i>EXOC2</i>	Pituitary	1.79E-05	0.000696	8.67E-08	increasing	0
<i>EZH1</i>	Pituitary	2.53E-08	0.0002	0.180289	other	0
<i>EZH2</i>	Pituitary	8.99E-10	-0.00077	8.92E-09	decreasing	0
<i>FADS2</i>	Pituitary	1.99E-07	-0.00068	2.14E-07	decreasing	0
<i>FAM107B</i>	Pituitary	4.93E-09	-0.00078	3.59E-10	decreasing	0
<i>FAM171A1</i>	Pituitary	2.24E-07	-0.00025	0.08909	other	0
<i>FAM49A</i>	Pituitary	1.86E-07	-8.63E-05	0.571467	other	0
<i>FAM64A</i>	Pituitary	3.49E-09	-0.00057	4.34E-05	decreasing	0
<i>FANCI</i>	Pituitary	3.49E-08	-0.00052	0.000236	other	0
<i>FBN2</i>	Pituitary	3.29E-10	-0.00068	1.64E-07	decreasing	1
<i>FBXL7</i>	Pituitary	2.19E-14	-0.00086	3.25E-13	decreasing	0
<i>FCHSD2</i>	Pituitary	1.43E-09	0.000549	0.000133	other	0
<i>FGF1</i>	Pituitary	7.71E-08	0.000152	0.299614	other	0
<i>FGF9</i>	Pituitary	9.34E-08	-0.00047	0.00145	other	0
<i>FILIP1</i>	Pituitary	5.10E-08	9.96E-05	0.512384	other	0
<i>FLRT3</i>	Pituitary	9.49E-08	-0.00029	0.044883	other	0
<i>FOXP2</i>	Pituitary	1.25E-09	-0.0002	0.185594	other	0
<i>FOXP1</i>	Pituitary	6.05E-10	0.000186	0.216935	other	1
<i>FRMD4A</i>	Pituitary	2.66E-07	-0.00072	1.97E-08	decreasing	0



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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>FRRS1L</i>	Pituitary	1.93E-07	0.000557	4.57E-05	increasing	0
<i>FSTL1</i>	Pituitary	1.94E-12	-0.00064	1.29E-06	decreasing	0
<i>FUT8</i>	Pituitary	8.11E-10	-0.00063	6.41E-06	decreasing	0
<i>FUT9</i>	Pituitary	2.77E-09	-0.00077	6.20E-10	decreasing	0
<i>GABRD</i>	Pituitary	5.96E-07	0.000761	1.09E-08	increasing	0
<i>GAREML</i>	Pituitary	5.17E-08	-0.00066	1.24E-06	decreasing	0
<i>GBE1</i>	Pituitary	8.28E-09	0.000652	2.72E-06	increasing	0
<i>GBGT1</i>	Pituitary	1.04E-09	0.000651	1.95E-06	increasing	0
<i>GDPD1</i>	Pituitary	7.59E-09	-0.00054	8.96E-05	decreasing	0
<i>GFOD1</i>	Pituitary	9.88E-06	0.00072	9.25E-08	increasing	0
<i>GHR</i>	Pituitary	5.18E-12	-0.00074	7.62E-09	decreasing	0
<i>GML</i>	Pituitary	1.58E-07	-0.00055	6.59E-05	decreasing	0
<i>GNAL</i>	Pituitary	1.04E-09	0.000736	8.32E-09	increasing	0
<i>GOLGA2</i>	Pituitary	3.83E-08	0.000472	0.00074	other	0
<i>GPC3</i>	Pituitary	9.32E-07	-0.00073	9.47E-09	decreasing	0
<i>GPNMB</i>	Pituitary	1.11E-07	0.000329	0.028274	other	0
<i>GPR37</i>	Pituitary	3.41E-08	-0.00064	1.82E-06	decreasing	0
<i>GPR61</i>	Pituitary	1.45E-10	0.000744	5.01E-09	increasing	0
<i>GPR64</i>	Pituitary	2.43E-07	-0.00068	1.70E-07	decreasing	0
<i>GPRASP1</i>	Pituitary	1.67E-07	0.000583	2.87E-05	increasing	0
<i>GPSM2</i>	Pituitary	1.31E-09	-0.00063	2.68E-06	decreasing	0
<i>GPX7</i>	Pituitary	8.63E-10	-0.0007	8.81E-08	decreasing	0
<i>GRB7</i>	Pituitary	1.29E-09	-0.00082	1.91E-10	decreasing	0
<i>GRIN1</i>	Pituitary	1.35E-07	0.00036	0.014831	other	0
<i>GTDC1</i>	Pituitary	1.77E-13	-0.00077	5.19E-09	decreasing	0
<i>GTSE1</i>	Pituitary	1.13E-08	-0.00035	0.018126	other	0
<i>H3F3B</i>	Pituitary	8.42E-07	-0.0007	2.06E-07	decreasing	0
<i>HERC3</i>	Pituitary	5.16E-08	0.000618	1.10E-05	increasing	0
<i>HEY1</i>	Pituitary	4.36E-06	-0.00069	1.04E-07	decreasing	1
<i>HIF1AN</i>	Pituitary	1.18E-07	0.000579	2.02E-05	increasing	0
<i>HJURP</i>	Pituitary	1.38E-11	-0.00079	1.40E-10	decreasing	0
<i>HMGA2</i>	Pituitary	1.02E-11	-0.00055	9.95E-05	decreasing	0
<i>HMGB2</i>	Pituitary	8.34E-10	-0.00071	5.42E-08	decreasing	0
<i>HMMR</i>	Pituitary	9.97E-10	-0.00064	2.60E-06	decreasing	0
<i>HPGD</i>	Pituitary	1.78E-08	0.000453	0.00146	other	0
<i>HPSE2</i>	Pituitary	1.40E-13	0.00084	1.12E-11	increasing	0
<i>HS6ST3</i>	Pituitary	2.86E-08	0.000774	6.30E-10	increasing	0
<i>HSF4</i>	Pituitary	7.76E-10	0.000579	1.97E-05	increasing	0
<i>HSPA12A</i>	Pituitary	1.31E-09	0.000709	2.13E-07	increasing	0
<i>HSPA12B</i>	Pituitary	2.07E-07	4.90E-05	0.748949	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>HTR2C</i>	Pituitary	3.36E-09	-0.00067	2.83E-07	decreasing	0
<i>ID2</i>	Pituitary	3.96E-07	-0.00072	1.45E-07	decreasing	0
<i>IDH2</i>	Pituitary	3.87E-06	-0.0007	7.38E-08	decreasing	0
<i>IGF2BP2</i>	Pituitary	3.89E-19	-0.00074	1.89E-08	decreasing	0
<i>IGF2BP3</i>	Pituitary	8.72E-14	-0.00071	1.51E-07	decreasing	1
<i>IGSF9</i>	Pituitary	3.17E-08	-0.00073	1.35E-08	decreasing	0
<i>IL12RB2</i>	Pituitary	1.73E-10	0.000669	3.67E-07	increasing	0
<i>IMPAD1</i>	Pituitary	2.31E-07	0.000108	0.478114	other	0
<i>INPP5B</i>	Pituitary	8.39E-08	0.000625	8.67E-06	increasing	0
<i>INSM2</i>	Pituitary	3.80E-08	-0.00047	0.000706	other	0
<i>IQGAP3</i>	Pituitary	1.75E-14	-0.00069	1.25E-07	decreasing	0
<i>IQSEC1</i>	Pituitary	6.79E-06	0.000699	1.54E-07	increasing	0
<i>IRAK1BP1</i>	Pituitary	2.82E-09	-0.00033	0.025494	other	0
<i>IVD</i>	Pituitary	2.30E-07	0.00049	0.000784	other	0
<i>JADE2</i>	Pituitary	1.80E-10	0.000765	3.86E-09	increasing	0
<i>KCNJ16</i>	Pituitary	1.57E-08	-0.00058	1.88E-05	decreasing	0
<i>KCNK4</i>	Pituitary	4.04E-09	8.03E-05	0.597249	other	0
<i>KCNMB2</i>	Pituitary	2.27E-07	-0.00057	3.16E-05	decreasing	1
<i>KCNMB4</i>	Pituitary	7.91E-08	-0.00074	4.57E-08	decreasing	0
<i>KIAA0101</i>	Pituitary	1.49E-10	-0.00065	1.39E-06	decreasing	0
<i>KIF11</i>	Pituitary	3.68E-09	-0.00066	1.01E-06	decreasing	0
<i>KIF14</i>	Pituitary	1.33E-12	-0.00066	1.02E-06	decreasing	0
<i>KIF15</i>	Pituitary	7.87E-11	-0.00065	1.28E-06	decreasing	0
<i>KIF18A</i>	Pituitary	3.70E-09	-0.00065	1.69E-06	decreasing	0
<i>KIF18B</i>	Pituitary	1.01E-10	-0.00063	4.46E-06	decreasing	0
<i>KIF20A</i>	Pituitary	7.11E-12	-0.0007	5.52E-08	decreasing	0
<i>KIF22</i>	Pituitary	2.40E-07	-0.00032	0.030378	other	0
<i>KIF23</i>	Pituitary	4.40E-12	-0.00076	1.43E-09	decreasing	0
<i>KIF24</i>	Pituitary	2.47E-08	-0.00063	3.31E-06	decreasing	0
<i>KIF4A</i>	Pituitary	5.40E-08	-0.00049	0.000419	other	0
<i>KIFC1</i>	Pituitary	3.81E-12	-0.00073	1.32E-08	decreasing	0
<i>KLF11</i>	Pituitary	6.24E-09	-0.00072	7.62E-08	decreasing	0
<i>KLF9</i>	Pituitary	4.08E-07	-0.0007	2.24E-07	decreasing	0
<i>KLHL35</i>	Pituitary	3.38E-08	9.22E-06	0.949937	other	0
<i>KNSTRN</i>	Pituitary	5.95E-08	-0.00053	0.000227	other	0
<i>KRT222</i>	Pituitary	1.44E-08	0.000616	4.32E-06	increasing	0
<i>L3MBTL4</i>	Pituitary	3.11E-06	0.000691	1.16E-07	increasing	0
<i>LAMP5</i>	Pituitary	1.21E-07	0.000655	7.23E-07	increasing	0
<i>LARGE</i>	Pituitary	1.96E-07	0.000133	0.37348	other	0
<i>LCTL</i>	Pituitary	6.70E-09	0.000566	7.12E-05	increasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LEPRE1</i>	Pituitary	1.89E-07	0.000109	0.473458	other	0
<i>LHB</i>	Pituitary	9.19E-09	0.000586	2.04E-05	increasing	0
<i>LHX1</i>	Pituitary	9.37E-11	0.000777	5.69E-10	increasing	0
<i>LMNB1</i>	Pituitary	1.54E-10	-0.00073	2.82E-08	decreasing	0
<i>LOC103214618</i>	Pituitary	1.50E-07	-8.53E-05	0.574564	other	0
<i>LOC103214631</i>	Pituitary	1.42E-11	-0.00076	2.09E-09	decreasing	0
<i>LOC103214728</i>	Pituitary	1.96E-07	-0.00019	0.201796	other	0
<i>LOC103215200</i>	Pituitary	3.20E-08	0.000771	2.09E-09	increasing	0
<i>LOC103216175</i>	Pituitary	1.78E-10	-0.00071	4.31E-08	decreasing	0
<i>LOC103217048</i>	Pituitary	1.98E-07	-0.00019	0.195206	other	0
<i>LOC103217216</i>	Pituitary	2.21E-07	-0.00068	4.96E-07	decreasing	0
<i>LOC103217305</i>	Pituitary	8.86E-09	0.000221	0.146041	other	0
<i>LOC103218075</i>	Pituitary	8.60E-11	0.000589	1.78E-05	increasing	0
<i>LOC103218076</i>	Pituitary	3.13E-10	0.000486	0.00048	other	0
<i>LOC103218277</i>	Pituitary	1.71E-07	0.000512	0.000367	other	0
<i>LOC103218335</i>	Pituitary	3.34E-11	0.000442	0.001678	other	0
<i>LOC103218411</i>	Pituitary	2.94E-16	-0.00086	2.83E-13	decreasing	0
<i>LOC103218542</i>	Pituitary	2.63E-08	0.000589	3.08E-05	increasing	0
<i>LOC103219103</i>	Pituitary	3.54E-08	8.92E-05	0.495257	other	0
<i>LOC103219120</i>	Pituitary	3.54E-10	-0.00068	7.66E-07	decreasing	0
<i>LOC103219315</i>	Pituitary	1.14E-07	-0.00018	0.238379	other	0
<i>LOC103219354</i>	Pituitary	3.44E-11	0.000795	1.26E-10	increasing	0
<i>LOC103219428</i>	Pituitary	2.13E-07	0.000403	0.005925	other	0
<i>LOC103219460</i>	Pituitary	1.28E-09	-0.00069	2.14E-07	decreasing	0
<i>LOC103219462</i>	Pituitary	5.11E-08	5.09E-05	0.73726	other	0
<i>LOC103219590</i>	Pituitary	1.77E-07	-0.00037	0.001841	other	0
<i>LOC103219792</i>	Pituitary	1.09E-06	0.000687	1.41E-07	increasing	0
<i>LOC103219855</i>	Pituitary	4.87E-08	-0.00074	5.39E-09	decreasing	0
<i>LOC103219911</i>	Pituitary	1.02E-07	0.000627	8.85E-06	increasing	0
<i>LOC103219975</i>	Pituitary	1.79E-07	-1.01E-05	0.945764	other	0
<i>LOC103220165</i>	Pituitary	3.31E-08	-2.11E-05	0.889454	other	0
<i>LOC103220998</i>	Pituitary	4.00E-08	-9.57E-05	0.531582	other	0
<i>LOC103221024</i>	Pituitary	1.05E-07	-0.0006	2.14E-05	decreasing	0
<i>LOC103221138</i>	Pituitary	4.79E-09	0.000604	1.55E-05	increasing	1
<i>LOC103221174</i>	Pituitary	7.60E-08	-9.88E-05	0.51972	other	0
<i>LOC103221872</i>	Pituitary	6.93E-08	-6.92E-05	0.651738	other	0
<i>LOC103221955</i>	Pituitary	1.78E-06	-0.00071	2.47E-07	decreasing	0
<i>LOC103222369</i>	Pituitary	3.34E-08	-0.00038	0.011209	other	0
<i>LOC103222606</i>	Pituitary	3.32E-08	0.000158	0.278407	other	0
<i>LOC103222782</i>	Pituitary	2.19E-07	-0.00055	8.81E-05	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103222981	Pituitary	2.47E-09	0.000738	4.26E-08	increasing	0
LOC103222983	Pituitary	4.55E-09	0.000764	1.09E-08	increasing	0
LOC103223289	Pituitary	8.27E-08	-0.00067	1.77E-06	decreasing	0
LOC103223587	Pituitary	9.21E-08	-0.00073	5.96E-08	decreasing	0
LOC103224129	Pituitary	2.46E-07	-0.00055	7.53E-05	decreasing	0
LOC103224287	Pituitary	3.04E-08	0.000694	9.53E-08	increasing	0
LOC103224472	Pituitary	7.86E-08	9.61E-05	0.527648	other	0
LOC103225055	Pituitary	2.71E-08	-0.00014	0.345271	other	0
LOC103225142	Pituitary	9.18E-09	0.000201	0.180355	other	0
LOC103225340	Pituitary	6.65E-09	-0.00016	0.296274	other	0
LOC103225920	Pituitary	2.65E-08	0.000628	2.60E-06	increasing	0
LOC103225927	Pituitary	1.53E-08	0.000536	0.00021	other	0
LOC103226240	Pituitary	1.76E-09	-0.00069	1.32E-07	decreasing	1
LOC103226832	Pituitary	7.26E-08	-0.00019	0.19036	other	0
LOC103227289	Pituitary	1.28E-07	-0.00036	0.010676	other	0
LOC103227374	Pituitary	2.06E-09	-2.63E-05	0.860944	other	0
LOC103227574	Pituitary	6.38E-08	5.42E-05	0.722817	other	0
LOC103227729	Pituitary	1.88E-07	9.88E-05	0.518053	other	0
LOC103228401	Pituitary	3.93E-12	-0.00026	0.081612	other	0
LOC103228968	Pituitary	6.43E-09	-0.00055	5.62E-05	decreasing	0
LOC103229111	Pituitary	1.34E-07	-0.00051	0.000396	other	0
LOC103229159	Pituitary	7.55E-08	8.33E-05	0.587156	other	0
LOC103229280	Pituitary	8.16E-08	-0.00024	0.107457	other	0
LOC103229506	Pituitary	6.06E-08	-0.00041	0.00589	other	0
LOC103230251	Pituitary	6.26E-08	-0.00012	0.436205	other	0
LOC103230509	Pituitary	1.83E-07	0.000206	0.156064	other	0
LOC103231548	Pituitary	6.61E-15	-0.00081	4.56E-11	decreasing	0
LOC103231594	Pituitary	7.50E-09	-0.00076	1.34E-09	decreasing	0
LOC103231881	Pituitary	1.45E-07	-0.00028	0.06546	other	0
LOC103231992	Pituitary	4.28E-09	-0.00056	5.97E-05	decreasing	0
LOC103232002	Pituitary	1.18E-07	-0.00064	1.28E-06	decreasing	0
LOC103232225	Pituitary	4.77E-09	0.000542	7.95E-05	increasing	0
LOC103232226	Pituitary	2.34E-08	-0.0003	0.038708	other	0
LOC103232245	Pituitary	8.52E-08	-0.00031	0.035828	other	0
LOC103232333	Pituitary	1.47E-07	-9.65E-05	0.529292	other	0
LOC103232555	Pituitary	7.00E-08	0.000164	0.284849	other	0
LOC103232871	Pituitary	1.19E-07	2.79E-06	0.98538	other	0
LOC103232947	Pituitary	1.15E-07	-0.00019	0.197767	other	0
LOC103232983	Pituitary	2.34E-07	-0.00066	8.95E-07	decreasing	0
LOC103233707	Pituitary	6.64E-08	-0.0008	1.19E-09	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
LOC103234108	Pituitary	1.09E-07	0.000535	3.96E-08	increasing	0
LOC103234274	Pituitary	8.56E-11	-0.00068	1.63E-07	decreasing	0
LOC103234284	Pituitary	1.32E-07	-0.00069	3.88E-07	decreasing	0
LOC103235307	Pituitary	8.57E-07	-0.00074	1.99E-08	decreasing	0
LOC103235309	Pituitary	9.64E-08	-0.00059	1.46E-05	decreasing	0
LOC103235467	Pituitary	1.39E-07	0.000171	0.261698	other	0
LOC103236002	Pituitary	1.17E-07	-0.00028	0.057752	other	0
LOC103236199	Pituitary	9.03E-13	-0.0008	1.41E-10	decreasing	0
LOC103236243	Pituitary	3.37E-09	-0.00015	0.317606	other	0
LOC103236840	Pituitary	6.21E-08	0.000354	0.013291	other	0
LOC103236916	Pituitary	2.49E-07	0.00045	0.001552	other	0
LOC103237276	Pituitary	9.40E-08	0.000171	0.2624	other	0
LOC103237807	Pituitary	1.39E-07	0.000276	0.066719	other	1
LOC103238262	Pituitary	7.66E-07	-0.00069	2.40E-07	decreasing	1
LOC103238634	Pituitary	1.63E-07	-3.22E-05	0.826266	other	0
LOC103238842	Pituitary	8.91E-09	-7.52E-05	0.620709	other	0
LOC103238939	Pituitary	1.43E-07	-2.02E-05	0.893057	other	0
LOC103239026	Pituitary	2.43E-07	-0.00051	0.000473	other	0
LOC103239517	Pituitary	1.75E-07	7.52E-05	0.622125	other	0
LOC103239658	Pituitary	2.44E-09	0.00016	0.280692	other	0
LOC103239792	Pituitary	3.44E-09	4.13E-05	0.785355	other	0
LOC103239878	Pituitary	2.21E-09	-6.47E-05	0.670011	other	0
LOC103240211	Pituitary	1.21E-07	3.83E-05	0.803313	other	0
LOC103240224	Pituitary	1.63E-07	-0.0002	0.163017	other	0
LOC103240328	Pituitary	5.79E-08	-9.03E-05	0.551426	other	0
LOC103240641	Pituitary	1.77E-11	-0.00064	1.56E-06	decreasing	0
LOC103240855	Pituitary	2.52E-08	0.000142	0.331933	other	0
LOC103241031	Pituitary	3.81E-08	9.78E-05	0.522686	other	0
LOC103241174	Pituitary	3.20E-08	-0.00049	0.000392	other	0
LOC103241267	Pituitary	4.04E-08	0.000723	1.84E-08	increasing	0
LOC103241849	Pituitary	6.15E-08	-0.00057	2.94E-05	decreasing	0
LOC103241853	Pituitary	2.76E-08	0.00039	0.006704	other	0
LOC103241917	Pituitary	5.03E-08	4.72E-05	0.758372	other	0
LOC103242103	Pituitary	1.17E-09	0.000454	0.001522	other	0
LOC103242222	Pituitary	9.12E-08	-0.00051	0.000509	other	0
LOC103242242	Pituitary	1.84E-07	0.000699	7.38E-08	increasing	1
LOC103242515	Pituitary	1.52E-09	0.00069	5.09E-07	increasing	0
LOC103243079	Pituitary	4.22E-10	0.000743	2.37E-08	increasing	0
LOC103243406	Pituitary	4.49E-08	-0.00018	0.227996	other	0
LOC103243446	Pituitary	3.31E-08	-0.00071	1.46E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>LOC103243499</i>	Pituitary	4.51E-08	0.000253	0.081332	other	0
<i>LOC103243892</i>	Pituitary	6.62E-08	-0.00075	2.50E-08	decreasing	0
<i>LOC103243906</i>	Pituitary	2.45E-08	-0.00018	0.212245	other	0
<i>LOC103243977</i>	Pituitary	1.22E-07	-0.00061	1.48E-05	decreasing	0
<i>LOC103244172</i>	Pituitary	8.41E-09	-8.62E-05	0.571624	other	0
<i>LOC103244309</i>	Pituitary	8.66E-09	-4.57E-05	0.764355	other	0
<i>LOC103244593</i>	Pituitary	2.60E-07	-0.00026	0.068328	other	0
<i>LOC103244645</i>	Pituitary	5.48E-10	0.000742	5.57E-09	increasing	0
<i>LOC103244685</i>	Pituitary	5.89E-08	0.000685	2.40E-07	increasing	0
<i>LOC103244696</i>	Pituitary	5.59E-10	0.000788	1.20E-09	increasing	0
<i>LOC103245138</i>	Pituitary	1.36E-12	0.000698	2.97E-07	increasing	0
<i>LOC103245179</i>	Pituitary	2.10E-07	0.000554	0.000114	other	1
<i>LOC103245450</i>	Pituitary	2.28E-08	5.80E-05	0.705125	other	0
<i>LOC103245680</i>	Pituitary	9.49E-08	-0.00027	0.071303	other	0
<i>LOC103246064</i>	Pituitary	7.73E-08	-0.00068	2.17E-07	decreasing	0
<i>LOC103246132</i>	Pituitary	6.84E-08	-5.32E-05	0.728237	other	0
<i>LOC103246527</i>	Pituitary	3.32E-08	-0.0002	0.170428	other	1
<i>LOC103246578</i>	Pituitary	1.33E-07	0.000607	1.13E-05	increasing	0
<i>LOC103246876</i>	Pituitary	8.57E-08	-0.00063	7.47E-06	decreasing	0
<i>LOC103248222</i>	Pituitary	7.68E-08	-4.11E-05	0.788388	other	0
<i>LPAR4</i>	Pituitary	7.98E-09	-0.00074	8.28E-09	decreasing	0
<i>LPIN1</i>	Pituitary	1.27E-07	0.000594	1.74E-05	increasing	0
<i>LRAT</i>	Pituitary	7.08E-08	0.000532	0.000242	other	0
<i>LRRC10B</i>	Pituitary	1.51E-07	0.000469	0.000807	other	0
<i>LRRC48</i>	Pituitary	1.37E-07	0.000225	0.132195	other	0
<i>LRRC4C</i>	Pituitary	4.34E-10	-0.00047	0.00096	other	0
<i>LUZP2</i>	Pituitary	7.34E-09	-0.00073	6.25E-08	decreasing	1
<i>MAP1A</i>	Pituitary	4.96E-06	0.000725	5.13E-08	increasing	0
<i>MAP2K6</i>	Pituitary	5.89E-10	-0.00062	3.75E-06	decreasing	0
<i>MARCH1</i>	Pituitary	1.84E-07	0.00078	2.83E-09	increasing	0
<i>MARCKSL1</i>	Pituitary	1.30E-07	-0.00075	2.79E-09	decreasing	0
<i>MCM3</i>	Pituitary	8.26E-08	-0.00055	6.60E-05	decreasing	0
<i>MCM5</i>	Pituitary	8.97E-08	-0.00056	5.37E-05	decreasing	0
<i>MCTP2</i>	Pituitary	8.07E-06	0.000696	8.59E-08	increasing	0
<i>MEGF10</i>	Pituitary	1.22E-07	0.0003	0.037269	other	0
<i>MELK</i>	Pituitary	1.29E-10	-0.00069	1.21E-07	decreasing	0
<i>MFAP2</i>	Pituitary	6.58E-11	-0.00079	1.99E-10	decreasing	0
<i>MIS18BP1</i>	Pituitary	3.41E-08	-0.00042	0.003531	other	0
<i>MKI67</i>	Pituitary	2.07E-10	-0.00068	3.55E-07	decreasing	0
<i>MKRN3</i>	Pituitary	6.84E-09	-0.00062	1.07E-05	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>MMP14</i>	Pituitary	4.24E-06	-0.00071	4.10E-08	decreasing	0
<i>MMP16</i>	Pituitary	3.48E-08	-0.00054	8.44E-05	decreasing	0
<i>MOXD1</i>	Pituitary	1.63E-07	-0.00069	9.53E-08	decreasing	0
<i>MPPED2</i>	Pituitary	3.38E-10	-0.00078	2.56E-09	decreasing	0
<i>MSI1</i>	Pituitary	2.00E-06	-0.00072	2.07E-08	decreasing	0
<i>MUC15</i>	Pituitary	3.01E-11	-0.00073	2.24E-08	decreasing	0
<i>MXD3</i>	Pituitary	1.61E-07	-0.00049	0.000371	other	0
<i>MYADML2</i>	Pituitary	1.32E-09	-0.00042	0.004321	other	0
<i>MYBL2</i>	Pituitary	2.77E-12	-0.00074	5.86E-09	decreasing	0
<i>MYCN</i>	Pituitary	1.79E-10	-0.00074	2.16E-08	decreasing	0
<i>NASP</i>	Pituitary	6.80E-10	-0.00071	1.70E-07	decreasing	0
<i>NAT16</i>	Pituitary	2.30E-07	0.000444	0.001584	other	0
<i>NCAPG</i>	Pituitary	8.37E-08	-0.00077	3.81E-09	decreasing	0
<i>NDC80</i>	Pituitary	3.99E-11	-0.00072	1.88E-08	decreasing	0
<i>NECAB1</i>	Pituitary	3.60E-08	0.000673	1.23E-06	increasing	0
<i>NEFH</i>	Pituitary	3.55E-15	0.000774	6.06E-10	increasing	0
<i>NEFL</i>	Pituitary	4.41E-18	0.000855	6.10E-13	increasing	0
<i>NEFM</i>	Pituitary	6.64E-11	0.00066	5.61E-07	increasing	0
<i>NEIL3</i>	Pituitary	3.47E-08	-0.00055	6.86E-05	decreasing	0
<i>NEK2</i>	Pituitary	1.41E-08	-0.00061	8.48E-06	decreasing	0
<i>NFIA</i>	Pituitary	3.06E-08	-0.00041	0.003857	other	0
<i>NHSL1</i>	Pituitary	9.63E-08	-0.00077	1.11E-08	decreasing	0
<i>NKX2.8</i>	Pituitary	2.33E-07	0.000782	1.55E-09	increasing	0
<i>NLGN3</i>	Pituitary	5.56E-08	-0.00073	9.77E-09	decreasing	0
<i>NOP9</i>	Pituitary	2.88E-08	0.000278	0.066323	other	0
<i>NPW</i>	Pituitary	6.13E-08	0.000455	0.001974	other	0
<i>NREP</i>	Pituitary	2.23E-19	-0.00089	1.11E-14	decreasing	0
<i>NRG2</i>	Pituitary	5.41E-10	0.000699	1.14E-07	increasing	0
<i>NRTN</i>	Pituitary	1.52E-08	-0.00075	4.68E-09	decreasing	0
<i>NT5DC2</i>	Pituitary	5.93E-08	-0.00053	0.0002	other	0
<i>NTF3</i>	Pituitary	1.21E-09	-0.00068	1.79E-07	decreasing	0
<i>NTM</i>	Pituitary	1.87E-07	-0.0003	0.045251	other	0
<i>NUCKS1</i>	Pituitary	2.27E-07	8.24E-06	0.95526	other	0
<i>NUF2</i>	Pituitary	2.66E-11	-0.00071	4.95E-08	decreasing	0
<i>NUP155</i>	Pituitary	1.02E-07	3.94E-05	0.796819	other	0
<i>NUSAP1</i>	Pituitary	8.59E-12	-0.00078	1.45E-09	decreasing	0
<i>NXPE3</i>	Pituitary	6.21E-08	0.000537	9.36E-05	increasing	0
<i>ODC1</i>	Pituitary	2.62E-09	-0.00075	1.10E-08	decreasing	0
<i>OSBPL2</i>	Pituitary	9.30E-10	0.000752	2.88E-09	increasing	0
<i>P2RY1</i>	Pituitary	1.04E-11	-0.00077	9.31E-10	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>PADI2</i>	Pituitary	1.26E-08	-0.00067	3.05E-07	decreasing	0
<i>PARP4</i>	Pituitary	8.74E-08	0.000713	1.63E-07	increasing	1
<i>PBK</i>	Pituitary	1.18E-13	-0.0007	1.28E-07	decreasing	0
<i>PCCB</i>	Pituitary	2.04E-08	0.000433	0.002132	other	0
<i>PCDH11X</i>	Pituitary	6.15E-08	-0.00073	1.49E-08	decreasing	0
<i>PCDH20</i>	Pituitary	4.06E-10	-8.35E-05	0.581363	other	0
<i>PCDH8</i>	Pituitary	4.87E-10	0.000464	0.001592	other	0
<i>PCDH9</i>	Pituitary	3.49E-09	-0.00047	0.00078	other	0
<i>PCLO</i>	Pituitary	2.13E-06	0.000693	1.00E-07	increasing	0
<i>PDCD1</i>	Pituitary	9.98E-08	0.000482	0.000986	other	0
<i>PDF</i>	Pituitary	9.23E-08	0.000131	0.388336	other	0
<i>PDPN</i>	Pituitary	2.42E-08	-0.00071	3.47E-08	decreasing	0
<i>PGBD5</i>	Pituitary	4.95E-10	0.000756	2.20E-09	increasing	0
<i>PHGDH</i>	Pituitary	3.11E-10	-0.00079	9.71E-10	decreasing	0
<i>PI4KA</i>	Pituitary	2.52E-10	0.000801	2.53E-10	increasing	0
<i>PIBF1</i>	Pituitary	2.35E-07	-0.00043	0.002455	other	0
<i>PINLYP</i>	Pituitary	1.20E-07	0.000586	1.50E-05	increasing	0
<i>PLD2</i>	Pituitary	4.25E-06	-0.00072	1.92E-08	decreasing	0
<i>PLEKHA5</i>	Pituitary	2.06E-07	-0.00043	0.00203	other	0
<i>PLS1</i>	Pituitary	1.22E-08	0.0006	8.50E-06	increasing	0
<i>PNOC</i>	Pituitary	2.51E-08	-0.00068	1.98E-07	decreasing	0
<i>PNPLA5</i>	Pituitary	1.60E-07	0.000349	0.014724	other	0
<i>PNPO</i>	Pituitary	6.31E-08	0.000277	0.055606	other	0
<i>POC1A</i>	Pituitary	2.03E-08	-0.00068	1.93E-07	decreasing	0
<i>POLE2</i>	Pituitary	1.23E-08	-0.00055	9.79E-05	decreasing	0
<i>POU6F2</i>	Pituitary	3.55E-12	0.000631	2.29E-06	increasing	0
<i>PPARGC1A</i>	Pituitary	2.24E-07	-0.00057	2.44E-05	decreasing	0
<i>PPP2R2C</i>	Pituitary	4.72E-07	0.000702	6.29E-08	increasing	0
<i>PRICKLE1</i>	Pituitary	1.33E-09	-1.49E-06	0.992032	other	0
<i>PRLHR</i>	Pituitary	1.07E-05	0.00068	2.08E-07	increasing	0
<i>PRRT4</i>	Pituitary	6.87E-07	-0.00073	8.53E-08	decreasing	0
<i>PTCHD4</i>	Pituitary	2.58E-08	0.000514	0.000204	other	0
<i>PTGFRN</i>	Pituitary	1.98E-08	-0.00056	4.82E-05	decreasing	1
<i>PVRL3</i>	Pituitary	9.96E-08	-0.00053	0.000107	other	0
<i>QRFPR</i>	Pituitary	1.29E-12	-0.00076	1.71E-09	decreasing	0
<i>QSOX2</i>	Pituitary	3.72E-08	0.000372	0.008981	other	0
<i>RAB29</i>	Pituitary	2.57E-07	0.000512	0.000387	other	0
<i>RAI1</i>	Pituitary	2.85E-07	0.000712	1.20E-07	increasing	0
<i>RALGPS2</i>	Pituitary	1.66E-06	0.000721	2.01E-08	increasing	0
<i>RBBP8</i>	Pituitary	7.33E-12	-0.00068	8.76E-07	decreasing	0



**Supplementary Table 9. Genes with a significant age effect from either ANOVA or linear regression. Beta is the regression coefficient, Pval is the p-value for the regression coefficient of expression on age (in days). Effect category is increasing if beta is positive and significant, decreasing if beta is negative and significant, and other if the ANOVA were significant rather than the linear regression. Local eQTL is 1 if the gene had a significant local eQTL**

Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>RBM20</i>	Pituitary	2.48E-11	0.000805	8.83E-10	increasing	0
<i>RBM7</i>	Pituitary	8.24E-08	-7.36E-05	0.624091	other	0
<i>RBMS1</i>	Pituitary	2.27E-07	-0.00065	1.03E-06	decreasing	0
<i>RBP4</i>	Pituitary	1.39E-11	0.000279	0.053863	other	0
<i>RCN1</i>	Pituitary	5.73E-10	-0.00071	3.20E-08	decreasing	0
<i>RCN2</i>	Pituitary	2.85E-07	-0.00075	4.23E-09	decreasing	0
<i>RGS13</i>	Pituitary	6.22E-08	-0.00073	2.27E-08	decreasing	0
<i>RHOU</i>	Pituitary	5.74E-10	-0.0006	1.40E-05	decreasing	0
<i>RIMS2</i>	Pituitary	1.55E-05	0.00069	1.22E-07	increasing	0
<i>RIMS4</i>	Pituitary	4.48E-08	0.000481	0.000891	other	0
<i>RIN1</i>	Pituitary	4.49E-09	0.000618	1.15E-05	increasing	0
<i>RIT1</i>	Pituitary	2.44E-07	-0.00038	0.008693	other	0
<i>RMI1</i>	Pituitary	1.08E-08	-0.00027	0.05804	other	0
<i>RMI2</i>	Pituitary	8.12E-09	-0.00062	5.77E-06	decreasing	0
<i>RRP12</i>	Pituitary	3.28E-08	0.000292	0.045528	other	0
<i>RSPO2</i>	Pituitary	1.33E-05	0.000713	1.84E-07	increasing	0
<i>RTKN2</i>	Pituitary	3.83E-08	0.000128	0.401169	other	0
<i>RUNX3</i>	Pituitary	3.24E-09	0.000544	0.000122	other	0
<i>SCARB2</i>	Pituitary	7.41E-08	-0.00069	1.14E-07	decreasing	0
<i>SCN2A</i>	Pituitary	2.33E-07	0.000721	2.10E-08	increasing	0
<i>SEC16B</i>	Pituitary	7.27E-10	0.000471	0.000747	other	0
<i>SEPT8</i>	Pituitary	2.57E-09	0.000346	0.020116	other	0
<i>SERINC2</i>	Pituitary	5.48E-10	-0.00072	8.62E-08	decreasing	0
<i>SGOL1</i>	Pituitary	4.68E-11	-0.00064	3.27E-06	decreasing	0
<i>SGOL2</i>	Pituitary	7.37E-10	-0.00067	5.02E-07	decreasing	0
<i>SHH</i>	Pituitary	1.67E-08	-0.00051	0.000223	other	0
<i>SKA2</i>	Pituitary	7.83E-09	-0.00043	0.003094	other	0
<i>SKA3</i>	Pituitary	1.11E-07	-0.00043	0.002514	other	0
<i>SKAP2</i>	Pituitary	1.17E-15	0.000831	3.22E-11	increasing	1
<i>SLC15A1</i>	Pituitary	6.02E-09	-0.00076	1.01E-08	decreasing	0
<i>SLC16A9</i>	Pituitary	5.76E-08	-0.00066	1.20E-06	decreasing	0
<i>SLC25A45</i>	Pituitary	2.04E-10	0.000546	0.000112	other	0
<i>SLC39A10</i>	Pituitary	1.11E-07	-0.0006	7.55E-06	decreasing	0
<i>SLC46A3</i>	Pituitary	7.93E-08	0.0007	2.74E-07	increasing	1
<i>SLC6A5</i>	Pituitary	6.51E-08	0.000567	4.03E-05	increasing	0
<i>SLC8A2</i>	Pituitary	1.28E-06	0.000706	4.95E-08	increasing	0
<i>SLC9A6</i>	Pituitary	1.95E-07	-0.00057	2.99E-05	decreasing	0
<i>SLCO1C1</i>	Pituitary	3.07E-10	-0.00071	4.48E-08	decreasing	0
<i>SLITRK1</i>	Pituitary	3.10E-10	-0.00074	8.00E-09	decreasing	0
<i>SLITRK5</i>	Pituitary	1.71E-07	-0.00055	0.000134	other	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>SMARCA2</i>	Pituitary	2.68E-05	0.000696	8.52E-08	increasing	0
<i>SMEK2</i>	Pituitary	1.66E-07	-0.00022	0.149273	other	0
<i>SMPDL3A</i>	Pituitary	4.48E-09	-0.00063	2.85E-06	decreasing	0
<i>SNRPA1</i>	Pituitary	1.38E-07	-0.00056	4.98E-05	decreasing	0
<i>SNX1</i>	Pituitary	4.03E-08	0.000235	0.122224	other	0
<i>SOX11</i>	Pituitary	1.38E-12	-0.00072	2.70E-08	decreasing	1
<i>SPARC</i>	Pituitary	4.93E-08	-0.00063	1.91E-06	decreasing	0
<i>SPATS2L</i>	Pituitary	1.80E-08	-0.00068	2.67E-07	decreasing	0
<i>SPC25</i>	Pituitary	1.78E-12	-0.00073	1.57E-08	decreasing	0
<i>SPINK2</i>	Pituitary	1.06E-10	-0.00071	8.91E-08	decreasing	0
<i>SPR</i>	Pituitary	7.17E-08	0.000116	0.446065	other	0
<i>SPTBN4</i>	Pituitary	3.03E-08	0.000607	6.50E-06	increasing	0
<i>SPTSSA</i>	Pituitary	5.44E-09	-0.00064	1.76E-06	decreasing	0
<i>SREK1IP1</i>	Pituitary	1.39E-08	-1.79E-05	0.906728	other	0
<i>ST6GAL2</i>	Pituitary	1.55E-08	-0.00055	5.12E-05	decreasing	0
<i>ST8SIA4</i>	Pituitary	2.24E-07	-0.00057	3.52E-05	decreasing	0
<i>STAT4</i>	Pituitary	1.94E-08	0.000726	1.48E-08	increasing	0
<i>STAT5B</i>	Pituitary	1.13E-07	0.000472	0.000722	other	0
<i>STEAP2</i>	Pituitary	1.86E-07	0.000722	3.26E-08	increasing	0
<i>STMN4</i>	Pituitary	6.68E-09	-0.00072	1.48E-07	decreasing	0
<i>SWAP70</i>	Pituitary	3.10E-08	-0.00039	0.00561	other	0
<i>SYCE3</i>	Pituitary	1.12E-07	-0.00061	5.61E-06	decreasing	0
<i>SYNE1</i>	Pituitary	5.54E-09	0.000761	1.53E-09	increasing	0
<i>SYT7</i>	Pituitary	2.79E-08	0.000612	5.25E-06	increasing	0
<i>TAC1</i>	Pituitary	4.31E-11	0.000233	0.117846	other	0
<i>TACC3</i>	Pituitary	5.40E-10	-0.00053	0.000158	other	0
<i>TBC1D1</i>	Pituitary	3.59E-10	0.000643	3.09E-06	increasing	0
<i>TBX1</i>	Pituitary	2.63E-08	0.00014	0.360831	other	0
<i>TBX20</i>	Pituitary	2.40E-09	-0.00067	5.99E-07	decreasing	0
<i>TCF19</i>	Pituitary	2.22E-07	-0.00058	2.84E-05	decreasing	0
<i>TEX40</i>	Pituitary	1.34E-07	-2.35E-05	0.876543	other	0
<i>TICRR</i>	Pituitary	1.45E-07	-0.0006	1.12E-05	decreasing	0
<i>TK1</i>	Pituitary	1.68E-07	-0.00063	2.45E-06	decreasing	0
<i>TMEFF1</i>	Pituitary	2.46E-09	-0.00063	4.98E-06	decreasing	0
<i>TMEM114</i>	Pituitary	6.53E-08	0.000364	0.010832	other	0
<i>TMEM155</i>	Pituitary	2.03E-09	-0.00075	2.40E-09	decreasing	0
<i>TMEM191C</i>	Pituitary	2.39E-08	0.000291	0.046088	other	0
<i>TMEM238</i>	Pituitary	3.96E-09	0.000149	0.327797	other	0
<i>TMEM257</i>	Pituitary	3.08E-08	-0.00066	4.96E-07	decreasing	0
<i>TMEM74</i>	Pituitary	2.14E-08	-0.00068	3.12E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>TMEM86B</i>	Pituitary	1.84E-07	0.000469	0.001153	other	0
<i>TMOD1</i>	Pituitary	9.91E-08	0.000608	6.20E-06	increasing	0
<i>TMPO</i>	Pituitary	1.59E-08	-0.00058	1.97E-05	decreasing	0
<i>TMSB15A</i>	Pituitary	2.82E-09	-0.00043	0.002583	other	0
<i>TMSB15B</i>	Pituitary	1.61E-11	-0.00079	6.92E-10	decreasing	0
<i>TNFRSF10B</i>	Pituitary	1.94E-09	0.000429	0.003745	other	0
<i>TNFRSF19</i>	Pituitary	5.46E-09	-0.00069	1.22E-07	decreasing	0
<i>TOP2A</i>	Pituitary	8.71E-12	-0.00072	1.87E-08	decreasing	0
<i>TPH2</i>	Pituitary	4.67E-09	0.000401	0.004683	other	0
<i>TPX2</i>	Pituitary	2.36E-11	-0.00076	1.21E-09	decreasing	0
<i>TRADD</i>	Pituitary	1.70E-07	0.000322	0.029594	other	0
<i>TROAP</i>	Pituitary	4.05E-13	-0.00067	6.64E-07	decreasing	0
<i>TRPV3</i>	Pituitary	2.41E-07	0.000678	9.63E-07	increasing	0
<i>TSHB</i>	Pituitary	6.78E-08	6.48E-05	0.658726	other	0
<i>TSHZ3</i>	Pituitary	1.44E-09	0.000828	1.68E-10	increasing	0
<i>TSPAN2</i>	Pituitary	4.99E-06	-0.00071	1.68E-07	decreasing	0
<i>TSPYL1</i>	Pituitary	1.01E-07	0.000618	6.52E-06	increasing	1
<i>TSPYL2</i>	Pituitary	1.38E-08	0.000657	6.73E-07	increasing	0
<i>TTC39A</i>	Pituitary	1.08E-08	0.000649	9.57E-07	increasing	0
<i>TTK</i>	Pituitary	2.81E-08	-0.00058	3.08E-05	decreasing	0
<i>TUBA8</i>	Pituitary	5.80E-06	0.000689	1.28E-07	increasing	1
<i>TUBB1</i>	Pituitary	5.06E-08	-0.00034	0.022517	other	0
<i>UBE2C</i>	Pituitary	8.73E-10	-0.00066	1.33E-06	decreasing	0
<i>UCP3</i>	Pituitary	5.63E-08	-0.00043	0.002436	other	0
<i>UGCG</i>	Pituitary	1.55E-07	-0.00023	0.111464	other	0
<i>UHRF1</i>	Pituitary	7.38E-10	-0.00077	1.08E-09	decreasing	0
<i>USP11</i>	Pituitary	9.94E-08	0.000747	7.36E-09	increasing	0
<i>VEGFC</i>	Pituitary	7.34E-08	-0.00071	3.16E-08	decreasing	0
<i>VSIG1</i>	Pituitary	3.26E-12	-0.00068	7.33E-07	decreasing	0
<i>VSNL1</i>	Pituitary	2.27E-07	0.000689	4.70E-07	increasing	0
<i>VSTM2A</i>	Pituitary	7.20E-12	-0.0008	8.85E-10	decreasing	0
<i>WEE1</i>	Pituitary	5.58E-08	-0.00068	5.53E-07	decreasing	0
<i>WFS1</i>	Pituitary	6.83E-08	0.00062	3.74E-06	increasing	0
<i>WNT1</i>	Pituitary	1.25E-09	-0.00019	0.191262	other	0
<i>WNT10B</i>	Pituitary	3.74E-10	-0.00016	0.273472	other	0
<i>WNT5A</i>	Pituitary	6.07E-12	-0.0008	1.00E-09	decreasing	0
<i>XPC</i>	Pituitary	1.91E-07	-1.19E-05	0.937335	other	0
<i>XPR1</i>	Pituitary	1.87E-07	-0.00038	0.00817	other	0
<i>ZFP42</i>	Pituitary	1.61E-10	-0.00071	1.95E-07	decreasing	1
<i>ZNF185</i>	Pituitary	1.05E-07	-0.00072	1.38E-07	decreasing	0

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Gene	Tissue	Anova.pval	Beta	Pval	EffectCategory	Local eQTL
<i>ZNF22</i>	Pituitary	1.25E-08	-0.00064	3.80E-06	decreasing	0
<i>ZNF311</i>	Pituitary	1.68E-06	-0.00073	1.48E-08	decreasing	0
<i>ZNF367</i>	Pituitary	1.25E-10	-0.00053	0.000104	other	0
<i>ZNF521</i>	Pituitary	5.28E-17	-0.00083	4.53E-12	decreasing	0
<i>ZNF543</i>	Pituitary	5.74E-09	7.94E-05	0.604762	other	0
<i>ZNF596</i>	Pituitary	1.77E-07	-0.00029	0.041848	other	0
<i>ZNF711</i>	Pituitary	4.03E-09	-0.00069	2.27E-07	decreasing	0
<i>ZWINT</i>	Pituitary	4.86E-08	-0.00044	0.00228	other	0

**Supplementary Table 10. The proportion of Bonferroni-significant eQTL from Dataset 2 to fall in four SNP MAF bins**

	eQTL MAF bin			
	10-20%	20-30%	30-40%	40-50%
<b>Local eQTL</b>				
Adrenal	0.018	0.172	0.354	0.456
BA46	0.021	0.191	0.359	0.429
Blood	0.004	0.248	0.312	0.435
Caudate	0.015	0.158	0.354	0.472
Fibroblast	0.025	0.175	0.347	0.453
Hippocampus	0.02	0.16	0.351	0.468
Pituitary	0.017	0.182	0.389	0.412
<b>Distant eQTL</b>				
Adrenal	0.003	0.283	0.387	0.327
BA46	0.007	0.262	0.51	0.222
Blood	0	0.5	0.333	0.167
Caudate	0.014	0.161	0.437	0.388
Fibroblast	0.018	0.125	0.539	0.318
Hippocampus	0.018	0.246	0.294	0.441
Pituitary	0.067	0.143	0.258	0.532

**Supplementary Table 11. Investigation of enrichment of local eQTL in genes with significant age effect**

Tissue	EffectCategory	OR	Pval
Adrenal	decreasing	0.25	3.33E-08
Adrenal	increasing	0.38	0.001864
Adrenal	other	0.27	1.56E-08
BA46	decreasing	0.55	8.38E-05
BA46	increasing	0.48	2.47E-05
BA46	other	0.63	0.050519
Caudate	decreasing	0.35	6.97E-17
Caudate	increasing	0.53	2.26E-09
Caudate	other	0.30	1.36E-27
Pituitary	decreasing	0.34	2.82E-05
Pituitary	increasing	0.53	0.07869
Pituitary	other	0.23	2.70E-06

**Supplementary Table 12. Comparison of specific genes with local eQTL in Vervet Dataset 2 to GTEx. The number of genes with at least one significant local eQTL in Vervet (at Bonferroni thresholds) are presented**

Tissue	# Local eQTL Vervet Genes <sup>a</sup>	# Vervet Genes with Human Ortholog	# Genes Tested in GTEx <sup>b</sup>	% Tested Genes p<0.05	% Tested Genes p<0.05/#tested Genes	% Tested Genes significant genome-wide in GTEx <sup>d</sup>
Adrenal	555	317	279	100%	49.10%	25.80%
Blood	60	16	14	100%	100%	35.70%
Caudate	441	225	196	100%	50.00%	18.40%
Hippocampus	361	187	168	100%	49.40%	14.30%
Pituitary	596	303	282	100%	45.00%	18.70%

<sup>a</sup>The number of genes with at least one significant local eQTL in Vervet, at Bonferroni corrected threshold ( $p < 6.5 \times 10^{-10}$ )

<sup>b</sup>Vervet genes with a human ortholog that were not tested in GTEx were filtered by their QC procedures

<sup>c</sup>The threshold for significance corrected for the number of genes compared between Vervet and GTEx (column 4).

<sup>d</sup>Genes were declared significant in GTEx at an FDR of 0.05

**Supplementary Table 13. Comparison of Vervet eQTL with Common Mind Consortium (CMC)****Vervet local eQTL at Bonferroni  
Thresholds**

Tissue	# Local eQTL Vervet Genes	# Vervet Genes with Human Ortholog	# Genes Tested in CMC	% Tested Genes CMC FDR<0.20	% Tested Genes significant genome- wide in CMC
BA46	307	183	130	100%	90.77%
Caudate	441	225	151	100%	87.42%
Hippocampus	361	187	137	99%	87.59%

**Vervet eQTL at FDR thresholds**

BA46	2251	1346	1079	99%	88.60%
Caudate	3079	1712	1316	99%	87.61%
Hippocampus	2377	1391	1115	99%	88.25%



**Supplementary Table 14. Counts of local eQTL in regions indicated by regulatory regions/features**

<b>Feature</b>	<b>Local+/Feature+</b>	<b>Local+/Feature-</b>	<b>Local-/Feature+</b>	<b>Local-/Feature-</b>
Exon	44	1158	433	16829
Intron	587	615	6879	10383
Flank	52	1150	448	16814
Intergenic	519	683	9501	7761
Liver Me <sup>a</sup>	7	1195	32	17230
Liver Ac <sup>b</sup>	78	1124	582	16680
Rhesus caudate Ac <sup>c</sup>	60	1142	391	16871
Rhesus prefrontal Ac <sup>d</sup>	41	1161	308	16954

<sup>a</sup>H3K4me3 marks in vervet liver

<sup>b</sup>H3K27ac marks in vervet liver

<sup>c</sup>vervet orthologous location of HDK27ac epigenetic marks in rhesus macaque caudate

<sup>d</sup>vervet orthologous location of HDK27ac epigenetic marks in rhesus macaque prefrontal cortex

Supplementary Table 15. Genes with distant eQTL on vervet chromosome 9. Gene position is given as the start of the probe that interrogates the gene, in base pairs (bp). N.distant.eQTL=number of distant eQTL for each gene in Dataset 1. SNPStart (bp) and SNPEnd (bp) present the range of positions for the associated SNPs. MinP.RNASeq.Blood is the minimum p-value obtained in evaluating association of SNPs and gene expression in Dataset 2 (RNA-Seq data). N.p<0.05 are the number of N.distant.eQTL SNPs with p<0.05 in RNA Seq analysis of gene expression in blood in Dataset 2. Pct Var is the range of percent variance in gene expression explained by SNPs in Dataset 1

VervetGeneSymbol	GeneChr	GeneStart (bp)	N.distant.eQTL	SNPChr	SNPStart (bp)	SNPEnd (bp)	MinP.RNASeq.Blood	N.p<0.05	Pct Var
<i>LCMT1</i>	chr5	22869269	76	chr9	82109236	83568492	9.90E-03	15	18%-35%
<i>UQCR10</i>	chr19	12644416	76	chr9	82109236	83568492	9.61E-02	0	15%-34%
<i>ST7</i>	chr21	85897845	152	chr9	82109236	83568492	8.28E-06	150	17%-33%
<i>YPEL4</i>	chr1	15584795	61	chr9	82109236	83568492	1.97E-06	61	16%-37%
<i>TMEM57</i>	chr20	107272832	15	chr9	82159100	83514443	8.92E-03	8	18%-25%
<i>UBALD1</i>	chr5	4295792	19	chr9	82159100	83514443	1.46E-01	0	18%-24%
<i>RANBP10</i>	chr5	59710718	42	chr9	82529804	83514443	2.07E-04	24	18%-23%
<i>NARF</i>	chr16	74400831	13	chr9	82542787	83514443	5.72E-03	9	16%-25%
<i>STXBP1</i>	chr12	10448338	11	chr9	82542787	82852576	2.10E-02	8	16%-21%
<i>CNN3</i>	chr20	38356395	16	chr9	82544812	83514443	2.17E-01	0	16%-28%
<i>DEDD2</i>	chr6	36402731	4	chr9	82632170	82694171	2.05E-02	2	16%-20%
<i>HMBS</i>	chr1	110460930	8	chr9	82632170	82870235	2.54E-01	0	17%-20%
<i>THBS4</i>	chr4	74274870	5	chr9	82632170	82852576	1.76E-01	0	19%-22%
<i>SUGT1</i>	chr3	30439128	1	chr9	82694171	82694171	4.79E-01	0	22%

**Supplementary Table 16. SNP-Probe combinations to have Bonferroni significant replication of microarray CAE9 distant eQTL in RNA-Seq data. There are 27 unique SNPs associated to two genes.**

SNP	Probe	VervetSymbol	Microarray Beta	Microarray P-value	RNA-Seq Beta	RNA-Seq P-value
CAE9_82105141	ILMN_1702175	ST7	0.54	2.68E-13	0.73	1.65E-05
CAE9_82106171	ILMN_1702175	ST7	0.50	1.65E-12	0.72	2.09E-05
CAE9_82115648	ILMN_1702175	ST7	0.55	2.21E-13	0.73	1.65E-05
CAE9_82671816	ILMN_1702175	ST7	0.63	2.79E-15	0.73	1.70E-05
CAE9_82159980	ILMN_1702175	ST7	0.50	8.86E-13	0.72	2.09E-05
CAE9_82171963	ILMN_1702175	ST7	0.55	2.06E-13	0.73	1.65E-05
CAE9_82197823	ILMN_1702175	ST7	0.50	8.86E-13	0.72	2.09E-05
CAE9_82252528	ILMN_1702175	ST7	0.55	1.07E-13	0.73	1.65E-05
CAE9_82462519	ILMN_1702175	ST7	0.55	1.07E-13	0.73	1.65E-05
CAE9_83183703	ILMN_1702175	ST7	0.51	2.32E-12	0.73	1.20E-05
CAE9_82753918	ILMN_1702175	ST7	0.63	9.65E-18	0.74	8.28E-06
CAE9_82792461	ILMN_1702175	ST7	0.63	9.65E-18	0.74	8.28E-06
CAE9_83279014	ILMN_1702175	ST7	0.55	3.98E-14	0.75	1.07E-05
CAE9_82115648	ILMN_1707763	ST7	0.62	4.23E-14	0.73	1.65E-05
CAE9_82120987	ILMN_1707763	ST7	0.64	2.65E-12	0.75	7.60E-06
CAE9_82171963	ILMN_1707763	ST7	0.63	1.84E-14	0.73	1.65E-05
CAE9_82179403	ILMN_1707763	ST7	0.62	7.24E-12	0.75	7.60E-06
CAE9_82197823	ILMN_1707763	ST7	0.54	2.77E-12	0.72	2.09E-05
CAE9_82159980	ILMN_1707763	ST7	0.54	2.77E-12	0.72	2.09E-05
CAE9_83183703	ILMN_1707763	ST7	0.60	5.92E-14	0.73	1.20E-05
CAE9_82252528	ILMN_1707763	ST7	0.64	7.30E-15	0.73	1.65E-05
CAE9_82308161	ILMN_1707763	ST7	0.65	3.56E-13	0.73	1.70E-05
CAE9_82462519	ILMN_1707763	ST7	0.64	7.30E-15	0.73	1.65E-05
CAE9_82671816	ILMN_1707763	ST7	0.75	1.59E-17	0.73	1.70E-05
CAE9_82753918	ILMN_1707763	ST7	0.72	7.10E-19	0.74	8.28E-06
CAE9_82792461	ILMN_1707763	ST7	0.72	7.10E-19	0.74	8.28E-06
CAE9_82105141	ILMN_1707763	ST7	0.62	3.74E-14	0.73	1.65E-05
CAE9_82106171	ILMN_1707763	ST7	0.54	6.26E-12	0.72	2.09E-05
CAE9_83248692	ILMN_1707763	ST7	0.59	3.36E-12	0.73	1.33E-05
CAE9_83279014	ILMN_1707763	ST7	0.65	2.18E-16	0.75	1.07E-05
CAE9_83429364	ILMN_1707763	ST7	0.58	7.68E-12	0.73	1.68E-05
CAE9_83183703	ILMN_1726624	YPEL4	0.57	9.14E-13	0.74	4.99E-06
CAE9_82792461	ILMN_1726624	YPEL4	0.67	3.50E-16	0.77	1.97E-06
CAE9_82853104	ILMN_1726624	YPEL4	0.62	8.82E-15	0.73	6.65E-06
CAE9_82015581	ILMN_1726624	YPEL4	0.66	6.65E-12	0.92	2.96E-06
CAE9_82105141	ILMN_1726624	YPEL4	0.60	5.02E-13	0.74	6.08E-06
CAE9_82115648	ILMN_1726624	YPEL4	0.60	8.44E-13	0.74	6.08E-06
CAE9_82116623	ILMN_1726624	YPEL4	0.57	4.68E-12	0.71	1.78E-05
CAE9_82171963	ILMN_1726624	YPEL4	0.60	3.13E-13	0.74	6.08E-06
CAE9_82252528	ILMN_1726624	YPEL4	0.60	3.43E-13	0.74	6.08E-06
CAE9_82302393	ILMN_1726624	YPEL4	0.57	1.95E-12	0.71	1.78E-05
CAE9_82308161	ILMN_1726624	YPEL4	0.68	2.07E-14	0.78	1.98E-06
CAE9_82404232	ILMN_1726624	YPEL4	0.63	4.21E-13	0.73	8.56E-06
CAE9_82439232	ILMN_1726624	YPEL4	0.57	1.95E-12	0.71	1.78E-05
CAE9_82462519	ILMN_1726624	YPEL4	0.60	3.43E-13	0.74	6.08E-06
CAE9_82671816	ILMN_1726624	YPEL4	0.77	3.89E-18	0.78	1.98E-06
CAE9_82694171	ILMN_1726624	YPEL4	1.03	2.99E-27	0.90	7.85E-06
CAE9_82747272	ILMN_1726624	YPEL4	0.59	7.01E-14	0.73	6.65E-06
CAE9_82753918	ILMN_1726624	YPEL4	0.67	3.50E-16	0.77	1.97E-06
CAE9_83248692	ILMN_1726624	YPEL4	0.62	1.38E-13	0.77	1.77E-06
CAE9_83279014	ILMN_1726624	YPEL4	0.60	1.27E-13	0.73	1.09E-05
CAE9_83321719	ILMN_1726624	YPEL4	0.62	1.58E-13	0.74	6.07E-06
CAE9_83429364	ILMN_1726624	YPEL4	0.64	3.33E-14	0.79	9.43E-07

**Supplementary Table 17. Genetic correlation of expression of *IFIT1B* (ILMN\_1759155) with 14 genes with distant eQTL on CAE9, in Dataset 1.**

<b>VervetGeneSymbol</b>	<b>Probe</b>	<b>rhoG</b>	<b>rhoGSE</b>	<b>P-value for rhoG=0</b>	<b>P-value for rhoG=1</b>
<i>RANBP10</i>	ILMN_1667306	0.912	0.038	4.92E-11	1.77E-03
<i>SUGT1</i>	ILMN_1687675	0.670	0.089	6.50E-07	9.55E-10
<i>LCMT1</i>	ILMN_1688452	0.830	0.063	2.79E-10	6.21E-05
<i>HMBS</i>	ILMN_1694476	0.899	0.065	3.86E-07	8.17E-02
<i>ST7</i>	ILMN_1702175	0.874	0.064	9.20E-12	4.95E-03
<i>ST7</i>	ILMN_1707763	0.921	0.054	7.30E-13	3.82E-02
<i>TMEM57</i>	ILMN_1718831	0.845	0.055	4.15E-09	1.03E-04
<i>YPEL4</i>	ILMN_1726624	0.940	0.030	5.53E-13	5.39E-03
<i>NARF</i>	ILMN_1726884	0.789	0.058	1.47E-10	1.56E-10
<i>UBALD1</i>	ILMN_1733863	0.852	0.053	1.18E-10	3.10E-06
<i>THBS4</i>	ILMN_1736078	0.822	0.063	1.52E-11	1.10E-05
<i>DEDD3</i>	ILMN_1768031	0.649	0.098	8.25E-06	2.00E-07
<i>UQCR10</i>	ILMN_1781986	0.873	0.056	6.70E-14	6.30E-04
<i>CNN3</i>	ILMN_1782439	0.710	0.089	1.15E-05	7.62E-05
<i>STXBP1</i>	ILMN_1810657	0.705	0.077	1.72E-07	4.95E-09

**Supplementary Table 18. Association analysis of CAE9\_82694171 with gene expression of 14 genes, in Dataset 1. Analysis is also done conditional on expression of gene *IFIT1B*, for which CAE9\_82694171 is a local eQTL**

Probe	VervetGeneSymbol	Unconditional analysis			Conditional on <i>IFIT1B</i> expression		
		Beta	P-value	Variance Explained	Beta	P-value	Variance Explained
ILMN_1667306	<i>RANBP10</i>	-0.81	5.33E-17	22.64%	0.12	5.23E-02	1.21%
ILMN_1687675	<i>SUGT1</i>	-0.73	1.53E-15	21.58%	-0.25	6.83E-03	3.22%
ILMN_1688452	<i>LCMT1</i>	-1.05	5.74E-28	35.12%	-0.45	1.40E-07	8.85%
ILMN_1694476	<i>HMBS</i>	-0.74	3.09E-15	19.68%	0.06	4.09E-01	0.26%
ILMN_1702175	<i>ST7</i>	-0.84	9.06E-23	30.18%	-0.44	1.66E-07	7.61%
ILMN_1707763	<i>ST7</i>	-0.96	2.00E-24	33.18%	-0.51	1.55E-08	9.95%
ILMN_1718831	<i>TMEM57</i>	-0.88	1.03E-18	25.37%	-0.06	4.15E-01	0.26%
ILMN_1726624	<i>YPEL4</i>	-1.03	4.47E-29	36.55%	-0.27	3.50E-05	4.81%
ILMN_1726884	<i>NARF</i>	-0.81	3.07E-16	24.94%	-0.21	1.94E-02	1.76%
ILMN_1733863	<i>UBALD1</i>	-0.69	7.95E-18	23.31%	-0.12	8.15E-02	0.79%
ILMN_1736078	<i>THBS4</i>	-0.69	5.19E-13	18.59%	-0.14	1.22E-01	0.43%
ILMN_1768031	<i>DEDD2</i>	-0.70	5.48E-13	19.55%	-0.19	5.05E-02	1.99%
ILMN_1781986	<i>UQCR10</i>	-0.90	5.81E-25	31.93%	-0.45	7.96E-08	9.04%
ILMN_1782439	<i>CNN3</i>	-0.90	1.12E-19	27.77%	-0.27	4.43E-03	3.51%
ILMN_1810657	<i>STXBP1</i>	-0.79	2.67E-15	20.92%	-0.07	4.08E-01	0.48%

**Supplementary Table 19. (A) Unconditional (univariate) analyses of hippocampal expression of three genes as a function of lead SNPs for each gene. (B) Conditional (multivariate) analysis of hippocampal expression of three genes as a function of the gene's lead SNP and the lead SNP for one of the other genes. Lead SNPs are colored as: red=*LOC103222765* ; blue=*LOC103222769* ; green=*LOC103222771***

A. Unconditional (Univariate) Analysis			
Response Variable	Explanatory Variable	Beta	P-value
<i>LOC103222765</i>	CAE18_68730707	-1.152	1.10E-10
	CAE18_68915135	0.219	0.204
	CAE18_68931864	-0.210	0.275
<i>LOC103222769</i>	CAE18_68730707	0.227	0.237
	CAE18_68915135	-0.901	3.67E-11
	CAE18_68931864	-0.920	3.66E-08
<i>LOC103222771</i>	CAE18_68730707	-0.499	0.011
	CAE18_68915135	-0.662	1.06E-05
	CAE18_68931864	-0.953	7.83E-10
B. Conditional (Multivariate) Analyses			
Response Variable	Explanatory Variables	Beta	P-value
<i>LOC103222765</i>	CAE18_68730707	-1.1652	3.48E-10
	CAE18_68915135	-0.0349	0.776
	CAE18_68730707	-1.1412	2.60E-10
	CAE18_68931864	-0.0667	0.616
<i>LOC103222769</i>	CAE18_68915135	-0.9108	1.06E-10
	CAE18_68730707	-0.0454	0.735
	CAE18_68915135	-0.6925	5.37E-05
	CAE18_68931864	-0.3288	0.078
<i>LOC103222771</i>	CAE18_68931864	-0.9084	9.19E-10
	CAE18_68730707	-0.361	0.010
	CAE18_68931864	-0.9135	1.96E-05
	CAE18_68915135	-0.0479	0.785

**Supplementary Table 20. RNA-seq summary by Tissue**

<b>Tissue type</b>	<b>RNA extraction method</b>	<b>cDNA libraries and RNA-seq reads</b>	<b>Average Input Reads [Mln]</b>	<b>% of uniquely aligned reads</b>
Adrenal	PerfectPure (N=57) and miRNeasy (N=3)	polyA (no RiboZero) 2x100bp, 2x120bp	56.4	90
BA46	PerfectPure (N=55) and miRNeasy (N=3)	total RNA (RiboZero) 2x120bp	58	77.3
Blood	PaxGene (N=60)	total RNA (RiboZero) 2x100bp	56.5	78
Caudate	PerfectPure (N=54), miRNeasy (N=5)	total RNA (RiboZero) 2x100bp	60.3	86.8
Fibroblast	miRNeasy (N=60)	polyA (no RiboZero) 2x100bp, 2x120bp	60.9	89.2
Hippocampus	PerfectPure (N=56) and miRNeasy (N=3)	total RNA (RiboZero) 2x100bp	45.1	78.9
Pituitary	PerfectPure (N=55) and miRNeasy (N=5)	polyA (no RiboZero) 2x100bp, 2x120bp	59.3	90.1

**Supplementary Table 21. Approximate chronologic age correspondence between Vervet and Human**

<b>Human Age*</b>	<b>Human Developmental Period*</b>	<b>Vervet Age</b>	<b>Vervet Category</b>	<b>Vervet Transcriptome Age Categories**</b>
Birth-5 months	Early infancy	0 to 1 month	Neonates	1d, <b>7d</b> , 30d
6-18 months	Late infancy	1.5 to 4.5 months	Young infants	60d, <b>90d</b>
19 months-5 yrs	Early childhood	6 months to 1.25 years	Older infants to young juveniles	180d, 270d, <b>1y, 1.25y</b>
6-11 yrs	Late childhood	1.5 to 2.75 years	Older juveniles	<b>1.5y, 1.75y, 2y, 2.5y</b>
12-19 yrs	Adolescence	3 to 4.75 years	Adolescents	<b>3y, 4y</b>
20-60+ yrs	Adulthood	5 years +	Adults	<b>5y or older</b>

\* BrainSpan Atlas [Kang et al] [PMID: 22031440]

\*\*in bold vervet age categories used for comparison



**Supplementary Table 22. Approximate chronologic age  
correspondence between vervet and rhesus macaque**

<b>Age rhesus macaques*</b>	<b>Age Vervet in Dataset 2</b>
0m	Infants 7 days
3m	Infants 90 days
12m	Infants 1 and 1.25 year old
48m	Adults 4+ years

\* Blueprint Non-Human Primate (NHP) Atlas [Bakken et al] [ PMID: 27409810]

**Supplementary Table 23. Matching tissues in Vervet Dataset 2 and human and rhesus macaque**

<b>Vervet tissue</b>	<b>Human tissue*</b>	<b>Rhesus tissue**</b>
BA46	Dorsolateral Prefrontal Cortex (DLPFC)	Medial Prefrontal Cortex
Caudate	Striatum	Basal ganglia
Hippocampus	Hippocampus	Hippocampus

\* BrainSpan Atlas [Kang et al PMID: 22031440]

\*\* Blueprint Non-Human Primate (NHP) Atlas [Bakken et al PMID: 27409810].

**Supplementary Table 24. Primers and probes for qRT-PCR**

Gene Symbol	Accession No.	Primer & Hydrolysis Probe Sequences (5'–3')	Reporter	Amplicon Size (bp)	Tm (°C)	Slope	Intercept	R <sup>2</sup>	Reference Stability (Std. Dev.)
<i>LOC103222765</i>	XR_493563.1	Forward: TGAATGCAACCTCAGGAACTG Reverse: CCTTCCTCTCAGCTTGCTTTATTC Probe: CTGGGCAACCAACCTG	FAM	89	60	-3.3809	34.17	0.98995	N/A
<i>LOC103222769</i>	XR_493565.1	Forward: CCGGCGAATCAGGCCTC Reverse: TGGATCTGAACTGCTGTTTGAAT Probe: ACAGCCAGGGAACCAAG	FAM	81	60	-3.8631	32.03	0.99879	N/A
<i>LOC103222771</i>	XR_493567.1 XR_493568.1 XR_493570.1 XR_493569.1	Forward: GCTGTTTCCAAGCCCCTAG Reverse: CCCAAAGACACAGGTTTATATGAAGT Probe: CAGCCCCGATGTCCTT	FAM	97	60	-3.5545	35.168	0.99143	N/A
<i>HPRT1</i>	XM_007992743.1	Forward: CCAGGTTATGACCTTGATTTATTTTGGCA Reverse: CAAGACGTTTCAGTCTGTCCATAAT Probe: CACCCTTTCCAAATCC	FAM	106	60	-3.4116	28.3	0.99911	0.25
<i>GAPDH*</i>	XM_007967342.1	Forward: CCACAGTCCACGCCATCA Reverse: CCATCACGCCACAGTTTGC Probe: CTGCCACCCAGAAGAC	FAM	70	60	-3.7975	23.8	0.99879	0.08
<i>B2M</i>	XM_008016776.1	Forward: CGTGCTCCAAGATTCAGGTTT Reverse: CCCAGACACATAGCAATTCAGGAAA Probe: ACTCACGCCATCCACC	FAM	81	60	-3.4614	25.14	0.99911	0.48

\*Assay also amplifies pseudogene.