Supplemental Information for: Lindblad-Toh et al: "A high-resolution map of evolutionary constraint in the human genome based on 29 eutherian mammals."

Contents

Supplementary Notes

This supplementary information follows the structure and layout of the main paper. Here we describe the methodology in detail and include additional analysis not covered in depth in the main text.

Supplementary Section S1: Samples and sequencing

Supplementary Methods 1.1 - Sequencing strategy:

Our goal was to identify constrained elements in the human genome based on evolutionary constraint across eutherian mammals. To obtain the maximum power at a reasonable cost we developed a strategy of sequencing genomes to 2x coverage instead of the standard 8x[1]. At 2x, theoretically ~85% of the sequence should be recovered, although in smaller pieces.

Supplementary Methods 1.2 - Species selection and preparation:

Species were selected to generate the maximum novel branch length, while spanning all the four major clades. When appropriate the relevance of the species as a model organism was taken into account. For non-endangered species, 8 females were selected and heterozygosity tested across 200 loci. The individual with the lowest level of polymorphism was selected for sequencing. All individuals sequenced are female. Most species had heterozygosity rates of 1/500-1/1000 bp, while the elephant, guinea pig and rabbit had extremely low heterozygosity. DNA was prepared from blood or available tissues using standard protocols for high molecular weight DNA. To determine the amount of sequence required for 2x coverage of each genome, ~50,000 Fosmid pairs were generated and an estimation of the euchromatic genome size was performed by placing these Fosmid pairs on the canine genome and estimating the relative genome size.

Supplementary Methods 1.3 - Sequencing coverage:

Eight of the nine high coverage draft or finished genomes were previously described (Table S1). Guinea pig was sequenced with a standard mix of paired end reads (4kb and 10kb plasmids, 40-kb Fosmid and BAC ends[2]) totaling 6.8x coverage of the genome and assembled using ARACHNE2[3].

For each of the organisms sequenced to low coverage, ~2x coverage of sequence typically was generated from 4kb paired end reads (~1.8x) and 40kb Fosmids (~0.2x) using ABI3730 sequencers. Species and sample source information is described in Table S1.

Supplementary Section S2: Assembly

Supplementary Methods 2.1 - Genome assembly strategy:

All 2x genomes were assembled using an assisted assembly method[4] where the *de novo* assembly is improved by placing all reads on related genomes (in this case on dog, CanFam2.0 and human, hg18) and leveraging the placement information to support and extend information in the *de novo* assembly.

Importantly, no novel information was introduced in the assemblies based on the alignment to the related genomes. Instead, read-read alignments confirmed by read placement on related genomes

were used to extend existing contigs; and confirmed single links were allowed to join different scaffolds, hence improving contiguity. Moreover, read pairs aligning onto the reference uniquely and consistently were used to detect and eventually fix misassemblies introduced in an earlier stage due to the presence of weak joins. All assembly statistics are described in Table S1 and assemblies are available at **http://www.broadinstitute.org/ftp/pub/assemblies/mammals/**.

Supplementary Text 2.2 – 2x sequencing versus next generation sequencing:

The 2x genomes utilized here were produced over a time span of several years, but to achieve consistency in the data set we utilized the same sequencing and assembly strategy throughout. The current availability of next generation sequencing technologies will reduce the cost of genome sequencing by an order of magnitude and allow sequencing to high coverage of many mammals. For comparative genome analysis understanding the quality of the assemblies, alignments and error modes in the data are important and so while future mammalian analysis will be less expensive and time consuming, they should still be performed in a consistent manner.

Supplementary Section S3: Error estimation and error correction

A detailed analysis of sequencing errors in the 2x genomes, including both miscalled bases and erroneous indels, has been published as a satellite paper[5], with key results summarized briefly below.

Supplementary Text 3.1 - Quality score distribution for assembly:

Even with only 2x average genomic coverage, these assemblies predominantly consist of high-quality bases. Roughly 82% of bases, across all of the assemblies, have quality scores >45, and only ~4% have scores <20.

Supplementary Text 3.2 - Comparison with ENCODE assemblies to estimate error rates:

The mismatch rates for aligned 2x and ENCODE bases ranged from 2.6 (elephant) to 25.1 (hedgehog) mismatches per kb, while the indel rates showed somewhat less variation. These rates generally decreased with increasing quality scores, as expected, but the limiting rates—at the highest quality scores—differed considerably among species.

At the highest quality scores, mismatch rates were highest for hedgehog, for which separate species were sequenced in the ENCODE and 2X project, and microbat, known to show elevated levels of intraspecific genetic variation[5]. The smallest mismatch rates occurred with the African savannah elephant, which has been reported to have low average genetic diversity[5].

We thus used observed difference rates at the highest quality bases (quality score >45) as rough estimates of polymorphism rates, and subtracted these estimates from the overall observed rates to obtain approximate polymorphism-corrected error rates. After this adjustment, the estimated base-call error rates were much more concordant across species, at 0.72–3.43 per kb.

The 2x species with slightly higher coverage, such as megabat (2.6x) and rock hyrax (2.2x), have the lowest residual error rates, as expected.

Supplementary Text 3.3 - Generation of error-corrected assemblies and alignments:

Given the localized nature of sequencing errors, with a large majority of errors coming from a small minority of bases, we developed automatic methods to generate a version of the alignments that mitigate the effects of errors for downstream analyses. These are available from http://compgen.bscb.cornell.edu/projects/32way-masked/

Supplementary Section S4: Alignment details

Supplementary Text S4.1 - Alignment choice in the detection of constraint:

Although we have used MultiZ alignments for the main bulk of this work, we also evaluated the use of Enredo and Pecan[6] to build an alternative set of alignments, for the specific purpose of evaluating segmental duplications, since MultiZ was not designed to handle them. In short, Enredo is a graph-based method that defines sets of co-linear genomic sequences and Pecan, a consistency-based multiple aligner, aligns them. On the one hand MultiZ provides a higher coverage of the genome. On the other hand Pecan works in a global fashion and, together with Enredo, can provide alignments on segmental duplications.

We compared the sets of phastCons constrained elements we obtain from both sets of alignments. We restricted the comparison to the regions covered by the Pecan alignments. Globally, we found approximately the same amount of genome under constraint: 4.34% on the MultiZ alignments vs. 4.01% on the Pecan alignments. When comparing the constrained regions at the base pair level, we found that 83.48% of the bases called by phastCons on the Pecan alignments are also detected as constrained when looking at the MultiZ alignments. The majority of the conflicting elements are shorter than 20 nucleotides. For instance, 93% of the MultiZ-phastCons elements of at least 30bp overlap with a Pecan-phastCons element (Fig S2).

We next focused on the human segmental duplications as defined by Enredo where Pecan and MultiZ alignments are likely to be more different. In these regions, Pecan assigned all the human copies of the genomic segmental duplication to the same alignment. We observed a drop in the amount of nucleotides under constraint in the MultiZ alignments (from 4.34% to 2.71%) while we see an increase in constraint in the Pecan alignments (from 4.01% to 4.94%). Again, both sets of elements tend to disagree more on smaller elements, but this time a third of the elements longer than 50 nucleotides are found in the Pecan-phastCons set only (Fig S2). PhastCons can over-predict constrained regions on Pecan alignments where long insertions have happened. We remove these from the final set by ensuring that all constrained elements have no more than 10% gaps in the human sequence and at least 80% informative nucleotides (non gaps or Ns) in at least one other sequence.

In segmental duplications, we note a reduction in the amount of detectable constrained elements. In some examples, we see how Pecan-phastCons elements can detect coding exons missed in the MultiZ-phastCons set, although we note that phastCons is not designed to study segmental duplications. Importantly, the constrained elements detected on both sets of alignments are comparable for the non-duplicated portion of the genome. For the remaining analysis in this paper we use the MultiZ alignments.

Supplementary Section S5: Estimating constraint

Supplementary Methods S5.1 - Neutral tree estimation:

For each chromosome we extracted 4-fold third codon positions from all Ensembl genes annotated as protein that had a single homolog in both mouse and dog. We used PAML (version 4, June 2007)[7] with default parameters to estimate branch lengths fixing the tree topology. The estimated nucleotide substitution rate matrix and tree branch lengths were used as the neutral model for constraint estimation.

Supplementary methods S5.2 - Supplementary methods - Estimates of selection - Siphy-ω, Siphy-π:

We used Siphy[8] for constraint estimation, at a resolution of 12bp and 50bp as previously described. Constraint was estimated in the full 29way-alignment, an alignment containing only a subset of species Human-Mouse-Rat-Dog (HMRD), and an alignment containing high coverage genomes for the ENCODE regions. Constraint was estimated using both a rate based method (Siphy-ω) and a biased substitution based method (Siphy-π).

Supplementary Text S5.3 - Challenges of varying branch length:

As a measure of constraint for the Siphy-π method, the log-odds scores were used. For a given strength of constraint, elements with log-odds scores are proportional to alignment depth, and as a result, elements with higher branch length will receive higher score. Since Ancestral Repeats tend to have lower branch length, this may lead to an over-estimation of the excess under constraint. To conservatively estimate constraint purely based on differences in substitution patterns, we have employed a branch length correction. Briefly, genomic windows were divided to bins based on their average branch length. In each bin, the mean (mu) and standard deviation (s) of the log-odds scores were computed for the Ancestral Repeats background sets. All scores in a bin were standardized by subtracting the mean and then dividing by the standard deviation to produce a Z-score. All Z-scores from all bins were then collected to produce one genomic distribution and one Ancestral Repeat distribution. Constraint was called based on these distributions as described in the previous section. The correction we have employed eliminates the bias towards windows with higher branch length.

Supplementary Methods S5.4 - Comparison with Encode:

In its most recent data freeze (January 2009) the ENCODE dataset includes a multiple alignment of a superset of the species used in this paper. This alignment consist of assemblies sequenced at "comparative analysis grade" offer us the possibility to benchmark the impact of low coverage data on our predictions.

The usage of 2x mammals presents potential challenges and biases in comparing the background set to the entire genome, due to problematic alignability issues and varying branch lengths. To assess the impact of the incomplete data resulting from low coverage

assemblies we compared predictions in the ENCODE regions using both alignments: The ENCODE alignment composed of high coverage assemblies and the genome wide alignment composed of low coverage assemblies restricted to the ENCODE regions. The ENCODE alignments are missing 6 species from our sets, and these species were excluded for the purpose of this comparison, resulting in the comparison of 23 species.

Supplementary Text 5.5 - Notes for Table S2 - Constraint Estimation and Detection statistics:

We used three different methods for detection and estimation of constrained elements (blue, red, green). The first (SiPhy-ω) is looking for a reduction in the neutral divergence rate estimate ω, and setting a cutoff on the value of ω. The second (Siphy-ω lods) is looking at ω, but setting a cutoff on the log odds probability that ω is less than 1. The third (Siphy-π) is looking at the log odds probability that the stationary distribution of the mutation matrix is different from uniform. We applied all three methods to 12-mers across the 29-way alignment using ancestral repeats as the background (top row), to 12-mers across the 29-way alignments using ancestral repeats that are conserved over species covering the same branch length as the elements, thus correcting for the varying branch lengths across the genome, but possibly being too stringent because some of the conservation of ancestral repeats is due to selection (second row), to 12-mers across the four mammals human, mouse, rat, dog (third row), and to 50-mers across the four mammals (last row).

Supplementary Section S6: Detection of constrained elements

Supplementary Text 6.1 - Detecting constraint elements:

We used a window-based approach to call constrained elements.

First, we divided the genome into (overlapping) kmers. Each kmer was scored using SiPhy to get S(i) the score of k-mer i. Since neutral evolutionary rate differ between different chromosomes, subsequent analysis was done separately for each chromosome. For each chromosome we constructed two histograms, a genomic histogram comprising all scores of k-mers for this chromosome, and a background histogram, comprising scores of all k-mers overlapping Ancestral Repeats for this chromosome. The two histograms were then used to compute an empirical FDR cutoff ω_c at level 10%, defined as the maximum value such that the ratio of areas to the right of this value is no more than 10%. Windows with $S(i) > w_c$ were declared as significant k-mers. Finally, we clustered overlapping significant k-mers to yield larger elements. The above procedure was repeated for two different window sizes (12bp and 50bp), different conservation scores (SiPhy-ω, SiPhy-π) and different alignments (29way, HMRD and ENCODE comparative grade).

The different alignments gave vastly different significance cutoffs. For example, when calling elements at a 10% FDR level and using the full 29way alignments at a 12bp resolution, the average constraint cutoff across all chromosomes was $\omega \sim 0.29$ - hence a roughly 3.4-fold reduction in average substitution rate was sufficient to declare an individual 12-mer as constrained. Using the HMRD alignment, a much stricter cutoff of essentially $\omega=0$ (no observed substitutions in the alignment) was required to declare a 12-mer as constrained at the same 10% FDR level.

Supplementary Text S6.2 - Comparison of SiPhy-ω, SiPhy-π and PhastCons elements:

We set out to examine the robustness of the set of elements called based on the method used. We have used both SiPhy versions, as well as elements called using phastCons. Overall, there was a strong agreement between the different methods. PhastCons elements overlap 93% of SiPhy-ω (5% FDR) bases, whereas phastCons overlap only 75% of SiPhy-ω (10% FDR) bases. This suggests that the core data set is similar but that 10% FDR of SiPhy-ω elements allows the inclusion of additional bases not found in the phastCons elements. This is supported by the fact that when these three data sets are compared, the SiPhy-ω 5% FDR contains 1,674 elements unique to this data set, whereas phastCons has 285,039 unique elements and SiPhy-ω 5% FDR has 1,449,816. While some of these elements may be false positive due to the higher FDR, this dataset should contain many novel elements.

Supplementary Text S6.3: Correlation between 29 mammals and previously defined constrained elements:

For each Megabase in the genome we computed HMRD 50mer based element and 29-way eutherian 12mer based (SiPhy-ω 10% FDR) element density, and found a very strong correlation between the two, suggesting that newly discovered elements have a similar genome-wide distribution as previously discovered elements (Figure S6).

In addition, we compared the elements detected for 29 mammals with both SiPhy omega and pi at 5% and 10% FDR and PhastCons elements and compared the overlap for both elements and bases with the HMRD 50 bp set, the Siepel five vertebrate data set and the union of these elements. While the union of the Siepel and HMRD elements cover a larger fraction on the genome, the overlap with the 29 mammals elements is only marginally bigger (see Supplemental Table S3 and Figure S4).

Supplementary Text S6.4: Identification of newly-detected elements: Within intronic and intergenic elements, the majority of constraint sequence was not previously detected as constraint with HMRD. Taking the lack of granularity of the 50mer HMRD analysis into account, we identify 55.3% of elements as potentially part of elements previously detected by HMRD (overlapping or falling within 50 bp of a previously detected constraint element). An additional 19.4% of elements fall 50 to 500 bp from previously identified elements suggesting they could be part of the same regulatory unit. The remaining 25.3% of elements (~916,000 elements), fall >500 bp from previously identified constraint elements, suggesting that they may be novel entities.

To examine the clustering of elements on a larger scale we examined the element numbers in 10kb windows of the genome. Under Poisson distribution the 95 percentile for the number of elements contained in a 10K window is 18. Since there are 300K such windows in the genome, we expect about 15K windows having 18 or more elements. We observe ~5x this number which indicates that elements do indeed tend to cluster

Supplementary Section S7: Constraint vs. polymorphism

Supplementary Methods S7.1 - SNP analysis methods:

For all analysis we have used an unbiased SNP set from Keinan et al.[9]. To allow the maximal divergence between human populations we have used the Yoruban (YRI) SNP set. Each position in the 29way-alignment was collapsed to the IUPAC code symbol closest to the Siphy-π vector for this position. A total of 92,906 SNPs for which Siphy-π indicated a two-fold degenerate site were used for comparison with the human SNPs.

Supplementary Methods S7.2 - SNP density vs. constraint:

We computed the average SNP density in both masked genomic regions, and in constrained elements and performed a correlation.

Supplementary Methods S7.3 - Shifted allelic spectrum for two-fold mutating sites:

We counted the joint frequency of all di-nucleotide patterns in the mammalian phylogeny for the ancestral and derived allele in the human YRI populations.

The value C(ij,kl) represent the counts in which the two mammalian alleles are i and j, the human ancestral allele is k and the derived allele is l.

We computed an enrichment matrix E(ij,kl) given by:

$$E(ij,kl) = C(ij,kl) / C(ij)*C(kl)$$

where C(ij) is the marginal frequency of the di-nucleotide pattern (ij) in the mammalian phylogeny, and C(kl) is the marginal frequency in the human ancestral and derived alleles. This enrichment matrix measures the tendency of the non-human allele and the derived allele to coincide, with E(ij,kl) = 1 representing no enrichment beyond background.

Supplementary Section S8: Protein-coding genes

Supplementary Methods S8.1 - Exon prediction:

To predict novel conserved exons, we applied an enhanced version of CONGO, an algorithm we previously developed for the same purpose in *Drosophila* genomes[10]. Briefly, CONGO incorporates discriminative metrics of protein-coding evolutionary signatures -- including reading frame conservation and codon substitution frequencies[11] -- within the framework of a semi-Markov conditional random field (SMCRF), a type of probabilistic graphical model that can combine such metrics in order to produce a segmentation of the genome into predicted exons and non-coding regions. The enhancements to the previous version are mainly adaptations to the mammalian exon prediction task, including a semi-Markov feature to model the short length distribution of mammalian exons, a synteny feature helpful for recognizing duplicated and pseudogenic regions, and an alternative training objective function similar to Conrad's[12], which improves the accuracy of the algorithm given the unbalanced prediction task (only ~1.5% of the human genome being protein-coding).

We applied CONGO to the MULTIZ alignments of 29 eutherian genomes, which we also postprocessed to mask likely sequencing errors[5]. We trained CONGO's SMCRF using the GENCODE

annotations of the ENCODE 'random' regions[13], approximately 0.5% of the human genome. We then applied the trained model to decode each human chromosome assembly. From the ~175,000 resulting exon predictions, we subtracted those overlapping any annotated coding exon from the major human gene catalogs (including RefSeq, Ensembl, GENCODE and UCSC Genes downloaded on March 27, 2010 – see supplementary data), leaving the 3,788 predictions reported in the main text.

Supplementary Methods S8.2 – Transcript models

We next used Scripture[14] to reconstruct transcript models based on high-throughput transcriptome sequencing in 16 human tissues by Illumina, Inc (BodyMap2). We used the resulting transcript models to assess expression evidence and tissue specificity for the predicted exons, and also to 'link' them with known gene structures annotated by GENCODE, as described in the main text. We also collected several other lines of evidence not used by CONGO to provide initial support for the exon predictions, including existing EST/cDNA expression evidence, similarity to Pfam protein domains identified using HMMER[15], and coding gene-associated chromatin states[16-17].

Supplementary Section S9: Readthrough and synonymous constraint elements

We searched for potential examples of stop codon readthrough in mammals by searching for continued protein-coding evolutionary signatures in the regions immediately downstream of the stop codon in known human coding transcripts. This follows our previous approach in 12 Drosophila genomes[10]. In addition to known selenoprotein-encoding genes, we found four novel candidates (*OPRK1*, *OPRL1*, *BRI3BP*, and *SACM1L*) with no apparent alternative explanations other than translational readthrough (such as splicing or RNA editing). Further analysis of these mammalian examples, and many others in animal species, are reported in a separate manuscript (Jungreis et al., "Evidence of widespread stop codon readthrough in *Drosophila* and other metazoa", in revision).

To identify protein-coding regions under selection for additional, overlapping functions, we developed a method based on phylogenetic codon models to measure synonymous substitution rates in short windows and report the statistical significance of their reduction. We applied this method to all human CCDS ORFs and identified more than 10,000 "Synonymous Constraint Elements" (SCEs) with resolution for nine-codon windows, covering about 2% of all synonymous sites (FDR < 0.01). A typical example shows a 77% reduced synonymous rate compared to genome-wide averages across placental mammals. The SCEs show strong positional enrichments for exon and ORF boundaries, suggesting widespread constraints on splicing and translational regulatory elements embedded within mammalian ORFs. Many SCEs can also be associated with other overlapping functions such as miRNA targeting, dual-coding regions, A-to-I editing, and RNA secondary structures, but further study will be needed in order to associate most with biological functions. Full details of this work are reported in a companion papers[18-19].

Supplementary Section S10: RNA structures

Supplementary Text 10.1 - EvoFold screen

The EvoFold RNA structure screen was based on a 41 species subset of the genome-wide 44-way multiZ alignment, which includes additional vertebrate genomes and is available from the UCSC

Genome Browser. We used a 31-way subset for the structure prediction and profile-model training, consisting of 28 of the 29 eutherian mammals, together with opossum, chicken, and tetraodon as outgroups. An additional 10 species that were not used for structure inference, consisting of primarily non-mammalian vertebrates and a single eutherian mammal, were used as an independent test set for structure validation.

The screen was restricted to a set of conserved alignment segments based on the PhastCons predicted elements[20], which span 5.56% of the genome. Since EvoFold is sensitive to misaligned sequences, we applied a conservative sequence filter to the extracted alignment segments, which discards sequences with a surprising number of mismatches given the branch-lengths of the relating phylogenetic tree (see Alignment Filtering below). EvoFold (v.2.0)[21] was then applied to these filtered alignments in both their forward and reverse directions. Low-confidence predictions that are short (< 6 base-pairs); harbor excessive amount of bulges; based on shallow or low quality alignments; or overlap repeats or pseudogenes were eliminated from the prediction set. See supplement of[22] for details on the screen.

The UCSC Genes set (as of May 25, 2009) was used to define genomic regions. Each prediction was assigned to the genomic region it had the greatest overlap with. Protein-coding regions were excluded from the study to focus it on non-coding regions.

Supplementary Text 10.2 - EvoFam clustering pipeline

We clustered the EvoFold predictions into candidate families using a novel approach (EvoFam), as described below. A probabilistic model based on a profile stochastic context free grammar (pSCFG), a.k.a. a covariance model, was built from each EvoFold prediction, using the Infernal RNA tools v 1.0 (cmbuild utility)[23]. An all-against-all similarity (homology) comparison between structural RNA predictions was performed, based on a probabilistic similarity measure between pairs of pSCFG models. This new similarity measure is based on a form of Kullback-Leibler divergence, modified to correct for varying false positive rates due to varying model size and complexity (see[22]).

A similarity graph was defined with vertices corresponding to the pSCFG models of RNA structures and with edges connecting pairs of models with a dissimilarity below a threshold selected to control false discovery rate (FDR). Families were defined as highly connected subgraphs, where a highly connected subgraph (HCS) is defined as a subgraph S of n vertices with edge connectivity $k(S)>n/2$, with edge connectivity $k(S)$ defined as the minimum number of edges whose removal disconnects S. These families were computed using the iterated HCS algorithm of[24].

Additional paralogous matches to the UTR EvoFold predictions were detected by searching the conserved UTR regions of the human genome with the corresponding pSCFG (using cmsearch with global search option). The paralogous hits were filtered by requiring E-value < 0.1 (relative to a 1 Megabase database) and strong double substitution evidence (p-value < 0.2; Monte Carlo test applied to all species excluding human). Repeat regions and known pseudogene matches were removed. For the analysis limited to UTR regions, this set of putative paralogs was then combined with the original EvoFold set and analyzed by the subsequent family identification stages.

Supplementary Text 10.3 - Filtered candidate families

After initial definition of the candidate families through cluster analysis, we further evaluated the statistical significance and biological evidence for the candidate sets. The disjunction of a series of enrichment tests was used to produce the final high confidence filtered sets:

(i) We evaluated the statistical significance of the compensatory substitutions supporting each member of a family using a Monte Carlo test on the 31-way alignment and, importantly, on the independent set of ten held-out species not used for structure inference. The test, called EvoP, measures how surprising it is to achieve the observed number of double substitutions, given the total number of substitutions and a random substitution process on the branches of the tree relating the aligned species (see S10.5 – EvoP double substitution significance test). Considering each member as an independent test for the overall significance of a family, the p-values of all family members were combined multiplicatively using the Fisher method and used as an overall measure of evidence as well as for ranking.

(ii) For predictions within known protein-coding genes (i.e. UTR and intronic genomic regions), gene ontology (GO) enrichment statistics were computed for each cluster with three or more members, using the topGO library[25]. We additionally required that an enriched GO term had evidential support in two or more family members to prevent a single unusual gene flagging the entire family. The GO analysis was conducted against a background set of the original EvoFold structure predictions, and so estimated the additional enrichment of families beyond the possible enrichments or biases of the original EvoFold set. Families were filtered based on the most significant p-value in each ontology.

(iii) The degree of enrichment of family members for a particular genomic region (5′UTR, 3′UTR, intron, intergenic) was computed by chi-squared statistic relative to the background proportions of the entire EvoFold prediction set.

(iv) We calculated the mean structure length in terms of pairing bases for each family: longer structures have a lower prior probability and thus higher confidence.

(v) Enrichment relative to an immunity-related gene set consisting of the human homologues of mouse macrophage-related genes as defined in[26] was estimated by Fisher's exact test.

We defined a final set of high-confidence predictions as the disjunction of the families deemed biologically significant via any of these significance estimates: those for which any of the following measures had p-value smaller than a defined threshold (0.05 for double substitution p-values; < 0.005 for region enrichment; < 0.01 for maximal GO enrichment p-values); or mean base-pair length > 11. Combining these statistical measures of confidence, the original full set of candidate families was filtered to a smaller set of high-confidence families.

Supplementary Text 10.4 - Alignment filtering

Since both the EvoFold RNA structure screen and the EvoFam family identification pipeline are sensitive to the assumption that the alignments are correct, we filter sequences that are likely to be misaligned from the alignments before using them. We filter an alignment by first identifying every outer branch on which there is significantly more substitutions than expected given its length and

the substitution rate in the rest of the tree. If such a branch exists, with at least two substitutions and more than 5-fold rate change relative to expected, we then mark the entire sequence from the species to which they lead as unobserved in the given alignment.

Both the number of substitutions on the outer branches and the substitution rate in the remaining tree are estimated using PAML[7].

Supplementary Text 10.5 - EvoP double substitution significance test

We have developed a new, easily interpretable p-value for evaluating and ranking the predicted structures based purely on substitution evidence. See supplement of[22] for details.

For a given predicted structure and an alignment that corresponds to the stem bases of this predicted structure, the p-value measures how probable it would be to see at least as many double substitutions in the aligned sequences if they do not encode a structural RNA (assuming the total number of substitutions in the alignment is fixed). We applied a previously-defined methodology[27], but whereas most current methods for counting substitutions are based on pairwise sequence comparisons, the counts for this p-value are performed on the underlying phylogenetic tree to take into account the treelike nature of evolution. Similarly, we only count a pair of substitutions as a double substitution if the two substitutions occur not only in the same base-pair, but also on the same branch in the tree, since the two substitutions are only likely to be correlated if they happen in close proximity time-wise. All of the substitution counts are based on the most probable ancestral tree which we infer using PAML[7].

When calculating the p-values we assume that if the aligned sequences do not encode a structural RNA each of the substitutions will have happened with equal probability along the sequence, with probabilities proportional to the branch lengths along the phylogenetic tree and with equal probabilities to all different types of substitutions. These are estimated using a Monte Carlo approach.

When a structure prediction is based on only a subset S of the species in the alignment, we use a very similar approach to assess to what extent the additional species support the original prediction. The only difference to the p-value defined above is that we include only the branches that do not connect the species in S in our analyses.

Supplementary Text 10.6 - Summary and enrichment statistics

To evaluate the statistical evidence for the entire predictions sets, we calculated the following summary and enrichment statistics (Figure 9a), which in all cases are based on the subset of novel predictions as defined in [22]: (1) EvoFold score: mean EvoFold log-odds score of novel structures in the sets. (2) RNAz overlap enrichment: Enrichment in overlap of novel EvoFold predictions with RNAz predictions compared to a random null set. (3) DNase hypersensitivity overlap: % overlap of novel intergenic predictions with DNase I hypersensitivity sites compared to random conserved regions (see [22] for details). (4) Avg. correlation of tissue-specific expression within families: The average Pearson correlation coefficient of expression of novel structures within families, across tissues based on a multi-tissue RNA-seq dataset (Illumina Body Map 2 data) (P-values based on

shuffled null) (see [22] for details). (5) Intergenic expression enrichment*:* The expression of novel conserved intergenic elements relative to randomly selected intergenic regions.

Using the Illumina BodyMap 2 ribo-depleted, non-polyA selected, total RNA dataset [Illumina], we compared the expression evidence overlying the novel intergenic structures compared with a shuffled set of random structure positions chosen from the conserved intergenic regions of the genome. For the expression analysis, regions overlapping RNA repeat elements and known pseudogenes were removed from both unshuffled and random background sets, as reads are often wrongly mapped in these regions giving false expression signals. Similarly, we removed regions showing mitochondrial chromosome homology as they have increased probability of representing either ribosomal RNA or tRNA pseudogenes. 1000 shuffles were used to estimate p-values by permutation test (see [22] for details).

Compared to the random background, the fold increase in expression (mean reads per base) of intergenic elements that show any expression for the EvoFold, GW unfiltered, and GW filtered input sets was 1.20 X (P<1E-3), 1.46 X (P<1E-3), and 2.33 X (P<1E-3), respectively. Similarly, the fold increase of the average expression levels for the entire predictions sets (including elements with no expression evidence) were 1.02 X (P<0.21), 1.20 X (P<6E-3), and 1.70 X (P<1E-3), respectively, for the EvoFold, GW unfiltered, and GW filtered input sets.

Supplementary Text 10.7 - Thermodynamic analysis of EvoFold predictions using RNAz

We used RNAz 2.0[28-29] to analyze the initial EvoFold predictions as well as the structures in the clustered families before and after filtering. RNAz was run on the same alignments as EvoFold. However, since the classification algorithm of RNAz is not trained for short structures, we added flanking regions to all EvoFold predictions shorter than 120 nt to obtain a minimum length of 120.

As positive control, we used a set of 356 known structural RNAs. As negative controls we (i) chose random locations within the PhastCons conserved regions that were used as input for the EvoFold analysis, (ii) we shuffled the alignment[30] (iii) we simulated random alignments preserving the dinucleotide content in the alignment[31].

We focused on two metrics calculated by RNAz: the z-score and the classification score. The z-score is a normalized value measuring the thermodynamic stability of an RNA structure. It is the number of standard deviations a given RNA structure is more/less stable than structures for random sequences of the same length and dinucleotide content. RNAz calculates the average z-score of all sequences in an alignment. By convention, negative z-scores denote more stable structures. RNAz combines the stability z-score with an evolutionary score measuring the structural conservation and uses a support vector machine to classify an alignment as "Functional RNA" or "other".

The results of the z-score analysis show that EvoFold predictions are significantly more stable than the random controls and that the clustering and the filtering of clusters enrich for even more stable RNA secondary structures (Supplementary Fig. S10a). The same trend can be observed for the RNAz classification (Supplementary Fig. S10b). While only 1-2% of the random controls are predicted as functional RNA, 11% of the EvoFold predictions are supported by RNAz. For the

clustered families this fraction increases to 15% and 24%, for the unfiltered and filtered sets, respectively.[22]

Supplementary Text 10.8 - Data availability

The complete set of structure predictions from the EvoFold screen as well as the candidate family predictions sets can be downloaded in bulk or browsed through a UCSC Genome Mirror from the following web-site: http://moma.ki.au.dk/prj/mammals/. In addition, individual families are listed and annotated in[22] and its supplement.

Supplementary Section S11: Patterns of promoter constraint

Supplementary Text 11.1 - Identification of peaks in constraint in the core promoters of transcripts

A peak in constraint was defined by an increase in Siphy-π value over the surrounding region. Raw π-scores were smoothed with a windowed-mean algorithm in 8 bp windows. Local maxima were identified in the smoothed signal, and a peak recorded if the conservation score at the maximum was ≥1.5X the average score at the base of the peak. To reduce spurious signals produced by low conservation, peaks with smoothed π -score less than 4 (roughly the genome-wide average) were discarded.

Supplementary Text 11.2 - GO enrichment

Enrichments for Gene Ontology (GO) terms were run using the topGO package, version 1.16.2 from BioConductor[25]. Gene Ontology annotations for human transcripts were collected from version 58 of the Ensembl database using the Ensembl Perl API: each term within the Biological Process ontology annotated by Ensembl as being associated with a given transcript was collected, along with all of its ancestor terms, with the associated transcript and gene name. In order to avoid a lack of power due to small numbers of annotated genes, all GO annotations were used regardless of evidence code. Each independent list of genes was tested for GO term enrichment using the entire set of human transcripts as the universe, using the "classic" algorithm and Fisher's exact test statistic as implemented in topGO. P-values for enrichment were corrected for multiple testing using the Bonferroni method.

Supplementary Text 11.3 - Comparison to CpG and TATA-box promoter classifications

To evaluate the relationship between the observed promoter constraint patterns with CpG and non-CpG promoters, we defined CpG promoters as those with an annotated CpG island within 200 bp of the TSS (CpG island coordinates were downloaded from UCSC) and compared these to our groups of promoter classification. CpG promoters were abundant in all classes; 66% of genes with both 'high' and 'intermittent' constraint were CpG promoters (5,083 and 9,342 genes respectively), while 41% (1,188 genes) of 'low' constraint genes were CpG promoters. In total, 63% (15,613) of the genes in our set are associated with a

CpG island. For reference, genes with TATA boxes of the "right" distance and orientation in the promoter are represented at 2-3% in each of the 3 categories.

Supplementary Section S12: Regulatory motif discovery

Supplemental Methods S12.1 – Regulatory motif instance identification

We use a method similar to Kheradpour[32] with extensions for using position frequency matrices (PFMs). We build a catalog of 688 motifs (for 345 factors) from TRANSFAC (version 11.3)[33], Jaspar (version 2008)[34], and large scale systematic motifs generated by Protein Binding Microarrays[35-37].

For each motif, 100 shuffled motifs are generated by randomly shuffling the columns of each PFM. Because the way the information content is ordered may affect the background level of conservation (e.g. a group of specified bases surrounded by unspecified bases may be more likely to be conserved by chance than the converse due to conservation typically being "blocky"), we create three bins of information content and shuffle only within each bin. Each of the 100 shuffled motifs is then matched to the human genome and only those that have +/- 20% the number of matches are considered. The remaining motifs are then clustered at a 0.8 correlation and up to 10 control motifs are chosen in random order, allowing only one motif per cluster. Together, these procedures attempt to choose control motifs that have the same base-composition and similar higher-order compositions (through frequency matching), while being diverse.

A branch length score (BLS) is computed for each motif match in human by computing the branch length of the smallest subtree that contains human and the informant species that contain an aligned motif match. We then produce a mapping between BLS and confidence (1 – false discovery rate) for each branch length score using $1 - r_c / r$ where r and r_c are the fraction of motif instances and control instances, respectively, that reach at least the specified BLS. Wilson score interval with z=1 is applied to both r (correcting downward) and r_c (correcting upward) in order to produce a conservative estimate of confidence in situations with few instances.

We also permit motif movement by repeating the procedure for each of the 32 windows w=0, 5, 10, 20, …, 100, 120, …, 500 allowing both the motif and the control motifs to move w bases in the informant genomes relative to the position aligned to human. Consequently, for each confidence cutoff from 0.1, 0.2, …, 0.9 the BLS and w combination that results in the highest sensitivity is chosen.

The computation of the confidence mapping benefits from having homogeneity in the regions scanned. It is important to exclude regions that may have other sources of evolutionary constraint (e.g. coding sequence) and regions that are difficult to align (e.g. repeats). Consequently, we exclude all simple repeats and repeat masked regions (downloaded from the UCSC genome browser on April 13, 2006) and use the Ensembl gene annotations (downloaded from UCSC on September 18, 2007) to exclude coding regions, 3' untranslated regions and exons from non-coding genes.

Confidence prediction is done on only autosomes, and then instances are identified on the chromosome X using the mapping produced on the autosomes but with a tree produced on

chromosome X. This is important to correct for the higher background level of conservation of chromosome X. Chromosome Y is ignored. Scaling analysis ignores instances on chromosome X.

When matching the PFMs we use a uniform background and a pseudo count of 0.001. The analysis in this paper is done at a match p-value of 4^{-8} as determined by TFM-Pvalue[38]. Of the 688 motifs that we started with, 630 (representing 335 factors) were able to be matched at this stringency and have at least one shuffle motif.

Supplementary Text S12.2 - Statistics on motif instances (Table S6). Matching motifs against the genome generally matches a very large proportion of the 1,558,114,353 bases we scanned. Only considering conserved motif instances, even at a low stringency, dramatically reduces the number of bases matching a motif. Statistics also reported for best motif for each factor (i.e. the one with the highest number of instances).

Supplementary Text S12.3 - Datasets and motifs used in motif analysis. Datasets were identified from the literature and peaks identified in the study were used after mapping to the appropriate assembly (if necessary). For factors that also had a dataset available in mouse, we also show the number of peaks found in human that were conserved in mouse. When multiple motifs were available for a factor, we chose the one with the highest enrichment in the human dataset (ignoring conservation).

Supplementary Section S13: Chromatin state information

Supplementary Methods S13.1 – Overlap with 51 chromatin states in CD4 cells. For the chromatin state analysis we first masked the portion of the genome corresponding to coding exons, RNAs, regions +/-2kb of a TSS, and pseudogenes (see Figure S18). We then evaluated the overlap of unmasked Siphy-ω 10% FDR elements with a set of 51 chromatin states previously defined in CD4T cells based on the maximum posterior state assignments[16]. For each state we computed the ratio of the number of bases of unmasked conserved elements to the total number of bases in the state, which fell in the region that was unmasked. The reported fold enrichment was this ratio relative to the fraction of bases in unmasked regions, which overlapped unmasked bases of Siphy-ω elements.

Supplementary Methods S13.2 – Overlap with 15 chromatin states across nine cell types. We also evaluated overlap of Siphy-ω elements with a set of 15 chromatin states defined across 9 cell types (Figure S19). As the same location may be assigned to different chromatin states in different cell types we ordered the chromatin states in a greedy manner, that is selecting the chromatin state with the maximum enrichment for conserved bases after excluding masked regions and chromatin states previously selected. A location was associated with a state if it was assigned to that state in at least one cell type and was not assigned to any previously selected state in any cell type. Using that same ordering of states we also evaluated the cumulative enrichment for unmasked Siphy-ω bases for locations assigned to that state or a higher ranking state in at least N cell types for N=1,...,9 (Figure S20).

Supplementary Section S14: Overall accounting of constrained elements

Supplementary Text S14.1 Supplementary Methods

Bases in constrained elements were assigned in a hierarchical manner based on the Gencode Version 2 (Levels 1-3) annotations from hg18, such that if a constrained base overlapped multiple categories, it was assigned only to the first annotation on the list it overlapped. The annotations used and their order were: coding exons, 5' UTR, 3' UTR, core promoter (200 bp of transcription start), extended promoter (2 kb of transcription start), RNA genes, pseudogenes, introns and intergenic sequence. RNA genes consisted of both linc RNAs[14] and structural RNAs as defined in http://moma.ki.au.dk/~jsp/data/rna/. Among the constrained elements not accounted from this set, chromatin states were considered to account for unconstrained elements if they overlapped one of the 20 chromatin states with the greatest conservation in the CD4T model or one of the eight candidate promoter, enhancer, and insulator states in at least one cell type of the nine cell type model. Motif instances at the 40% confidence were used to account for constrained elements after the chromatin states.

Supplementary Section S15: Disease-associated variants

Supplementary Methods 15.1

To investigate the overlap between genomic variants associated with clinical phenotypes and mammalian conservation, we used results from the genome-wide association study (GWAS) database curated by NHGRI and accessed on May 30, 2011[39]. The overlap between GWAS hits and SiPhy-ω 10% FDR elements was calculated for the autosomes and X chromosome, excluding regions that were masked during prediction of the SiPhy-ω elements, exons, and regions within 2kb of the starts of transcripts as defined by GENCODE version 3c[40]. We also calculated the enrichment relative to conservation of HapMap phase 2 and 3 SNPs that were assayed in the Utah residents with ancestry from northern and western Europe (the CEPH population, abbreviated CEU), from release 28 [41]. Significance of the fold enrichment was expressed as a binomial p-value.

To find examples of conservation and regulatory motif instances overlapping GWAS-linked SNPs, we used LD from HapMap release 27[41]. We first used r^2 measures from the CEU population to list blocks of SNPs in perfect linkage ($r^2 = 1.0$) with each of the GWAS results, and scanned them against SiPhy-ω elements and the library of motif instances described in Supplementary Section S12.

Supplementary Section S16: Codon-specific positive selection

Supplementary Methods S16.1 - Phylogenetic analysis with the sitewise likelihood ratio

Sitewise dN/dS values were estimated by running the Sitewise Likelihood Ratio (SLR) software[42] on the trees and alignments from each of the parallel datasets produced by the pipeline described below. Characterizing the sitewise behavior of protein evolution in mammals was of primary interest, as the increased phylogenetic depth afforded by the added low-coverage genomes was

expected to give enough evolutionary branch length to make a sitewise analysis sensitive and specific enough to discover new regions subject to pervasive positive selection pressures within the mammalian clade. The SLR method was employed for this study, as it has been shown in simulation experiments to have desirable performance when compared to the sitewise Bayes Empirical Bayes decoding implemented in PAML, especially with regards to consistent performance between different genes[42].

A brief overview of SLR's sitewise inference is as follows: first, all gene-wide parameters are estimated for a probabilistic codon model of evolution (including branch lengths, equilibrium codon frequencies, the transition/transversion ratio, and dN/dSgene corresponding to the overall dN/dS across the gene) using information from all sites in the gene. The dN/dSi at each site is then individually and independently re-estimated while holding all other parameters fixed, and a per-site likelihood ratio test is performed, calculating the independently maximized likelihood scores for each site given the null model (neutrality, dN/dS=1) and the alternative model (dN/dS ≠1) and comparing the resulting test statistic (twice the log-likelihood difference between the null and alternative model) to a χ^2 distribution. The Banjamini-Hochberg procedure is employed to correct for multiple tests. In addition to the likelihood ratio test results, SLR provides the estimated dN/dSi at each site and the lower and upper limits of an approximate 95% confidence interval on dN/dS formed by thresholding the likelihood curve. See[42] for more information and results on the size and power of the SLR test.We refer to these sitewise patterns of positive selection are as localized positive selection.

Supplementary Methods S16.2 - Ensembl Compara gene trees pipeline

Orthologous gene trees were generated from gene family trees in the Ensembl Compara v57 database. The Ensembl Compara gene trees pipeline[43] generates gene families and alignments with the following steps: (1) run all-against-all BLASTP sequence similarity searches using all annotated Ensembl proteins, (2) generate sequence family clusters from the resulting BLAST similarity matrix using the hcluster_sg algorithm, (3) align sequences using Mcoffee's meta-alignment method, and (4) calculate gene trees using TreeBeST, which uses a given known species tree and multiple evolutionary models (including protein, codon, and DNA models) to guide the creation of gene family trees with resolved duplication events. TreeBeST combines different evolutionary models into one final gene tree topology that is then fixed. Finally, branch lengths are optimized with maximum likelihood using the HKY model. The ability of TreeBeST to combine information from multiple evolutionary models is especially important in obtaining robust tree topologies from the often partial gene predictions resulting from the low-coverage genomes in this dataset.

The Ensembl pipeline uses a novel gene-building pipeline for its annotation of low-coverage shotgun genome assemblies, as the nature of low-coverage genomes causes problems with the standard pipeline[44]. Ensembl's low-coverage gene building pipeline is based on whole-genome alignments of each low-coverage genome to an annotated reference genome (human in the case of the present mammalian genomes), built using BLASTz and axtTools. Scaffolds are arranged into “gene-scaffolds” based on the reference genome annotation, and frame-shifting indels in the low-coverage sequence (which are the result of sequence / assembly error in the vast majority of cases) are corrected by inserting 1- or 2-bp “frame-shifting” introns into the low-coverage gene model.

When the whole-genome alignment implies that the low-coverage sequence is missing an entire internal exon, a run of 'X's is inserted into the gene model in order to produce the correct translation length.

Supplementary Methods S16.3 - Isolating nearly-orthologous mammalian sub-trees

The full Compara gene family trees represent the deep evolutionary history of a gene, including duplication and speciation events going as far back as the protein-protein BLAST searches will reach. As a result, some gene trees comprise several hundred sequences with many nearly complete sets of orthologous sub-trees related by ancient duplication events. Although this property of the trees may be useful for other analysis, we wished to avoid measuring functional divergence following gene duplication in this study. Furthermore, we also wanted to restrict our analysis to genes that are well-represented in mammals to avoid including artifactual lineage-specific genes resulting from over-annotation or assembly error.

To mitigate both of the above issues for this analysis, a simple algorithm was used to filter out trees without sufficient taxonomic coverage and to split trees with ancient duplication events into roughly orthologous sub-trees. For each node starting from the root, the tree was split into two sub-trees and both sub-trees were included in the analysis if they both satisfied the following criteria: (1) contained genes from at least two out of four mammalian families (Primates, Glires, Laurasiatheria, Afrotheria) and (2) contained at least one gene from one of the outgroup species (chicken, tetraodon, opossum). If the entire tree did not satisfy the two conditions, it was dropped from the analysis. The application of this tree-splitting algorithm to the Ensembl Compara v57 database, which contains 19,298 full gene trees covering 21,317 human genes, yielded the set of 15,451 trees (or sub-trees) containing 17,709 human genes used in this analysis.

Supplementary Methods S16.4 - Sequence quality and alignment filtering

The accuracy of homology assignments is a major concern in all evolutionary studies, and the issue becomes critically important in site-wise analyses: because there is no averaging of evolutionary measures over the length of a gene, a single mis-aligned codon could directly lead to a false positive in the sitewise analysis of selective pressures, artificially raising the proportion of observed positively-selected codons. In the present study, there was also concern that the higher sequencing error rates in low-coverage genomes could lead to elevated estimates of evolutionary rates and dN/dS ratios.

In order to minimize these potential sources of error, we masked out regions of the multiple alignments based on sequence quality scores and an alignment quality metric. For sequence quality, we masked out codons (replacing the codon's nucleotides with 'N' characters) in low-coverage genomes where any of the three nucleotides in the codon had a PHRED or PHRED-equivalent score equal to or below 20. Quality scores for the source assemblies in Ensembl v57 were retrieved from Ensembl, UCSC or the source sequencing centers. For alignment quality, we used the approach employed by Pollard et al[45] of filtering out alignment columns which did not contain at least 3 Primate sequences, 2 Glires sequences, and 1 outgroup sequence. Outgroup species were defined as any species not within the Primate, Glires, or Laurasiatheria clades.

Supplementary Methods S16.5 - Clade-specific datasets

Although the SLR method does not include models comparable to PAML's branch-site models[46] for lineage-specific sitewise analysis, the mammalian evolutionary tree contains a number of similarly-sized and closely-related clades which are amenable to independent evolutionary analysis. In order to investigate independent sitewise selective pressures in mammalian sub-clades, we ran the sitewise pipeline on alignments restricted to each of the Primates, Glires, and Laurasiatheria clades. Although the Afrotheria clade is also situated nearby in the mammalian tree, it was excluded from this analysis due to the low number of available genomes (3). Each sub-clade pipeline run used alignments generated from the full mammalian gene alignments by removing any sequences from species outside the clade, and subsequently removing any columns containing only gaps. The sequence and alignment quality filtering was applied to the full mammalian alignments, and any masked sequences or alignment columns were carried over to the sub-clade alignments.

Supplementary Methods S16.5 - Gene Ontology term enrichment analysis

The topGO package for R/Bioconductor[25] was used to evaluate genes containing elevated dN/dS or positively-selected codons for enrichment in Gene Ontology (GO) terms. GO term annotations from v60 of the Ensembl human annotation set were used. Two sets of genes were defined: genes under weak constraint having dN/dS[gene] > 0.4, and genes undergoing significant positive selection with at least one confidently positively selected codon (at FDR < 0.05). The topGO package was used to perform a series of Fisher's exact tests for enrichment, using the set of all genes analyzed in this study as the gene 'universe'. A Bonferroni correction was applied to enrichment p-values to correct for multiple testing, and only terms enriched at $p < 0.05$ after correction were retained.

Supplementary Methods S16.6 - Pfam protein domain analysis

Alignment sites were annotated with Pfam domains using v57 of the Ensembl human annotation set, yielding 2.2 million sitewise values annotated with 3,116 Pfam IDs. Each Pfam domain was summarized according to its number of annotated sites, number of genes covered, mean estimated dN/dS value, and fraction of positively-selected sites. Because the overall proportion of positive selection in mammals is quite low, domains covering either fewer than 500 sites or fewer than 5 genes were dropped from the analysis to avoid spurious results from a small number of misalignments or stochastic effects.

For the present analysis, domains were separately sorted by the mean dN/dS value and the fraction of positive selection. In order to separate domains best characterized by weak selective constraint and intermittent positive selection from those best characterized by strong constraint and localized selection, the top 10 domains for each sorting criterion were compared; results are shown in Table 5.1.3a. Domains placed within the top 10 under both sorting criteria are shaded in grey, and potentially interesting domains under the fraction of positive selection criterion are highlighted in bold.

Supplementary Methods S16.7 - Data availability

See http://www.ebi.ac.uk/~greg/mammals/ for data resulting from the sitewise analysis. Summary statistics and plots for each gene can be accessed online, and all data generated (including trees, alignments, sitewise results, and tables of domains & GO terms) are available either to download in bulk or as UCSC browser tracks.

Supplemental Text S16.8 (Table S9) - Summary of sitewise selection pressures in mammals, primates, glires, and laurasiatheria

Notes: A number of summary calculations were performed on each of the four sitewise datasets. Columns labeled 'dN/dS X' contain the fraction of sites where the maximum-likelihood estimate of dN/dS is above or below the given value. 'Domain instances' shows the total number of Pfam domain instances gathered from Ensembl v57, and 'Domain types' shows the number of unique Pfam IDs gathered. 'Positive domain instances' and 'Positive domain types' show the same calculations for the subset of domain instances containing significantly positively-selected sites. 'Positive genes' and 'Positive sites' similarly show the number of genes and sites containing significant evidence for positive selection (after multiple-testing correction).

Supplemental Text S16.10 (Table S12) - GO enrichments

Notes: All terms were first sorted by 'pval.fis.bonf' (the Bonferroni-corrected p-value for enrichment) and a threshold of $p<0.05$ was applied. Terms were subsequently sorted by 'pval.elim' for display purposes. Terms mentioned in the text are in bold.

Tables containing complete results for all GO enrichments are available from the above webpage.

Supplemental Text S16.11 (Table S13) - Domain analysis

Notes: Rows were sorted either by mean dN/dS or by fraction of positive sites, and the top 10 domains for each set were retained. Those domains showing up in the top 10 on both lists were grayed out. Domains mentioned in the text are in bold.

Supplementary Section S17: Exaptation of ancestral repeat elements

Supplementary Methods S17.1 - A detailed analysis of mobile elements exapted to act as putative regulatory elements in the human genome is described in a companion paper[47].

To create a subset of putative regulatory regions we began with the set of conserved elements defined by phastCons[20]. We then removed all conserved elements that overlap protein-coding exons, untranslated regions, or exons from non-coding RNA genes. The resulting set consists of ~2.6 million conserved non-exonic elements (CNEEs). These CNEEs are under selection, but do not appear in mature transcripts, suggesting that they are likely to be functional at the DNA level and act to regulate the expression of nearby genes[48].

To understand which of these putative regulatory elements in the human genome are the results of mobile element insertions we examined the overlap of our CNEEs with mobile element annotations generated by RepeatMasker (www.repeatmasker.org). To be conservative, we did not keep all CNEEs that overlapped a mobile element insertion, but only those, which had a majority of the

bases annotated as originating in a SINE, LINE, LTR, or DNA transposon insertion. This resulted in a set of 284,857 conserved non-exonic elements, totaling nearly 7Mb of sequence, which have been exapted from mobile element insertions.

To date exaptation events we used the genome-wide multi-species alignment. For each exaptation we began with the most divergent group of species and calculated if half, or more, of the bases in the CNEE were aligning to any species in the group. This was iterated with progressively closer species until more than half of the CNEE bases were present in the most recent common ancestor of human and the group of species being used. The exaptation event was placed on the branch of the human lineage above the ancestor that appears to have contained at least half of the CNEE bases.

Supplementary Section S18: Human and Primate accelerated regions

Supplementary Text S18.1 - Human acceleration in Primate conserved elements

A second set of HARs was identified using candidate elements that were only required to show conservation in primates (though many are also more deeply conserved). These 920,486 primate-conserved sequences are similar in their genomic distribution to the 1.3 million mammalian-conserved regions used in the primary HAR analysis. They are 92.4% non-coding, with 11.1% overlapping experimentally identified enhancers. Interestingly, a much larger proportion of these primate-conserved regions are accelerated in human (1930 or 0.2% of primate-conserved elements vs. 0.04% of mammalian-conserved elements), suggesting that lineage-specific evolution is more common in less deeply conserved functional elements. Like the primary set of HARs, these 1,930 HARs are slightly depleted in coding sequences and occur as often as expected in enhancers compared to the set of primate-conserved regions from which they were identified.

Supplementary Text S18.2 – Evidence of biased gene conversion in accelerated regions

GC-biased gene conversion (gBGC) is a non-adaptive, recombination-associated process that increases the rate of fixation of AT to GC polymorphisms (i.e., weak-to-strong changes). Since gBGC can mimic selection and accelerate the overall rate of substitutions, we checked for biases in the pattern of human substitutions in HARs in order to assess evidence that these regions could have been shaped by gBGC.

On average, HAR sequence GC-content is nearly identical in human (39.0%) and the inferred human-chimp ancestor (38.1%). Of 550 HARs with sufficient outgroup alignment data to count substitutions of each type, 284 (51.6%) have more weak-to-strong than strong-to-weak substitutions on the human lineage. These HARs, and not any others, show an increase in GC-content on the human lineage. On average, this change represents a 1% increase in GC-content. A few HARs show more extreme patterns of weak-to-strong bias and larger increases in GC-content. Human substitutions in seventy-three HARs (13.3%) are all weak-to-strong (compared to 6.4% all strong-to-weak) and result in greater than 5% increases in GC-content on the human lineage. Since HAR ancestral GC-content is 38.1%, there is greater mutational opportunity for weak-to-strong compared to strong-to-weak changes on the human lineage. Hence, these findings suggest that while gBGC may have shaped the evolution of some HARs, most of the signal of human acceleration in HARs cannot be explained by gBGC or other GC-biased mutation or fixation processes.

We did not conduct a parallel analysis of substitutions in PARs, because gBGC is not a likely explanation for the substitution patterns in these elements. In particular, our filtering and statistical testing methods ensure that most PARs have higher than expected rates of substitutions in multiple primate lineages. Since recombination rates are highly variable at the PAR length-scale (hundreds of base pairs) between even closely related primates and recombination hotspots are not expected to occur at the same place on multiple branches on the primate phylogeny, it is highly unlikely that gBGC would have shaped substitutions across the primates.

Supplementary Text S18.3 - Gene Ontology (GO) enrichment analysis of accelerated regions versus positively and negatively selected codons

To explore potential functional effects of sequence changes in fast-evolving regions of the mammalian genome, we conducted statistical enrichment analyses of Gene Ontology (GO) terms associated with HARs and PARs (which are mostly non-coding) and compared these results with those for positively and negatively selected codons. Interestingly, there are many more enriched terms in common between the HARs or PARs and negatively selected codons than between HARs or PARs and positively selected codons. One notable exception is a set of GO terms associated with extra-cellular signaling (e.g., “cell surface”, “extra cellular space”, “receptor activity”, “signal transducer activity”) that are enriched in loci that are fast-evolving at both the coding and non-coding levels. Also, terms related to immunity feature in both sets, albeit somewhat distinct aspects of the immune system. In contrast, developmental pathways and processes (e.g., “axon guidance”, “ureteric bud development”) are much more commonly enriched in the HARs and PARs, suggesting a prominent role for developmental gene expression divergence in primate and human adaptations.

Although these results could be affected by myriad factors including gene density and genome-scale mutation rate heterogeneity, they seem to suggest that regulatory changes tend to occur more frequently in genes under strong purifying constraint, and rarely in genes experiencing adaptive or diversifying selection. Thus, distinct processes and pathways appear to have been under selection at the regulatory versus protein level in mammals.

Supplementary Text S18.4 - Gene Ontology (GO) enrichment analysis of HARs versus PARs

Contrasting the HAR and PAR GO enrichment results may indicate specific functions underlying human-specific biology. In fact, HARs and PARs are associated with largely different sets of enriched GO terms, although they share a small number of terms including “homophilic cell adhesion” and “astacin activity”. Interestingly, HARs are preferentially enriched for GO terms related to transcriptional regulation, the cell cycle, and MHC receptor activity compared to PARs. Furthermore, while HARs are enriched for some neuronal terms, they do not show strong enrichment for annotations related to axonogenesis, which are highly enriched among PARs. These results are not sensitive to the use of a 1Kb versus 100Kb window for mapping GO terms onto HARs and PARs. These findings indicate that although some biological systems are universally fast-evolving, adaptation appears to occur through somewhat distinct mechanisms in different clades.

Supplementary Methods S18.5 - HAR and PAR detection

Genomic regions with accelerated substitution rates in the human and primate lineages were identified by first defining candidate elements conserved across all mammals excluding the lineage of interest (human or primates). Conserved elements were identified using the phastCons program from the PHAST package (http://compgen.bscb.cornell.edu/phast) with expected length = 45, target coverage = 0.3, and expected conservation level = 0.3. Conserved elements were filtered to remove potential alignment and assembly errors using annotations from the UCSC genome browser database. Our strict inclusion criteria were: level 1 or level 2 non-gap synteny between human and all of macaque, mouse, and dog (netSynteny); no pseudogenes (luNega and pseudoYale); no segmental duplications (genomicSupDups); no repeat elements (rmsk); and no human paralogs (selfChain). After filtering, there were 1,322,576 mammalian conserved elements for human lineage-specific tests and 1,255,037 for primate clade-specific tests. Note that the exclusion of either human or all primates when running phastCons means that these sets are not identical to each other or to the set of phastCons elements used elsewhere in this study.

These sets of filtered conserved elements were scored for accelerated substitution rates in the subtree of interest (human or primates) compared to the rest of the tree using the likelihood ratio test (LRT) method implemented in the phyloP program from the PHAST package[45,49]. Acceleration p-values were adjusted for multiple comparisons using the FDR-controlling method of Benjamini and Hochberg[50].

Intersections with genome annotations and experimentally identified enhancers were performed using the featureBits program from the kent libraries and custom scripts. Genomic coordinates of experimentally identified enhancers obtained from the supplemental materials of Visel *et al.*[51] and Heintzman *et al.*[52] were mapped to the human genome assembly (hg18) using the liftOver program from the kent libraries and alignment chains from the UCSC genome browser database.

Transcription factor binding sites were predicted on both strands of the human and chimpanzee sequences of each HAR using position specific weight matrices derived from motifs of the 11 JASPAR transcription factor families with pseudo-counts[34]. For each family, statistically significant binding potential was determined using the balanced cutoff method of Rahmann *et al.*[53]. The total number of predicted binding sites was determined separately for human and chimp in each HAR for each JASPAR family. For each HAR and each family, these counts were transformed into a divergence score by taking the absolute difference in the number of sites between human and chimp and dividing by the length of the HAR. The minimum, maximum, and mean values of the divergence score across all HARs were computed for each family and for all families together.

Supplementary Methods S18.6 – Checking HARs for evidence of gBGC

To check if the accelerated substitution rates in HARs might be driven by GC-baised gene conversion, we calculated GC content and proportion of changes from weak-to-weak, weak-to-strong, strong-to-strong, and strong-to-weak along the human branch for each HAR. To do so, we first reconstructed the ancestral sequence, using chimp, gorilla, and organutan as outgroups. The procedure for reconstructing the ancestral sequence was majority rule parsimony, but also minimized the number of changes from weak to strong and strong to weak in cases where there was no majority. Specifically, the procedure was as follows: If any one outgroup nucleotide

matched the ingroup, the ancestral nucleotide was assigned that nucleotide. However, if none of the outgroup nucleotides matched the ingroup, the nucleotide with the maximum number of outgroup species in agreement was used (e.g., ingroup = A, outgroups = {CCG}; ancestor is assigned C). If there was no majority, the nucleotide was assigned based on whether the ingroup nucleotide was weak or strong (e.g., ingroup = A, outgroups = {C,G,T}; ancestor is assigned T).

Supplementary Methods S18.7 - Gene Ontology enrichment analyses

Functional enrichment/depletion analysis of fast-evolving regions was conducted by mapping Gene Ontology (GO) terms onto our data sets as follows. In all cases, we considered both the full set of GO terms and the GOSlim subset from the GOA project (ftp://ftp.ebi.ac.uk/pub/databases/GO/goa/goslim/).

We first mapped GO terms to UCSC known genes using the go.goaPart table of the UCSC genome browser. Then, we associated a term with any of the 1.32 million candidate phastCons elements located within 1Kb (or 100Kb) of a transcribed known gene annotated with that term. In this case, the "universe" for enrichment/depletion analysis is the set of candidate phastCons elements and the "foreground" set is the subset of these elements that is significantly accelerated in humans (HARs). By conducting enrichment/depletion tests at the level of phastCons elements, we automatically account for the many-to-many mappings of these elements to genes and GO terms. A parallel mapping pipeline was applied to the PARs. Both pipelines were implemented using Perl and MySQL (DBI) with local copies of the UCSC databases.

Each GO term was tested for enrichment and depletion in each of the "universe" versus "foreground" comparisons described above using two one-sided Fisher exact tests implemented in custom R (http://r-project.org) scripts. Unadjusted and Bonferroni-corrected p-values were used to evaluate statistical significance.

Supplemental Text S18.7 – Explanation of Table S15-predicted transcription factor binding sites per 100bp across all HARs for each of the 11 JASPAR families. Min=minimum number of hits for a given family in a single HAR. Max=maximum number of hits for a given family in a single HAR. Mean=average number of hits for a given family per HAR.

Supplementary Data Sets

Data access: A complete set of data files can be downloaded from or viewed in:
1. The Broad website (https://www.broadinstitute.org/scientific-community/science/projects/mammals-models/29-mammals-project-supplementary-info)
2. UCSC (http://genomewiki.cse.ucsc.edu/index.php/29mammals)
3. IGV (http://www.broadinstitute.org/igv/projects/29mammals).

Constrained Elements (SiPhy -omega, & pi)
Summary: Lists of constrained elements. For each 12-mer in the human genome a measure of constraint was scored using SiPhy (see reference below), both as a rate-based score (omega), and a measure that includes biased substitution patterns (pi). Those falling in annotated Ancestral Repeats were used as a background. An empirical cutoff score was set corresponding to 10% FDR, and all 12-mers above this score were considered significant. Overlapping significant 12-mers were clustered to yield larger elements. The HMRD SiPhy –omega 50-bp set used for comparison is also made available.

Files:
29way_omega_lods_elements_12mers.chr_specific.fdr_0.1_with_scores.txt.gz
29way_pi_lods_elements_12mers.chr_specific.fdr_0.1_with_scores.txt.gz
HMRD_omega_lods_elements_50mers.chr_specific.fdr_0.1_with_scores.txt.gz
Format: 'Chromosome Start End Lods-score Branch-length'
Format note: coordinates are 0-based, inclusive (meaning the End position is considered part of the element), and on hg18

Contact: Or Zuk <orzuk@broad.mit.edu>, Manuel Garber <mgarber@broadinstitute.org>

Reference: Garber, M. *et al.* Identifying novel constrained elements by exploiting biased substitution patterns. *Bioinformatics* **25**, i54-62, doi:btp190 [pii] 10.1093/bioinformatics/btp190 (2009).

Heights (omega,pi)
Summary: Base-level measure of constraint scored using SiPhy (see reference above), both as a rate-based score (omega) and a measure that includes biased substitution patterns (pi).

Files:
omega.12mers.wig.gz
Format: 'position log_odds_score'
pi.ewig.gz
Format: 'postion %A %C %G %G log_odds_score'

Format note: coordinates on hg18

Contact: Manuel Garber <mgarber@broadinstitute.org>

Protein-coding exons
Summary: A list of identified previous annotation and (Reference annotation) novel conserved exons (Congo). Exons were identified using a version of CONGO (previously developed for the *Drosophila* genomes, see reference below) enhanced to handle mammalian exon prediction. The enhancements include a semi-Markov feature to model the short length distribution of mammalian exons, a synteny feature for recognizing duplicated regions, and an alternative training function to improve accuracy when performing an unbalanced prediction task (only ~1.5% of the human genome is protein-coding).

Files: ReferenceAnnotation_hg18.20101019.new.syn.gtf
CONGO_hg18.20101019.new.syn.gtf
Format: GTF
Format note: coordinates on hg18

Contact: Mike Lin <mikelin@mit.edu>

Reference: Lin, M. F. *et al.* Revisiting the protein-coding gene catalog of Drosophila melanogaster using 12 fly genomes. *Genome Res* **17**, 1823-1836, doi:gr.6679507 [pii] 10.1101/gr.6679507 (2007).

Synonymous Constraint Elements
Summary: Identified coding regions with a very low synonymous substitution rate – indicating additional sequence constraints beyond the amino acid level. The Synonymous Constraint Elements (SCEs) are defined at three different resolutions (9-, 15-, and 30-codon). There is also a bedGraph track for the local estimate of the synonymous substitution rate (lambda_s). Also available at: http://compbio.mit.edu/SCE/

File: SynonymousConstraintElements.tar.gz
Files in archive:
SCE9.hg18.bed.gz
SCE15.hg18.bed.gzSCE30.hg18.bed.gz
lambda_s_ORF.hg18.bedGraph.gz
File formats: BED, bedGraph
Format note: coordinates are on hg18

Contact: Mike Lin <mikelin@mit.edu>

RNA structures
Summary: The list of candidate predictions for structural RNA families. EvoFold structural predictions were based on a 31-way subset of the genome-wide 44-way multiZ alignment

(consisting of 28 of the 29 eutherian mammals, together with opossum, chicken, and tetraodon as outgroups) and clustered into candidate families using the novel EvoFam algorithm. This data, as well as the complete set of structure predictions from the EvoFold screen can be downloaded in bulk or browsed through a UCSC Genome Mirror from the following web- site: http://moma.ki.au.dk/prj/mammals/.

In addition, individual families are listed and annotated in the following reference and its supplement.

File: StructuralRNAfamilies.tar.gz
Files in archive:
Genome_wide_prediction_set
Genome_wide_with_paralogs_prediction_set
UTR_with_paralogs_prediction_set
data_format.txt
Format: described in the file: data_format.txt
Format note: coordinates are hg18

Contacts: Brian Parker bparker@binf.ku.dk, Jakob Skou Pedersen jakob.skou@ki.au.dk

Reference: Parker, B. J. *et al.* New families of human regulatory RNA structures identified by comparative analysis of vertebrate genomes. *Genome Research* (2011).

Constraint Structure in Promoters
Summary: A list of local maxima identified from the smoothed pi-scores in the core promoters of genes.

File: peaks.positions.gz
Format: 'Chromosome Start End Score'
Format note: Coordinates are 1-based and exclusive (meaning the End base is not included in the peak position). All positions are at a single base, and are on hg18.

Contact: Evan Mauceli <evan@broadinstitute.org>

Motif instances
Summary: A list of instances of identified regulatory motifs. A motif catalog was built from TRANSFAC, Jaspar, and Protein Binding Microarrays using a method similar to that described in the reference below, with extensions for position frequency matricies. Motif instances were identified genome-wide using a FDR of 60%.

File: instances-thresh8-0.4.txt.gz
Format: Motif-name Chromosome Start End Strand
Format note: coordinates are 1-based, inclusive (meaning the End position is considered part of the element), and on hg18

Contact: Pouya Kheradpour pouyak@mit.edu

Reference: Kheradpour, P., Stark, A., Roy, S. & Kellis, M. Reliable prediction of regulator targets using 12 Drosophila genomes. *Genome Res* **17**, 1919-1931, doi:gr.7090407 [pii] 10.1101/gr.7090407 (2007).

Chromatin Mark Data

Summary: ENCODE segmentation of hg18 into chromatin states for each of nine human cell types. States were learned using a Hidden Markov Model that computationally integrated ChIP-seq data into fifteen states associated with different types of functionality. This data is available from UCSC at:
http://genome-preview.ucsc.edu/cgi-bin/hgTrackUi?hgsid=2563118&c=chrX&g=wgEncodeBroadHmm

A similar segmentation based on the CD4T cell line is also provided in the file:

Files:

map_allstates.bed.txt.gz – segmentation based on CD4T cell line
chromatinMarks.tar.gz

Files in archive:

wgEncodeBroadHmmGm12878HMM.bed – modelling in GM12878 cells
wgEncodeBroadHmmH1hescHMM.bed – modelling in H1-hESC cells
wgEncodeBroadHmmHmecHMM.bed – modelling in HMEC cells
wgEncodeBroadHmmHsmmHMM.bed – modelling in HSMM cells
wgEncodeBroadHmmHuvecHMM.bed – modelling in HUVEC cells
wgEncodeBroadHmmHepg2HMM.bed – modelling in HepG2 cells
wgEncodeBroadHmmNhekHMM.bed – modelling in NHEK cells
wgEncodeBroadHmmK562HMM.bed – modelling in K562 cells
wgEncodeBroadHmmNhlfHMM.bed – modelling in NHLF cells

File format: BED

Contact: Jason Ernst jernst@mit.edu

References:

Ernst J and Kellis M. Discovery and characterization of chromatin states for systematic annotation of the human genome. *Nature Biotechnology* 2010 Jul 25;28:817-825.

J. Ernst, P. Kheradpour, T.S. Mikkelsen, N. Shoresh, L.D. Ward, C.B. Epstein, X. Zhang, L. Wang, R. Issner, M. Coyne, M. Ku, T. Durham, M. Kellis, B.E. Bernstein
Mapping and analysis of chromatin state dynamics in nine human cell types.
Nature 473: 43-49, 2011.

Accounting for conserved elements

Summary: A list of each conserved element (omega), the chromatin state it resides in, and, if applicable, any genic annotation it overlaps, as well as any overlapping motif instances.

File: elementPartition.txt.gz
File Format:
Column 1: 'ELEMENT:'
Column 2-6: 'Chromosome Start End Lods-score Branch-length'
Column 3-4*: 'chromatin: 'cell-type:chromatin-state-' for 9 cell types. *if a conserved element overlaps multiple chromatin states, then the consecutive states appear in consecutive columns
Column 5-6 (if applicable): 'gencode:' annotation
Column 7-8 (if applicable); 'motifs:' overlapping motifs for this element

Chromatin state numbers and candidate annotations:
State 1 – Active Promoter
State 2 – Weak Promoter
State 3 – Inactive/Poised Promoter
State 4,5 – Strong enhancer
State 6,7 – Weak enhancer
State 8 – Insulator
State 9 – Transcriptional transition
State 10 – Transcriptional elongation
State 11 – Weak transcribed
State 12 – Polycomb-repressed
State 13 – Heterochromatin; low signal
State 14,15 – Repetitive/Copy Number Variation

Contact: Evan Mauceli evan@broadinstitute.org

Associated GWAs SNPs overlapping constraint
Summary: SNPs and data from the NHGRI GWAS catalog, 5/30/11
File: conserved_gwas.xlsx
File format: Microsoft Excel Workbook

Contact: Luke Ward lucas.d.ward@gmail.com

Positively selected codons
Summary: Main data files and backing data for the analysis identifying positively selected codons. This data and updates are available for download from here:
http://www.ebi.ac.uk/goldman-srv/mammals/

File: PositivelySelectedCodons.tar.gz
Files in archive:
Pol_sel_score.bed - one region per Ensembl gene analyzed, with a score corresponding to the negative log of an overall p-value for positive selection at that gene based on mammalian alignments.

Overall_dN_dS.bed - one region per Ensembl gene analyzed, with a score corresponding to the overall dN/dS at that gene based on mammalian alignments.

Sites.bedGraph - one value per codon analyzed, with a score corresponding to the signed sitewise likelihood ratio statistic for non-neutral selection. Values above zero indicate evidence for positive selection, values below zero indicate evidence for negative selection. The statistic is approximately chi-square distributed when the data is neutrally evolving. The bedGraph file looks best when displayed on UCSC the following track parameters:

```
type=bigWig
lineMark=0
lineOnOff=on
autoScale=off
viewLimits=-20:10
minLimit=-20
maxLimit=10
visibility=full
```

mammals_e57_sitewise_tables.Rdata - the .Rdata file which contains the main results tables (genes and sites)

web/ – directory containing the 'complete archive' package which contains alignments, PDFs, and other data used during the analysis

File formats: BED, bedGraph, Rdata
Format note: coordinates are on hg18

Contact: Gregory Jordan greg@ebi.ac.uk

Exapted repeats

Summary: List of exapted elements identified as described in the following reference.

File: exaptedElements.bed.gz
File format: BED
Format note: coordinates are on hg18
.
Contact: Craig Lowe craiglowe@gmail.com

Reference: Lowe, C. B. & Haussler, D. 29 mammalian genomes reveal novel exaptations of mobile elements for likely regulatory functions in the human genome. *In preparation* (2011).

Human and Primate Accelerated Regions

Summary: Lists of human accelerated regions (HARs) and primate accelerated regions (PARs). Regions with accelerated substitution rates in either lineage were identified by first defining candidate elements using the phastCons program (not including the lineage of interest) and then scoring those elements for accelerated substitution rates in the subtree (human or primate) of interest.

Files:
2xHARs.bed
2xPARs.bed
Format: BED
Format note: coordinates are on hg18

Contact: Katherine Pollard <katherine.pollard@gladstone.ucsf.edu>

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Table S1. Information on the 29 mammalian assemblies

Common name	Scientific name	Assembly	Sample source	Data generation center	GenBank accession number	Coverage (x-fold)	Total contig length (Gb)	N50 contig (kb)	N50 scaffold (gapped, kb)
Human	*Homo sapiens*	hg18	n/a	multiple	NCBI36	FINISHED	2.83	38,500	N/A
Chimpanze	*Pan troglodytus*	panTro2	n/a	multiple	AADA01000000	6.0	2.97	29	9,700
Rhesus Macaque	*Macaca mulatta*	rheMac2	n/a	multiple	AANU01000000	5.1	2.87	26	5,870
Tarsier	*Tarsier syrichta*	tarSyr1	Duke University Primate Center	WUSG	ABRT000000000	2.1	2.77	2.9	12
Mouse Lemur	*Microcebus murinus*	micMur1	Caltech	Broad	ABDC01000000	1.9	1.86	3.5	140
Bushbaby (Northern Greater Galago)	*Otolemur garnetti*	otoGar1	Duke University Primate Center	Broad	AAQR01000000	1.9	1.97	3.1	137
Tree Shrew	*Tupaia belangeri*	tupBel1	German Primate Center, Goettingen	Broad	AAPY01000000	1.9	2.14	3	124
Mouse	*Mus musculus*	mm9	n/a	multiple	Build 37	FINISHED	2.72	39,294	N/A
Rat	*Rattus norvegicus*	rn4	n/a	BCM	Baylor3.4	7.3	2.49	18,985	N/A
Kangaroo Rat	*Dipodomys ordii*	dipOrd1	Museum of Vertebrate Zoology, University of California, Berkeley,	BCM	ABRO01000000	1.8	1.84	4.3	33
Guinea Pig	*Cavia porcellus*	cavPor2	Covance Research	Broad	AAKN01000000	1.9	1.95	81	28,000
Squirrel, Thirteen-lined Ground	*Spermophilis* tridecemlineatus	speTri1	National Institute of Neurological Disorders and Stroke	Broad	AAQQ01000000	1.9	1.91	2.7	95
Rabbit	*Oryctolagus cuniculus*	oryCun1	Covance Research	Broad	AAGW02000000	2.0	2.08	3.3	55
Pika	*Ochotona princeps*	ochPri2	New Mexico Museum of Natural History	Broad	AAYZ01000000	1.9	1.92	3.3	88
Alpaca	*Vicugna pacos*	vicPac1	Binghamton University	WUSC	ABRR01000000	2.9	1.92	3.9	22
Dolphin, Bottlenosed	*Tursiops truncatus*	turTru1	Portland State University	BCM	ABRN01000000	2.8	2.30	9.7	16
Cow	*Bos taurus*	bosTau4	n/a	BCM	AAFC03000000	5.4	2.87	49	1920
Horse	*Equus caballus*	equCab2	n/a	Broad	AAWR02000000	6.8	2.43	112	47,000
Cat, Domestic	*Felis catus*	felCat3	n/a	Agencourt	AANG01000000	1.9	1.64	2.4	113
Dog, Domestic	*Canis familaiaris*	canFam2	n/a	Broad	AACN010000000	7.6	2.39	180	45,000
Little Brown Bat (Microbat)	*Myotis lucifugus*	myoLuc1	Center for Ecology and Conservation Biology, Boston University	Broad	AAPE01000000	1.8	1.67	3.1	93
Fruit Bat (Megabat, Flying Fox)	*Pteropus vampyrus*	pteVam1	Lubee Bat Conservancy, Gainsville	BCM	ABRP01000000	2.9	1.84	8.5	121
Hedgehog, European	*Erinaceus europeaus*	eriEur1	University of East Anglia, Norwich, UK	Broad	AANN01000000	1.9	2.13	2.8	33
Shrew, Common	*Sorex araneus*	sorAra1	Cornell University, Ithaca	Broad	AALT00000000	1.9	1.83	3.2	48
Elephant, African Savannah	*Loxodonta africana*	loxAfr2	San Diego Zoo's CRES	Broad	AAGU02000000	1.9	2.45	2.9	64
Hyrax, Rock	*Procavia capensis*	proCap1	The Dallas Zoo	BCM	ABRQ01000000	2.4	2.40	3.4	24
Tenrec	*Echinops telfari*	echTel1	Institute of Anatomy, University of Munich, Germany	Broad	AAIY01000000	1.9	2.11	3.1	48
Nine-banded Armadillo	*Dasypus novemicinctus*	dasNov2	School of Veterinary Medicine, Louisiana State University	Broad	AAGV020000000	2.3	2.37	2.4	55
Sloth, Two-toed	*Choloepus hoffmanni*	choHof1	San Diego Zoo's CRES	WUSG	ABVD01000000	2.2	2.06	2.3	10

Table S2. Constraint estimation and detection statistics

Stat	29way ω 12mers	29way ω-lods 12mers	29way π-lods 12mers
#called (kmers) fdr=0.1	44,931,962	**81,923,925**	110,250,366
frac called (kmers)	1.46%	**2.66%**	3.58%
# elements	2,759,895	**3,621,583**	4,463,319
# bases	80,384,823	**128,766,046**	165,088,933
frac. called (bases)	2.61%	**4.18%**	5.36%
frac. constrained (kmers)	5.34%	XX	11.99%
frac. constrained (kmers, chr-shifted)	**5.44%**	XX	**12.33%**

Stat	29way ω 12mers (BL-corr.)	29way ω-lods 12mers (BL-corr.)	29way π-lods 12mers (BL-corr.)
#called (kmers) fdr=0.1	38,744,951	14,409,822	5,411,300
frac called (kmers)	1.26%	0.47%	0.18%
# elements	2,760,769	1,232,883	471,773
# bases	74,366,747	30,098,017	11,803,440
frac. called (bases)	2.41%	0.98%	0.38%
frac. constrained (kmers)	4.18%	XX	56.33%
frac. constrained (kmers, chr-shifted)	4.22%	XX	5.63%

Stat	HMRD ω 12mers	HMRD ω-lods 12mers	HMRD π-lods 12mers
#called (kmers) fdr=0.1	965,648	12,163,613	21,385,019
frac called (kmers)	0.03%	0.39%	0.69%
# elements	295,134	1,583,803	2,546,071
# bases	4,225,299	30,086,694	54,526,055
frac. called (bases)	0.14%	0.98%	1.77%
frac. constrained (kmers)	XX	XX	10.40%
frac. constrained (kmers, chr-shifted)	XX	XX	10.52%

Stat	HMRD ω 50mers	HMRD ω-lods 50mers	HMRD π-lods 50mers
#called (kmers) fdr=0.1	42,521,200	68,775,126	82,962,293
frac called (kmers)	1.38%	2.23%	2.69%
# elements	789,570	817,021	35,057
# bases	87,972,128	114,540,295	4,646,148
frac. called (bases)	2.86%	3.72%	0.15%
frac. constrained (kmers)	5.34%	XX	11.76%
frac. constrained (kmers, chr-shifted)	5.36%	XX	11.94%

XX = Unreliable estimate due to noisy curve or lack of distinction from Gaussian
Genome len: 3,080,436,051

Table S3. Comparison of SiPhy and Phastcons elements to HMRD and vertebrate Siepel elements

a. Element description

	Elements	Total bases (Mb)	Median element size (bp)	Mean element size (bp)	Maximum element size (bp)	Minimum element size (bp)
A. 29 mammals SiPhy-omega (10%FDR)	3,621,583	129	19	36	4,182	12
B. 29 mammals SiPhy-omega (5%FDR)	1,985,021	69	20	35	2,503	12
C. 29 mammals SiPhy-pi (10%FDR)	4,463,319	165	18	37	17,137	12
D. 29 mammals SiPhy-pi (5%FDR)	2,261,877	99	21	44	5,832	12
E. 29 mammals Phastcons	2,040,420	112	29	55	3,895	1
F. MRH.D SiPhy - 50 bp	488,089	60	89	123	6,275	49
G. 5 vertebrate Phastcons - syntenic elements (Siepel 2005)	1,183,203	123	69	104	4,922	1
H. Union of HMRD and 5 vertebrates (F + G)	1,188,513	137	77	115	6,280	1

b. Overlap of sets of elements

	A	B	C	D	E	F	G	H
A. 29 mammals SiPhy-omega (10%FDR)	0	1,292,279	2,939,856	1,924,733	2,084,383	688,122	1,581,042	1,666,254
B. 29 mammals SiPhy-omega (5%FDR)	1,958,119	0	1,904,076	1,879,787	1,878,647	801,002	1,452,392	1,508,727
C. 29 mammals SiPhy-pi (10%FDR)	2,378,558	998,510	0	1,598,747	1,594,852	504,997	1,347,895	1,411,653
D. 29 mammals SiPhy-pi (5%FDR)	1,994,844	1,302,081	2,198,146	0	1,646,898	582,943	1,275,799	1,333,626
E. 29 mammals Phastcons	1,739,288	1,161,052	1,668,545	1,391,162	0	570,218	1,151,100	1,200,484
F. MRH.D SiPhy - 50 bp	421,408	384,403	411,641	403,453	426,654	0	421,603	488,089
G. 5 vertebrate Phastcons - syntenic elements (Siepel 2005)	850,816	657,568	869,285	739,129	806,837	415,833	0	1,183,203
H. Union of HMRD and 5 vertebrates (F + G)	819,674	623,443	837,631	703,506	778,697	421,163	1,122,066	0

c. Intersection between sets in basepairs

	A	B	C	D	E	F	G	H
A. 29 mammals SiPhy-omega (10%FDR)	0	67,627,303	113,238,367	89,400,914	92,714,916	44,242,045	78,301,827	82,952,319
B. 29 mammals SiPhy-omega (5%FDR)	67,627,303	0	65,981,370	66,004,495	64,535,015	35,334,387	54,961,790	57,415,163
C. 29 mammals SiPhy-pi (10%FDR)	113,238,367	65,981,370	0	95,843,873	89,646,311	46,473,954	83,096,502	89,168,007
D. 29 mammals SiPhy-pi (5%FDR)	89,400,914	66,004,495	95,843,873	0	76,958,066	43,091,056	68,617,675	73,290,379
E. 29 mammals Phastcons	92,714,916	64,535,015	89,646,311	76,958,066	0	43,205,177	75,124,448	79,480,139
F. MRH.D SiPhy - 50 bp	44,242,045	35,334,387	46,473,954	43,091,056	43,205,177	0	45,823,368	59,825,356
G. 5 vertebrate Phastcons - syntenic elements (Siepel 2005)	78,301,827	54,961,790	83,096,502	68,617,675	75,124,448	45,823,368	0	122,814,031
H. Union of HMRD and 5 vertebrates (F + G)	82,952,319	57,415,163	89,168,007	73,290,379	79,480,139	59,825,356	122,814,031	0

Table S4. Statistics on new exon predictions by CONGO and supporting evidence

Total new predictions	3789	100.00%	All new predictions, not overlapping protein-coding exons or pseudogenes in Gencode/EnsEMBL, RefSeq, or UCSC known genes

Breakdown by genomic territory:	1375	36.29%	Intergenic
	728	19.21%	Intron
	482	12.72%	UTR
	481	12.69%	NCExon
	76	2.01%	NCIntron
	114	3.01%	AntisenseCDS
	313	8.26%	AntisenseIntron
	103	2.72%	AntisenseUTR
	45	1.19%	AntisenseNCExon
	71	1.87%	AntisenseNCIntron

Predictions supported by different lines of evidence (not mutually exclusive):			
	394	10.40%	Pfam domain
	895	23.62%	Mrna (cDNA)
	1318	34.78%	IntronEst
	1640	43.28%	Scripture transcripts (Illuminua human body map)

Table S5. Predicted new protein-coding exons by CONGO

id	chrom	start	end	strand	phase	length_nt	CONGO_score	territory	segdup	Pfam domains	mrna	intronEst	ScriptureTU	ScriptureLinkage	ScriptureLinkageTo
CONGO_chr1_000849675_517_p0	chr1	849675	850191	+	0	517	1048.16	UTR		SAND		1	TU689	SpliceToPCG	ENSG00000187634
CONGO_chr1_000906021_252_m0	chr1	906021	906272	-	0	252	512.23	Intron					TU690	SpliceToPCG	ENSG00000187642
CONGO_chr1_000959799_148_p0	chr1	959799	959946	+	0	148	704.49	NCExon				1	TU691	SpliceToPCG	ENSG00000188157
CONGO_chr1_002351817_112_p0	chr1	2351817	2351928	+	0	112	56.39	NCExon			1		TU694	SpliceToPCG	ENSG00000149527
CONGO_chr1_002706469_119_m1	chr1	2706469	2706587	-	1	119	550.24	Intergenic							
CONGO_chr1_002706737_513_m0	chr1	2706737	2707249	-	0	513	2692.97	Intergenic							
CONGO_chr1_006048712_212_p0	chr1	6048712	6048923	+	0	212	1139.1	Intron							
CONGO_chr1_006437081_645_p0	chr1	6437081	6437725	+	0	645	2611.29	Intron	1						
CONGO_chr1_006437885_960_p0	chr1	6437885	6438844	+	0	960	3025.77	Intron	1					NovelUnspliced	
CONGO_chr1_006488673_133_m0	chr1	6488673	6488805	-	0	133	663.25	Intron							
CONGO_chr1_007743250_179_p0	chr1	7743250	7743428	+	0	179	5.26	Intron					TU695	SpliceToPCG	ENSG00000049245
CONGO_chr1_008596909_126_p1	chr1	8596909	8597034	+	1	126	132.74	AntisenseIntron	1						
CONGO_chr1_008853471_59_m2	chr1	8853471	8853529	-	2	59	464.44	UTR			1	1	TU696	SpliceToPCG	ENSG00000074800
CONGO_chr1_009933876_67_m0	chr1	9933876	9933942	-	0	67	469.19	AntisenseIntron							
CONGO_chr1_009935031_84_m2	chr1	9935031	9935114	-	2	84	407.43	AntisenseIntron							
CONGO_chr1_009938466_80_m1	chr1	9938466	9938545	-	1	80	394.73	AntisenseIntron					TU697	NovelMultiExon	
CONGO_chr1_009943359_74_m0	chr1	9943359	9943432	-	0	74	263.51	AntisenseIntron							
CONGO_chr1_010089867_153_p1	chr1	10089867	10090019	+	1	153	100.13	NCExon				1	TU698	SpliceToPCG	ENSG00000130939
CONGO_chr1_010326735_201_p2	chr1	10326735	10326935	+	2	201	326.92	Intron							
CONGO_chr1_010624667_223_m0	chr1	10624667	10624889	-	0	223	111.23	Intron					TU699	SpliceToPCG	ENSG00000130940
CONGO_chr1_010703959_110_m2	chr1	10703959	10704068	-	2	110	34.12	Intron							
CONGO_chr1_010928863_172_m1	chr1	10928863	10929034	-	1	172	1.34	Intergenic							
CONGO_chr1_012938056_264_m1	chr1	12938056	12938319	-	1	264	237.3	Intron	1						
CONGO_chr1_016409222_118_m0	chr1	16409222	16409339	-	0	118	191.28	Intron							
CONGO_chr1_021746484_119_p0	chr1	21746484	21746602	+	0	119	501.95	Intron				1			
CONGO_chr1_022067965_84_m0	chr1	22067965	22068048	-	0	84	243.46	Intron					TU124	SpliceToPCG	ENSG00000142798
CONGO_chr1_022068546_198_m0	chr1	22068546	22068743	-	0	198	285.39	Intron					TU124	SpliceToPCG	ENSG00000142798
CONGO_chr1_022069914_39_m0	chr1	22069914	22069952	-	0	39	25.31	Intron					TU124	SpliceToPCG	ENSG00000142798
CONGO_chr1_022149815_165_m0	chr1	22149815	22149979	-	0	165	748.93	Intergenic							
CONGO_chr1_022150126_154_m0	chr1	22150126	22150279	-	0	154	51.12	Intergenic							
CONGO_chr1_022150402_125_m0	chr1	22150402	22150526	-	0	125	105.62	Intergenic							
CONGO_chr1_023293410_51_m1	chr1	23293410	23293460	-	1	51	32.32	UTR			1	1	TU700	SpliceToPCG	ENSG00000169641
CONGO_chr1_024160045_167_p0	chr1	24160045	24160211	+	0	167	122.13	UTR	1		1	1	TU701	SpliceToPCG	ENSG00000189266
CONGO_chr1_026363239_295_m1	chr1	26363239	26363533	-	1	295	891.37	Intergenic							
CONGO_chr1_026364904_98_m0	chr1	26364904	26365001	-	0	98	452.66	Intergenic							
CONGO_chr1_026365113_84_m0	chr1	26365113	26365196	-	0	84	382.41	Intergenic							
CONGO_chr1_026367494_86_m2	chr1	26367494	26367579	-	2	86	352.18	Intergenic							
CONGO_chr1_026370267_147_m0	chr1	26370267	26370413	-	0	147	737.94	AntisenseUTR				1			
CONGO_chr1_026370695_45_m0	chr1	26370695	26370739	-	0	45	175.02	AntisenseUTR				1			
CONGO_chr1_026553738_126_m0	chr1	26553738	26553863	-	0	126	15.66	Intergenic							
CONGO_chr1_026555537_64_m1	chr1	26555537	26555600	-	1	64	62.88	Intergenic							
CONGO_chr1_026671455_115_p1	chr1	26671455	26671569	+	1	115	32.19	UTR			1	1	TU702	SpliceToPCG	ENSG00000198830
CONGO_chr1_026922591_97_m2	chr1	26922591	26922687	-	2	97	55.5	AntisenseIntron							
CONGO_chr1_027050207_42_m0	chr1	27050207	27050248	-	0	42	51.02	AntisenseCDS				1			
CONGO_chr1_027770933_92_m2	chr1	27770933	27771024	-	2	92	63.34	Intron					TU703	SpliceToPCG	ENSG00000126705
CONGO_chr1_027824198_52_m1	chr1	27824198	27824249	-	1	52	3.73	UTR			1	1	TU704	SpliceToPCG	ENSG00000000938
CONGO_chr1_028791611_233_p0	chr1	28791611	28791843	+	0	233	886.32	UTR		Ras	1	1	TU705	SpliceToPCG	ENSG00000188060
CONGO_chr1_028823045_72_m0	chr1	28823045	28823116	-	0	72	132.53	NCExon				1	TU706	SpliceToPCG	ENSG00000120656
CONGO_chr1_029086139_171_p0	chr1	29086139	29086309	+	0	171	71.17	UTR			1	1	TU125	SpliceToPCG	ENSG00000159023
CONGO_chr1_029267832_51_p0	chr1	29267832	29267882	+	0	51	30.96	Intron					TU125	SpliceToPCG	ENSG00000159023
CONGO_chr1_029268265_129_p0	chr1	29268265	29268393	+	0	129	463.29	Intron					TU125	SpliceToPCG	ENSG00000159023
CONGO_chr1_029269571_144_p0	chr1	29269571	29269714	+	0	144	102.51	Intron						NovelUnspliced	
CONGO_chr1_029365874_92_m1	chr1	29365874	29365965	-	1	92	107.11	NCExon			1	1	TU707	SpliceToPCG	ENSG00000116350
CONGO_chr1_032157755_92_m0	chr1	32157755	32157846	-	0	92	34.1	UTR			1	1	TU708	SpliceToPCG	ENSG00000184007
CONGO_chr1_032282949_60_p0	chr1	32282949	32283008	+	0	60	97.99	NCIntron							
CONGO_chr1_032565594_53_p1	chr1	32565594	32565646	+	1	53	55.09	NCExon				1	TU709	SpliceToPCG	ENSG00000116478
CONGO_chr1_035422839_65_p1	chr1	35422839	35422903	+	1	65	5.09	AntisenseIntron							
CONGO_chr1_035422908_94_m0	chr1	35422908	35423001	-	0	94	200.1	Intron					TU710	SpliceToPCG	ENSG00000116560
CONGO_chr1_036323353_115_m1	chr1	36323353	36323467	-	1	115	965	AntisenseCDS							
CONGO_chr1_036532238_84_p1	chr1	36532238	36532321	+	1	84	46.39	NCExon					TU712	SpliceToPCG	ENSG00000054118
CONGO_chr1_037216344_96_p2	chr1	37216344	37216439	+	2	96	59.27	AntisenseIntron							
CONGO_chr1_037479084_87_p0	chr1	37479084	37479170	+	0	87	36.33	Intergenic							
CONGO_chr1_038509057_81_m0	chr1	38509057	38509137	-	0	81	8.95	Intergenic							
CONGO_chr1_038619746_54_m2	chr1	38619746	38619799	-	2	54	66.46	Intergenic							
CONGO_chr1_038785616_97_m1	chr1	38785616	38785712	-	1	97	26.48	Intergenic							
CONGO_chr1_038800099_92_p0	chr1	38800099	38800190	+	0	92	11.71	Intergenic							
CONGO_chr1_039397228_52_p0	chr1	39397228	39397279	+	0	52	204.48	Intron					TU713	SpliceToPCG	ENSG00000127603
CONGO_chr1_039490105_96_p0	chr1	39490105	39490200	+	0	96	75.1	Intron					TU714	SpliceToPCG	ENSG00000127603
CONGO_chr1_039507395_115_m2	chr1	39507395	39507509	-	2	115	430.7	AntisenseCDS							
CONGO_chr1_039537191_73_p2	chr1	39537191	39537263	+	2	73	7.64	Intron							
CONGO_chr1_040860353_141_m0	chr1	40860353	40860493	-	0	141	6	UTR			1		TU716	SpliceToPCG	ENSG00000117016
CONGO_chr1_040947438_31_p2	chr1	40947438	40947468	+	2	31	1.24	Intron							
CONGO_chr1_040947526_137_m2	chr1	40947526	40947662	-	2	137	56.83	AntisenseUTR							
CONGO_chr1_041867007_68_m0	chr1	41867007	41867074	-	0	68	391.27	UTR			1		TU717	SpliceToPCG	ENSG00000127124
CONGO_chr1_044512393_176_p2	chr1	44512393	44512568	+	2	176	38.82	AntisenseIntron							
CONGO_chr1_044762974_108_p0	chr1	44762974	44763081	+	0	108	19.53	Intron							
CONGO_chr1_046771316_475_m1	chr1	46771316	46771790	-	1	475	1021.18	Intergenic							
CONGO_chr1_047206029_100_m1	chr1	47206029	47206128	-	1	100	104.95	AntisenseIntron		p450					
CONGO_chr1_047716491_140_m2	chr1	47716491	47716630	-	2	140	45.8	Intergenic							
CONGO_chr1_048004161_205_m1	chr1	48004161	48004365	-	1	205	602.98	NCExon					TU21	SpliceToNCG	ENSG00000204018
CONGO_chr1_048013429_270_m1	chr1	48013429	48013698	-	1	270	2206.81	NCExon					TU21	SpliceToPCG	ENSG00000231033
CONGO_chr1_048016713_91_m2	chr1	48016713	48016803	-	2	91	1081.65	NCExon				1	TU21	SpliceToPCG	ENSG00000231033
CONGO_chr1_048032845_175_m0	chr1	48032845	48033019	-	0	175	1167.02	NCExon				1	TU21	SpliceToPCG	ENSG00000231033
CONGO_chr1_048039732_147_m0	chr1	48039732	48039878	-	0	147	1459.99	NCExon				1	TU21	SpliceToPCG	ENSG00000231033
CONGO_chr1_048234947_103_m1	chr1	48234947	48235049	-	1	103	51.38	NCExon				1	TU21	SpliceToPCG	ENSG00000231033
CONGO_chr1_049172241_64_p0	chr1	49172241	49172304	+	0	64	211.04	AntisenseIntron							
CONGO_chr1_050440719_120_p0	chr1	50440719	50440838	+	0	120	7.21	UTR			1		TU721	SpliceToPCG	ENSG00000162374
CONGO_chr1_050461375_47_p0	chr1	50461375	50461421	+	0	47	13.56	AntisenseNCExon							
CONGO_chr1_050871773_155_p2	chr1	50871773	50871927	+	2	155	8.35	AntisenseIntron							
CONGO_chr1_050942137_123_p0	chr1	50942137	50942259	+	0	123	72.77	AntisenseIntron							
CONGO_chr1_051792988_86_m0	chr1	51792988	51793073	-	0	86	70.12	AntisenseNCIntron							
CONGO_chr1_053838362_178_m2	chr1	53838362	53838539	-	2	178	1199.92	UTR			1	1	TU240	SpliceToPCG	ENSG00000174332
CONGO_chr1_053976067_301_m0	chr1	53976067	53976367	-	0	301	1189.42	Intergenic					TU240	SpliceToPCG	ENSG00000174332
CONGO_chr1_054371229_327_m0	chr1	54371229	54371555	-	0	327	2217.36	Intergenic				1			
CONGO_chr1_054374891_179_m2	chr1	54374891	54375069	-	2	179	853.9	Intergenic				1			
CONGO_chr1_060461523_76_p0	chr1	60461523	60461598	+	0	76	64.49	Intergenic							
CONGO_chr1_060467874_141_m2	chr1	60467874	60468014	-	2	141	32.12	Intergenic							
CONGO_chr1_061348979_99_m0	chr1	61348979	61349077	-	0	99	7.92	AntisenseIntron							
CONGO_chr1_061419367_97_p1	chr1	61419367	61419463	+	1	97	103.32	Intron							
CONGO_chr1_061436970_63_p0	chr1	61436970	61437032	+	0	63	42.35	Intron							
CONGO_chr1_061482669_59_p2	chr1	61482669	61482727	+	2	59	142.97	Intron							
CONGO_chr1_062391618_124_p1	chr1	62391618	62391741	+	1	124	229.17	NCExon			1		TU723	SpliceToPCG	ENSG00000132849
CONGO_chr1_063142203_77_m0	chr1	63142203	63142279	-	0	77	123.53	Intergenic							
CONGO_chr1_063238640_90_m1	chr1	63238640	63238729	-	1	90	140.58	Intergenic							
CONGO_chr1_071771112_67_m2	chr1	71771112	71771178	-	2	67	63.22	Intron							
CONGO_chr1_072062085_66_p2	chr1	72062085	72062150	+	2	66	116.52	AntisenseIntron							
CONGO_chr1_075372893_81_p0	chr1	75372893	75372973	+	0	81	146.96	Intron							
CONGO_chr1_078184803_97_m2	chr1	78184803	78184899	-	2	97	93.76	NCExon			1	1	TU241	SpliceToPCG	ENSG00000162613
CONGO_chr1_078185728_139_p1	chr1	78185728	78185866	+	1	139	0.79	AntisenseCDS				1	TU724	SpliceToPCG	ENSG00000162614
CONGO_chr1_078186670_69_m0	chr1	78186670	78186738	-	0	69	20.56	UTR			1	1	TU241	SpliceToPCG	ENSG00000162613
CONGO_chr1_079177922_150_m2	chr1	79177922	79178071	-	2	150	330.75	Intron							
CONGO_chr1_081544764_37_m0	chr1	81544764	81544800	-	0	37	14.61	AntisenseUTR				1			
CONGO_chr1_082253611_99_p2	chr1	82253611	82253709	+	2	99	39.08	Intergenic							
CONGO_chr1_083118344_109_p1	chr1	83118344	83118452	+	1	109	29.28	Intergenic							
CONGO_chr1_083930328_87_m1	chr1	83930328	83930414	-	1	87	16.79	NCIntron							
CONGO_chr1_084582949_87_p0	chr1	84582949	84583035	+	0	87	460.24	NCExon		DnaJ	1				
CONGO_chr1_084583379_108_p0	chr1	84583379	84583486	+	0	108	175.77	NCExon			1				
CONGO_chr1_085439723_136_m0	chr1	85439723	85439858	-	0	136	149.9	UTR							
CONGO_chr1_087394497_55_p2	chr1	87394497	87394551	+	2	55	2.15	Intron							
CONGO_chr1_087441126_59_m0	chr1	87441126	87441184	-	0	59	151.05	Intergenic							
CONGO_chr1_087539179_69_m0	chr1	87539179	87539247	-	0	69	4.32	Intergenic							
CONGO_chr1_087567328_188_p1	chr1	87567328	87567515	+	1	188	42.06	UTR			1	1	TU725	SpliceToPCG	ENSG00000143013

CONGO_chr1_087579530_134_p0	chr1	87579530	87579663	+	0	134	37.94	Intron								
CONGO_chr1_087788988_144_m0	chr1	87788988	87789131	-	0	144	129.08	Intergenic								
CONGO_chr1_087801703_122_m2	chr1	87801703	87801824	-	2	122	55.16	Intergenic								
CONGO_chr1_087802440_82_m0	chr1	87802440	87802521	-	0	82	19.51	Intergenic								
CONGO_chr1_087838306_70_m2	chr1	87838306	87838375	-	2	70	60.95	Intergenic								
CONGO_chr1_087923434_107_m2	chr1	87923434	87923540	-	2	107	88.68	Intergenic								
CONGO_chr1_088215489_53_m2	chr1	88215489	88215541	-	2	53	31.17	Intergenic								
CONGO_chr1_088419980_94_m1	chr1	88419980	88420073	-	1	94	30.16	Intergenic								
CONGO_chr1_088614813_135_p0	chr1	88614813	88614947	+	0	135	152.38	Intergenic								
CONGO_chr1_088649056_93_p0	chr1	88649056	88649148	+	0	93	35.61	Intergenic								
CONGO_chr1_088700446_146_m2	chr1	88700446	88700591	-	2	146	19.56	Intergenic								
CONGO_chr1_089817738_64_p1	chr1	89817738	89817801	+	1	64	161	UTR			1	1	TU726	SpliceToPCG	ENSG00000197147	
CONGO_chr1_090436957_99_m0	chr1	90436957	90437055	-	0	99	11.48	Intergenic								
CONGO_chr1_090775825_103_m1	chr1	90775825	90775927	-	1	103	3.86	Intergenic								
CONGO_chr1_090861442_181_m1	chr1	90861442	90861622	-	1	181	27.52	Intergenic								
CONGO_chr1_090968267_137_m1	chr1	90968267	90968403	-	1	137	137.15	Intergenic								
CONGO_chr1_090968727_114_m1	chr1	90968727	90968840	-	1	114	17.94	Intergenic								
CONGO_chr1_091073375_155_m2	chr1	91073375	91073529	-	2	155	51.43	NCIntron								
CONGO_chr1_091079133_119_m2	chr1	91079133	91079251	-	2	119	120.55	NCIntron								
CONGO_chr1_091182200_68_p2	chr1	91182200	91182267	+	2	68	145.41	AntisenseIntron								
CONGO_chr1_096446173_90_p0	chr1	96446173	96446262	+	0	90	65.28	Intergenic								
CONGO_chr1_096446679_65_p1	chr1	96446679	96446743	+	1	65	25.78	Intergenic								
CONGO_chr1_097383491_156_m2	chr1	97383491	97383646	-	2	156	88.78	Intron								
CONGO_chr1_098690327_112_m1	chr1	98690327	98690438	-	1	112	61.06	Intergenic								
CONGO_chr1_099135399_101_m2	chr1	99135399	99135499	-	2	101	22.24	Intron								
CONGO_chr1_099353735_78_m0	chr1	99353735	99353812	-	0	78	355.68	AntisenseNCIntron								
CONGO_chr1_100563904_94_p0	chr1	100563904	100563997	+	0	94	3.76	Intergenic								
CONGO_chr1_103895862_38_m2	chr1	103895862	103895899	-	2	38	99.12	AntisenseCDS				1				
CONGO_chr1_107484550_149_p2	chr1	107484550	107484698	+	2	149	130.28	Intron					TU727	SpliceToPCG	ENSG00000162631	
CONGO_chr1_107826966_37_p1	chr1	107826966	107827002	+	1	37	31.86	UTR					TU728	SpliceToPCG	ENSG00000162631	
CONGO_chr1_107920537_84_m2	chr1	107920537	107920620	-	2	84	233.37	Intron			1					
CONGO_chr1_108839623_107_m2	chr1	108839623	108839729	-	2	107	349.6	Intergenic								
CONGO_chr1_109037651_137_p1	chr1	109037651	109037787	+	1	137	37.2	UTR			1	1	TU729	SpliceToPCG	ENSG00000134186	
CONGO_chr1_109042068_104_m0	chr1	109042068	109042171	-	0	104	5.4	AntisenseNCExon					TU730	NovelMultiExon		
CONGO_chr1_110572678_167_p2	chr1	110572678	110572844	+	2	167	359.51	Intron								
CONGO_chr1_110690878_84_p2	chr1	110690878	110690961	+	2	84	43.81	Intergenic			1		TU731	SpliceToPCG	ENSG00000162775	
CONGO_chr1_111511251_85_p1	chr1	111511251	111511335	+	1	85	11.48	Intron					TU732	SpliceToPCG	ENSG00000134255	
CONGO_chr1_111626716_166_p1	chr1	111626716	111626881	+	1	166	215	NCExon		Glyco_hydro_18	1	1	TU73	SpliceToPCG	ENSG00000134216	
CONGO_chr1_111627126_125_p0	chr1	111627126	111627250	+	0	125	207	NCExon		Glyco_hydro_18	1	1	TU73	SpliceToPCG	ENSG00000134216	
CONGO_chr1_111627483_72_p0	chr1	111627483	111627554	+	0	72	63.46	NCExon			1	1	TU73	SpliceToPCG	ENSG00000134216	
CONGO_chr1_111628276_119_p2	chr1	111628276	111628394	+	2	119	118.93	NCExon		Glyco_hydro_18	1	1	TU73	SpliceToPCG	ENSG00000134216	
CONGO_chr1_112871598_108_m2	chr1	112871598	112871705	-	2	108	185.83	Intron					TU733	SpliceToPCG	ENSG00000007341	
CONGO_chr1_115102046_74_p0	chr1	115102046	115102119	+	0	74	0.15	AntisenseUTR				1				
CONGO_chr1_116267080_100_m1	chr1	116267080	116267179	-	1	100	23.88	AntisenseNCIntron					TU734	NovelMultiExon		
CONGO_chr1_119817802_148_p1	chr1	119817802	119817949	+	1	148	6.58	Intergenic								
CONGO_chr1_142491437_138_p2	chr1	142491437	142491574	+	2	138	258.71	NCExon	1			1				
CONGO_chr1_142496534_236_p1	chr1	142496534	142496769	+	1	236	665.78	NCExon	1		1	1				
CONGO_chr1_143176221_236_m1	chr1	143176221	143176456	-	1	236	134.49	NCExon	1		1	1				
CONGO_chr1_143181392_143_m1	chr1	143181392	143181534	-	1	143	74.22	NCExon	1		1	1				
CONGO_chr1_145214476_64_m1	chr1	145214476	145214539	-	1	64	38.32	AntisenseCDS			1	1				
CONGO_chr1_145384087_86_p2	chr1	145384087	145384172	+	2	86	12.1	AntisenseIntron								
CONGO_chr1_147959571_132_m2	chr1	147959571	147959702	-	2	132	95.2	NCExon	1			1				
CONGO_chr1_147967540_236_m1	chr1	147967540	147967775	-	1	236	323.56	Intergenic	1			1	TU736	NovelMultiExon		
CONGO_chr1_148566640_96_p1	chr1	148566640	148566735	+	1	96	171.21	UTR			1	1	TU738	SpliceToPCG	ENSG00000117360	
CONGO_chr1_148603661_136_m2	chr1	148603661	148603796	-	2	136	92.42	AntisenseUTR					TU739	UnsplicedMergeWithPCG	ENSG00000163125	
CONGO_chr1_149151415_101_p0	chr1	149151415	149151515	+	0	101	310.3	Intergenic								
CONGO_chr1_149586261_103_p1	chr1	149586261	149586363	+	1	103	26.86	AntisenseUTR				1	TU740	SpliceToNCG	ENSG00000237976	
CONGO_chr1_150044330_67_m0	chr1	150044330	150044396	-	0	67	72.12	UTR			1		TU741	SpliceToPCG	ENSG00000143365	
CONGO_chr1_151099798_253_p0	chr1	151099798	151100050	+	0	253	69.96	Intergenic								
CONGO_chr1_151187637_341_p0	chr1	151187637	151187977	+	0	341	1353.29	AntisenseNCIntron								
CONGO_chr1_151873368_76_p0	chr1	151873368	151873443	+	0	76	8.84	UTR			1	1	TU243	SpliceToPCG	ENSG00000143553	
CONGO_chr1_151878468_84_p0	chr1	151878468	151878551	+	0	84	26.39	Intron				1	TU243	SpliceToPCG	ENSG00000160679	
CONGO_chr1_152502395_93_m2	chr1	152502395	152502487	-	2	93	36.21	AntisenseUTR				1		UnsplicedMergeWithPCG	ENSG00000143569	
CONGO_chr1_153559817_411_p2	chr1	153559817	153560227	+	2	411	584.13	UTR			1	1	TU743	SpliceToPCG	ENSG00000160753	
CONGO_chr1_154205949_68_m2	chr1	154205949	154206016	-	2	68	19.93	NCExon				1	TU746	SpliceToPCG	ENSG00000116584	
CONGO_chr1_154225649_63_m0	chr1	154225649	154225711	-	0	63	5.89	UTR			1	1	TU747	SpliceToPCG	ENSG00000116584	
CONGO_chr1_154243353_102_m0	chr1	154243353	154243454	-	0	102	87.67	NCExon				1				
CONGO_chr1_154964848_216_m0	chr1	154964848	154965063	-	0	216	466.63	UTR			1	1	TU748	SpliceToPCG	ENSG00000143319	
CONGO_chr1_155718144_101_p1	chr1	155718144	155718244	+	1	101	167.51	Intergenic								
CONGO_chr1_156728417_136_p2	chr1	156728417	156728552	+	2	136	543.23	AntisenseNCIntron			1					
CONGO_chr1_157378013_86_m2	chr1	157378013	157378098	-	2	86	105.57	Intron								
CONGO_chr1_157587699_722_p1	chr1	157587699	157588420	+	1	722	2112.86	Intron		7tm_1						
CONGO_chr1_157603043_289_p0	chr1	157603043	157603331	+	0	289	1130.59	Intron		7tm_1						
CONGO_chr1_157603376_128_p2	chr1	157603376	157603503	+	2	128	376.58	Intron								
CONGO_chr1_157669228_325_p1	chr1	157669228	157669552	+	1	325	1160.32	Intron		7tm_1						
CONGO_chr1_159398157_141_p0	chr1	159398157	159398297	+	0	141	257.74	UTR			1					
CONGO_chr1_159542098_117_m0	chr1	159542098	159542214	-	0	117	548.42	UTR			1	1	TU750	SpliceToPCG	ENSG00000158887	
CONGO_chr1_161708976_173_p2	chr1	161708976	161709148	+	2	173	16.54	Intergenic								
CONGO_chr1_162904523_103_m2	chr1	162904523	162904625	-	2	103	11.47	AntisenseIntron								
CONGO_chr1_163779899_112_m1	chr1	163779899	163780010	-	1	112	102.58	AntisenseUTR								
CONGO_chr1_168157467_54_p2	chr1	168157467	168157520	+	2	54	60.01	AntisenseCDS			1	1				
CONGO_chr1_169444717_153_p0	chr1	169444717	169444869	+	0	153	950.07	UTR		FMO-like	1		TU754	SpliceToPCG	ENSG00000094963	
CONGO_chr1_169825131_237_p0	chr1	169825131	169825367	+	0	237	743.86	NCExon			1	1	TU755	SpliceToPCG	ENSG00000117523	
CONGO_chr1_169862308_53_m0	chr1	169862308	169862360	-	0	53	18.45	AntisenseNCExon								
CONGO_chr1_176469454_185_p1	chr1	176469454	176469638	+	1	185	62.57	Intron								
CONGO_chr1_176607961_125_p2	chr1	176607961	176608085	+	2	125	192.03	Intron					TU756	SpliceToPCG	ENSG00000075391	
CONGO_chr1_176714470_104_m2	chr1	176714470	176714573	-	2	104	18.99	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000075391	
CONGO_chr1_176715293_81_m0	chr1	176715293	176715373	-	0	81	206.32	Intergenic					TU246	NovelMultiExon		
CONGO_chr1_176718070_86_m2	chr1	176718070	176718155	-	2	86	143.4	Intergenic					TU246	NovelMultiExon		
CONGO_chr1_176725830_366_m2	chr1	176725830	176726195	-	2	366	790	Intergenic		Lectin_C						
CONGO_chr1_179648906_434_p0	chr1	179648906	179649339	+	0	434	726.55	UTR			1		TU757	UnsplicedMergeWithPCG	ENSG00000198216	
CONGO_chr1_180015202_97_p1	chr1	180015202	180015298	+	1	97	288.25	Intron								
CONGO_chr1_180626255_323_m0	chr1	180626255	180626577	-	0	323	522.52	UTR			1	1	TU758	SpliceToPCG	ENSG00000135821	
CONGO_chr1_194765148_71_m0	chr1	194765148	194765218	-	0	71	65.33	Intron								
CONGO_chr1_196531195_117_m0	chr1	196531195	196531311	-	0	117	170	AntisenseIntron								
CONGO_chr1_196534606_85_m1	chr1	196534606	196534690	-	1	85	17.41	AntisenseIntron								
CONGO_chr1_198311990_126_m0	chr1	198311990	198312115	-	0	126	12.03	AntisenseIntron						NovelUnspliced		
CONGO_chr1_198648363_42_m0	chr1	198648363	198648404	-	0	42	112.95	AntisenseNCIntron				1				
CONGO_chr1_199156206_65_p2	chr1	199156206	199156270	+	2	65	263.56	Intergenic					TU759	NovelMultiExon		
CONGO_chr1_199209276_50_p0	chr1	199209276	199209325	+	0	50	19.83	AntisenseCDS				1	TU763	NovelMultiExon		
CONGO_chr1_200680797_183_p1	chr1	200680797	200680979	+	1	183	216.31	NCExon				1	TU764	SpliceToPCG	ENSG00000077157	
CONGO_chr1_200775891_102_p0	chr1	200775891	200775992	+	0	102	701.7	Intron	1				TU765	SpliceToPCG	ENSG00000077157	
CONGO_chr1_202033324_1091_p1	chr1	202033324	202034414	+	1	1091	5840.75	Intron		zf-BED			TU50	SpliceToPCG	ENSG00000058673	
CONGO_chr1_202034433_347_p2	chr1	202034433	202034779	+	2	347	1679.91	UTR			1		TU50	SpliceToPCG	ENSG00000058673	
CONGO_chr1_202034859_744_p2	chr1	202034859	202035602	+	2	744	3304.39	UTR			1		TU50	SpliceToPCG	ENSG00000058673	
CONGO_chr1_202035604_185_p1	chr1	202035604	202035788	+	1	185	301.53	UTR			1		TU50	SpliceToPCG	ENSG00000058673	
CONGO_chr1_202035848_296_p0	chr1	202035848	202036143	+	0	296	674.64	UTR		hATC	1		TU50	SpliceToPCG	ENSG00000058673	
CONGO_chr1_202478865_150_m0	chr1	202478865	202479014	-	0	150	707.56	NCExon			1		TU51	SpliceToPCG	ENSG00000143850	
CONGO_chr1_202510480_81_m1	chr1	202510480	202510560	-	1	81	625.01	UTR			1	1	TU51	SpliceToPCG	ENSG00000143850	
CONGO_chr1_202512747_32_m0	chr1	202512747	202512778	-	0	32	218	AntisenseNCExon				1				
CONGO_chr1_202603550_58_m2	chr1	202603550	202603607	-	2	58	332.06	NCExon					TU51	SpliceToPCG	ENSG00000143850	
CONGO_chr1_202607281_77_m1	chr1	202607281	202607357	-	1	77	427.9	NCExon					TU51	SpliceToPCG	ENSG00000143850	
CONGO_chr1_202613334_83_m0	chr1	202613334	202613416	-	0	83	392.32	NCExon					TU51	SpliceToPCG	ENSG00000143850	
CONGO_chr1_203492956_162_p0	chr1	203492956	203493117	+	0	162	535.87	UTR			1	1				
CONGO_chr1_203592284_37_m0	chr1	203592284	203592320	-	0	37	9.72	UTR			1	1	TU767	SpliceToPCG	ENSG00000162873	
CONGO_chr1_203676676_102_m0	chr1	203676676	203676777	-	0	102	447.69	Intron				1				
CONGO_chr1_204758344_157_p0	chr1	204758344	204758500	+	0	157	808.43	Intron								
CONGO_chr1_208255972_138_p0	chr1	208255972	208256109	+	0	138	821.65	Intron					TU769	SpliceToPCG	ENSG00000143469	
CONGO_chr1_211522324_45_m2	chr1	211522324	211522368	-	2	45	1.68	Intergenic								
CONGO_chr1_212023340_57_m0	chr1	212023340	212023396	-	0	57	6.17	AntisenseNCIntron								
CONGO_chr1_212236393_360_m0	chr1	212236393	212236752	-	0	360	1072.16	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000117707	
CONGO_chr1_212242630_115_m1	chr1	212242630	212242744	-	1	115	47.27	AntisenseIntron								
CONGO_chr1_212270682_113_m2	chr1	212270682	212270794	-	2	113	12.99	AntisenseIntron			1					
CONGO_chr1_212291203_94_p2	chr1	212291203	212291296	+	2	94	21.18	Intergenic								
CONGO_chr1_214203813_96_m0	chr1	214203813	214203908	-	0	96	44.86	Intron								

CONGO_chr1_214488580_52_m1	chr1	214488580	214488631	-	1	52	8.01	Intron								
CONGO_chr1_214790282_43_m1	chr1	214790282	214790324	-	1	43	0.94	Intron								
CONGO_chr1_214870658_153_m0	chr1	214870658	214870810	-	0	153	159.76	Intron								
CONGO_chr1_214963463_100_p0	chr1	214963463	214963562	+	0	100	164.93	AntisenseIntron								
CONGO_chr1_215083666_104_p1	chr1	215083666	215083769	+	1	104	10.24	AntisenseIntron								
CONGO_chr1_215329828_112_p0	chr1	215329828	215329939	+	0	112	34.99	AntisenseIntron								
CONGO_chr1_215793976_111_p0	chr1	215793976	215794086	+	0	111	70.94	AntisenseIntron								
CONGO_chr1_216115315_103_m0	chr1	216115315	216115417	-	0	103	67.75	Intergenic								
CONGO_chr1_216274648_98_p2	chr1	216274648	216274745	+	2	98	40.04	Intergenic								
CONGO_chr1_216304578_190_p1	chr1	216304578	216304767	+	1	190	96.6	Intergenic								
CONGO_chr1_216348056_117_m2	chr1	216348056	216348172	-	2	117	71.09	Intergenic								
CONGO_chr1_218198533_451_m0	chr1	218198533	218198983	-	0	451	5253.62	NCExon		Cation_efflux	1	1	TU770	SpliceToPCG	ENSG00000196660	
CONGO_chr1_219116661_183_p0	chr1	219116661	219116843	+	0	183	16.85	Intergenic								
CONGO_chr1_219949092_125_m2	chr1	219949092	219949216	-	2	125	104.5	Intron								
CONGO_chr1_223778924_63_m1	chr1	223778924	223778986	-	1	63	60.81	Intron					TU771	SpliceToPCG	ENSG00000154380	
CONGO_chr1_225473570_175_m1	chr1	225473570	225473744	-	1	175	53.54	NCExon				1	TU772	SpliceToPCG	ENSG00000143776	
CONGO_chr1_228627967_331_m0	chr1	228627967	228628297	-	0	331	319.72	UTR				1	TU774	SpliceToPCG	ENSG00000177614	
CONGO_chr1_232926664_145_p1	chr1	232926664	232926808	+	1	145	23.55	Intergenic								
CONGO_chr1_236170742_167_m2	chr1	236170742	236170908	-	2	167	457.6	Intergenic		COX1						
CONGO_chr1_236171714_128_m2	chr1	236171714	236171841	-	2	128	56.01	Intergenic								
CONGO_chr1_236171915_158_m2	chr1	236171915	236172072	-	2	158	187.28	Intergenic								
CONGO_chr1_236172762_242_m2	chr1	236172762	236173003	-	2	242	878.45	Intergenic		NADHdh						
CONGO_chr1_236173059_155_m2	chr1	236173059	236173213	-	2	155	494.51	Intergenic		NADHdh						
CONGO_chr1_236173215_257_m2	chr1	236173215	236173471	-	2	257	884.93	Intergenic		NADHdh						
CONGO_chr1_238437497_344_m1	chr1	238437497	238437840	-	1	344	2077.62	AntisenseCDS	1							
CONGO_chr1_239908112_30_p0	chr1	239908112	239908141	+	0	30	240.09	NCExon					TU775	SpliceToPCG	ENSG00000162843	
CONGO_chr1_241484972_111_m0	chr1	241484972	241485082	-	0	111	5.55	UTR			1	1	TU776	SpliceToPCG	ENSG00000143702	
CONGO_chr1_241626851_108_m1	chr1	241626851	241626958	-	1	108	0.78	AntisenseIntron								
CONGO_chr1_241646288_159_p0	chr1	241646288	241646446	+	0	159	10.72	Intron								
CONGO_chr1_241943526_114_p0	chr1	241943526	241943639	+	0	114	113.01	AntisenseIntron								
CONGO_chr1_242079086_147_p0	chr1	242079086	242079232	+	0	147	7.4	AntisenseIntron								
CONGO_chr1_242190162_79_m1	chr1	242190162	242190240	-	1	79	25.57	AntisenseNCIntron								
CONGO_chr1_242337177_198_m0	chr1	242337177	242337374	-	0	198	7.09	AntisenseNCExon								
CONGO_chr1_242960489_252_m0	chr1	242960489	242960740	-	0	252	189.81	Intergenic								
CONGO_chr1_245001834_83_m0	chr1	245001834	245001916	-	0	83	252.8	Intergenic					TU777	SpliceToPCG	ENSG00000223519	
CONGO_chr1_245015918_108_m0	chr1	245015918	245016025	-	0	108	774.58	UTR				1				
CONGO_chr1_245016939_80_m2	chr1	245016939	245017018	-	2	80	125.28	UTR				1				
CONGO_chr1_245019512_145_m0	chr1	245019512	245019656	-	0	145	1680	UTR								
CONGO_chr1_245020596_124_m1	chr1	245020596	245020719	-	1	124	805.46	AntisenseNCExon				1		UnsplicedMergeWithNCG	ENSG00000227953	
CONGO_chr1_245022202_55_m2	chr1	245022202	245022256	-	2	55	367.39	AntisenseNCExon				1				
CONGO_chr1_245081917_47_m0	chr1	245081917	245081963	-	0	47	109.03	NCExon			1	1	TU778	SpliceToPCG	ENSG00000153207	
CONGO_chr1_246926955_177_p2	chr1	246926955	246927131	+	2	177	442.52	NCExon				1	TU779	SpliceToNCG	ENSG00000229703	
CONGO_chr10_005794363_146_p2	chr10	5794363	5794508	+	2	146	215.64	NCExon				1	TU42	SpliceToPCG	ENSG00000108021	
CONGO_chr10_005794792_96_p0	chr10	5794792	5794887	+	0	96	392.2	UTR			1	1	TU42	SpliceToPCG	ENSG00000108021	
CONGO_chr10_005796104_73_p0	chr10	5796104	5796176	+	0	73	81.66	NCExon				1	TU42	SpliceToPCG	ENSG00000108021	
CONGO_chr10_005799628_92_p2	chr10	5799628	5799719	+	2	92	118.42	UTR			1	1	TU42	SpliceToPCG	ENSG00000108021	
CONGO_chr10_005802229_138_p0	chr10	5802229	5802366	+	0	138	288.56	Intron					TU42	SpliceToPCG	ENSG00000108021	
CONGO_chr10_008745383_86_m2	chr10	8745383	8745468	-	2	86	24.93	Intergenic								
CONGO_chr10_010880734_53_p0	chr10	10880734	10880786	+	0	53	91.17	Intergenic				1	TU338	NovelMultiExon		
CONGO_chr10_011001933_36_p1	chr10	11001933	11001968	+	1	36	171.53	Intergenic				1	TU155	SpliceToPCG	ENSG00000048740	
CONGO_chr10_011412425_129_p0	chr10	11412425	11412553	+	0	129	0.64	UTR			1	1	TU155	SpliceToPCG	ENSG00000048740	
CONGO_chr10_011655611_73_m0	chr10	11655611	11655683	-	0	73	220.67	Intron				1				
CONGO_chr10_013728943_99_m1	chr10	13728943	13729041	-	1	99	414.73	UTR			1	1	TU339	SpliceToPCG	ENSG00000151474	
CONGO_chr10_014106359_66_m0	chr10	14106359	14106424	-	0	66	497.44	Intron				1	TU340	SpliceToPCG	ENSG00000151474	
CONGO_chr10_018620612_81_p0	chr10	18620612	18620692	+	0	81	68.68	Intron				1				
CONGO_chr10_019465509_208_p0	chr10	19465509	19465716	+	0	208	721.89	Intergenic		Ldl_recept_a						
CONGO_chr10_019484010_98_p2	chr10	19484010	19484107	+	2	98	280.71	Intergenic					TU341	NovelMultiExon		
CONGO_chr10_019494572_174_p0	chr10	19494572	19494745	+	0	174	372.46	Intergenic								
CONGO_chr10_019504143_121_p0	chr10	19504143	19504263	+	0	121	195.9	Intergenic								
CONGO_chr10_022665520_92_p1	chr10	22665520	22665611	+	1	92	17.61	AntisenseIntron								
CONGO_chr10_023526713_158_m2	chr10	23526713	23526870	-	2	158	48.23	Intergenic								
CONGO_chr10_023579390_66_m1	chr10	23579390	23579455	-	1	66	325.36	UTR					TU342	SpliceToPCG	ENSG00000179133	
CONGO_chr10_024371220_211_p0	chr10	24371220	24371430	+	0	211	783.74	Intron				1	TU343	SpliceToPCG	ENSG00000120549	
CONGO_chr10_024696066_69_p0	chr10	24696066	24696134	+	0	69	208.79	Intron				1	TU344	SpliceToPCG	ENSG00000120549	
CONGO_chr10_024919272_143_m2	chr10	24919272	24919414	-	2	143	351.32	NCExon			1		TU345	SpliceToPCG	ENSG00000107863	
CONGO_chr10_025035447_84_m0	chr10	25035447	25035530	-	0	84	381.53	Intron								
CONGO_chr10_026993205_123_m0	chr10	26993205	26993327	-	0	123	41.13	NCExon				1				
CONGO_chr10_026996494_88_m2	chr10	26996494	26996581	-	2	88	12.11	NCIntron								
CONGO_chr10_028438666_42_m0	chr10	28438666	28438707	-	0	42	30.05	Intron								
CONGO_chr10_029836672_78_m0	chr10	29836672	29836749	-	0	78	81.34	Intron	1				TU347	SpliceToPCG	ENSG00000197321	
CONGO_chr10_029892136_92_m1	chr10	29892136	29892227	-	1	92	4.47	UTR	1		1	1	TU348	SpliceToPCG	ENSG00000197321	
CONGO_chr10_029899903_61_m0	chr10	29899903	29899963	-	0	61	19.44	Intron	1							
CONGO_chr10_035007795_106_m1	chr10	35007795	35007900	-	1	106	280.04	Intron								
CONGO_chr10_046319057_120_p2	chr10	46319057	46319176	+	2	120	203.16	UTR	1				TU159	SpliceToPCG	ENSG00000165874	
CONGO_chr10_046324340_108_p2	chr10	46324340	46324447	+	2	108	363.2	UTR	1				TU159	SpliceToPCG	ENSG00000165874	
CONGO_chr10_046338175_173_p2	chr10	46338175	46338347	+	2	173	391.42	UTR	1		1	1	TU351	SpliceToPCG	ENSG00000165874	
CONGO_chr10_047128721_32_p0	chr10	47128721	47128752	+	0	32	18.42	NCExon	1		1	1	TU27	SpliceToNCG	ENSG00000198250	
CONGO_chr10_047133300_72_p1	chr10	47133300	47133371	+	1	72	267.46	NCExon	1		1	1	TU27	SpliceToNCG	ENSG00000198250	
CONGO_chr10_047135071_72_p1	chr10	47135071	47135142	+	1	72	434.3	NCExon	1		1	1	TU27	SpliceToNCG	ENSG00000198250	
CONGO_chr10_047138494_77_p2	chr10	47138494	47138570	+	2	77	41.78	NCExon	1		1	1	TU27	SpliceToNCG	ENSG00000198250	
CONGO_chr10_047138648_69_p0	chr10	47138648	47138716	+	0	69	180.85	NCExon	1		1		TU27	SpliceToNCG	ENSG00000198250	
CONGO_chr10_047139073_81_p0	chr10	47139073	47139153	+	0	81	12.87	NCExon	1		1		TU27	SpliceToNCG	ENSG00000198250	
CONGO_chr10_049034142_73_m2	chr10	49034142	49034214	-	2	73	0.09	NCExon	1							
CONGO_chr10_049530285_52_m0	chr10	49530285	49530336	-	0	52	70.22	UTR			1	1	TU353	SpliceToPCG	ENSG00000128805	
CONGO_chr10_050083977_82_m1	chr10	50083977	50084058	-	1	82	25.8	Intergenic								
CONGO_chr10_050378154_198_m0	chr10	50378154	50378351	-	0	198	70.65	Intron								
CONGO_chr10_050402300_122_p1	chr10	50402300	50402421	+	1	122	337.68	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000225830	
CONGO_chr10_053558222_69_p0	chr10	53558222	53558290	+	0	69	34.7	Intron					TU354	SpliceToPCG	ENSG00000185532	
CONGO_chr10_053723681_53_m1	chr10	53723681	53723733	-	1	53	159.02	AntisenseUTR			1	1	TU355	SpliceToNCG	ENSG00000236671	
CONGO_chr10_059765607_68_p1	chr10	59765607	59765674	+	1	68	83.14	Intron								
CONGO_chr10_061166824_141_m0	chr10	61166824	61166964	-	0	141	544.62	NCExon			1	1	TU356	SpliceToNCG	ENSG00000227877	
CONGO_chr10_061473838_60_m0	chr10	61473838	61473897	-	0	60	223.47	NCExon			1		TU88	SpliceToPCG	ENSG00000151150	
CONGO_chr10_061474029_84_m0	chr10	61474029	61474112	-	0	84	332.44	NCExon			1		TU88	SpliceToPCG	ENSG00000151150	
CONGO_chr10_061481239_73_m1	chr10	61481239	61481311	-	1	73	275.65	NCExon					TU88	SpliceToPCG	ENSG00000151150	
CONGO_chr10_061498485_65_p2	chr10	61498485	61498549	+	2	65	219.87	AntisenseCDS								
CONGO_chr10_061499433_137_p2	chr10	61499433	61499569	+	2	137	76.53	AntisenseCDS								
CONGO_chr10_061499635_97_p1	chr10	61499635	61499731	+	1	97	37.6	AntisenseCDS								
CONGO_chr10_061511955_75_p0	chr10	61511955	61512029	+	0	75	21.07	AntisenseIntron								
CONGO_chr10_061537952_110_m0	chr10	61537952	61538061	-	0	110	52.28	NCExon				1				
CONGO_chr10_062002229_68_m2	chr10	62002229	62002296	-	2	68	406.98	UTR			1	1	TU357	SpliceToPCG	ENSG00000151150	
CONGO_chr10_063404496_103_m1	chr10	63404496	63404598	-	1	103	28.33	AntisenseIntron								
CONGO_chr10_064202197_105_m1	chr10	64202197	64202301	-	1	105	19.51	Intergenic								
CONGO_chr10_069496848_90_m0	chr10	69496848	69496937	-	0	90	17.9	Intron				1	TU358	SpliceToPCG	ENSG00000148634	
CONGO_chr10_070030353_162_m0	chr10	70030353	70030514	-	0	162	36.51	AntisenseIntron						NovelUnspliced		
CONGO_chr10_070257810_223_p0	chr10	70257810	70258032	+	0	223	601.72	Intron								
CONGO_chr10_071383710_78_p0	chr10	71383710	71383787	+	0	78	174.63	Intron				1	TU359	SpliceToPCG	ENSG00000197467	
CONGO_chr10_076113662_55_m0	chr10	76113662	76113716	-	0	55	87.41	AntisenseIntron								
CONGO_chr10_076528795_221_m0	chr10	76528795	76529015	-	0	221	4.02	NCExon					TU361	SpliceToPCG	ENSG00000079393	
CONGO_chr10_076725321_157_p1	chr10	76725321	76725477	+	1	157	178.97	Intergenic				1				
CONGO_chr10_076880655_108_m0	chr10	76880655	76880762	-	0	108	35.34	AntisenseIntron								
CONGO_chr10_077027498_118_p0	chr10	77027498	77027615	+	0	118	32.51	Intron								
CONGO_chr10_077138138_97_p0	chr10	77138138	77138234	+	0	97	105.1	Intron								
CONGO_chr10_077140124_101_p2	chr10	77140124	77140224	+	2	101	64.28	Intron								
CONGO_chr10_077151473_88_p2	chr10	77151473	77151560	+	2	88	15.59	Intron								
CONGO_chr10_077166030_135_m0	chr10	77166030	77166164	-	0	135	15.47	AntisenseIntron								
CONGO_chr10_077212649_81_m2	chr10	77212649	77212729	-	2	81	37.93	AntisenseUTR								
CONGO_chr10_077234102_111_m1	chr10	77234102	77234212	-	1	111	30.77	AntisenseIntron								
CONGO_chr10_077334367_159_p0	chr10	77334367	77334525	+	0	159	10.81	Intron								
CONGO_chr10_077354179_85_m1	chr10	77354179	77354263	-	1	85	23.66	AntisenseIntron								
CONGO_chr10_077358250_81_m0	chr10	77358250	77358330	-	0	81	20.57	AntisenseIntron								
CONGO_chr10_077367680_113_p2	chr10	77367680	77367792	+	2	113	55.56	Intron								
CONGO_chr10_078198866_32_p0	chr10	78198866	78198897	+	0	32	42.19	Intergenic								
CONGO_chr10_078357431_105_p2	chr10	78357431	78357535	+	2	105	53.11	AntisenseIntron								
CONGO_chr10_078538050_92_m0	chr10	78538050	78538141	-	0	92	310.17	Intron								
CONGO_chr10_078570058_211_m0	chr10	78570058	78570268	-	0	211	950.94	Intron				1				

CONGO_chr10_078674719_51_p0	chr10	78674719	78674769	+	0	51	59.55	AntisenseIntron								
CONGO_chr10_086201970_72_p0	chr10	86201970	86202041	+	0	72	94.87	NCExon					1	TU362	SpliceToPCG	ENSG00000107771
CONGO_chr10_093799716_82_m1	chr10	93799716	93799797	-	1	82	287.56	UTR			1			TU162	SpliceToPCG	ENSG00000107864
CONGO_chr10_093992957_56_m2	chr10	93992957	93993012	-	2	56	15.68	UTR			1		1	TU162	SpliceToPCG	ENSG00000107864
CONGO_chr10_096032541_39_p0	chr10	96032541	96032579	+	0	39	42.44	Intron						TU364	SpliceToPCG	ENSG00000138193
CONGO_chr10_096284087_198_m0	chr10	96284087	96284284	-	0	198	171.51	AntisenseUTR							UnsplicedMergeWithPCG	ENSG00000108239
CONGO_chr10_097699643_210_p0	chr10	97699643	97699852	+	0	210	558.33	NCExon						TU89	SpliceToPCG	ENSG00000173088
CONGO_chr10_097705141_98_p0	chr10	97705141	97705238	+	0	98	117.45	NCExon						TU89	SpliceToPCG	ENSG00000173088
CONGO_chr10_097711576_141_p1	chr10	97711576	97711716	+	1	141	844.79	NCExon						TU89	SpliceToPCG	ENSG00000173088
CONGO_chr10_097718471_178_p1	chr10	97718471	97718648	+	1	178	425.62	NCExon					1	TU28	SpliceToPCG	ENSG00000188649
CONGO_chr10_097721813_151_p0	chr10	97721813	97721963	+	0	151	267.87	Intron					1	TU28	SpliceToPCG	ENSG00000188649
CONGO_chr10_097723756_148_p2	chr10	97723756	97723903	+	2	148	781.23	UTR			1		1	TU28	SpliceToPCG	ENSG00000173088
CONGO_chr10_097731722_139_p1	chr10	97731722	97731860	+	1	139	471.44	UTR			1		1	TU28	SpliceToPCG	ENSG00000173088
CONGO_chr10_097733353_204_p0	chr10	97733353	97733556	+	0	204	672.06	UTR			1		1	TU28	SpliceToPCG	ENSG00000173088
CONGO_chr10_097745890_110_p0	chr10	97745890	97745999	+	0	110	395.44	UTR			1			TU28	SpliceToPCG	ENSG00000173088
CONGO_chr10_098581913_234_p2	chr10	98581913	98582146	+	2	234	12.14	UTR			1		1	TU58	SpliceToPCG	ENSG00000196233
CONGO_chr10_098657012_66_p2	chr10	98657012	98657077	+	2	66	152.74	UTR			1		1	TU58	SpliceToPCG	ENSG00000196233
CONGO_chr10_098657415_80_p2	chr10	98657415	98657494	+	2	80	177.35	UTR			1		1	TU58	SpliceToPCG	ENSG00000196233
CONGO_chr10_098693860_133_p0	chr10	98693860	98693992	+	0	133	19.11	UTR			1		1	TU58	SpliceToPCG	ENSG00000196233
CONGO_chr10_098704657_179_m1	chr10	98704657	98704835	-	1	179	181.15	AntisenseCDS			1				UnsplicedMergeWithPCG	ENSG00000196233
CONGO_chr10_099339569_79_m1	chr10	99339569	99339647	-	1	79	86.11	AntisenseCDS							UnsplicedMergeWithPCG	ENSG00000203942
CONGO_chr10_099615472_66_p0	chr10	99615472	99615537	+	0	66	57.33	UTR			1		1	TU365	SpliceToPCG	ENSG00000155265
CONGO_chr10_101118365_63_p2	chr10	101118365	101118427	+	2	63	130.29	NCExon			1		1	TU366	SpliceToPCG	ENSG00000119946
CONGO_chr10_101855508_43_m2	chr10	101855508	101855550	-	2	43	84.96	Intergenic								
CONGO_chr10_101872235_81_m0	chr10	101872235	101872315	-	0	81	66.99	Intergenic								
CONGO_chr10_101885098_163_m0	chr10	101885098	101885260	-	0	163	670.77	Intergenic		p450						
CONGO_chr10_102321174_118_p2	chr10	102321174	102321291	+	2	118	44.42	Intergenic								
CONGO_chr10_102532407_83_p2	chr10	102532407	102532489	+	2	83	15.05	Intron								
CONGO_chr10_102542701_81_p2	chr10	102542701	102542781	+	2	81	54.07	Intron								
CONGO_chr10_102614382_100_p1	chr10	102614382	102614481	+	1	100	3.39	Intergenic								
CONGO_chr10_102631983_121_p0	chr10	102631983	102632103	+	0	121	110.22	Intergenic								
CONGO_chr10_102977314_102_p1	chr10	102977314	102977415	+	1	102	638.25	AntisenseCDS								
CONGO_chr10_103233986_95_p0	chr10	103233986	103234080	+	0	95	42.98	Intron								
CONGO_chr10_103235685_138_m0	chr10	103235685	103235822	-	0	138	4.29	AntisenseIntron								
CONGO_chr10_103235926_128_m0	chr10	103235926	103236053	-	0	128	106.57	AntisenseIntron								
CONGO_chr10_103458025_149_m2	chr10	103458025	103458173	-	2	149	73.18	NCExon					1			
CONGO_chr10_103543050_96_m0	chr10	103543050	103543145	-	0	96	49.46	NCExon			1			TU90	SpliceToPCG	ENSG00000198408
CONGO_chr10_103543433_59_m2	chr10	103543433	103543491	-	2	59	15.93	NCExon			1		1	TU90	SpliceToPCG	ENSG00000198408
CONGO_chr10_103545156_163_m1	chr10	103545156	103545318	-	1	163	30.92	NCExon			1		1	TU90	SpliceToPCG	ENSG00000198408
CONGO_chr10_103584014_103_m0	chr10	103584014	103584116	-	0	103	357.53	Intron								
CONGO_chr10_104104117_75_p0	chr10	104104117	104104191	+	0	75	64.65	Intron			1			TU367	SpliceToPCG	ENSG00000107862
CONGO_chr10_105763380_72_p0	chr10	105763380	105763451	+	0	72	357.26	Intron						TU368	SpliceToPCG	ENSG00000065613
CONGO_chr10_106391025_318_m1	chr10	106391025	106391342	-	1	318	43.84	AntisenseCDS								
CONGO_chr10_111755704_126_m0	chr10	111755704	111755829	-	0	126	510.33	UTR			1		1	TU369	SpliceToPCG	ENSG00000203876
CONGO_chr10_112650108_167_m2	chr10	112650108	112650274	-	2	167	191.92	NCExon			1		1	TU163	SpliceToNCG	ENSG00000214413
CONGO_chr10_112651286_46_m0	chr10	112651286	112651331	-	0	46	249.04	NCExon			1		1	TU163	SpliceToNCG	ENSG00000214413
CONGO_chr10_114240547_102_m1	chr10	114240547	114240648	-	1	102	31.86	AntisenseIntron								
CONGO_chr10_114285444_96_m1	chr10	114285444	114285539	-	1	96	69.77	AntisenseIntron								
CONGO_chr10_114286661_131_p1	chr10	114286661	114286791	+	1	131	12.81	Intron								
CONGO_chr10_114288221_78_m0	chr10	114288221	114288298	-	0	78	34.91	AntisenseNCExon								
CONGO_chr10_114727251_130_m0	chr10	114727251	114727380	-	0	130	301.06	AntisenseIntron								
CONGO_chr10_114879614_123_p0	chr10	114879614	114879736	+	0	123	244.71	Intron			1		1	TU370	SpliceToPCG	ENSG00000148737
CONGO_chr10_115349082_78_m0	chr10	115349082	115349159	-	0	78	5.69	Intron								
CONGO_chr10_118584436_88_m0	chr10	118584436	118584523	-	0	88	671.58	UTR			1		1	TU371	SpliceToPCG	ENSG00000165868
CONGO_chr10_119471519_103_p0	chr10	119471519	119471621	+	0	103	4.12	Intergenic								
CONGO_chr10_119653240_124_m1	chr10	119653240	119653363	-	1	124	29.87	Intergenic								
CONGO_chr10_121330071_86_p1	chr10	121330071	121330156	+	1	86	38.41	AntisenseUTR								
CONGO_chr10_121342954_62_m2	chr10	121342954	121343015	-	2	62	60.61	UTR			1		1	TU372	SpliceToPCG	ENSG00000151923
CONGO_chr10_121568315_321_p0	chr10	121568315	121568635	+	0	321	2175.1	UTR		VMA21	1		1	TU373	SpliceToPCG	ENSG00000198825
CONGO_chr10_123229555_63_m0	chr10	123229555	123229617	-	0	63	356.17	NCExon			1			TU374	SpliceToPCG	ENSG00000066468
CONGO_chr10_123698917_76_p1	chr10	123698917	123698992	+	1	76	30.13	NCIntron						TU375	SpliceToNCG	ENSG00000226864
CONGO_chr10_123782599_60_p0	chr10	123782599	123782658	+	0	60	84.58	NCExon						TU376	SpliceToPCG	ENSG00000138162
CONGO_chr10_124318101_58_p2	chr10	124318101	124318158	+	2	58	77.51	Intron								
CONGO_chr10_124318195_218_p1	chr10	124318195	124318412	+	1	218	776.75	Intron		SRCR						
CONGO_chr10_124374040_232_p2	chr10	124374040	124374271	+	2	232	645.93	Intron		SRCR						
CONGO_chr10_124842493_90_m0	chr10	124842493	124842582	-	0	90	134.66	Intergenic								
CONGO_chr10_125179155_127_m1	chr10	125179155	125179281	-	1	127	45.28	AntisenseNCIntron								
CONGO_chr10_125200608_49_m2	chr10	125200608	125200656	-	2	49	42.67	AntisenseNCIntron								
CONGO_chr10_130722548_67_p1	chr10	130722548	130722614	+	1	67	30.05	Intergenic								
CONGO_chr10_130924538_50_p1	chr10	130924538	130924587	+	1	50	44.66	Intergenic								
CONGO_chr10_131011293_75_m2	chr10	131011293	131011367	-	2	75	185.42	Intergenic								
CONGO_chr10_131259848_62_m2	chr10	131259848	131259909	-	2	62	19.27	AntisenseIntron								
CONGO_chr10_131532853_153_m0	chr10	131532853	131533005	-	0	153	57.31	Intron								
CONGO_chr10_131539307_213_p2	chr10	131539307	131539519	+	2	213	60.49	AntisenseIntron								
CONGO_chr10_131567890_166_m1	chr10	131567890	131568055	-	1	166	115.75	Intron								
CONGO_chr10_131581325_110_p1	chr10	131581325	131581434	+	1	110	163.24	AntisenseIntron								
CONGO_chr10_131640757_255_p2	chr10	131640757	131641011	+	2	255	119.1	AntisenseIntron								
CONGO_chr10_131767820_63_m0	chr10	131767820	131767882	-	0	63	263.57	NCExon			1		1	TU92	SpliceToNCG	ENSG00000237489
CONGO_chr10_131768102_54_m0	chr10	131768102	131768155	-	0	54	86.23	NCExon			1		1	TU92	SpliceToNCG	ENSG00000237489
CONGO_chr10_131798958_69_m0	chr10	131798958	131799026	-	0	69	7.69	NCExon			1		1	TU92	SpliceToNCG	ENSG00000237489
CONGO_chr11_000188457_120_m1	chr11	188457	188576	-	1	120	263.46	AntisenseCDS								
CONGO_chr11_001169458_274_p1	chr11	1169458	1169731	+	1	274	143.67	NCExon			1			TU4	SpliceToPCG	ENSG00000117983
CONGO_chr11_001169852_475_p0	chr11	1169852	1170326	+	0	475	2793.25	NCExon			1			TU4	SpliceToPCG	ENSG00000117983
CONGO_chr11_001170584_200_p2	chr11	1170584	1170783	+	2	200	716.72	NCExon			1			TU4	SpliceToPCG	ENSG00000117983
CONGO_chr11_001171287_175_p0	chr11	1171287	1171461	+	0	175	680.64	NCExon			1			TU4	SpliceToPCG	ENSG00000117983
CONGO_chr11_001171912_251_p2	chr11	1171912	1172162	+	2	251	1938.67	NCExon		VWD	1			TU4	SpliceToPCG	ENSG00000117983
CONGO_chr11_001172289_184_p0	chr11	1172289	1172472	+	0	184	1509.65	NCExon		VWD	1		1	TU4	SpliceToPCG	ENSG00000117983
CONGO_chr11_001172814_88_p2	chr11	1172814	1172901	+	2	88	363.28	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001173678_174_p1	chr11	1173678	1173851	+	1	174	1044.79	NCExon		C8	1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001174419_104_p1	chr11	1174419	1174522	+	1	104	369.01	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001175270_172_p0	chr11	1175270	1175441	+	0	172	765.75	NCExon			1			TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001176070_38_p2	chr11	1176070	1176107	+	2	38	34.74	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001176676_123_p0	chr11	1176676	1176798	+	0	123	375.37	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001176889_99_p0	chr11	1176889	1176987	+	0	99	341.71	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001177173_120_p0	chr11	1177173	1177292	+	0	120	430.66	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001177497_70_p0	chr11	1177497	1177566	+	0	70	65.08	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001177657_115_p2	chr11	1177657	1177771	+	2	115	324.43	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_001178240_153_p1	chr11	1178240	1178392	+	1	153	613.4	NCExon			1		1	TU4	SpliceToNCG	ENSG00000215182
CONGO_chr11_004219862_528_m0	chr11	4219862	4220389	-	0	528	424.8	Intergenic	1	Ssu72						
CONGO_chr11_004696433_238_p0	chr11	4696433	4696670	+	0	238	804.57	NCIntron		7tm_1						
CONGO_chr11_004696724_102_p0	chr11	4696724	4696825	+	0	102	382.88	NCIntron		7tm_1						
CONGO_chr11_004696863_438_p2	chr11	4696863	4697300	+	2	438	1804.3	NCIntron		7tm_1						
CONGO_chr11_004729929_343_m1	chr11	4729929	4730271	-	1	343	2016.87	AntisenseNCIntron								
CONGO_chr11_004730325_459_m0	chr11	4730325	4730783	-	0	459	2112.46	AntisenseNCIntron		7tm_1						
CONGO_chr11_005409193_216_m0	chr11	5409193	5409408	-	0	216	863.21	Intron								
CONGO_chr11_005492401_146_m2	chr11	5492401	5492546	-	2	146	296.66	UTR		UBA	1				UnsplicedMergeWithPCG	ENSG00000175518
CONGO_chr11_005492709_111_m2	chr11	5492709	5492819	-	2	111	118.97	UTR			1				UnsplicedMergeWithPCG	ENSG00000175518
CONGO_chr11_005505107_390_m0	chr11	5505107	5505496	-	0	390	1922.36	Intron								
CONGO_chr11_005505568_72_m0	chr11	5505568	5505639	-	0	72	238.49	Intron								
CONGO_chr11_005530130_273_m0	chr11	5530130	5530402	-	0	273	1036.46	Intron		7tm_1						
CONGO_chr11_005914674_605_p2	chr11	5914674	5915278	+	2	605	778.04	AntisenseUTR	1				1			
CONGO_chr11_006023656_134_m0	chr11	6023656	6023789	-	0	134	604.25	Intergenic								
CONGO_chr11_006023824_421_m0	chr11	6023824	6024244	-	0	421	1451.44	Intergenic								
CONGO_chr11_006459064_63_p2	chr11	6459064	6459126	+	2	63	3.64	AntisenseUTR					1	TU378	SpliceToPCG	ENSG00000132286
CONGO_chr11_006698226_155_m2	chr11	6698226	6698380	-	2	155	43.08	UTR			1			TU167	NovelMultiExon	
CONGO_chr11_006698556_97_m1	chr11	6698556	6698652	-	1	97	85.3	UTR			1			TU167	NovelMultiExon	
CONGO_chr11_007555398_48_p0	chr11	7555398	7555445	+	0	48	94.55	NCExon			1		1	TU379	SpliceToPCG	ENSG00000166387
CONGO_chr11_007594919_127_p0	chr11	7594919	7595045	+	0	127	237.58	Intron						TU380	SpliceToPCG	ENSG00000166387
CONGO_chr11_007826823_313_p0	chr11	7826823	7827135	+	0	313	1779.26	Intergenic		7tm_1						
CONGO_chr11_008040196_159_p1	chr11	8040196	8040354	+	1	159	28.85	NCExon			1		1			
CONGO_chr11_008293661_82_m2	chr11	8293661	8293742	-	2	82	46.39	Intergenic								
CONGO_chr11_008708775_174_p0	chr11	8708775	8708948	+	0	174	663.16	AntisenseCDS								
CONGO_chr11_008982472_46_m0	chr11	8982472	8982517	-	0	46	146.11	Intergenic						TU381	SpliceToPCG	ENSG00000175348
CONGO_chr11_009389164_45_p0	chr11	9389164	9389208	+	0	45	11.09	Intron								
CONGO_chr11_009806249_96_m2	chr11	9806249	9806344	-	2	96	1.69	Intron					1	TU382	SpliceToPCG	ENSG00000133812

CONGO_chr11_010835985_43_m1	chr11	10835985	10836027	-	1	43	254.17	UTR			1	1	TU383	SpliceToPCG	ENSG00000236287
CONGO_chr11_012254109_181_p2	chr11	12254109	12254289	+	2	181	583.34	Intergenic				1	TU168	SpliceToPCG	ENSG00000133808
CONGO_chr11_012265213_75_p2	chr11	12265213	12265287	+	2	75	38	UTR			1	1	TU168	SpliceToPCG	ENSG00000133808
CONGO_chr11_012411969_70_p1	chr11	12411969	12412038	+	1	70	114.19	Intron							
CONGO_chr11_012781038_48_m1	chr11	12781038	12781085	-	1	48	69.45	AntisenseIntron							
CONGO_chr11_012822900_57_m0	chr11	12822900	12822956	-	0	57	121.34	AntisenseIntron							
CONGO_chr11_012824013_51_m2	chr11	12824013	12824063	-	2	51	24.93	AntisenseIntron							
CONGO_chr11_012842809_63_p0	chr11	12842809	12842871	+	0	63	63.49	NCExon			1	1	TU384	SpliceToPCG	ENSG00000187079
CONGO_chr11_015544251_87_p1	chr11	15544251	15544337	+	1	87	39.68	Intergenic							
CONGO_chr11_015735320_180_p0	chr11	15735320	15735499	+	0	180	53.22	Intergenic							
CONGO_chr11_015754607_99_m0	chr11	15754607	15754705	-	0	99	36.77	Intergenic							
CONGO_chr11_015779977_158_p2	chr11	15779977	15780134	+	2	158	67.54	Intergenic							
CONGO_chr11_015996710_161_p2	chr11	15996710	15996870	+	2	161	5.95	AntisenseIntron							
CONGO_chr11_016268916_187_p1	chr11	16268916	16269102	+	1	187	120.56	AntisenseIntron							
CONGO_chr11_016381110_75_p0	chr11	16381110	16381184	+	0	75	161.06	AntisenseIntron							
CONGO_chr11_016381309_92_m0	chr11	16381309	16381400	-	0	92	25.67	Intron							
CONGO_chr11_016590204_180_m1	chr11	16590204	16590383	-	1	180	111.21	NCExon			1	1	TU385	NovelMultiExon	
CONGO_chr11_016759075_101_m2	chr11	16759075	16759175	-	2	101	62.91	Intergenic				1	TU29	SpliceToPCG	ENSG00000166689
CONGO_chr11_016760877_143_m1	chr11	16760877	16761019	-	1	143	1106.97	Intergenic			1	1	TU29	SpliceToPCG	ENSG00000166689
CONGO_chr11_016761823_134_m0	chr11	16761823	16761956	-	0	134	1719.04	Intergenic			1	1	TU29	SpliceToPCG	ENSG00000166689
CONGO_chr11_016764352_159_m0	chr11	16764352	16764510	-	0	159	1254.44	Intergenic			1	1	TU29	SpliceToPCG	ENSG00000166689
CONGO_chr11_016785267_81_m0	chr11	16785267	16785347	-	0	81	44.43	Intron					TU29	SpliceToPCG	ENSG00000166689
CONGO_chr11_016793298_120_m0	chr11	16793298	16793417	-	0	120	518.51	Intron					TU29	SpliceToPCG	ENSG00000166689
CONGO_chr11_016891516_92_m0	chr11	16891516	16891607	-	0	92	195.68	Intron							
CONGO_chr11_017511842_69_m0	chr11	17511842	17511910	-	0	69	263.31	Intron				1			
CONGO_chr11_017631845_155_p2	chr11	17631845	17631999	+	2	155	109.36	Intergenic							
CONGO_chr11_018578052_69_p0	chr11	18578052	18578120	+	0	69	353.81	NCExon			1	1	TU93	NovelMultiExon	
CONGO_chr11_018581247_72_p0	chr11	18581247	18581318	+	0	72	321.13	NCExon			1	1	TU93	NovelMultiExon	
CONGO_chr11_018581895_51_p0	chr11	18581895	18581945	+	0	51	236.77	NCExon			1	1	TU93	NovelMultiExon	
CONGO_chr11_018934394_157_m1	chr11	18934394	18934550	-	1	157	55.95	Intron							
CONGO_chr11_018949918_322_m1	chr11	18949918	18950239	-	1	322	137.82	Intron							
CONGO_chr11_019386072_88_m1	chr11	19386072	19386159	-	1	88	2.26	AntisenseIntron							
CONGO_chr11_019755585_55_p1	chr11	19755585	19755639	+	1	55	54.31	Intron			1				
CONGO_chr11_019791906_72_p0	chr11	19791906	19791977	+	0	72	319.24	Intron							
CONGO_chr11_019820780_46_p2	chr11	19820780	19820825	+	2	46	189.79	Intron							
CONGO_chr11_021262717_298_p0	chr11	21262717	21263014	+	0	298	684.52	Intron						UnsplicedMergeWithPCG	ENSG00000225477
CONGO_chr11_022836044_105_m0	chr11	22836044	22836148	-	0	105	59	AntisenseNCIntron					TU94	NovelMultiExon	
CONGO_chr11_022837574_45_m0	chr11	22837574	22837618	-	0	45	107.16	AntisenseNCIntron					TU94	NovelMultiExon	
CONGO_chr11_022838499_45_m0	chr11	22838499	22838543	-	0	45	13.27	AntisenseNCIntron					TU94	NovelMultiExon	
CONGO_chr11_026287768_75_p2	chr11	26287768	26287842	+	2	75	19.66	Intergenic			1	1	TU386	SpliceToPCG	ENSG00000134343
CONGO_chr11_030613725_107_m2	chr11	30613725	30613831	-	2	107	64.78	Intergenic							
CONGO_chr11_031219573_167_m2	chr11	31219573	31219739	-	2	167	288	UTR			1	1	TU387	SpliceToPCG	ENSG00000188682
CONGO_chr11_031741599_110_m2	chr11	31741599	31741708	-	2	110	104.76	AntisenseCDS				1			
CONGO_chr11_031742609_100_m0	chr11	31742609	31742708	-	0	100	11.18	AntisenseIntron							
CONGO_chr11_031789449_145_p0	chr11	31789449	31789593	+	0	145	41.65	AntisenseUTR							
CONGO_chr11_032871248_209_p0	chr11	32871248	32871456	+	0	209	52.7	UTR			1	1	TU169	SpliceToPCG	ENSG00000060749
CONGO_chr11_032905279_113_p1	chr11	32905279	32905391	+	1	113	318.99	UTR			1	1	TU169	SpliceToPCG	ENSG00000060749
CONGO_chr11_033519924_345_p2	chr11	33519924	33520268	+	2	345	652.58	Intergenic				1	TU389	SpliceToPCG	ENSG00000110427
CONGO_chr11_034502900_98_m0	chr11	34502900	34502997	-	0	98	262.69	Intergenic							
CONGO_chr11_041438249_112_m1	chr11	41438249	41438360	-	1	112	39.5	Intergenic							
CONGO_chr11_045204122_706_p2	chr11	45204122	45204827	+	2	706	6658.04	Intergenic					TU170	SpliceToPCG	ENSG00000019485
CONGO_chr11_045204838_1449_p0	chr11	45204838	45206286	+	0	1449	12574.43	Intergenic			1		TU170	SpliceToPCG	ENSG00000019485
CONGO_chr11_045973722_75_m2	chr11	45973722	45973796	-	2	75	81.71	Intron							
CONGO_chr11_047446898_122_m2	chr11	47446898	47447019	-	2	122	41.55	UTR			1	1	TU390	SpliceToPCG	ENSG00000149187
CONGO_chr11_047710245_103_m0	chr11	47710245	47710347	-	0	103	109.77	NCExon			1	1	TU391	SpliceToPCG	ENSG00000109920
CONGO_chr11_048205557_110_p0	chr11	48205557	48205666	+	0	110	43.94	Intergenic							
CONGO_chr11_048205699_261_p1	chr11	48205699	48205959	+	1	261	635.93	Intergenic							
CONGO_chr11_048206020_164_p0	chr11	48206020	48206183	+	0	164	347.72	Intergenic							
CONGO_chr11_048442210_830_m1	chr11	48442210	48443039	-	1	830	2572.51	Intergenic	1	7tm_1					
CONGO_chr11_048474733_657_p0	chr11	48474733	48475389	+	0	657	853.86	Intergenic	1	7tm_1					
CONGO_chr11_048491062_284_p0	chr11	48491062	48491345	+	0	284	264.44	Intergenic	1	7tm_1					
CONGO_chr11_048504301_181_p0	chr11	48504301	48504481	+	0	181	286.41	Intergenic	1						
CONGO_chr11_048504642_388_p2	chr11	48504642	48505029	+	2	388	220.97	Intergenic	1						
CONGO_chr11_048567960_529_p0	chr11	48567960	48568488	+	0	529	22.64	Intergenic		7tm_1					
CONGO_chr11_048588191_671_p0	chr11	48588191	48588861	+	0	671	764.51	Intergenic	1	7tm_1					
CONGO_chr11_048588863_156_p1	chr11	48588863	48589018	+	1	156	1.97	Intergenic	1						
CONGO_chr11_051340186_242_p0	chr11	51340186	51340427	+	0	242	183.15	Intergenic	1	7tm_1					
CONGO_chr11_054842663_189_p0	chr11	54842663	54842851	+	0	189	81.86	Intergenic		7tm_1					
CONGO_chr11_054842897_282_p0	chr11	54842897	54843178	+	0	282	117.46	Intergenic		7tm_1					
CONGO_chr11_054843193_197_p2	chr11	54843193	54843389	+	2	197	45.59	Intergenic							
CONGO_chr11_054849833_182_p2	chr11	54849833	54850014	+	2	182	112.66	Intergenic		7tm_1					
CONGO_chr11_054850154_87_p0	chr11	54850154	54850240	+	0	87	53.39	Intergenic		7tm_1					
CONGO_chr11_054850415_215_p2	chr11	54850415	54850629	+	2	215	326.67	Intergenic							
CONGO_chr11_054912730_262_p1	chr11	54912730	54912991	+	1	262	30.84	Intergenic		7tm_1					
CONGO_chr11_054956033_365_p0	chr11	54956033	54956397	+	0	365	478.42	Intergenic							
CONGO_chr11_054968487_191_p0	chr11	54968487	54968677	+	0	191	91.53	Intergenic							
CONGO_chr11_054969017_198_p0	chr11	54969017	54969214	+	0	198	21.33	Intergenic							
CONGO_chr11_054969255_128_p1	chr11	54969255	54969382	+	1	128	37.8	Intergenic							
CONGO_chr11_055002193_302_p0	chr11	55002193	55002494	+	0	302	231.24	Intergenic							
CONGO_chr11_055033856_436_p0	chr11	55033856	55034291	+	0	436	1945.34	Intergenic		7tm_1	1				
CONGO_chr11_055034316_348_p0	chr11	55034316	55034663	+	0	348	2522	Intergenic		7tm_1	1				
CONGO_chr11_055197876_85_p0	chr11	55197876	55197960	+	0	85	287.55	Intergenic							
CONGO_chr11_055197970_60_p0	chr11	55197970	55198029	+	0	60	41.75	Intergenic							
CONGO_chr11_055198347_50_p2	chr11	55198347	55198396	+	2	50	254.24	Intergenic							
CONGO_chr11_055198438_119_p2	chr11	55198438	55198556	+	2	119	659.89	Intergenic							
CONGO_chr11_055238850_426_p1	chr11	55238850	55239275	+	1	426	2008.34	Intergenic		7tm_1					
CONGO_chr11_055239510_233_p0	chr11	55239510	55239742	+	0	233	1312.4	Intergenic							
CONGO_chr11_055311078_293_p2	chr11	55311078	55311370	+	2	293	1387.04	Intergenic		7tm_1					
CONGO_chr11_055311423_508_p2	chr11	55311423	55311930	+	2	508	1754.4	Intergenic							
CONGO_chr11_055472357_326_m0	chr11	55472357	55472682	-	0	326	738.13	Intergenic							
CONGO_chr11_055472764_140_m2	chr11	55472764	55472903	-	2	140	408.09	Intergenic							
CONGO_chr11_055595854_209_p2	chr11	55595854	55596062	+	2	209	856.96	Intergenic							
CONGO_chr11_055689596_381_p0	chr11	55689596	55689976	+	0	381	406.18	Intergenic							
CONGO_chr11_055734985_648_m0	chr11	55734985	55735632	-	0	648	4096.71	Intergenic		7tm_1					
CONGO_chr11_055735697_143_m0	chr11	55735697	55735839	-	0	143	686.35	Intergenic							
CONGO_chr11_055820784_192_m2	chr11	55820784	55820975	-	2	192	503.5	Intergenic							
CONGO_chr11_055821120_370_m0	chr11	55821120	55821489	-	0	370	684.26	Intergenic		7tm_1					
CONGO_chr11_055859194_150_p0	chr11	55859194	55859343	+	0	150	67.43	Intergenic							
CONGO_chr11_055859387_178_p1	chr11	55859387	55859564	+	1	178	438.91	Intergenic							
CONGO_chr11_055859607_108_p2	chr11	55859607	55859714	+	2	108	93.62	Intergenic							
CONGO_chr11_055859930_135_p2	chr11	55859930	55860064	+	2	135	537.06	Intergenic							
CONGO_chr11_055905809_400_p2	chr11	55905809	55906208	+	2	400	1003.83	Intron		7tm_1					
CONGO_chr11_055906307_187_p2	chr11	55906307	55906493	+	2	187	338.29	Intron							
CONGO_chr11_055906532_65_p2	chr11	55906532	55906596	+	2	65	22.55	Intron							
CONGO_chr11_055917814_291_p0	chr11	55917814	55918104	+	0	291	988.12	Intron		7tm_1					
CONGO_chr11_055918128_327_p0	chr11	55918128	55918454	+	0	327	1611.68	Intron		7tm_1					
CONGO_chr11_055918473_191_p2	chr11	55918473	55918663	+	2	191	1099.67	Intron		7tm_1					
CONGO_chr11_056004303_176_m0	chr11	56004303	56004478	-	0	176	928.86	AntisenseIntron							
CONGO_chr11_056143846_347_m2	chr11	56143846	56144192	-	2	347	965.25	AntisenseIntron		7tm_1					
CONGO_chr11_056144482_241_m0	chr11	56144482	56144722	-	0	241	523.22	AntisenseIntron							
CONGO_chr11_056157390_162_m1	chr11	56157390	56157551	-	1	162	509.33	AntisenseIntron							
CONGO_chr11_056157591_465_m0	chr11	56157591	56158055	-	0	465	1197.9	AntisenseIntron		7tm_1					
CONGO_chr11_056275068_256_m2	chr11	56275068	56275323	-	2	256	1208.23	Intergenic							
CONGO_chr11_056275421_219_m0	chr11	56275421	56275639	-	0	219	869.82	Intergenic							
CONGO_chr11_056275689_253_m2	chr11	56275689	56275941	-	2	253	1097.1	Intergenic							
CONGO_chr11_056314281_413_m0	chr11	56314281	56314693	-	0	413	2444.64	Intergenic							
CONGO_chr11_056314701_293_m0	chr11	56314701	56314993	-	0	293	1412.45	Intergenic							
CONGO_chr11_056414905_81_p0	chr11	56414905	56414985	+	0	81	435.08	Intergenic		Cyt-b5					
CONGO_chr11_056424091_111_p0	chr11	56424091	56424201	+	0	111	474.74	Intergenic							
CONGO_chr11_056426924_206_p0	chr11	56426924	56427129	+	0	206	277.25	Intergenic							
CONGO_chr11_056428460_102_p0	chr11	56428460	56428561	+	0	102	309.62	Intergenic							
CONGO_chr11_056435138_126_p0	chr11	56435138	56435263	+	0	126	438.23	Intergenic							
CONGO_chr11_056440290_61_p0	chr11	56440290	56440350	+	0	61	391.31	Intergenic							
CONGO_chr11_056446358_77_p2	chr11	56446358	56446434	+	2	77	126.62	Intergenic							
CONGO_chr11_056447743_97_p1	chr11	56447743	56447839	+	1	97	313.73	Intergenic							

CONGO_chr11_056450389_126_p1	chr11	56450389	56450514	+	1	126	920.44	Intergenic		FA_desaturase						
CONGO_chr11_056451891_52_p1	chr11	56451891	56451942	+	1	52	24.05	Intergenic								
CONGO_chr11_056542208_729_p0	chr11	56542208	56542936	+	0	729	1484.82	Intergenic		7tm_1						
CONGO_chr11_056542947_126_p0	chr11	56542947	56543072	+	0	126	247.05	Intergenic								
CONGO_chr11_056561825_73_p0	chr11	56561825	56561897	+	0	73	172.01	Intergenic								
CONGO_chr11_056561913_310_p1	chr11	56561913	56562222	+	1	310	996.55	Intergenic		7tm_1	1					
CONGO_chr11_056562293_220_p1	chr11	56562293	56562512	+	1	220	537.48	Intergenic			1					
CONGO_chr11_056835288_126_m0	chr11	56835288	56835413	-	0	126	521.51	Intron				1	TU392	SpliceToPCG	ENSG00000149115	
CONGO_chr11_057191774_48_p1	chr11	57191774	57191821	+	1	48	17.84	Intergenic				1				
CONGO_chr11_057315523_47_m2	chr11	57315523	57315569	-	2	47	239.18	AntisenseCDS				1				
CONGO_chr11_057390368_341_m2	chr11	57390368	57390708	-	2	341	893.68	Intergenic		7tm_1						
CONGO_chr11_057390781_526_m0	chr11	57390781	57391306	-	0	526	1506.96	Intergenic		7tm_1						
CONGO_chr11_057469675_174_m0	chr11	57469675	57469848	-	0	174	260.13	Intergenic								
CONGO_chr11_057632794_213_m2	chr11	57632794	57633006	-	2	213	252.7	AntisenseIntron								
CONGO_chr11_057815915_469_m0	chr11	57815915	57816383	-	0	469	2607.1	Intergenic		7tm_1						
CONGO_chr11_057816404_389_m2	chr11	57816404	57816792	-	2	389	1652.22	Intergenic		7tm_1						
CONGO_chr11_057841733_299_m2	chr11	57841733	57842031	-	2	299	977.25	Intergenic		7tm_1						
CONGO_chr11_057842219_211_m0	chr11	57842219	57842429	-	0	211	498.39	Intergenic								
CONGO_chr11_057867868_224_m2	chr11	57867868	57868091	-	2	224	298.5	Intergenic								
CONGO_chr11_057872971_473_m2	chr11	57872971	57873443	-	2	473	643.15	Intergenic		7tm_1						
CONGO_chr11_057873727_136_m0	chr11	57873727	57873862	-	0	136	174.73	Intergenic								
CONGO_chr11_057912110_371_m2	chr11	57912110	57912480	-	2	371	182.31	Intergenic		7tm_1						
CONGO_chr11_058273108_338_m1	chr11	58273108	58273445	-	1	338	930.28	Intergenic		Gly_acyl_tr_C/N						
CONGO_chr11_058281554_172_m2	chr11	58281554	58281725	-	2	172	42.85	Intergenic		Gly_acyl_tr_N						
CONGO_chr11_058282574_127_m0	chr11	58282574	58282700	-	0	127	232.19	Intergenic		Gly_acyl_tr_N			TU393	SpliceToPCG	ENSG00000149124	
CONGO_chr11_058677310_72_m0	chr11	58677310	58677381	-	0	72	45.24	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000166801	
CONGO_chr11_058811953_1212_m2	chr11	58811953	58813164	-	2	1212	2414.15	Intergenic		MACPF			TU394	SpliceToPCG	ENSG00000197629	
CONGO_chr11_058813308_151_m2	chr11	58813308	58813458	-	2	151	144.85	Intergenic						NovelUnspliced		
CONGO_chr11_058856890_112_m2	chr11	58856890	58857001	-	2	112	24.11	Intergenic								
CONGO_chr11_058857005_237_m0	chr11	58857005	58857241	-	0	237	418.54	Intergenic								
CONGO_chr11_058857801_182_m1	chr11	58857801	58857982	-	1	182	259.94	Intergenic								
CONGO_chr11_058915429_93_m0	chr11	58915429	58915521	-	0	93	119.99	Intergenic								
CONGO_chr11_059055850_360_p2	chr11	59055850	59056209	+	2	360	1352.38	Intergenic		7tm_1						
CONGO_chr11_059056383_204_p0	chr11	59056383	59056586	+	0	204	909.77	Intergenic								
CONGO_chr11_059056639_78_p1	chr11	59056639	59056716	+	1	78	89.98	Intergenic								
CONGO_chr11_059181154_75_p0	chr11	59181154	59181228	+	0	75	89.11	AntisenseIntron								
CONGO_chr11_059252770_211_p0	chr11	59252770	59252980	+	0	211	615.81	Intergenic		7tm_1						
CONGO_chr11_059272863_483_p0	chr11	59272863	59273345	+	0	483	2005.15	Intergenic								
CONGO_chr11_059273479_148_p1	chr11	59273479	59273626	+	1	148	455.11	Intergenic								
CONGO_chr11_059327276_69_p0	chr11	59327276	59327344	+	0	69	78.24	Intergenic			1		TU395	SpliceToPCG	ENSG00000166900	
CONGO_chr11_061070674_255_p2	chr11	61070674	61070928	+	2	255	6.28	AntisenseIntron								
CONGO_chr11_061071225_265_m2	chr11	61071225	61071489	-	2	265	203.35	NCExon			1	1	TU396	SpliceToPCG	ENSG00000011347	
CONGO_chr11_061429441_144_m0	chr11	61429441	61429584	-	0	144	277.46	Intron					TU397	SpliceToPCG	ENSG00000167994	
CONGO_chr11_062189179_39_m0	chr11	62189179	62189217	-	0	39	319.33	Intron			1	1	TU398	SpliceToPCG	ENSG00000162191	
CONGO_chr11_062323586_76_p2	chr11	62323586	62323661	+	2	76	76.99	AntisenseUTR					TU399	SpliceToPCG	ENSG00000162227	
CONGO_chr11_062356424_156_m0	chr11	62356424	62356579	-	0	156	445.17	Intergenic					TU400	SpliceToPCG	ENSG00000133316	
CONGO_chr11_063765673_453_p0	chr11	63765673	63766125	+	0	453	1930.58	Intron				1	TU401	SpliceToPCG	ENSG00000110011	
CONGO_chr11_064592075_92_m0	chr11	64592075	64592166	-	0	92	170.89	Intergenic				1	TU402	SpliceToPCG	ENSG00000146670	
CONGO_chr11_064612906_174_m0	chr11	64612906	64613079	-	0	174	885.05	Intergenic			1	1	TU403	SpliceToPCG	ENSG00000187066	
CONGO_chr11_064646138_94_m1	chr11	64646138	64646231	-	1	94	12.14	UTR			1	1	TU404	SpliceToPCG	ENSG00000149806	
CONGO_chr11_065304489_150_m0	chr11	65304489	65304638	-	0	150	890.7	Intergenic				1	TU172	SpliceToPCG	ENSG00000172922	
CONGO_chr11_066242490_178_m0	chr11	66242490	66242667	-	0	178	1100.45	Intron			1		TU405	SpliceToPCG	ENSG00000173898	
CONGO_chr11_067048259_165_m0	chr11	67048259	67048423	-	0	165	722.31	Intergenic								
CONGO_chr11_067064559_79_p1	chr11	67064559	67064637	+	1	79	63.24	Intergenic								
CONGO_chr11_067140058_202_m0	chr11	67140058	67140259	-	0	202	220.75	Intergenic				1				
CONGO_chr11_067191520_110_m2	chr11	67191520	67191629	-	2	110	374.09	UTR			1	1				
CONGO_chr11_068681891_156_p0	chr11	68681891	68682046	+	0	156	742.34	NCIntron								
CONGO_chr11_069634880_66_p2	chr11	69634880	69634945	+	2	66	264.71	Intron				1	TU406	SpliceToPCG	ENSG00000131620	
CONGO_chr11_069856776_75_p0	chr11	69856776	69856850	+	0	75	134.69	NCExon			1		TU407	SpliceToPCG	ENSG00000131626	
CONGO_chr11_070241414_67_m0	chr11	70241414	70241480	-	0	67	90.32	Intron								
CONGO_chr11_070419150_171_m2	chr11	70419150	70419320	-	2	171	381.17	Intron								
CONGO_chr11_071304843_104_m2	chr11	71304843	71304946	-	2	104	736.66	NCExon				1	TU408	SpliceToPCG	ENSG00000196763	
CONGO_chr11_071477034_41_p1	chr11	71477034	71477074	+	1	41	4.31	UTR			1	1	TU409	SpliceToPCG	ENSG00000184154	
CONGO_chr11_071565474_174_p0	chr11	71565474	71565647	+	0	174	174.81	Intergenic		Folate_rec		1				
CONGO_chr11_071566173_136_p0	chr11	71566173	71566308	+	0	136	152.48	Intergenic		Folate_rec						
CONGO_chr11_071728848_71_m2	chr11	71728848	71728918	-	2	71	35.36	Intron								
CONGO_chr11_072731845_126_p0	chr11	72731845	72731970	+	0	126	391.58	Intron				1	TU410	SpliceToPCG	ENSG00000110237	
CONGO_chr11_072795310_128_m2	chr11	72795310	72795437	-	2	128	100.5	UTR			1	1	TU411	SpliceToPCG	ENSG00000054965	
CONGO_chr11_074333711_68_m0	chr11	74333711	74333778	-	0	68	247	UTR			1	1	TU173	SpliceToPCG	ENSG00000166435	
CONGO_chr11_074337621_70_m1	chr11	74337621	74337690	-	1	70	267.32	UTR			1	1	TU173	SpliceToPCG	ENSG00000166435	
CONGO_chr11_074400726_315_m0	chr11	74400726	74401040	-	0	315	145.68	Intergenic								
CONGO_chr11_074519831_243_m0	chr11	74519831	74520073	-	0	243	274.4	Intergenic								
CONGO_chr11_075620930_73_m2	chr11	75620930	75621002	-	2	73	3.26	Intergenic								
CONGO_chr11_076082733_95_m2	chr11	76082733	76082827	-	2	95	209.32	NCExon								
CONGO_chr11_076084103_103_m2	chr11	76084103	76084205	-	2	103	142.88	NCExon		Guanylate_cyc						
CONGO_chr11_076085433_175_m0	chr11	76085433	76085607	-	0	175	867.15	NCExon		Guanylate_cyc						
CONGO_chr11_076096197_63_m0	chr11	76096197	76096259	-	0	63	217.01	NCExon		Pkinase_Tyr						
CONGO_chr11_076096272_63_m1	chr11	76096272	76096334	-	1	63	7.55	NCExon								
CONGO_chr11_076101007_101_m2	chr11	76101007	76101107	-	2	101	124.13	NCExon								
CONGO_chr11_076101421_87_m0	chr11	76101421	76101507	-	0	87	392.49	NCExon					TU412	NovelMultiExon		
CONGO_chr11_076101831_48_m0	chr11	76101831	76101878	-	0	48	64.08	NCIntron								
CONGO_chr11_076103604_89_m0	chr11	76103604	76103692	-	0	89	239.95	NCIntron								
CONGO_chr11_076105101_53_m0	chr11	76105101	76105153	-	0	53	43.59	NCExon								
CONGO_chr11_076105238_97_m1	chr11	76105238	76105334	-	1	97	19.86	NCExon								
CONGO_chr11_076108260_254_m2	chr11	76108260	76108513	-	2	254	88.67	NCExon								
CONGO_chr11_076527049_63_p0	chr11	76527049	76527111	+	0	63	182.63	Intron								
CONGO_chr11_076555633_54_p0	chr11	76555633	76555686	+	0	54	200.77	Intron								
CONGO_chr11_078350836_211_m0	chr11	78350836	78351046	-	0	211	243.22	Intron				1				
CONGO_chr11_078537429_71_m2	chr11	78537429	78537499	-	2	71	37.44	UTR			1	1	TU413	SpliceToPCG	ENSG00000149256	
CONGO_chr11_082145922_118_p1	chr11	82145922	82146039	+	1	118	93.22	Intergenic								
CONGO_chr11_082545814_104_m2	chr11	82545814	82545917	-	2	104	72.2	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000165494	
CONGO_chr11_082556409_180_p2	chr11	82556409	82556588	+	2	180	165.07	Intron			1	1	TU414	SpliceToPCG	ENSG00000165494	
CONGO_chr11_082869063_42_m2	chr11	82869063	82869104	-	2	42	187.56	UTR			1	1	TU174	SpliceToPCG	ENSG00000150672	
CONGO_chr11_083826079_78_m0	chr11	83826079	83826156	-	0	78	387.61	Intron				1				
CONGO_chr11_084108987_84_m0	chr11	84108987	84109070	-	0	84	6.61	Intron					TU174	SpliceToPCG	ENSG00000150672	
CONGO_chr11_085103085_73_p2	chr11	85103085	85103157	+	2	73	120.53	AntisenseCDS								
CONGO_chr11_085349376_93_m0	chr11	85349376	85349468	-	0	93	254.58	Intron				1	TU415	SpliceToPCG	ENSG00000073921	
CONGO_chr11_085633755_145_m2	chr11	85633755	85633899	-	2	145	477.92	AntisenseUTR								
CONGO_chr11_085820983_103_p0	chr11	85820983	85821085	+	0	103	20.16	Intergenic								
CONGO_chr11_085821109_121_p2	chr11	85821109	85821229	+	2	121	174.98	Intergenic				1				
CONGO_chr11_089017819_187_p1	chr11	89017819	89018005	+	1	187	54.89	Intergenic	1			1	TU44	NovelMultiExon		
CONGO_chr11_089025312_102_p0	chr11	89025312	89025413	+	0	102	261.93	NCExon	1		1	1	TU44	SpliceToPCG	ENSG00000134612	
CONGO_chr11_089031435_126_p0	chr11	89031435	89031560	+	0	126	763.2	NCExon	1		1	1	TU44	SpliceToPCG	ENSG00000134612	
CONGO_chr11_089032354_187_p0	chr11	89032354	89032540	+	0	187	1102.78	UTR	1	PA	1	1	TU44	SpliceToPCG	ENSG00000134612	
CONGO_chr11_089034966_94_p2	chr11	89034966	89035059	+	2	94	351.17	UTR	1		1	1	TU44	SpliceToPCG	ENSG00000134612	
CONGO_chr11_092138321_69_p2	chr11	92138321	92138389	+	2	69	145.09	Intron					TU416	SpliceToPCG	ENSG00000165323	
CONGO_chr11_093890397_105_p2	chr11	93890397	93890501	+	2	105	431.99	Intergenic				1	TU175	SpliceToPCG	ENSG00000168876	
CONGO_chr11_093900898_126_p2	chr11	93900898	93901023	+	2	126	360.11	Intergenic				1	TU175	NovelMultiExon		
CONGO_chr11_094101785_85_p0	chr11	94101785	94101869	+	0	85	142.52	Intergenic				1	TU176	SpliceToPCG	ENSG00000166025	
CONGO_chr11_094113752_51_p2	chr11	94113752	94113802	+	2	51	123.64	Intergenic				1	TU176	SpliceToPCG	ENSG00000166025	
CONGO_chr11_094422279_978_p0	chr11	94422279	94423256	+	0	978	4075.9	Intergenic		JmjC, JmjN						
CONGO_chr11_104471919_165_m2	chr11	104471919	104472083	-	2	165	8.11	Intron	1	Peptidase_C14						
CONGO_chr11_105321400_39_p0	chr11	105321400	105321438	+	0	39	31.63	NCExon			1	1				
CONGO_chr11_105677533_128_m2	chr11	105677533	105677660	-	2	128	55.16	Intergenic								
CONGO_chr11_107598653_107_p0	chr11	107598653	107598759	+	0	107	14	Intergenic			1					
CONGO_chr11_110631918_110_p2	chr11	110631918	110632027	+	2	110	574.93	UTR			1	1				
CONGO_chr11_110676462_95_p2	chr11	110676462	110676556	+	2	95	576.1	UTR			1	1	TU177	SpliceToPCG	ENSG00000214290	
CONGO_chr11_110680863_55_p0	chr11	110680863	110680917	+	0	55	32.96	UTR			1	1	TU177	SpliceToPCG	ENSG00000214290	
CONGO_chr11_110824385_218_p2	chr11	110824385	110824602	+	2	218	510.79	Intergenic								
CONGO_chr11_110825268_63_p0	chr11	110825268	110825330	+	0	63	133.48	Intergenic								
CONGO_chr11_110825358_71_p2	chr11	110825358	110825428	+	2	71	26.64	Intergenic								
CONGO_chr11_110826275_106_p0	chr11	110826275	110826380	+	0	106	607.48	Intergenic								
CONGO_chr11_110826979_91_p2	chr11	110826979	110827069	+	2	91	339	Intergenic								
CONGO_chr11_110831320_236_p0	chr11	110831320	110831555	+	0	236	329.46	Intron								
CONGO_chr11_110832484_191_p1	chr11	110832484	110832674	+	1	191	795.2	UTR			1					

CONGO_chr11_110832999_283_p2	chr11	110832999	110833281	+	2	283	1194.07	Intergenic				1				
CONGO_chr11_110833780_92_p2	chr11	110833780	110833871	+	2	92	114.98	Intergenic				1				
CONGO_chr11_110834052_109_p0	chr11	110834052	110834160	+	0	109	380.48	Intergenic				1				
CONGO_chr11_110835562_166_p0	chr11	110835562	110835727	+	0	166	670.02	Intergenic								
CONGO_chr11_110836147_158_p2	chr11	110836147	110836304	+	2	158	655.98	Intergenic								
CONGO_chr11_110838251_118_p0	chr11	110838251	110838368	+	0	118	159.81	Intergenic								
CONGO_chr11_110838980_126_p0	chr11	110838980	110839105	+	0	126	316.99	Intergenic								
CONGO_chr11_110839244_181_p0	chr11	110839244	110839424	+	0	181	308.08	Intergenic								
CONGO_chr11_110842764_61_p1	chr11	110842764	110842824	+	1	61	205.16	Intergenic					1	TU417	NovelMultiExon	
CONGO_chr11_110845135_145_p1	chr11	110845135	110845279	+	1	145	394.73	AntisenseIntron					1			
CONGO_chr11_110845722_198_p0	chr11	110845722	110845919	+	0	198	48.88	AntisenseIntron					1			
CONGO_chr11_112337283_170_p1	chr11	112337283	112337452	+	1	170	15.39	UTR				1	1	TU418	NovelMultiExon	
CONGO_chr11_113183883_134_m2	chr11	113183883	113184016	-	2	134	430.27	Intron					1	TU419	SpliceToPCG	ENSG00000048028
CONGO_chr11_113538937_135_p0	chr11	113538937	113539071	+	0	135	11.75	Intron								
CONGO_chr11_113621649_84_m0	chr11	113621649	113621732	-	0	84	115.44	AntisenseIntron							NovelUnspliced	
CONGO_chr11_114150900_42_p0	chr11	114150900	114150941	+	0	42	12.12	Intergenic								
CONGO_chr11_114515704_66_m0	chr11	114515704	114515769	-	0	66	41.34	Intergenic								
CONGO_chr11_114555949_80_p2	chr11	114555949	114556028	+	2	80	24.09	AntisenseIntron								
CONGO_chr11_114796381_111_p0	chr11	114796381	114796491	+	0	111	65.67	AntisenseIntron								
CONGO_chr11_116730858_301_p0	chr11	116730858	116731158	+	0	301	121.47	Intron				1	1	TU178	SpliceToPCG	ENSG00000110274
CONGO_chr11_116732118_199_p0	chr11	116732118	116732316	+	0	199	581.41	Intron				1		TU178	SpliceToPCG	ENSG00000110274
CONGO_chr11_117290534_39_m0	chr11	117290534	117290572	-	0	39	20.14	Intron								
CONGO_chr11_117389706_100_m1	chr11	117389706	117389805	-	1	100	319.19	Intergenic					1	TU420	NovelMultiExon	
CONGO_chr11_117391618_117_m2	chr11	117391618	117391734	-	2	117	725.38	NCExon				1	1	TU421	NovelMultiExon	
CONGO_chr11_117902183_49_m0	chr11	117902183	117902231	-	0	49	1.45	AntisenseNCExon							UnsplicedMergeWithPCG	ENSG00000118058
CONGO_chr11_117940890_97_m0	chr11	117940890	117940986	-	0	97	442.86	UTR				1	1	TU422	SpliceToPCG	ENSG00000118096
CONGO_chr11_118063952_153_m0	chr11	118063952	118064104	-	0	153	3.45	Intergenic	1	Trehalase						
CONGO_chr11_118443757_180_m1	chr11	118443757	118443936	-	1	180	779.73	AntisenseCDS						TU423	NovelMultiExon	
CONGO_chr11_118875595_52_m2	chr11	118875595	118875646	-	2	52	6.09	AntisenseUTR								
CONGO_chr11_119492877_99_m2	chr11	119492877	119492975	-	2	99	101.86	Intron				1	1	TU424	SpliceToPCG	ENSG00000137699
CONGO_chr11_122856734_78_p1	chr11	122856734	122856811	+	1	78	614.89	Intergenic					1	TU425	SpliceToPCG	ENSG00000023171
CONGO_chr11_122867768_110_p0	chr11	122867768	122867877	+	0	110	324.16	Intergenic								
CONGO_chr11_122886571_76_p2	chr11	122886571	122886646	+	2	76	220.36	Intergenic								
CONGO_chr11_122967313_147_p0	chr11	122967313	122967459	+	0	147	385.63	Intron								
CONGO_chr11_123216936_554_m2	chr11	123216936	123217489	-	2	554	2606.5	Intergenic		7tm_1						
CONGO_chr11_123217491_262_m0	chr11	123217491	123217752	-	0	262	1087.1	Intergenic		7tm_1						
CONGO_chr11_123237768_82_m2	chr11	123237768	123237849	-	2	82	117.31	Intergenic								
CONGO_chr11_123237982_291_m0	chr11	123237982	123238272	-	0	291	392.81	Intergenic								
CONGO_chr11_123535013_201_p0	chr11	123535013	123535213	+	0	201	2125.91	Intergenic				1				
CONGO_chr11_123614357_200_p2	chr11	123614357	123614556	+	2	200	97.96	Intron		7tm_1						
CONGO_chr11_123699972_230_m1	chr11	123699972	123700201	-	1	230	5.45	Intergenic								
CONGO_chr11_123714195_189_m0	chr11	123714195	123714383	-	0	189	57.99	Intergenic								
CONGO_chr11_123741335_323_m0	chr11	123741335	123741657	-	0	323	1002.5	Intergenic		7tm_1						
CONGO_chr11_123891498_370_m2	chr11	123891498	123891867	-	2	370	548.58	Intergenic								
CONGO_chr11_123891993_259_m2	chr11	123891993	123892251	-	2	259	990.65	Intergenic		7tm_1						
CONGO_chr11_123906746_221_p2	chr11	123906746	123906966	+	2	221	251.51	Intergenic		7tm_1						
CONGO_chr11_124543464_97_p1	chr11	124543464	124543560	+	1	97	7.03	Intron								
CONGO_chr11_124659602_73_p1	chr11	124659602	124659674	+	1	73	21.39	Intron								
CONGO_chr11_125278275_76_m2	chr11	125278275	125278350	-	2	76	27.66	UTR				1	1	TU426	SpliceToPCG	ENSG00000110060
CONGO_chr11_125322791_351_p2	chr11	125322791	125323141	+	2	351	823.73	Intergenic								
CONGO_chr11_125323410_98_p2	chr11	125323410	125323507	+	2	98	473.34	Intergenic								
CONGO_chr11_125323586_100_p0	chr11	125323586	125323685	+	0	100	209.25	Intergenic								
CONGO_chr11_125325119_276_p2	chr11	125325119	125325394	+	2	276	915.56	Intergenic		ig		1				
CONGO_chr11_125328505_291_p2	chr11	125328505	125328795	+	2	291	380.39	Intron		ig		1		TU427	NovelMultiExon	
CONGO_chr11_125329192_284_p2	chr11	125329192	125329475	+	2	284	910.57	Intron		fn3			1	TU428	NovelMultiExon	
CONGO_chr11_125330162_123_p2	chr11	125330162	125330284	+	2	123	851.39	Intron								
CONGO_chr11_127611327_89_m0	chr11	127611327	127611415	-	0	89	204.41	Intergenic								
CONGO_chr11_127872678_102_m2	chr11	127872678	127872779	-	2	102	56.03	Intron						TU429	SpliceToPCG	ENSG00000134954
CONGO_chr11_128061768_39_p0	chr11	128061768	128061806	+	0	39	73.01	AntisenseNCExon				1	1			
CONGO_chr11_128498993_42_m1	chr11	128498993	128499034	-	1	42	235.37	Intron					1	TU430	SpliceToPCG	ENSG00000134909
CONGO_chr11_129377827_53_m2	chr11	129377827	129377879	-	2	53	5.79	UTR				1	1	TU431	SpliceToPCG	ENSG00000170325
CONGO_chr11_131213066_99_m0	chr11	131213066	131213164	-	0	99	166.73	AntisenseIntron								
CONGO_chr11_133284174_209_m2	chr11	133284174	133284382	-	2	209	2005.47	Intergenic					1	TU95	SpliceToPCG	ENSG00000080854
CONGO_chr11_133286991_122_m1	chr11	133286991	133287112	-	1	122	303.59	Intergenic					1	TU95	SpliceToPCG	ENSG00000080854
CONGO_chr11_133293362_46_m1	chr11	133293362	133293407	-	1	46	4.4	UTR				1		TU95	SpliceToPCG	ENSG00000080854
CONGO_chr12_000880988_101_p2	chr12	880988	881088	+	2	101	298	NCExon				1		TU432	SpliceToPCG	ENSG00000060237
CONGO_chr12_002705959_93_m0	chr12	2705959	2706051	-	0	93	305.68	Intergenic						TU433	NovelMultiExon	
CONGO_chr12_002706235_161_m0	chr12	2706235	2706395	-	0	161	468.65	Intergenic								
CONGO_chr12_002706433_56_m2	chr12	2706433	2706488	-	2	56	19.11	Intergenic								
CONGO_chr12_002747331_160_m0	chr12	2747331	2747490	-	0	160	101.58	Intergenic					1			
CONGO_chr12_002749736_145_m0	chr12	2749736	2749880	-	0	145	130.18	Intergenic					1	TU434	NovelMultiExon	
CONGO_chr12_002754987_99_m0	chr12	2754987	2755085	-	0	99	279.99	Intergenic								
CONGO_chr12_003282764_67_m1	chr12	3282764	3282830	-	1	67	52.69	Intergenic								
CONGO_chr12_003283209_77_m2	chr12	3283209	3283285	-	2	77	66.34	Intergenic								
CONGO_chr12_003286191_105_m0	chr12	3286191	3286295	-	0	105	459.51	Intergenic						TU435	NovelMultiExon	
CONGO_chr12_003302779_101_p0	chr12	3302779	3302879	+	0	101	177.47	NCExon				1				
CONGO_chr12_003316542_99_m2	chr12	3316542	3316640	-	2	99	120.65	Intergenic								
CONGO_chr12_008823227_173_p2	chr12	8823227	8823399	+	2	173	64.5	NCExon				1		TU179	SpliceToPCG	ENSG00000166532
CONGO_chr12_008823898_78_p2	chr12	8823898	8823975	+	2	78	35.18	NCExon				1	1	TU179	SpliceToPCG	ENSG00000166532
CONGO_chr12_009273235_42_m2	chr12	9273235	9273276	-	2	42	52.21	Intergenic								
CONGO_chr12_009274116_103_m0	chr12	9274116	9274218	-	0	103	103.24	Intergenic		A2M_recep				TU180	NovelMultiExon	
CONGO_chr12_009274873_69_m0	chr12	9274873	9274941	-	0	69	140.8	Intergenic						TU180	NovelMultiExon	
CONGO_chr12_009275492_51_p2	chr12	9275492	9275542	+	2	51	102.23	Intergenic					1			
CONGO_chr12_009275918_131_m0	chr12	9275918	9276048	-	0	131	415.06	Intergenic						TU181	NovelMultiExon	
CONGO_chr12_009276225_219_m0	chr12	9276225	9276443	-	0	219	1020.11	Intergenic					1	TU181	NovelMultiExon	
CONGO_chr12_009277332_177_m0	chr12	9277332	9277508	-	0	177	814.18	Intergenic		A2M_comp			1			
CONGO_chr12_009277998_178_m0	chr12	9277998	9278175	-	0	178	448.01	Intergenic		A2M_comp			1			
CONGO_chr12_009278464_57_m0	chr12	9278464	9278520	-	0	57	111.27	Intergenic								
CONGO_chr12_009278955_135_m0	chr12	9278955	9279089	-	0	135	137.39	Intergenic		A2M_comp				TU436	SpliceToPCG	ENSG00000175899
CONGO_chr12_009279766_72_m2	chr12	9279766	9279837	-	2	72	204.38	Intergenic		A2M_comp						
CONGO_chr12_009280128_177_m2	chr12	9280128	9280304	-	2	177	877.7	Intergenic		Thiol-ester_cl						
CONGO_chr12_009280837_84_m2	chr12	9280837	9280920	-	2	84	110.38	Intergenic								
CONGO_chr12_009284526_52_m0	chr12	9284526	9284577	-	0	52	118.52	AntisenseNCIntron								
CONGO_chr12_009284795_122_m2	chr12	9284795	9284916	-	2	122	565.01	AntisenseNCIntron						TU182	NovelMultiExon	
CONGO_chr12_009285117_127_m0	chr12	9285117	9285243	-	0	127	380.24	AntisenseNCExon						TU182	NovelMultiExon	
CONGO_chr12_009285747_198_m0	chr12	9285747	9285944	-	0	198	990.32	AntisenseNCExon		A2M					NovelUnspliced	
CONGO_chr12_009286486_55_m2	chr12	9286486	9286540	-	2	55	196.7	AntisenseNCExon							NovelUnspliced	
CONGO_chr12_009297468_150_m0	chr12	9297468	9297617	-	0	150	1527.82	Intergenic		A2M_N_2			1			
CONGO_chr12_009300507_143_m2	chr12	9300507	9300649	-	2	143	420.97	Intergenic		A2M_N_2			1			
CONGO_chr12_009306393_147_m0	chr12	9306393	9306539	-	0	147	143.01	Intergenic					1			
CONGO_chr12_009309504_110_m2	chr12	9309504	9309613	-	2	110	482.43	Intergenic					1			
CONGO_chr12_009311862_115_m0	chr12	9311862	9311976	-	0	115	156.38	Intergenic					1			
CONGO_chr12_009315432_85_m2	chr12	9315432	9315516	-	2	85	435.59	Intergenic								
CONGO_chr12_009316912_169_m0	chr12	9316912	9317080	-	0	169	570.2	Intergenic								
CONGO_chr12_009318102_53_m2	chr12	9318102	9318154	-	2	53	63.93	Intergenic								
CONGO_chr12_009318301_154_m0	chr12	9318301	9318454	-	0	154	594.73	Intergenic		A2M_N						
CONGO_chr12_009319588_93_m0	chr12	9319588	9319680	-	0	93	183.28	Intergenic								
CONGO_chr12_009584222_112_p0	chr12	9584222	9584333	+	0	112	16.98	Intron	1				1			
CONGO_chr12_009598858_130_p0	chr12	9598858	9598987	+	0	130	74.6	Intergenic	1				1	TU183	NovelMultiExon	
CONGO_chr12_009600562_119_p2	chr12	9600562	9600680	+	2	119	59.25	Intergenic	1				1	TU183	NovelMultiExon	
CONGO_chr12_009601392_52_p0	chr12	9601392	9601443	+	0	52	64.62	NCExon	1			1	1			
CONGO_chr12_009603038_174_p2	chr12	9603038	9603211	+	2	174	678.55	NCExon	1	Thiol-ester_cl		1	1	TU437	NovelMultiExon	
CONGO_chr12_009603973_82_p2	chr12	9603973	9604054	+	2	82	9.69	NCExon	1	A2M_comp		1	1			
CONGO_chr12_009604680_157_p1	chr12	9604680	9604836	+	1	157	49.35	NCExon	1	A2M_comp		1	1			
CONGO_chr12_009606808_47_p0	chr12	9606808	9606854	+	0	47	53.18	NCExon	1			1	1			
CONGO_chr12_009608023_166_p0	chr12	9608023	9608188	+	0	166	448.05	NCExon	1	A2M_comp		1	1			
CONGO_chr12_009608955_212_p2	chr12	9608955	9609166	+	2	212	481.26	NCExon	1	A2M_comp		1	1			
CONGO_chr12_009614654_102_p0	chr12	9614654	9614755	+	0	102	70.01	NCExon	1			1	1	TU438	SpliceToPCG	ENSG00000139088
CONGO_chr12_010085348_139_p1	chr12	10085348	10085486	+	1	139	171.48	UTR				1	1	TU439	SpliceToPCG	ENSG00000197992
CONGO_chr12_010554258_44_m2	chr12	10554258	10554301	-	2	44	65.01	AntisenseIntron								
CONGO_chr12_011215261_157_p1	chr12	11215261	11215417	+	1	157	516.76	AntisenseUTR				1	1	TU440	UnsplicedMergeWithPCG	ENSG00000212127
CONGO_chr12_011843152_109_m1	chr12	11843152	11843260	-	1	109	112.86	AntisenseIntron								
CONGO_chr12_016502205_103_p1	chr12	16502205	16502307	+	1	103	3.67	Intergenic								
CONGO_chr12_018406965_123_p1	chr12	18406965	18407087	+	1	123	523.95	Intron				1	1	TU441	SpliceToPCG	ENSG00000139144
CONGO_chr12_022170830_110_m1	chr12	22170830	22170939	-	1	110	219.3	Intergenic								

CONGO_chr12_022559160_65_m1	chr12	22559160	22559224	-	1	65	12.07	Intron					TU442	SpliceToPCG	ENSG00000111731
CONGO_chr12_024125654_75_m0	chr12	24125654	24125728	-	0	75	54.83	Intron							
CONGO_chr12_024372630_75_m0	chr12	24372630	24372704	-	0	75	48.99	Intron							
CONGO_chr12_024804615_63_m0	chr12	24804615	24804677	-	0	63	32.14	Intergenic							
CONGO_chr12_025048570_150_p0	chr12	25048570	25048719	+	0	150	234.43	Intergenic							
CONGO_chr12_025061335_159_p1	chr12	25061335	25061493	+	1	159	552.9	Intergenic				1			
CONGO_chr12_025074479_57_p0	chr12	25074479	25074535	+	0	57	171.14	Intergenic				1			
CONGO_chr12_025076506_65_p0	chr12	25076506	25076570	+	0	65	69.1	Intergenic				1			
CONGO_chr12_025078049_100_p1	chr12	25078049	25078148	+	1	100	18.92	Intergenic				1			
CONGO_chr12_025097062_96_p2	chr12	25097062	25097157	+	2	96	31.46	UTR			1	1	TU443	SpliceToPCG	ENSG00000118308
CONGO_chr12_029827650_321_m1	chr12	29827650	29827970	-	1	321	110.16	Intron			1	1	TU444	SpliceToPCG	ENSG00000133687
CONGO_chr12_030350265_91_p0	chr12	30350265	30350355	+	0	91	388.79	Intergenic							
CONGO_chr12_031081488_159_m0	chr12	31081488	31081646	-	0	159	161.91	NCIntron							
CONGO_chr12_032443995_104_p0	chr12	32443995	32444098	+	0	104	54.76	Intergenic				1			
CONGO_chr12_032608390_101_p1	chr12	32608390	32608490	+	1	101	29.88	UTR			1	1	TU445	SpliceToPCG	ENSG00000139132
CONGO_chr12_046470256_170_m1	chr12	46470256	46470425	-	1	170	30.9	NCExon			1		TU446	SpliceToPCG	ENSG00000061273
CONGO_chr12_047035877_141_m1	chr12	47035877	47036017	-	1	141	207.81	Intergenic							
CONGO_chr12_047036542_96_m0	chr12	47036542	47036637	-	0	96	75.03	Intergenic							
CONGO_chr12_047065476_200_m2	chr12	47065476	47065675	-	2	200	202.03	Intergenic							
CONGO_chr12_047065908_171_m0	chr12	47065908	47066078	-	0	171	34.08	Intergenic							
CONGO_chr12_047396728_55_p1	chr12	47396728	47396782	+	1	55	180.65	AntisenseUTR					TU447	NovelMultiExon	
CONGO_chr12_047667083_94_p1	chr12	47667083	47667176	+	1	94	29.3	Intergenic							
CONGO_chr12_048246790_102_m0	chr12	48246790	48246891	-	0	102	92.3	UTR			1	1	TU448	SpliceToPCG	ENSG00000187778
CONGO_chr12_048338301_85_m0	chr12	48338301	48338385	-	0	85	88.82	Intron					TU449	SpliceToPCG	ENSG00000161791
CONGO_chr12_048753635_301_p0	chr12	48753635	48753935	+	0	301	622.65	Intron		ASC					
CONGO_chr12_048753953_342_p0	chr12	48753953	48754294	+	0	342	2336.15	Intron		ASC					
CONGO_chr12_049877820_254_m2	chr12	49877820	49878073	-	2	254	1860.24	UTR			1	1	TU45	SpliceToPCG	ENSG00000170545
CONGO_chr12_049878600_226_m0	chr12	49878600	49878825	-	0	226	610.19	UTR			1	1	TU45	SpliceToPCG	ENSG00000170545
CONGO_chr12_049879797_135_m0	chr12	49879797	49879931	-	0	135	769.35	UTR			1	1	TU45	SpliceToPCG	ENSG00000170545
CONGO_chr12_049884223_196_m0	chr12	49884223	49884418	-	0	196	1051.32	UTR			1	1	TU45	SpliceToPCG	ENSG00000170545
CONGO_chr12_049886840_48_m0	chr12	49886840	49886887	-	0	48	243	UTR			1	1	TU45	SpliceToPCG	ENSG00000170545
CONGO_chr12_050494264_681_m0	chr12	50494264	50494944	-	0	681	943.99	Intergenic							
CONGO_chr12_050946597_152_p0	chr12	50946597	50946748	+	0	152	138.78	Intergenic		Filament					
CONGO_chr12_050947014_117_p0	chr12	50947014	50947130	+	0	117	46.56	Intergenic							
CONGO_chr12_050947396_197_p0	chr12	50947396	50947592	+	0	197	141.3	Intergenic							
CONGO_chr12_050955872_105_p0	chr12	50955872	50955976	+	0	105	420.32	UTR			1	1	TU450	SpliceToPCG	ENSG00000170442
CONGO_chr12_051021373_295_p1	chr12	51021373	51021667	+	1	295	914.71	Intergenic							
CONGO_chr12_051024272_209_p0	chr12	51024272	51024480	+	0	209	489.46	Intergenic		Filament		1			
CONGO_chr12_051026223_61_p1	chr12	51026223	51026283	+	1	61	494.58	Intergenic							
CONGO_chr12_051027314_45_p0	chr12	51027314	51027358	+	0	45	97.12	Intergenic							
CONGO_chr12_051028052_87_p0	chr12	51028052	51028138	+	0	87	347.69	Intergenic							
CONGO_chr12_051028156_45_m0	chr12	51028156	51028200	-	0	45	18.01	Intergenic				1			
CONGO_chr12_051028438_126_p0	chr12	51028438	51028563	+	0	126	14.96	Intergenic							
CONGO_chr12_051030164_221_p0	chr12	51030164	51030384	+	0	221	1312.66	Intergenic		Filament					
CONGO_chr12_051033172_32_p1	chr12	51033172	51033203	+	1	32	261.82	Intergenic							
CONGO_chr12_051091804_186_m2	chr12	51091804	51091989	-	2	186	172.87	Intergenic							
CONGO_chr12_051094012_152_m0	chr12	51094012	51094163	-	0	152	541.77	Intergenic		Filament			TU451	SpliceToPCG	ENSG00000170421
CONGO_chr12_051096025_143_m0	chr12	51096025	51096167	-	0	143	342.04	Intergenic		Filament					
CONGO_chr12_051098402_78_m0	chr12	51098402	51098479	-	0	78	8.32	Intergenic				1			
CONGO_chr12_051101710_209_m0	chr12	51101710	51101918	-	0	209	581.48	Intergenic		Filament					
CONGO_chr12_051313513_74_m0	chr12	51313513	51313586	-	0	74	7.01	Intergenic							
CONGO_chr12_051395628_161_m0	chr12	51395628	51395788	-	0	161	520.56	Intergenic		Filament					
CONGO_chr12_051396516_126_m0	chr12	51396516	51396641	-	0	126	406.56	Intergenic		Filament					
CONGO_chr12_051397787_84_m0	chr12	51397787	51397870	-	0	84	133.36	Intergenic							
CONGO_chr12_051398219_100_m0	chr12	51398219	51398318	-	0	100	75.15	Intergenic							
CONGO_chr12_051399020_61_m1	chr12	51399020	51399080	-	1	61	417.62	Intergenic							
CONGO_chr12_051401216_291_m0	chr12	51401216	51401506	-	0	291	44.18	Intergenic				1			
CONGO_chr12_051428282_83_m2	chr12	51428282	51428364	-	2	83	1.42	Intergenic							
CONGO_chr12_051433360_152_m0	chr12	51433360	51433511	-	0	152	295.53	Intergenic							
CONGO_chr12_051724637_75_p0	chr12	51724637	51724711	+	0	75	160.67	AntisenseUTR						NovelUnspliced	
CONGO_chr12_051921974_277_p0	chr12	51921974	51922250	+	0	277	423.03	Intergenic							
CONGO_chr12_052132158_270_p2	chr12	52132158	52132427	+	2	270	64.29	UTR			1	1	TU184	SpliceToPCG	ENSG00000197111
CONGO_chr12_052154920_349_p1	chr12	52154920	52155268	+	1	349	369.52	Intron				1	TU184	SpliceToPCG	ENSG00000197111
CONGO_chr12_052696814_142_p2	chr12	52696814	52696955	+	2	142	66.26	UTR					TU185	SpliceToPCG	ENSG00000172789
CONGO_chr12_052708503_56_p1	chr12	52708503	52708558	+	1	56	72.88	UTR			1		TU185	SpliceToPCG	ENSG00000172789
CONGO_chr12_053032379_91_p1	chr12	53032379	53032469	+	1	91	59.77	Intergenic							
CONGO_chr12_053796384_142_p1	chr12	53796384	53796525	+	1	142	468.75	Intergenic							
CONGO_chr12_053874319_234_m0	chr12	53874319	53874552	-	0	234	1242.35	Intergenic		7tm_1					
CONGO_chr12_053874620_110_m2	chr12	53874620	53874729	-	2	110	183.54	Intergenic		7tm_1					
CONGO_chr12_053874761_107_m0	chr12	53874761	53874867	-	0	107	85.87	Intergenic							
CONGO_chr12_054022914_408_p2	chr12	54022914	54023321	+	2	408	2157.8	Intergenic		7tm_1					
CONGO_chr12_054023337_80_p1	chr12	54023337	54023416	+	1	80	146.33	Intergenic							
CONGO_chr12_054023472_351_p2	chr12	54023472	54023822	+	2	351	2032.79	Intergenic		7tm_1					
CONGO_chr12_054291674_281_p0	chr12	54291674	54291954	+	0	281	1016.17	Intergenic		7tm_1					
CONGO_chr12_054291998_563_p2	chr12	54291998	54292560	+	2	563	2207.98	Intergenic		7tm_1					
CONGO_chr12_054431554_33_m0	chr12	54431554	54431586	-	0	33	30.85	AntisenseUTR					TU453	SpliceToPCG	ENSG00000135392
CONGO_chr12_054698189_40_p0	chr12	54698189	54698228	+	0	40	37.03	Intergenic			1	1	TU455	SpliceToPCG	ENSG00000123411
CONGO_chr12_054701432_63_m1	chr12	54701432	54701494	-	1	63	182.36	AntisenseCDS				1			
CONGO_chr12_054701520_133_m2	chr12	54701520	54701652	-	2	133	55.7	AntisenseCDS				1			
CONGO_chr12_054798284_86_p1	chr12	54798284	54798369	+	1	86	98.92	UTR			1	1	TU187	SpliceToPCG	ENSG00000092841
CONGO_chr12_054799139_64_p2	chr12	54799139	54799202	+	2	64	105.49	UTR			1	1	TU187	SpliceToPCG	ENSG00000092841
CONGO_chr12_054919829_86_p2	chr12	54919829	54919914	+	2	86	14.63	AntisenseUTR					TU456	UnsplicedMergeWithPCG	ENSG00000139645
CONGO_chr12_055368185_122_p1	chr12	55368185	55368306	+	1	122	151.04	AntisenseUTR							
CONGO_chr12_055663545_114_m1	chr12	55663545	55663658	-	1	114	366.79	Intergenic	1						
CONGO_chr12_055665733_97_m2	chr12	55665733	55665829	-	2	97	5.66	Intergenic	1						
CONGO_chr12_055665923_89_m0	chr12	55665923	55666011	-	0	89	56.74	Intergenic	1						
CONGO_chr12_055848235_51_p2	chr12	55848235	55848285	+	2	51	274.36	NCExon			1		TU457	SpliceToPCG	ENSG00000123384
CONGO_chr12_056209294_73_m2	chr12	56209294	56209366	-	2	73	115.21	AntisenseUTR				1	TU458	SpliceToPCG	ENSG00000175203
CONGO_chr12_056299620_309_p2	chr12	56299620	56299928	+	2	309	573.21	NCExon				1	TU459	SpliceToPCG	ENSG00000135502
CONGO_chr12_056304781_63_p0	chr12	56304781	56304843	+	0	63	33.64	NCExon			1		TU460	SpliceToPCG	ENSG00000135502
CONGO_chr12_061054438_146_p1	chr12	61054438	61054583	+	1	146	87.76	Intron				1	TU461	SpliceToPCG	ENSG00000135655
CONGO_chr12_063213315_67_p0	chr12	63213315	63213381	+	0	67	192	Intergenic							
CONGO_chr12_063221628_125_p2	chr12	63221628	63221752	+	2	125	381.44	Intergenic							
CONGO_chr12_065484100_133_m0	chr12	65484100	65484232	-	0	133	852.95	Intergenic			1	1			
CONGO_chr12_068505565_46_p0	chr12	68505565	68505610	+	0	46	394.84	Intergenic				1	TU462	SpliceToPCG	ENSG00000127328
CONGO_chr12_068535327_91_p2	chr12	68535327	68535417	+	2	91	590.13	Intergenic				1	TU188	NovelMultiExon	
CONGO_chr12_068559075_68_p1	chr12	68559075	68559142	+	1	68	620.14	Intergenic					TU188	NovelMultiExon	
CONGO_chr12_068559242_259_p2	chr12	68559242	68559500	+	2	259	361.85	Intergenic							
CONGO_chr12_068560248_92_p1	chr12	68560248	68560339	+	1	92	92.81	Intergenic					TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068566867_151_p2	chr12	68566867	68567017	+	2	151	204.98	Intergenic					TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068571018_196_p1	chr12	68571018	68571213	+	1	196	847.34	Intergenic		NDT80_PhoG			TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068573811_77_p0	chr12	68573811	68573887	+	0	77	460.76	Intergenic					TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068575418_111_p1	chr12	68575418	68575528	+	1	111	1318.3	Intergenic		NDT80_PhoG			TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068577203_91_p1	chr12	68577203	68577293	+	1	91	703.94	Intergenic					TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068583691_201_p0	chr12	68583691	68583891	+	0	201	1441.14	Intergenic					TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068590016_109_p0	chr12	68590016	68590124	+	0	109	897	Intergenic				1	TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068590868_110_p2	chr12	68590868	68590977	+	2	110	653.73	Intergenic				1	TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068606618_164_p0	chr12	68606618	68606781	+	0	164	1576.54	UTR			1	1	TU8	SpliceToPCG	ENSG00000166268
CONGO_chr12_068974248_94_p0	chr12	68974248	68974341	+	0	94	20.9	UTR			1	1	TU463	SpliceToPCG	ENSG00000111596
CONGO_chr12_069127180_381_m0	chr12	69127180	69127560	-	0	381	727.42	Intergenic		RVT_1					
CONGO_chr12_069128111_208_m1	chr12	69128111	69128318	-	1	208	240.4	Intergenic		dUTPase					
CONGO_chr12_076954775_221_p0	chr12	76954775	76954995	+	0	221	1582.65	Intron			1				
CONGO_chr12_076955006_292_p0	chr12	76955006	76955297	+	0	292	2791.57	Intron			1				
CONGO_chr12_078695429_135_m0	chr12	78695429	78695563	-	0	135	64.02	Intron					TU189	SpliceToPCG	ENSG00000058272
CONGO_chr12_078728306_117_m0	chr12	78728306	78728422	-	0	117	209.56	Intron					TU189	SpliceToPCG	ENSG00000058272
CONGO_chr12_079129860_49_p1	chr12	79129860	79129908	+	1	49	41.24	Intergenic							
CONGO_chr12_079135509_67_p0	chr12	79135509	79135575	+	0	67	436.39	Intergenic							
CONGO_chr12_079137725_99_p2	chr12	79137725	79137823	+	2	99	661.47	Intergenic							
CONGO_chr12_079140002_155_p2	chr12	79140002	79140156	+	2	155	842.15	Intergenic		VWD					
CONGO_chr12_079147168_122_p0	chr12	79147168	79147289	+	0	122	819.58	Intergenic							
CONGO_chr12_079150803_206_p1	chr12	79150803	79151008	+	1	206	1399.17	Intergenic		VWD					
CONGO_chr12_079156764_126_p0	chr12	79156764	79156889	+	0	126	370.98	Intergenic							
CONGO_chr12_079174248_124_p0	chr12	79174248	79174371	+	0	124	747.07	Intergenic					TU190	NovelMultiExon	
CONGO_chr12_079175736_178_p2	chr12	79175736	79175913	+	2	178	1266.35	Intergenic		VWD			TU190	NovelMultiExon	
CONGO_chr12_079196939_139_p1	chr12	79196939	79197077	+	1	139	1487.38	Intergenic		VWD			TU464	NovelMultiExon	

CONGO_chr12_079214774_99_p0	chr12	79214774	79214872	+	0	99	489	Intergenic								
CONGO_chr12_079220545_150_p0	chr12	79220545	79220694	+	0	150	874.45	Intergenic								
CONGO_chr12_079223487_120_p0	chr12	79223487	79223606	+	0	120	950.28	Intergenic		VWD						
CONGO_chr12_079228522_117_p0	chr12	79228522	79228638	+	0	117	632.55	Intergenic								
CONGO_chr12_079253874_178_p0	chr12	79253874	79254051	+	0	178	1228.45	Intergenic					TU465	SpliceToPCG	ENSG00000165899	
CONGO_chr12_079558485_45_p1	chr12	79558485	79558529	+	1	45	198.44	Intron								
CONGO_chr12_080287532_87_m0	chr12	80287532	80287618	-	0	87	50.38	Intron					TU466	SpliceToPCG	ENSG00000139220	
CONGO_chr12_084180824_146_p2	chr12	84180824	84180969	+	2	146	205.85	Intergenic				1	TU467	SpliceToPCG	ENSG00000133640	
CONGO_chr12_086961521_98_m0	chr12	86961521	86961618	-	0	98	134.94	AntisenseCDS				1				
CONGO_chr12_088264363_64_p1	chr12	88264363	88264426	+	1	64	22.02	Intergenic								
CONGO_chr12_091646900_128_p1	chr12	91646900	91647027	+	1	128	194.28	Intergenic				1	TU468	NovelMultiExon		
CONGO_chr12_091654389_96_p0	chr12	91654389	91654484	+	0	96	70.48	UTR			1	1	TU469	SpliceToPCG	ENSG00000187510	
CONGO_chr12_094258280_117_m0	chr12	94258280	94258396	-	0	117	98.99	Intergenic								
CONGO_chr12_094323262_130_m2	chr12	94323262	94323391	-	2	130	171.77	Intergenic				1				
CONGO_chr12_095482553_122_p2	chr12	95482553	95482674	+	2	122	214.12	Intron					TU96	NovelMultiExon		
CONGO_chr12_095494494_177_p0	chr12	95494494	95494670	+	0	177	1099.12	UTR			1	1	TU96	NovelMultiExon		
CONGO_chr12_095498506_93_p0	chr12	95498506	95498598	+	0	93	574.84	UTR			1		TU96	NovelMultiExon		
CONGO_chr12_095565784_143_p1	chr12	95565784	95565926	+	1	143	526.15	UTR			1	1	TU191	SpliceToPCG	ENSG00000188596	
CONGO_chr12_095600095_151_p0	chr12	95600095	95600245	+	0	151	1241.47	Intron					TU191	SpliceToPCG	ENSG00000188596	
CONGO_chr12_095702705_95_p1	chr12	95702705	95702799	+	1	95	463.23	Intergenic				1	TU30	SpliceToPCG	ENSG00000188596	
CONGO_chr12_095704584_224_p2	chr12	95704584	95704807	+	2	224	515.25	Intergenic				1	TU30	SpliceToPCG	ENSG00000188596	
CONGO_chr12_095710322_87_p0	chr12	95710322	95710408	+	0	87	394.41	Intergenic				1	TU30	SpliceToPCG	ENSG00000188596	
CONGO_chr12_095735684_139_p1	chr12	95735684	95735822	+	1	139	165.22	Intergenic				1	TU30	SpliceToPCG	ENSG00000188596	
CONGO_chr12_095746923_75_p0	chr12	95746923	95746997	+	0	75	86.67	Intergenic				1	TU30	SpliceToPCG	ENSG00000139350	
CONGO_chr12_095778728_120_p0	chr12	95778728	95778847	+	0	120	852.66	Intergenic				1	TU30	SpliceToPCG	ENSG00000139350	
CONGO_chr12_096303974_76_m0	chr12	96303974	96304049	-	0	76	7.58	Intergenic								
CONGO_chr12_096455474_89_m0	chr12	96455474	96455562	-	0	89	14.41	AntisenseNCIntron								
CONGO_chr12_099651683_84_p2	chr12	99651683	99651766	+	2	84	876.97	Intergenic			1	1				
CONGO_chr12_099657763_252_p2	chr12	99657763	99658014	+	2	252	1609.2	Intergenic			1	1				
CONGO_chr12_102096037_70_m2	chr12	102096037	102096106	-	2	70	36.96	AntisenseIntron				1				
CONGO_chr12_102208206_64_m0	chr12	102208206	102208269	-	0	64	60.54	Intron						NovelUnspliced		
CONGO_chr12_102630288_56_m0	chr12	102630288	102630343	-	0	56	484.6	AntisenseCDS								
CONGO_chr12_102807389_160_m2	chr12	102807389	102807548	-	2	160	390	NCExon				1				
CONGO_chr12_102810863_442_m0	chr12	102810863	102811304	-	0	442	782.65	NCExon				1	TU59	NovelMultiExon		
CONGO_chr12_102814879_161_m2	chr12	102814879	102815039	-	2	161	291.69	NCExon				1	TU59	NovelMultiExon		
CONGO_chr12_102824046_215_m1	chr12	102824046	102824260	-	1	215	953.48	NCExon					TU59	NovelMultiExon		
CONGO_chr12_102829226_104_m0	chr12	102829226	102829329	-	0	104	113.11	NCExon					TU59	NovelMultiExon		
CONGO_chr12_102833039_317_m0	chr12	102833039	102833355	-	0	317	1015.7	UTR			1					
CONGO_chr12_102869485_47_p1	chr12	102869485	102869531	+	1	47	148.07	AntisenseCDS				1	TU470	SpliceToPCG	ENSG00000166598	
CONGO_chr12_105796834_227_m2	chr12	105796834	105797060	-	2	227	115.73	AntisenseUTR				1				
CONGO_chr12_109505333_85_p2	chr12	109505333	109505417	+	2	85	10.5	AntisenseUTR								
CONGO_chr12_110971695_104_m2	chr12	110971695	110971798	-	2	104	55.9	NCExon			1		TU471	SpliceToPCG	ENSG00000111300	
CONGO_chr12_111230940_139_m1	chr12	111230940	111231078	-	1	139	1342.73	Intergenic				1	TU31	SpliceToPCG	ENSG00000173064	
CONGO_chr12_111231748_109_m2	chr12	111231748	111231856	-	2	109	754.85	Intergenic				1	TU31	SpliceToPCG	ENSG00000173064	
CONGO_chr12_111235204_131_m1	chr12	111235204	111235334	-	1	131	1180.92	Intergenic				1	TU31	SpliceToPCG	ENSG00000173064	
CONGO_chr12_111236644_90_m1	chr12	111236644	111236733	-	1	90	1101.41	Intergenic				1	TU31	SpliceToPCG	ENSG00000173064	
CONGO_chr12_111241412_518_m0	chr12	111241412	111241929	-	0	518	4336.88	Intergenic				1	TU31	SpliceToPCG	ENSG00000173064	
CONGO_chr12_111304139_177_m0	chr12	111304139	111304315	-	0	177	712.78	Intergenic				1	TU31	SpliceToPCG	ENSG00000173064	
CONGO_chr12_115527237_71_p1	chr12	115527237	115527307	+	1	71	73.19	Intergenic								
CONGO_chr12_115803350_294_p0	chr12	115803350	115803643	+	0	294	62.19	AntisenseCDS								
CONGO_chr12_117112377_213_p0	chr12	117112377	117112589	+	0	213	36.46	AntisenseUTR					TU473	NovelMultiExon		
CONGO_chr12_118171890_146_m0	chr12	118171890	118172035	-	0	146	13.13	Intergenic								
CONGO_chr12_119976088_144_m0	chr12	119976088	119976231	-	0	144	131.36	Intergenic								
CONGO_chr12_121276930_135_m0	chr12	121276930	121277064	-	0	135	230.98	UTR			1	1	TU474	SpliceToPCG	ENSG00000184047	
CONGO_chr12_121372614_2268_m0	chr12	121372614	121374881	-	0	2268	13630.55	Intron					TU475	SpliceToPCG	ENSG00000130779	
CONGO_chr12_122273538_85_m1	chr12	122273538	122273622	-	1	85	506.52	UTR			1	1	TU192	SpliceToPCG	ENSG00000051825	
CONGO_chr12_122277963_154_m1	chr12	122277963	122278116	-	1	154	559.1	UTR			1	1	TU192	SpliceToPCG	ENSG00000051825	
CONGO_chr12_122844442_171_p0	chr12	122844442	122844612	+	0	171	2646.02	Intron			1		TU476	SpliceToPCG	ENSG00000197653	
CONGO_chr12_126394755_144_m0	chr12	126394755	126394898	-	0	144	193.67	Intergenic					TU477	NovelMultiExon		
CONGO_chr12_126674660_192_p0	chr12	126674660	126674851	+	0	192	197.57	Intergenic				1				
CONGO_chr12_129447859_189_m0	chr12	129447859	129448047	-	0	189	281.61	UTR			1	1	TU60	SpliceToPCG	ENSG00000060709	
CONGO_chr12_129474640_175_m1	chr12	129474640	129474814	-	1	175	783.53	Intron					TU60	SpliceToPCG	ENSG00000060709	
CONGO_chr12_129474838_448_m1	chr12	129474838	129475285	-	1	448	1620.06	Intron								
CONGO_chr12_129521191_51_m0	chr12	129521191	129521241	-	0	51	49.68	UTR			1	1	TU60	SpliceToPCG	ENSG00000060709	
CONGO_chr12_129557146_123_m0	chr12	129557146	129557268	-	0	123	16.29	UTR			1	1	TU60	SpliceToPCG	ENSG00000060709	
CONGO_chr12_130019475_96_p2	chr12	130019475	130019570	+	2	96	153.95	Intron			1	1	TU478	SpliceToPCG	ENSG00000111452	
CONGO_chr12_131595825_256_p0	chr12	131595825	131596080	+	0	256	154.53	Intron				1	TU61	SpliceToPCG	ENSG00000112787	
CONGO_chr12_131596120_986_p2	chr12	131596120	131597105	+	2	986	2924.51	Intron	1		1	1	TU61	SpliceToPCG	ENSG00000112787	
CONGO_chr12_131657727_164_p2	chr12	131657727	131657890	+	2	164	17.72	Intron				1	TU61	SpliceToPCG	ENSG00000112787	
CONGO_chr12_131660749_69_p0	chr12	131660749	131660817	+	0	69	455.35	Intron				1	TU61	SpliceToPCG	ENSG00000112787	
CONGO_chr13_024821700_83_p2	chr13	24821700	24821782	+	2	83	28.92	NCExon				1	TU485	SpliceToPCG	ENSG00000139496	
CONGO_chr13_025566862_93_m2	chr13	25566862	25566954	-	2	93	160.07	Intergenic								
CONGO_chr13_027294741_58_m0	chr13	27294741	27294798	-	0	58	23.59	Intergenic								
CONGO_chr13_027294806_99_p0	chr13	27294806	27294904	+	0	99	18.18	Intergenic								
CONGO_chr13_029938117_135_m2	chr13	29938117	29938251	-	2	135	49.74	Intron				1				
CONGO_chr13_030487455_84_p0	chr13	30487455	30487538	+	0	84	1.37	Intergenic								
CONGO_chr13_030537115_118_p1	chr13	30537115	30537232	+	1	118	299.86	Intergenic								
CONGO_chr13_031418114_205_p0	chr13	31418114	31418318	+	0	205	1231.06	NCExon			1	1	TU487	SpliceToPCG	ENSG00000073910	
CONGO_chr13_034568133_106_p2	chr13	34568133	34568238	+	2	106	19.12	Intron	1				TU488	SpliceToPCG	ENSG00000172915	
CONGO_chr13_034987048_170_m2	chr13	34987048	34987217	-	2	170	99.91	AntisenseIntron								
CONGO_chr13_035603251_162_m1	chr13	35603251	35603412	-	1	162	20.32	UTR			1	1	TU489	SpliceToPCG	ENSG00000133083	
CONGO_chr13_042921018_58_m0	chr13	42921018	42921075	-	0	58	176.61	Intron								
CONGO_chr13_045748726_65_p1	chr13	45748726	45748790	+	1	65	146.17	Intergenic					TU490	SpliceToPCG	ENSG00000173988	
CONGO_chr13_050476390_102_m2	chr13	50476390	50476491	-	2	102	255.06	UTR			1	1				
CONGO_chr13_050506244_53_m2	chr13	50506244	50506296	-	2	53	20.59	UTR			1	1				
CONGO_chr13_050520357_95_m1	chr13	50520357	50520451	-	1	95	631.12	UTR			1	1				
CONGO_chr13_050534958_74_m0	chr13	50534958	50535031	-	0	74	524.36	UTR		HNOB	1	1				
CONGO_chr13_050556288_175_m1	chr13	50556288	50556462	-	1	175	778.83	AntisenseNCExon				1				
CONGO_chr13_050557456_241_m2	chr13	50557456	50557696	-	2	241	1854.84	NCExon				1				
CONGO_chr13_050560065_148_m0	chr13	50560065	50560212	-	0	148	1686.32	NCExon				1				
CONGO_chr13_050582933_414_m0	chr13	50582933	50583346	-	0	414	1925.38	NCExon				1				
CONGO_chr13_051533956_135_m2	chr13	51533956	51534090	-	2	135	634.28	NCExon				1	TU491	SpliceToPCG	ENSG00000197168	
CONGO_chr13_057181804_84_p2	chr13	57181804	57181887	+	2	84	46.37	Intron				1	TU493	SpliceToPCG	ENSG00000118946	
CONGO_chr13_067327808_99_m1	chr13	67327808	67327906	-	1	99	85.08	Intergenic								
CONGO_chr13_070431551_135_m0	chr13	70431551	70431685	-	0	135	104.48	Intergenic								
CONGO_chr13_070996949_99_p0	chr13	70996949	70997047	+	0	99	54.6	AntisenseIntron								
CONGO_chr13_070997150_87_p0	chr13	70997150	70997236	+	0	87	99.34	AntisenseIntron								
CONGO_chr13_070997335_120_m0	chr13	70997335	70997454	-	0	120	10.79	Intron								
CONGO_chr13_071115765_119_m0	chr13	71115765	71115883	-	0	119	76.43	Intron								
CONGO_chr13_071245851_113_p2	chr13	71245851	71245963	+	2	113	46.15	AntisenseIntron								
CONGO_chr13_071262142_35_m0	chr13	71262142	71262176	-	0	35	72.03	Intron								
CONGO_chr13_071325997_128_p0	chr13	71325997	71326124	+	0	128	60.05	AntisenseIntron								
CONGO_chr13_071671102_84_p0	chr13	71671102	71671185	+	0	84	0.53	Intergenic								
CONGO_chr13_071900038_111_p0	chr13	71900038	71900148	+	0	111	96.79	Intergenic								
CONGO_chr13_073778134_90_m0	chr13	73778134	73778223	-	0	90	46.87	Intergenic				1				
CONGO_chr13_075328751_103_p1	chr13	75328751	75328853	+	1	103	59.18	NCExon			1	1	TU494	SpliceToPCG	ENSG00000136153	
CONGO_chr13_076575345_102_m2	chr13	76575345	76575446	-	2	102	139.4	NCExon				1	TU495	SpliceToPCG	ENSG00000005810	
CONGO_chr13_077688365_63_m0	chr13	77688365	77688427	-	0	63	13.42	AntisenseNCIntron								
CONGO_chr13_078185141_160_p0	chr13	78185141	78185300	+	0	160	110.33	Intergenic								
CONGO_chr13_078246322_140_p2	chr13	78246322	78246461	+	2	140	82.91	Intergenic								
CONGO_chr13_078251873_96_m0	chr13	78251873	78251968	-	0	96	50.74	Intergenic								
CONGO_chr13_078517364_60_m2	chr13	78517364	78517423	-	2	60	13.59	NCIntron								
CONGO_chr13_078557285_42_m0	chr13	78557285	78557326	-	0	42	49.87	NCIntron								
CONGO_chr13_078793370_68_m0	chr13	78793370	78793437	-	0	68	26.39	Intron			1		TU496	SpliceToPCG	ENSG00000139746	
CONGO_chr13_079255125_128_m2	chr13	79255125	79255252	-	2	128	13.28	Intergenic								
CONGO_chr13_085191730_41_p1	chr13	85191730	85191770	+	1	41	71.43	Intergenic								
CONGO_chr13_085271487_51_p0	chr13	85271487	85271537	+	0	51	22.12	Intergenic								
CONGO_chr13_090586358_74_p2	chr13	90586358	90586431	+	2	74	14.37	Intergenic								
CONGO_chr13_093853675_101_p2	chr13	93853675	93853775	+	2	101	7.98	UTR			1	1	TU497	SpliceToPCG	ENSG00000183098	
CONGO_chr13_094157151_288_m0	chr13	94157151	94157438	-	0	288	10.37	Intergenic						NovelUnspliced		
CONGO_chr13_094245728_105_m0	chr13	94245728	94245832	-	0	105	64.35	AntisenseNCIntron								
CONGO_chr13_096806932_129_m0	chr13	96806932	96807060	-	0	129	210.82	AntisenseCDS								
CONGO_chr13_097846514_161_p0	chr13	97846514	97846674	+	0	161	564.16	Intron						NovelUnspliced		
CONGO_chr13_098304822_174_m0	chr13	98304822	98304995	-	0	174	714.79	Intron								
CONGO_chr13_106007920_156_p2	chr13	106007920	106008075	+	2	156	42.88	AntisenseCDS					TU498	NovelMultiExon		

CONGO_chr13_111129421_60_m2	chr13	111129421	111129480	-	2	60	26.05	Intergenic								
CONGO_chr13_111679304_153_m0	chr13	111679304	111679456	-	0	153	124.03	Intergenic								
CONGO_chr13_113105694_126_m0	chr13	113105694	113105819	-	0	126	550.52	Intergenic			1		TU101	SpliceToPCG	ENSG00000150401	
CONGO_chr13_113108987_283_m0	chr13	113108987	113109269	-	0	283	907.95	Intergenic					TU101	SpliceToPCG	ENSG00000150401	
CONGO_chr13_113109659_878_m1	chr13	113109659	113110536	-	1	878	4531.95	Intergenic					TU101	SpliceToPCG	ENSG00000150401	
CONGO_chr13_113761321_190_m0	chr13	113761321	113761510	-	0	190	623.13	Intergenic								
CONGO_chr13_113979973_81_p0	chr13	113979973	113980053	+	0	81	283.9	Intergenic				1	TU194	SpliceToPCG	ENSG00000130177	
CONGO_chr13_113983902_119_p0	chr13	113983902	113984020	+	0	119	400.93	Intergenic				1	TU194	NovelMultiExon		
CONGO_chr14_019717391_72_p0	chr14	19717391	19717462	+	0	72	85.19	Intergenic								
CONGO_chr14_019717501_476_p0	chr14	19717501	19717976	+	0	476	2140.04	Intergenic		7tm_1						
CONGO_chr14_019717992_106_p0	chr14	19717992	19718097	+	0	106	627.05	Intergenic								
CONGO_chr14_019747292_195_p1	chr14	19747292	19747486	+	1	195	726.09	Intergenic		7tm_1						
CONGO_chr14_019747512_426_p0	chr14	19747512	19747937	+	0	426	901.59	Intergenic		7tm_1						
CONGO_chr14_019747941_103_p2	chr14	19747941	19748043	+	2	103	410.78	Intergenic								
CONGO_chr14_019767391_570_p1	chr14	19767391	19767960	+	1	570	1254.28	Intergenic		7tm_1	1					
CONGO_chr14_019768082_235_p0	chr14	19768082	19768316	+	0	235	647.05	Intergenic								
CONGO_chr14_020296210_189_p0	chr14	20296210	20296398	+	0	189	54.66	Intergenic		Gag_p30						
CONGO_chr14_021139889_643_m0	chr14	21139889	21140531	-	0	643	2690.47	Intergenic	1	7tm_1						
CONGO_chr14_021140571_246_m0	chr14	21140571	21140816	-	0	246	612.62	Intergenic	1	7tm_1						
CONGO_chr14_021399752_106_p2	chr14	21399752	21399857	+	2	106	6.07	Intron				1	TU499	SpliceToNCG	ENSG00000211787	
CONGO_chr14_021442449_166_p0	chr14	21442449	21442614	+	0	166	344.21	NCExon			1	1				
CONGO_chr14_021693146_183_p0	chr14	21693146	21693328	+	0	183	170.48	Intron								
CONGO_chr14_021988914_58_p0	chr14	21988914	21988971	+	0	58	32.76	UTR			1	1	TU62	SpliceToPCG	ENSG00000229164	
CONGO_chr14_022017709_55_p0	chr14	22017709	22017763	+	0	55	23.39	UTR			1	1	TU62	SpliceToPCG	ENSG00000229164	
CONGO_chr14_022029310_72_p2	chr14	22029310	22029381	+	2	72	139.19	UTR			1	1	TU62	SpliceToPCG	ENSG00000229164	
CONGO_chr14_022055105_45_p2	chr14	22055105	22055149	+	2	45	119.63	UTR			1	1	TU62	SpliceToPCG	ENSG00000229164	
CONGO_chr14_022076405_61_p0	chr14	22076405	22076465	+	0	61	71.03	NCExon			1		TU500	SpliceToPCG	ENSG00000229164	
CONGO_chr14_022606349_141_p2	chr14	22606349	22606489	+	2	141	111.58	AntisenseNCExon				1	TU501	NovelMultiExon		
CONGO_chr14_022639551_180_m1	chr14	22639551	22639730	-	1	180	117.72	UTR			1					
CONGO_chr14_022640341_273_m0	chr14	22640341	22640613	-	0	273	533.47	UTR			1		TU502	NovelMultiExon		
CONGO_chr14_022641975_126_m0	chr14	22641975	22642100	-	0	126	278.81	Intron								
CONGO_chr14_022846241_88_p2	chr14	22846241	22846328	+	2	88	68.1	UTR			1	1	TU503	SpliceToPCG	ENSG00000100836	
CONGO_chr14_022891695_115_m1	chr14	22891695	22891809	-	1	115	20.18	UTR			1	1	TU504	SpliceToPCG	ENSG00000092096	
CONGO_chr14_023052287_72_p0	chr14	23052287	23052358	+	0	72	6.64	NCIntron				1	TU505	SpliceToPCG	ENSG00000157306	
CONGO_chr14_023366335_88_m1	chr14	23366335	23366422	-	1	88	159.96	Intergenic								
CONGO_chr14_025295583_111_p0	chr14	25295583	25295693	+	0	111	35.2	Intergenic								
CONGO_chr14_025295723_57_p1	chr14	25295723	25295779	+	1	57	132.21	Intergenic								
CONGO_chr14_025417512_106_m0	chr14	25417512	25417617	-	0	106	16.94	Intergenic								
CONGO_chr14_025447787_173_p2	chr14	25447787	25447959	+	2	173	53.17	Intergenic								
CONGO_chr14_025669319_85_p2	chr14	25669319	25669403	+	2	85	32.69	Intergenic								
CONGO_chr14_025933637_48_m0	chr14	25933637	25933684	-	0	48	14.54	Intergenic								
CONGO_chr14_025983938_81_m0	chr14	25983938	25984018	-	0	81	9.11	Intergenic			1		TU102	SpliceToPCG	ENSG00000139910	
CONGO_chr14_025986293_94_m0	chr14	25986293	25986386	-	0	94	12.59	UTR			1		TU102	SpliceToPCG	ENSG00000139910	
CONGO_chr14_025986612_118_p0	chr14	25986612	25986729	+	0	118	42.59	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000139910	
CONGO_chr14_026088783_45_m0	chr14	26088783	26088827	-	0	45	59.42	UTR			1	1	TU102	SpliceToPCG	ENSG00000139910	
CONGO_chr14_027173616_72_p0	chr14	27173616	27173687	+	0	72	206.62	NCIntron								
CONGO_chr14_028340486_91_m1	chr14	28340486	28340576	-	1	91	119.53	Intergenic								
CONGO_chr14_028415066_117_m0	chr14	28415066	28415182	-	0	117	140.19	Intergenic								
CONGO_chr14_028755277_116_m2	chr14	28755277	28755392	-	2	116	69.39	Intergenic								
CONGO_chr14_028781914_138_p0	chr14	28781914	28782051	+	0	138	13.35	Intergenic								
CONGO_chr14_028930926_90_m1	chr14	28930926	28931015	-	1	90	58.48	Intergenic								
CONGO_chr14_028931248_77_m0	chr14	28931248	28931324	-	0	77	30.97	Intergenic								
CONGO_chr14_029766484_115_m1	chr14	29766484	29766598	-	1	115	7.72	Intergenic								
CONGO_chr14_029812341_119_p2	chr14	29812341	29812459	+	2	119	51.58	Intergenic								
CONGO_chr14_030668138_148_p0	chr14	30668138	30668285	+	0	148	203.57	AntisenseCDS								
CONGO_chr14_031868154_112_p1	chr14	31868154	31868265	+	1	112	35.84	UTR				1	TU195	SpliceToPCG	ENSG00000151320	
CONGO_chr14_031868274_92_p2	chr14	31868274	31868365	+	2	92	30.44	UTR			1	1	TU195	SpliceToPCG	ENSG00000151320	
CONGO_chr14_032185720_36_p2	chr14	32185720	32185755	+	2	36	36.68	Intron								
CONGO_chr14_032264142_108_p2	chr14	32264142	32264249	+	2	108	0.76	Intron								
CONGO_chr14_032473829_132_p1	chr14	32473829	32473960	+	1	132	79.88	Intergenic				1	TU506	SpliceToPCG	ENSG00000151322	
CONGO_chr14_032863049_181_m1	chr14	32863049	32863229	-	1	181	4.96	AntisenseIntron								
CONGO_chr14_032933156_46_p1	chr14	32933156	32933201	+	1	46	98.05	Intron								
CONGO_chr14_033101002_95_m2	chr14	33101002	33101096	-	2	95	10.57	AntisenseIntron								
CONGO_chr14_033105287_59_m1	chr14	33105287	33105345	-	1	59	59.52	AntisenseIntron								
CONGO_chr14_033106418_140_p1	chr14	33106418	33106557	+	1	140	17.59	Intron								
CONGO_chr14_033155782_75_m1	chr14	33155782	33155856	-	1	75	2.33	AntisenseIntron								
CONGO_chr14_033182441_103_m1	chr14	33182441	33182543	-	1	103	22.96	AntisenseIntron								
CONGO_chr14_033232976_117_p2	chr14	33232976	33233092	+	2	117	8.61	Intron								
CONGO_chr14_033272319_158_m1	chr14	33272319	33272476	-	1	158	10.62	AntisenseIntron								
CONGO_chr14_033342695_81_m2	chr14	33342695	33342775	-	2	81	99.61	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000151322	
CONGO_chr14_033342999_108_m0	chr14	33342999	33343106	-	0	108	2.1	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000151322	
CONGO_chr14_034502886_42_m0	chr14	34502886	34502927	-	0	42	68.77	Intergenic				1	TU103	NovelMultiExon		
CONGO_chr14_034504518_96_m0	chr14	34504518	34504613	-	0	96	305.31	Intergenic								
CONGO_chr14_034508127_52_m0	chr14	34508127	34508178	-	0	52	74.47	Intergenic				1	TU103	NovelMultiExon		
CONGO_chr14_034521387_80_m1	chr14	34521387	34521466	-	1	80	589.92	Intergenic				1	TU103	NovelMultiExon		
CONGO_chr14_035078503_83_p0	chr14	35078503	35078585	+	0	83	487.25	AntisenseCDS	1			1		UnsplicedMergeWithPCG	ENSG00000174373	
CONGO_chr14_035227416_661_m0	chr14	35227416	35228076	-	0	661	1237.39	Intron			1		TU196	SpliceToPCG	ENSG00000174373	
CONGO_chr14_035228505_266_m1	chr14	35228505	35228770	-	1	266	304.11	Intron				1	TU196	SpliceToPCG	ENSG00000174373	
CONGO_chr14_035559225_84_m0	chr14	35559225	35559308	-	0	84	36.16	Intergenic								
CONGO_chr14_035982334_64_m1	chr14	35982334	35982397	-	1	64	83.25	Intergenic								
CONGO_chr14_036058424_145_m2	chr14	36058424	36058568	-	2	145	69.53	UTR			1	1	TU507	SpliceToPCG	ENSG00000136352	
CONGO_chr14_036094585_63_p0	chr14	36094585	36094647	+	0	63	67.43	Intergenic								
CONGO_chr14_036224060_139_m1	chr14	36224060	36224198	-	1	139	14.27	Intron								
CONGO_chr14_037161006_131_p0	chr14	37161006	37161136	+	0	131	277.6	NCExon			1	1				
CONGO_chr14_037161307_158_p2	chr14	37161307	37161464	+	2	158	277.7	NCExon			1	1				
CONGO_chr14_037161686_274_p1	chr14	37161686	37161959	+	1	274	236.12	NCExon			1		TU508	NovelMultiExon		
CONGO_chr14_037240288_195_p1	chr14	37240288	37240482	+	1	195	158.04	NCExon			1		TU46	SpliceToPCG	ENSG00000139865	
CONGO_chr14_037263854_105_p0	chr14	37263854	37263958	+	0	105	81.48	NCExon			1		TU46	SpliceToPCG	ENSG00000139865	
CONGO_chr14_037288297_61_p1	chr14	37288297	37288357	+	1	61	345.23	NCIntron				1	TU46	SpliceToPCG	ENSG00000139865	
CONGO_chr14_037288670_130_p0	chr14	37288670	37288799	+	0	130	440.34	NCIntron					TU46	SpliceToPCG	ENSG00000139865	
CONGO_chr14_037290009_173_p2	chr14	37290009	37290181	+	2	173	896.65	NCIntron					TU46	SpliceToPCG	ENSG00000139865	
CONGO_chr14_038937134_107_m0	chr14	38937134	38937240	-	0	107	26.54	UTR			1		TU509	SpliceToPCG	ENSG00000165355	
CONGO_chr14_041305926_57_p2	chr14	41305926	41305982	+	2	57	13.34	UTR			1	1	TU510	SpliceToPCG	ENSG00000165379	
CONGO_chr14_052632585_102_m2	chr14	52632585	52632686	-	2	102	115.56	Intron					TU511	SpliceToPCG	ENSG00000100523	
CONGO_chr14_053325334_54_m0	chr14	53325334	53325387	-	0	54	38.9	NCIntron								
CONGO_chr14_053350864_40_p0	chr14	53350864	53350903	+	0	40	66.45	AntisenseNCIntron								
CONGO_chr14_053756855_57_m0	chr14	53756855	53756911	-	0	57	58.05	Intergenic								
CONGO_chr14_054222955_65_m1	chr14	54222955	54223019	-	1	65	6.64	Intron					TU512	NovelMultiExon		
CONGO_chr14_056185172_144_m0	chr14	56185172	56185315	-	0	144	45.65	AntisenseUTR					TU197	UnsplicedMergeWithPCG	ENSG00000070269	
CONGO_chr14_056185446_120_m2	chr14	56185446	56185565	-	2	120	223.65	AntisenseUTR				1	TU197	UnsplicedMergeWithPCG	ENSG00000070269	
CONGO_chr14_056267110_68_p2	chr14	56267110	56267177	+	2	68	33.39	Intergenic								
CONGO_chr14_056546167_102_p0	chr14	56546167	56546268	+	0	102	201.24	Intergenic								
CONGO_chr14_056827462_92_p2	chr14	56827462	56827553	+	2	92	1.77	NCExon			1		TU513	SpliceToPCG	ENSG00000053770	
CONGO_chr14_057402194_103_m0	chr14	57402194	57402296	-	0	103	251.05	Intergenic				1				
CONGO_chr14_057867662_214_m2	chr14	57867662	57867875	-	2	214	166.24	AntisenseUTR								
CONGO_chr14_057887987_96_m1	chr14	57887987	57888082	-	1	96	40.3	AntisenseIntron								
CONGO_chr14_059889981_74_m2	chr14	59889981	59890054	-	2	74	11.56	Intergenic								
CONGO_chr14_060684612_54_m0	chr14	60684612	60684665	-	0	54	12.06	Intergenic								
CONGO_chr14_061506603_180_p2	chr14	61506603	61506782	+	2	180	216.51	Intergenic				1	TU514	SpliceToPCG	ENSG00000139973	
CONGO_chr14_061664268_116_p2	chr14	61664268	61664383	+	2	116	17.29	UTR			1	1	TU515	SpliceToPCG	ENSG00000139973	
CONGO_chr14_062854162_60_p0	chr14	62854162	62854221	+	0	60	428.42	AntisenseCDS								
CONGO_chr14_066023128_153_p1	chr14	66023128	66023280	+	1	153	744.16	NCExon			1	1	TU63	SpliceToNCG	ENSG00000196553	
CONGO_chr14_066024631_97_p1	chr14	66024631	66024727	+	1	97	638.86	NCExon			1	1	TU63	SpliceToNCG	ENSG00000196553	
CONGO_chr14_066025458_51_p0	chr14	66025458	66025508	+	0	51	62.41	NCExon			1	1	TU63	SpliceToNCG	ENSG00000196553	
CONGO_chr14_066028524_142_p0	chr14	66028524	66028665	+	0	142	88.17	NCExon			1	1	TU63	SpliceToNCG	ENSG00000196553	
CONGO_chr14_070857592_60_p1	chr14	70857592	70857651	+	1	60	110.28	Intergenic				1	TU516	SpliceToPCG	ENSG00000197555	
CONGO_chr14_072089772_46_p0	chr14	72089772	72089817	+	0	46	86.01	Intron			1					
CONGO_chr14_073149029_414_p0	chr14	73149029	73149442	+	0	414	475.19	Intergenic		Bile_Hydr_Trans						
CONGO_chr14_073255299_166_m1	chr14	73255299	73255464	-	1	166	1435.92	UTR			1		TU517	SpliceToPCG	ENSG00000156030	
CONGO_chr14_073459101_53_p0	chr14	73459101	73459153	+	0	53	16.19	NCExon			1	1	TU518	SpliceToPCG	ENSG00000119725	
CONGO_chr14_074614024_228_p0	chr14	74614024	74614251	+	0	228	1261.74	UTR			1	1	TU519	SpliceToPCG	ENSG00000119703	
CONGO_chr14_075611886_48_p2	chr14	75611886	75611933	+	2	48	36.33	Intron								
CONGO_chr14_075912498_50_p0	chr14	75912498	75912547	+	0	50	15.71	Intron				1				
CONGO_chr14_076211454_131_p1	chr14	76211454	76211584	+	1	131	22.52	Intergenic								
CONGO_chr14_076350403_100_m0	chr14	76350403	76350502	-	0	100	200.27	Intergenic				1	TU520	SpliceToPCG	ENSG00000013523	

CONGO_chr14_076561307_91_m1	chr14	76561307	76561397	-	1	91	69.7	UTR			1			UnsplicedMergeWithPCG	ENSG00000119669
CONGO_chr14_077779185_314_p2	chr14	77779185	77779498	+	2	314	2330.42	NCExon		Laminin_G_2	1		TU105	SpliceToPCG	ENSG00000021645
CONGO_chr14_077779526_373_p0	chr14	77779526	77779898	+	0	373	3531.17	NCExon		EGF, Laminin_G_2	1	1	TU105	SpliceToPCG	ENSG00000021645
CONGO_chr14_078344705_60_m2	chr14	78344705	78344764	-	2	60	132.59	AntisenseIntron							
CONGO_chr14_079389635_110_p2	chr14	79389635	79389744	+	2	110	222.03	NCExon			1	1	TU105	SpliceToPCG	ENSG00000021645
CONGO_chr14_080804511_84_m0	chr14	80804511	80804594	-	0	84	522.82	Intron				1	TU521	SpliceToPCG	ENSG00000140022
CONGO_chr14_090141685_171_m2	chr14	90141685	90141855	-	2	171	337.01	Intron				1	TU522	SpliceToPCG	ENSG00000165914
CONGO_chr14_090821767_133_m1	chr14	90821767	90821899	-	1	133	176.05	Intron				1	TU523	SpliceToPCG	ENSG00000015133
CONGO_chr14_092966755_243_m0	chr14	92966755	92966997	-	0	243	187.27	AntisenseIntron							
CONGO_chr14_093002896_103_p0	chr14	93002896	93002998	+	0	103	13.61	Intron							
CONGO_chr14_093156991_150_p2	chr14	93156991	93157140	+	2	150	119.54	Intron				1	TU524	SpliceToPCG	ENSG00000133958
CONGO_chr14_093544708_62_p0	chr14	93544708	93544769	+	0	62	26.75	UTR			1		TU525	SpliceToPCG	ENSG00000175699
CONGO_chr14_093883636_185_m0	chr14	93883636	93883820	-	0	185	162.97	Intergenic							
CONGO_chr14_094729409_97_m1	chr14	94729409	94729505	-	1	97	3.9	Intron				1	TU526	SpliceToPCG	ENSG00000165959
CONGO_chr14_095458871_186_p0	chr14	95458871	95459056	+	0	186	1914.25	NCExon			1	1		NovelUnspliced	
CONGO_chr14_097109420_144_p0	chr14	97109420	97109563	+	0	144	61.88	Intergenic							
CONGO_chr14_097169388_59_p2	chr14	97169388	97169446	+	2	59	7.07	AntisenseUTR							
CONGO_chr14_098169608_77_p1	chr14	98169608	98169684	+	1	77	48.14	Intergenic							
CONGO_chr14_098346292_100_p2	chr14	98346292	98346391	+	2	100	29.42	Intergenic							
CONGO_chr14_099428229_57_p2	chr14	99428229	99428285	+	2	57	402.85	Intron					TU527	SpliceToPCG	ENSG00000066629
CONGO_chr14_099814047_128_m0	chr14	99814047	99814174	-	0	128	9.68	AntisenseUTR				1	TU528	SpliceToPCG	ENSG00000197119
CONGO_chr14_100086510_90_m1	chr14	100086510	100086599	-	1	90	16.51	Intron							
CONGO_chr14_100113442_332_m1	chr14	100113442	100113773	-	1	332	208.79	Intergenic							
CONGO_chr14_102624175_157_p0	chr14	102624175	102624331	+	0	157	590.21	Intergenic					TU529	NovelMultiExon	
CONGO_chr14_103476896_298_m1	chr14	103476896	103477193	-	1	298	1465.18	NCExon				1	TU198	SpliceToPCG	ENSG00000156411
CONGO_chr14_103477487_281_m0	chr14	103477487	103477767	-	0	281	1776.66	NCExon				1	TU198	SpliceToPCG	ENSG00000156411
CONGO_chr14_103672555_138_p0	chr14	103672555	103672692	+	0	138	70.21	Intergenic							
CONGO_chr14_105159294_84_m0	chr14	105159294	105159377	-	0	84	114.19	Intron	1				TU199	NovelMultiExon	
CONGO_chr14_105160450_131_m2	chr14	105160450	105160580	-	2	131	431.45	Intron	1				TU199	NovelMultiExon	
CONGO_chr14_105178347_84_m0	chr14	105178347	105178430	-	0	84	13.58	NCExon	1		1	1	TU200	NovelMultiExon	
CONGO_chr14_105179161_131_m2	chr14	105179161	105179291	-	2	131	89.81	NCExon	1		1	1	TU200	NovelMultiExon	
CONGO_chr15_023124120_92_p2	chr15	23124120	23124211	+	2	92	7.72	NCIntron							
CONGO_chr15_026662711_132_p2	chr15	26662711	26662842	+	2	132	131.44	Intergenic	1			1	TU106	NovelMultiExon	
CONGO_chr15_026673453_136_p0	chr15	26673453	26673588	+	0	136	215.75	Intergenic	1			1	TU106	NovelMultiExon	
CONGO_chr15_026676824_171_p2	chr15	26676824	26676994	+	2	171	201.81	Intergenic	1	Cyt-b5		1	TU106	SpliceToPCG	ENSG00000206149
CONGO_chr15_026715918_126_p2	chr15	26715918	26716043	+	2	126	189.36	UTR	1		1	1	TU107	SpliceToPCG	ENSG00000206149
CONGO_chr15_026717867_102_p1	chr15	26717867	26717968	+	1	102	148.11	Intron	1			1	TU107	SpliceToPCG	ENSG00000206149
CONGO_chr15_026718075_140_p1	chr15	26718075	26718214	+	1	140	111.94	UTR	1	ZZ	1	1	TU107	SpliceToPCG	ENSG00000206149
CONGO_chr15_028035727_133_m1	chr15	28035727	28035859	-	1	133	1555.61	NCExon				1	TU531	SpliceToPCG	ENSG00000104067
CONGO_chr15_028152115_97_m0	chr15	28152115	28152211	-	0	97	296.33	NCExon				1			
CONGO_chr15_029240401_54_m0	chr15	29240401	29240454	-	0	54	406.53	Intergenic			1				
CONGO_chr15_031198742_120_m2	chr15	31198742	31198861	-	2	120	146.26	Intron							
CONGO_chr15_033333263_160_p1	chr15	33333263	33333422	+	1	160	1.33	Intergenic							
CONGO_chr15_033333721_75_m2	chr15	33333721	33333795	-	2	75	30.38	Intergenic							
CONGO_chr15_033645385_147_m0	chr15	33645385	33645531	-	0	147	33.87	AntisenseNCIntron							
CONGO_chr15_033832569_85_m1	chr15	33832569	33832653	-	1	85	28	AntisenseNCIntron							
CONGO_chr15_033918414_64_m2	chr15	33918414	33918477	-	2	64	8.09	AntisenseNCIntron							
CONGO_chr15_034575049_220_m1	chr15	34575049	34575268	-	1	220	74.45	Intergenic							
CONGO_chr15_034973571_115_m1	chr15	34973571	34973685	-	1	115	11.18	Intron					TU532	SpliceToPCG	ENSG00000134138
CONGO_chr15_035028469_68_p1	chr15	35028469	35028536	+	1	68	194.81	AntisenseIntron							
CONGO_chr15_035028585_181_m1	chr15	35028585	35028765	-	1	181	55.34	Intron							
CONGO_chr15_035028891_108_p0	chr15	35028891	35028998	+	0	108	69.59	AntisenseIntron							
CONGO_chr15_035136929_67_p2	chr15	35136929	35136995	+	2	67	20.31	AntisenseIntron							
CONGO_chr15_035161635_99_m1	chr15	35161635	35161733	-	1	99	106.97	Intron							
CONGO_chr15_035301017_92_p1	chr15	35301017	35301108	+	1	92	11.43	Intergenic							
CONGO_chr15_035438962_113_m2	chr15	35438962	35439074	-	2	113	15.25	Intergenic							
CONGO_chr15_035441177_147_m0	chr15	35441177	35441323	-	0	147	38.3	Intergenic							
CONGO_chr15_035959557_104_m2	chr15	35959557	35959660	-	2	104	19.64	Intergenic							
CONGO_chr15_035983897_138_m0	chr15	35983897	35984034	-	0	138	4.84	Intergenic							
CONGO_chr15_038403549_462_p0	chr15	38403549	38404010	+	0	462	270.58	NCExon			1		TU533	NovelMultiExon	
CONGO_chr15_038992229_61_m2	chr15	38992229	38992289	-	2	61	40.42	Intergenic							
CONGO_chr15_039299320_69_m2	chr15	39299320	39299388	-	2	69	456.72	Intron			1	1	TU201	SpliceToPCG	ENSG00000178997
CONGO_chr15_039305933_133_m0	chr15	39305933	39306065	-	0	133	399.96	Intron			1	1	TU201	SpliceToPCG	ENSG00000178997
CONGO_chr15_040453777_114_p0	chr15	40453777	40453890	+	0	114	463.59	Intron							
CONGO_chr15_041648676_150_m0	chr15	41648676	41648825	-	0	150	242.66	NCExon	1						
CONGO_chr15_041958989_172_m0	chr15	41958989	41959160	-	0	172	758.96	Intron					TU534	SpliceToPCG	ENSG00000171877
CONGO_chr15_045444453_40_m0	chr15	45444453	45444492	-	0	40	45.02	AntisenseIntron							
CONGO_chr15_046305368_69_p2	chr15	46305368	46305436	+	2	69	0.87	UTR			1	1	TU535	SpliceToPCG	ENSG00000074803
CONGO_chr15_048580190_63_m1	chr15	48580190	48580252	-	1	63	1.05	UTR				1	TU537	SpliceToPCG	ENSG00000092439
CONGO_chr15_050003529_105_m0	chr15	50003529	50003633	-	0	105	182.79	AntisenseNCIntron					TU65	SpliceToPCG	ENSG00000166477
CONGO_chr15_050005234_135_m1	chr15	50005234	50005368	-	1	135	771.48	AntisenseNCIntron		Leo1			TU65	SpliceToPCG	ENSG00000166477
CONGO_chr15_050006267_95_m0	chr15	50006267	50006361	-	0	95	414.95	AntisenseNCIntron		Leo1			TU65	SpliceToPCG	ENSG00000166477
CONGO_chr15_050008822_146_m0	chr15	50008822	50008967	-	0	146	11.78	AntisenseNCExon					TU65	SpliceToPCG	ENSG00000166477
CONGO_chr15_050125319_70_p1	chr15	50125319	50125388	+	1	70	141.78	UTR	1		1	1	TU538	SpliceToPCG	ENSG00000069956
CONGO_chr15_051056351_63_p0	chr15	51056351	51056413	+	0	63	27.49	Intergenic							
CONGO_chr15_053397118_165_m0	chr15	53397118	53397282	-	0	165	151.15	NCExon			1	1	TU539	SpliceToPCG	ENSG00000069974
CONGO_chr15_053699351_136_m1	chr15	53699351	53699486	-	1	136	169.14	UTR			1		TU540	SpliceToPCG	ENSG00000166450
CONGO_chr15_055820716_111_m0	chr15	55820716	55820826	-	0	111	4.75	AntisenseNCIntron							
CONGO_chr15_058283898_63_m0	chr15	58283898	58283960	-	0	63	3.55	Intergenic							
CONGO_chr15_058343875_73_m1	chr15	58343875	58343947	-	1	73	92.83	Intergenic							
CONGO_chr15_058604967_48_m2	chr15	58604967	58605014	-	2	48	100.9	Intron							
CONGO_chr15_058756642_82_m1	chr15	58756642	58756723	-	1	82	170.87	Intron				1			
CONGO_chr15_061679949_234_p1	chr15	61679949	61680182	+	1	234	485.73	UTR			1	1	TU541	SpliceToPCG	ENSG00000140455
CONGO_chr15_062002122_474_m0	chr15	62002122	62002595	-	0	474	2567.48	Intron					TU542	SpliceToPCG	ENSG00000035664
CONGO_chr15_063991474_119_m2	chr15	63991474	63991592	-	2	119	131.13	NCExon				1	TU543	SpliceToPCG	ENSG00000157890
CONGO_chr15_064986651_101_m2	chr15	64986651	64986751	-	2	101	63.54	Intergenic							
CONGO_chr15_065800214_74_p0	chr15	65800214	65800287	+	0	74	0.63	Intron							
CONGO_chr15_067504675_42_p1	chr15	67504675	67504716	+	1	42	33.8	NCExon			1	1	TU544	SpliceToPCG	ENSG00000137807
CONGO_chr15_070576186_68_p2	chr15	70576186	70576253	+	2	68	210.51	Intron				1	TU545	SpliceToPCG	ENSG00000166233
CONGO_chr15_073305452_107_m2	chr15	73305452	73305558	-	2	107	14.79	Intergenic	1						
CONGO_chr15_075975765_1034_p1	chr15	75975765	75976798	+	1	1034	2757.52	Intergenic	1	Laminin_G_2					
CONGO_chr15_075976862_887_p0	chr15	75976862	75977748	+	0	887	2682.95	Intergenic	1						
CONGO_chr15_075977774_162_p0	chr15	75977774	75977935	+	0	162	264.87	Intergenic	1						
CONGO_chr15_075977958_291_p0	chr15	75977958	75978248	+	0	291	697.3	Intergenic	1						
CONGO_chr15_075978286_105_p0	chr15	75978286	75978390	+	0	105	398.79	Intergenic	1						
CONGO_chr15_075978406_110_p2	chr15	75978406	75978515	+	2	110	2.42	Intergenic	1						
CONGO_chr15_075978532_477_p0	chr15	75978532	75979008	+	0	477	975.99	Intergenic	1				TU203	NovelMultiExon	
CONGO_chr15_075980732_470_p0	chr15	75980732	75981201	+	0	470	972.01	Intergenic	1			1	TU203	NovelMultiExon	
CONGO_chr15_075981553_135_p0	chr15	75981553	75981687	+	0	135	203.75	Intergenic	1			1	TU204	NovelMultiExon	
CONGO_chr15_075983323_199_p0	chr15	75983323	75983521	+	0	199	434.1	Intergenic	1			1	TU204	NovelMultiExon	
CONGO_chr15_078281167_180_m0	chr15	78281167	78281346	-	0	180	1157.73	Intergenic				1	TU546	NovelMultiExon	
CONGO_chr15_079262253_40_p0	chr15	79262253	79262292	+	0	40	24.08	UTR			1	1	TU547	SpliceToPCG	ENSG00000172349
CONGO_chr15_080344965_184_p1	chr15	80344965	80345148	+	1	184	613.15	Intron	1		1	1	TU548	SpliceToPCG	ENSG00000188659
CONGO_chr15_081165440_242_m0	chr15	81165440	81165681	-	0	242	804.2	Intron							
CONGO_chr15_081176989_180_m0	chr15	81176989	81177168	-	0	180	30.52	NCExon			1		TU205	SpliceToNCG	ENSG00000228141
CONGO_chr15_081177612_72_m0	chr15	81177612	81177683	-	0	72	15.72	NCExon			1	1	TU205	SpliceToNCG	ENSG00000228141
CONGO_chr15_082512870_554_m2	chr15	82512870	82513423	-	2	554	1804.4	Intergenic	1						
CONGO_chr15_082513483_329_m2	chr15	82513483	82513811	-	2	329	443.82	Intergenic	1						
CONGO_chr15_082562653_116_p2	chr15	82562653	82562768	+	2	116	76.34	Intergenic	1				TU206	SpliceToPCG	ENSG00000205242
CONGO_chr15_082564361_215_p0	chr15	82564361	82564575	+	0	215	638.42	Intergenic	1			1	TU206	NovelMultiExon	
CONGO_chr15_082572590_137_p1	chr15	82572590	82572726	+	1	137	311.18	Intergenic	1				TU32	NovelMultiExon	
CONGO_chr15_082573321_143_p1	chr15	82573321	82573463	+	1	143	543.79	Intergenic	1			1	TU32	NovelMultiExon	
CONGO_chr15_082575801_100_p2	chr15	82575801	82575900	+	2	100	68.41	Intergenic	1			1	TU32	NovelMultiExon	
CONGO_chr15_082580846_152_p1	chr15	82580846	82580997	+	1	152	486.86	Intergenic	1			1	TU32	NovelMultiExon	
CONGO_chr15_082581259_167_p2	chr15	82581259	82581425	+	2	167	422.72	Intergenic	1			1	TU32	NovelMultiExon	
CONGO_chr15_082586218_139_p0	chr15	82586218	82586356	+	0	139	352.58	Intergenic	1				TU32	NovelMultiExon	
CONGO_chr15_084021211_123_p2	chr15	84021211	84021333	+	2	123	307.78	UTR			1		TU549	SpliceToPCG	ENSG00000170776
CONGO_chr15_084034265_75_p0	chr15	84034265	84034339	+	0	75	249.39	Intron				1	TU550	SpliceToPCG	ENSG00000170776
CONGO_chr15_084424208_51_p0	chr15	84424208	84424258	+	0	51	280.16	Intergenic							
CONGO_chr15_085251322_135_p1	chr15	85251322	85251456	+	1	135	461.14	Intron							
CONGO_chr15_087212451_114_p2	chr15	87212451	87212564	+	2	114	320.58	NCExon		EGF	1	1	TU551	SpliceToPCG	ENSG00000157766
CONGO_chr15_089278573_211_p2	chr15	89278573	89278783	+	2	211	1051.17	UTR			1	1	TU207	SpliceToPCG	ENSG00000140553
CONGO_chr15_089279178_86_p1	chr15	89279178	89279263	+	1	86	284.42	UTR			1	1	TU207	SpliceToPCG	ENSG00000140553
CONGO_chr15_091248454_117_p1	chr15	91248454	91248570	+	1	117	97.05	Intron							
CONGO_chr15_093640371_59_m1	chr15	93640371	93640429	-	1	59	0.04	NCIntron							

CONGO_chr15_093721308_98_p2	chr15	93721308	93721405	+	2	98	3.12	Intergenic								
CONGO_chr15_093842028_162_p0	chr15	93842028	93842189	+	0	162	8.49	NCExon			1	1	TU552	NovelMultiExon		
CONGO_chr15_093876299_140_p1	chr15	93876299	93876438	+	1	140	30.82	Intergenic								
CONGO_chr15_093894757_76_p0	chr15	93894757	93894832	+	0	76	32.29	Intergenic								
CONGO_chr15_093901182_84_p0	chr15	93901182	93901265	+	0	84	37.69	Intergenic								
CONGO_chr15_093948115_105_m0	chr15	93948115	93948219	-	0	105	90.69	Intergenic								
CONGO_chr15_094971259_86_m0	chr15	94971259	94971344	-	0	86	18.07	Intergenic								
CONGO_chr15_094989974_61_m0	chr15	94989974	94990034	-	0	61	17.45	Intergenic								
CONGO_chr15_095072492_76_p1	chr15	95072492	95072567	+	1	76	40.14	Intergenic								
CONGO_chr15_096806780_101_m2	chr15	96806780	96806880	-	2	101	199.58	Intron								
CONGO_chr15_096881008_131_m2	chr15	96881008	96881138	-	2	131	568.73	Intergenic								
CONGO_chr16_000530191_182_p0	chr16	530191	530372	+	0	182	900.25	Intron					TU553	SpliceToPCG	ENSG00000103326	
CONGO_chr16_001248385_114_p0	chr16	1248385	1248498	+	0	114	64.16	UTR	1	Trypsin	1	1	TU554	SpliceToPCG	ENSG00000095917	
CONGO_chr16_001263910_164_m2	chr16	1263910	1264073	-	2	164	272.14	Intron								
CONGO_chr16_001276372_143_m0	chr16	1276372	1276514	-	0	143	479.13	Intergenic		Trypsin						
CONGO_chr16_001276609_173_m2	chr16	1276609	1276781	-	2	173	255.94	Intergenic								
CONGO_chr16_001278249_275_m1	chr16	1278249	1278523	-	1	275	1023.04	Intergenic		Trypsin						
CONGO_chr16_001278671_165_m0	chr16	1278671	1278835	-	0	165	365.8	Intergenic		Trypsin						
CONGO_chr16_002981050_54_p2	chr16	2981050	2981103	+	2	54	42.92	NCExon			1	1				
CONGO_chr16_002986498_36_p2	chr16	2986498	2986533	+	2	36	66.67	Intergenic								
CONGO_chr16_002989904_42_p2	chr16	2989904	2989945	+	2	42	115.04	Intergenic				1				
CONGO_chr16_002990088_33_p2	chr16	2990088	2990120	+	2	33	16.55	Intergenic				1				
CONGO_chr16_002990716_114_p2	chr16	2990716	2990829	+	2	114	101.47	Intergenic								
CONGO_chr16_002994243_406_p0	chr16	2994243	2994648	+	0	406	426.17	Intergenic								
CONGO_chr16_003021412_87_m0	chr16	3021412	3021498	-	0	87	418.6	UTR			1		TU557	SpliceToPCG	ENSG00000162069	
CONGO_chr16_003134017_75_p0	chr16	3134017	3134091	+	0	75	325.85	Intergenic								
CONGO_chr16_003134186_141_p0	chr16	3134186	3134326	+	0	141	180.01	UTR			1	1				
CONGO_chr16_003134745_89_p2	chr16	3134745	3134833	+	2	89	39.18	UTR			1	1				
CONGO_chr16_003298608_230_p2	chr16	3298608	3298837	+	2	230	243.33	NCExon		SCAN	1	1	TU558	SpliceToPCG	ENSG00000162086	
CONGO_chr16_004197128_131_p0	chr16	4197128	4197258	+	0	131	114.75	AntisenseCDS								
CONGO_chr16_005138436_112_m0	chr16	5138436	5138547	-	0	112	35.87	Intergenic	1							
CONGO_chr16_006306997_63_p0	chr16	6306997	6307059	+	0	63	254.59	UTR			1	1	TU209	SpliceToPCG	ENSG00000078328	
CONGO_chr16_006644605_48_p0	chr16	6644605	6644652	+	0	48	212.8	UTR			1	1	TU209	SpliceToPCG	ENSG00000078328	
CONGO_chr16_007294389_99_p0	chr16	7294389	7294487	+	0	99	141.28	Intron				1	TU559	SpliceToPCG	ENSG00000078328	
CONGO_chr16_010183235_191_m0	chr16	10183235	10183425	-	0	191	13.44	UTR			1	1	TU560	SpliceToPCG	ENSG00000183454	
CONGO_chr16_011385000_142_m0	chr16	11385000	11385141	-	0	142	183.42	Intergenic				1	TU561	NovelMultiExon		
CONGO_chr16_011385574_110_m2	chr16	11385574	11385683	-	2	110	341.8	Intergenic				1	TU210	NovelMultiExon		
CONGO_chr16_011386246_70_m0	chr16	11386246	11386315	-	0	70	34.44	Intergenic				1	TU210	NovelMultiExon		
CONGO_chr16_011386569_206_m2	chr16	11386569	11386774	-	2	206	34.93	Intergenic				1	TU562	NovelMultiExon		
CONGO_chr16_011391463_98_m0	chr16	11391463	11391560	-	0	98	203.99	Intergenic					TU211	NovelMultiExon		
CONGO_chr16_011391637_185_m2	chr16	11391637	11391821	-	2	185	104.11	Intergenic					TU211	NovelMultiExon		
CONGO_chr16_011394749_169_m0	chr16	11394749	11394917	-	0	169	25.42	Intergenic								
CONGO_chr16_011402623_141_m0	chr16	11402623	11402763	-	0	141	7.62	Intergenic				1				
CONGO_chr16_011412603_82_m1	chr16	11412603	11412684	-	1	82	27.62	Intergenic								
CONGO_chr16_011418989_208_m0	chr16	11418989	11419196	-	0	208	36.69	Intergenic								
CONGO_chr16_011432393_175_m0	chr16	11432393	11432567	-	0	175	399.76	Intergenic								
CONGO_chr16_011437019_218_m0	chr16	11437019	11437236	-	0	218	223.24	Intergenic								
CONGO_chr16_011442296_138_m0	chr16	11442296	11442433	-	0	138	203.21	Intergenic								
CONGO_chr16_011470865_160_m0	chr16	11470865	11471024	-	0	160	143.55	UTR			1		TU563	SpliceToPCG	ENSG00000188897	
CONGO_chr16_011473011_164_m2	chr16	11473011	11473174	-	2	164	346.85	UTR			1					
CONGO_chr16_011476981_92_m1	chr16	11476981	11477072	-	1	92	24.81	UTR			1					
CONGO_chr16_011478121_183_m1	chr16	11478121	11478303	-	1	183	327.16	UTR			1					
CONGO_chr16_011479178_185_m0	chr16	11479178	11479362	-	0	185	449.13	UTR			1		TU212	SpliceToPCG	ENSG00000188897	
CONGO_chr16_011479887_156_m0	chr16	11479887	11480042	-	0	156	353.46	UTR			1	1	TU212	SpliceToPCG	ENSG00000188897	
CONGO_chr16_011488619_125_m2	chr16	11488619	11488743	-	2	125	266.24	Intron				1				
CONGO_chr16_011490066_159_m2	chr16	11490066	11490224	-	2	159	651.37	UTR			1	1				
CONGO_chr16_011493058_149_m1	chr16	11493058	11493206	-	1	149	357.19	UTR			1	1				
CONGO_chr16_011495001_153_m0	chr16	11495001	11495153	-	0	153	309.34	Intergenic				1	TU213	NovelMultiExon		
CONGO_chr16_011495932_186_m0	chr16	11495932	11496117	-	0	186	388.88	Intergenic				1	TU213	NovelMultiExon		
CONGO_chr16_011502161_166_m1	chr16	11502161	11502326	-	1	166	310.57	Intergenic				1				
CONGO_chr16_011503434_104_m0	chr16	11503434	11503537	-	0	104	19.25	Intergenic								
CONGO_chr16_011510073_140_m2	chr16	11510073	11510212	-	2	140	280.77	Intergenic								
CONGO_chr16_011515716_181_m0	chr16	11515716	11515896	-	0	181	102	Intergenic								
CONGO_chr16_011517286_135_m0	chr16	11517286	11517420	-	0	135	226.32	AntisenseIntron				1				
CONGO_chr16_011517499_166_m1	chr16	11517499	11517664	-	1	166	265.85	AntisenseIntron		Vitellogenin_N		1				
CONGO_chr16_017352050_39_p0	chr16	17352050	17352088	+	0	39	158.58	AntisenseIntron								
CONGO_chr16_018728192_165_p0	chr16	18728192	18728356	+	0	165	1.1	AntisenseUTR					TU564	UnsplicedMergeWithPCG	ENSG00000157106	
CONGO_chr16_020506790_120_m0	chr16	20506790	20506909	-	0	120	377.33	Intergenic	1				TU108	NovelMultiExon		
CONGO_chr16_020509345_100_m1	chr16	20509345	20509444	-	1	100	425.82	Intergenic		1 AMP-binding			TU108	NovelMultiExon		
CONGO_chr16_020509533_128_m0	chr16	20509533	20509660	-	0	128	139.07	Intergenic		1 AMP-binding			TU108	NovelMultiExon		
CONGO_chr16_020512653_124_m1	chr16	20512653	20512776	-	1	124	486.24	Intergenic		1 AMP-binding			TU214	NovelMultiExon		
CONGO_chr16_020514588_80_m0	chr16	20514588	20514667	-	0	80	19.68	Intergenic	1				TU214	NovelMultiExon		
CONGO_chr16_020630296_208_p2	chr16	20630296	20630503	+	2	208	387.74	Intergenic				1				
CONGO_chr16_020637173_144_p1	chr16	20637173	20637316	+	1	144	397.95	Intergenic				1	TU13	SpliceToPCG	ENSG00000005187	
CONGO_chr16_020638070_138_p0	chr16	20638070	20638207	+	0	138	247.4	Intergenic					TU13	NovelMultiExon		
CONGO_chr16_020644185_80_p0	chr16	20644185	20644264	+	0	80	469.29	Intergenic								
CONGO_chr16_020646166_124_p1	chr16	20646166	20646289	+	1	124	818.2	Intergenic		AMP-binding			TU13	SpliceToPCG	ENSG00000005187	
CONGO_chr16_020647211_108_p0	chr16	20647211	20647318	+	0	108	263.35	Intergenic					TU13	NovelMultiExon		
CONGO_chr16_020648053_128_p0	chr16	20648053	20648180	+	0	128	204.73	Intergenic		AMP-binding			TU13	SpliceToPCG	ENSG00000005187	
CONGO_chr16_020648277_100_p1	chr16	20648277	20648376	+	1	100	925.68	Intergenic		AMP-binding			TU13	SpliceToPCG	ENSG00000005187	
CONGO_chr16_020650443_81_p0	chr16	20650443	20650523	+	0	81	69.25	Intergenic					TU13	NovelMultiExon		
CONGO_chr16_020651730_51_p0	chr16	20651730	20651780	+	0	51	20.97	Intergenic					TU13	NovelMultiExon		
CONGO_chr16_021257278_71_p0	chr16	21257278	21257348	+	0	71	5.89	Intergenic								
CONGO_chr16_021257743_118_p0	chr16	21257743	21257860	+	0	118	365.81	Intergenic								
CONGO_chr16_021857687_188_p0	chr16	21857687	21857874	+	0	188	548.83	Intergenic								
CONGO_chr16_021858504_171_p1	chr16	21858504	21858674	+	1	171	680.32	Intergenic								
CONGO_chr16_021859099_182_p1	chr16	21859099	21859280	+	1	182	594.77	Intergenic				1				
CONGO_chr16_021863685_78_p0	chr16	21863685	21863762	+	0	78	185.51	Intergenic				1				
CONGO_chr16_028178047_278_p0	chr16	28178047	28178324	+	0	278	462.38	Intergenic								
CONGO_chr16_030451321_528_m0	chr16	30451321	30451848	-	0	528	1234.41	UTR		zf-C2H2	1	1	TU565	SpliceToPCG	ENSG00000156853	
CONGO_chr16_030660563_168_p0	chr16	30660563	30660730	+	0	168	334.74	UTR			1	1	TU215	SpliceToPCG	ENSG00000080603	
CONGO_chr16_030662604_162_p0	chr16	30662604	30662765	+	0	162	224.81	UTR			1	1	TU215	SpliceToPCG	ENSG00000080603	
CONGO_chr16_030694694_107_m0	chr16	30694694	30694800	-	0	107	185.07	AntisenseUTR			1		TU566	UnsplicedMergeWithPCG	ENSG00000103549	
CONGO_chr16_030841890_85_p0	chr16	30841890	30841974	+	0	85	2.9	AntisenseCDS			1	1	TU567	SpliceToPCG	ENSG00000099364	
CONGO_chr16_046466136_83_m1	chr16	46466136	46466218	-	1	83	29.63	NCIntron								
CONGO_chr16_046823244_69_p1	chr16	46823244	46823312	+	1	69	37.03	AntisenseCDS								
CONGO_chr16_048151769_155_p2	chr16	48151769	48151923	+	2	155	1.25	AntisenseIntron								
CONGO_chr16_048181069_110_m1	chr16	48181069	48181178	-	1	110	29.85	Intron								
CONGO_chr16_048290301_159_p0	chr16	48290301	48290459	+	0	159	28.54	AntisenseIntron								
CONGO_chr16_049735701_143_p2	chr16	49735701	49735843	+	2	143	35.13	AntisenseIntron								
CONGO_chr16_049744895_72_p0	chr16	49744895	49744966	+	0	72	46.24	Intergenic								
CONGO_chr16_050050032_69_p0	chr16	50050032	50050100	+	0	69	136.65	Intergenic								
CONGO_chr16_050344164_90_p0	chr16	50344164	50344253	+	0	90	13.14	Intergenic								
CONGO_chr16_050349108_93_p0	chr16	50349108	50349200	+	0	93	27.01	Intergenic								
CONGO_chr16_050516351_105_p1	chr16	50516351	50516455	+	1	105	28.53	Intergenic								
CONGO_chr16_050530815_163_p0	chr16	50530815	50530977	+	0	163	38.29	Intergenic								
CONGO_chr16_051051935_71_p0	chr16	51051935	51052005	+	0	71	126.17	AntisenseIntron								
CONGO_chr16_051052210_125_p0	chr16	51052210	51052334	+	0	125	1.8	AntisenseIntron								
CONGO_chr16_051053768_111_p2	chr16	51053768	51053878	+	2	111	90.73	AntisenseIntron								
CONGO_chr16_051058715_66_p0	chr16	51058715	51058780	+	0	66	12.62	AntisenseIntron								
CONGO_chr16_051183546_108_m0	chr16	51183546	51183653	-	0	108	12.07	NCIntron								
CONGO_chr16_051635413_159_m0	chr16	51635413	51635571	-	0	159	166.1	Intron						NovelUnspliced		
CONGO_chr16_051799645_128_m2	chr16	51799645	51799772	-	2	128	42.47	AntisenseCDS			1		TU568	NovelMultiExon		
CONGO_chr16_051814863_58_p1	chr16	51814863	51814920	+	1	58	123.41	Intron				1	TU569	SpliceToPCG	ENSG00000177200	
CONGO_chr16_052258334_116_p0	chr16	52258334	52258449	+	0	116	3.58	AntisenseIntron								
CONGO_chr16_052314510_81_m2	chr16	52314510	52314590	-	2	81	14.86	AntisenseIntron								
CONGO_chr16_052538681_76_p1	chr16	52538681	52538756	+	1	76	91.88	Intron								
CONGO_chr16_052544765_123_p0	chr16	52544765	52544887	+	0	123	23.4	Intron								
CONGO_chr16_052582987_97_m1	chr16	52582987	52583083	-	1	97	30.9	AntisenseIntron								
CONGO_chr16_052652781_119_p2	chr16	52652781	52652899	+	2	119	25.85	Intron								
CONGO_chr16_052654126_141_m0	chr16	52654126	52654266	-	0	141	99.78	AntisenseIntron								
CONGO_chr16_053132656_38_p0	chr16	53132656	53132693	+	0	38	3.51	Intron								
CONGO_chr16_053208640_55_p0	chr16	53208640	53208694	+	0	55	137.71	Intron								
CONGO_chr16_053208855_107_m2	chr16	53208855	53208961	-	2	107	13.51	AntisenseIntron								
CONGO_chr16_053281649_71_p2	chr16	53281649	53281719	+	2	71	52.71	Intergenic								

CONGO_chr16_053648287_168_p1	chr16	53648287	53648454	+	1	168	38.85	Intergenic									
CONGO_chr16_054319530_145_p1	chr16	54319530	54319674	+	1	145	442.36	Intergenic	1	COesterase				TU19	SpliceToPCG	ENSG00000196959	
CONGO_chr16_054321745_134_p0	chr16	54321745	54321878	+	0	134	338.41	Intergenic	1	COesterase			1	TU19	SpliceToPCG	ENSG00000196959	
CONGO_chr16_054324819_105_p0	chr16	54324819	54324923	+	0	105	229.81	Intergenic	1	COesterase			1	TU19	SpliceToPCG	ENSG00000196959	
CONGO_chr16_054331816_141_p0	chr16	54331816	54331956	+	0	141	358.07	Intergenic	1	COesterase				TU570	SpliceToPCG	ENSG00000196959	
CONGO_chr16_054334232_109_p0	chr16	54334232	54334340	+	0	109	34.95	Intergenic	1				1	TU571	NovelMultiExon		
CONGO_chr16_054338171_132_p2	chr16	54338171	54338302	+	2	132	524.97	Intergenic	1	COesterase				TU109	SpliceToPCG	ENSG00000196959	
CONGO_chr16_054340974_73_p2	chr16	54340974	54341046	+	2	73	50.82	Intergenic	1					TU109	SpliceToPCG	ENSG00000196959	
CONGO_chr16_054341343_109_p1	chr16	54341343	54341451	+	1	109	107.02	Intergenic	1	COesterase				TU109	SpliceToPCG	ENSG00000196959	
CONGO_chr16_056134060_55_p1	chr16	56134060	56134114	+	1	55	115.24	UTR			1		1	TU572	SpliceToPCG	ENSG00000159618	
CONGO_chr16_056376877_203_m2	chr16	56376877	56377079	-	2	203	589.94	Intron			1		1	TU216	SpliceToPCG	ENSG00000140859	
CONGO_chr16_056379988_139_m0	chr16	56379988	56380126	-	0	139	177.37	UTR			1		1	TU216	SpliceToPCG	ENSG00000140859	
CONGO_chr16_056528497_202_m0	chr16	56528497	56528698	-	0	202	291.19	Intron					1	TU573	SpliceToPCG	ENSG00000070729	
CONGO_chr16_062652099_32_m0	chr16	62652099	62652130	-	0	32	24.76	Intergenic									
CONGO_chr16_066522508_74_p1	chr16	66522508	66522581	+	1	74	79	AntisenseCDS					1		UnsplicedMergeWithPCG	ENSG00000141086	
CONGO_chr16_068238825_66_m2	chr16	68238825	68238890	-	2	66	52.35	AntisenseCDS							UnsplicedMergeWithPCG	ENSG00000102908	
CONGO_chr16_068289653_110_p2	chr16	68289653	68289762	+	2	110	10.25	UTR			1			TU574	SpliceToPCG	ENSG00000102908	
CONGO_chr16_070021666_105_m0	chr16	70021666	70021770	-	0	105	533.17	Intergenic						TU217	SpliceToPCG	ENSG00000235418	
CONGO_chr16_070022072_74_m2	chr16	70022072	70022145	-	2	74	213.53	Intergenic						TU217	SpliceToPCG	ENSG00000235418	
CONGO_chr16_070024069_59_m2	chr16	70024069	70024127	-	2	59	15.33	Intergenic									
CONGO_chr16_070315173_99_m0	chr16	70315173	70315271	-	0	99	122.51	UTR			1		1	TU575	SpliceToPCG	ENSG00000040199	
CONGO_chr16_070472721_88_m1	chr16	70472721	70472808	-	1	88	14	UTR			1		1	TU576	SpliceToPCG	ENSG00000102984	
CONGO_chr16_071018790_68_m2	chr16	71018790	71018857	-	2	68	174.7	AntisenseNCExon					1		NovelUnspliced		
CONGO_chr16_071205078_45_p2	chr16	71205078	71205122	+	2	45	13.35	Intergenic									
CONGO_chr16_071449979_137_p0	chr16	71449979	71450115	+	0	137	76.67	AntisenseIntron									
CONGO_chr16_071493654_62_p2	chr16	71493654	71493715	+	2	62	94.52	AntisenseIntron									
CONGO_chr16_071946300_99_m0	chr16	71946300	71946398	-	0	99	62.35	Intergenic									
CONGO_chr16_072071738_38_m0	chr16	72071738	72071775	-	0	38	45.06	Intergenic									
CONGO_chr16_072563001_103_m1	chr16	72563001	72563103	-	1	103	50.74	Intergenic									
CONGO_chr16_072936246_125_m2	chr16	72936246	72936370	-	2	125	581.23	UTR	1		1		1	TU218	SpliceToPCG	ENSG00000214331	
CONGO_chr16_072941141_118_m0	chr16	72941141	72941258	-	0	118	129.16	Intron	1					TU218	SpliceToPCG	ENSG00000214331	
CONGO_chr16_073491097_57_m0	chr16	73491097	73491153	-	0	57	174.4	Intron					1	TU577	SpliceToPCG	ENSG00000103091	
CONGO_chr16_074091184_174_m0	chr16	74091184	74091357	-	0	174	284.62	Intergenic		NAcGluc_Transf							
CONGO_chr16_077189246_103_p0	chr16	77189246	77189348	+	0	103	0.64	Intron									
CONGO_chr16_077201525_150_p0	chr16	77201525	77201674	+	0	150	132.35	Intron									
CONGO_chr16_077256411_79_p1	chr16	77256411	77256489	+	1	79	22.84	Intron									
CONGO_chr16_077549792_60_m2	chr16	77549792	77549851	-	2	60	18.72	AntisenseIntron									
CONGO_chr16_078196408_74_m1	chr16	78196408	78196481	-	1	74	107.16	Intergenic									
CONGO_chr16_078508034_110_m2	chr16	78508034	78508143	-	2	110	55.06	Intergenic									
CONGO_chr16_083760632_2283_p0	chr16	83760632	83762914	+	0	2283	7578.46	Intergenic					1	TU219	SpliceToPCG	ENSG00000131149	
CONGO_chr16_083948570_181_p0	chr16	83948570	83948750	+	0	181	623.74	Intergenic						TU219	SpliceToPCG	ENSG00000131149	
CONGO_chr16_085902257_63_m0	chr16	85902257	85902319	-	0	63	24.75	Intron					1	TU578	SpliceToPCG	ENSG00000103264	
CONGO_chr16_085949518_87_m2	chr16	85949518	85949604	-	2	87	665.9	Intron						TU579	SpliceToPCG	ENSG00000103264	
CONGO_chr16_088199212_90_m2	chr16	88199212	88199301	-	2	90	107.54	Intergenic									
CONGO_chr16_088564297_203_m2	chr16	88564297	88564499	-	2	203	262.3	UTR		DDE	1				UnsplicedMergeWithPCG	ENSG00000177946	
CONGO_chr16_088579355_125_p0	chr16	88579355	88579479	+	0	125	842.93	NCIntron						TU6	SpliceToNCG	ENSG00000223959	
CONGO_chr16_088582606_157_p1	chr16	88582606	88582762	+	1	157	430.14	NCExon			1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088582795_66_p0	chr16	88582795	88582860	+	0	66	98.67	NCExon			1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088584775_138_p0	chr16	88584775	88584912	+	0	138	1034.55	NCExon		AAA	1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088585138_159_p1	chr16	88585138	88585296	+	1	159	238.2	NCIntron		AAA			1				
CONGO_chr16_088586630_108_p2	chr16	88586630	88586737	+	2	108	871.74	NCExon		AAA	1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088587677_126_p2	chr16	88587677	88587802	+	2	126	755.68	NCExon			1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088590653_149_p1	chr16	88590653	88590801	+	1	149	283.94	NCIntron						TU6	SpliceToNCG	ENSG00000223959	
CONGO_chr16_088593105_116_p2	chr16	88593105	88593220	+	2	116	394.44	NCExon		Peptidase_M41	1				UnsplicedMergeWithNCG	ENSG00000223959	
CONGO_chr16_088593733_131_p0	chr16	88593733	88593863	+	0	131	763.01	NCExon		Peptidase_M41	1			TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088593877_57_p0	chr16	88593877	88593933	+	0	57	341.95	NCExon			1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088594012_195_p0	chr16	88594012	88594206	+	0	195	678.44	NCExon			1		1	TU6	SpliceToPCG	ENSG00000141013	
CONGO_chr16_088594358_200_p0	chr16	88594358	88594557	+	0	200	654.1	NCExon			1		1	TU6	SpliceToNCG	ENSG00000223959	
CONGO_chr16_088640866_140_m0	chr16	88640866	88641005	-	0	140	672.19	UTR		Transthyretin	1		1	TU580	SpliceToPCG	ENSG00000222019	
CONGO_chr17_000881588_144_m0	chr17	881588	881731	-	0	144	835.95	Intron			1		1	TU581	SpliceToPCG	ENSG00000159842	
CONGO_chr17_001078837_349_m0	chr17	1078837	1079185	-	0	349	1003.91	Intergenic					1	TU582	SpliceToPCG	ENSG00000159842	
CONGO_chr17_001079534_141_m0	chr17	1079534	1079674	-	0	141	262.91	Intergenic									
CONGO_chr17_001754698_75_m1	chr17	1754698	1754772	-	1	75	60.27	Intergenic									
CONGO_chr17_001921936_105_p1	chr17	1921936	1922040	+	1	105	236.51	AntisenseIntron									
CONGO_chr17_002024905_69_m0	chr17	2024905	2024973	-	0	69	31.17	Intron									
CONGO_chr17_002025159_51_p0	chr17	2025159	2025209	+	0	51	27.83	AntisenseIntron									
CONGO_chr17_002026968_79_p1	chr17	2026968	2027046	+	1	79	10.03	AntisenseIntron									
CONGO_chr17_002041953_135_p2	chr17	2041953	2042087	+	2	135	10.9	AntisenseIntron									
CONGO_chr17_002065405_106_p1	chr17	2065405	2065510	+	1	106	16.29	AntisenseIntron									
CONGO_chr17_002065518_127_m1	chr17	2065518	2065644	-	1	127	18.81	NCExon					1				
CONGO_chr17_002561606_100_m0	chr17	2561606	2561705	-	0	100	61.7	UTR					1	TU583	SpliceToPCG	ENSG00000132361	
CONGO_chr17_002620373_117_p1	chr17	2620373	2620489	+	1	117	1297.49	Intergenic									
CONGO_chr17_002704040_107_p0	chr17	2704040	2704146	+	0	107	177.27	Intron						TU584	SpliceToPCG	ENSG00000132359	
CONGO_chr17_003003934_438_m0	chr17	3003934	3004371	-	0	438	2419.78	Intergenic		7tm_1							
CONGO_chr17_003004453_425_m2	chr17	3004453	3004877	-	2	425	1915.12	Intergenic		7tm_1							
CONGO_chr17_003091260_287_p0	chr17	3091260	3091546	+	0	287	1123.59	UTR	1		1						
CONGO_chr17_003115688_414_p0	chr17	3115688	3116101	+	0	414	1146.87	Intergenic		7tm_1							
CONGO_chr17_003116149_332_p0	chr17	3116149	3116480	+	0	332	982.92	Intergenic		7tm_1							
CONGO_chr17_003161813_166_p1	chr17	3161813	3161978	+	1	166	847.9	Intergenic									
CONGO_chr17_003535554_70_m0	chr17	3535554	3535623	-	0	70	198.36	Intron		P2X_receptor			1	TU585	SpliceToPCG	ENSG00000083454	
CONGO_chr17_003662589_109_m1	chr17	3662589	3662697	-	1	109	3.73	UTR			1		1	TU586	SpliceToPCG	ENSG00000074356	
CONGO_chr17_004651542_143_m2	chr17	4651542	4651684	-	2	143	616.7	Intergenic					1	TU587	NovelMultiExon		
CONGO_chr17_004734299_87_p0	chr17	4734299	4734385	+	0	87	122.57	UTR			1		1	TU588	SpliceToPCG	ENSG00000141503	
CONGO_chr17_005325335_93_p0	chr17	5325335	5325427	+	0	93	443.47	AntisenseCDS			1			TU589	NovelMultiExon		
CONGO_chr17_006481223_74_m2	chr17	6481223	6481296	-	2	74	39.92	Intron									
CONGO_chr17_006483695_603_m0	chr17	6483695	6484297	-	0	603	1922.13	Intron									
CONGO_chr17_006501905_123_p1	chr17	6501905	6502027	+	1	123	107.93	Intergenic	1				1	TU66	SpliceToPCG	ENSG00000212734	
CONGO_chr17_006502797_161_p2	chr17	6502797	6502957	+	2	161	252.84	Intergenic	1	Lipoxygenase			1	TU66	NovelMultiExon		
CONGO_chr17_006503968_144_p0	chr17	6503968	6504111	+	0	144	5.54	Intergenic	1	Lipoxygenase			1	TU66	NovelMultiExon		
CONGO_chr17_006505247_210_p0	chr17	6505247	6505456	+	0	210	160.51	Intergenic	1	Lipoxygenase				TU66	NovelMultiExon		
CONGO_chr17_006738361_202_p0	chr17	6738361	6738562	+	0	202	161.37	NCExon		PLAT	1		1	TU590	NovelMultiExon		
CONGO_chr17_006738927_123_p1	chr17	6738927	6739049	+	1	123	167.9	NCExon			1		1	TU220	NovelMultiExon		
CONGO_chr17_006739409_138_p0	chr17	6739409	6739546	+	0	138	73.74	NCExon		Lipoxygenase	1		1	TU220	NovelMultiExon		
CONGO_chr17_006740359_144_p0	chr17	6740359	6740502	+	0	144	324.77	NCExon		Lipoxygenase	1		1	TU110	NovelMultiExon		
CONGO_chr17_006740657_150_p0	chr17	6740657	6740806	+	0	150	441.96	NCExon		Lipoxygenase	1		1	TU110	NovelMultiExon		
CONGO_chr17_006742572_114_p0	chr17	6742572	6742685	+	0	114	75.26	NCExon		Lipoxygenase	1		1	TU110	NovelMultiExon		
CONGO_chr17_006743434_100_p1	chr17	6743434	6743533	+	1	100	78.93	NCExon		Lipoxygenase	1		1	TU111	NovelMultiExon		
CONGO_chr17_006743636_168_p0	chr17	6743636	6743803	+	0	168	312.98	NCExon		Lipoxygenase	1		1	TU111	NovelMultiExon		
CONGO_chr17_006743911_122_p0	chr17	6743911	6744032	+	0	122	140.22	NCExon		Lipoxygenase	1		1	TU111	NovelMultiExon		
CONGO_chr17_007272999_85_p1	chr17	7272999	7273083	+	1	85	117.97	Intergenic						TU112	SpliceToPCG	ENSG00000181284	
CONGO_chr17_007274858_175_p1	chr17	7274858	7275032	+	1	175	264.06	Intergenic						TU112	SpliceToPCG	ENSG00000181284	
CONGO_chr17_007276458_239_p0	chr17	7276458	7276696	+	0	239	272.73	Intergenic						TU112	SpliceToPCG	ENSG00000169992	
CONGO_chr17_008188962_124_p0	chr17	8188962	8189085	+	0	124	19.61	Intron						TU591	SpliceToPCG	ENSG00000184650	
CONGO_chr17_008872593_163_p1	chr17	8872593	8872755	+	1	163	10.01	Intron									
CONGO_chr17_010647793_213_m0	chr17	10647793	10648005	-	0	213	793.92	NCExon			1		1	TU592	SpliceToNCG	ENSG00000205351	
CONGO_chr17_014145339_111_p0	chr17	14145339	14145449	+	0	111	110.41	UTR			1			TU594	SpliceToPCG	ENSG00000125430	
CONGO_chr17_016982312_157_p2	chr17	16982312	16982468	+	2	157	774.77	Intron					1	TU595	SpliceToPCG	ENSG00000133030	
CONGO_chr17_017967283_150_p0	chr17	17967283	17967432	+	0	150	687.43	Intron			1						
CONGO_chr17_019459693_109_p0	chr17	19459693	19459801	+	0	109	852.2	Intergenic		MatE				TU596	SpliceToNCG	ENSG00000243820	
CONGO_chr17_019468778_70_p1	chr17	19468778	19468847	+	1	70	337.64	Intergenic									
CONGO_chr17_019469746_133_p0	chr17	19469746	19469878	+	0	133	781.26	Intergenic		MatE							
CONGO_chr17_019474572_95_p2	chr17	19474572	19474666	+	2	95	355.13	NCExon					1	TU113	SpliceToNCG	ENSG00000231625	
CONGO_chr17_019476602_55_p0	chr17	19476602	19476656	+	0	55	71.42	NCExon					1	TU113	SpliceToNCG	ENSG00000231625	
CONGO_chr17_019476966_185_p2	chr17	19476966	19477150	+	2	185	354.36	NCExon					1	TU113	SpliceToNCG	ENSG00000231625	
CONGO_chr17_022659757_79_p1	chr17	22659757	22659835	+	1	79	9.11	UTR			1		1	TU597	SpliceToPCG	ENSG00000109046	
CONGO_chr17_022807827_201_p0	chr17	22807827	22808027	+	0	201	561.13	Intergenic	1				1	TU222	SpliceToPCG	ENSG00000141068	
CONGO_chr17_022917610_117_p0	chr17	22917610	22917726	+	0	117	161.07	Intron									
CONGO_chr17_022972346_82_p1	chr17	22972346	22972427	+	1	82	181.38	Intron					1	TU222	SpliceToPCG	ENSG00000141068	
CONGO_chr17_023100937_111_p0	chr17	23100937	23101047	+	0	111	211.62	Intergenic	1	Gal-bind_lectin			1				
CONGO_chr17_023105749_89_p0	chr17	23105749	23105837	+	0	89	41.4	Intergenic	1	Gal-bind_lectin							
CONGO_chr17_023144741_107_m0	chr17	23144741	23144847	-	0	107	195.23	Intron					1				
CONGO_chr17_023385585_30_m2	chr17	23385585	23385614	-	2	30	51	Intergenic									
CONGO_chr17_024068473_381_m0	chr17	24068473	24068853	-	0	381	1632.66	UTR			1		1	TU598	SpliceToPCG	ENSG00000109113	
CONGO_chr17_024302611_142_m1	chr17	24302611	24302752	-	1	142	57.74	UTR			1		1	TU599	SpliceToPCG	ENSG00000109118	
CONGO_chr17_024371359_85_p1	chr17	24371359	24371443	+	1	85	10.88	Intergenic									

CONGO_chr17_024430875_1270_m1	chr17	24430875	24432144	-	1	1270	9466.29	Intron					1	TU67	SpliceToPCG	ENSG00000196535
CONGO_chr17_024477037_75_m0	chr17	24477037	24477111	-	0	75	29.42	Intron					1	TU67	SpliceToPCG	ENSG00000196535
CONGO_chr17_024479219_432_m1	chr17	24479219	24479650	-	1	432	1582.74	UTR			1		1	TU67	SpliceToPCG	ENSG00000196535
CONGO_chr17_024482527_60_m0	chr17	24482527	24482586	-	0	60	190.23	Intron					1	TU67	SpliceToPCG	ENSG00000196535
CONGO_chr17_024638477_59_p2	chr17	24638477	24638535	+	2	59	147	AntisenseCDS					1	TU600	NovelMultiExon	
CONGO_chr17_027573891_144_p1	chr17	27573891	27574034	+	1	144	310.79	Intron						TU601	SpliceToPCG	ENSG00000126858
CONGO_chr17_027729047_66_p0	chr17	27729047	27729112	+	0	66	32.37	UTR			1		1	TU602	SpliceToPCG	ENSG00000010244
CONGO_chr17_031975581_80_p2	chr17	31975581	31975660	+	2	80	89.7	UTR			1		1	TU603	SpliceToPCG	ENSG00000005955
CONGO_chr17_032384498_110_m2	chr17	32384498	32384607	-	2	110	646.1	AntisenseCDS					1	TU604	NovelMultiExon	
CONGO_chr17_032410584_167_m0	chr17	32410584	32410750	-	0	167	129.82	AntisenseIntron								
CONGO_chr17_032424328_138_m0	chr17	32424328	32424465	-	0	138	29.64	AntisenseIntron								
CONGO_chr17_032534210_106_p1	chr17	32534210	32534315	+	1	106	93.11	AntisenseIntron								
CONGO_chr17_032540993_93_p0	chr17	32540993	32541085	+	0	93	1.52	AntisenseIntron								
CONGO_chr17_032601474_81_p1	chr17	32601474	32601554	+	1	81	80.62	AntisenseIntron								
CONGO_chr17_033618861_122_m2	chr17	33618861	33618982	-	2	122	193.8	NCExon	1	Peptidase_M1	1		1	TU114	NovelMultiExon	
CONGO_chr17_033628903_78_m2	chr17	33628903	33628980	-	2	78	186.96	NCExon	1		1		1	TU114	NovelMultiExon	
CONGO_chr17_033652033_85_m0	chr17	33652033	33652117	-	0	85	211.3	NCExon	1		1		1	TU114	NovelMultiExon	
CONGO_chr17_033955035_186_m0	chr17	33955035	33955220	-	0	186	341.88	Intron					1	TU605	SpliceToPCG	ENSG00000017373
CONGO_chr17_034005846_63_m2	chr17	34005846	34005908	-	2	63	217.42	Intron								
CONGO_chr17_034335473_78_p0	chr17	34335473	34335550	+	0	78	248.26	NCExon			1		1	TU606	NovelMultiExon	
CONGO_chr17_034647610_83_p0	chr17	34647610	34647692	+	0	83	106.68	Intron						TU607	SpliceToPCG	ENSG00000223399
CONGO_chr17_034972746_181_m1	chr17	34972746	34972926	-	1	181	18.48	Intergenic								
CONGO_chr17_035017615_157_p1	chr17	35017615	35017771	+	1	157	34.76	AntisenseUTR								
CONGO_chr17_035109664_137_m1	chr17	35109664	35109800	-	1	137	27.23	AntisenseUTR								
CONGO_chr17_035541016_62_m0	chr17	35541016	35541077	-	0	62	208.01	AntisenseUTR							NovelUnspliced	
CONGO_chr17_035722243_100_p1	chr17	35722243	35722342	+	1	100	35.72	Intron								
CONGO_chr17_036569744_196_m1	chr17	36569744	36569939	-	1	196	97.88	UTR		Keratin_B2	1					
CONGO_chr17_036622729_208_p2	chr17	36622729	36622936	+	2	208	293.82	Intron								
CONGO_chr17_037036568_50_m1	chr17	37036568	37036617	-	1	50	155.08	NCExon	1		1			TU223	SpliceToNCG	ENSG00000214514
CONGO_chr17_037043650_99_m0	chr17	37043650	37043748	-	0	99	53.54	NCIntron								
CONGO_chr17_037422966_222_m2	chr17	37422966	37423187	-	2	222	91.55	UTR			1		1	TU609	SpliceToPCG	ENSG00000168259
CONGO_chr17_037445249_771_m0	chr17	37445249	37446019	-	0	771	2854.17	Intron								
CONGO_chr17_037446047_687_m0	chr17	37446047	37446733	-	0	687	1428.35	Intron					1			
CONGO_chr17_037448378_190_m1	chr17	37448378	37448567	-	1	190	288.18	Intron					1			
CONGO_chr17_037448611_310_m0	chr17	37448611	37448920	-	0	310	766.92	Intron					1			
CONGO_chr17_037908338_75_p0	chr17	37908338	37908412	+	0	75	85.07	Intron					1	TU610	SpliceToPCG	ENSG00000033627
CONGO_chr17_038277948_286_p2	chr17	38277948	38278233	+	2	286	779.8	Intergenic		Cu_amine_oxid			1	TU115	SpliceToPCG	ENSG00000131467
CONGO_chr17_038278936_130_p1	chr17	38278936	38279065	+	1	130	347.49	Intergenic		Cu_amine_oxid			1	TU115	SpliceToPCG	ENSG00000131467
CONGO_chr17_038279637_189_p0	chr17	38279637	38279825	+	0	189	628.9	Intergenic		Cu_amine_oxid			1	TU115	SpliceToPCG	ENSG00000131467
CONGO_chr17_038736027_105_m0	chr17	38736027	38736131	-	0	105	423.66	NCExon			1		1	TU611	SpliceToNCG	ENSG00000236383
CONGO_chr17_038975865_76_m0	chr17	38975865	38975940	-	0	76	19.76	Intron								
CONGO_chr17_039371122_170_p0	chr17	39371122	39371291	+	0	170	150.21	Intergenic					1	TU612	NovelMultiExon	
CONGO_chr17_039499410_134_p1	chr17	39499410	39499543	+	1	134	48.61	AntisenseCDS					1		UnsplicedMergeWithPCG	ENSG00000161654
CONGO_chr17_039871408_202_m0	chr17	39871408	39871609	-	0	202	27.45	UTR			1		1	TU613	SpliceToPCG	ENSG00000186566
CONGO_chr17_040113493_45_p0	chr17	40113493	40113537	+	0	45	25.83	AntisenseCDS			1		1			
CONGO_chr17_040843381_57_m0	chr17	40843381	40843437	-	0	57	64.55	UTR			1		1	TU615	SpliceToPCG	ENSG00000159314
CONGO_chr17_040948349_153_m2	chr17	40948349	40948501	-	2	153	69.02	UTR	1		1		1	TU616	SpliceToPCG	ENSG00000214420
CONGO_chr17_043414788_99_p0	chr17	43414788	43414886	+	0	99	20.16	Intergenic								
CONGO_chr17_043486618_163_p1	chr17	43486618	43486780	+	1	163	26.48	Intron					1	TU618	SpliceToPCG	ENSG00000082641
CONGO_chr17_043581913_102_p2	chr17	43581913	43582014	+	2	102	60.5	AntisenseIntron								
CONGO_chr17_043585696_130_m0	chr17	43585696	43585825	-	0	130	102.22	Intron								
CONGO_chr17_043593092_83_p2	chr17	43593092	43593174	+	2	83	23.16	AntisenseIntron								
CONGO_chr17_043610956_63_m2	chr17	43610956	43611018	-	2	63	80.51	Intron								
CONGO_chr17_043726700_118_m1	chr17	43726700	43726817	-	1	118	39.46	AntisenseNCExon								
CONGO_chr17_043987892_88_m1	chr17	43987892	43987979	-	1	88	16.13	UTR			1		1	TU619	SpliceToPCG	ENSG00000108511
CONGO_chr17_044287194_75_p0	chr17	44287194	44287268	+	0	75	34.35	Intron						TU620	SpliceToPCG	ENSG00000136436
CONGO_chr17_046183648_114_m0	chr17	46183648	46183761	-	0	114	39.86	AntisenseUTR					1		UnsplicedMergeWithPCG	ENSG00000108848
CONGO_chr17_046500292_81_m0	chr17	46500292	46500372	-	0	81	277.65	Intron					1	TU621	SpliceToPCG	ENSG00000008294
CONGO_chr17_046618385_184_m0	chr17	46618385	46618568	-	0	184	103.73	Intron			1			TU622	SpliceToPCG	ENSG00000011258
CONGO_chr17_050943419_276_m0	chr17	50943419	50943694	-	0	276	1635.86	Intergenic								
CONGO_chr17_051394422_110_p0	chr17	51394422	51394531	+	0	110	464.13	Intergenic								
CONGO_chr17_051397939_98_p1	chr17	51397939	51398036	+	1	98	262.11	Intergenic								
CONGO_chr17_051478599_61_p0	chr17	51478599	51478659	+	0	61	213.51	Intergenic								
CONGO_chr17_053437396_54_p1	chr17	53437396	53437449	+	1	54	36.92	AntisenseUTR					1	TU623	NovelMultiExon	
CONGO_chr17_054785465_33_m0	chr17	54785465	54785497	-	0	33	104.01	AntisenseUTR								
CONGO_chr17_056264448_96_m2	chr17	56264448	56264543	-	2	96	24.12	AntisenseIntron								
CONGO_chr17_056577258_164_m0	chr17	56577258	56577421	-	0	164	136.56	AntisenseIntron								
CONGO_chr17_056768309_118_m0	chr17	56768309	56768426	-	0	118	23.61	AntisenseIntron								
CONGO_chr17_056799096_104_m0	chr17	56799096	56799199	-	0	104	28.94	AntisenseIntron								
CONGO_chr17_057679149_148_m0	chr17	57679149	57679296	-	0	148	70.99	Intergenic	1					TU624	NovelMultiExon	
CONGO_chr17_057740518_54_p2	chr17	57740518	57740571	+	2	54	56.19	Intergenic								
CONGO_chr17_057741035_105_p2	chr17	57741035	57741139	+	2	105	162.78	Intergenic								
CONGO_chr17_057772215_105_p2	chr17	57772215	57772319	+	2	105	178	Intergenic								
CONGO_chr17_057772981_54_p2	chr17	57772981	57773034	+	2	54	61.64	Intergenic								
CONGO_chr17_057781764_105_p2	chr17	57781764	57781868	+	2	105	184.26	Intergenic								
CONGO_chr17_057800263_54_p2	chr17	57800263	57800316	+	2	54	151.72	Intergenic								
CONGO_chr17_058181296_254_m0	chr17	58181296	58181549	-	0	254	1496.45	Intron						TU225	SpliceToPCG	ENSG00000173838
CONGO_chr17_058181559_71_m2	chr17	58181559	58181629	-	2	71	117.5	Intron						TU225	SpliceToPCG	ENSG00000173838
CONGO_chr17_058530342_109_p0	chr17	58530342	58530450	+	0	109	299.85	Intron					1	TU226	SpliceToPCG	ENSG00000170921
CONGO_chr17_058582363_111_p2	chr17	58582363	58582473	+	2	111	256.63	Intron			1		1	TU226	SpliceToPCG	ENSG00000170921
CONGO_chr17_059927361_95_p2	chr17	59927361	59927455	+	2	95	48.82	AntisenseIntron					1	TU116	UnsplicedMergeWithPCG	ENSG00000108654
CONGO_chr17_059927883_80_p2	chr17	59927883	59927962	+	2	80	145.04	AntisenseIntron					1	TU116	NovelMultiExon	
CONGO_chr17_059928347_163_p1	chr17	59928347	59928509	+	1	163	3.95	AntisenseIntron					1	TU116	NovelMultiExon	
CONGO_chr17_060176496_93_m0	chr17	60176496	60176588	-	0	93	27.63	UTR	1		1		1	TU68	SpliceToPCG	ENSG00000215769
CONGO_chr17_060178387_150_m0	chr17	60178387	60178536	-	0	150	589.47	UTR	1		1		1	TU68	SpliceToPCG	ENSG00000215769
CONGO_chr17_060188496_132_m1	chr17	60188496	60188627	-	1	132	25.95	UTR	1		1		1	TU68	SpliceToPCG	ENSG00000215769
CONGO_chr17_060188935_356_m0	chr17	60188935	60189290	-	0	356	495.76	UTR	1		1		1	TU68	SpliceToPCG	ENSG00000215769
CONGO_chr17_060380257_397_p0	chr17	60380257	60380653	+	0	397	1109.12	Intergenic	1				1			
CONGO_chr17_060394898_64_m0	chr17	60394898	60394961	-	0	64	34.78	NCExon	1		1		1	TU33	SpliceToNCG	ENSG00000214174
CONGO_chr17_060395895_121_m1	chr17	60395895	60396015	-	1	121	402.53	NCIntron	1				1	TU33	SpliceToNCG	ENSG00000214174
CONGO_chr17_060399114_129_m2	chr17	60399114	60399242	-	2	129	332.07	NCExon	1		1		1	TU33	SpliceToNCG	ENSG00000214174
CONGO_chr17_060399334_155_m1	chr17	60399334	60399488	-	1	155	575.4	NCExon	1		1		1	TU33	SpliceToNCG	ENSG00000214174
CONGO_chr17_060399822_111_m2	chr17	60399822	60399932	-	2	111	125.14	NCExon	1		1		1	TU33	SpliceToNCG	ENSG00000214174
CONGO_chr17_060399965_133_m0	chr17	60399965	60400097	-	0	133	336.38	NCExon	1		1		1	TU33	SpliceToNCG	ENSG00000214174
CONGO_chr17_061312631_93_m0	chr17	61312631	61312723	-	0	93	31.13	Intron						TU625	SpliceToPCG	ENSG00000154240
CONGO_chr17_062223028_48_p0	chr17	62223028	62223075	+	0	48	166.18	Intron						TU626	SpliceToPCG	ENSG00000154229
CONGO_chr17_063355518_181_p0	chr17	63355518	63355698	+	0	181	292.97	Intron	1				1	TU627	SpliceToPCG	ENSG00000171634
CONGO_chr17_063420002_484_m0	chr17	63420002	63420485	-	0	484	2.62	UTR	1		1		1	TU229	SpliceToPCG	ENSG00000186665
CONGO_chr17_063422701_76_m0	chr17	63422701	63422776	-	0	76	239.89	AntisenseNCIntron	1					TU229	NovelMultiExon	
CONGO_chr17_064922381_129_m2	chr17	64922381	64922509	-	2	129	80.65	AntisenseUTR								
CONGO_chr17_064922893_121_p2	chr17	64922893	64923013	+	2	121	144.25	Intron								
CONGO_chr17_065676499_95_p2	chr17	65676499	65676593	+	2	95	17.81	UTR			1		1		NovelUnspliced	
CONGO_chr17_066512017_61_m0	chr17	66512017	66512077	-	0	61	14.4	Intergenic								
CONGO_chr17_066948172_70_p1	chr17	66948172	66948241	+	1	70	29.94	Intergenic								
CONGO_chr17_067002298_59_m2	chr17	67002298	67002356	-	2	59	22.08	Intergenic								
CONGO_chr17_067019478_123_p2	chr17	67019478	67019600	+	2	123	38.56	Intergenic								
CONGO_chr17_071095773_151_p0	chr17	71095773	71095923	+	0	151	55.62	UTR			1					
CONGO_chr17_071098302_64_p1	chr17	71098302	71098365	+	1	64	10.56	UTR			1		1	TU117	SpliceToPCG	ENSG00000188126
CONGO_chr17_071098583_110_p0	chr17	71098583	71098692	+	0	110	198.5	UTR			1		1	TU117	SpliceToPCG	ENSG00000188126
CONGO_chr17_071100104_114_p0	chr17	71100104	71100217	+	0	114	537.28	UTR		Myosin_head	1		1	TU117	SpliceToPCG	ENSG00000188126
CONGO_chr17_071443308_42_m2	chr17	71443308	71443349	-	2	42	234.5	Intron			1		1	TU629	SpliceToPCG	ENSG00000188878
CONGO_chr17_071815306_369_m0	chr17	71815306	71815674	-	0	369	594.69	UTR			1			TU630	SpliceToPCG	ENSG00000129646
CONGO_chr17_072076639_682_m1	chr17	72076639	72077320	-	1	682	3002.05	Intron			1					
CONGO_chr17_072243449_104_m2	chr17	72243449	72243552	-	2	104	113.81	UTR			1		1	TU631	SpliceToPCG	ENSG00000161547
CONGO_chr17_073100363_134_p2	chr17	73100363	73100496	+	2	134	110.21	Intergenic								
CONGO_chr17_073465178_90_p0	chr17	73465178	73465267	+	0	90	13.45	Intergenic								
CONGO_chr17_073511846_100_p1	chr17	73511846	73511945	+	1	100	151.94	UTR			1		1	TU118	SpliceToPCG	ENSG00000078687
CONGO_chr17_073512697_59_p1	chr17	73512697	73512755	+	1	59	31.96	UTR			1		1	TU118	SpliceToPCG	ENSG00000078687
CONGO_chr17_073539192_327_p2	chr17	73539192	73539518	+	2	327	1516.24	UTR			1		1	TU118	SpliceToPCG	ENSG00000078687
CONGO_chr17_073741571_81_p2	chr17	73741571	73741651	+	2	81	13.96	Intron					1	TU632	SpliceToPCG	ENSG00000204278
CONGO_chr17_074314813_161_p1	chr17	74314813	74314973	+	1	161	105.78	AntisenseCDS								
CONGO_chr17_076709655_351_p1	chr17	76709655	76710005	+	1	351	949.21	AntisenseCDS								
CONGO_chr17_076770365_104_m0	chr17	76770365	76770468	-	0	104	24.9	AntisenseNCExon								
CONGO_chr17_076983884_147_p0	chr17	76983884	76984030	+	0	147	11.95	Intergenic								
CONGO_chr18_003486448_57_m0	chr18	3486448	3486504	-	0	57	29.06	UTR			1			TU634	SpliceToPCG	ENSG00000170579

CONGO_chr18_003864614_93_m0	chr18	3864614	3864706	-	0	93	4.54	NCExon			1	1	TU635	SpliceToPCG	ENSG00000170579
CONGO_chr18_005388650_735_m0	chr18	5388650	5389384	-	0	735	5337.33	Intron			1		TU69	SpliceToPCG	ENSG00000082397
CONGO_chr18_005390496_99_m0	chr18	5390496	5390594	-	0	99	9.6	Intron			1	1	TU69	SpliceToPCG	ENSG00000082397
CONGO_chr18_005390968_75_m0	chr18	5390968	5391042	-	0	75	104.1	Intron			1	1	TU69	SpliceToPCG	ENSG00000082397
CONGO_chr18_005397436_66_m0	chr18	5397436	5397501	-	0	66	77.46	Intron					TU69	SpliceToPCG	ENSG00000082397
CONGO_chr18_008112240_75_p2	chr18	8112240	8112314	+	2	75	104.13	Intron			1	1	TU230	SpliceToPCG	ENSG00000173482
CONGO_chr18_008361758_51_p0	chr18	8361758	8361808	+	0	51	117.71	Intron				1	TU230	SpliceToPCG	ENSG00000173482
CONGO_chr18_010698273_165_m1	chr18	10698273	10698437	-	1	165	837.9	Intron				1			
CONGO_chr18_010725230_99_m0	chr18	10725230	10725328	-	0	99	378.16	Intron							
CONGO_chr18_012449754_174_m0	chr18	12449754	12449927	-	0	174	486.18	NCExon				1	TU636	SpliceToPCG	ENSG00000134278
CONGO_chr18_020490614_64_m1	chr18	20490614	20490677	-	1	64	54.62	AntisenseNCIntron							
CONGO_chr18_020815478_91_p1	chr18	20815478	20815568	+	1	91	117.11	Intergenic							
CONGO_chr18_020895562_98_m2	chr18	20895562	20895659	-	2	98	10.51	Intergenic							
CONGO_chr18_020911972_105_m0	chr18	20911972	20912076	-	0	105	61.99	Intron							
CONGO_chr18_020924158_125_m0	chr18	20924158	20924282	-	0	125	241.66	Intron							
CONGO_chr18_020946704_116_p2	chr18	20946704	20946819	+	2	116	109.03	AntisenseIntron							
CONGO_chr18_020974330_72_p1	chr18	20974330	20974401	+	1	72	9.3	AntisenseIntron							
CONGO_chr18_021023500_109_m2	chr18	21023500	21023608	-	2	109	4.77	Intron							
CONGO_chr18_021023981_91_p0	chr18	21023981	21024071	+	0	91	100.55	AntisenseIntron							
CONGO_chr18_021119077_101_p0	chr18	21119077	21119177	+	0	101	38.11	AntisenseIntron							
CONGO_chr18_021119951_199_p1	chr18	21119951	21120149	+	1	199	3.23	AntisenseIntron							
CONGO_chr18_021121439_45_p2	chr18	21121439	21121483	+	2	45	0.56	AntisenseIntron							
CONGO_chr18_021352100_53_m2	chr18	21352100	21352152	-	2	53	107.71	Intergenic							
CONGO_chr18_021647947_89_p2	chr18	21647947	21648035	+	2	89	5.76	Intergenic							
CONGO_chr18_022491322_124_m0	chr18	22491322	22491445	-	0	124	107.49	Intergenic				1	TU637	SpliceToPCG	ENSG00000134504
CONGO_chr18_022491744_155_p2	chr18	22491744	22491898	+	2	155	5.16	Intergenic							
CONGO_chr18_022690086_83_m2	chr18	22690086	22690168	-	2	83	45.95	UTR			1	1	TU638	SpliceToPCG	ENSG00000171885
CONGO_chr18_025497696_95_p0	chr18	25497696	25497790	+	0	95	49.07	Intergenic							
CONGO_chr18_027152095_58_m0	chr18	27152095	27152152	-	0	58	99.31	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000134760
CONGO_chr18_028532389_61_p1	chr18	28532389	28532449	+	1	61	36.85	AntisenseIntron							
CONGO_chr18_028576813_92_p0	chr18	28576813	28576904	+	0	92	27.88	AntisenseIntron							
CONGO_chr18_029460960_73_p0	chr18	29460960	29461032	+	0	73	18.56	Intron				1	TU639	SpliceToPCG	ENSG00000141431
CONGO_chr18_029504179_68_m2	chr18	29504179	29504246	-	2	68	3.45	AntisenseIntron							
CONGO_chr18_030426946_64_p0	chr18	30426946	30427009	+	0	64	132.13	Intron							
CONGO_chr18_030724239_63_m1	chr18	30724239	30724301	-	1	63	62.79	AntisenseCDS				1		UnsplicedMergeWithPCG	ENSG00000134769
CONGO_chr18_032483277_90_p1	chr18	32483277	32483366	+	1	90	326.97	Intron					TU119	SpliceToPCG	ENSG00000134775
CONGO_chr18_032486766_125_p0	chr18	32486766	32486890	+	0	125	614.64	Intron					TU119	SpliceToPCG	ENSG00000134775
CONGO_chr18_032487303_75_p1	chr18	32487303	32487377	+	1	75	17.43	Intron					TU119	SpliceToPCG	ENSG00000134775
CONGO_chr18_033077715_106_p0	chr18	33077715	33077820	+	0	106	59.93	AntisenseUTR			1		TU641	UnsplicedMergeWithPCG	ENSG00000101489
CONGO_chr18_033218236_88_m1	chr18	33218236	33218323	-	1	88	26.52	Intron							
CONGO_chr18_033819070_116_m0	chr18	33819070	33819185	-	0	116	13.64	Intergenic							
CONGO_chr18_034893219_58_m1	chr18	34893219	34893276	-	1	58	49.83	Intergenic							
CONGO_chr18_035825679_53_p2	chr18	35825679	35825731	+	2	53	13.41	Intergenic							
CONGO_chr18_036432331_97_p2	chr18	36432331	36432427	+	2	97	84.4	Intergenic							
CONGO_chr18_037491358_138_m0	chr18	37491358	37491495	-	0	138	38.84	Intergenic							
CONGO_chr18_037555076_37_p2	chr18	37555076	37555112	+	2	37	19.9	Intergenic							
CONGO_chr18_037713412_102_p0	chr18	37713412	37713513	+	0	102	28.66	Intergenic							
CONGO_chr18_037720245_134_p2	chr18	37720245	37720378	+	2	134	15.43	Intergenic							
CONGO_chr18_039190830_364_p2	chr18	39190830	39191193	+	2	364	57.28	Intergenic							
CONGO_chr18_039191544_212_p2	chr18	39191544	39191755	+	2	212	177.12	Intergenic							
CONGO_chr18_042916823_57_p1	chr18	42916823	42916879	+	1	57	20.04	AntisenseIntron							
CONGO_chr18_042992458_63_m0	chr18	42992458	42992520	-	0	63	340.92	NCExon			1		TU642	NovelMultiExon	
CONGO_chr18_043447232_92_m2	chr18	43447232	43447323	-	2	92	40.15	Intergenic							
CONGO_chr18_049968082_124_m2	chr18	49968082	49968205	-	2	124	205.73	Intron				1	TU643	SpliceToPCG	ENSG00000134046
CONGO_chr18_050195604_96_p0	chr18	50195604	50195699	+	0	96	72.8	Intergenic							
CONGO_chr18_050196349_177_p0	chr18	50196349	50196525	+	0	177	295.69	Intergenic							
CONGO_chr18_051118688_202_p0	chr18	51118688	51118889	+	0	202	21.01	AntisenseIntron							
CONGO_chr18_051118971_110_m0	chr18	51118971	51119080	-	0	110	55.86	Intron							
CONGO_chr18_051212148_68_p2	chr18	51212148	51212215	+	2	68	65.48	AntisenseIntron							
CONGO_chr18_051219943_159_m0	chr18	51219943	51220101	-	0	159	89.72	Intron				1	TU231	SpliceToPCG	ENSG00000196628
CONGO_chr18_051348579_100_m1	chr18	51348579	51348678	-	1	100	5.66	Intron							
CONGO_chr18_051407940_138_m0	chr18	51407940	51408077	-	0	138	38.84	UTR			1	1	TU231	SpliceToPCG	ENSG00000196628
CONGO_chr18_054073853_209_p0	chr18	54073853	54074061	+	0	209	1178.38	Intron					TU47	SpliceToPCG	ENSG00000049759
CONGO_chr18_054074081_491_p0	chr18	54074081	54074571	+	0	491	3294.14	Intron					TU47	SpliceToPCG	ENSG00000049759
CONGO_chr18_054074588_399_p0	chr18	54074588	54074986	+	0	399	3632.81	Intron					TU47	SpliceToPCG	ENSG00000049759
CONGO_chr18_054169358_54_p2	chr18	54169358	54169411	+	2	54	131.09	Intron					TU47	SpliceToPCG	ENSG00000049759
CONGO_chr18_054214755_66_p2	chr18	54214755	54214820	+	2	66	57.96	UTR			1	1	TU47	SpliceToPCG	ENSG00000049759
CONGO_chr18_054683121_78_p1	chr18	54683121	54683198	+	1	78	13.85	UTR			1	1	TU644	SpliceToPCG	ENSG00000074657
CONGO_chr18_058050738_76_p0	chr18	58050738	58050813	+	0	76	36.54	Intron					TU646	SpliceToPCG	ENSG00000134444
CONGO_chr18_070486694_76_p1	chr18	70486694	70486769	+	1	76	11.23	Intron						NovelUnspliced	
CONGO_chr18_070742980_111_m0	chr18	70742980	70743090	-	0	111	174.08	AntisenseIntron							
CONGO_chr18_070846022_120_p0	chr18	70846022	70846141	+	0	120	60.5	Intron							
CONGO_chr18_071040779_111_m0	chr18	71040779	71040889	-	0	111	3.48	UTR			1		TU647	SpliceToPCG	ENSG00000180011
CONGO_chr18_071059201_102_p0	chr18	71059201	71059302	+	0	102	7.41	Intron							
CONGO_chr18_071071537_70_p2	chr18	71071537	71071606	+	2	70	3.45	Intron							
CONGO_chr18_071204198_130_p1	chr18	71204198	71204327	+	1	130	41.71	Intergenic							
CONGO_chr18_072054122_89_m0	chr18	72054122	72054210	-	0	89	74.19	Intergenic							
CONGO_chr18_072772011_182_p2	chr18	72772011	72772192	+	2	182	389.89	Intron							
CONGO_chr18_073626038_87_p0	chr18	73626038	73626124	+	0	87	122.03	Intergenic							
CONGO_chr18_074562943_152_m2	chr18	74562943	74563094	-	2	152	3.73	Intergenic							
CONGO_chr19_001018572_102_p0	chr19	1018572	1018673	+	0	102	73.9	UTR			1	1			
CONGO_chr19_003265759_96_p0	chr19	3265759	3265854	+	0	96	228.56	Intergenic							
CONGO_chr19_003434200_175_m0	chr19	3434200	3434374	-	0	175	679.78	Intergenic							
CONGO_chr19_003588534_78_m0	chr19	3588534	3588611	-	0	78	120.31	Intron			1		TU648	SpliceToPCG	ENSG00000186111
CONGO_chr19_004469234_68_m2	chr19	4469234	4469301	-	2	68	74.74	Intergenic					TU649	SpliceToPCG	ENSG00000167676
CONGO_chr19_005518676_260_m0	chr19	5518676	5518935	-	0	260	407.84	NCExon			1	1			
CONGO_chr19_005890522_72_m2	chr19	5890522	5890593	-	2	72	52.22	Intron							
CONGO_chr19_006156040_89_p0	chr19	6156040	6156128	+	0	89	242.37	Intergenic							
CONGO_chr19_006849318_150_p2	chr19	6849318	6849467	+	2	150	239.61	Intron	1				TU650	SpliceToPCG	ENSG00000174837
CONGO_chr19_007759682_105_p2	chr19	7759682	7759786	+	2	105	107.55	NCExon	1		1	1	TU120	NovelMultiExon	
CONGO_chr19_007760095_90_p2	chr19	7760095	7760184	+	2	90	67.56	NCExon	1		1	1	TU120	NovelMultiExon	
CONGO_chr19_007760646_86_p0	chr19	7760646	7760731	+	0	86	136.18	NCExon	1		1	1	TU120	NovelMultiExon	
CONGO_chr19_009162969_182_p2	chr19	9162969	9163150	+	2	182	17.1	Intergenic		7tm_1					
CONGO_chr19_009163644_191_p2	chr19	9163644	9163834	+	2	191	8.38	Intergenic							
CONGO_chr19_009206851_145_p2	chr19	9206851	9206995	+	2	145	151.38	Intergenic							
CONGO_chr19_009885159_135_m0	chr19	9885159	9885293	-	0	135	75.48	Intron				1	TU651	SpliceToPCG	ENSG00000105088
CONGO_chr19_011203861_105_m0	chr19	11203861	11203965	-	0	105	708.96	Intron			1	1	TU652	SpliceToPCG	ENSG00000130158
CONGO_chr19_012659863_93_p0	chr19	12659863	12659955	+	0	93	609.78	Intergenic			1	1			
CONGO_chr19_012660060_127_p1	chr19	12660060	12660186	+	1	127	306.69	Intergenic		G-gamma	1	1			
CONGO_chr19_012775918_200_p2	chr19	12775918	12776117	+	2	200	608.46	Intergenic					TU653	SpliceToPCG	ENSG00000104889
CONGO_chr19_013571567_123_m1	chr19	13571567	13571689	-	1	123	356.92	Intergenic				1			
CONGO_chr19_013903550_151_m1	chr19	13903550	13903700	-	1	151	816.34	UTR			1	1	TU233	SpliceToPCG	ENSG00000132000
CONGO_chr19_013903777_149_m0	chr19	13903777	13903925	-	0	149	721.35	UTR			1	1	TU233	SpliceToPCG	ENSG00000132000
CONGO_chr19_014084136_153_m0	chr19	14084136	14084288	-	0	153	89.31	Intron			1	1	TU654	SpliceToPCG	ENSG00000072062
CONGO_chr19_014823844_270_m0	chr19	14823844	14824113	-	0	270	234.36	Intergenic		7tm_1					
CONGO_chr19_014824487_239_m2	chr19	14824487	14824725	-	2	239	242.63	Intergenic		7tm_1					
CONGO_chr19_014863794_134_m2	chr19	14863794	14863927	-	2	134	168.32	Intergenic							
CONGO_chr19_014864112_505_m0	chr19	14864112	14864616	-	0	505	691.28	Intergenic		7tm_1					
CONGO_chr19_015370441_137_m1	chr19	15370441	15370577	-	1	137	60.79	NCExon			1	1	TU655	SpliceToPCG	ENSG00000011243
CONGO_chr19_015400017_303_m2	chr19	15400017	15400319	-	2	303	376.31	NCExon			1	1	TU234	SpliceToPCG	ENSG00000011451
CONGO_chr19_015414487_73_m2	chr19	15414487	15414559	-	2	73	79.34	Intron					TU234	SpliceToPCG	ENSG00000011451
CONGO_chr19_015535883_149_p1	chr19	15535883	15536031	+	1	149	432.1	Intergenic				1			
CONGO_chr19_015543545_145_p0	chr19	15543545	15543689	+	0	145	564.21	Intergenic				1			
CONGO_chr19_015545549_128_p2	chr19	15545549	15545676	+	2	128	712.51	Intergenic		p450					
CONGO_chr19_015547525_122_p0	chr19	15547525	15547646	+	0	122	423.28	Intergenic							
CONGO_chr19_015548385_262_p1	chr19	15548385	15548646	+	1	262	837.62	Intergenic		p450					
CONGO_chr19_015548984_67_p0	chr19	15548984	15549050	+	0	67	177.37	Intergenic							
CONGO_chr19_015549242_130_p2	chr19	15549242	15549371	+	2	130	652.91	Intergenic		p450					
CONGO_chr19_015555161_134_p1	chr19	15555161	15555294	+	1	134	357.66	Intergenic		p450		1			
CONGO_chr19_015555935_83_p0	chr19	15555935	15556017	+	0	83	186.21	Intergenic				1	TU656	SpliceToPCG	ENSG00000186529
CONGO_chr19_015556386_162_p0	chr19	15556386	15556547	+	0	162	275.31	Intergenic		p450		1			
CONGO_chr19_016024262_66_p1	chr19	16024262	16024327	+	1	66	2.14	Intergenic							
CONGO_chr19_016024344_177_p0	chr19	16024344	16024520	+	0	177	357.64	Intergenic							
CONGO_chr19_016699367_118_p0	chr19	16699367	16699484	+	0	118	525.51	Intron							
CONGO_chr19_017149606_90_p1	chr19	17149606	17149695	+	1	90	0.44	Intron				1	TU657	SpliceToPCG	ENSG00000099331

CONGO_chr19_017362322_147_m1	chr19	17362322	17362468	-	1	147	911.28	Intergenic								
CONGO_chr19_017363020_133_m2	chr19	17363020	17363152	-	2	133	568.19	Intergenic			1		TU658	SpliceToPCG	ENSG00000130303	
CONGO_chr19_017365644_324_m0	chr19	17365644	17365967	-	0	324	1677.34	Intron			1					
CONGO_chr19_017408267_114_m0	chr19	17408267	17408380	-	0	114	153.54	Intergenic				1	TU659	SpliceToPCG	ENSG00000188051	
CONGO_chr19_018082462_90_p1	chr19	18082462	18082551	+	1	90	344.29	Intron					TU660	SpliceToPCG	ENSG00000099308	
CONGO_chr19_018089976_89_p0	chr19	18089976	18090064	+	0	89	187.06	Intron					TU661	SpliceToPCG	ENSG00000099308	
CONGO_chr19_018208733_139_m0	chr19	18208733	18208871	-	0	139	247.62	UTR			1	1				
CONGO_chr19_018222122_161_m2	chr19	18222122	18222282	-	2	161	306.07	UTR			1	1	TU662	NovelMultiExon		
CONGO_chr19_035071899_71_m2	chr19	35071899	35071969	-	2	71	48.77	Intergenic								
CONGO_chr19_035533544_42_p0	chr19	35533544	35533585	+	0	42	88.35	Intergenic								
CONGO_chr19_035774817_132_p0	chr19	35774817	35774948	+	0	132	31.25	Intergenic								
CONGO_chr19_035893504_245_p2	chr19	35893504	35893748	+	2	245	1558.49	Intergenic					TU663	SpliceToPCG	ENSG00000198597	
CONGO_chr19_036031581_102_p0	chr19	36031581	36031682	+	0	102	31.13	Intergenic								
CONGO_chr19_036457616_56_p2	chr19	36457616	36457671	+	2	56	9.35	Intergenic								
CONGO_chr19_036499304_66_m0	chr19	36499304	36499369	-	0	66	22.25	Intron								
CONGO_chr19_038008990_114_p1	chr19	38008990	38009103	+	1	114	811.33	NCExon			1	1	TU70	SpliceToPCG	ENSG00000173809	
CONGO_chr19_038009191_154_p1	chr19	38009191	38009344	+	1	154	1195.18	NCExon			1	1	TU70	SpliceToPCG	ENSG00000173809	
CONGO_chr19_038009429_67_p0	chr19	38009429	38009495	+	0	67	734.87	NCExon			1	1	TU70	SpliceToPCG	ENSG00000173809	
CONGO_chr19_038009940_66_p2	chr19	38009940	38010005	+	2	66	158.16	NCExon			1		TU70	SpliceToPCG	ENSG00000173809	
CONGO_chr19_040415150_543_m0	chr19	40415150	40415692	-	0	543	1421.09	Intergenic								
CONGO_chr19_040769002_282_p0	chr19	40769002	40769283	+	0	282	352.86	Intergenic								
CONGO_chr19_040769763_114_p0	chr19	40769763	40769876	+	0	114	168.01	Intergenic								
CONGO_chr19_040950262_244_p1	chr19	40950262	40950505	+	1	244	211.81	Intron			1	1	TU664	SpliceToPCG	ENSG00000167595	
CONGO_chr19_040973063_194_m2	chr19	40973063	40973256	-	2	194	515.6	NCIntron								
CONGO_chr19_040973329_120_m2	chr19	40973329	40973448	-	2	120	405.64	NCExon			1					
CONGO_chr19_040973759_77_m0	chr19	40973759	40973835	-	0	77	124.85	NCExon			1					
CONGO_chr19_040974009_87_m1	chr19	40974009	40974095	-	1	87	98.61	NCExon			1	1				
CONGO_chr19_040974502_93_m1	chr19	40974502	40974594	-	1	93	185.14	NCExon			1	1				
CONGO_chr19_040975130_55_m0	chr19	40975130	40975184	-	0	55	164.27	NCExon			1	1				
CONGO_chr19_040975261_87_m0	chr19	40975261	40975347	-	0	87	115	NCIntron								
CONGO_chr19_040975815_115_m2	chr19	40975815	40975929	-	2	115	169.65	NCIntron								
CONGO_chr19_040979532_160_m0	chr19	40979532	40979691	-	0	160	443.47	NCIntron								
CONGO_chr19_041083184_62_m1	chr19	41083184	41083245	-	1	62	119.94	UTR			1	1	TU665	SpliceToPCG	ENSG00000167604	
CONGO_chr19_043012356_130_m2	chr19	43012356	43012485	-	2	130	269.95	AntisenseNCExon					TU48	SpliceToPCG	ENSG00000189144	
CONGO_chr19_043012564_261_m2	chr19	43012564	43012824	-	2	261	274.63	AntisenseNCExon		WD40			TU48	SpliceToPCG	ENSG00000189144	
CONGO_chr19_043013088_693_m1	chr19	43013088	43013780	-	1	693	1183.72	AntisenseNCExon					TU48	SpliceToPCG	ENSG00000189144	
CONGO_chr19_043013797_356_m1	chr19	43013797	43014152	-	1	356	666.59	AntisenseNCExon					TU48	SpliceToPCG	ENSG00000189144	
CONGO_chr19_043015827_130_m1	chr19	43015827	43015956	-	1	130	140.34	UTR			1	1	TU48	SpliceToPCG	ENSG00000189144	
CONGO_chr19_043893756_86_p2	chr19	43893756	43893841	+	2	86	53.76	NCExon				1	TU666	SpliceToPCG	ENSG00000130402	
CONGO_chr19_044056366_103_m0	chr19	44056366	44056468	-	0	103	270.48	UTR			1	1	TU235	SpliceToPCG	ENSG00000187994	
CONGO_chr19_044058811_144_m0	chr19	44058811	44058954	-	0	144	200.24	UTR			1	1	TU235	SpliceToPCG	ENSG00000187994	
CONGO_chr19_044091716_90_m0	chr19	44091716	44091805	-	0	90	577.4	Intergenic				1				
CONGO_chr19_044093043_200_m2	chr19	44093043	44093242	-	2	200	138.65	Intergenic				1				
CONGO_chr19_044093293_182_m0	chr19	44093293	44093474	-	0	182	133.77	Intergenic				1				
CONGO_chr19_044094046_88_m0	chr19	44094046	44094133	-	0	88	447.71	Intergenic				1				
CONGO_chr19_044094292_41_m2	chr19	44094292	44094332	-	2	41	198.72	Intergenic				1				
CONGO_chr19_044429613_99_m0	chr19	44429613	44429711	-	0	99	210.25	Intergenic	1							
CONGO_chr19_044429869_75_m0	chr19	44429869	44429943	-	0	75	3.49	Intergenic	1							
CONGO_chr19_044430188_144_m0	chr19	44430188	44430331	-	0	144	272.32	Intergenic	1							
CONGO_chr19_044430404_72_m0	chr19	44430404	44430475	-	0	72	204.37	Intergenic	1							
CONGO_chr19_044448199_99_p0	chr19	44448199	44448297	+	0	99	35.91	Intergenic	1							
CONGO_chr19_045420054_166_m1	chr19	45420054	45420219	-	1	166	442.07	UTR			1					
CONGO_chr19_045519023_75_m2	chr19	45519023	45519097	-	2	75	6.05	UTR			1	1	TU667	SpliceToPCG	ENSG00000105221	
CONGO_chr19_045605905_99_m0	chr19	45605905	45606003	-	0	99	142.77	UTR			1	1	TU668	SpliceToPCG	ENSG00000105227	
CONGO_chr19_045623357_39_p1	chr19	45623357	45623395	+	1	39	32.53	AntisenseIntron								
CONGO_chr19_046248194_182_m2	chr19	46248194	46248375	-	2	182	1135.42	Intergenic	1	p450						
CONGO_chr19_046249769_142_m0	chr19	46249769	46249910	-	0	142	1072.83	Intergenic	1	p450						
CONGO_chr19_046252947_142_m0	chr19	46252947	46253088	-	0	142	1680.76	Intergenic	1	p450		1				
CONGO_chr19_046254435_177_m0	chr19	46254435	46254611	-	0	177	1152.46	Intergenic	1	p450						
CONGO_chr19_046255191_161_m2	chr19	46255191	46255351	-	2	161	1113.73	Intergenic	1	p450						
CONGO_chr19_046257034_76_m0	chr19	46257034	46257109	-	0	76	692.18	Intergenic	1	p450						
CONGO_chr19_046259255_163_m0	chr19	46259255	46259417	-	0	163	1066.66	Intergenic	1	p450						
CONGO_chr19_046260010_93_m0	chr19	46260010	46260102	-	0	93	698.11	Intergenic	1	p450						
CONGO_chr19_047104220_449_m2	chr19	47104220	47104668	-	2	449	1007.99	AntisenseIntron				1	TU236	SpliceToPCG	ENSG00000105404	
CONGO_chr19_047105052_118_m0	chr19	47105052	47105169	-	0	118	268.18	AntisenseIntron				1	TU236	SpliceToPCG	ENSG00000105404	
CONGO_chr19_047312701_297_m0	chr19	47312701	47312997	-	0	297	1344.88	Intron				1				
CONGO_chr19_047356324_61_m1	chr19	47356324	47356384	-	1	61	30.05	Intergenic				1	TU669	SpliceToPCG	ENSG00000028277	
CONGO_chr19_047357951_96_p0	chr19	47357951	47358046	+	0	96	15.61	Intergenic								
CONGO_chr19_047467766_2504_p1	chr19	47467766	47470269	+	1	2504	19047.16	Intergenic					TU237	SpliceToPCG	ENSG00000079432	
CONGO_chr19_047470275_295_p0	chr19	47470275	47470569	+	0	295	2125.5	Intergenic				1	TU237	SpliceToPCG	ENSG00000079432	
CONGO_chr19_047519833_321_p0	chr19	47519833	47520153	+	0	321	577.69	Intron								
CONGO_chr19_048570367_141_m2	chr19	48570367	48570507	-	2	141	19.92	Intergenic	1				TU670	NovelMultiExon		
CONGO_chr19_050382429_111_p2	chr19	50382429	50382539	+	2	111	160.91	Intergenic				1	TU671	SpliceToPCG	ENSG00000189114	
CONGO_chr19_050429291_634_m2	chr19	50429291	50429924	-	2	634	968.3	UTR		Sec6	1		TU238	SpliceToPCG	ENSG00000130201	
CONGO_chr19_050433621_539_m1	chr19	50433621	50434159	-	1	539	2704.02	Intergenic				1	TU238	SpliceToPCG	ENSG00000130201	
CONGO_chr19_050957037_245_p0	chr19	50957037	50957281	+	0	245	922.26	Intergenic					TU122	SpliceToPCG	ENSG00000237452	
CONGO_chr19_050958436_90_p1	chr19	50958436	50958525	+	1	90	1046.08	Intergenic					TU122	SpliceToPCG	ENSG00000237452	
CONGO_chr19_050959069_144_p1	chr19	50959069	50959212	+	1	144	417.09	Intergenic					TU122	SpliceToPCG	ENSG00000237452	
CONGO_chr19_051622846_664_m2	chr19	51622846	51623509	-	2	664	1932.95	Intergenic					TU672	NovelMultiExon		
CONGO_chr19_051805441_49_p2	chr19	51805441	51805489	+	2	49	11.4	UTR			1		TU673	SpliceToPCG	ENSG00000160014	
CONGO_chr19_052305736_90_m0	chr19	52305736	52305825	-	0	90	156.32	Intron								
CONGO_chr19_052468454_104_p2	chr19	52468454	52468557	+	2	104	292.01	Intergenic					TU674	SpliceToPCG	ENSG00000105321	
CONGO_chr19_052865512_51_p0	chr19	52865512	52865562	+	0	51	79.21	UTR			1	1	TU675	SpliceToPCG	ENSG00000063169	
CONGO_chr19_053055217_135_p0	chr19	53055217	53055351	+	0	135	142.39	Intergenic		Homeobox	1					
CONGO_chr19_053391412_485_p2	chr19	53391412	53391896	+	2	485	2165.1	Intron					TU676	SpliceToPCG	ENSG00000185453	
CONGO_chr19_053446872_146_p0	chr19	53446872	53447017	+	0	146	177.87	AntisenseIntron		V1R						
CONGO_chr19_054213037_171_m0	chr19	54213037	54213207	-	0	171	622.67	Intergenic	1			1				
CONGO_chr19_054213942_128_m0	chr19	54213942	54214069	-	0	128	894.49	Intergenic	1			1				
CONGO_chr19_054214978_201_m0	chr19	54214978	54215178	-	0	201	306.23	Intergenic	1							
CONGO_chr19_054215444_141_m0	chr19	54215444	54215584	-	0	141	190.6	Intergenic	1							
CONGO_chr19_054298478_49_p2	chr19	54298478	54298526	+	2	49	89.44	UTR			1		TU677	SpliceToPCG	ENSG00000104852	
CONGO_chr19_054450549_118_m0	chr19	54450549	54450666	-	0	118	118.05	Intergenic								
CONGO_chr19_054450748_158_m2	chr19	54450748	54450905	-	2	158	912.22	Intergenic								
CONGO_chr19_054451082_82_m0	chr19	54451082	54451163	-	0	82	110.64	Intergenic		SNF						
CONGO_chr19_054534727_268_p0	chr19	54534727	54534994	+	0	268	50.74	UTR			1	1	TU678	SpliceToPCG	ENSG00000104894	
CONGO_chr19_054622578_105_p2	chr19	54622578	54622682	+	2	105	47.17	Intergenic				1				
CONGO_chr19_054623015_174_p2	chr19	54623015	54623188	+	2	174	555.81	Intergenic				1				
CONGO_chr19_054623688_200_p2	chr19	54623688	54623887	+	2	200	1036.39	Intergenic				1				
CONGO_chr19_055261355_99_m2	chr19	55261355	55261453	-	2	99	18.72	AntisenseUTR								
CONGO_chr19_055398711_30_p0	chr19	55398711	55398740	+	0	30	101.05	UTR			1	1	TU679	SpliceToPCG	ENSG00000105357	
CONGO_chr19_055661968_57_m0	chr19	55661968	55662024	-	0	57	114.57	UTR			1	1	TU680	SpliceToPCG	ENSG00000142530	
CONGO_chr19_055981011_60_m0	chr19	55981011	55981070	-	0	60	343.62	Intergenic			1	1	TU681	SpliceToPCG	ENSG00000167747	
CONGO_chr19_056003696_132_m2	chr19	56003696	56003827	-	2	132	316	Intergenic								
CONGO_chr19_056012996_110_p1	chr19	56012996	56013105	+	1	110	43.91	UTR			1	1	TU682	SpliceToPCG	ENSG00000180279	
CONGO_chr19_056406860_279_p2	chr19	56406860	56407138	+	2	279	130	Intergenic	1	ig		1	TU683	NovelMultiExon		
CONGO_chr19_056477554_105_p2	chr19	56477554	56477658	+	2	105	13.31	Intergenic								
CONGO_chr19_056477986_103_p2	chr19	56477986	56478088	+	2	103	139.26	Intergenic								
CONGO_chr19_056889543_78_p2	chr19	56889543	56889620	+	2	78	444.95	NCExon			1	1	TU72	SpliceToPCG	ENSG00000182310	
CONGO_chr19_056896723_69_p2	chr19	56896723	56896791	+	2	69	18.49	NCExon			1	1	TU72	SpliceToPCG	ENSG00000182310	
CONGO_chr19_056898086_78_p2	chr19	56898086	56898163	+	2	78	195.06	NCExon			1	1	TU72	SpliceToPCG	ENSG00000182310	
CONGO_chr19_056898293_110_p2	chr19	56898293	56898402	+	2	110	468.82	NCExon			1	1	TU72	SpliceToPCG	ENSG00000182310	
CONGO_chr19_057110171_672_m1	chr19	57110171	57110842	-	1	672	758.56	Intergenic		zf-C2H2						
CONGO_chr19_057112642_109_m0	chr19	57112642	57112750	-	0	109	20.26	Intergenic		KRAB						
CONGO_chr19_057848290_606_m2	chr19	57848290	57848895	-	2	606	420.92	Intron		zf-C2H2	1		TU684	SpliceToPCG	ENSG00000167766	
CONGO_chr19_057875361_127_m0	chr19	57875361	57875487	-	0	127	74.18	Intron		KRAB						
CONGO_chr19_058102060_458_m1	chr19	58102060	58102517	-	1	458	13.86	Intron		zf-C2H2			TU685	SpliceToPCG	ENSG00000180257	
CONGO_chr19_058799469_98_m0	chr19	58799469	58799566	-	0	98	619.15	Intergenic								
CONGO_chr19_058801199_97_m0	chr19	58801199	58801295	-	0	97	449.41	Intergenic								
CONGO_chr19_058801502_89_m0	chr19	58801502	58801590	-	0	89	375.18	Intergenic								
CONGO_chr19_058801619_122_m2	chr19	58801619	58801740	-	2	122	303.04	Intergenic								
CONGO_chr19_058802008_113_m1	chr19	58802008	58802120	-	1	113	629.56	Intergenic								
CONGO_chr19_058803333_181_m2	chr19	58803333	58803513	-	2	181	416.89	Intergenic								
CONGO_chr19_060666910_233_m0	chr19	60666910	60667142	-	0	233	595.28	Intergenic				1				
CONGO_chr19_060667561_173_m0	chr19	60667561	60667733	-	0	173	801.45	Intergenic				1				
CONGO_chr19_060819230_747_p0	chr19	60819230	60819976	+	0	747	5273.38	Intergenic		zf-C2H2				UnsplicedMergeWithPCG	ENSG00000227571	

CONGO_chr19_061447347_261_p0	chr19	61447347	61447607	+	0	261	561.95	AntisenseIntron		SCAN						
CONGO_chr19_061476043_58_p0	chr19	61476043	61476100	+	0	58	127.68	AntisenseIntron				1				
CONGO_chr19_061816992_127_p0	chr19	61816992	61817118	+	0	127	401.72	Intron		KRAB		1	TU686	SpliceToPCG	ENSG00000196867	
CONGO_chr19_061848848_169_p0	chr19	61848848	61849016	+	0	169	547.13	NCExon			1	1	TU123	NovelMultiExon		
CONGO_chr19_061850738_77_p2	chr19	61850738	61850814	+	2	77	371.91	NCExon			1	1	TU123	NovelMultiExon		
CONGO_chr19_061858283_111_p0	chr19	61858283	61858393	+	0	111	380.28	NCExon			1	1	TU123	NovelMultiExon		
CONGO_chr19_061964082_334_p1	chr19	61964082	61964415	+	1	334	1938.14	Intergenic				1				
CONGO_chr19_061996193_154_m0	chr19	61996193	61996346	-	0	154	129.89	Intron		SCAN						
CONGO_chr19_062755807_96_m2	chr19	62755807	62755902	-	2	96	123.87	AntisenseUTR			1	1	TU687	SpliceToPCG	ENSG00000105132	
CONGO_chr19_063522945_184_p0	chr19	63522945	63523128	+	0	184	28.28	Intergenic		zf-C2H2						
CONGO_chr19_063523139_270_p1	chr19	63523139	63523408	+	1	270	53.17	Intergenic		zf-C2H2						
CONGO_chr19_063784624_284_p0	chr19	63784624	63784907	+	0	284	939.91	NCExon			1	1	TU239	SpliceToPCG	ENSG00000213753	
CONGO_chr19_063785224_133_p2	chr19	63785224	63785356	+	2	133	0.27	NCExon			1	1	TU239	SpliceToPCG	ENSG00000213753	
CONGO_chr2_002314320_135_p0	chr2	2314320	2314454	+	0	135	24.35	Intergenic								
CONGO_chr2_011242256_91_m1	chr2	11242256	11242346	-	1	91	68.23	Intron					TU257	SpliceToPCG	ENSG00000134318	
CONGO_chr2_011254270_171_m2	chr2	11254270	11254440	-	2	171	527.81	Intron					TU257	SpliceToPCG	ENSG00000134318	
CONGO_chr2_011735225_81_p0	chr2	11735225	11735305	+	0	81	83.82	Intergenic			1	1				
CONGO_chr2_011771333_57_p0	chr2	11771333	11771389	+	0	57	641.58	Intergenic			1	1	TU830	SpliceToPCG	ENSG00000134324	
CONGO_chr2_016271744_106_m0	chr2	16271744	16271849	-	0	106	58.91	NCExon				1				
CONGO_chr2_016719091_72_m2	chr2	16719091	16719162	-	2	72	0.99	Intergenic								
CONGO_chr2_018821990_65_p0	chr2	18821990	18822054	+	0	65	15.18	Intergenic								
CONGO_chr2_019918705_81_p0	chr2	19918705	19918785	+	0	81	31.31	Intergenic								
CONGO_chr2_020388292_72_m2	chr2	20388292	20388363	-	2	72	62.87	Intron					TU831	SpliceToPCG	ENSG00000055917	
CONGO_chr2_021666512_64_p0	chr2	21666512	21666575	+	0	64	66.73	NCIntron								
CONGO_chr2_023512893_87_p0	chr2	23512893	23512979	+	0	87	67.71	Intron								
CONGO_chr2_023551935_108_p0	chr2	23551935	23552042	+	0	108	325.95	UTR				1	TU832	NovelMultiExon		
CONGO_chr2_023877818_54_m0	chr2	23877818	23877871	-	0	54	138.9	Intron					TU833	SpliceToPCG	ENSG00000119778	
CONGO_chr2_023904172_63_m1	chr2	23904172	23904234	-	1	63	1.4	UTR			1	1	TU834	SpliceToPCG	ENSG00000119778	
CONGO_chr2_027213287_118_m1	chr2	27213287	27213404	-	1	118	60.88	UTR			1		TU835	SpliceToPCG	ENSG00000186143	
CONGO_chr2_031965361_106_m2	chr2	31965361	31965466	-	2	106	59.64	Intron					TU836	SpliceToPCG	ENSG00000162959	
CONGO_chr2_036965167_87_m2	chr2	36965167	36965253	-	2	87	1.33	Intron					TU837	SpliceToPCG	ENSG00000115808	
CONGO_chr2_038956696_60_p2	chr2	38956696	38956755	+	2	60	85.09	UTR			1	1	TU258	SpliceToPCG	ENSG00000188010	
CONGO_chr2_038960824_51_p2	chr2	38960824	38960874	+	2	51	139.45	UTR			1	1	TU258	SpliceToPCG	ENSG00000188010	
CONGO_chr2_043544201_86_p2	chr2	43544201	43544286	+	2	86	21.05	AntisenseIntron								
CONGO_chr2_043986621_54_p0	chr2	43986621	43986674	+	0	54	21.67	AntisenseIntron								
CONGO_chr2_044660055_102_m1	chr2	44660055	44660156	-	1	102	92.58	AntisenseIntron								
CONGO_chr2_044698796_60_p0	chr2	44698796	44698855	+	0	60	17.39	Intron								
CONGO_chr2_044699132_131_m2	chr2	44699132	44699262	-	2	131	7.45	AntisenseIntron								
CONGO_chr2_044920737_134_p2	chr2	44920737	44920870	+	2	134	41.31	Intergenic								
CONGO_chr2_045003383_63_p0	chr2	45003383	45003445	+	0	63	18.77	AntisenseNCExon				1				
CONGO_chr2_047888167_131_m0	chr2	47888167	47888297	-	0	131	4.38	UTR			1	1	TU838	SpliceToPCG	ENSG00000138081	
CONGO_chr2_050427708_92_m0	chr2	50427708	50427799	-	0	92	18.29	UTR			1	1				
CONGO_chr2_053994512_61_m2	chr2	53994512	53994572	-	2	61	151.43	Intron			1		TU839	SpliceToPCG	ENSG00000068878	
CONGO_chr2_055362984_91_p1	chr2	55362984	55363074	+	1	91	625.97	NCExon			1		TU840	UnsplicedMergeWithNCG	ENSG00000162997	
CONGO_chr2_055364643_435_p0	chr2	55364643	55365077	+	0	435	1282.89	NCExon		YbaK	1			UnsplicedMergeWithNCG	ENSG00000162997	
CONGO_chr2_056460389_99_p0	chr2	56460389	56460487	+	0	99	242.24	Intron					TU841	SpliceToPCG	ENSG00000055813	
CONGO_chr2_057821673_133_p1	chr2	57821673	57821805	+	1	133	64.34	Intergenic								
CONGO_chr2_057840200_189_m0	chr2	57840200	57840388	-	0	189	26.54	Intergenic								
CONGO_chr2_057950491_189_p0	chr2	57950491	57950679	+	0	189	14.82	Intergenic								
CONGO_chr2_058040048_74_p1	chr2	58040048	58040121	+	1	74	181.88	Intron								
CONGO_chr2_058664347_59_p0	chr2	58664347	58664405	+	0	59	67.41	NCIntron								
CONGO_chr2_058711893_64_p2	chr2	58711893	58711956	+	2	64	0.41	NCIntron								
CONGO_chr2_058745511_100_m0	chr2	58745511	58745610	-	0	100	24.59	AntisenseNCIntron								
CONGO_chr2_058987360_87_p0	chr2	58987360	58987446	+	0	87	36.86	NCIntron								
CONGO_chr2_058987531_62_m2	chr2	58987531	58987592	-	2	62	3.43	AntisenseNCIntron								
CONGO_chr2_059375666_83_p2	chr2	59375666	59375748	+	2	83	13.91	AntisenseNCIntron								
CONGO_chr2_059395010_87_p1	chr2	59395010	59395096	+	1	87	51.73	AntisenseNCIntron								
CONGO_chr2_059745900_126_m0	chr2	59745900	59746025	-	0	126	99.22	NCIntron								
CONGO_chr2_059960181_51_m0	chr2	59960181	59960231	-	0	51	52.67	Intergenic								
CONGO_chr2_059990224_73_p0	chr2	59990224	59990296	+	0	73	0.53	Intergenic								
CONGO_chr2_060295302_161_p2	chr2	60295302	60295462	+	2	161	39.52	Intergenic								
CONGO_chr2_060615654_103_p1	chr2	60615654	60615756	+	1	103	97.16	AntisenseIntron								
CONGO_chr2_060625883_102_m0	chr2	60625883	60625984	-	0	102	55.9	Intron					TU842	SpliceToPCG	ENSG00000119866	
CONGO_chr2_060649197_83_p2	chr2	60649197	60649279	+	2	83	81.17	Intergenic								
CONGO_chr2_060728835_154_m1	chr2	60728835	60728988	-	1	154	41.13	Intergenic								
CONGO_chr2_061268219_101_p2	chr2	61268219	61268319	+	2	101	4.42	AntisenseUTR			1		TU843	SpliceToPCG	ENSG00000162929	
CONGO_chr2_061295004_94_p2	chr2	61295004	61295097	+	2	94	215.69	AntisenseCDS				1	TU844	NovelMultiExon		
CONGO_chr2_062177593_264_m2	chr2	62177593	62177856	-	2	264	74.28	AntisenseIntron		RVT_1						
CONGO_chr2_063075119_96_m0	chr2	63075119	63075214	-	0	96	31.55	AntisenseIntron								
CONGO_chr2_063131447_55_m2	chr2	63131447	63131501	-	2	55	0.55	AntisenseUTR								
CONGO_chr2_063515383_85_m1	chr2	63515383	63515467	-	1	85	5.86	Intron								
CONGO_chr2_064716069_85_m2	chr2	64716069	64716153	-	2	85	14.12	UTR			1		TU845	SpliceToPCG	ENSG00000179833	
CONGO_chr2_065153255_101_m2	chr2	65153255	65153355	-	2	101	139.3	AntisenseCDS				1	TU846	NovelMultiExon		
CONGO_chr2_065168939_81_p0	chr2	65168939	65169019	+	0	81	95.53	AntisenseUTR				1	TU847	SpliceToPCG	ENSG00000011523	
CONGO_chr2_065768833_100_m1	chr2	65768833	65768932	-	1	100	6.31	AntisenseNCIntron								
CONGO_chr2_066251524_108_p0	chr2	66251524	66251631	+	0	108	53.98	Intergenic								
CONGO_chr2_066515672_148_m0	chr2	66515672	66515819	-	0	148	58.07	AntisenseNCExon								
CONGO_chr2_066617761_74_p2	chr2	66617761	66617834	+	2	74	3.76	Intron								
CONGO_chr2_066652394_139_m1	chr2	66652394	66652532	-	1	139	26.87	AntisenseUTR				1		UnsplicedMergeWithPCG	ENSG00000143995	
CONGO_chr2_066746316_138_p2	chr2	66746316	66746453	+	2	138	73.02	NCExon				1	TU848	UnsplicedMergeWithNCG	ENSG00000232046	
CONGO_chr2_066772308_52_p2	chr2	66772308	66772359	+	2	52	45.54	NCExon				1	TU849	SpliceToNCG	ENSG00000232046	
CONGO_chr2_066776148_92_p0	chr2	66776148	66776239	+	0	92	47.49	NCExon			1	1		UnsplicedMergeWithNCG	ENSG00000232046	
CONGO_chr2_066778762_221_m2	chr2	66778762	66778982	-	2	221	62.92	NCIntron						NovelUnspliced		
CONGO_chr2_066924373_96_m0	chr2	66924373	66924468	-	0	96	33.63	Intergenic								
CONGO_chr2_066924605_100_m0	chr2	66924605	66924704	-	0	100	101.49	Intergenic								
CONGO_chr2_066931060_71_m0	chr2	66931060	66931130	-	0	71	28.51	Intergenic								
CONGO_chr2_067134931_101_p1	chr2	67134931	67135031	+	1	101	130.59	Intergenic								
CONGO_chr2_067135552_183_m2	chr2	67135552	67135734	-	2	183	76.84	Intergenic								
CONGO_chr2_067597057_120_p0	chr2	67597057	67597176	+	0	120	156.16	Intergenic								
CONGO_chr2_067806405_176_p2	chr2	67806405	67806580	+	2	176	17.78	Intergenic								
CONGO_chr2_068880586_95_p1	chr2	68880586	68880680	+	1	95	53.64	Intron					TU850	SpliceToPCG	ENSG00000163219	
CONGO_chr2_069005193_108_p0	chr2	69005193	69005300	+	0	108	118.63	Intergenic		BRICHOS						
CONGO_chr2_069006321_142_p0	chr2	69006321	69006462	+	0	142	218.1	Intergenic		BRICHOS						
CONGO_chr2_069007376_95_p2	chr2	69007376	69007470	+	2	95	298.75	Intergenic								
CONGO_chr2_070889569_138_m0	chr2	70889569	70889706	-	0	138	121.52	UTR		Lectin_C	1					
CONGO_chr2_071938553_38_m2	chr2	71938553	71938590	-	2	38	13.87	Intergenic								
CONGO_chr2_072415699_47_m2	chr2	72415699	72415745	-	2	47	39	Intron								
CONGO_chr2_073017273_100_p2	chr2	73017273	73017372	+	2	100	178.88	Intergenic					TU851	SpliceToPCG	ENSG00000135638	
CONGO_chr2_073160913_262_m1	chr2	73160913	73161174	-	1	262	45.81	Intron					TU259	SpliceToPCG	ENSG00000135631	
CONGO_chr2_073161261_408_m0	chr2	73161261	73161668	-	0	408	915.51	NCExon					TU259	SpliceToPCG	ENSG00000135631	
CONGO_chr2_073973579_108_p2	chr2	73973579	73973686	+	2	108	272.79	UTR			1	1	TU852	SpliceToPCG	ENSG00000163017	
CONGO_chr2_074067039_303_p0	chr2	74067039	74067341	+	0	303	2215.55	NCExon		zf-CXXC		1	TU853	SpliceToPCG	ENSG00000187605	
CONGO_chr2_074299262_166_m1	chr2	74299262	74299427	-	1	166	993.05	UTR			1		TU854	SpliceToPCG	ENSG00000188687	
CONGO_chr2_074507286_109_m2	chr2	74507286	74507394	-	2	109	336.68	Intron					TU855	SpliceToPCG	ENSG00000114993	
CONGO_chr2_083957184_360_m0	chr2	83957184	83957543	-	0	360	714.62	Intergenic	1	rve						
CONGO_chr2_085134278_207_m2	chr2	85134278	85134484	-	2	207	60.45	AntisenseUTR				1		UnsplicedMergeWithPCG	ENSG00000176407	
CONGO_chr2_085511172_115_p0	chr2	85511172	85511286	+	0	115	120.56	UTR			1					
CONGO_chr2_085625257_160_m0	chr2	85625257	85625416	-	0	160	13.78	AntisenseUTR	1			1	TU856	SpliceToPCG	ENSG00000115486	
CONGO_chr2_086300604_144_m0	chr2	86300604	86300747	-	0	144	363.94	Intron					TU857	SpliceToPCG	ENSG00000068615	
CONGO_chr2_086541413_53_p0	chr2	86541413	86541465	+	0	53	110.02	NCExon				1	TU858	SpliceToPCG	ENSG00000115548	
CONGO_chr2_088465606_190_p2	chr2	88465606	88465795	+	2	190	68.84	Intergenic								
CONGO_chr2_095241093_103_p0	chr2	95241093	95241195	+	0	103	343.92	NCExon				1	TU859	SpliceToNCG	ENSG00000233757	
CONGO_chr2_095244159_920_p2	chr2	95244159	95245078	+	2	920	6644.32	NCExon		zf-C2H2		1		UnsplicedMergeWithNCG	ENSG00000233757	
CONGO_chr2_095347321_115_p0	chr2	95347321	95347435	+	0	115	165.65	Intron								
CONGO_chr2_096683910_51_p0	chr2	96683910	96683960	+	0	51	182.3	UTR			1	1				
CONGO_chr2_096830536_63_p2	chr2	96830536	96830598	+	2	63	94.45	Intron					TU860	SpliceToPCG	ENSG00000158158	
CONGO_chr2_097684049_151_p2	chr2	97684049	97684199	+	2	151	447.54	NCExon			1	1	TU261	SpliceToNCG	ENSG00000228486	
CONGO_chr2_097685564_133_p1	chr2	97685564	97685696	+	1	133	57.31	NCExon			1	1	TU261	SpliceToNCG	ENSG00000228486	
CONGO_chr2_099093745_66_m0	chr2	99093745	99093810	-	0	66	93.24	UTR			1	1	TU262	SpliceToPCG	ENSG00000135951	
CONGO_chr2_099100439_216_m0	chr2	99100439	99100654	-	0	216	265.06	UTR			1	1	TU262	SpliceToPCG	ENSG00000135951	
CONGO_chr2_099414635_138_m1	chr2	99414635	99414772	-	1	138	17.84	NCExon				1	TU861	SpliceToPCG	ENSG00000135945	
CONGO_chr2_102915443_153_p0	chr2	102915443	102915595	+	0	153	89.24	Intergenic								
CONGO_chr2_103276274_159_p1	chr2	103276274	103276432	+	1	159	78.1	Intergenic								
CONGO_chr2_103726461_98_p1	chr2	103726461	103726558	+	1	98	26.42	Intergenic								
CONGO_chr2_104621550_169_m1	chr2	104621550	104621718	-	1	169	18.47	Intergenic								

CONGO_chr2_104622098_115_m1	chr2	104622098	104622212	-	1	115	39.54	Intergenic								
CONGO_chr2_104685635_92_m2	chr2	104685635	104685726	-	2	92	33.88	Intergenic								
CONGO_chr2_104884351_99_p2	chr2	104884351	104884449	+	2	99	5.67	Intergenic								
CONGO_chr2_104919596_60_m0	chr2	104919596	104919655	-	0	60	85.95	NCExon				1		UnsplicedMergeWithNCG	ENSG00000224509	
CONGO_chr2_105063996_74_p2	chr2	105063996	105064069	+	2	74	21.19	Intron								
CONGO_chr2_108312307_98_p2	chr2	108312307	108312404	+	2	98	224.6	NCExon		Sulfotransfer_1	1	1				
CONGO_chr2_108663857_148_p1	chr2	108663857	108664004	+	1	148	399.12	NCExon	1		1	1	TU862	SpliceToPCG	ENSG00000169756	
CONGO_chr2_108752148_78_p2	chr2	108752148	108752225	+	2	78	42.06	Intron	1			1	TU863	SpliceToPCG	ENSG00000153201	
CONGO_chr2_110327221_171_m0	chr2	110327221	110327391	-	0	171	707.84	NCExon			1	1	TU864	SpliceToNCG	ENSG00000175701	
CONGO_chr2_112914444_206_m0	chr2	112914444	112914649	-	0	206	689.49	Intergenic	1							
CONGO_chr2_118526183_56_p2	chr2	118526183	118526238	+	2	56	121.75	Intergenic								
CONGO_chr2_118622936_110_m0	chr2	118622936	118623045	-	0	110	11.04	NCIntron								
CONGO_chr2_118657239_130_m1	chr2	118657239	118657368	-	1	130	34.95	NCExon				1	TU866	SpliceToNCG	ENSG00000226856	
CONGO_chr2_118850341_82_m0	chr2	118850341	118850422	-	0	82	11.64	Intergenic								
CONGO_chr2_121888187_63_m2	chr2	121888187	121888249	-	2	63	179.25	Intron								
CONGO_chr2_127372965_199_p0	chr2	127372965	127373163	+	0	199	473.93	NCExon				1	TU76	SpliceToNCG	ENSG00000237524	
CONGO_chr2_127373263_75_p2	chr2	127373263	127373337	+	2	75	462.85	NCExon				1	TU76	SpliceToNCG	ENSG00000237524	
CONGO_chr2_127373569_90_p2	chr2	127373569	127373658	+	2	90	197.41	NCExon				1	TU76	SpliceToNCG	ENSG00000237524	
CONGO_chr2_127373982_84_p2	chr2	127373982	127374065	+	2	84	49.21	NCExon				1	TU76	SpliceToNCG	ENSG00000237524	
CONGO_chr2_127679942_141_m0	chr2	127679942	127680082	-	0	141	494.65	Intron					TU867	SpliceToPCG	ENSG00000186684	
CONGO_chr2_127694035_150_m0	chr2	127694035	127694184	-	0	150	13.06	UTR			1	1				
CONGO_chr2_127959951_111_m0	chr2	127959951	127960061	-	0	111	279.59	Intron		IWS1_C		1	TU868	SpliceToPCG	ENSG00000163166	
CONGO_chr2_128339950_109_m0	chr2	128339950	128340058	-	0	109	172.34	Intron					TU869	SpliceToPCG	ENSG00000144233	
CONGO_chr2_133039723_434_m1	chr2	133039723	133040156	-	1	434	29.98	AntisenseIntron								
CONGO_chr2_134728303_49_p1	chr2	134728303	134728351	+	1	49	24.28	UTR			1	1	TU870	SpliceToPCG	ENSG00000152127	
CONGO_chr2_135420271_77_m1	chr2	135420271	135420347	-	1	77	53.88	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000082258	
CONGO_chr2_135501572_159_m0	chr2	135501572	135501730	-	0	159	640.71	Intron								
CONGO_chr2_135504352_136_m1	chr2	135504352	135504487	-	1	136	596.65	UTR			1	1	TU871	UnsplicedMergeWithPCG	ENSG00000176601	
CONGO_chr2_135514403_174_m0	chr2	135514403	135514576	-	0	174	579.11	UTR			1	1	TU872	SpliceToPCG	ENSG00000176601	
CONGO_chr2_142605047_66_p0	chr2	142605047	142605112	+	0	66	26.39	AntisenseUTR								
CONGO_chr2_143631275_105_m0	chr2	143631275	143631379	-	0	105	65.9	AntisenseIntron								
CONGO_chr2_143832049_157_p0	chr2	143832049	143832205	+	0	157	25.4	Intron								
CONGO_chr2_143832234_102_m2	chr2	143832234	143832335	-	2	102	88.99	AntisenseIntron								
CONGO_chr2_143876021_189_p2	chr2	143876021	143876209	+	2	189	70.82	Intron								
CONGO_chr2_144097922_87_m0	chr2	144097922	144098008	-	0	87	90.2	AntisenseIntron								
CONGO_chr2_144123587_89_m2	chr2	144123587	144123675	-	2	89	68.01	AntisenseIntron								
CONGO_chr2_144153789_125_p2	chr2	144153789	144153913	+	2	125	7.84	Intron								
CONGO_chr2_144156051_85_p0	chr2	144156051	144156135	+	0	85	27.34	Intron								
CONGO_chr2_144351999_61_m2	chr2	144351999	144352059	-	2	61	55.57	Intergenic								
CONGO_chr2_144420573_55_p1	chr2	144420573	144420627	+	1	55	4.83	AntisenseUTR					TU263	SpliceToNCG	ENSG00000232377	
CONGO_chr2_144421015_65_p2	chr2	144421015	144421079	+	2	65	37.29	AntisenseUTR				1	TU263	SpliceToNCG	ENSG00000232377	
CONGO_chr2_144424942_108_m0	chr2	144424942	144425049	-	0	108	28.77	NCExon			1					
CONGO_chr2_144479006_126_p0	chr2	144479006	144479131	+	0	126	224.4	AntisenseIntron								
CONGO_chr2_144862667_101_m2	chr2	144862667	144862767	-	2	101	23.76	UTR	1		1		TU131	SpliceToPCG	ENSG00000169554	
CONGO_chr2_144863378_59_p1	chr2	144863378	144863436	+	1	59	99.87	AntisenseUTR	1					UnsplicedMergeWithPCG	ENSG00000169554	
CONGO_chr2_144905606_96_m2	chr2	144905606	144905701	-	2	96	142.36	Intron								
CONGO_chr2_144944456_80_m1	chr2	144944456	144944535	-	1	80	113.51	Intron					TU131	SpliceToPCG	ENSG00000169554	
CONGO_chr2_144953820_183_m0	chr2	144953820	144954002	-	0	183	21.93	Intron								
CONGO_chr2_144968813_90_m0	chr2	144968813	144968902	-	0	90	66.77	Intron			1					
CONGO_chr2_144974301_192_m0	chr2	144974301	144974492	-	0	192	77.45	Intron								
CONGO_chr2_144978528_136_p1	chr2	144978528	144978663	+	1	136	210.8	AntisenseNCExon								
CONGO_chr2_144984549_61_m1	chr2	144984549	144984609	-	1	61	5.53	Intron								
CONGO_chr2_144984878_125_p2	chr2	144984878	144985002	+	2	125	150.38	AntisenseIntron								
CONGO_chr2_144993976_161_m2	chr2	144993976	144994136	-	2	161	81.42	UTR			1	1	TU131	SpliceToPCG	ENSG00000169554	
CONGO_chr2_145055150_118_p1	chr2	145055150	145055267	+	1	118	116.73	Intergenic								
CONGO_chr2_145055351_100_m1	chr2	145055351	145055450	-	1	100	30.39	Intergenic								
CONGO_chr2_145056991_86_p0	chr2	145056991	145057076	+	0	86	184.36	Intergenic								
CONGO_chr2_145082167_79_m0	chr2	145082167	145082245	-	0	79	60.84	Intergenic								
CONGO_chr2_145125092_112_m1	chr2	145125092	145125203	-	1	112	29.33	Intergenic								
CONGO_chr2_145348260_100_m0	chr2	145348260	145348359	-	0	100	130.35	AntisenseNCIntron								
CONGO_chr2_145591593_98_p1	chr2	145591593	145591690	+	1	98	11.03	NCExon			1	1				
CONGO_chr2_146409308_92_p1	chr2	146409308	146409399	+	1	92	102.11	Intergenic								
CONGO_chr2_146515574_113_m2	chr2	146515574	146515686	-	2	113	34.76	Intergenic								
CONGO_chr2_147098678_67_m1	chr2	147098678	147098744	-	1	67	10.29	Intergenic								
CONGO_chr2_147672576_213_m1	chr2	147672576	147672788	-	1	213	86.21	Intergenic								
CONGO_chr2_152027940_77_m2	chr2	152027940	152028016	-	2	77	29.8	AntisenseCDS				1		UnsplicedMergeWithPCG	ENSG00000080345	
CONGO_chr2_152403509_79_p0	chr2	152403509	152403587	+	0	79	128.57	AntisenseUTR								
CONGO_chr2_153279310_80_m0	chr2	153279310	153279389	-	0	80	21.13	NCExon				1	TU873	SpliceToPCG	ENSG00000196504	
CONGO_chr2_156108878_125_m2	chr2	156108878	156109002	-	2	125	2.25	Intergenic								
CONGO_chr2_156471169_47_p0	chr2	156471169	156471215	+	0	47	18.68	Intergenic								
CONGO_chr2_156699965_166_p0	chr2	156699965	156700130	+	0	166	57.94	AntisenseNCIntron								
CONGO_chr2_157158012_62_p2	chr2	157158012	157158073	+	2	62	5.16	Intron								
CONGO_chr2_157299591_62_p1	chr2	157299591	157299652	+	1	62	110.39	Intergenic								
CONGO_chr2_157349145_42_p0	chr2	157349145	157349186	+	0	42	35.49	Intergenic								
CONGO_chr2_157429086_93_m0	chr2	157429086	157429178	-	0	93	30.07	Intergenic								
CONGO_chr2_157429205_130_m0	chr2	157429205	157429334	-	0	130	186.46	Intergenic								
CONGO_chr2_157569782_114_m0	chr2	157569782	157569895	-	0	114	170.9	Intergenic								
CONGO_chr2_157714209_100_p1	chr2	157714209	157714308	+	1	100	2.27	Intergenic								
CONGO_chr2_160081327_93_m0	chr2	160081327	160081419	-	0	93	1.68	UTR			1	1				
CONGO_chr2_160181214_45_p2	chr2	160181214	160181258	+	2	45	68.86	AntisenseUTR			1	1	TU874	SpliceToNCG	ENSG00000224152	
CONGO_chr2_160182591_54_m2	chr2	160182591	160182644	-	2	54	25.32	Intron					TU875	SpliceToPCG	ENSG00000123636	
CONGO_chr2_161764929_71_p1	chr2	161764929	161764999	+	1	71	81.31	Intron						NovelUnspliced		
CONGO_chr2_161813281_62_m2	chr2	161813281	161813342	-	2	62	119.84	NCExon				1	TU876	SpliceToNCG	ENSG00000235724	
CONGO_chr2_161946893_259_m1	chr2	161946893	161947151	-	1	259	99.42	AntisenseNCExon								
CONGO_chr2_162865821_127_p0	chr2	162865821	162865947	+	0	127	195.9	AntisenseIntron								
CONGO_chr2_162986382_64_m0	chr2	162986382	162986445	-	0	64	6.33	Intron								
CONGO_chr2_163812276_76_m1	chr2	163812276	163812351	-	1	76	22.61	Intergenic								
CONGO_chr2_163813524_251_p2	chr2	163813524	163813774	+	2	251	51.05	Intergenic								
CONGO_chr2_164028517_49_p2	chr2	164028517	164028565	+	2	49	27.4	Intergenic								
CONGO_chr2_164030504_105_p0	chr2	164030504	164030608	+	0	105	22.01	Intergenic								
CONGO_chr2_164177085_103_m0	chr2	164177085	164177187	-	0	103	25.53	Intron					TU877	SpliceToPCG	ENSG00000182263	
CONGO_chr2_164177194_96_p1	chr2	164177194	164177289	+	1	96	42.14	AntisenseIntron								
CONGO_chr2_164278826_132_p0	chr2	164278826	164278957	+	0	132	152.48	AntisenseIntron								
CONGO_chr2_164298357_97_p0	chr2	164298357	164298453	+	0	97	33.9	AntisenseIntron								
CONGO_chr2_164300594_173_m2	chr2	164300594	164300766	-	2	173	84.42	UTR			1	1	TU878	SpliceToPCG	ENSG00000182263	
CONGO_chr2_164619578_137_p1	chr2	164619578	164619714	+	1	137	38.35	AntisenseNCIntron								
CONGO_chr2_164630969_240_p2	chr2	164630969	164631208	+	2	240	143.28	AntisenseNCIntron								
CONGO_chr2_164817457_101_m2	chr2	164817457	164817557	-	2	101	132.01	NCIntron								
CONGO_chr2_165014929_146_p2	chr2	165014929	165015074	+	2	146	105.4	Intergenic								
CONGO_chr2_165133071_63_m0	chr2	165133071	165133133	-	0	63	391.99	NCExon			1	1	TU879	SpliceToPCG	ENSG00000115290	
CONGO_chr2_165893160_135_p0	chr2	165893160	165893294	+	0	135	211.22	Intron								
CONGO_chr2_167857998_93_p2	chr2	167857998	167858090	+	2	93	33.41	NCExon				1				
CONGO_chr2_170706535_46_p2	chr2	170706535	170706580	+	2	46	169.42	Intergenic								
CONGO_chr2_171587826_157_p1	chr2	171587826	171587982	+	1	157	42.9	AntisenseCDS				1	TU880	NovelMultiExon		
CONGO_chr2_172288519_157_m1	chr2	172288519	172288675	-	1	157	2.04	AntisenseIntron								
CONGO_chr2_172645115_128_p2	chr2	172645115	172645242	+	2	128	67.85	Intron								
CONGO_chr2_172645760_104_m2	chr2	172645760	172645863	-	2	104	97.63	AntisenseIntron								
CONGO_chr2_172666314_44_m1	chr2	172666314	172666357	-	1	44	39.01	Intergenic								
CONGO_chr2_173771111_65_p1	chr2	173771111	173771175	+	1	65	134.25	AntisenseNCExon						UnsplicedMergeWithNCG	ENSG00000238133	
CONGO_chr2_173771277_116_p2	chr2	173771277	173771392	+	2	116	185.55	AntisenseNCExon						UnsplicedMergeWithNCG	ENSG00000238133	
CONGO_chr2_173771505_160_p1	chr2	173771505	173771664	+	1	160	41.96	AntisenseNCExon								
CONGO_chr2_174226269_81_m2	chr2	174226269	174226349	-	2	81	41.95	Intergenic								
CONGO_chr2_174697329_93_m0	chr2	174697329	174697421	-	0	93	80.69	Intron								
CONGO_chr2_174731980_116_p2	chr2	174731980	174732095	+	2	116	49.94	AntisenseIntron								
CONGO_chr2_174733709_136_m1	chr2	174733709	174733844	-	1	136	11.65	Intron								
CONGO_chr2_174912062_139_p1	chr2	174912062	174912200	+	1	139	4.72	Intergenic								
CONGO_chr2_176462783_164_p2	chr2	176462783	176462946	+	2	164	24.59	Intergenic								
CONGO_chr2_176646836_81_p0	chr2	176646836	176646916	+	0	81	197.69	Intergenic								
CONGO_chr2_176648804_83_m1	chr2	176648804	176648886	-	1	83	64.59	Intergenic								
CONGO_chr2_176657028_74_p0	chr2	176657028	176657101	+	0	74	51.59	AntisenseUTR								
CONGO_chr2_176657252_105_p0	chr2	176657252	176657356	+	0	105	3.77	Intergenic								
CONGO_chr2_176690278_112_m1	chr2	176690278	176690389	-	1	112	274.93	AntisenseCDS				1		UnsplicedMergeWithPCG	ENSG00000128710	
CONGO_chr2_176738162_127_m1	chr2	176738162	176738288	-	1	127	20.23	AntisenseIntron								
CONGO_chr2_177795034_74_p1	chr2	177795034	177795107	+	1	74	5.82	UTR	1		1	1	TU881	SpliceToPCG	ENSG00000170144	
CONGO_chr2_178645652_113_m0	chr2	178645652	178645764	-	0	113	84.86	UTR			1					

CONGO_chr2_179225625_84_m2	chr2	179225625	179225708	-	2	84	259.74	Intron			1	1	TU77	NovelMultiExon	
CONGO_chr2_179225820_84_m2	chr2	179225820	179225903	-	2	84	109.73	Intron					TU77	NovelMultiExon	
CONGO_chr2_179226013_84_m2	chr2	179226013	179226096	-	2	84	78.88	Intron					TU77	NovelMultiExon	
CONGO_chr2_179248643_84_m2	chr2	179248643	179248726	-	2	84	57.55	Intron					TU77	NovelMultiExon	
CONGO_chr2_179250173_87_m2	chr2	179250173	179250259	-	2	87	205.49	NCExon			1	1	TU882	NovelMultiExon	
CONGO_chr2_179325146_122_m0	chr2	179325146	179325267	-	0	122	142.47	Intron					TU883	NovelMultiExon	
CONGO_chr2_181899893_69_p0	chr2	181899893	181899961	+	0	69	67.87	NCIntron							
CONGO_chr2_182247579_129_p0	chr2	182247579	182247707	+	0	129	77.03	AntisenseIntron							
CONGO_chr2_183576705_80_m0	chr2	183576705	183576784	-	0	80	15.48	Intron					TU884	SpliceToPCG	ENSG00000061676
CONGO_chr2_187709879_71_m0	chr2	187709879	187709949	-	0	71	26.72	AntisenseNCIntron							
CONGO_chr2_190234492_90_p0	chr2	190234492	190234581	+	0	90	271.35	UTR			1	1	TU78	SpliceToPCG	ENSG00000138381
CONGO_chr2_190236872_54_p0	chr2	190236872	190236925	+	0	54	296.55	UTR			1	1	TU78	SpliceToPCG	ENSG00000138381
CONGO_chr2_190238347_76_p0	chr2	190238347	190238422	+	0	76	465.28	UTR			1	1	TU78	SpliceToPCG	ENSG00000138381
CONGO_chr2_190239012_71_p2	chr2	190239012	190239082	+	2	71	60.46	UTR			1	1	TU78	SpliceToPCG	ENSG00000138381
CONGO_chr2_190633791_57_m0	chr2	190633791	190633847	-	0	57	96.28	Intron							
CONGO_chr2_197563649_248_m2	chr2	197563649	197563896	-	2	248	734.73	NCExon				1	TU885	SpliceToPCG	ENSG00000065413
CONGO_chr2_198358025_170_m2	chr2	198358025	198358194	-	2	170	82.52	UTR			1	1	TU886	SpliceToPCG	ENSG00000152430
CONGO_chr2_199236062_108_p0	chr2	199236062	199236169	+	0	108	24.4	AntisenseNCIntron							
CONGO_chr2_200030307_105_m2	chr2	200030307	200030411	-	2	105	87.41	UTR			1	1	TU887	SpliceToPCG	ENSG00000119042
CONGO_chr2_200392540_186_m2	chr2	200392540	200392725	-	2	186	175.68	NCExon				1	TU888	SpliceToNCG	ENSG00000226124
CONGO_chr2_200424932_65_p0	chr2	200424932	200424996	+	0	65	102	Intergenic							
CONGO_chr2_201433125_242_p2	chr2	201433125	201433366	+	2	242	43.98	AntisenseCDS				1			
CONGO_chr2_202775397_139_p1	chr2	202775397	202775535	+	1	139	228.14	Intergenic					TU889	SpliceToPCG	ENSG00000182329
CONGO_chr2_203670515_87_p0	chr2	203670515	203670601	+	0	87	207.15	NCExon					TU890	SpliceToPCG	ENSG00000144426
CONGO_chr2_204654859_87_m1	chr2	204654859	204654945	-	1	87	58.62	Intergenic							
CONGO_chr2_206255590_72_m1	chr2	206255590	206255661	-	1	72	66.01	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000118257
CONGO_chr2_206279169_87_m1	chr2	206279169	206279255	-	1	87	23.15	AntisenseIntron							
CONGO_chr2_206400859_93_m0	chr2	206400859	206400951	-	0	93	11.66	Intergenic							
CONGO_chr2_206465115_81_p2	chr2	206465115	206465195	+	2	81	14.25	Intergenic							
CONGO_chr2_207243456_75_m0	chr2	207243456	207243530	-	0	75	527.62	Intron							
CONGO_chr2_207686605_107_m2	chr2	207686605	207686711	-	2	107	11.36	Intron							
CONGO_chr2_208102784_204_p1	chr2	208102784	208102987	+	1	204	37.19	UTR			1	1	TU891	SpliceToPCG	ENSG00000118260
CONGO_chr2_208543541_92_p2	chr2	208543541	208543632	+	2	92	15.36	AntisenseIntron							
CONGO_chr2_210260688_243_p2	chr2	210260688	210260930	+	2	243	472.86	Intron							
CONGO_chr2_210467176_160_p0	chr2	210467176	210467335	+	0	160	287.68	Intron					TU893	SpliceToPCG	ENSG00000144406
CONGO_chr2_210543942_82_m1	chr2	210543942	210544023	-	1	82	37.32	AntisenseIntron							
CONGO_chr2_213720440_67_m0	chr2	213720440	213720506	-	0	67	109.99	UTR							
CONGO_chr2_215953801_141_p1	chr2	215953801	215953941	+	1	141	261.17	AntisenseCDS				1	TU894	NovelMultiExon	
CONGO_chr2_218583068_117_m0	chr2	218583068	218583184	-	0	117	146.38	Intergenic					TU895	SpliceToPCG	ENSG00000079308
CONGO_chr2_220019233_67_p1	chr2	220019233	220019299	+	1	67	28.03	Intron							
CONGO_chr2_221998896_55_p1	chr2	221998896	221998950	+	1	55	40.71	AntisenseUTR				1		UnsplicedMergeWithPCG	ENSG00000116106
CONGO_chr2_222841904_108_p0	chr2	222841904	222842011	+	0	108	6.03	AntisenseIntron							
CONGO_chr2_222891991_876_m0	chr2	222891991	222892866	-	0	876	1443.63	AntisenseNCExon		zf-C3HC4					
CONGO_chr2_225410272_46_m0	chr2	225410272	225410317	-	0	46	66.45	Intron							
CONGO_chr2_225555168_162_m0	chr2	225555168	225555329	-	0	162	721.06	NCExon				1	TU897	SpliceToPCG	ENSG00000135905
CONGO_chr2_227960643_267_m0	chr2	227960643	227960909	-	0	267	356.09	Intergenic							
CONGO_chr2_228171850_182_m0	chr2	228171850	228172031	-	0	182	415.13	Intergenic							
CONGO_chr2_228172038_178_p1	chr2	228172038	228172215	+	1	178	49.16	Intergenic							
CONGO_chr2_228181744_140_p0	chr2	228181744	228181883	+	0	140	11.2	Intergenic							
CONGO_chr2_228187498_303_m0	chr2	228187498	228187800	-	0	303	366.54	Intron							
CONGO_chr2_228190458_318_p0	chr2	228190458	228190775	+	0	318	502.69	AntisenseNCExon				1		UnsplicedMergeWithNCG	ENSG00000236116
CONGO_chr2_228221234_162_m0	chr2	228221234	228221395	-	0	162	387.7	Intergenic		Folate_carrier			TU898	SpliceToPCG	ENSG00000135917
CONGO_chr2_228297400_318_m0	chr2	228297400	228297717	-	0	318	424.86	Intergenic							
CONGO_chr2_228301295_291_p0	chr2	228301295	228301585	+	0	291	474.53	Intergenic							
CONGO_chr2_228318854_327_p0	chr2	228318854	228319180	+	0	327	450.46	Intergenic							
CONGO_chr2_230711598_139_p2	chr2	230711598	230711736	+	2	139	468.22	NCIntron							
CONGO_chr2_231563652_421_p0	chr2	231563652	231564072	+	0	421	707.36	AntisenseNCIntron					TU899	SpliceToPCG	ENSG00000173699
CONGO_chr2_232066788_239_m1	chr2	232066788	232067026	-	1	239	3.62	Intergenic						NovelUnspliced	
CONGO_chr2_233093553_97_p0	chr2	233093553	233093649	+	0	97	25.52	Intergenic				1			
CONGO_chr2_233094275_108_p2	chr2	233094275	233094382	+	2	108	495.38	Intergenic				1			
CONGO_chr2_233094770_51_p2	chr2	233094770	233094820	+	2	51	212.61	Intergenic				1			
CONGO_chr2_233094925_190_p2	chr2	233094925	233095114	+	2	190	1116.33	Intergenic		Trypsin		1			
CONGO_chr2_233095469_100_p1	chr2	233095469	233095568	+	1	100	461.34	Intergenic				1			
CONGO_chr2_233095656_160_p0	chr2	233095656	233095815	+	0	160	739.93	Intergenic		Trypsin		1			
CONGO_chr2_233096014_143_p2	chr2	233096014	233096156	+	2	143	1105.28	Intergenic		Trypsin		1			
CONGO_chr2_233096370_163_p0	chr2	233096370	233096532	+	0	163	1224.14	Intergenic		Trypsin		1			
CONGO_chr2_238303162_67_p0	chr2	238303162	238303228	+	0	67	162.54	Intron					TU901	SpliceToPCG	ENSG00000124831
CONGO_chr2_241156812_393_p0	chr2	241156812	241157204	+	0	393	335.56	UTR			1	1	TU266	SpliceToPCG	ENSG00000142327
CONGO_chr2_241160513_141_p0	chr2	241160513	241160653	+	0	141	978.68	UTR		Peptidase_M1	1	1	TU266	SpliceToPCG	ENSG00000142327
CONGO_chr2_241494604_78_p0	chr2	241494604	241494681	+	0	78	93.38	Intergenic							
CONGO_chr20_000503362_119_m0	chr20	503362	503480	-	0	119	28.48	Intergenic							
CONGO_chr20_005520484_49_m2	chr20	5520484	5520532	-	2	49	31.87	Intron				1	TU783	SpliceToPCG	ENSG00000125772
CONGO_chr20_007445455_117_m0	chr20	7445455	7445571	-	0	117	59.72	Intergenic							
CONGO_chr20_010224831_75_p1	chr20	10224831	10224905	+	1	75	38.49	NCExon			1			UnsplicedMergeWithPCG	ENSG00000132639
CONGO_chr20_010342417_119_m0	chr20	10342417	10342535	-	0	119	246.35	UTR			1	1	TU784	SpliceToPCG	ENSG00000125863
CONGO_chr20_013444987_87_m0	chr20	13444987	13445073	-	0	87	84.93	Intron							
CONGO_chr20_015821572_84_p2	chr20	15821572	15821655	+	2	84	327.57	AntisenseUTR							
CONGO_chr20_016576582_62_m2	chr20	16576582	16576643	-	2	62	13.07	Intergenic							
CONGO_chr20_020421347_105_p0	chr20	20421347	20421451	+	0	105	83.33	AntisenseIntron							
CONGO_chr20_020527323_141_m2	chr20	20527323	20527463	-	2	141	659.14	NCExon			1		TU785	SpliceToPCG	ENSG00000188559
CONGO_chr20_021019080_126_p0	chr20	21019080	21019205	+	0	126	9.39	Intergenic				1			
CONGO_chr20_029472994_149_m2	chr20	29472994	29473142	-	2	149	10.25	NCExon		Defensin_beta	1				
CONGO_chr20_031257288_64_p0	chr20	31257288	31257351	+	0	64	111.47	NCExon			1				
CONGO_chr20_033328931_219_m0	chr20	33328931	33329149	-	0	219	404.58	NCExon				1	TU787	SpliceToPCG	ENSG00000088298
CONGO_chr20_037768313_82_m0	chr20	37768313	37768394	-	0	82	23.89	Intergenic							
CONGO_chr20_038774627_62_m2	chr20	38774627	38774688	-	2	62	122.72	Intergenic							
CONGO_chr20_040144036_55_p0	chr20	40144036	40144090	+	0	55	387.2	AntisenseCDS				1	TU789	NovelMultiExon	
CONGO_chr20_043200573_77_m2	chr20	43200573	43200649	-	2	77	182.22	Intergenic					TU248	NovelMultiExon	
CONGO_chr20_043200666_64_m2	chr20	43200666	43200729	-	2	64	120.29	Intergenic					TU248	NovelMultiExon	
CONGO_chr20_043996754_97_p0	chr20	43996754	43996850	+	0	97	51.17	AntisenseCDS			1	1	TU791	SpliceToPCG	ENSG00000100982
CONGO_chr20_050203254_134_p0	chr20	50203254	50203387	+	0	134	399.46	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000020256
CONGO_chr20_050838572_90_m0	chr20	50838572	50838661	-	0	90	7.15	Intergenic							
CONGO_chr20_051120698_83_p1	chr20	51120698	51120780	+	1	83	46.2	Intron							
CONGO_chr20_051436319_156_m0	chr20	51436319	51436474	-	0	156	48.2	AntisenseIntron							
CONGO_chr20_051538809_68_m0	chr20	51538809	51538876	-	0	68	27.45	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000182463
CONGO_chr20_055718415_200_m2	chr20	55718415	55718614	-	2	200	8.68	UTR					TU793	SpliceToPCG	ENSG00000124225
CONGO_chr20_056898331_336_p0	chr20	56898331	56898666	+	0	336	569.46	Intron							
CONGO_chr20_056898703_94_p2	chr20	56898703	56898796	+	2	94	291.37	Intron							
CONGO_chr20_056898801_388_p1	chr20	56898801	56899188	+	1	388	380.47	NCExon				1			
CONGO_chr20_062139724_276_p0	chr20	62139724	62139999	+	0	276	697.86	UTR			1	1			
CONGO_chr20_062200601_83_p2	chr20	62200601	62200683	+	2	83	406.19	UTR			1		TU794	SpliceToPCG	ENSG00000125510
CONGO_chr20_062291860_98_p2	chr20	62291860	62291957	+	2	98	196.29	UTR			1	1	TU795	SpliceToPCG	ENSG00000196132
CONGO_chr21_014985090_55_p1	chr21	14985090	14985144	+	1	55	13.2	Intergenic							
CONGO_chr21_015297801_199_p1	chr21	15297801	15297999	+	1	199	140.58	AntisenseIntron							
CONGO_chr21_016873851_97_m2	chr21	16873851	16873947	-	2	97	25.71	AntisenseIntron							
CONGO_chr21_016882730_209_p0	chr21	16882730	16882938	+	0	209	93.04	Intron				1	TU796	SpliceToPCG	ENSG00000215386
CONGO_chr21_016899923_55_p1	chr21	16899923	16899977	+	1	55	9.72	Intron							
CONGO_chr21_017136967_140_p2	chr21	17136967	17137106	+	2	140	52.57	Intergenic							
CONGO_chr21_017137158_46_p0	chr21	17137158	17137203	+	0	46	22.68	Intergenic							
CONGO_chr21_022496808_79_m0	chr21	22496808	22496886	-	0	79	159.87	Intergenic							
CONGO_chr21_026029139_78_p0	chr21	26029139	26029216	+	0	78	101.92	UTR			1	1	TU797	SpliceToPCG	ENSG00000154727
CONGO_chr21_031454633_87_m0	chr21	31454633	31454719	-	0	87	446.59	Intron					TU798	SpliceToPCG	ENSG00000156299
CONGO_chr21_031570919_54_m0	chr21	31570919	31570972	-	0	54	36.22	UTR			1	1	TU799	SpliceToPCG	ENSG00000156299
CONGO_chr21_033865927_38_p2	chr21	33865927	33865964	+	2	38	108.71	UTR			1		TU800	SpliceToPCG	ENSG00000159140
CONGO_chr21_037807611_87_p1	chr21	37807611	37807697	+	1	87	7.26	UTR			1		TU801	SpliceToPCG	ENSG00000157540
CONGO_chr21_039792398_81_p0	chr21	39792398	39792478	+	0	81	222.51	Intron							
CONGO_chr21_043196638_77_m2	chr21	43196638	43196714	-	2	77	499.42	AntisenseCDS			1	1			
CONGO_chr21_044184558_83_p0	chr21	44184558	44184640	+	0	83	274.11	Intron					TU802	SpliceToPCG	ENSG00000160216
CONGO_chr21_045396952_100_p0	chr21	45396952	45397051	+	0	100	367.66	Intron			1				
CONGO_chr22_016656495_66_m2	chr22	16656495	16656560	-	2	66	37.24	Intron					TU803	SpliceToPCG	ENSG00000093100
CONGO_chr22_016666577_51_m2	chr22	16666577	16666627	-	2	51	18.9	Intron				1	TU249	SpliceToPCG	ENSG00000093100
CONGO_chr22_016689220_63_m2	chr22	16689220	16689282	-	2	63	305.27	Intron				1	TU249	SpliceToPCG	ENSG00000093100
CONGO_chr22_017397037_216_p0	chr22	17397037	17397252	+	0	216	804.07	NCIntron	1						
CONGO_chr22_017397310_425_p2	chr22	17397310	17397734	+	2	425	1028.08	NCIntron	1						
CONGO_chr22_018453210_78_p0	chr22	18453210	18453287	+	0	78	5.42	UTR			1	1	TU804	SpliceToPCG	ENSG00000099901

CONGO_chr22_019695673_207_m2	chr22	19695673	19695879	-	2	207	744.85	NCExon	1		1	1	TU129	SpliceToNCG	ENSG00000161149
CONGO_chr22_019696816_132_m2	chr22	19696816	19696947	-	2	132	179.52	Intron	1						
CONGO_chr22_019749751_217_p1	chr22	19749751	19749967	+	1	217	448.04	AntisenseIntron		Tubulin					
CONGO_chr22_019751240_142_p2	chr22	19751240	19751381	+	2	142	229.77	AntisenseIntron		Tubulin					
CONGO_chr22_019751705_223_p0	chr22	19751705	19751927	+	0	223	257.83	AntisenseIntron		Tubulin		1	TU807	SpliceToNCG	ENSG00000230513
CONGO_chr22_019754090_297_p0	chr22	19754090	19754386	+	0	297	427.01	AntisenseIntron							
CONGO_chr22_020342070_285_p0	chr22	20342070	20342354	+	0	285	546.59	AntisenseIntron					TU250	SpliceToPCG	ENSG00000100023
CONGO_chr22_020342555_105_p0	chr22	20342555	20342659	+	0	105	355.87	NCExon				1	TU250	SpliceToPCG	ENSG00000100023
CONGO_chr22_020678541_392_m0	chr22	20678541	20678932	-	0	392	617.42	NCExon			1		TU808	UnsplicedMergeWithNCG	ENSG00000197549
CONGO_chr22_020679059_112_m1	chr22	20679059	20679170	-	1	112	32.13	NCExon			1	1			
CONGO_chr22_020679530_300_m1	chr22	20679530	20679829	-	1	300	391.73	NCExon			1	1			
CONGO_chr22_023838145_285_p0	chr22	23838145	23838429	+	0	285	2871.51	AntisenseCDS					TU811	SpliceToPCG	ENSG00000197077
CONGO_chr22_025729653_194_m0	chr22	25729653	25729846	-	0	194	8.17	Intergenic							
CONGO_chr22_025772116_115_p0	chr22	25772116	25772230	+	0	115	28.45	Intergenic							
CONGO_chr22_027168874_71_m2	chr22	27168874	27168944	-	2	71	101.28	NCExon					TU812	SpliceToPCG	ENSG00000100154
CONGO_chr22_027806138_144_p2	chr22	27806138	27806281	+	2	144	94.2	Intron							
CONGO_chr22_029530015_76_p0	chr22	29530015	29530090	+	0	76	53.23	Intron							
CONGO_chr22_029536667_97_p0	chr22	29536667	29536763	+	0	97	300.24	Intron							
CONGO_chr22_029695377_428_p2	chr22	29695377	29695804	+	2	428	1213.89	NCExon					TU813	SpliceToPCG	ENSG00000182457
CONGO_chr22_030054787_104_p2	chr22	30054787	30054890	+	2	104	25.04	AntisenseCDS				1	TU814	NovelMultiExon	
CONGO_chr22_034267194_300_p0	chr22	34267194	34267493	+	0	300	318.08	UTR			1	1	TU815	SpliceToPCG	ENSG00000100302
CONGO_chr22_034476128_126_m0	chr22	34476128	34476253	-	0	126	70.2	Intron							
CONGO_chr22_034478606_43_m1	chr22	34478606	34478648	-	1	43	89.23	NCExon				1	TU252	SpliceToPCG	ENSG00000100320
CONGO_chr22_034575565_45_m0	chr22	34575565	34575609	-	0	45	21.73	Intron				1	TU252	SpliceToPCG	ENSG00000100320
CONGO_chr22_035034800_63_m2	chr22	35034800	35034862	-	2	63	78.97	Intron					TU816	SpliceToPCG	ENSG00000100345
CONGO_chr22_035429852_132_p1	chr22	35429852	35429983	+	1	132	55.63	NCExon			1	1			
CONGO_chr22_036115755_134_m2	chr22	36115755	36115888	-	2	134	66.66	Intron							
CONGO_chr22_036710292_103_m1	chr22	36710292	36710394	-	1	103	89.24	UTR			1	1	TU817	SpliceToPCG	ENSG00000100146
CONGO_chr22_037021339_61_m0	chr22	37021339	37021399	-	0	61	141.72	UTR				1	TU253	SpliceToPCG	ENSG00000213923
CONGO_chr22_037023836_115_m1	chr22	37023836	37023950	-	1	115	67.67	UTR			1	1	TU253	SpliceToPCG	ENSG00000213923
CONGO_chr22_037215177_180_p0	chr22	37215177	37215356	+	0	180	115.59	AntisenseUTR				1	TU818	NovelMultiExon	
CONGO_chr22_037817558_190_p0	chr22	37817558	37817747	+	0	190	35.42	NCExon				1	TU819	UnsplicedMergeWithNCG	ENSG00000225720
CONGO_chr22_038230154_241_p1	chr22	38230154	38230394	+	1	241	1154.62	UTR		Complex1_LYR	1	1	TU820	SpliceToPCG	ENSG00000100324
CONGO_chr22_038843005_74_p1	chr22	38843005	38843078	+	1	74	11.91	UTR			1	1	TU821	SpliceToPCG	ENSG00000100354
CONGO_chr22_039217937_92_m1	chr22	39217937	39218028	-	1	92	192.06	Intron							
CONGO_chr22_039259540_46_m0	chr22	39259540	39259585	-	0	46	136.47	UTR				1	TU822	SpliceToPCG	ENSG00000196588
CONGO_chr22_039278056_262_m0	chr22	39278056	39278317	-	0	262	1515.76	UTR			1	1	TU823	SpliceToPCG	ENSG00000196588
CONGO_chr22_040121676_88_m1	chr22	40121676	40121763	-	1	88	1046.87	AntisenseCDS			1	1	TU824	UnsplicedMergeWithPCG	ENSG00000167074
CONGO_chr22_040422836_98_p0	chr22	40422836	40422933	+	0	98	505.94	UTR			1		TU825	SpliceToPCG	ENSG00000184208
CONGO_chr22_040635715_383_m2	chr22	40635715	40636097	-	2	383	1633.65	AntisenseIntron					TU254	SpliceToPCG	ENSG00000159958
CONGO_chr22_040636358_147_m2	chr22	40636358	40636504	-	2	147	751.82	AntisenseIntron					TU254	SpliceToPCG	ENSG00000159958
CONGO_chr22_040683622_221_p2	chr22	40683622	40683842	+	2	221	1302.34	UTR			1	1	TU826	SpliceToPCG	ENSG00000205704
CONGO_chr22_040697474_328_p2	chr22	40697474	40697801	+	2	328	689.25	Intergenic							
CONGO_chr22_040805849_68_m1	chr22	40805849	40805916	-	1	68	59.37	AntisenseCDS			1	1	TU827	NovelMultiExon	
CONGO_chr22_041300683_86_m2	chr22	41300683	41300768	-	2	86	484.66	NCExon	1		1	1	TU256	SpliceToPCG	ENSG00000189306
CONGO_chr22_041301881_196_m0	chr22	41301881	41302076	-	0	196	1779.55	NCExon	1		1	1	TU256	SpliceToPCG	ENSG00000189306
CONGO_chr22_041302462_98_m2	chr22	41302462	41302559	-	2	98	743.34	NCExon	1		1	1	TU75	SpliceToPCG	ENSG00000189306
CONGO_chr22_041302931_118_m0	chr22	41302931	41303048	-	0	118	764.44	NCExon	1		1	1	TU75	SpliceToPCG	ENSG00000189306
CONGO_chr22_041306167_143_m2	chr22	41306167	41306309	-	2	143	750.56	NCExon	1		1	1	TU75	SpliceToPCG	ENSG00000189306
CONGO_chr22_041307879_73_m0	chr22	41307879	41307951	-	0	73	182	NCExon	1		1	1	TU75	SpliceToPCG	ENSG00000189306
CONGO_chr22_042524458_107_m0	chr22	42524458	42524564	-	0	107	49.63	NCExon				1			
CONGO_chr22_048567245_90_p1	chr22	48567245	48567334	+	1	90	52.32	AntisenseCDS							
CONGO_chr22_048793101_102_m0	chr22	48793101	48793202	-	0	102	112.42	UTR			1	1			
CONGO_chr22_049036361_103_p1	chr22	49036361	49036463	+	1	103	221.75	AntisenseCDS			1	1			
CONGO_chr22_049331548_164_p0	chr22	49331548	49331711	+	0	164	725.05	NCExon							
CONGO_chr3_009450039_159_m2	chr3	9450039	9450197	-	2	159	127.66	AntisenseCDS							
CONGO_chr3_009450719_123_m0	chr3	9450719	9450841	-	0	123	45.16	AntisenseCDS							
CONGO_chr3_009451274_41_p2	chr3	9451274	9451314	+	2	41	24.24	NCExon				1	TU267	SpliceToPCG	OTTHUMG00000150491
CONGO_chr3_009466164_95_p2	chr3	9466164	9466258	+	2	95	4.79	NCExon					TU267	SpliceToPCG	OTTHUMG00000150491
CONGO_chr3_010352813_172_m0	chr3	10352813	10352984	-	0	172	347.75	NCExon			1	1	TU902	SpliceToPCG	OTTHUMG00000128679
CONGO_chr3_012556749_184_m1	chr3	12556749	12556932	-	1	184	1125.9	Intergenic					TU268	NovelMultiExon	
CONGO_chr3_012558359_163_m2	chr3	12558359	12558521	-	2	163	1247.71	Intergenic				1	TU268	NovelMultiExon	
CONGO_chr3_012559679_50_m1	chr3	12559679	12559728	-	1	50	656.87	Intergenic				1	TU269	NovelMultiExon	
CONGO_chr3_012561746_218_m0	chr3	12561746	12561963	-	0	218	1276.66	Intergenic				1	TU269	NovelMultiExon	
CONGO_chr3_012765159_62_p0	chr3	12765159	12765220	+	0	62	342.64	AntisenseCDS			1	1		UnsplicedMergeWithPCG	OTTHUMG00000129801
CONGO_chr3_013038533_68_m0	chr3	13038533	13038600	-	0	68	112.13	Intron					TU903	SpliceToPCG	OTTHUMG00000155398
CONGO_chr3_013058787_77_m0	chr3	13058787	13058863	-	0	77	235.93	Intron							
CONGO_chr3_013063978_45_m1	chr3	13063978	13064022	-	1	45	12.03	Intron				1	TU270	SpliceToPCG	OTTHUMG00000155398
CONGO_chr3_013180604_30_m1	chr3	13180604	13180633	-	1	30	81.61	Intergenic				1	TU270	SpliceToPCG	OTTHUMG00000155398
CONGO_chr3_014572411_55_m0	chr3	14572411	14572465	-	0	55	93.39	Intergenic							
CONGO_chr3_014836173_170_m2	chr3	14836173	14836342	-	2	170	10.41	AntisenseCDS	1						
CONGO_chr3_014978944_60_p0	chr3	14978944	14979003	+	0	60	30.96	UTR				1	TU904	SpliceToPCG	OTTHUMG00000129839
CONGO_chr3_015684756_61_m1	chr3	15684756	15684816	-	1	61	1.78	UTR			1	1	TU905	SpliceToPCG	OTTHUMG00000155379
CONGO_chr3_017853485_151_p1	chr3	17853485	17853635	+	1	151	92.4	AntisenseNCIntron							
CONGO_chr3_017963461_110_p2	chr3	17963461	17963570	+	2	110	17.86	AntisenseNCIntron							
CONGO_chr3_018129954_170_m1	chr3	18129954	18130123	-	1	170	132.05	AntisenseIntron							
CONGO_chr3_018144579_151_m1	chr3	18144579	18144729	-	1	151	31.27	AntisenseIntron							
CONGO_chr3_018459276_66_p0	chr3	18459276	18459341	+	0	66	2.38	AntisenseIntron							
CONGO_chr3_018651454_133_p1	chr3	18651454	18651586	+	1	133	11.63	Intergenic							
CONGO_chr3_018675008_139_p0	chr3	18675008	18675146	+	0	139	60.2	Intergenic							
CONGO_chr3_018675170_108_p0	chr3	18675170	18675277	+	0	108	125.55	Intergenic							
CONGO_chr3_018819440_134_m0	chr3	18819440	18819573	-	0	134	86.62	AntisenseNCIntron							
CONGO_chr3_018892136_177_m2	chr3	18892136	18892312	-	2	177	38.95	AntisenseNCIntron							
CONGO_chr3_022185313_219_m2	chr3	22185313	22185531	-	2	219	1245.92	NCExon			1	1	TU272	SpliceToPCG	OTTHUMG00000130484
CONGO_chr3_022388945_106_m0	chr3	22388945	22389050	-	0	106	8	NCExon			1	1	TU272	SpliceToPCG	OTTHUMG00000130484
CONGO_chr3_024135581_44_m1	chr3	24135581	24135624	-	1	44	51.28	UTR			1		TU906	SpliceToPCG	OTTHUMG00000130478
CONGO_chr3_025308160_151_m1	chr3	25308160	25308310	-	1	151	43.94	AntisenseIntron							
CONGO_chr3_025444765_145_p2	chr3	25444765	25444909	+	2	145	229.12	UTR			1	1	TU273	SpliceToPCG	OTTHUMG00000130480
CONGO_chr3_025444914_113_p1	chr3	25444914	25445026	+	1	113	17.07	UTR			1	1	TU273	SpliceToPCG	OTTHUMG00000130480
CONGO_chr3_028592768_224_p2	chr3	28592768	28592991	+	2	224	535.64	NCExon				1	TU274	SpliceToPCG	OTTHUMG00000155699
CONGO_chr3_028881719_69_p0	chr3	28881719	28881787	+	0	69	337.03	NCExon				1	TU274	SpliceToNCG	OTTHUMG00000155718
CONGO_chr3_029199451_174_p0	chr3	29199451	29199624	+	0	174	847.1	NCExon				1			
CONGO_chr3_031725749_84_m0	chr3	31725749	31725832	-	0	84	208.59	AntisenseNCExon							
CONGO_chr3_031867891_117_m0	chr3	31867891	31868007	-	0	117	94.77	Intron							
CONGO_chr3_032712186_138_p2	chr3	32712186	32712323	+	2	138	340.84	NCExon			1	1	TU907	SpliceToPCG	OTTHUMG00000130748
CONGO_chr3_033593698_63_m2	chr3	33593698	33593760	-	2	63	108.21	NCExon			1	1	TU908	SpliceToPCG	OTTHUMG00000156489
CONGO_chr3_033661982_64_p2	chr3	33661982	33662045	+	2	64	22.18	AntisenseIntron							
CONGO_chr3_035696283_90_p0	chr3	35696283	35696372	+	0	90	44.72	UTR			1	1	TU275	SpliceToPCG	OTTHUMG00000130795
CONGO_chr3_035810652_41_p0	chr3	35810652	35810692	+	0	41	2.8	UTR			1	1	TU275	SpliceToPCG	OTTHUMG00000130795
CONGO_chr3_036924818_132_m1	chr3	36924818	36924949	-	1	132	146.4	NCExon				1	TU909	SpliceToPCG	OTTHUMG00000155848
CONGO_chr3_042103795_102_p2	chr3	42103795	42103896	+	2	102	300.83	NCExon				1	TU911	SpliceToPCG	OTTHUMG00000131795
CONGO_chr3_042226690_52_m1	chr3	42226690	42226741	-	1	52	16.82	AntisenseCDS			1	1		UnsplicedMergeWithPCG	OTTHUMG00000131795
CONGO_chr3_042646992_72_m1	chr3	42646992	42647063	-	1	72	106	AntisenseCDS				1		UnsplicedMergeWithPCG	OTTHUMG00000133037
CONGO_chr3_046012218_38_m1	chr3	46012218	46012255	-	1	38	9.57	UTR			1	1	TU912	SpliceToPCG	OTTHUMG00000133447
CONGO_chr3_046633680_143_p0	chr3	46633680	46633822	+	0	143	1138.7	NCExon			1	1	TU277	SpliceToNCG	OTTHUMG00000156446
CONGO_chr3_046641622_91_p1	chr3	46641622	46641712	+	1	91	440.11	NCExon			1		TU277	SpliceToNCG	OTTHUMG00000156446
CONGO_chr3_046736337_161_m0	chr3	46736337	46736497	-	0	161	681.8	UTR		Trypsin	1	1	TU132	SpliceToPCG	OTTHUMG00000133480
CONGO_chr3_046750130_139_m0	chr3	46750130	46750268	-	0	139	235.43	UTR		Trypsin	1	1	TU132	SpliceToPCG	OTTHUMG00000133480
CONGO_chr3_046750559_178_m2	chr3	46750559	46750736	-	2	178	565.38	NCExon		Trypsin	1	1	TU132	SpliceToPCG	OTTHUMG00000133480
CONGO_chr3_046770253_163_m0	chr3	46770253	46770415	-	0	163	177.01	Intron		Trypsin		1	TU133	SpliceToPCG	OTTHUMG00000133480
CONGO_chr3_046772536_157_m2	chr3	46772536	46772692	-	2	157	191.66	UTR		Trypsin	1	1	TU133	SpliceToPCG	OTTHUMG00000133480
CONGO_chr3_047140544_66_p2	chr3	47140544	47140609	+	2	66	161.93	AntisenseCDS						UnsplicedMergeWithPCG	OTTHUMG00000133514
CONGO_chr3_048675287_59_p1	chr3	48675287	48675345	+	1	59	16.28	AntisenseUTR							
CONGO_chr3_049104834_60_m1	chr3	49104834	49104893	-	1	60	195.13	UTR			1	1	TU913	SpliceToPCG	OTTHUMG00000156771
CONGO_chr3_049555428_297_p0	chr3	49555428	49555724	+	0	297	240.59	Intergenic		Gag_p30					
CONGO_chr3_049979598_101_m2	chr3	49979598	49979698	-	2	101	18.44	AntisenseUTR				1	TU914	NovelMultiExon	
CONGO_chr3_050115325_135_m0	chr3	50115325	50115459	-	0	135	63.81	AntisenseNCExon						UnsplicedMergeWithPCG	OTTHUMG00000156785
CONGO_chr3_052761245_68_p2	chr3	52761245	52761312	+	2	68	5.04	AntisenseCDS				1		UnsplicedMergeWithPCG	ENSG00000114904
CONGO_chr3_053338402_110_p1	chr3	53338402	53338511	+	1	110	93.44	AntisenseIntron							
CONGO_chr3_053749486_60_p0	chr3	53749486	53749545	+	0	60	369.3	Intron							
CONGO_chr3_053805408_60_p0	chr3	53805408	53805467	+	0	60	42.48	Intron			1	1			
CONGO_chr3_055527623_133_m1	chr3	55527623	55527755	-	1	133	52.25	Intron							
CONGO_chr3_056642774_98_p2	chr3	56642774	56642871	+	2	98	62.78	AntisenseCDS					TU916	UnsplicedMergeWithPCG	ENSG00000163946
CONGO_chr3_056925377_51_m0	chr3	56925377	56925427	-	0	51	40.46	Intron			1	1	TU917	SpliceToPCG	ENSG00000163947
CONGO_chr3_057889695_60_p0	chr3	57889695	57889754	+	0	60	19.86	UTR			1		TU918	SpliceToPCG	OTTHUMG00000133764

CONGO_chr3_058141129_131_p0	chr3	58141129	58141259	+	0	131	255.82	Intergenic								
CONGO_chr3_059000323_73_m2	chr3	59000323	59000395	-	2	73	238.07	UTR			1	1	TU134	SpliceToPCG	ENSG00000163689	
CONGO_chr3_059006995_94_m0	chr3	59006995	59007088	-	0	94	597.29	UTR			1	1	TU134	SpliceToPCG	ENSG00000163689	
CONGO_chr3_059007931_90_m0	chr3	59007931	59008020	-	0	90	612.91	UTR			1	1	TU134	SpliceToPCG	ENSG00000163689	
CONGO_chr3_062326146_175_p1	chr3	62326146	62326320	+	1	175	38.52	AntisenseNCIntron								
CONGO_chr3_062335013_32_m2	chr3	62335013	62335044	-	2	32	50.94	UTR					TU919	SpliceToPCG	OTTHUMG00000158705	
CONGO_chr3_062382162_112_p1	chr3	62382162	62382273	+	1	112	31.02	AntisenseIntron								
CONGO_chr3_062411985_53_m0	chr3	62411985	62412037	-	0	53	64.34	Intron								
CONGO_chr3_062495291_138_m0	chr3	62495291	62495428	-	0	138	35.51	Intron								
CONGO_chr3_064405199_86_m0	chr3	64405199	64405284	-	0	86	608.19	NCExon				1	TU920	SpliceToNCG	OTTHUMG00000158710	
CONGO_chr3_069304883_92_m1	chr3	69304883	69304974	-	1	92	22.97	Intron					TU921	SpliceToPCG	OTTHUMG00000158772	
CONGO_chr3_070020287_60_m2	chr3	70020287	70020346	-	2	60	22.12	AntisenseIntron					TU922	NovelMultiExon		
CONGO_chr3_070328767_260_m2	chr3	70328767	70329026	-	2	260	1900.95	NCExon				1				
CONGO_chr3_070338410_222_m2	chr3	70338410	70338631	-	2	222	721.97	NCExon				1				
CONGO_chr3_070443727_88_m0	chr3	70443727	70443814	-	0	88	259.28	Intergenic								
CONGO_chr3_070518743_85_p2	chr3	70518743	70518827	+	2	85	88.75	Intergenic								
CONGO_chr3_071103852_94_m0	chr3	71103852	71103945	-	0	94	49.79	UTR			1		TU923	SpliceToPCG	OTTHUMG00000158803	
CONGO_chr3_071180890_86_p1	chr3	71180890	71180975	+	1	86	27.59	AntisenseIntron								
CONGO_chr3_071265273_97_p1	chr3	71265273	71265369	+	1	97	93	AntisenseIntron								
CONGO_chr3_071298842_165_p0	chr3	71298842	71299006	+	0	165	4.62	AntisenseIntron								
CONGO_chr3_071505812_100_m2	chr3	71505812	71505911	-	2	100	23.08	Intron								
CONGO_chr3_071576334_76_p1	chr3	71576334	71576409	+	1	76	8.62	AntisenseIntron								
CONGO_chr3_073565480_69_m0	chr3	73565480	73565548	-	0	69	393.95	Intron			1	1	TU924	SpliceToPCG	ENSG00000121440	
CONGO_chr3_076443129_130_p0	chr3	76443129	76443258	+	0	130	77.44	Intron				1				
CONGO_chr3_077734776_126_p2	chr3	77734776	77734901	+	2	126	290.12	Intron				1	TU925	SpliceToPCG	ENSG00000185008	
CONGO_chr3_077764315_183_p2	chr3	77764315	77764497	+	2	183	602.97	Intron			1	1	TU926	SpliceToPCG	ENSG00000185008	
CONGO_chr3_077774512_273_p2	chr3	77774512	77774784	+	2	273	936.9	Intron				1	TU927	SpliceToPCG	ENSG00000185008	
CONGO_chr3_079543761_109_m0	chr3	79543761	79543869	-	0	109	214.03	Intron								
CONGO_chr3_081226819_95_p1	chr3	81226819	81226913	+	1	95	2.65	Intergenic								
CONGO_chr3_086111050_99_m0	chr3	86111050	86111148	-	0	99	7.36	AntisenseCDS								
CONGO_chr3_088191160_186_p0	chr3	88191160	88191345	+	0	186	486.76	AntisenseIntron				1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088218097_146_p0	chr3	88218097	88218242	+	0	146	1069.69	AntisenseIntron				1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088244955_82_p1	chr3	88244955	88245036	+	1	82	481.54	AntisenseIntron				1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088257974_136_p0	chr3	88257974	88258109	+	0	136	378.12	AntisenseIntron	1			1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088260649_203_p2	chr3	88260649	88260851	+	2	203	725.44	AntisenseIntron				1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088261527_140_p0	chr3	88261527	88261666	+	0	140	794.4	AntisenseIntron				1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088266901_142_p1	chr3	88266901	88267042	+	1	142	566.4	AntisenseIntron				1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088270545_415_p0	chr3	88270545	88270959	+	0	415	1595.81	UTR			1	1	TU16	SpliceToPCG	ENSG00000175105	
CONGO_chr3_088598468_287_p2	chr3	88598468	88598754	+	2	287	356.31	Intergenic					TU928	NovelMultiExon		
CONGO_chr3_088599048_110_m2	chr3	88599048	88599157	-	2	110	174.92	Intergenic								
CONGO_chr3_098649659_48_p0	chr3	98649659	98649706	+	0	48	119.66	Intron				1				
CONGO_chr3_099023741_149_p0	chr3	99023741	99023889	+	0	149	193.21	Intergenic			1	1	TU36	SpliceToPCG	ENSG00000080200	
CONGO_chr3_099044729_67_p1	chr3	99044729	99044795	+	1	67	229.1	Intergenic			1	1	TU36	SpliceToPCG	ENSG00000080200	
CONGO_chr3_099065843_170_p1	chr3	99065843	99066012	+	1	170	432.97	Intergenic			1	1	TU36	SpliceToPCG	ENSG00000080200	
CONGO_chr3_099066091_91_p2	chr3	99066091	99066181	+	2	91	382	Intergenic			1		TU36	SpliceToPCG	ENSG00000080200	
CONGO_chr3_099073376_103_p1	chr3	99073376	99073478	+	1	103	299.32	Intergenic			1		TU36	SpliceToPCG	ENSG00000080200	
CONGO_chr3_099078474_67_p0	chr3	99078474	99078540	+	0	67	171.32	UTR			1		TU36	SpliceToPCG	ENSG00000080200	
CONGO_chr3_099306349_343_p2	chr3	99306349	99306691	+	2	343	941.59	Intergenic		7tm_1				NovelUnspliced		
CONGO_chr3_099306893_285_p2	chr3	99306893	99307177	+	2	285	901.4	Intergenic		7tm_1						
CONGO_chr3_099399073_109_p2	chr3	99399073	99399181	+	2	109	58.22	Intergenic	1	7tm_1						
CONGO_chr3_099399331_150_p0	chr3	99399331	99399480	+	0	150	34.92	Intergenic	1			1				
CONGO_chr3_099399511_140_p0	chr3	99399511	99399650	+	0	140	162.07	Intergenic	1			1				
CONGO_chr3_099409023_367_p0	chr3	99409023	99409389	+	0	367	304.61	Intergenic		7tm_1						
CONGO_chr3_099409394_460_p2	chr3	99409394	99409853	+	2	460	407.65	Intergenic								
CONGO_chr3_099423905_556_p1	chr3	99423905	99424460	+	1	556	341.9	Intergenic								
CONGO_chr3_101031952_92_m0	chr3	101031952	101032043	-	0	92	46.31	AntisenseIntron				1	TU929	SpliceToPCG	ENSG00000168386	
CONGO_chr3_101409573_172_p0	chr3	101409573	101409744	+	0	172	553.39	Intergenic		CDC50						
CONGO_chr3_101413110_118_p2	chr3	101413110	101413227	+	2	118	163.93	Intergenic		CDC50						
CONGO_chr3_107070446_110_m1	chr3	107070446	107070555	-	1	110	189	UTR			1	1	TU930	SpliceToPCG	OTTHUMG00000150654	
CONGO_chr3_113151332_96_p0	chr3	113151332	113151427	+	0	96	382.33	Intron					TU931	SpliceToPCG	ENSG00000144824	
CONGO_chr3_113200784_103_p0	chr3	113200784	113200886	+	0	103	42.17	UTR			1	1	TU932	SpliceToPCG	ENSG00000144834	
CONGO_chr3_113236383_48_p0	chr3	113236383	113236430	+	0	48	1.61	Intergenic								
CONGO_chr3_113239609_250_p0	chr3	113239609	113239858	+	0	250	977.42	UTR				1				
CONGO_chr3_113248511_39_p2	chr3	113248511	113248549	+	2	39	296.12	NCExon				1				
CONGO_chr3_115539733_107_m2	chr3	115539733	115539839	-	2	107	11.46	UTR			1		TU278	SpliceToPCG	ENSG00000181722	
CONGO_chr3_115577331_43_p1	chr3	115577331	115577373	+	1	43	130.92	NCExon			1	1	TU933	NovelMultiExon		
CONGO_chr3_115620632_73_m1	chr3	115620632	115620704	-	1	73	23.53	Intron				1				
CONGO_chr3_115766880_162_m0	chr3	115766880	115767041	-	0	162	73.49	Intron						NovelUnspliced		
CONGO_chr3_115826414_186_m2	chr3	115826414	115826599	-	2	186	40.03	UTR			1	1	TU278	SpliceToPCG	ENSG00000181722	
CONGO_chr3_115916205_103_m1	chr3	115916205	115916307	-	1	103	0.07	Intron						NovelUnspliced		
CONGO_chr3_116301724_46_p2	chr3	116301724	116301769	+	2	46	61.1	AntisenseIntron								
CONGO_chr3_117018151_33_m2	chr3	117018151	117018183	-	2	33	56.11	Intron			1		TU934	SpliceToPCG	ENSG00000185565	
CONGO_chr3_120495857_99_p2	chr3	120495857	120495955	+	2	99	14.32	UTR			1		TU935	SpliceToPCG	ENSG00000031081	
CONGO_chr3_121567997_154_p2	chr3	121567997	121568150	+	2	154	76.45	Intergenic				1				
CONGO_chr3_121568171_222_p2	chr3	121568171	121568392	+	2	222	428.14	Intergenic				1				
CONGO_chr3_121569449_174_p2	chr3	121569449	121569622	+	2	174	931.24	Intergenic				1				
CONGO_chr3_123941909_73_p1	chr3	123941909	123941981	+	1	73	193.1	AntisenseCDS			1	1				
CONGO_chr3_126216247_300_m2	chr3	126216247	126216546	-	2	300	750.44	Intron			1	1	TU936	SpliceToPCG	ENSG00000173706	
CONGO_chr3_128361140_144_m0	chr3	128361140	128361283	-	0	144	12.28	Intergenic								
CONGO_chr3_130597750_110_m0	chr3	130597750	130597859	-	0	110	57.55	UTR	1	Ribosomal_L32e	1	1	TU937	SpliceToPCG	ENSGR0000183611	
CONGO_chr3_130995857_39_m0	chr3	130995857	130995895	-	0	39	117.59	Intron			1	1	TU938	SpliceToPCG	ENSG00000172765	
CONGO_chr3_132052355_108_p0	chr3	132052355	132052462	+	0	108	654.9	Intergenic			1	1	TU280	SpliceToPCG	ENSG00000017260	
CONGO_chr3_132096124_55_p0	chr3	132096124	132096178	+	0	55	9.54	UTR			1	1	TU280	SpliceToPCG	ENSG00000017260	
CONGO_chr3_132564890_130_p1	chr3	132564890	132565019	+	1	130	14.44	NCExon			1	1	TU939	SpliceToPCG	ENSG00000206369	
CONGO_chr3_134889726_154_p2	chr3	134889726	134889879	+	2	154	227.39	Intergenic		Transferrin		1				
CONGO_chr3_134893257_109_p0	chr3	134893257	134893365	+	0	109	652.66	Intergenic		Transferrin						
CONGO_chr3_134895750_147_p2	chr3	134895750	134895896	+	2	147	281.22	Intergenic		Transferrin						
CONGO_chr3_134900979_116_p2	chr3	134900979	134901094	+	2	116	260.58	Intergenic		Transferrin						
CONGO_chr3_134902416_125_p0	chr3	134902416	134902540	+	0	125	560.88	UTR		Transferrin	1	1				
CONGO_chr3_134905758_91_p0	chr3	134905758	134905848	+	0	91	575.05	Intron		Transferrin						
CONGO_chr3_134911110_93_p2	chr3	134911110	134911202	+	2	93	145.79	UTR		Transferrin	1					
CONGO_chr3_134914195_151_p2	chr3	134914195	134914345	+	2	151	342.42	UTR		Transferrin	1					
CONGO_chr3_138465894_89_p0	chr3	138465894	138465982	+	0	89	26.21	Intergenic								
CONGO_chr3_138843933_160_p1	chr3	138843933	138844092	+	1	160	54.43	Intergenic								
CONGO_chr3_139389087_45_p0	chr3	139389087	139389131	+	0	45	29.94	UTR			1	1	TU940	SpliceToPCG	ENSG00000114098	
CONGO_chr3_142168466_103_p1	chr3	142168466	142168568	+	1	103	103.66	UTR			1	1	TU941	SpliceToPCG	ENSG00000114120	
CONGO_chr3_142605459_50_p2	chr3	142605459	142605508	+	2	50	10.95	UTR			1	1	TU942	SpliceToPCG	ENSG00000177311	
CONGO_chr3_142864624_180_p0	chr3	142864624	142864803	+	0	180	695.58	Intergenic				1	TU281	NovelMultiExon		
CONGO_chr3_142868312_153_p0	chr3	142868312	142868464	+	0	153	810.79	Intergenic				1	TU281	NovelMultiExon		
CONGO_chr3_142883017_149_p0	chr3	142883017	142883165	+	0	149	373.09	Intergenic				1				
CONGO_chr3_142886591_141_p1	chr3	142886591	142886731	+	1	141	535.99	Intergenic				1				
CONGO_chr3_142887404_146_p1	chr3	142887404	142887549	+	1	146	326.03	Intergenic				1				
CONGO_chr3_142922551_80_p1	chr3	142922551	142922630	+	1	80	77.28	Intergenic				1				
CONGO_chr3_142930823_113_p2	chr3	142930823	142930935	+	2	113	389.37	Intergenic								
CONGO_chr3_147596237_162_m0	chr3	147596237	147596398	-	0	162	306.47	Intergenic		Scramblase		1	TU282	NovelMultiExon		
CONGO_chr3_147599170_129_m0	chr3	147599170	147599298	-	0	129	125.87	Intergenic		Scramblase						
CONGO_chr3_147601837_200_m2	chr3	147601837	147602036	-	2	200	370.41	Intergenic		Scramblase		1	TU282	NovelMultiExon		
CONGO_chr3_147799262_82_p0	chr3	147799262	147799343	+	0	82	46.09	AntisenseIntron					TU943	NovelMultiExon		
CONGO_chr3_148532521_114_p0	chr3	148532521	148532634	+	0	114	17.77	Intergenic								
CONGO_chr3_148608556_137_m2	chr3	148608556	148608692	-	2	137	31	Intergenic								
CONGO_chr3_149071038_89_p1	chr3	149071038	149071126	+	1	89	3.29	Intergenic								
CONGO_chr3_149135077_83_p2	chr3	149135077	149135159	+	2	83	29.16	Intergenic								
CONGO_chr3_150441839_140_m2	chr3	150441839	150441978	-	2	140	629.09	Intergenic				1	TU944	SpliceToPCG	OTTHUMG00000150306	
CONGO_chr3_150449499_140_m1	chr3	150449499	150449638	-	1	140	98.75	Intergenic								
CONGO_chr3_150453323_213_m2	chr3	150453323	150453535	-	2	213	445.72	Intergenic								
CONGO_chr3_150456407_212_m2	chr3	150456407	150456618	-	2	212	555.94	Intergenic								
CONGO_chr3_150467343_172_m2	chr3	150467343	150467514	-	2	172	71.43	Intergenic								
CONGO_chr3_150470297_243_m2	chr3	150470297	150470539	-	2	243	266.25	Intergenic								
CONGO_chr3_150475940_114_m2	chr3	150475940	150476053	-	2	114	89.85	Intergenic								
CONGO_chr3_150476987_114_m1	chr3	150476987	150477100	-	1	114	6.34	Intergenic				1				
CONGO_chr3_152105804_113_m0	chr3	152105804	152105916	-	0	113	150.42	Intergenic								
CONGO_chr3_152500615_62_m2	chr3	152500615	152500676	-	2	62	52.48	UTR			1	1	TU945	SpliceToPCG	ENSG00000138271	
CONGO_chr3_152603406_51_p0	chr3	152603406	152603456	+	0	51	13.09	Intron					TU946	SpliceToPCG	ENSG00000144893	
CONGO_chr3_152973908_223_p0	chr3	152973908	152974130	+	0	223	510.07	NCIntron				1				
CONGO_chr3_152977282_172_p1	chr3	152977282	152977453	+	1	172	674.41	NCIntron		Abhydrolase_3		1	TU283	NovelMultiExon		

CONGO_chr3_152984310_188_p0	chr3	152984310	152984497	+	0	188	227.44	NCExon			1	1	TU283	NovelMultiExon	
CONGO_chr3_152984614_138_p1	chr3	152984614	152984751	+	1	138	568.39	NCExon			1	1			
CONGO_chr3_153499884_55_p1	chr3	153499884	153499938	+	1	55	3.28	UTR			1	1	TU947	SpliceToPCG	ENSG00000152601
CONGO_chr3_156491427_95_m2	chr3	156491427	156491521	-	2	95	37.39	NCExon			1	1	TU948	SpliceToNCG	OTTHUMG00000158471
CONGO_chr3_156904629_79_m0	chr3	156904629	156904707	-	0	79	301.74	UTR			1	1	TU949	SpliceToPCG	OTTHUMG00000158477
CONGO_chr3_159632443_70_p0	chr3	159632443	159632512	+	0	70	96.03	Intron							
CONGO_chr3_159632604_157_m2	chr3	159632604	159632760	-	2	157	128.54	AntisenseIntron							
CONGO_chr3_160041634_184_m1	chr3	160041634	160041817	-	1	184	435.36	Intergenic			1				
CONGO_chr3_160041906_383_m0	chr3	160041906	160042288	-	0	383	618.53	Intergenic		7tm_1	1				
CONGO_chr3_160932818_80_p2	chr3	160932818	160932897	+	2	80	49.22	Intron				1	TU950	SpliceToPCG	ENSG00000151967
CONGO_chr3_169113268_119_p2	chr3	169113268	169113386	+	2	119	223.65	NCExon			1	1	TU136	SpliceToNCG	OTTHUMG00000158502
CONGO_chr3_169115543_143_p0	chr3	169115543	169115685	+	0	143	737.1	NCExon			1	1	TU136	SpliceToNCG	OTTHUMG00000158502
CONGO_chr3_169117781_198_p1	chr3	169117781	169117978	+	1	198	437.94	NCIntron					TU136	SpliceToNCG	OTTHUMG00000158503
CONGO_chr3_169413563_57_m1	chr3	169413563	169413619	-	1	57	3.41	Intergenic							
CONGO_chr3_170316314_104_p1	chr3	170316314	170316417	+	1	104	513.95	AntisenseCDS							
CONGO_chr3_170316802_113_p2	chr3	170316802	170316914	+	2	113	432.05	AntisenseCDS						UnsplicedMergeWithPCG	OTTHUMG00000158596
CONGO_chr3_170442969_101_p1	chr3	170442969	170443069	+	1	101	2.81	AntisenseIntron							
CONGO_chr3_170565195_63_p0	chr3	170565195	170565257	+	0	63	87.64	AntisenseIntron							
CONGO_chr3_170600778_66_m0	chr3	170600778	170600843	-	0	66	16.89	Intron							
CONGO_chr3_170600869_81_m0	chr3	170600869	170600949	-	0	81	0.09	Intron							
CONGO_chr3_170676968_98_p2	chr3	170676968	170677065	+	2	98	23.61	AntisenseIntron						NovelUnspliced	
CONGO_chr3_170678512_105_m0	chr3	170678512	170678616	-	0	105	89.54	Intron							
CONGO_chr3_170775007_116_m1	chr3	170775007	170775122	-	1	116	116.81	Intron							
CONGO_chr3_170782017_74_p1	chr3	170782017	170782090	+	1	74	134.18	AntisenseIntron							
CONGO_chr3_174805774_75_m0	chr3	174805774	174805848	-	0	75	5.45	AntisenseIntron							
CONGO_chr3_181944661_265_m0	chr3	181944661	181944925	-	0	265	3	Intron						NovelUnspliced	
CONGO_chr3_182375145_140_m2	chr3	182375145	182375284	-	2	140	90.42	AntisenseNCIntron							
CONGO_chr3_182375431_58_m2	chr3	182375431	182375488	-	2	58	18.14	AntisenseNCIntron							
CONGO_chr3_182927354_224_p0	chr3	182927354	182927577	+	0	224	61.04	NCIntron							
CONGO_chr3_182952927_68_p1	chr3	182952927	182952994	+	1	68	46.01	NCIntron							
CONGO_chr3_183224362_106_m1	chr3	183224362	183224467	-	1	106	39.93	Intergenic							
CONGO_chr3_183461555_80_m1	chr3	183461555	183461634	-	1	80	43.6	Intergenic							
CONGO_chr3_183472039_171_p0	chr3	183472039	183472209	+	0	171	25.16	Intergenic							
CONGO_chr3_184333299_140_m2	chr3	184333299	184333438	-	2	140	122.09	Intron		Lamp			TU953	SpliceToPCG	OTTHUMG00000158355
CONGO_chr3_185700227_245_m0	chr3	185700227	185700471	-	0	245	486.83	AntisenseIntron							
CONGO_chr3_185700502_135_m0	chr3	185700502	185700636	-	0	135	452.6	AntisenseIntron							
CONGO_chr3_185700779_74_m0	chr3	185700779	185700852	-	0	74	94.7	AntisenseIntron						NovelUnspliced	
CONGO_chr3_188922291_73_m0	chr3	188922291	188922363	-	0	73	56.13	UTR			1		TU956	SpliceToPCG	OTTHUMG00000156441
CONGO_chr3_189552868_62_p0	chr3	189552868	189552929	+	0	62	30.42	Intron							
CONGO_chr3_197119963_495_m0	chr3	197119963	197120457	-	0	495	1488.68	UTR			1	1	TU957	SpliceToPCG	OTTHUMG00000155737
CONGO_chr4_000558694_1158_m0	chr4	558694	559851	-	0	1158	1870.43	Intergenic						NovelUnspliced	
CONGO_chr4_001386720_884_m2	chr4	1386720	1387603	-	2	884	2104.43	Intergenic		Homeobox	1				
CONGO_chr4_001389768_463_m0	chr4	1389768	1390230	-	0	463	937.92	Intergenic							
CONGO_chr4_001913923_66_m0	chr4	1913923	1913988	-	0	66	79.54	AntisenseCDS				1		UnsplicedMergeWithPCG	OTTHUMG00000121147
CONGO_chr4_002416729_105_p0	chr4	2416729	2416833	+	0	105	725.92	Intron				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002422472_72_p0	chr4	2422472	2422543	+	0	72	263.02	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002422789_89_p0	chr4	2422789	2422877	+	0	89	446.13	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002423667_205_p1	chr4	2423667	2423871	+	1	205	1414.57	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002430248_142_p0	chr4	2430248	2430389	+	0	142	823.73	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002430632_152_p2	chr4	2430632	2430783	+	2	152	670.57	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002431562_206_p0	chr4	2431562	2431767	+	0	206	2709.21	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002433968_163_p1	chr4	2433968	2434130	+	1	163	855.92	Intergenic				1	TU17	SpliceToPCG	ENSG00000206113
CONGO_chr4_002567609_246_p0	chr4	2567609	2567854	+	0	246	1995.85	UTR			1	1	TU137	SpliceToPCG	ENSG00000125386
CONGO_chr4_002596787_134_p0	chr4	2596787	2596920	+	0	134	1465.04	UTR			1	1	TU137	SpliceToPCG	ENSG00000125386
CONGO_chr4_002597935_168_p1	chr4	2597935	2598102	+	1	168	2002.55	UTR			1	1	TU137	SpliceToPCG	ENSG00000125386
CONGO_chr4_003379014_85_p0	chr4	3379014	3379098	+	0	85	27.07	Intron					TU958	SpliceToPCG	OTTHUMG00000090277
CONGO_chr4_004574583_122_p2	chr4	4574583	4574704	+	2	122	21.25	AntisenseIntron							
CONGO_chr4_006041332_494_m2	chr4	6041332	6041825	-	2	494	1093.29	NCExon			1			UnsplicedMergeWithNCG	OTTHUMG00000125490
CONGO_chr4_006060624_537_m0	chr4	6060624	6061160	-	0	537	942.73	Intergenic							
CONGO_chr4_006064458_139_m1	chr4	6064458	6064596	-	1	139	612.73	Intergenic							
CONGO_chr4_006070773_287_m0	chr4	6070773	6071059	-	0	287	1292.75	Intergenic							
CONGO_chr4_006122685_106_m0	chr4	6122685	6122790	-	0	106	616.15	Intron							
CONGO_chr4_008063057_120_m2	chr4	8063057	8063176	-	2	120	187.25	Intron				1	TU959	SpliceToPCG	ENSG00000163995
CONGO_chr4_008493450_96_p0	chr4	8493450	8493545	+	0	96	263.27	Intron				1	TU284	SpliceToPCG	OTTHUMG00000128484
CONGO_chr4_008493783_286_p0	chr4	8493783	8494068	+	0	286	372.38	UTR			1	1	TU284	SpliceToPCG	ENSG00000205959
CONGO_chr4_014613795_209_m2	chr4	14613795	14614003	-	2	209	23.47	Intergenic						NovelUnspliced	
CONGO_chr4_015807379_32_m2	chr4	15807379	15807410	-	2	32	5.77	Intron				1	TU960	SpliceToPCG	ENSG00000169762
CONGO_chr4_017485898_120_m0	chr4	17485898	17486017	-	0	120	455.85	Intron						UnsplicedMergeWithPCG	ENSG00000215273
CONGO_chr4_017486231_253_m1	chr4	17486231	17486483	-	1	253	745.33	Intron						UnsplicedMergeWithPCG	ENSG00000215273
CONGO_chr4_017486750_88_m1	chr4	17486750	17486837	-	1	88	234.64	Intron							
CONGO_chr4_017487100_299_m1	chr4	17487100	17487398	-	1	299	189.54	Intron						NovelUnspliced	
CONGO_chr4_017487805_318_m2	chr4	17487805	17488122	-	2	318	668.68	Intron						NovelUnspliced	
CONGO_chr4_020091095_78_m1	chr4	20091095	20091172	-	1	78	45.74	AntisenseIntron							
CONGO_chr4_023846359_116_p0	chr4	23846359	23846474	+	0	116	46	Intergenic							
CONGO_chr4_024083096_90_m0	chr4	24083096	24083185	-	0	90	7.1	Intergenic				1		NovelUnspliced	
CONGO_chr4_024147975_99_m0	chr4	24147975	24148073	-	0	99	163.48	UTR			1	1	TU961	SpliceToPCG	ENSG00000109606
CONGO_chr4_024341118_63_p2	chr4	24341118	24341180	+	2	63	21.54	Intergenic							
CONGO_chr4_025774303_32_p0	chr4	25774303	25774334	+	0	32	95.2	Intergenic				1	TU962	SpliceToPCG	OTTHUMG00000097793
CONGO_chr4_030397447_70_p0	chr4	30397447	30397516	+	0	70	1.02	Intron					TU963	SpliceToPCG	ENSG00000169851
CONGO_chr4_030560840_89_p2	chr4	30560840	30560928	+	2	89	116.14	Intron				1	TU964	SpliceToPCG	ENSG00000169851
CONGO_chr4_035959776_208_p0	chr4	35959776	35959983	+	0	208	501.72	UTR			1			UnsplicedMergeWithPCG	ENSG00000197057
CONGO_chr4_038351775_81_m0	chr4	38351775	38351855	-	0	81	2.73	AntisenseIntron							
CONGO_chr4_041444983_107_m0	chr4	41444983	41445089	-	0	107	57.78	Intron							
CONGO_chr4_041554195_143_m0	chr4	41554195	41554337	-	0	143	15.92	Intergenic							
CONGO_chr4_041554379_152_p2	chr4	41554379	41554530	+	2	152	61.53	Intergenic							
CONGO_chr4_041569824_152_m2	chr4	41569824	41569975	-	2	152	19.76	Intergenic					TU965	NovelMultiExon	
CONGO_chr4_046643817_83_p2	chr4	46643817	46643899	+	2	83	23.26	AntisenseIntron							
CONGO_chr4_048091319_109_p0	chr4	48091319	48091427	+	0	109	149.94	Intron				1	TU966	SpliceToPCG	ENSG00000109171
CONGO_chr4_048295603_45_m0	chr4	48295603	48295647	-	0	45	175.21	Intron					TU967	SpliceToPCG	ENSG00000075539
CONGO_chr4_052555772_67_p2	chr4	52555772	52555838	+	2	67	217.43	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000188993
CONGO_chr4_056380950_121_p0	chr4	56380950	56381070	+	0	121	641.96	UTR			1		TU968	NovelMultiExon	
CONGO_chr4_056833244_172_p2	chr4	56833244	56833415	+	2	172	619.82	UTR			1	1	TU969	SpliceToPCG	ENSG00000109265
CONGO_chr4_056971694_80_p0	chr4	56971694	56971773	+	0	80	0.9	AntisenseIntron			1	1	TU970	NovelMultiExon	
CONGO_chr4_056980594_212_p2	chr4	56980594	56980805	+	2	212	199.66	AntisenseIntron			1	1			
CONGO_chr4_057113484_54_p1	chr4	57113484	57113537	+	1	54	222.74	Intergenic				1	TU138	NovelMultiExon	
CONGO_chr4_057120315_129_p1	chr4	57120315	57120443	+	1	129	266.33	Intergenic				1	TU138	NovelMultiExon	
CONGO_chr4_057136428_96_p1	chr4	57136428	57136523	+	1	96	97.87	Intergenic				1	TU138	NovelMultiExon	
CONGO_chr4_057145446_89_p2	chr4	57145446	57145534	+	2	89	134.66	Intergenic				1		NovelUnspliced	
CONGO_chr4_057157423_132_p0	chr4	57157423	57157554	+	0	132	617.07	Intergenic				1	TU285	NovelMultiExon	
CONGO_chr4_057161857_176_p0	chr4	57161857	57162032	+	0	176	1298.37	Intergenic				1	TU285	NovelMultiExon	
CONGO_chr4_057164132_115_p1	chr4	57164132	57164246	+	1	115	725.44	Intergenic				1			
CONGO_chr4_062611818_129_p2	chr4	62611818	62611946	+	2	129	163.71	Intron		Latrophilin		1	TU971	SpliceToPCG	ENSG00000150471
CONGO_chr4_062616439_44_m0	chr4	62616439	62616482	-	0	44	98.73	AntisenseCDS							
CONGO_chr4_063002558_94_m1	chr4	63002558	63002651	-	1	94	96.05	Intergenic							
CONGO_chr4_068732451_117_m0	chr4	68732451	68732567	-	0	117	299.62	AntisenseNCIntron				1			
CONGO_chr4_068733680_120_m0	chr4	68733680	68733799	-	0	120	631.23	AntisenseNCIntron		Trypsin					
CONGO_chr4_068734287_260_m1	chr4	68734287	68734546	-	1	260	1032.44	AntisenseNCIntron		Trypsin		1			
CONGO_chr4_068735301_88_m2	chr4	68735301	68735388	-	2	88	24.87	AntisenseNCIntron		Trypsin					
CONGO_chr4_068735425_51_m2	chr4	68735425	68735475	-	2	51	60.32	AntisenseNCIntron							
CONGO_chr4_068736737_161_m1	chr4	68736737	68736897	-	1	161	148.1	UTR		SEA	1	1			
CONGO_chr4_069252960_228_m1	chr4	69252960	69253187	-	1	228	239.82	Intergenic	1	UDPGT					
CONGO_chr4_069256961_208_m2	chr4	69256961	69257168	-	2	208	436.59	Intergenic	1	UDPGT					
CONGO_chr4_069260680_129_m0	chr4	69260680	69260808	-	0	129	88.96	Intergenic	1	UDPGT					
CONGO_chr4_069815285_224_m1	chr4	69815285	69815508	-	1	224	236.93	NCExon	1	UDPGT			TU972	UnsplicedMergeWithNCG	ENSG00000205660
CONGO_chr4_069905200_243_m1	chr4	69905200	69905442	-	1	243	286.26	Intergenic	1	UDPGT					
CONGO_chr4_069909164_220_m2	chr4	69909164	69909383	-	2	220	505.25	Intergenic	1	UDPGT		1	TU973	SpliceToPCG	ENSG00000156096
CONGO_chr4_069910223_88_m0	chr4	69910223	69910310	-	0	88	29.87	Intergenic	1	UDPGT		1			
CONGO_chr4_069914330_132_m0	chr4	69914330	69914461	-	0	132	128.39	Intergenic	1	UDPGT					
CONGO_chr4_069919971_270_m2	chr4	69919971	69920240	-	2	270	112.34	Intergenic	1	UDPGT					
CONGO_chr4_069920516_162_m0	chr4	69920516	69920677	-	0	162	4.45	Intergenic	1	UDPGT					
CONGO_chr4_069928144_156_p0	chr4	69928144	69928299	+	0	156	148.81	Intergenic		UDPGT					
CONGO_chr4_069935652_96_p0	chr4	69935652	69935747	+	0	96	91.95	Intergenic	1	UDPGT					
CONGO_chr4_069939477_197_p2	chr4	69939477	69939673	+	2	197	63.89	Intergenic	1	UDPGT			TU974	NovelMultiExon	
CONGO_chr4_070257562_206_p2	chr4	70257562	70257767	+	2	206	67.23	Intergenic	1	UDPGT					
CONGO_chr4_070289855_223_p1	chr4	70289855	70290077	+	1	223	12.99	UTR	1	UDPGT					

CONGO_chr4_070290248_270_p2	chr4	70290248	70290517	+	2	270	523.9	Intron		1	UDPGT					
CONGO_chr4_070298914_88_p0	chr4	70298914	70299001	+	0	88	107.62	Intergenic		1	UDPGT			TU139	SpliceToPCG	ENSG00000215110
CONGO_chr4_070299839_220_p2	chr4	70299839	70300058	+	2	220	690.95	Intergenic		1	UDPGT			TU975	SpliceToPCG	ENSG00000109181
CONGO_chr4_070302111_243_p1	chr4	70302111	70302353	+	1	243	482.47	Intergenic		1	UDPGT		1	TU976	SpliceToPCG	OTTHUMG00000129404
CONGO_chr4_070309144_156_p0	chr4	70309144	70309299	+	0	156	132.99	Intergenic		1	UDPGT					
CONGO_chr4_070309552_313_p0	chr4	70309552	70309864	+	0	313	5.77	Intergenic		1	UDPGT					
CONGO_chr4_070318325_88_p0	chr4	70318325	70318412	+	0	88	146.11	UTR		1	UDPGT		1	TU139	SpliceToPCG	ENSG00000215110
CONGO_chr4_070319253_220_p2	chr4	70319253	70319472	+	2	220	327.88	UTR		1	UDPGT			TU139	SpliceToPCG	ENSG00000215110
CONGO_chr4_070323194_228_p1	chr4	70323194	70323421	+	1	228	242.93	UTR		1	UDPGT			TU977	SpliceToPCG	OTTHUMG00000129401
CONGO_chr4_071826208_54_p2	chr4	71826208	71826261	+	2	54	133.41	Intron				1	1	TU978	SpliceToPCG	OTTHUMG00000129910
CONGO_chr4_072271857_126_p1	chr4	72271857	72271982	+	1	126	0.45	UTR				1	1	TU979	SpliceToPCG	OTTHUMG00000129907
CONGO_chr4_072453670_62_m2	chr4	72453670	72453731	-	2	62	177.2	AntisenseIntron								
CONGO_chr4_073391995_84_m2	chr4	73391995	73392078	-	2	84	268.73	Intron								
CONGO_chr4_077287656_162_m2	chr4	77287656	77287817	-	2	162	304.73	UTR				1	1	TU980	NovelMultiExon	
CONGO_chr4_077779740_80_p0	chr4	77779740	77779819	+	0	80	105.99	NCExon					1			
CONGO_chr4_078959768_108_m2	chr4	78959768	78959875	-	2	108	110.88	Intergenic					1	TU981	SpliceToPCG	ENSG00000138767
CONGO_chr4_080351842_67_m2	chr4	80351842	80351908	-	2	67	74.77	AntisenseNCIntron							NovelUnspliced	
CONGO_chr4_080763354_52_p2	chr4	80763354	80763405	+	2	52	1.97	Intergenic						TU982	NovelUnspliced	
CONGO_chr4_080787332_105_m0	chr4	80787332	80787436	-	0	105	62.37	Intergenic								
CONGO_chr4_082743017_84_m0	chr4	82743017	82743100	-	0	84	425.17	Intergenic					1	TU286	NovelMultiExon	
CONGO_chr4_082964695_54_m0	chr4	82964695	82964748	-	0	54	257.87	Intergenic					1	TU286	NovelMultiExon	
CONGO_chr4_083055488_48_m0	chr4	83055488	83055535	-	0	48	129.56	Intergenic					1			
CONGO_chr4_083430681_71_p0	chr4	83430681	83430751	+	0	71	106.97	Intergenic								
CONGO_chr4_083435868_97_p1	chr4	83435868	83435964	+	1	97	182.98	Intergenic						TU983	NovelMultiExon	
CONGO_chr4_083494270_62_m2	chr4	83494270	83494331	-	2	62	24.88	UTR				1	1	TU287	SpliceToPCG	OTTHUMG00000130290
CONGO_chr4_083495072_107_m0	chr4	83495072	83495178	-	0	107	4	UTR				1	1	TU287	SpliceToPCG	OTTHUMG00000130290
CONGO_chr4_084790957_60_p0	chr4	84790957	84791016	+	0	60	33.2	Intergenic								
CONGO_chr4_084919215_136_m1	chr4	84919215	84919350	-	1	136	6.83	Intergenic								
CONGO_chr4_084919647_55_p1	chr4	84919647	84919701	+	1	55	58.11	Intergenic								
CONGO_chr4_088607985_78_m0	chr4	88607985	88608062	-	0	78	143.68	Intergenic								
CONGO_chr4_090169803_71_p1	chr4	90169803	90169873	+	1	71	200.19	AntisenseCDS				1			UnsplicedMergeWithPCG	ENSG00000138640
CONGO_chr4_094946889_159_p0	chr4	94946889	94947047	+	0	159	719.7	Intergenic								
CONGO_chr4_094974770_82_p1	chr4	94974770	94974851	+	1	82	16.92	Intergenic								
CONGO_chr4_096327476_86_m0	chr4	96327476	96327561	-	0	86	96.73	Intron								
CONGO_chr4_099127060_108_m0	chr4	99127060	99127167	-	0	108	21.98	Intron								
CONGO_chr4_099272686_92_m0	chr4	99272686	99272777	-	0	92	182.4	Intron						TU984	SpliceToPCG	OTTHUMG00000131009
CONGO_chr4_099527610_72_p0	chr4	99527610	99527681	+	0	72	120.04	Intron					1	TU985	SpliceToPCG	ENSG00000138698
CONGO_chr4_100790632_880_m1	chr4	100790632	100791511	-	1	880	7635.73	UTR				1		TU140	NovelMultiExon	
CONGO_chr4_100791517_1637_m2	chr4	100791517	100793153	-	2	1637	13260.39	Intergenic						TU140	NovelMultiExon	
CONGO_chr4_100793224_584_m2	chr4	100793224	100793807	-	2	584	2205.61	Intergenic						TU140	NovelMultiExon	
CONGO_chr4_100793901_167_m1	chr4	100793901	100794067	-	1	167	279.67	Intergenic							NovelUnspliced	
CONGO_chr4_102164524_199_m1	chr4	102164524	102164722	-	1	199	52.54	UTR				1		TU986	SpliceToPCG	OTTHUMG00000133839
CONGO_chr4_104283078_206_m2	chr4	104283078	104283283	-	2	206	193.58	Intron								
CONGO_chr4_107498789_261_m0	chr4	107498789	107499049	-	0	261	572.64	Intergenic					1			
CONGO_chr4_107507649_395_m2	chr4	107507649	107508043	-	2	395	1861.59	Intergenic					1			
CONGO_chr4_109314024_101_p1	chr4	109314024	109314124	+	1	101	150.54	NCExon				1	1	TU987	NovelMultiExon	
CONGO_chr4_109960417_87_m0	chr4	109960417	109960503	-	0	87	477.31	NCExon				1		TU988	SpliceToPCG	OTTHUMG00000150039
CONGO_chr4_110988842_81_p1	chr4	110988842	110988922	+	1	81	300.76	Intergenic								
CONGO_chr4_113590411_50_m1	chr4	113590411	113590460	-	1	50	22.9	Intergenic								
CONGO_chr4_114254328_57_p0	chr4	114254328	114254384	+	0	57	150.16	Intron								
CONGO_chr4_114257895_129_p0	chr4	114257895	114258023	+	0	129	1218.99	Intron					1	TU989	SpliceToPCG	OTTHUMG00000132912
CONGO_chr4_114286474_135_p0	chr4	114286474	114286608	+	0	135	760.12	Intron				1	1	TU990	SpliceToPCG	OTTHUMG00000132912
CONGO_chr4_119419710_31_p0	chr4	119419710	119419740	+	0	31	40.61	NCExon				1	1	TU991	UnsplicedMergeWithNCG	ENSG00000206823
CONGO_chr4_121148234_114_m0	chr4	121148234	121148347	-	0	114	62.8	Intergenic		RhoGAP						
CONGO_chr4_122323281_121_m1	chr4	122323281	122323401	-	1	121	173.59	UTR				1	1	TU992	NovelMultiExon	
CONGO_chr4_122357020_86_m0	chr4	122357020	122357105	-	0	86	66.65	UTR				1	1			
CONGO_chr4_122905519_192_m0	chr4	122905519	122905710	-	0	192	776.23	UTR				1	1	TU993	SpliceToPCG	OTTHUMG00000133035
CONGO_chr4_128763992_105_p1	chr4	128763992	128764096	+	1	105	268.01	Intergenic					1			
CONGO_chr4_129202445_380_p1	chr4	129202445	129202824	+	1	380	41.59	Intron					1	TU289	SpliceToPCG	OTTHUMG00000133343
CONGO_chr4_129215065_59_p2	chr4	129215065	129215123	+	2	59	56.13	UTR				1	1	TU289	SpliceToPCG	OTTHUMG00000133343
CONGO_chr4_139843278_160_m1	chr4	139843278	139843437	-	1	160	27.49	Intergenic								
CONGO_chr4_140988758_50_m2	chr4	140988758	140988807	-	2	50	37.27	Intron							NovelUnspliced	
CONGO_chr4_141600116_115_m0	chr4	141600116	141600230	-	0	115	227.74	NCExon		Glyco_transf_54		1	1	TU38	SpliceToPCG	ENSG00000205301
CONGO_chr4_141602533_76_m1	chr4	141602533	141602608	-	1	76	256.24	NCExon		Glyco_transf_54		1	1	TU38	SpliceToPCG	ENSG00000205301
CONGO_chr4_141605500_114_m1	chr4	141605500	141605613	-	1	114	72.89	NCExon				1	1	TU38	SpliceToPCG	ENSG00000205301
CONGO_chr4_141612379_47_m0	chr4	141612379	141612425	-	0	47	16.47	NCExon				1	1	TU38	SpliceToPCG	ENSG00000205301
CONGO_chr4_141615417_134_m2	chr4	141615417	141615550	-	2	134	871.62	NCIntron		Glyco_transf_54			1	TU38	NovelMultiExon	
CONGO_chr4_141638733_94_m0	chr4	141638733	141638826	-	0	94	58.55	NCExon				1	1	TU38	NovelMultiExon	
CONGO_chr4_143170731_175_m1	chr4	143170731	143170905	-	1	175	949.49	Intron					1	TU994	SpliceToPCG	ENSG00000109452
CONGO_chr4_144574717_55_p2	chr4	144574717	144574771	+	2	55	195.78	Intron					1	TU290	SpliceToPCG	ENSG00000109458
CONGO_chr4_147357555_208_p0	chr4	147357555	147357762	+	0	208	314.38	Intergenic								
CONGO_chr4_147362959_223_p2	chr4	147362959	147363181	+	2	223	720.18	Intergenic		Reeler				TU995	NovelMultiExon	
CONGO_chr4_147370849_160_p0	chr4	147370849	147371008	+	0	160	133.74	Intergenic						TU996	NovelMultiExon	
CONGO_chr4_147558507_69_p0	chr4	147558507	147558575	+	0	69	7.69	AntisenseIntron								
CONGO_chr4_147795423_96_p2	chr4	147795423	147795518	+	2	96	44.58	Intergenic								
CONGO_chr4_147909377_126_m1	chr4	147909377	147909502	-	1	126	37.46	Intron								
CONGO_chr4_148155662_81_p2	chr4	148155662	148155742	+	2	81	59.17	Intergenic								
CONGO_chr4_148177763_75_p2	chr4	148177763	148177837	+	2	75	30.98	Intergenic								
CONGO_chr4_148377220_73_p0	chr4	148377220	148377292	+	0	73	218.48	Intergenic								
CONGO_chr4_148379956_53_p0	chr4	148379956	148380008	+	0	53	70.61	Intergenic								
CONGO_chr4_150492620_49_m2	chr4	150492620	150492668	-	2	49	64.46	Intergenic					1	TU291	NovelMultiExon	
CONGO_chr4_150573998_112_m0	chr4	150573998	150574109	-	0	112	245.44	NCExon				1	1	TU291	NovelMultiExon	
CONGO_chr4_150689057_135_m2	chr4	150689057	150689191	-	2	135	557.1	NCExon				1	1	TU79	NovelMultiExon	
CONGO_chr4_150693745_145_m0	chr4	150693745	150693889	-	0	145	455.73	NCExon				1	1	TU79	NovelMultiExon	
CONGO_chr4_150704294_72_m0	chr4	150704294	150704365	-	0	72	5.06	NCExon				1	1	TU79	NovelMultiExon	
CONGO_chr4_150875978_83_m2	chr4	150875978	150876060	-	2	83	171.67	NCExon				1	1	TU79	NovelMultiExon	
CONGO_chr4_151496746_129_m0	chr4	151496746	151496874	-	0	129	23.85	Intron								
CONGO_chr4_151507346_144_p0	chr4	151507346	151507489	+	0	144	49.03	AntisenseIntron								
CONGO_chr4_151713564_135_m2	chr4	151713564	151713698	-	2	135	1.82	Intron							NovelUnspliced	
CONGO_chr4_151723532_88_m1	chr4	151723532	151723619	-	1	88	151.72	AntisenseUTR								
CONGO_chr4_151740148_158_m1	chr4	151740148	151740305	-	1	158	65.59	Intron								
CONGO_chr4_151820640_176_p0	chr4	151820640	151820815	+	0	176	4.69	AntisenseIntron								
CONGO_chr4_152316166_111_m2	chr4	152316166	152316276	-	2	111	204.37	UTR				1	1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_152317127_163_m0	chr4	152317127	152317289	-	0	163	785.98	UTR				1	1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_152317419_139_m1	chr4	152317419	152317557	-	1	139	1024.89	UTR				1	1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_152319957_43_m2	chr4	152319957	152319999	-	2	43	207.31	UTR				1	1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_152328025_41_m1	chr4	152328025	152328065	-	1	41	168.44	UTR				1	1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_152366649_40_m2	chr4	152366649	152366688	-	2	40	470.89	UTR				1	1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_152465843_112_m0	chr4	152465843	152465954	-	0	112	448.19	Intergenic					1	TU24	SpliceToPCG	OTTHUMG00000154051
CONGO_chr4_153132602_106_m0	chr4	153132602	153132707	-	0	106	22.78	Intergenic								
CONGO_chr4_153589054_55_m1	chr4	153589054	153589108	-	1	55	104.08	Intron								
CONGO_chr4_154819986_166_p0	chr4	154819986	154820151	+	0	166	73.52	Intergenic				1		TU997	NovelMultiExon	
CONGO_chr4_154820372_193_p1	chr4	154820372	154820564	+	1	193	353.46	Intergenic		TIR		1			NovelUnspliced	
CONGO_chr4_155960965_60_p0	chr4	155960965	155961024	+	0	60	15.3	Intron				1	1	TU998	SpliceToPCG	ENSG00000151962
CONGO_chr4_158504037_117_p0	chr4	158504037	158504153	+	0	117	360.1	UTR				1	1	TU999	SpliceToPCG	OTTHUMG00000133836
CONGO_chr4_159946850_176_p0	chr4	159946850	159947025	+	0	176	97.44	Intron				1	1	TU1000	SpliceToPCG	ENSG00000052795
CONGO_chr4_160327244_71_p0	chr4	160327244	160327314	+	0	71	838.41	Intergenic					1	TU39	SpliceToPCG	ENSG00000109756
CONGO_chr4_160333802_58_p1	chr4	160333802	160333859	+	1	58	360	Intergenic					1	TU39	SpliceToPCG	ENSG00000109756
CONGO_chr4_160351102_84_p1	chr4	160351102	160351185	+	1	84	976.48	Intergenic					1	TU39	SpliceToPCG	ENSG00000109756
CONGO_chr4_160379411_76_p1	chr4	160379411	160379486	+	1	76	610.31	Intergenic					1	TU39	SpliceToPCG	ENSG00000109756
CONGO_chr4_160381803_168_p0	chr4	160381803	160381970	+	0	168	1675.25	Intergenic					1	TU39	SpliceToPCG	ENSG00000109756
CONGO_chr4_160407789_123_p2	chr4	160407789	160407911	+	2	123	47.95	Intergenic					1			
CONGO_chr4_160500678_63_p0	chr4	160500678	160500740	+	0	63	50.47	UTR				1		TU39	SpliceToPCG	ENSG00000109756
CONGO_chr4_164753237_150_m2	chr4	164753237	164753386	-	2	150	266.98	Intron				1	1	TU292	SpliceToPCG	ENSG00000145416
CONGO_chr4_164753555_86_m1	chr4	164753555	164753640	-	1	86	169.04	Intron					1	TU292	SpliceToPCG	ENSG00000145416
CONGO_chr4_165129103_84_m0	chr4	165129103	165129186	-	0	84	279.8	Intron					1	TU1001	SpliceToPCG	ENSG00000145416
CONGO_chr4_165911046_112_p0	chr4	165911046	165911157	+	0	112	798.18	NCExon				1	1	TU1002	NovelMultiExon	
CONGO_chr4_166019522_89_p2	chr4	166019522	166019610	+	2	89	329.23	NCExon				1	1			
CONGO_chr4_174455521_183_p1	chr4	174455521	174455703	+	1	183	755.5	Intron				1	1	TU1003	SpliceToPCG	ENSG00000109586
CONGO_chr4_175076955_88_p2	chr4	175076955	175077042	+	2	88	92.42	Intergenic								
CONGO_chr4_175361366_66_p0	chr4	175361366	175361431	+	0	66	21.94	AntisenseNCIntron								
CONGO_chr4_177389308_61_m0	chr4	177389308	177389368	-	0	61	258.65	Intron								
CONGO_chr4_182509440_121_p2	chr4	182509440	182509560	+	2	121	16.86	Intergenic								
CONGO_chr4_182666029_109_m0	chr4	182666029	182666137	-	0	109	21.71	Intergenic								
CONGO_chr4_183607203_279_m0	chr4	183607203	183607481	-	0	279	146.95	AntisenseIntron								

CONGO_chr4_183653951_104_m0	chr4	183653951	183654054	-	0	104	8.46	AntisenseIntron								
CONGO_chr4_184955851_352_p0	chr4	184955851	184956202	+	0	352	852.93	Intergenic				1				
CONGO_chr4_186758096_108_m0	chr4	186758096	186758203	-	0	108	147.29	Intron								
CONGO_chr4_186892247_56_m0	chr4	186892247	186892302	-	0	56	213.64	UTR				1	TU1004	SpliceToPCG	OTTHUMG00000157215	
CONGO_chr4_187263225_270_p0	chr4	187263225	187263494	+	0	270	586.9	Intergenic								
CONGO_chr4_187263663_128_p0	chr4	187263663	187263790	+	0	128	269.66	Intergenic				1	TU1005	SpliceToPCG	ENSG00000109794	
CONGO_chr4_187792883_69_m2	chr4	187792883	187792951	-	2	69	35.53	Intron								
CONGO_chr4_190707326_37_m2	chr4	190707326	190707362	-	2	37	9.37	Intergenic	1							
CONGO_chr5_003481341_146_m2	chr5	3481341	3481486	-	2	146	26.38	NCIntron								
CONGO_chr5_003565540_32_m2	chr5	3565540	3565571	-	2	32	1.44	AntisenseIntron								
CONGO_chr5_004372877_82_p1	chr5	4372877	4372958	+	1	82	30.78	Intron								
CONGO_chr5_006767409_404_p0	chr5	6767409	6767812	+	0	404	232.24	UTR			1	1	TU1006	SpliceToPCG	ENSG00000112941	
CONGO_chr5_030783559_78_m0	chr5	30783559	30783636	-	0	78	21.46	Intergenic								
CONGO_chr5_035932047_102_m0	chr5	35932047	35932148	-	0	102	516.75	Intergenic								
CONGO_chr5_036244484_66_m0	chr5	36244484	36244549	-	0	66	49.1	Intron			1	1	TU1007	SpliceToPCG	ENSG00000152620	
CONGO_chr5_036665835_69_p0	chr5	36665835	36665903	+	0	69	43.13	Intron				1	TU1008	SpliceToPCG	ENSG00000079215	
CONGO_chr5_036912725_204_m0	chr5	36912725	36912928	-	0	204	124.08	AntisenseUTR								
CONGO_chr5_037851325_173_m2	chr5	37851325	37851497	-	2	173	12.26	UTR					TU1009	SpliceToPCG	ENSG00000168621	
CONGO_chr5_042836701_74_p2	chr5	42836701	42836774	+	2	74	6.28	AntisenseCDS			1	1	TU1010	SpliceToPCG	ENSG00000198865	
CONGO_chr5_050312476_52_p1	chr5	50312476	50312527	+	1	52	1.63	Intergenic								
CONGO_chr5_050427210_76_m1	chr5	50427210	50427285	-	1	76	26.38	Intergenic								
CONGO_chr5_051290288_83_m2	chr5	51290288	51290370	-	2	83	10.33	Intergenic								
CONGO_chr5_053546885_147_m0	chr5	53546885	53547031	-	0	147	61.85	Intron								
CONGO_chr5_054188150_177_m0	chr5	54188150	54188326	-	0	177	447.23	Intergenic								
CONGO_chr5_054198157_186_m0	chr5	54198157	54198342	-	0	186	12.1	Intergenic			1					
CONGO_chr5_054200296_306_m0	chr5	54200296	54200601	-	0	306	802.94	Intergenic								
CONGO_chr5_054200638_162_m0	chr5	54200638	54200799	-	0	162	217.2	Intergenic								
CONGO_chr5_054201775_182_m1	chr5	54201775	54201956	-	1	182	487.98	Intergenic								
CONGO_chr5_058761877_125_m0	chr5	58761877	58762001	-	0	125	573.17	Intron								
CONGO_chr5_059017489_38_m0	chr5	59017489	59017526	-	0	38	39.98	Intron								
CONGO_chr5_060357734_90_m0	chr5	60357734	60357823	-	0	90	36.34	AntisenseIntron								
CONGO_chr5_060828081_161_p2	chr5	60828081	60828241	+	2	161	28.27	Intron								
CONGO_chr5_060956818_57_p2	chr5	60956818	60956874	+	2	57	5.93	AntisenseNCExon						NovelUnspliced		
CONGO_chr5_060956879_52_m2	chr5	60956879	60956930	-	2	52	15.48	NCExon			1	1				
CONGO_chr5_061014595_88_m0	chr5	61014595	61014682	-	0	88	48.47	AntisenseIntron								
CONGO_chr5_061069470_113_p2	chr5	61069470	61069582	+	2	113	33.04	Intergenic								
CONGO_chr5_065320219_48_p0	chr5	65320219	65320266	+	0	48	3.7	UTR			1	1	TU1011	SpliceToPCG	ENSG00000112851	
CONGO_chr5_068951923_120_p2	chr5	68951923	68952042	+	2	120	102.07	NCExon	1	BIR	1	1				
CONGO_chr5_069454877_100_m2	chr5	69454877	69454976	-	2	100	30.41	NCExon	1	BIR	1	1				
CONGO_chr5_069807064_120_p2	chr5	69807064	69807183	+	2	120	158.66	NCExon	1	BIR	1	1				
CONGO_chr5_071839035_59_m0	chr5	71839035	71839093	-	0	59	143.11	Intergenic				1				
CONGO_chr5_072231734_74_p1	chr5	72231734	72231807	+	1	74	95.74	Intron					TU1012	SpliceToPCG	ENSG00000083312	
CONGO_chr5_072613187_46_p1	chr5	72613187	72613232	+	1	46	60.51	Intergenic								
CONGO_chr5_074948385_104_p2	chr5	74948385	74948488	+	2	104	161.34	NCIntron				1				
CONGO_chr5_076927038_133_p1	chr5	76927038	76927170	+	1	133	52.58	Intergenic								
CONGO_chr5_077175932_175_m1	chr5	77175932	77176106	-	1	175	35.77	Intergenic								
CONGO_chr5_077179370_77_p2	chr5	77179370	77179446	+	2	77	13.23	Intergenic								
CONGO_chr5_077200359_119_m0	chr5	77200359	77200477	-	0	119	17.97	Intergenic				1				
CONGO_chr5_077206011_100_m2	chr5	77206011	77206110	-	2	100	83.41	Intergenic								
CONGO_chr5_077289962_103_p1	chr5	77289962	77290064	+	1	103	20.52	Intergenic								
CONGO_chr5_077348588_159_p0	chr5	77348588	77348746	+	0	159	46.46	AntisenseIntron								
CONGO_chr5_077394306_72_m1	chr5	77394306	77394377	-	1	72	65.14	Intron								
CONGO_chr5_081183166_113_m1	chr5	81183166	81183278	-	1	113	92.9	Intergenic								
CONGO_chr5_081636252_174_p1	chr5	81636252	81636425	+	1	174	326.12	UTR			1	1	TU1014	SpliceToPCG	ENSG00000205464	
CONGO_chr5_087100842_101_m2	chr5	87100842	87100942	-	2	101	90.51	Intergenic								
CONGO_chr5_087120066_63_m0	chr5	87120066	87120128	-	0	63	15.62	Intergenic								
CONGO_chr5_087204372_97_m1	chr5	87204372	87204468	-	1	97	24.27	Intergenic								
CONGO_chr5_087204520_95_m2	chr5	87204520	87204614	-	2	95	10.85	Intergenic								
CONGO_chr5_087276214_124_m1	chr5	87276214	87276337	-	1	124	39.05	Intergenic								
CONGO_chr5_087995550_148_p0	chr5	87995550	87995697	+	0	148	63.23	AntisenseNCIntron								
CONGO_chr5_087997517_131_p2	chr5	87997517	87997647	+	2	131	7.06	AntisenseUTR								
CONGO_chr5_088054057_81_m0	chr5	88054057	88054137	-	0	81	97.05	UTR			1	1	TU1015	SpliceToPCG	ENSG00000081189	
CONGO_chr5_088235511_53_p1	chr5	88235511	88235563	+	1	53	115.8	AntisenseUTR	1			1				
CONGO_chr5_088260957_165_p0	chr5	88260957	88261121	+	0	165	38.69	NCIntron								
CONGO_chr5_088461600_60_m0	chr5	88461600	88461659	-	0	60	10.31	Intergenic								
CONGO_chr5_089088602_100_m0	chr5	89088602	89088701	-	0	100	46.92	Intergenic								
CONGO_chr5_089972409_33_p1	chr5	89972409	89972441	+	1	33	215.8	Intron				1				
CONGO_chr5_091054585_74_p1	chr5	91054585	91054658	+	1	74	12.6	Intergenic								
CONGO_chr5_091444889_175_m1	chr5	91444889	91445063	-	1	175	18.52	Intergenic								
CONGO_chr5_091967166_115_m1	chr5	91967166	91967280	-	1	115	38.34	Intergenic								
CONGO_chr5_091996298_123_p0	chr5	91996298	91996420	+	0	123	154	Intergenic								
CONGO_chr5_092339689_93_p0	chr5	92339689	92339781	+	0	93	106.6	Intergenic								
CONGO_chr5_092408963_70_p1	chr5	92408963	92409032	+	1	70	133.57	Intergenic								
CONGO_chr5_092641189_153_p0	chr5	92641189	92641341	+	0	153	71.38	Intergenic								
CONGO_chr5_092977294_135_m0	chr5	92977294	92977428	-	0	135	38.68	Intergenic					TU1016	SpliceToPCG	ENSG00000113391	
CONGO_chr5_093037492_113_p2	chr5	93037492	93037604	+	2	113	41.28	AntisenseIntron								
CONGO_chr5_093248610_99_p0	chr5	93248610	93248708	+	0	99	0.11	AntisenseIntron								
CONGO_chr5_093571277_58_p0	chr5	93571277	93571334	+	0	58	13.55	AntisenseIntron								
CONGO_chr5_093676186_107_p2	chr5	93676186	93676292	+	2	107	24.07	AntisenseIntron								
CONGO_chr5_094253708_145_m1	chr5	94253708	94253852	-	1	145	1.03	Intron								
CONGO_chr5_106685360_78_m0	chr5	106685360	106685437	-	0	78	41.64	Intergenic								
CONGO_chr5_106736758_34_m0	chr5	106736758	106736791	-	0	34	23.32	Intergenic								
CONGO_chr5_106765529_143_m2	chr5	106765529	106765671	-	2	143	21.65	Intron								
CONGO_chr5_107348604_84_m0	chr5	107348604	107348687	-	0	84	13.71	Intron								
CONGO_chr5_108288353_37_p1	chr5	108288353	108288389	+	1	37	118.09	Intron				1				
CONGO_chr5_112186903_54_p2	chr5	112186903	112186956	+	2	54	95.84	Intron			1		TU1017	SpliceToPCG	ENSG00000134982	
CONGO_chr5_113725560_100_p2	chr5	113725560	113725659	+	2	100	30.68	Intergenic					TU1018	SpliceToPCG	ENSG00000080709	
CONGO_chr5_115270417_41_p2	chr5	115270417	115270457	+	2	41	40.75	Intron				1	TU1019	SpliceToPCG	ENSG00000177879	
CONGO_chr5_115417610_140_p0	chr5	115417610	115417749	+	0	140	1367.38	Intergenic				1				
CONGO_chr5_115422321_223_p1	chr5	115422321	115422543	+	1	223	2264.71	Intergenic				1				
CONGO_chr5_118542169_87_p2	chr5	118542169	118542255	+	2	87	4.68	Intron					TU1020	SpliceToPCG	ENSG00000172869	
CONGO_chr5_121543150_175_p0	chr5	121543150	121543324	+	0	175	1172.64	Intergenic				1	TU293	SpliceToPCG	ENSG00000164185	
CONGO_chr5_121546085_152_p2	chr5	121546085	121546236	+	2	152	646.65	Intergenic				1	TU293	SpliceToPCG	ENSG00000164185	
CONGO_chr5_121737106_74_p0	chr5	121737106	121737179	+	0	74	82.65	Intron								
CONGO_chr5_121737199_334_p1	chr5	121737199	121737532	+	1	334	817.64	Intron								
CONGO_chr5_121737744_267_p2	chr5	121737744	121738010	+	2	267	559.89	Intron								
CONGO_chr5_122469540_210_p2	chr5	122469540	122469749	+	2	210	318.61	Intron								
CONGO_chr5_124344338_135_m2	chr5	124344338	124344472	-	2	135	199.54	Intergenic								
CONGO_chr5_124775758_75_m1	chr5	124775758	124775832	-	1	75	88.28	Intergenic								
CONGO_chr5_124776571_63_m1	chr5	124776571	124776633	-	1	63	57.97	Intergenic								
CONGO_chr5_125735034_125_p0	chr5	125735034	125735158	+	0	125	83.5	Intron			1	1	TU1021	SpliceToPCG	ENSG00000155324	
CONGO_chr5_127012946_34_p0	chr5	127012946	127012979	+	0	34	30.37	UTR			1	1	TU1022	SpliceToPCG	ENSG00000205279	
CONGO_chr5_128761926_50_m0	chr5	128761926	128761975	-	0	50	29.43	Intergenic								
CONGO_chr5_129111771_177_p0	chr5	129111771	129111947	+	0	177	1040.41	Intergenic								
CONGO_chr5_130895693_54_m0	chr5	130895693	130895746	-	0	54	172.12	Intron			1	1	TU1023	SpliceToPCG	ENSG00000158987	
CONGO_chr5_132004241_178_m1	chr5	132004241	132004418	-	1	178	613	AntisenseCDS				1	TU1024	SpliceToNCG	ENSG00000223442	
CONGO_chr5_133504386_93_p1	chr5	133504386	133504478	+	1	93	341.59	Intron			1	1	TU1025	SpliceToPCG	ENSG00000081059	
CONGO_chr5_134301205_87_m0	chr5	134301205	134301291	-	0	87	31.82	AntisenseIntron								
CONGO_chr5_135576367_35_p2	chr5	135576367	135576401	+	2	35	83.59	Intergenic								
CONGO_chr5_137219938_99_p1	chr5	137219938	137220036	+	1	99	34.13	Intergenic					TU294	NovelMultiExon		
CONGO_chr5_137220753_63_p0	chr5	137220753	137220815	+	0	63	81.49	Intergenic					TU294	NovelMultiExon		
CONGO_chr5_137225477_56_p0	chr5	137225477	137225532	+	0	56	47.92	Intergenic					TU1027	SpliceToPCG	ENSG00000120729	
CONGO_chr5_139588499_107_p2	chr5	139588499	139588605	+	2	107	390.88	Intron				1	TU1028	SpliceToPCG	ENSG00000120306	
CONGO_chr5_139925642_99_p0	chr5	139925642	139925740	+	0	99	717.73	UTR			1	1	TU295	SpliceToPCG	ENSG00000176087	
CONGO_chr5_139926334_198_p0	chr5	139926334	139926531	+	0	198	1295.4	UTR			1	1	TU295	SpliceToPCG	ENSG00000176087	
CONGO_chr5_140221150_266_p0	chr5	140221150	140221415	+	0	266	775.82	AntisenseUTR		Cadherin_2						
CONGO_chr5_140221456_93_p2	chr5	140221456	140221548	+	2	93	278.41	AntisenseUTR								
CONGO_chr5_140221606_83_p2	chr5	140221606	140221688	+	2	83	225.11	AntisenseUTR								
CONGO_chr5_140221707_102_p2	chr5	140221707	140221808	+	2	102	144.54	AntisenseUTR								
CONGO_chr5_140221939_90_p0	chr5	140221939	140222028	+	0	90	310.03	AntisenseUTR								
CONGO_chr5_140222034_117_p0	chr5	140222034	140222150	+	0	117	670.77	AntisenseUTR								
CONGO_chr5_140222231_97_p1	chr5	140222231	140222327	+	1	97	119.54	AntisenseUTR								
CONGO_chr5_140222354_179_p0	chr5	140222354	140222532	+	0	179	364.13	AntisenseUTR								
CONGO_chr5_140222819_362_p0	chr5	140222819	140223180	+	0	362	781.02	AntisenseCDS								
CONGO_chr5_140223190_101_p0	chr5	140223190	140223290	+	0	101	52.3	AntisenseUTR								

CONGO_chr5_140599744_291_p0	chr5	140599744	140600034	+	0	291	615.91	NCExon		Cadherin_2	1					
CONGO_chr5_140600119_281_p2	chr5	140600119	140600399	+	2	281	1761.27	NCExon		Cadherin	1					
CONGO_chr5_140600406_91_p0	chr5	140600406	140600496	+	0	91	393.85	NCExon		Cadherin	1	1				
CONGO_chr5_140600532_284_p2	chr5	140600532	140600815	+	2	284	1165.36	NCExon	1	Cadherin	1	1				
CONGO_chr5_140600889_113_p2	chr5	140600889	140601001	+	2	113	626.5	NCExon	1		1					
CONGO_chr5_140601124_183_p0	chr5	140601124	140601306	+	0	183	977.54	NCExon	1	Cadherin	1	1				
CONGO_chr5_140601574_219_p0	chr5	140601574	140601792	+	0	219	721.71	NCExon	1		1	1				
CONGO_chr5_140601850_119_p2	chr5	140601850	140601968	+	2	119	218.75	NCExon	1		1					
CONGO_chr5_140786083_125_p2	chr5	140786083	140786207	+	2	125	114.19	UTR		Cadherin_2	1					
CONGO_chr5_140786237_78_p1	chr5	140786237	140786314	+	1	78	154.65	UTR		Cadherin_2	1					
CONGO_chr5_141167165_151_p0	chr5	141167165	141167315	+	0	151	31.29	Intergenic						NovelUnspliced		
CONGO_chr5_141851139_171_m0	chr5	141851139	141851309	-	0	171	29.41	AntisenseNCIntron								
CONGO_chr5_145821783_120_p0	chr5	145821783	145821902	+	0	120	3.54	Intron					1	TU296	SpliceToPCG	ENSG00000113649
CONGO_chr5_145869823_94_p2	chr5	145869823	145869916	+	2	94	92.39	Intron			1		1	TU296	SpliceToPCG	ENSG00000113649
CONGO_chr5_145874653_139_p0	chr5	145874653	145874791	+	0	139	374.84	AntisenseCDS								
CONGO_chr5_146440815_78_m2	chr5	146440815	146440892	-	2	78	517.07	UTR			1		1	TU1029	SpliceToPCG	ENSG00000156475
CONGO_chr5_147603019_288_p1	chr5	147603019	147603306	+	1	288	47.11	Intergenic								
CONGO_chr5_150155196_183_p0	chr5	150155196	150155378	+	0	183	950.36	UTR			1		1	TU1030	SpliceToPCG	ENSG00000181368
CONGO_chr5_150290735_312_m1	chr5	150290735	150291046	-	1	312	115.07	UTR	1	zf-C2H2	1			TU1031	SpliceToPCG	ENSG00000145908
CONGO_chr5_156714000_66_p0	chr5	156714000	156714065	+	0	66	118.74	Intron						TU1032	SpliceToPCG	ENSG00000055163
CONGO_chr5_157562529_30_m0	chr5	157562529	157562558	-	0	30	1.79	Intergenic								
CONGO_chr5_157811349_88_m1	chr5	157811349	157811436	-	1	88	9.51	Intergenic								
CONGO_chr5_158085099_95_m0	chr5	158085099	158085193	-	0	95	40.79	Intron								
CONGO_chr5_158091930_67_p0	chr5	158091930	158091996	+	0	67	6.25	AntisenseIntron								
CONGO_chr5_158120371_96_p0	chr5	158120371	158120466	+	0	96	32.91	AntisenseIntron								
CONGO_chr5_158274332_96_m1	chr5	158274332	158274427	-	1	96	113.44	Intron								
CONGO_chr5_159468130_70_m1	chr5	159468130	159468199	-	1	70	89.94	Intron						TU1033	SpliceToPCG	ENSG00000170234
CONGO_chr5_163858259_82_p1	chr5	163858259	163858340	+	1	82	22.94	NCIntron								
CONGO_chr5_166338679_223_p2	chr5	166338679	166338901	+	2	223	196.86	Intergenic								
CONGO_chr5_166449890_99_p2	chr5	166449890	166449988	+	2	99	14.48	Intergenic								
CONGO_chr5_167384234_39_p0	chr5	167384234	167384272	+	0	39	39.94	Intron								
CONGO_chr5_170040651_109_p0	chr5	170040651	170040759	+	0	109	618.57	Intron						TU1034	SpliceToPCG	ENSG00000182132
CONGO_chr5_170491302_74_p1	chr5	170491302	170491375	+	1	74	21.22	Intron								
CONGO_chr5_170521016_60_p0	chr5	170521016	170521075	+	0	60	25.02	NCExon			1		1	TU1035	SpliceToPCG	ENSG00000204764
CONGO_chr5_170560954_172_m1	chr5	170560954	170561125	-	1	172	139.13	AntisenseIntron								
CONGO_chr5_170562201_171_p0	chr5	170562201	170562371	+	0	171	43.77	Intron								
CONGO_chr5_170682283_80_p2	chr5	170682283	170682362	+	2	80	22.42	Intergenic								
CONGO_chr5_171356499_68_m0	chr5	171356499	171356566	-	0	68	3.35	Intron			1		1	TU1036	SpliceToPCG	ENSG00000072803
CONGO_chr5_171716300_84_m2	chr5	171716300	171716383	-	2	84	254.54	Intron								
CONGO_chr5_175067388_126_p1	chr5	175067388	175067513	+	1	126	222.53	Intergenic						TU1037	SpliceToPCG	ENSG00000113749
CONGO_chr5_176229202_187_p0	chr5	176229202	176229388	+	0	187	309.69	Intron		TSP_1			1	TU1038	SpliceToPCG	ENSG00000113763
CONGO_chr5_176912775_95_m0	chr5	176912775	176912869	-	0	95	93.73	UTR			1		1	TU1039	SpliceToPCG	ENSG00000146067
CONGO_chr5_177625262_72_m0	chr5	177625262	177625333	-	0	72	208.91	Intron						TU1040	SpliceToPCG	ENSG00000050767
CONGO_chr5_178978908_128_p2	chr5	178978908	178979035	+	2	128	127.65	AntisenseCDS					1	TU1041	NovelMultiExon	
CONGO_chr5_179279923_110_m2	chr5	179279923	179280032	-	2	110	1161.6	Intergenic					1	TU1042	SpliceToPCG	ENSG00000113269
CONGO_chr6_002689129_141_m0	chr6	2689129	2689269	-	0	141	164.62	Intron								
CONGO_chr6_004006248_133_p0	chr6	4006248	4006380	+	0	133	32.78	UTR	1		1		1	TU1045	SpliceToPCG	ENSG00000112739
CONGO_chr6_008414034_191_p2	chr6	8414034	8414224	+	2	191	60.48	NCIntron								
CONGO_chr6_009718856_84_m2	chr6	9718856	9718939	-	2	84	1.16	NCExon								
CONGO_chr6_009781254_33_m0	chr6	9781254	9781286	-	0	33	65.41	NCExon								
CONGO_chr6_009948456_99_m0	chr6	9948456	9948554	-	0	99	347.21	UTR			1					
CONGO_chr6_010881253_75_m2	chr6	10881253	10881327	-	2	75	438.32	Intron						TU1046	SpliceToPCG	ENSG00000111837
CONGO_chr6_011242707_83_m2	chr6	11242707	11242789	-	2	83	160.67	AntisenseCDS					1		UnsplicedMergeWithNCG	ENSG00000224531
CONGO_chr6_013122167_191_p1	chr6	13122167	13122357	+	1	191	397.59	Intron						TU1047	SpliceToPCG	ENSG00000112137
CONGO_chr6_014609627_81_p0	chr6	14609627	14609707	+	0	81	65.82	Intergenic								
CONGO_chr6_015571131_77_m2	chr6	15571131	15571207	-	2	77	22.85	AntisenseIntron								
CONGO_chr6_016436552_90_m0	chr6	16436552	16436641	-	0	90	140.88	UTR			1			TU1048	SpliceToPCG	ENSG00000124788
CONGO_chr6_017047751_64_p0	chr6	17047751	17047814	+	0	64	22.76	Intergenic								
CONGO_chr6_017228868_105_p2	chr6	17228868	17228972	+	2	105	263.09	NCExon					1	TU141	SpliceToNCG	ENSG00000230873
CONGO_chr6_017237322_132_p0	chr6	17237322	17237453	+	0	132	584.76	NCExon			1		1	TU141	SpliceToNCG	ENSG00000230873
CONGO_chr6_017238804_288_p0	chr6	17238804	17239091	+	0	288	276.43	NCExon			1		1	TU141	SpliceToNCG	ENSG00000230873
CONGO_chr6_017393263_90_p0	chr6	17393263	17393352	+	0	90	37.63	Intron						TU1049	SpliceToPCG	ENSG00000112183
CONGO_chr6_017878956_42_m0	chr6	17878956	17878997	-	0	42	69.37	Intron			1			TU298	SpliceToPCG	ENSG00000137177
CONGO_chr6_017929996_120_m2	chr6	17929996	17930115	-	2	120	460.54	Intron						TU298	SpliceToPCG	ENSG00000137177
CONGO_chr6_019828043_58_p1	chr6	19828043	19828100	+	1	58	18.62	AntisenseNCIntron								
CONGO_chr6_021774776_80_p0	chr6	21774776	21774855	+	0	80	58.66	NCExon			1		1	TU1050	SpliceToNCG	ENSG00000238274
CONGO_chr6_025035375_183_m0	chr6	25035375	25035557	-	0	183	48.62	Intergenic							NovelUnspliced	
CONGO_chr6_025044045_61_m0	chr6	25044045	25044105	-	0	61	283.45	Intergenic			1		1	TU1051	SpliceToPCG	ENSG00000111913
CONGO_chr6_025150058_76_m0	chr6	25150058	25150133	-	0	76	1008.22	NCExon			1		1	TU1052	SpliceToPCG	ENSG00000111913
CONGO_chr6_026304570_166_p2	chr6	26304570	26304735	+	2	166	59.99	Intergenic			1					
CONGO_chr6_026484780_212_p2	chr6	26484780	26484991	+	2	212	181.11	UTR			1		1	TU299	SpliceToPCG	ENSG00000026950
CONGO_chr6_026485108_145_p1	chr6	26485108	26485252	+	1	145	157.8	UTR		SPRY	1		1	TU299	SpliceToPCG	ENSG00000026950
CONGO_chr6_030133330_144_m0	chr6	30133330	30133473	-	0	144	103.11	UTR			1		1	TU300	SpliceToNCG	ENSG00000204623
CONGO_chr6_030133871_76_m1	chr6	30133871	30133946	-	1	76	215.69	UTR			1		1	TU300	SpliceToNCG	ENSG00000204623
CONGO_chr6_031012957_101_p2	chr6	31012957	31013057	+	2	101	60.05	Intergenic								
CONGO_chr6_031610379_123_p0	chr6	31610379	31610501	+	0	123	27.41	AntisenseUTR						TU1056	NovelMultiExon	
CONGO_chr6_032084791_164_m2	chr6	32084791	32084954	-	2	164	393.15	UTR	1	Fibrinogen_C	1					
CONGO_chr6_032085032_162_m2	chr6	32085032	32085193	-	2	162	392.29	UTR	1	Fibrinogen_C	1		1	TU1057	SpliceToPCG	ENSG00000168477
CONGO_chr6_032085286_97_m0	chr6	32085286	32085382	-	0	97	108.59	UTR	1	Fibrinogen_C	1		1	TU303	UnsplicedMergeWithPCG	ENSG00000168477
CONGO_chr6_032085476_152_m2	chr6	32085476	32085627	-	2	152	350.45	NCExon	1	Fibrinogen_C	1		1	TU303	SpliceToPCG	ENSG00000168477
CONGO_chr6_032085720_133_m0	chr6	32085720	32085852	-	0	133	266.12	NCExon	1		1		1			
CONGO_chr6_032085972_131_m2	chr6	32085972	32086102	-	2	131	262.35	NCExon	1	fn3	1		1	TU1058	SpliceToPCG	ENSG00000168477
CONGO_chr6_032086196_144_m2	chr6	32086196	32086339	-	2	144	319.39	NCExon	1		1		1	TU1059	SpliceToPCG	ENSG00000168477
CONGO_chr6_032086908_123_m2	chr6	32086908	32087030	-	2	123	126.74	NCExon	1	fn3	1		1	TU1060	SpliceToPCG	ENSG00000168477
CONGO_chr6_032087282_336_m2	chr6	32087282	32087617	-	2	336	1191.25	NCExon	1	fn3	1		1			
CONGO_chr6_032087907_321_m2	chr6	32087907	32088227	-	2	321	198.48	NCExon	1	fn3	1		1	TU1061	SpliceToPCG	ENSG00000168477
CONGO_chr6_032089147_148_p2	chr6	32089147	32089294	+	2	148	327.8	NCExon	1	Stk19	1		1	TU1062	SpliceToPCG	ENSG00000204344
CONGO_chr6_032163006_741_m2	chr6	32163006	32163746	-	2	741	1750.53	Intron		fn3				TU1063	SpliceToPCG	ENSG00000168477
CONGO_chr6_033050776_92_p0	chr6	33050776	33050867	+	0	92	85.81	UTR			1		1	TU1064	SpliceToPCG	ENSG00000204256
CONGO_chr6_033340533_94_p1	chr6	33340533	33340626	+	1	94	180.39	AntisenseCDS					1	TU1065	NovelMultiExon	
CONGO_chr6_033395220_164_p2	chr6	33395220	33395383	+	2	164	351.1	AntisenseCDS					1	TU1066	NovelMultiExon	
CONGO_chr6_033404781_240_m0	chr6	33404781	33405020	-	0	240	682.67	UTR					1			
CONGO_chr6_034323436_78_m0	chr6	34323436	34323513	-	0	78	184.29	UTR			1		1	TU1067	SpliceToPCG	ENSG00000186577
CONGO_chr6_035048336_63_p0	chr6	35048336	35048398	+	0	63	152.75	NCExon			1			TU1068	SpliceToPCG	ENSG00000064999
CONGO_chr6_036675758_262_p1	chr6	36675758	36676019	+	1	262	27.69	NCExon			1		1	TU1069	SpliceToPCG	ENSG00000112081
CONGO_chr6_036793028_147_p1	chr6	36793028	36793174	+	1	147	1253.26	Intron					1	TU1070	SpliceToPCG	ENSG00000196624
CONGO_chr6_036793783_91_p1	chr6	36793783	36793873	+	1	91	426.77	Intron								
CONGO_chr6_041184113_114_p0	chr6	41184113	41184226	+	0	114	153.14	NCExon			1		1	TU40	SpliceToPCG	ENSG00000001167
CONGO_chr6_041184486_91_p0	chr6	41184486	41184576	+	0	91	148.67	NCIntron			1					
CONGO_chr6_042181846_127_p1	chr6	42181846	42181972	+	1	127	63.89	AntisenseCDS							UnsplicedMergeWithPCG	ENSG00000188112
CONGO_chr6_042376354_112_m2	chr6	42376354	42376465	-	2	112	153.66	UTR			1		1	TU1071	SpliceToPCG	ENSG00000124496
CONGO_chr6_045738830_608_p2	chr6	45738830	45739437	+	2	608	3747.06	Intergenic						TU1072	NovelMultiExon	
CONGO_chr6_047679454_74_p0	chr6	47679454	47679527	+	0	74	59.51	Intron						TU1073	SpliceToPCG	ENSG00000198087
CONGO_chr6_050789404_150_p0	chr6	50789404	50789553	+	0	150	49.02	UTR			1		1			
CONGO_chr6_050920064_63_p1	chr6	50920064	50920126	+	1	63	7.14	UTR						TU1074	SpliceToPCG	ENSG00000008196
CONGO_chr6_051698446_37_p0	chr6	51698446	51698482	+	0	37	4.49	AntisenseIntron								
CONGO_chr6_051966095_49_p2	chr6	51966095	51966143	+	2	49	54.5	AntisenseIntron								
CONGO_chr6_053014023_143_m2	chr6	53014023	53014165	-	2	143	310.64	UTR			1		1	TU1076	SpliceToPCG	ENSG00000112144
CONGO_chr6_053038359_72_p0	chr6	53038359	53038430	+	0	72	87.27	AntisenseCDS			1		1	TU1077	SpliceToPCG	ENSG00000112146
CONGO_chr6_056513600_730_m0	chr6	56513600	56514329	-	0	730	5232.94	Intron			1			TU1078	SpliceToPCG	ENSG00000151914
CONGO_chr6_056665771_136_m0	chr6	56665771	56665906	-	0	136	364.43	NCExon			1			TU1079	SpliceToPCG	ENSG00000151914
CONGO_chr6_056676405_99_m0	chr6	56676405	56676503	-	0	99	99.14	Intron						TU1080	SpliceToPCG	ENSG00000151914
CONGO_chr6_064344300_96_p0	chr6	64344300	64344395	+	0	96	72.36	UTR			1		1	TU1081	SpliceToPCG	ENSG00000112245
CONGO_chr6_073065514_88_p1	chr6	73065514	73065601	+	1	88	19.42	Intron						TU1082	SpliceToPCG	ENSG00000079841
CONGO_chr6_074284123_115_p0	chr6	74284123	74284237	+	0	115	31.83	AntisenseUTR	1		1		1	TU1083	NovelMultiExon	
CONGO_chr6_078457108_184_p0	chr6	78457108	78457291	+	0	184	610.26	NCExon					1	TU143	SpliceToNCG	ENSG00000214481
CONGO_chr6_078527784_318_p0	chr6	78527784	78528101	+	0	318	372.99	NCExon						TU143	SpliceToNCG	ENSG00000214481
CONGO_chr6_078595367_132_p0	chr6	78595367	78595498	+	0	132	309.43	NCExon						TU143	SpliceToNCG	ENSG00000214481
CONGO_chr6_079770834_146_p2	chr6	79770834	79770979	+	2	146	26.31	AntisenseIntron					1			
CONGO_chr6_085790338_114_p0	chr6	85790338	85790451	+	0	114	26.75	Intergenic								
CONGO_chr6_085880701_146_m0	chr6	85880701	85880846	-	0	146	19.91	Intergenic								
CONGO_chr6_086378100_73_m0	chr6	86378100	86378172	-	0	73	18.97	UTR			1			TU1084	SpliceToPCG	ENSG00000135316
CONGO_chr6_089018010_73_m0	chr6	89018010	89018082	-	0	73	81.82	Intergenic								
CONGO_chr6_091902020_95_p2	chr6	91902020	91902114	+	2	95	149.99	Intergenic								
CONGO_chr6_092339426_134_m2	chr6	92339426	92339559	-	2	134	65.86	Intergenic								

CONGO_chr6_097623442_94_m1	chr6	97623442	97623535	-	1	94	6.72	AntisenseIntron								
CONGO_chr6_097651793_83_m2	chr6	97651793	97651875	-	2	83	67.27	AntisenseIntron								
CONGO_chr6_097651985_65_p0	chr6	97651985	97652049	+	0	65	61.39	Intron								
CONGO_chr6_097678325_162_m0	chr6	97678325	97678486	-	0	162	40.1	AntisenseIntron								
CONGO_chr6_098015953_74_m1	chr6	98015953	98016026	-	1	74	32.46	AntisenseNCIntron								
CONGO_chr6_098223494_118_m1	chr6	98223494	98223611	-	1	118	50.21	AntisenseNCIntron								
CONGO_chr6_098439966_91_p0	chr6	98439966	98440056	+	0	91	35.69	Intergenic								
CONGO_chr6_098440080_81_m0	chr6	98440080	98440160	-	0	81	81.79	Intergenic								
CONGO_chr6_098599026_135_p0	chr6	98599026	98599160	+	0	135	55.75	Intergenic								
CONGO_chr6_098599164_77_p0	chr6	98599164	98599240	+	0	77	117.07	Intergenic								
CONGO_chr6_098826836_176_p0	chr6	98826836	98827011	+	0	176	30.38	Intergenic								
CONGO_chr6_099197148_101_m2	chr6	99197148	99197248	-	2	101	39.02	Intergenic								
CONGO_chr6_099532274_81_p2	chr6	99532274	99532354	+	2	81	4.35	Intergenic								
CONGO_chr6_099667872_74_p2	chr6	99667872	99667945	+	2	74	81.89	Intergenic								
CONGO_chr6_100086014_120_p2	chr6	100086014	100086133	+	2	120	26.85	NCExon	1			1	1	TU1085	SpliceToNCG	ENSG00000207017
CONGO_chr6_101959676_50_m1	chr6	101959676	101959725	-	1	50	8.1	AntisenseIntron								
CONGO_chr6_105505029_49_p2	chr6	105505029	105505077	+	2	49	26.25	Intergenic					1			
CONGO_chr6_106915477_173_p0	chr6	106915477	106915649	+	0	173	57.57	Intergenic				1	1	TU308	NovelMultiExon	
CONGO_chr6_107016356_153_p0	chr6	107016356	107016508	+	0	153	396.33	Intergenic								
CONGO_chr6_107065998_289_p0	chr6	107065998	107066286	+	0	289	696.72	UTR				1	1	TU308	NovelMultiExon	
CONGO_chr6_108252240_76_m0	chr6	108252240	108252315	-	0	76	79.04	Intergenic							SpliceToPCG	ENSG00000146285
CONGO_chr6_109611851_137_p0	chr6	109611851	109611987	+	0	137	193.23	NCExon					1			
CONGO_chr6_109615532_73_p1	chr6	109615532	109615604	+	1	73	433.91	NCExon					1			
CONGO_chr6_109615855_111_p0	chr6	109615855	109615965	+	0	111	557.02	NCExon					1			
CONGO_chr6_109624381_114_p0	chr6	109624381	109624494	+	0	114	152.91	NCExon					1			
CONGO_chr6_109624969_195_p0	chr6	109624969	109625163	+	0	195	1441.5	NCExon					1			
CONGO_chr6_109627429_158_p2	chr6	109627429	109627586	+	2	158	260.41	NCExon					1			
CONGO_chr6_109631611_153_p0	chr6	109631611	109631763	+	0	153	435.94	NCExon					1			
CONGO_chr6_109634248_102_p0	chr6	109634248	109634349	+	0	102	174.31	NCExon					1			
CONGO_chr6_109645142_141_p0	chr6	109645142	109645282	+	0	141	104.18	NCExon					1	TU1086	SpliceToNCG	ENSG00000243587
CONGO_chr6_109654955_136_p1	chr6	109654955	109655090	+	1	136	520.98	NCExon					1			
CONGO_chr6_109655342_204_p0	chr6	109655342	109655545	+	0	204	638.28	NCExon					1			
CONGO_chr6_109712371_104_p2	chr6	109712371	109712474	+	2	104	629.73	Intergenic								
CONGO_chr6_109713872_50_p0	chr6	109713872	109713921	+	0	50	293.49	Intergenic						TU309	NovelMultiExon	
CONGO_chr6_109714238_177_p1	chr6	109714238	109714414	+	1	177	1162.76	Intergenic						TU309	SpliceToPCG	ENSG00000203799
CONGO_chr6_109722243_100_m1	chr6	109722243	109722342	-	1	100	211.65	AntisenseCDS								
CONGO_chr6_109737398_99_p0	chr6	109737398	109737496	+	0	99	131.53	NCExon					1	TU1087	SpliceToPCG	ENSG00000203799
CONGO_chr6_109742031_158_p0	chr6	109742031	109742188	+	0	158	795.45	NCExon								
CONGO_chr6_109743176_139_p1	chr6	109743176	109743314	+	1	139	501.44	NCExon								
CONGO_chr6_109744744_121_p0	chr6	109744744	109744864	+	0	121	271.25	NCExon						TU1088	SpliceToPCG	ENSG00000203799
CONGO_chr6_109764264_150_p0	chr6	109764264	109764413	+	0	150	1278.93	Intergenic					1	TU1089	SpliceToPCG	ENSG00000203799
CONGO_chr6_109765292_54_p0	chr6	109765292	109765345	+	0	54	87.78	Intergenic						TU1090	SpliceToPCG	ENSG00000203798
CONGO_chr6_111201772_62_m1	chr6	111201772	111201833	-	1	62	55.09	UTR				1	1	TU1091	SpliceToPCG	ENSG00000155111
CONGO_chr6_111758082_127_m1	chr6	111758082	111758208	-	1	127	18.35	NCExon				1		TU310	SpliceToPCG	ENSG00000009413
CONGO_chr6_111792840_99_m1	chr6	111792840	111792938	-	1	99	38.64	Intron						TU310	SpliceToPCG	ENSG00000009413
CONGO_chr6_111802827_119_p2	chr6	111802827	111802945	+	2	119	496.79	AntisenseCDS							UnsplicedMergeWithPCG	ENSG00000009413
CONGO_chr6_119350943_42_m0	chr6	119350943	119350984	-	0	42	65.86	Intron								
CONGO_chr6_124045117_47_m2	chr6	124045117	124045163	-	2	47	43.3	Intergenic								
CONGO_chr6_127439437_124_m1	chr6	127439437	127439560	-	1	124	88.32	NCIntron								
CONGO_chr6_128368866_115_p0	chr6	128368866	128368980	+	0	115	30.78	AntisenseCDS								
CONGO_chr6_129655647_258_p0	chr6	129655647	129655904	+	0	258	710.85	Intron		Laminin_EGF				TU1092	SpliceToPCG	ENSG00000196569
CONGO_chr6_131245404_271_m1	chr6	131245404	131245674	-	1	271	1740.1	UTR				1		TU311	SpliceToPCG	ENSG00000079819
CONGO_chr6_131245788_204_m0	chr6	131245788	131245991	-	0	204	413.08	UTR				1		TU311	SpliceToPCG	ENSG00000079819
CONGO_chr6_133281916_135_m0	chr6	133281916	133282050	-	0	135	49.27	Intergenic								
CONGO_chr6_134316135_122_p0	chr6	134316135	134316256	+	0	122	319.5	UTR				1	1	TU1094	SpliceToPCG	ENSG00000028839
CONGO_chr6_135686236_30_p2	chr6	135686236	135686265	+	2	30	3.28	AntisenseIntron								
CONGO_chr6_136400974_131_m1	chr6	136400974	136401104	-	1	131	60.52	AntisenseUTR								
CONGO_chr6_137694267_71_m2	chr6	137694267	137694337	-	2	71	18.18	Intergenic								
CONGO_chr6_137716737_62_p1	chr6	137716737	137716798	+	1	62	279.77	Intergenic								
CONGO_chr6_138740903_111_p0	chr6	138740903	138741013	+	0	111	618.88	Intergenic						TU312	NovelMultiExon	
CONGO_chr6_138745330_348_p0	chr6	138745330	138745677	+	0	348	1494.38	Intergenic						TU312	NovelMultiExon	
CONGO_chr6_139055306_151_m0	chr6	139055306	139055456	-	0	151	128.24	NCExon					1			
CONGO_chr6_141925788_55_m1	chr6	141925788	141925842	-	1	55	59.11	Intergenic								
CONGO_chr6_142496680_183_p0	chr6	142496680	142496862	+	0	183	1264.57	NCExon								
CONGO_chr6_142497382_314_p2	chr6	142497382	142497695	+	2	314	552.99	NCExon		Connexin_CCC						
CONGO_chr6_143647205_65_p0	chr6	143647205	143647269	+	0	65	30.97	Intron								
CONGO_chr6_148310301_48_p0	chr6	148310301	148310348	+	0	48	6.11	NCExon					1			
CONGO_chr6_148882728_484_p1	chr6	148882728	148883211	+	1	484	2662.75	Intron					1	TU1095	SpliceToPCG	ENSG00000111961
CONGO_chr6_151049702_118_p0	chr6	151049702	151049819	+	0	118	665.74	Intron						TU1096	SpliceToPCG	ENSG00000120278
CONGO_chr6_151197807_137_p2	chr6	151197807	151197943	+	2	137	112.94	Intron						TU1097	SpliceToPCG	ENSG00000120278
CONGO_chr6_154562804_35_p1	chr6	154562804	154562838	+	1	35	2.48	AntisenseCDS								
CONGO_chr6_157513551_129_p1	chr6	157513551	157513679	+	1	129	13.03	UTR				1	1	TU1098	SpliceToPCG	ENSG00000049618
CONGO_chr6_158229591_90_p0	chr6	158229591	158229680	+	0	90	56.52	Intron				1	1	TU1099	SpliceToPCG	ENSG00000130340
CONGO_chr6_166044497_135_m2	chr6	166044497	166044631	-	2	135	496.19	Intergenic						TU1100	SpliceToPCG	ENSG00000112541
CONGO_chr6_166319586_106_m0	chr6	166319586	166319691	-	0	106	101.55	NCExon				1	1			
CONGO_chr6_167026271_51_m0	chr6	167026271	167026321	-	0	51	142.63	Intron								
CONGO_chr6_168076254_36_p0	chr6	168076254	168076289	+	0	36	187.85	Intron					1	TU1101	SpliceToPCG	ENSG00000130396
CONGO_chr6_168130394_66_p0	chr6	168130394	168130459	+	0	66	415.63	Intergenic								
CONGO_chr6_168137226_139_p0	chr6	168137226	168137364	+	0	139	261.54	AntisenseUTR								
CONGO_chr6_168140069_104_p2	chr6	168140069	168140172	+	2	104	600.04	AntisenseNCExon					1			
CONGO_chr6_168142761_89_p0	chr6	168142761	168142849	+	0	89	279.65	NCExon				1	1	TU1102	NovelMultiExon	
CONGO_chr6_168161502_68_p0	chr6	168161502	168161569	+	0	68	234.78	UTR				1	1	TU1103	SpliceToPCG	ENSG00000125337
CONGO_chr7_001244114_196_m1	chr7	1244114	1244309	-	1	196	40.02	Intergenic								
CONGO_chr7_002270450_96_p0	chr7	2270450	2270545	+	0	96	450.92	AntisenseCDS				1	1			
CONGO_chr7_002390753_81_p0	chr7	2390753	2390833	+	0	81	689.24	NCExon					1			
CONGO_chr7_002394703_111_p0	chr7	2394703	2394813	+	0	111	808.18	NCExon					1			
CONGO_chr7_005853533_164_p0	chr7	5853533	5853696	+	0	164	43.03	UTR	1			1	1		UnsplicedMergeWithNCG	ENSG00000235944
CONGO_chr7_012360501_138_m2	chr7	12360501	12360638	-	2	138	69.18	Intron		EGF_CA		1				
CONGO_chr7_013473165_163_p0	chr7	13473165	13473327	+	0	163	53.97	NCIntron								
CONGO_chr7_013616399_49_p0	chr7	13616399	13616447	+	0	49	2.22	NCIntron								
CONGO_chr7_013731030_71_p2	chr7	13731030	13731100	+	2	71	47.25	Intergenic								
CONGO_chr7_014346517_105_m2	chr7	14346517	14346621	-	2	105	61.43	Intron								
CONGO_chr7_019118903_93_p0	chr7	19118903	19118995	+	0	93	42.6	NCExon				1	1			
CONGO_chr7_019122217_63_m0	chr7	19122217	19122279	-	0	63	102.49	UTR				1	1	TU1104	SpliceToPCG	ENSG00000122691
CONGO_chr7_020939207_95_p2	chr7	20939207	20939301	+	2	95	0.4	NCIntron								
CONGO_chr7_020964768_195_m0	chr7	20964768	20964962	-	0	195	76.45	AntisenseNCIntron								
CONGO_chr7_020970211_113_p2	chr7	20970211	20970323	+	2	113	67.53	NCIntron								
CONGO_chr7_020970445_101_p2	chr7	20970445	20970545	+	2	101	123.5	NCIntron								
CONGO_chr7_021047981_134_m2	chr7	21047981	21048114	-	2	134	5.54	Intergenic								
CONGO_chr7_021206821_89_m2	chr7	21206821	21206909	-	2	89	80.43	Intergenic								
CONGO_chr7_021778143_83_m2	chr7	21778143	21778225	-	2	83	123.03	AntisenseIntron								
CONGO_chr7_025501713_171_m0	chr7	25501713	25501883	-	0	171	92.45	Intergenic								
CONGO_chr7_025662943_160_p1	chr7	25662943	25663102	+	1	160	126.42	AntisenseNCIntron								
CONGO_chr7_025759570_134_p2	chr7	25759570	25759703	+	2	134	5.31	AntisenseNCIntron								
CONGO_chr7_026196543_63_m0	chr7	26196543	26196605	-	0	63	42.85	UTR				1	1	TU1105	SpliceToPCG	ENSG00000122566
CONGO_chr7_026491851_126_p1	chr7	26491851	26491976	+	1	126	58.79	NCIntron								
CONGO_chr7_026661944_83_p2	chr7	26661944	26662026	+	2	83	20.85	Intergenic								
CONGO_chr7_026692880_121_p0	chr7	26692880	26693000	+	0	121	40.15	AntisenseIntron								
CONGO_chr7_026695849_219_p0	chr7	26695849	26696067	+	0	219	29.23	AntisenseIntron								
CONGO_chr7_027146426_69_m0	chr7	27146426	27146494	-	0	69	61.33	Intron								
CONGO_chr7_027147350_52_m2	chr7	27147350	27147401	-	2	52	31.15	UTR						TU1106	SpliceToPCG	ENSG00000105997
CONGO_chr7_027149808_146_p1	chr7	27149808	27149953	+	1	146	55.44	AntisenseUTR						TU1107	SpliceToNCG	ENSG00000235345
CONGO_chr7_027191300_141_m0	chr7	27191300	27191440	-	0	141	21.75	UTR				1	1	TU1108	SpliceToPCG	ENSG00000005073
CONGO_chr7_027522958_69_m2	chr7	27522958	27523026	-	2	69	47.02	Intergenic								
CONGO_chr7_027612468_59_p0	chr7	27612468	27612526	+	0	59	114.76	AntisenseIntron								
CONGO_chr7_031484642_47_m2	chr7	31484642	31484688	-	2	47	120.19	Intergenic								
CONGO_chr7_032434169_124_p2	chr7	32434169	32434292	+	2	124	47.25	Intergenic								
CONGO_chr7_037454988_89_m0	chr7	37454988	37455076	-	0	89	75.52	UTR				1	1	TU1111	SpliceToPCG	ENSG00000155849
CONGO_chr7_037802202_178_p1	chr7	37802202	37802379	+	1	178	589.42	NCIntron								
CONGO_chr7_037802794_222_p0	chr7	37802794	37803015	+	0	222	507.19	NCIntron							NovelUnspliced	
CONGO_chr7_038984114_70_p1	chr7	38984114	38984183	+	1	70	75.03	UTR					1			
CONGO_chr7_039090381_74_m0	chr7	39090381	39090454	-	0	74	74	AntisenseIntron								
CONGO_chr7_039232249_159_m0	chr7	39232249	39232407	-	0	159	11.81	AntisenseIntron								
CONGO_chr7_039242659_66_m0	chr7	39242659	39242724	-	0	66	76.62	AntisenseIntron								
CONGO_chr7_040533591_66_p0	chr7	40533591	40533656	+	0	66	128.99	Intron								

CONGO_chr7_041139898_78_m0	chr7	41139898	41139975	-	0	78	56.46	Intergenic								
CONGO_chr7_042159336_124_p1	chr7	42159336	42159459	+	1	124	40.97	AntisenseIntron								
CONGO_chr7_050662953_42_m0	chr7	50662953	50662994	-	0	42	0.56	Intron								
CONGO_chr7_051223105_45_m2	chr7	51223105	51223149	-	2	45	213.25	Intron					TU1112	SpliceToPCG	ENSG00000106078	
CONGO_chr7_063935148_426_m0	chr7	63935148	63935573	-	0	426	803.78	Intergenic	1	rve				UnsplicedMergeWithNCG	ENSG00000234338	
CONGO_chr7_063936927_191_m2	chr7	63936927	63937117	-	2	191	508.45	Intergenic	1					NovelUnspliced		
CONGO_chr7_069070679_48_p0	chr7	69070679	69070726	+	0	48	219.12	Intron					TU1115	SpliceToPCG	ENSG00000158321	
CONGO_chr7_069236980_211_m1	chr7	69236980	69237190	-	1	211	45.87	AntisenseIntron								
CONGO_chr7_069340975_55_p2	chr7	69340975	69341029	+	2	55	30.16	Intron								
CONGO_chr7_069397152_101_m2	chr7	69397152	69397252	-	2	101	46.3	AntisenseIntron								
CONGO_chr7_069441027_148_p2	chr7	69441027	69441174	+	2	148	186.3	Intron								
CONGO_chr7_069520309_75_m2	chr7	69520309	69520383	-	2	75	64.81	AntisenseIntron								
CONGO_chr7_069529499_127_p0	chr7	69529499	69529625	+	0	127	33.92	Intron								
CONGO_chr7_069733895_74_p0	chr7	69733895	69733968	+	0	74	8.85	Intron								
CONGO_chr7_072063100_93_m0	chr7	72063100	72063192	-	0	93	46.65	UTR	1		1	1	TU1116	SpliceToPCG	ENSG00000106133	
CONGO_chr7_072787717_49_p2	chr7	72787717	72787765	+	2	49	73.29	NCExon				1	TU147	SpliceToNCG	ENSG00000214738	
CONGO_chr7_072787994_121_p1	chr7	72787994	72788114	+	1	121	708.47	NCExon				1	TU147	SpliceToNCG	ENSG00000214738	
CONGO_chr7_072788196_61_p0	chr7	72788196	72788256	+	0	61	134.02	NCExon				1	TU147	SpliceToNCG	ENSG00000225969	
CONGO_chr7_073767379_44_p1	chr7	73767379	73767422	+	1	44	44.06	Intron					TU1117	SpliceToPCG	ENSG00000077809	
CONGO_chr7_074877587_93_p0	chr7	74877587	74877679	+	0	93	12.21	UTR	1		1	1	TU82	SpliceToPCG	ENSG00000178809	
CONGO_chr7_074877825_88_p0	chr7	74877825	74877912	+	0	88	51.29	UTR	1		1	1	TU82	SpliceToPCG	ENSG00000178809	
CONGO_chr7_074882099_139_p1	chr7	74882099	74882237	+	1	139	571.88	UTR	1		1	1	TU82	SpliceToPCG	ENSG00000178809	
CONGO_chr7_074882334_115_p2	chr7	74882334	74882448	+	2	115	46.8	UTR	1		1	1	TU82	SpliceToPCG	ENSG00000178809	
CONGO_chr7_080966210_125_m0	chr7	80966210	80966334	-	0	125	139.59	Intergenic								
CONGO_chr7_081027372_146_m2	chr7	81027372	81027517	-	2	146	338.27	NCExon				1				
CONGO_chr7_081027982_222_m2	chr7	81027982	81028203	-	2	222	199.73	NCExon		Cadherin		1				
CONGO_chr7_081041326_97_m1	chr7	81041326	81041422	-	1	97	234.34	Intergenic								
CONGO_chr7_081048974_183_m2	chr7	81048974	81049156	-	2	183	20.81	NCExon			1					
CONGO_chr7_081058224_95_m2	chr7	81058224	81058318	-	2	95	281.75	NCIntron								
CONGO_chr7_081064908_171_m2	chr7	81064908	81065078	-	2	171	592.47	NCExon			1					
CONGO_chr7_086619712_96_p2	chr7	86619712	86619807	+	2	96	102.05	UTR			1	1	TU1118	SpliceToPCG	ENSG00000135164	
CONGO_chr7_089786651_303_m0	chr7	89786651	89786953	-	0	303	736.88	AntisenseNCIntron								
CONGO_chr7_089954577_94_p0	chr7	89954577	89954670	+	0	94	71.83	NCExon				1	TU1119	SpliceToPCG	ENSG00000058091	
CONGO_chr7_090669159_87_p1	chr7	90669159	90669245	+	1	87	9.16	Intron								
CONGO_chr7_090887994_92_m1	chr7	90887994	90888085	-	1	92	33.09	NCIntron								
CONGO_chr7_092015986_66_m0	chr7	92015986	92016051	-	0	66	3.61	Intergenic								
CONGO_chr7_092017966_105_m2	chr7	92017966	92018070	-	2	105	177	Intergenic								
CONGO_chr7_092511688_42_m1	chr7	92511688	92511729	-	1	42	8.69	Intergenic								
CONGO_chr7_093977009_202_p0	chr7	93977009	93977210	+	0	202	75.33	UTR			1	1	TU1120	SpliceToPCG	ENSG00000127995	
CONGO_chr7_096185505_48_m1	chr7	96185505	96185552	-	1	48	35.58	Intergenic								
CONGO_chr7_096471388_70_m1	chr7	96471388	96471457	-	1	70	25.57	NCExon			1					
CONGO_chr7_096471527_87_p0	chr7	96471527	96471613	+	0	87	150.3	AntisenseNCExon								
CONGO_chr7_096479164_234_p0	chr7	96479164	96479397	+	0	234	3.49	AntisenseNCExon								
CONGO_chr7_096479468_84_m0	chr7	96479468	96479551	-	0	84	40.47	NCExon				1				
CONGO_chr7_099042307_147_p2	chr7	99042307	99042453	+	2	147	289.62	UTR				1	TU315	SpliceToPCG	ENSG00000197343	
CONGO_chr7_099043232_138_p2	chr7	99043232	99043369	+	2	138	251.45	UTR				1	TU315	SpliceToPCG	ENSG00000197343	
CONGO_chr7_101475232_117_p2	chr7	101475232	101475348	+	2	117	36.83	Intron	1							
CONGO_chr7_102531139_97_p1	chr7	102531139	102531235	+	1	97	88.52	AntisenseCDS			1	1		UnsplicedMergeWithPCG	ENSG00000161048	
CONGO_chr7_102909866_88_m1	chr7	102909866	102909953	-	1	88	63.1	NCExon				1				
CONGO_chr7_107170783_49_p0	chr7	107170783	107170831	+	0	49	187.78	NCExon				1		UnsplicedMergeWithNCG	ENSG00000241292	
CONGO_chr7_110989143_73_m2	chr7	110989143	110989215	-	2	73	91.14	UTR			1	1	TU1124	SpliceToPCG	ENSG00000184903	
CONGO_chr7_111877799_138_p0	chr7	111877799	111877936	+	0	138	112.09	UTR			1	1	TU1125	SpliceToPCG	ENSG00000006652	
CONGO_chr7_112229139_203_m2	chr7	112229139	112229341	-	2	203	14.77	Intergenic								
CONGO_chr7_113841517_155_m2	chr7	113841517	113841671	-	2	155	19.54	AntisenseUTR				1				
CONGO_chr7_114088172_148_p2	chr7	114088172	114088319	+	2	148	124.6	Intron								
CONGO_chr7_114921871_116_m1	chr7	114921871	114921986	-	1	116	30.46	Intergenic								
CONGO_chr7_114922204_78_m2	chr7	114922204	114922281	-	2	78	67.81	Intergenic								
CONGO_chr7_115135114_106_m1	chr7	115135114	115135219	-	1	106	10.97	Intergenic								
CONGO_chr7_116617423_136_p2	chr7	116617423	116617558	+	2	136	242.36	NCExon			1		TU1126	SpliceToPCG	ENSG00000004866	
CONGO_chr7_121731839_195_p0	chr7	121731839	121732033	+	0	195	105.32	NCExon			1	1				
CONGO_chr7_121756148_68_p2	chr7	121756148	121756215	+	2	68	91.97	AntisenseIntron								
CONGO_chr7_126801455_245_p2	chr7	126801455	126801699	+	2	245	175.04	AntisenseCDS								
CONGO_chr7_128293700_421_p0	chr7	128293700	128294120	+	0	421	1680.48	NCExon					TU316	SpliceToNCG	ENSG00000239815	
CONGO_chr7_128295956_110_p2	chr7	128295956	128296065	+	2	110	691.95	NCExon					TU316	SpliceToNCG	ENSG00000239815	
CONGO_chr7_128296302_67_m1	chr7	128296302	128296368	-	1	67	30.18	Intron				1	TU57	SpliceToPCG	ENSG00000135253	
CONGO_chr7_128296453_92_m0	chr7	128296453	128296544	-	0	92	141.03	Intron				1	TU57	SpliceToPCG	ENSG00000135253	
CONGO_chr7_128296913_127_m1	chr7	128296913	128297039	-	1	127	136.23	Intron					TU57	SpliceToPCG	ENSG00000135253	
CONGO_chr7_128307909_103_m0	chr7	128307909	128308011	-	0	103	199.95	NCExon			1	1	TU57	SpliceToPCG	ENSG00000135253	
CONGO_chr7_128308287_89_m2	chr7	128308287	128308375	-	2	89	317.58	Intron				1	TU57	SpliceToPCG	ENSG00000135253	
CONGO_chr7_128939324_195_p0	chr7	128939324	128939518	+	0	195	1156.38	NCExon			1	1	TU1127	SpliceToNCG	ENSG00000240204	
CONGO_chr7_129841758_46_m0	chr7	129841758	129841803	-	0	46	204.12	Intron								
CONGO_chr7_130525643_113_m0	chr7	130525643	130525755	-	0	113	20.47	AntisenseIntron								
CONGO_chr7_131911749_217_p0	chr7	131911749	131911965	+	0	217	49.67	AntisenseUTR				1	TU1128	NovelMultiExon		
CONGO_chr7_133543985_122_m2	chr7	133543985	133544106	-	2	122	214.18	AntisenseIntron								
CONGO_chr7_133544694_396_p0	chr7	133544694	133545089	+	0	396	1061.75	Intron								
CONGO_chr7_133545119_379_p1	chr7	133545119	133545497	+	1	379	197.25	Intron								
CONGO_chr7_133546150_110_p2	chr7	133546150	133546259	+	2	110	220.28	Intron								
CONGO_chr7_134580635_185_p0	chr7	134580635	134580819	+	0	185	867.22	Intron						UnsplicedMergeWithPCG	ENSG00000146857	
CONGO_chr7_134605311_96_m2	chr7	134605311	134605406	-	2	96	746.98	Intergenic								
CONGO_chr7_134605504_109_m0	chr7	134605504	134605612	-	0	109	680.18	Intergenic								
CONGO_chr7_134605945_102_m0	chr7	134605945	134606046	-	0	102	420.46	Intergenic		Xan_ur_permease						
CONGO_chr7_134623530_160_m1	chr7	134623530	134623689	-	1	160	1051.32	Intergenic								
CONGO_chr7_134642453_150_m0	chr7	134642453	134642602	-	0	150	361.89	Intergenic				1		NovelUnspliced		
CONGO_chr7_134645857_67_m1	chr7	134645857	134645923	-	1	67	138.31	Intergenic				1				
CONGO_chr7_138698462_84_p1	chr7	138698462	138698545	+	1	84	88.33	Intron				1	TU1129	SpliceToPCG	ENSG00000146963	
CONGO_chr7_140131958_120_m2	chr7	140131958	140132077	-	2	120	297.5	Intron			1		TU1130	SpliceToPCG	ENSG00000157764	
CONGO_chr7_140420580_382_p0	chr7	140420580	140420961	+	0	382	1727.04	Intergenic				1				
CONGO_chr7_140558860_114_p2	chr7	140558860	140558973	+	2	114	1240.16	Intergenic				1	TU1131	SpliceToPCG	ENSG00000230744	
CONGO_chr7_141633556_150_m0	chr7	141633556	141633705	-	0	150	639.23	AntisenseNCIntron		Trypsin						
CONGO_chr7_141634266_94_m0	chr7	141634266	141634359	-	0	94	279.91	AntisenseNCIntron				1				
CONGO_chr7_141634910_248_m1	chr7	141634910	141635157	-	1	248	596.9	AntisenseNCExon		Trypsin		1				
CONGO_chr7_141635939_89_m2	chr7	141635939	141636027	-	2	89	407.72	Intergenic								
CONGO_chr7_141705902_157_p0	chr7	141705902	141706058	+	0	157	36.83	NCExon	1		1	1				
CONGO_chr7_141924602_279_p2	chr7	141924602	141924880	+	2	279	157.06	NCExon		V-set	1	1	TU1133	NovelMultiExon		
CONGO_chr7_142150779_137_p2	chr7	142150779	142150915	+	2	137	332.23	Intron	1	Trypsin		1				
CONGO_chr7_142151217_114_p0	chr7	142151217	142151330	+	0	114	174.24	Intron	1	Trypsin		1				
CONGO_chr7_142169577_102_p2	chr7	142169577	142169678	+	2	102	104.22	Intron	1							
CONGO_chr7_142170795_254_p1	chr7	142170795	142171048	+	1	254	334.78	Intron	1	Trypsin						
CONGO_chr7_142171449_137_p2	chr7	142171449	142171585	+	2	137	153.89	Intron	1	Trypsin		1				
CONGO_chr7_142194809_68_p1	chr7	142194809	142194876	+	1	68	138.6	NCExon			1	1	TU1134	SpliceToNCG	ENSG00000211721	
CONGO_chr7_142200504_107_p2	chr7	142200504	142200610	+	2	107	873.3	NCExon			1	1	TU1135	SpliceToNCG	ENSG00000211764	
CONGO_chr7_149657912_188_p2	chr7	149657912	149658099	+	2	188	83.62	UTR			1		TU149	SpliceToPCG	ENSG00000127399	
CONGO_chr7_149658179_190_p2	chr7	149658179	149658368	+	2	190	65.78	UTR			1		TU149	SpliceToPCG	ENSG00000127399	
CONGO_chr7_149659162_122_p1	chr7	149659162	149659283	+	1	122	202.52	UTR			1		TU149	SpliceToPCG	ENSG00000127399	
CONGO_chr7_149735633_612_p0	chr7	149735633	149736244	+	0	612	2210.31	NCExon		zf-C2H2	1	1	TU1137	SpliceToPCG	ENSG00000196456	
CONGO_chr7_150409311_258_m2	chr7	150409311	150409568	-	2	258	201.36	UTR			1	1	TU1138	SpliceToPCG	ENSG00000164897	
CONGO_chr7_150459430_105_m0	chr7	150459430	150459534	-	0	105	0.28	AntisenseIntron								
CONGO_chr7_150519000_108_m0	chr7	150519000	150519107	-	0	108	345	NCExon				1				
CONGO_chr7_150519658_239_m2	chr7	150519658	150519896	-	2	239	940.42	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150520296_178_m0	chr7	150520296	150520473	-	0	178	2144.01	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150520763_87_m0	chr7	150520763	150520849	-	0	87	473.87	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150521311_200_m2	chr7	150521311	150521510	-	2	200	1263.13	NCExon		AAA		1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150522276_108_m2	chr7	150522276	150522383	-	2	108	877.16	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150522536_83_m1	chr7	150522536	150522618	-	1	83	269.41	NCExon					TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150523633_45_m0	chr7	150523633	150523677	-	0	45	255.5	NCExon					TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150524467_107_m2	chr7	150524467	150524573	-	2	107	112.64	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150524996_76_m0	chr7	150524996	150525071	-	0	76	301.47	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150525841_85_m1	chr7	150525841	150525925	-	1	85	459.85	NCExon				1	TU10	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150526817_146_m0	chr7	150526817	150526962	-	0	146	288.14	NCExon				1				
CONGO_chr7_150528402_72_m0	chr7	150528402	150528473	-	0	72	216.01	NCExon				1	TU317	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150530930_174_m0	chr7	150530930	150531103	-	0	174	1157.71	NCExon					TU317	SpliceToNCG	ENSG00000183016	
CONGO_chr7_150531414_120_m0	chr7	150531414	150531533	-	0	120	522.09	NCExon				1				
CONGO_chr7_150532528_328_m1	chr7	150532528	150532855	-	1	328	1599.47	NCExon				1				
CONGO_chr7_150538206_132_m0	chr7	150538206	150538337	-	0	132	341.12	Intron								
CONGO_chr7_150760187_118_m1	chr7	150760187	150760304	-	1	118	544.39	NCExon		Crystall	1		TU1139	SpliceToPCG	ENSG00000127377	

CONGO_chr7_150894633_86_m0	chr7	150894633	150894718	-	0	86	77.11	Intron					TU1140	SpliceToPCG	ENSG00000106617
CONGO_chr7_152739285_450_m0	chr7	152739285	152739734	-	0	450	294.36	NCExon	1	rve	1				
CONGO_chr7_153512591_53_p2	chr7	153512591	153512643	+	2	53	47.28	Intron							
CONGO_chr7_155031287_113_m2	chr7	155031287	155031399	-	2	113	452.98	Intergenic							
CONGO_chr7_156856219_105_p2	chr7	156856219	156856323	+	2	105	140.46	NCExon				1			
CONGO_chr7_156857602_174_p2	chr7	156857602	156857775	+	2	174	724.21	NCExon						UnsplicedMergeWithPCG	ENSG00000105993
CONGO_chr7_158242784_102_m0	chr7	158242784	158242885	-	0	102	39.02	Intron					TU1141	SpliceToPCG	ENSG00000117868
CONGO_chr8_001196258_33_p2	chr8	1196258	1196290	+	2	33	312.86	Intergenic				1	TU318	SpliceToPCG	ENSG00000198010
CONGO_chr8_001436939_66_p2	chr8	1436939	1437004	+	2	66	347.56	UTR			1		TU318	SpliceToPCG	ENSG00000198010
CONGO_chr8_008614331_120_m2	chr8	8614331	8614450	-	2	120	56.74	Intergenic							
CONGO_chr8_009510405_66_p0	chr8	9510405	9510470	+	0	66	73.87	Intron				1			
CONGO_chr8_010369779_198_m1	chr8	10369779	10369976	-	1	198	487.16	Intergenic		Trypsin					
CONGO_chr8_010391281_106_m0	chr8	10391281	10391386	-	0	106	604.47	NCIntron							
CONGO_chr8_010391555_123_m0	chr8	10391555	10391677	-	0	123	368.63	NCIntron						NovelUnspliced	
CONGO_chr8_010392632_260_m1	chr8	10392632	10392891	-	1	260	1162.39	NCExon		Trypsin	1	1		NovelUnspliced	
CONGO_chr8_010393536_193_m2	chr8	10393536	10393728	-	2	193	1205.48	NCExon		Trypsin	1	1		NovelUnspliced	
CONGO_chr8_010505352_97_p1	chr8	10505352	10505448	+	1	97	516.64	AntisenseCDS							
CONGO_chr8_010506112_73_p0	chr8	10506112	10506184	+	0	73	39.78	AntisenseCDS							
CONGO_chr8_011257814_76_m2	chr8	11257814	11257889	-	2	76	357.84	AntisenseCDS				1			
CONGO_chr8_011260502_140_p2	chr8	11260502	11260641	+	2	140	995.78	UTR			1	1		UnsplicedMergeWithPCG	ENSG00000154316
CONGO_chr8_011614151_40_p2	chr8	11614151	11614190	+	2	40	62.4	Intron						NovelUnspliced	
CONGO_chr8_018985996_92_m2	chr8	18985996	18986087	-	2	92	174.51	Intergenic				1			
CONGO_chr8_019750953_78_p1	chr8	19750953	19751030	+	1	78	227.55	Intron				1	TU1142	SpliceToPCG	ENSG00000104613
CONGO_chr8_021902180_111_p0	chr8	21902180	21902290	+	0	111	99.06	Intron				1	TU1143	SpliceToPCG	ENSG00000130227
CONGO_chr8_022752260_122_p2	chr8	22752260	22752381	+	2	122	29.28	AntisenseIntron							
CONGO_chr8_024266319_63_p0	chr8	24266319	24266381	+	0	63	316.83	Intron						NovelUnspliced	
CONGO_chr8_025497994_80_m2	chr8	25497994	25498073	-	2	80	52.32	AntisenseIntron							
CONGO_chr8_025559110_91_m1	chr8	25559110	25559200	-	1	91	104.07	AntisenseIntron							
CONGO_chr8_025845963_186_m0	chr8	25845963	25846148	-	0	186	86.35	Intron							
CONGO_chr8_025851506_150_p0	chr8	25851506	25851655	+	0	150	9.32	Intron							
CONGO_chr8_026205141_44_p0	chr8	26205141	26205184	+	0	44	57.02	UTR			1	1	TU1144	SpliceToPCG	ENSG00000221914
CONGO_chr8_027152660_54_m1	chr8	27152660	27152713	-	1	54	60.91	Intron			1	1	TU1145	SpliceToPCG	ENSG00000015592
CONGO_chr8_030533717_141_p0	chr8	30533717	30533857	+	0	141	21.37	Intron				1	TU1147	SpliceToPCG	ENSG00000157110
CONGO_chr8_030622369_288_p0	chr8	30622369	30622656	+	0	288	1986.82	AntisenseIntron				1	TU1148	NovelMultiExon	
CONGO_chr8_031008801_152_p0	chr8	31008801	31008952	+	0	152	120.78	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000172733
CONGO_chr8_031616363_127_p0	chr8	31616363	31616489	+	0	127	136.99	Intergenic							
CONGO_chr8_032624263_147_p0	chr8	32624263	32624409	+	0	147	458.87	UTR			1			UnsplicedMergeWithPCG	ENSG00000157168
CONGO_chr8_037050370_80_m2	chr8	37050370	37050449	-	2	80	32.8	Intergenic							
CONGO_chr8_037224523_84_p0	chr8	37224523	37224606	+	0	84	41.08	Intergenic							
CONGO_chr8_037302641_173_m2	chr8	37302641	37302813	-	2	173	1.21	Intergenic						NovelUnspliced	
CONGO_chr8_037306477_132_p0	chr8	37306477	37306608	+	0	132	10.81	Intergenic							
CONGO_chr8_037456127_162_p0	chr8	37456127	37456288	+	0	162	21.37	Intergenic							
CONGO_chr8_037542570_148_m1	chr8	37542570	37542717	-	1	148	113.33	Intergenic							
CONGO_chr8_037614885_124_p1	chr8	37614885	37615008	+	1	124	71.69	Intergenic							
CONGO_chr8_039513190_167_p0	chr8	39513190	39513356	+	0	167	178.17	Intergenic		Reprolysin					
CONGO_chr8_041286119_164_m1	chr8	41286119	41286282	-	1	164	29.06	UTR			1		TU1149	SpliceToPCG	ENSG00000104332
CONGO_chr8_041744017_77_m2	chr8	41744017	41744093	-	2	77	10.25	Intron							
CONGO_chr8_041744310_102_m2	chr8	41744310	41744411	-	2	102	9.78	Intron							
CONGO_chr8_049067001_310_m1	chr8	49067001	49067310	-	1	310	89.86	Intergenic							
CONGO_chr8_049067385_281_m2	chr8	49067385	49067665	-	2	281	473.33	Intergenic		rve					
CONGO_chr8_053300789_105_m0	chr8	53300789	53300893	-	0	105	37	Intron							
CONGO_chr8_053324471_173_m0	chr8	53324471	53324643	-	0	173	91.06	Intron				1			
CONGO_chr8_053329363_114_m2	chr8	53329363	53329476	-	2	114	36.55	Intron				1			
CONGO_chr8_053329654_120_p0	chr8	53329654	53329773	+	0	120	0.15	AntisenseIntron							
CONGO_chr8_053330042_106_p1	chr8	53330042	53330147	+	1	106	93.77	AntisenseIntron							
CONGO_chr8_053484476_90_m0	chr8	53484476	53484565	-	0	90	67.87	UTR			1	1	TU1150	SpliceToPCG	ENSG00000147488
CONGO_chr8_054304323_75_m0	chr8	54304323	54304397	-	0	75	399.15	UTR			1			UnsplicedMergeWithPCG	ENSG00000082556
CONGO_chr8_055253685_68_m0	chr8	55253685	55253752	-	0	68	38.12	Intergenic							
CONGO_chr8_055858661_164_p2	chr8	55858661	55858824	+	2	164	808.67	Intergenic				1	TU320	NovelMultiExon	
CONGO_chr8_055912564_220_p0	chr8	55912564	55912783	+	0	220	261.26	Intergenic		PLAT		1	TU320	NovelMultiExon	
CONGO_chr8_055927730_113_p2	chr8	55927730	55927842	+	2	113	308.47	Intergenic				1	TU83	NovelMultiExon	
CONGO_chr8_055932142_79_p0	chr8	55932142	55932220	+	0	79	214.52	Intergenic				1	TU83	NovelMultiExon	
CONGO_chr8_055940949_82_p2	chr8	55940949	55941030	+	2	82	244.63	Intergenic				1	TU83	NovelMultiExon	
CONGO_chr8_055944957_56_p1	chr8	55944957	55945012	+	1	56	226.4	Intergenic				1	TU83	NovelMultiExon	
CONGO_chr8_057237437_133_m1	chr8	57237437	57237569	-	1	133	63.98	UTR			1			UnsplicedMergeWithPCG	ENSG00000181690
CONGO_chr8_061867981_292_m2	chr8	61867981	61868272	-	2	292	116.12	AntisenseIntron							
CONGO_chr8_062092023_116_m2	chr8	62092023	62092138	-	2	116	84.2	Intergenic							
CONGO_chr8_064029015_71_p2	chr8	64029015	64029085	+	2	71	112.7	Intron					TU1151	NovelMultiExon	
CONGO_chr8_065342115_109_p0	chr8	65342115	65342223	+	0	109	73.16	Intergenic							
CONGO_chr8_065345457_121_p1	chr8	65345457	65345577	+	1	121	130.95	Intergenic							
CONGO_chr8_065680628_94_p1	chr8	65680628	65680721	+	1	94	3.11	AntisenseIntron							
CONGO_chr8_066220109_150_m0	chr8	66220109	66220258	-	0	150	9.74	Intergenic							
CONGO_chr8_066263134_160_p1	chr8	66263134	66263293	+	1	160	59.21	Intergenic							
CONGO_chr8_068022840_114_m0	chr8	68022840	68022953	-	0	114	295.9	Intergenic				1		NovelUnspliced	
CONGO_chr8_069993288_60_m0	chr8	69993288	69993347	-	0	60	15.47	NCIntron							
CONGO_chr8_073195300_290_p2	chr8	73195300	73195589	+	2	290	41.07	Intergenic		Gag_p30					
CONGO_chr8_076728512_69_p2	chr8	76728512	76728580	+	2	69	78.46	Intergenic							
CONGO_chr8_076912656_46_p0	chr8	76912656	76912701	+	0	46	20	Intergenic							
CONGO_chr8_077603344_78_p0	chr8	77603344	77603421	+	0	78	20.73	Intergenic							
CONGO_chr8_077654112_81_p1	chr8	77654112	77654192	+	1	81	40.7	Intergenic							
CONGO_chr8_077656496_176_p2	chr8	77656496	77656671	+	2	176	31.87	Intergenic							
CONGO_chr8_077745032_36_p1	chr8	77745032	77745067	+	1	36	26.99	AntisenseNCIntron							
CONGO_chr8_077747617_148_m1	chr8	77747617	77747764	-	1	148	155	NCExon			1	1	TU1152	NovelMultiExon	
CONGO_chr8_077758530_216_p1	chr8	77758530	77758745	+	1	216	93.6	Intron				1			
CONGO_chr8_077759816_93_p0	chr8	77759816	77759908	+	0	93	69.24	Intron							
CONGO_chr8_077761991_74_m0	chr8	77761991	77762064	-	0	74	116.91	AntisenseIntron							
CONGO_chr8_077773689_51_p2	chr8	77773689	77773739	+	2	51	15.66	Intron							
CONGO_chr8_077778818_211_m1	chr8	77778818	77779028	-	1	211	244.19	AntisenseCDS							
CONGO_chr8_077876958_180_p1	chr8	77876958	77877137	+	1	180	24.59	Intron							
CONGO_chr8_077940137_85_p2	chr8	77940137	77940221	+	2	85	35.33	UTR			1		TU1153	SpliceToPCG	ENSG00000091656
CONGO_chr8_078984487_143_m2	chr8	78984487	78984629	-	2	143	28.08	Intergenic							
CONGO_chr8_079721867_168_p0	chr8	79721867	79722034	+	0	168	293.66	Intergenic							
CONGO_chr8_081948334_469_m1	chr8	81948334	81948802	-	1	469	521.59	Intron				1	TU1154	SpliceToPCG	ENSG00000164684
CONGO_chr8_082681361_152_m1	chr8	82681361	82681512	-	1	152	1272.6	Intergenic		Inositol_P					
CONGO_chr8_082688511_108_m2	chr8	82688511	82688618	-	2	108	683.15	Intergenic				1	TU1155	NovelMultiExon	
CONGO_chr8_082694798_106_m0	chr8	82694798	82694903	-	0	106	502.05	Intergenic		Inositol_P		1	TU321	NovelMultiExon	
CONGO_chr8_082699147_103_m2	chr8	82699147	82699249	-	2	103	357.33	Intergenic		Inositol_P		1	TU321	SpliceToPCG	ENSG00000133731
CONGO_chr8_082700852_134_m0	chr8	82700852	82700985	-	0	134	88.23	Intergenic		Inositol_P		1			
CONGO_chr8_085258206_163_p0	chr8	85258206	85258368	+	0	163	36.39	UTR			1	1	TU1156	NovelMultiExon	
CONGO_chr8_088509890_68_p2	chr8	88509890	88509957	+	2	68	311.63	Intergenic				1	TU150	SpliceToPCG	ENSG00000176571
CONGO_chr8_088552592_60_p0	chr8	88552592	88552651	+	0	60	43.03	Intergenic				1	TU150	SpliceToPCG	ENSG00000176571
CONGO_chr8_088568932_117_p0	chr8	88568932	88569048	+	0	117	127.24	Intergenic				1	TU150	SpliceToPCG	ENSG00000176571
CONGO_chr8_092042146_107_m2	chr8	92042146	92042252	-	2	107	270.26	Intergenic				1	TU84	NovelMultiExon	
CONGO_chr8_092052470_76_m0	chr8	92052470	92052545	-	0	76	67.71	Intergenic				1	TU84	NovelMultiExon	
CONGO_chr8_092059983_74_m2	chr8	92059983	92060056	-	2	74	402.51	Intergenic				1	TU84	NovelMultiExon	
CONGO_chr8_092061767_99_m2	chr8	92061767	92061865	-	2	99	220.75	Intergenic				1	TU84	NovelMultiExon	
CONGO_chr8_093038649_146_p1	chr8	93038649	93038794	+	1	146	174.87	AntisenseNCExon						UnsplicedMergeWithPCG	ENSG00000079102
CONGO_chr8_093039063_84_m0	chr8	93039063	93039146	-	0	84	36.46	NCExon			1		TU1157	SpliceToPCG	ENSG00000079102
CONGO_chr8_093723994_63_p1	chr8	93723994	93724056	+	1	63	17.1	Intergenic							
CONGO_chr8_093724142_81_m2	chr8	93724142	93724222	-	2	81	112.18	Intergenic							
CONGO_chr8_093834857_57_m0	chr8	93834857	93834913	-	0	57	11.56	NCIntron							
CONGO_chr8_097136956_68_m2	chr8	97136956	97137023	-	2	68	21.08	Intergenic							
CONGO_chr8_098777608_90_p2	chr8	98777608	98777697	+	2	90	125.68	Intron					TU1158	SpliceToPCG	ENSG00000147649
CONGO_chr8_100718125_82_m1	chr8	100718125	100718206	-	1	82	45.66	AntisenseIntron							
CONGO_chr8_102518687_108_p0	chr8	102518687	102518794	+	0	108	38.04	Intergenic							
CONGO_chr8_102573854_101_m0	chr8	102573854	102573954	-	0	101	15.19	AntisenseUTR				1	TU1159	NovelMultiExon	
CONGO_chr8_103931465_84_m0	chr8	103931465	103931548	-	0	84	3.87	UTR			1	1	TU322	SpliceToPCG	ENSG00000155096
CONGO_chr8_103939450_105_m0	chr8	103939450	103939554	-	0	105	368.14	UTR			1	1	TU322	SpliceToPCG	ENSG00000155096
CONGO_chr8_105919705_51_p0	chr8	105919705	105919755	+	0	51	106.85	Intergenic							
CONGO_chr8_106031634_91_m1	chr8	106031634	106031724	-	1	91	97.76	Intergenic							
CONGO_chr8_106171781_79_p1	chr8	106171781	106171859	+	1	79	42.62	Intergenic							
CONGO_chr8_106651206_128_p2	chr8	106651206	106651333	+	2	128	3.67	Intron							
CONGO_chr8_106681428_104_p2	chr8	106681428	106681531	+	2	104	84.11	Intron							
CONGO_chr8_106715264_56_p2	chr8	106715264	106715319	+	2	56	19.14	Intron							
CONGO_chr8_106860865_119_p2	chr8	106860865	106860983	+	2	119	101.25	Intron							

CONGO_chr8_108579248_93_p2	chr8	108579248	108579340	+	2	93	31.53	AntisenseUTR								
CONGO_chr8_110859893_331_p2	chr8	110859893	110860223	+	2	331	267.32	Intergenic								
CONGO_chr8_110863445_193_p0	chr8	110863445	110863637	+	0	193	61.55	Intergenic								
CONGO_chr8_116510619_44_m2	chr8	116510619	116510662	-	2	44	52.16	Intron								
CONGO_chr8_116533205_81_m0	chr8	116533205	116533285	-	0	81	8.83	Intron								
CONGO_chr8_116860851_58_p2	chr8	116860851	116860908	+	2	58	42.76	AntisenseIntron								
CONGO_chr8_117739621_67_p2	chr8	117739621	117739687	+	2	67	106.81	AntisenseIntron								
CONGO_chr8_117739935_106_m1	chr8	117739935	117740040	-	1	106	12.8	Intron			1	1	TU1160	SpliceToPCG	ENSG00000147677	
CONGO_chr8_125033852_39_p1	chr8	125033852	125033890	+	1	39	133.08	Intron								
CONGO_chr8_130961804_83_m1	chr8	130961804	130961886	-	1	83	206.13	UTR			1	1	TU1161	SpliceToPCG	ENSG00000153310	
CONGO_chr8_133019654_91_p0	chr8	133019654	133019744	+	0	91	328.6	Intron								
CONGO_chr8_134557343_69_p2	chr8	134557343	134557411	+	2	69	136.08	AntisenseCDS			1	1				
CONGO_chr8_142333748_163_m1	chr8	142333748	142333910	-	1	163	12.87	Intergenic				1	TU1162	SpliceToPCG	ENSG00000022567	
CONGO_chr8_143350644_184_p0	chr8	143350644	143350827	+	0	184	45.21	AntisenseUTR								
CONGO_chr8_143359128_465_m2	chr8	143359128	143359592	-	2	465	598.31	Intron				1	TU1163	SpliceToPCG	ENSG00000171045	
CONGO_chr8_143652048_145_m1	chr8	143652048	143652192	-	1	145	532.65	AntisenseIntron								
CONGO_chr8_143652888_87_m0	chr8	143652888	143652974	-	0	87	355.35	AntisenseIntron								
CONGO_chr8_143654166_117_m0	chr8	143654166	143654282	-	0	117	222.52	AntisenseIntron				1				
CONGO_chr8_143876035_212_m2	chr8	143876035	143876246	-	2	212	820.51	Intergenic		UPAR_LY6						
CONGO_chr8_143879501_99_m2	chr8	143879501	143879599	-	2	99	404.26	Intergenic								
CONGO_chr8_144234003_117_p2	chr8	144234003	144234119	+	2	117	17.47	Intergenic					TU1164	NovelMultiExon		
CONGO_chr8_144891805_588_m0	chr8	144891805	144892392	-	0	588	1132.53	AntisenseIntron								
CONGO_chr8_145176255_534_p0	chr8	145176255	145176788	+	0	534	811.92	Intergenic				1	TU1165	NovelMultiExon		
CONGO_chr8_145177192_156_p2	chr8	145177192	145177347	+	2	156	77.13	Intergenic								
CONGO_chr8_145190591_235_m0	chr8	145190591	145190825	-	0	235	1027.93	Intergenic					TU1166	SpliceToPCG	ENSG00000178814	
CONGO_chr8_145434865_53_p2	chr8	145434865	145434917	+	2	53	77.04	UTR	1		1	1				
CONGO_chr8_145435334_108_p0	chr8	145435334	145435441	+	0	108	179.42	UTR	1		1	1	TU1167	SpliceToPCG	ENSG00000179832	
CONGO_chr8_145435756_120_p0	chr8	145435756	145435875	+	0	120	696.12	UTR	1		1	1				
CONGO_chr8_145436159_123_p0	chr8	145436159	145436281	+	0	123	366.31	UTR	1		1	1				
CONGO_chr8_145437133_147_p0	chr8	145437133	145437279	+	0	147	603.84	UTR	1		1	1				
CONGO_chr8_145438258_123_p0	chr8	145438258	145438380	+	0	123	621.27	UTR	1		1	1				
CONGO_chr8_145438627_80_p0	chr8	145438627	145438706	+	0	80	108.28	UTR	1		1	1				
CONGO_chr9_000917249_77_p1	chr9	917249	917325	+	1	77	95.73	Intron								
CONGO_chr9_000959295_64_m1	chr9	959295	959358	-	1	64	43.52	Intergenic								
CONGO_chr9_005738585_130_p2	chr9	5738585	5738714	+	2	130	13.15	UTR			1		TU1170	SpliceToPCG	ENSG00000107036	
CONGO_chr9_006976521_90_m2	chr9	6976521	6976610	-	2	90	11.58	AntisenseCDS				1	TU1171	NovelMultiExon		
CONGO_chr9_008085710_167_p2	chr9	8085710	8085876	+	2	167	4.79	Intergenic								
CONGO_chr9_008475639_86_m2	chr9	8475639	8475724	-	2	86	39.81	Intron					TU1172	SpliceToPCG	ENSG00000153707	
CONGO_chr9_008516048_160_m1	chr9	8516048	8516207	-	1	160	101.16	Intron								
CONGO_chr9_008774104_118_m1	chr9	8774104	8774221	-	1	118	31.59	Intron								
CONGO_chr9_014121571_105_p0	chr9	14121571	14121675	+	0	105	69.56	AntisenseIntron								
CONGO_chr9_014298022_170_p1	chr9	14298022	14298191	+	1	170	39.57	AntisenseIntron								
CONGO_chr9_015962299_88_p1	chr9	15962299	15962386	+	1	88	53.08	UTR			1		TU1173	SpliceToPCG	ENSG00000164989	
CONGO_chr9_016268491_100_m0	chr9	16268491	16268590	-	0	100	2.46	Intergenic								
CONGO_chr9_016402932_101_p1	chr9	16402932	16403032	+	1	101	81.1	AntisenseUTR						NovelUnspliced		
CONGO_chr9_016417988_110_m2	chr9	16417988	16418097	-	2	110	15.54	Intron						NovelUnspliced		
CONGO_chr9_016439378_96_p0	chr9	16439378	16439473	+	0	96	51.64	AntisenseIntron								
CONGO_chr9_016561574_91_m1	chr9	16561574	16561664	-	1	91	41.19	Intron								
CONGO_chr9_016561718_89_p0	chr9	16561718	16561806	+	0	89	13.52	AntisenseIntron								
CONGO_chr9_016671398_54_p0	chr9	16671398	16671451	+	0	54	216.44	AntisenseIntron								
CONGO_chr9_016671751_103_m1	chr9	16671751	16671853	-	1	103	5.94	Intron						NovelUnspliced		
CONGO_chr9_016700865_192_p0	chr9	16700865	16701056	+	0	192	89.92	AntisenseIntron								
CONGO_chr9_016818765_118_m1	chr9	16818765	16818882	-	1	118	10.13	Intron								
CONGO_chr9_016858086_168_m0	chr9	16858086	16858253	-	0	168	19.02	UTR			1	1				
CONGO_chr9_018153860_120_p0	chr9	18153860	18153979	+	0	120	303.57	Intergenic					TU1174	NovelMultiExon		
CONGO_chr9_018337921_83_p2	chr9	18337921	18338003	+	2	83	2.35	Intergenic								
CONGO_chr9_019930936_69_p0	chr9	19930936	19931004	+	0	69	19.59	Intergenic								
CONGO_chr9_021916345_251_p2	chr9	21916345	21916595	+	2	251	90.6	Intron								
CONGO_chr9_021918418_204_p0	chr9	21918418	21918621	+	0	204	431.43	Intron						NovelUnspliced		
CONGO_chr9_023681899_48_p0	chr9	23681899	23681946	+	0	48	7.13	AntisenseUTR								
CONGO_chr9_023755005_118_p0	chr9	23755005	23755122	+	0	118	16.86	AntisenseCDS				1				
CONGO_chr9_024825571_64_p2	chr9	24825571	24825634	+	2	64	13.18	Intergenic								
CONGO_chr9_026514454_97_m0	chr9	26514454	26514550	-	0	97	122.31	Intergenic								
CONGO_chr9_026685126_88_p1	chr9	26685126	26685213	+	1	88	85.33	Intergenic								
CONGO_chr9_032542433_45_p0	chr9	32542433	32542477	+	0	45	268.99	AntisenseCDS			1	1	TU323	SpliceToPCG	ENSG00000241043	
CONGO_chr9_032542799_123_p0	chr9	32542799	32542921	+	0	123	536.3	NCExon			1	1	TU323	SpliceToNCG	ENSG00000235453	
CONGO_chr9_034655031_157_m1	chr9	34655031	34655187	-	1	157	134.9	NCExon			1	1	TU1175	SpliceToNCG	ENSG00000187186	
CONGO_chr9_035098653_82_m1	chr9	35098653	35098734	-	1	82	12.71	UTR	1		1	1	TU1177	SpliceToPCG	ENSG00000005238	
CONGO_chr9_035290163_71_p1	chr9	35290163	35290233	+	1	71	40.74	Intron								
CONGO_chr9_035290776_76_p0	chr9	35290776	35290851	+	0	76	74.46	Intron								
CONGO_chr9_035290953_128_p0	chr9	35290953	35291080	+	0	128	97.03	Intron								
CONGO_chr9_035291337_94_p0	chr9	35291337	35291430	+	0	94	207.08	Intron								
CONGO_chr9_035293913_138_p1	chr9	35293913	35294050	+	1	138	42.94	Intron								
CONGO_chr9_035295517_48_p2	chr9	35295517	35295564	+	2	48	4.13	Intron								
CONGO_chr9_035331713_126_m2	chr9	35331713	35331838	-	2	126	81.06	AntisenseIntron								
CONGO_chr9_035341524_95_p0	chr9	35341524	35341618	+	0	95	144.98	Intron								
CONGO_chr9_035341929_359_p0	chr9	35341929	35342287	+	0	359	1548.41	Intron						NovelUnspliced		
CONGO_chr9_035342333_79_p1	chr9	35342333	35342411	+	1	79	210.4	Intron						NovelUnspliced		
CONGO_chr9_035342936_481_p1	chr9	35342936	35343416	+	1	481	1480.91	Intron						NovelUnspliced		
CONGO_chr9_035343611_197_p1	chr9	35343611	35343807	+	1	197	428.58	NCExon			1					
CONGO_chr9_036414610_71_m2	chr9	36414610	36414680	-	2	71	304.3	NCExon				1	TU324	SpliceToPCG	ENSG00000137075	
CONGO_chr9_036477305_253_m0	chr9	36477305	36477557	-	0	253	44.91	NCExon				1	TU324	SpliceToPCG	ENSG00000137075	
CONGO_chr9_036929517_103_m0	chr9	36929517	36929619	-	0	103	194.74	Intron								
CONGO_chr9_037169289_58_p0	chr9	37169289	37169346	+	0	58	18.11	Intron								
CONGO_chr9_037205353_78_m0	chr9	37205353	37205430	-	0	78	42.1	AntisenseIntron								
CONGO_chr9_038446115_76_p1	chr9	38446115	38446190	+	1	76	119.34	Intergenic				1				
CONGO_chr9_038452100_131_p1	chr9	38452100	38452230	+	1	131	764	Intergenic				1				
CONGO_chr9_038459844_119_p2	chr9	38459844	38459962	+	2	119	700.41	Intergenic								
CONGO_chr9_038461885_46_p1	chr9	38461885	38461930	+	1	46	253.2	Intergenic								
CONGO_chr9_070950440_116_p0	chr9	70950440	70950555	+	0	116	1108.14	Intron								
CONGO_chr9_070956387_72_p1	chr9	70956387	70956458	+	1	72	154.21	UTR			1	1	TU1178	SpliceToPCG	ENSG00000119139	
CONGO_chr9_071130046_414_p0	chr9	71130046	71130459	+	0	414	953.78	Intron				1	TU1179	SpliceToPCG	ENSG00000135063	
CONGO_chr9_071300074_45_m0	chr9	71300074	71300118	-	0	45	148.12	Intron								
CONGO_chr9_075400109_42_m0	chr9	75400109	75400150	-	0	42	49.86	Intergenic								
CONGO_chr9_075402069_68_m0	chr9	75402069	75402136	-	0	68	32.42	Intergenic								
CONGO_chr9_075888368_103_p2	chr9	75888368	75888470	+	2	103	73.09	Intergenic								
CONGO_chr9_078817461_57_p1	chr9	78817461	78817517	+	1	57	36.88	Intergenic								
CONGO_chr9_080483703_69_p0	chr9	80483703	80483771	+	0	69	35.94	Intergenic								
CONGO_chr9_081013837_123_p2	chr9	81013837	81013959	+	2	123	48.34	Intergenic								
CONGO_chr9_081384764_104_m2	chr9	81384764	81384867	-	2	104	82.11	AntisenseNCExon								
CONGO_chr9_081414799_105_p0	chr9	81414799	81414903	+	0	105	59.39	Intron								
CONGO_chr9_083200332_87_m0	chr9	83200332	83200418	-	0	87	70.09	Intergenic								
CONGO_chr9_083430931_84_p0	chr9	83430931	83431014	+	0	84	52.76	AntisenseIntron								
CONGO_chr9_084293389_125_m1	chr9	84293389	84293513	-	1	125	84.2	Intergenic								
CONGO_chr9_084699954_127_m2	chr9	84699954	84700080	-	2	127	80.86	Intergenic								
CONGO_chr9_085780266_148_p0	chr9	85780266	85780413	+	0	148	57.89	AntisenseUTR								
CONGO_chr9_088032397_159_m0	chr9	88032397	88032555	-	0	159	252.6	Intron					TU1180	SpliceToPCG	ENSG00000187753	
CONGO_chr9_089761039_146_p2	chr9	89761039	89761184	+	2	146	169.71	Intergenic						NovelUnspliced		
CONGO_chr9_094517291_54_p0	chr9	94517291	94517344	+	0	54	339.47	AntisenseCDS						UnsplicedMergeWithPCG	ENSG00000185963	
CONGO_chr9_095354210_55_p2	chr9	95354210	95354264	+	2	55	58.11	Intron					TU1181	SpliceToPCG	ENSG00000048828	
CONGO_chr9_096887443_119_p0	chr9	96887443	96887561	+	0	119	39.58	NCExon			1		TU1182	SpliceToPCG	ENSG00000148120	
CONGO_chr9_096887571_60_m0	chr9	96887571	96887630	-	0	60	13.86	AntisenseNCExon								
CONGO_chr9_097298380_139_p2	chr9	97298380	97298518	+	2	139	60.31	AntisenseIntron								
CONGO_chr9_098306201_66_m1	chr9	98306201	98306266	-	1	66	133.34	Intron					TU1183	SpliceToPCG	ENSG00000081377	
CONGO_chr9_099078672_129_p0	chr9	99078672	99078800	+	0	129	604.84	UTR			1	1	TU325	SpliceToPCG	ENSG00000197816	
CONGO_chr9_099079659_71_p0	chr9	99079659	99079729	+	0	71	537.95	UTR			1	1	TU325	SpliceToPCG	ENSG00000197816	
CONGO_chr9_100206392_58_m0	chr9	100206392	100206449	-	0	58	35.54	Intron								
CONGO_chr9_101581101_108_p0	chr9	101581101	101581208	+	0	108	41.44	AntisenseNCIntron								
CONGO_chr9_101627762_174_p2	chr9	101627762	101627935	+	2	174	162.3	UTR			1	1	TU1184	SpliceToPCG	ENSG00000119508	
CONGO_chr9_101661650_58_p2	chr9	101661650	101661707	+	2	58	38.55	Intron								
CONGO_chr9_106619328_79_m0	chr9	106619328	106619406	-	0	79	74.18	Intron					TU1185	SpliceToPCG	ENSG00000165029	
CONGO_chr9_108089280_64_m2	chr9	108089280	108089343	-	2	64	79.83	AntisenseNCIntron								
CONGO_chr9_108418287_65_m2	chr9	108418287	108418351	-	2	65	8.9	AntisenseNCExon								
CONGO_chr9_108666588_144_m0	chr9	108666588	108666731	-	0	144	33.77	AntisenseIntron						NovelUnspliced		
CONGO_chr9_108719124_82_p2	chr9	108719124	108719205	+	2	82	46.13	Intron								

CONGO_chr9_111340332_46_m0	chr9	111340332	111340377	-	0	46	101.29	Intergenic				1				
CONGO_chr9_115544232_116_m2	chr9	115544232	115544347	-	2	116	66.02	Intergenic								
CONGO_chr9_115767381_63_m2	chr9	115767381	115767443	-	2	63	10.92	AntisenseIntron								
CONGO_chr9_116468744_104_m2	chr9	116468744	116468847	-	2	104	45.61	NCExon				1	TU1186	SpliceToNCG	ENSG00000230601	
CONGO_chr9_120753205_68_p0	chr9	120753205	120753272	+	0	68	170.87	Intergenic					TU1187	NovelMultiExon		
CONGO_chr9_121441629_51_p0	chr9	121441629	121441679	+	0	51	76.31	Intergenic								
CONGO_chr9_122649393_60_p1	chr9	122649393	122649452	+	1	60	337.54	NCExon			1	1	TU1189	SpliceToNCG	ENSG00000226752	
CONGO_chr9_123503145_69_p1	chr9	123503145	123503213	+	1	69	161.48	Intron								
CONGO_chr9_123539637_146_p0	chr9	123539637	123539782	+	0	146	151.48	Intron					TU1190	SpliceToPCG	ENSG00000136848	
CONGO_chr9_124409964_114_p0	chr9	124409964	124410077	+	0	114	19.89	Intergenic								
CONGO_chr9_124647334_138_p0	chr9	124647334	124647471	+	0	138	20.06	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000056586	
CONGO_chr9_124924336_91_m1	chr9	124924336	124924426	-	1	91	5.01	UTR			1	1	TU1191	SpliceToPCG	ENSG00000165209	
CONGO_chr9_124925219_95_m2	chr9	124925219	124925313	-	2	95	85.35	UTR			1					
CONGO_chr9_125213876_54_m0	chr9	125213876	125213929	-	0	54	77.93	NCExon					TU1192	SpliceToPCG	ENSG00000119522	
CONGO_chr9_125240474_154_m1	chr9	125240474	125240627	-	1	154	108.38	Intron								
CONGO_chr9_125571872_197_m2	chr9	125571872	125572068	-	2	197	53	Intron								
CONGO_chr9_125577826_131_p2	chr9	125577826	125577956	+	2	131	59.28	AntisenseIntron								
CONGO_chr9_126163433_87_m2	chr9	126163433	126163519	-	2	87	43.23	Intron								
CONGO_chr9_126322287_48_m0	chr9	126322287	126322334	-	0	48	3.51	UTR			1		TU1193	SpliceToPCG	ENSG00000148200	
CONGO_chr9_126461283_88_m1	chr9	126461283	126461370	-	1	88	12.25	AntisenseNCExon								
CONGO_chr9_126462562_115_m0	chr9	126462562	126462676	-	0	115	98.37	AntisenseNCExon								
CONGO_chr9_127317482_129_m0	chr9	127317482	127317610	-	0	129	83.07	Intron								
CONGO_chr9_127344234_81_p0	chr9	127344234	127344314	+	0	81	60.51	AntisenseIntron					TU326	NovelMultiExon		
CONGO_chr9_127347992_117_m0	chr9	127347992	127348108	-	0	117	57.02	Intron								
CONGO_chr9_127348117_54_p0	chr9	127348117	127348170	+	0	54	50.3	AntisenseIntron					TU326	NovelMultiExon		
CONGO_chr9_127351788_106_p2	chr9	127351788	127351893	+	2	106	94.49	AntisenseIntron								
CONGO_chr9_127351939_103_p1	chr9	127351939	127352041	+	1	103	19.91	AntisenseIntron								
CONGO_chr9_127564799_87_m1	chr9	127564799	127564885	-	1	87	99.43	AntisenseIntron								
CONGO_chr9_127685959_140_m0	chr9	127685959	127686098	-	0	140	70.82	AntisenseIntron								
CONGO_chr9_127688527_119_p1	chr9	127688527	127688645	+	1	119	6.88	Intron								
CONGO_chr9_127706780_115_m1	chr9	127706780	127706894	-	1	115	28.25	AntisenseIntron						NovelUnspliced		
CONGO_chr9_127766138_90_p0	chr9	127766138	127766227	+	0	90	33.49	Intron					TU1194	SpliceToPCG	ENSG00000167081	
CONGO_chr9_127859593_120_p0	chr9	127859593	127859712	+	0	120	158.79	NCExon								
CONGO_chr9_127860207_110_m2	chr9	127860207	127860316	-	2	110	8	AntisenseNCIntron								
CONGO_chr9_127910075_139_p2	chr9	127910075	127910213	+	2	139	33.51	NCIntron								
CONGO_chr9_127961633_81_p2	chr9	127961633	127961713	+	2	81	60.66	NCExon								
CONGO_chr9_128037817_129_m1	chr9	128037817	128037945	-	1	129	18.16	Intergenic				1				
CONGO_chr9_128231638_78_m1	chr9	128231638	128231715	-	1	78	8.34	AntisenseIntron								
CONGO_chr9_130298006_65_p1	chr9	130298006	130298070	+	1	65	37.19	UTR			1	1	TU1195	SpliceToPCG	ENSG00000136811	
CONGO_chr9_130357449_51_p0	chr9	130357449	130357499	+	0	51	32.47	Intron			1	1	TU327	SpliceToPCG	ENSG00000197694	
CONGO_chr9_130374856_69_p0	chr9	130374856	130374924	+	0	69	430.25	Intron								
CONGO_chr9_130431225_63_p1	chr9	130431225	130431287	+	1	63	109.33	Intron					TU327	SpliceToPCG	ENSG00000197694	
CONGO_chr9_132227216_158_p2	chr9	132227216	132227373	+	2	158	964.81	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132228075_124_p0	chr9	132228075	132228198	+	0	124	890.78	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132229922_176_p2	chr9	132229922	132230097	+	2	176	878.9	Intergenic					TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132230839_97_p0	chr9	132230839	132230935	+	0	97	744	Intergenic					TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132231084_120_p2	chr9	132231084	132231203	+	2	120	662.36	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132233484_162_p2	chr9	132233484	132233645	+	2	162	604.5	Intergenic					TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132234778_282_p2	chr9	132234778	132235059	+	2	282	1446	Intergenic		I-set		1	TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132236172_168_p2	chr9	132236172	132236339	+	2	168	798.15	Intergenic				1	TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132237502_114_p2	chr9	132237502	132237615	+	2	114	516.69	NCExon		I-set		1	TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132238246_87_p2	chr9	132238246	132238332	+	2	87	591.14	NCExon				1	TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132239710_192_p2	chr9	132239710	132239901	+	2	192	832.21	Intergenic		I-set		1	TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132240771_174_p2	chr9	132240771	132240944	+	2	174	1038.91	Intergenic					TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132241084_114_p2	chr9	132241084	132241197	+	2	114	717.38	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132241724_143_p2	chr9	132241724	132241866	+	2	143	876.31	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132242857_151_p0	chr9	132242857	132243007	+	0	151	1336.41	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132244457_219_p2	chr9	132244457	132244675	+	2	219	1047.26	Intergenic					TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132247392_114_p2	chr9	132247392	132247505	+	2	114	1005.23	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132247887_188_p2	chr9	132247887	132248074	+	2	188	1181.72	Intergenic		I-set			TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_132248712_97_p0	chr9	132248712	132248808	+	0	97	1047.88	Intergenic					TU2	SpliceToPCG	ENSG00000148357	
CONGO_chr9_133419765_473_p2	chr9	133419765	133420237	+	2	473	1313.38	Intergenic								
CONGO_chr9_134096851_147_p2	chr9	134096851	134096997	+	2	147	76.64	Intron			1					
CONGO_chr9_134102685_46_p0	chr9	134102685	134102730	+	0	46	96.3	NCExon					TU1196	SpliceToPCG	ENSG00000196358	
CONGO_chr9_134485382_127_p2	chr9	134485382	134485508	+	2	127	55.35	AntisenseIntron						NovelUnspliced		
CONGO_chr9_134800241_63_m2	chr9	134800241	134800303	-	2	63	44.16	UTR			1	1	TU1197	SpliceToPCG	ENSG00000165699	
CONGO_chr9_135260600_90_p0	chr9	135260600	135260689	+	0	90	9.19	UTR			1		TU1198	SpliceToPCG	ENSG00000198870	
CONGO_chr9_135303722_173_p0	chr9	135303722	135303894	+	0	173	263.08	Intron								
CONGO_chr9_135340634_156_p0	chr9	135340634	135340789	+	0	156	422.16	Intergenic								
CONGO_chr9_135881691_255_p0	chr9	135881691	135881945	+	0	255	2431.39	NCExon			1	1	TU1199	SpliceToPCG	ENSG00000237769	
CONGO_chr9_136417906_152_p1	chr9	136417906	136418057	+	1	152	376.23	Intron								
CONGO_chr9_137645907_111_p0	chr9	137645907	137646017	+	0	111	125.56	NCExon								
CONGO_chr9_137647029_137_p0	chr9	137647029	137647165	+	0	137	335.61	NCExon					TU328	UnsplicedMergeWithNCG	ENSG00000236543	
CONGO_chr9_137648254_74_p1	chr9	137648254	137648327	+	1	74	97.8	Intergenic					TU328	SpliceToNCG	ENSG00000236543	
CONGO_chr9_137648576_108_p2	chr9	137648576	137648683	+	2	108	73.17	Intergenic					TU1200	NovelMultiExon		
CONGO_chr9_137655698_66_m0	chr9	137655698	137655763	-	0	66	108.89	UTR			1					
CONGO_chr9_138284373_110_m2	chr9	138284373	138284482	-	2	110	26	Intergenic					TU152	NovelMultiExon		
CONGO_chr9_138285334_138_m1	chr9	138285334	138285471	-	1	138	41.76	Intergenic					TU152	NovelMultiExon		
CONGO_chr9_138286392_248_m2	chr9	138286392	138286639	-	2	248	80.87	Intergenic					TU152	NovelMultiExon		
CONGO_chr9_138295289_177_m0	chr9	138295289	138295465	-	0	177	149.48	Intergenic					TU153	NovelMultiExon		
CONGO_chr9_138297623_88_m1	chr9	138297623	138297710	-	1	88	126.85	Intergenic					TU153	NovelMultiExon		
CONGO_chr9_138299051_128_m0	chr9	138299051	138299178	-	0	128	477.2	Intergenic					TU153	NovelMultiExon		
CONGO_chr9_138346285_164_p0	chr9	138346285	138346448	+	0	164	643.94	Intron								
CONGO_chr9_138999309_102_p2	chr9	138999309	138999410	+	2	102	197.06	UTR			1	1	TU1201	SpliceToPCG	ENSG00000107317	
CONGO_chr9_139185248_190_m1	chr9	139185248	139185437	-	1	190	290.68	NCExon				1	TU329	SpliceToNCG	ENSG00000185863	
CONGO_chr9_139185914_136_m2	chr9	139185914	139186049	-	2	136	1166.67	NCExon				1	TU329	SpliceToNCG	ENSG00000185863	
CONGO_chr9_139232309_567_p0	chr9	139232309	139232875	+	0	567	2449.44	UTR		zf-C3HC4			TU1202	SpliceToPCG	ENSG00000188566	
CONGO_chrX_009943700_199_p2	chrX	9943700	9943898	+	2	199	246.41	UTR		WW	1	1	TU1203	SpliceToPCG	ENSG00000047644	
CONGO_chrX_010504868_88_p0	chrX	10504868	10504955	+	0	88	12.84	AntisenseUTR						UnsplicedMergeWithPCG	ENSG00000101871	
CONGO_chrX_011805935_124_p2	chrX	11805935	11806058	+	2	124	315.53	Intergenic				1				
CONGO_chrX_017584180_226_p0	chrX	17584180	17584405	+	0	226	538.48	Intron								
CONGO_chrX_018551920_123_p0	chrX	18551920	18552042	+	0	123	152.15	Intron					TU330	SpliceToPCG	ENSG00000008086	
CONGO_chrX_018556634_165_p0	chrX	18556634	18556798	+	0	165	598.88	Intron					TU330	SpliceToPCG	ENSG00000008086	
CONGO_chrX_023269656_77_m0	chrX	23269656	23269732	-	0	77	59.47	AntisenseIntron								
CONGO_chrX_023712332_60_p0	chrX	23712332	23712391	+	0	60	93.36	UTR			1	1	TU1204	SpliceToPCG	ENSG00000130066	
CONGO_chrX_024077709_124_p0	chrX	24077709	24077832	+	0	124	34.17	UTR			1	1	TU1205	SpliceToPCG	ENSG00000005889	
CONGO_chrX_024669435_118_m2	chrX	24669435	24669552	-	2	118	163.54	AntisenseCDS								
CONGO_chrX_024804828_121_m1	chrX	24804828	24804948	-	1	121	48.14	AntisenseIntron								
CONGO_chrX_024804987_97_m0	chrX	24804987	24805083	-	0	97	45.31	AntisenseIntron								
CONGO_chrX_024827503_83_m2	chrX	24827503	24827585	-	2	83	43.38	AntisenseIntron								
CONGO_chrX_024856346_114_p0	chrX	24856346	24856459	+	0	114	2.4	Intron								
CONGO_chrX_024918451_148_p1	chrX	24918451	24918598	+	1	148	40.86	Intron								
CONGO_chrX_024920424_126_m2	chrX	24920424	24920549	-	2	126	33.51	AntisenseIntron								
CONGO_chrX_024927766_97_m0	chrX	24927766	24927862	-	0	97	4.31	Intergenic								
CONGO_chrX_028951490_52_m0	chrX	28951490	28951541	-	0	52	51.88	AntisenseIntron								
CONGO_chrX_035919889_93_p0	chrX	35919889	35919981	+	0	93	375.34	Intergenic					TU332	SpliceToPCG	ENSG00000165164	
CONGO_chrX_035921228_132_p0	chrX	35921228	35921359	+	0	132	424.11	Intergenic					TU332	NovelMultiExon		
CONGO_chrX_035925378_50_p2	chrX	35925378	35925427	+	2	50	56.63	Intergenic					TU1206	NovelMultiExon		
CONGO_chrX_036073257_135_p0	chrX	36073257	36073391	+	0	135	346.35	Intergenic				1	TU1207	SpliceToPCG	ENSG00000176034	
CONGO_chrX_036077146_116_p0	chrX	36077146	36077261	+	0	116	283.02	Intergenic				1				
CONGO_chrX_036088719_89_p0	chrX	36088719	36088807	+	0	89	66.72	Intergenic				1	TU1208	NovelMultiExon		
CONGO_chrX_036118089_146_p2	chrX	36118089	36118234	+	2	146	224.74	Intergenic				1	TU1209	NovelMultiExon		
CONGO_chrX_036128417_55_p0	chrX	36128417	36128471	+	0	55	159.5	Intergenic				1	TU333	NovelMultiExon		
CONGO_chrX_036129429_110_p2	chrX	36129429	36129538	+	2	110	688.07	Intergenic					TU333	NovelMultiExon		
CONGO_chrX_038763426_88_p1	chrX	38763426	38763513	+	1	88	65.97	Intergenic								
CONGO_chrX_053170180_231_p0	chrX	53170180	53170410	+	0	231	474.44	NCIntron						NovelUnspliced		
CONGO_chrX_053312876_96_m1	chrX	53312876	53312971	-	1	96	59.5	NCExon			1	1	TU1212	SpliceToPCG	ENSG00000124313	
CONGO_chrX_056772512_130_p0	chrX	56772512	56772641	+	0	130	148.73	NCExon			1	1	TU1213	SpliceToNCG	ENSG00000204272	
CONGO_chrX_056909014_127_p0	chrX	56909014	56909140	+	0	127	11.11	Intergenic								
CONGO_chrX_062891090_192_m0	chrX	62891090	62891281	-	0	192	320.57	UTR			1	1	TU1214	SpliceToPCG	ENSG00000131089	
CONGO_chrX_063542247_239_p0	chrX	63542247	63542485	+	0	239	435.22	Intergenic								
CONGO_chrX_063542497_168_p2	chrX	63542497	63542664	+	2	168	412.77	Intergenic								
CONGO_chrX_063984505_390_p0	chrX	63984505	63984894	+	0	390	119.79	Intergenic								
CONGO_chrX_070683027_146_p1	chrX	70683027	70683172	+	1	146	135.96	NCExon			1		TU1215	SpliceToPCG	ENSG00000147162	
CONGO_chrX_071216799_43_p0	chrX	71216799	71216841	+	0	43	3.78	Intron					TU1216	SpliceToPCG	ENSG00000204131	

CONGO_chrX_072139728_182_p2	chrX	72139728	72139909	+	2	182	79.93	Intergenic	1							
CONGO_chrX_072215976_393_p0	chrX	72215976	72216368	+	0	393	387.07	AntisenseUTR	1							
CONGO_chrX_096986885_590_p2	chrX	96986885	96987474	+	2	590	1622.77	Intergenic		RnaseH						
CONGO_chrX_096987500_177_p0	chrX	96987500	96987676	+	0	177	547.12	Intergenic								
CONGO_chrX_096988047_787_p2	chrX	96988047	96988833	+	2	787	4407.72	Intergenic		rve						
CONGO_chrX_102848808_119_m2	chrX	102848808	102848926	-	2	119	266	UTR		Neur_chan_memb						
CONGO_chrX_105079288_106_p0	chrX	105079288	105079393	+	0	106	49.94	Intron			1	1				
CONGO_chrX_106889378_195_m0	chrX	106889378	106889572	-	0	195	282.16	Intron								
CONGO_chrX_107104280_193_p0	chrX	107104280	107104472	+	0	193	137.39	Intergenic		NACHT						
CONGO_chrX_107104532_463_p0	chrX	107104532	107104994	+	0	463	275.79	Intergenic								
CONGO_chrX_107105043_294_p2	chrX	107105043	107105336	+	2	294	95.11	Intergenic								
CONGO_chrX_107114424_171_p1	chrX	107114424	107114594	+	1	171	76.02	Intergenic								
CONGO_chrX_107114709_171_p1	chrX	107114709	107114879	+	1	171	314.48	Intergenic								
CONGO_chrX_109328301_65_m2	chrX	109328301	109328365	-	2	65	3.79	UTR			1	1	TU1220	SpliceToPCG	ENSG00000101935	
CONGO_chrX_110542022_88_m0	chrX	110542022	110542109	-	0	88	178.6	UTR			1	1				
CONGO_chrX_110648742_273_p0	chrX	110648742	110649014	+	0	273	1670.81	NCExon			1		TU1221	NovelMultiExon		
CONGO_chrX_118270659_168_m1	chrX	118270659	118270826	-	1	168	268.74	NCExon					TU334	SpliceToNCG	ENSG00000214992	
CONGO_chrX_118272723_131_m0	chrX	118272723	118272853	-	0	131	708.62	NCExon				1	TU334	SpliceToNCG	ENSG00000214992	
CONGO_chrX_118274912_54_m0	chrX	118274912	118274965	-	0	54	266.62	NCExon				1				
CONGO_chrX_118275015_660_m1	chrX	118275015	118275674	-	1	660	3263.77	NCExon				1				
CONGO_chrX_118623718_165_m0	chrX	118623718	118623882	-	0	165	236.91	UTR			1	1	TU1222	SpliceToPCG	ENSG00000186416	
CONGO_chrX_119017424_155_m0	chrX	119017424	119017578	-	0	155	67.92	Intergenic								
CONGO_chrX_122441371_76_p1	chrX	122441371	122441446	+	1	76	38.6	Intron				1	TU1223	SpliceToPCG	ENSG00000125675	
CONGO_chrX_129477415_90_m0	chrX	129477415	129477504	-	0	90	271.61	NCExon			1	1				
CONGO_chrX_129485106_126_m0	chrX	129485106	129485231	-	0	126	59.09	NCIntron								
CONGO_chrX_129745202_144_m2	chrX	129745202	129745345	-	2	144	454.43	UTR			1	1	TU1224	SpliceToPCG	ENSG00000165675	
CONGO_chrX_130999956_64_p1	chrX	130999956	131000019	+	1	64	14.13	Intron								
CONGO_chrX_131165846_57_p0	chrX	131165846	131165902	+	0	57	4.97	AntisenseUTR								
CONGO_chrX_131796967_72_m0	chrX	131796967	131797038	-	0	72	26.52	Intron								
CONGO_chrX_132949893_79_p0	chrX	132949893	132949971	+	0	79	16.12	Intergenic	1							
CONGO_chrX_133563747_72_m2	chrX	133563747	133563818	-	2	72	31.14	UTR			1	1				
CONGO_chrX_133584064_78_p1	chrX	133584064	133584141	+	1	78	105.59	AntisenseIntron								
CONGO_chrX_134383723_222_p0	chrX	134383723	134383944	+	0	222	272.84	NCExon	1		1	1				
CONGO_chrX_136144990_160_m1	chrX	136144990	136145149	-	1	160	33.97	Intergenic								
CONGO_chrX_136796081_78_m0	chrX	136796081	136796158	-	0	78	103.01	Intergenic								
CONGO_chrX_138997769_127_m0	chrX	138997769	138997895	-	0	127	152.79	Intergenic								
CONGO_chrX_139421743_130_m1	chrX	139421743	139421872	-	1	130	11.25	Intergenic								
CONGO_chrX_147695577_102_p0	chrX	147695577	147695678	+	0	102	27.69	Intron								
CONGO_chrX_148438821_229_m1	chrX	148438821	148439049	-	1	229	977.95	AntisenseCDS	1			1	TU1225	SpliceToNCG	ENSG00000225261	
CONGO_chrX_148848775_229_p1	chrX	148848775	148849003	+	1	229	249.96	AntisenseCDS		1 HSF_DNA-bind		1	TU1226	SpliceToNCG	ENSG00000224871	
CONGO_chrX_154018568_76_p0	chrX	154018568	154018643	+	0	76	315.4	AntisenseIntron								

Table S6. Basic statistics on motif instances

Confidence	# of motifs reaching confidence	Total # of instances	# of examined bases covered	# of TFs with a motif reaching confidence	Total # of instances (best motif per TF)
0.0	630	55,021,406	80.6	335	35,366,716
0.1	540	15,817,545	45.3	294	11,181,918
0.2	492	8,385,913	26.0	270	6,068,955
0.3	435	4,697,272	14.3	252	3,495,271
0.4	375	2,675,802	7.7	225	2,050,302
0.5	293	1,449,752	3.9	188	1,175,237
0.6	216	707,141	1.7	151	595,984
0.7	129	269,944	0.6	101	240,849
0.8	56	90,464	0.2	45	80,138
0.9	16	33,822	0.1	14	29,080

Table S7. Listing of data sets and motifs used in analysis

Factor	Cell type	Technology	Num peaks	Motif used	Citation
CTCF	CD4+ T cells Embryonic stem (mouse)	Sequencing	21,544 8,546 (+mouse)	Jaspar MA0139.1	17512414 bern, unpub (mouse)
ER	MCF-7 breast cancer	Paired-end Tags	1,229	Transfac M00191	17542648
Fos	K562 CML	Sequencing	18,963	Transfac M00926	20139302
FOXA2	Liver	Promoter array	143 19 (+mouse)	Jaspar MA0047.2	17529977
HNF1	Liver	Promoter array	246 23 (+mouse)	Jaspar MA0046.1	17529977
HNF4	Liver	Promoter array	1,231 99 (+mouse)	Transfac M01036	17529977
HNF6	Liver	Promoter array	149 20 (+mouse)	Transfac M00639	17529977
Myc	K562 CML Embryonic stem (mouse)	Sequencing Promoter array (mouse)	15,749 2,399 (+mouse)	Transfac M00187	20139302 18358816 (mouse)
NF-κB	GM12878 B-Lymphocyte	Sequencing	38,559	Jaspar MA0061.1	20299548
NRSF	Jurkat T cell line	Sequencing	1,931	Transfac M00325	17540862
p53	HCT116 colon cancer	Paired-end Tags	62,939	Transfac M00034	16413492
STAT1	HeLa S3 cells	Sequencing	41,530	Transfac M00224	17558387
YY1	NT2/D1	Sequencing	11,018	Transfac M00651	Encode, unpub

Table S8. Coincidence of GWAS results with TSS-distal noncoding conserved elements

		Noncoding TSS-distal genome	Noncoding TSS-distal Hapmap CEU SNPs
All callable positions	*n*	1996107874	3464198
Conserved by SiPhy-ω	*n*	88530563	138260
GWAS hit in at least one study	*n*	3402	3390
Conserved GWAS	*n*	187	186
	fold enrichment	1.24	1.37
	p	1.6×10^{-3}	9.8×10^{-6}

Table S9. Summary of sitewise selective pressures

Data set	N sites	dN/dS <0.5	dN/dS <1	dN/dS >1	dN/dS >1.5	Domain instances	Domain types	Genes	Positive domain instances	Positive domain types	Positive genes	Positive sites	Fraction positive sites
Mammals	6,050,046	84%	94%	6%	2%	26,667	3,117	12,871	1,451	871	4,431	15,381	0.25423%
Primates	6,386,902	86%	91%	9%	6%	27,441	3,164	12,968	7	7	17	19	0.00030%
Glires	6,335,182	88%	95%	5%	2%	27,671	3,168	13,068	8	6	23	27	0.00043%
Laurasiatheria	6,313,057	85%	94%	6%	3%	27,120	3,146	12,860	89	77	369	468	0.00741%

Table S10. Simulation results for the power of site-wise analysis using three different mammalian trees

Tree	Indel rate	Spearman's rank correlation between inferred/true dN/dS	TPR at FDR <0.1	TP at FDR <0.1	TP at FDR <0.05	TPR at FDR <0.05	FPR at SLR default threshold	TP at SLR default threshold	FP at SLR default threshold	FDR at SLR default threshold
29 Eutherian	0	0.942	0.66400	3760	2990	0.528	0.00137	2900	0.00137	0.0423
9 high-coverage	0	0.849	0.13700	782	429	0.075	0.00248	1419	0.00248	0.1400
HMRD	0	0.749	0.00942	50	10	0.002	0.00538	802	0.00538	0.3860
29 Eutherian	0.05	0.831	0.43800	2433	1686	0.304	0.00176	2006	0.00176	0.0764
9 high-coverage	0.05	0.696	0.01760	98	86	0.015	0.00340	938	0.00340	0.2530
HMRD	0.05	0.570	0.00000	NA	NA	NA	0.00464	412	0.00464	0.5160

Table S11. Summaries of site-wise data in regions of high and low recombination rate, GC content, and evidence for non-neutral evolution

Variable	Quantile range	Low value	High value	Number of sites	Mean dN/dS	Mean signed LRT	Mean male recombination	Mean female recombination	Mean sex-averaged recombination	Fraction of sites under positive selection	GC content (10-kb window)
LRT Statistic											
signed_lrt	0-0.01	-188.187	-44.199	57,981	0.006	-50.660	1.522	1.812	1.681	0.00000	0.512
signed_lrt	0.01-0.25	-44.199	-19.594	1,391,549	0.015	-26.806	1.128	1.734	1.445	0.00000	0.475
signed_lrt	0.25-0.5	-19.594	-12.030	1,449,530	0.040	-15.607	0.971	1.657	1.333	0.00000	0.455
signed_lrt	0.5-0.75	-12.030	-4.926	1,449,521	0.128	-8.575	0.929	1.613	1.294	0.00000	0.451
signed_lrt	0.75-0.99	-4.926	3.648	1,391,529	0.694	-1.505	0.921	1.619	1.293	0.01338	0.454
signed_lrt	0.99-1	3.648	108.850	57,970	2.984	8.208	0.879	1.614	1.272	1.00000	0.454
Male Recombination											
recomb_m	0-0.01	-0.010	0.000	743,415	0.265	-12.265	0.000	0.991	0.648	0.01539	0.468
recomb_m	0.01-0.25	0.000	0.214	707,759	0.249	-12.617	0.102	1.192	0.647	0.01364	0.450
recomb_m	0.25-0.5	0.214	0.591	1,448,727	0.243	-12.865	0.414	1.469	0.942	0.01375	0.446
recomb_m	0.5-0.75	0.591	1.275	1,448,935	0.236	-13.168	0.882	1.809	1.345	0.01278	0.447
recomb_m	0.75-0.99	1.275	6.107	1,393,462	0.233	-14.509	2.402	2.288	2.345	0.01187	0.483
recomb_m	0.99-1	6.107	10.372	55,782	0.206	-16.616	8.010	1.562	4.787	0.00932	0.540
GC Content											
gc	0-0.01	0.071	0.332	58,204	0.233	-11.474	0.563	1.269	0.929	0.01347	0.322
gc	0.01-0.25	0.332	0.395	1,392,861	0.233	-11.936	0.750	1.492	1.141	0.01260	0.369
gc	0.25-0.5	0.395	0.447	1,449,024	0.256	-12.137	0.873	1.698	1.310	0.01461	0.419
gc	0.5-0.75	0.447	0.521	1,449,980	0.254	-13.575	0.987	1.778	1.402	0.01438	0.483
gc	0.75-0.99	0.521	0.644	1,390,064	0.225	-15.376	1.328	1.704	1.532	0.01125	0.564
gc	0.99-1	0.644	0.706	57,947	0.225	-16.780	2.147	0.775	1.466	0.01034	0.660
High GC, Male Recombination											
recomb_m	0-0.01	-0.010	0.000	98,083	0.230	-15.273	0.000	0.583	0.379	0.01139	0.608
recomb_m	0.01-0.25	0.000	0.242	47,884	0.207	-15.997	0.084	1.313	0.700	0.00892	0.593
recomb_m	0.25-0.5	0.242	0.987	151,389	0.196	-16.185	0.648	1.544	1.096	0.00816	0.599
recomb_m	0.5-0.75	0.987	2.081	139,459	0.209	-16.277	1.532	1.825	1.678	0.00994	0.604
recomb_m	0.75-0.99	2.081	8.735	141,879	0.202	-17.217	4.427	1.632	3.030	0.00841	0.610
recomb_m	0.99-1	8.735	10.372	2,811	0.348	-11.262	9.690	2.961	6.330	0.03380	0.585
High GC, Female Recombination											
recomb_f	0-0.01	-0.010	0.000	87,934	0.249	-15.971	0.698	0.000	0.349	0.01273	0.618
recomb_f	0.01-0.25	0.000	0.415	57,495	0.205	-16.672	2.991	0.211	1.602	0.00990	0.609
recomb_f	0.25-0.5	0.415	1.323	145,697	0.198	-16.101	1.632	0.771	1.202	0.00800	0.608
recomb_f	0.5-0.75	1.323	2.339	145,206	0.207	-15.733	1.171	1.784	1.529	0.00916	0.596
recomb_f	0.75-0.99	2.339	4.801	139,831	0.197	-16.924	2.309	3.095	2.705	0.00891	0.597
recomb_f	0.99-1	4.801	8.041	5,342	0.164	-18.475	1.319	5.943	3.734	0.00449	0.590

Table S12. GO enrichments for codon-wise and gene-wise positively selected genes

		GO term enrichments						
GO.ID	Term	Annotated	Significant	Expected	Rank in pval.elim	pval.fis	pval.elim	pval.fis.bonf
ENRICHMENTS FOR CODON-WISE POSITIVE SELECTION								
GO:0007018	microtubule-based movement	288	89	44.54	1	0	0	0
GO:0007026	negative regulation of microtubule depol...	60	29	9.28	2	0	0	0
GO:0006265	DNA topological change	65	29	10.05	3	0	0	0
GO:0000723	telomere maintenance	53	23	8.2	4	0	0	0.01
GO:0090161	Golgi ribbon formation	7	7	1.08	5	0	0	0.01
GO:0043044	ATP-dependent chromatin remodeling	17	11	2.63	6	0	0	0.03
GO:0055114	oxidation reduction	1553	303	240.18	7	0	0	0.04
GO:0055072	iron ion homeostasis	69	27	10.67	50	0	0	0.01
GO:0006974	response to DNA damage stimulus	1023	212	158.21	66	0	0.01	0.02
GO:0006259	DNA metabolic process	1523	311	235.54	153	0	0.03	0
GO:0002460	adaptive immune response based on somati...	208	66	32.17	347	0	0.1	0
GO:0002250	adaptive immune response	211	66	32.63	449	0	0.13	0
GO:0032886	regulation of microtubule-based process	124	45	19.18	915	0	0.29	0
GO:0002455	humoral immune response mediated by circ...	78	29	12.06	918	0	0.3	0.01
GO:0002443	leukocyte mediated immunity	269	70	41.6	991	0	0.32	0.03
GO:0070507	regulation of microtubule cytoskeleton o...	110	42	17.01	1172	0	0.4	0
GO:0007017	microtubule-based process	621	166	96.04	1269	0	0.43	0
GO:0043242	negative regulation of protein complex d...	97	34	15	2085	0	0.69	0.01
GO:0031110	regulation of microtubule polymerization...	75	31	11.6	2086	0	0.7	0
GO:0031109	microtubule polymerization or depolymeri...	86	31	13.3	3065	0	0.93	0.01
ENRICHMENTS FOR GENE-WISE POSITIVE SELECTION								
GO:0045132	meiotic chromosome segregation	29	23	1.11	1	9.10E-028	9.10E-028	5.19E-024
GO:0006355	regulation of transcription, DNA-depende...	4628	312	177.86	2	5.40E-024	5.40E-024	3.08E-020
GO:0042742	defense response to bacterium	186	34	7.15	3	0	0	0
GO:0006955	immune response	2043	168	78.52	4	8.30E-021	0	4.73E-017
GO:0050909	sensory perception of taste	55	20	2.11	5	6.10E-015	0	0
GO:0007217	tachykinin receptor signaling pathway	21	11	0.81	6	0	0	0
GO:0031103	axon regeneration	37	13	1.42	7	0	0	0
GO:0006526	activation of transmembrane receptor pro...	16	9	0.61	8	0	0	0
GO:0031640	killing of cells of another organism	33	12	1.27	9	0	0	0
GO:0042523	positive regulation of tyrosine phosphor...	12	8	0.46	10	0	0	0
GO:0007566	embryo implantation	38	12	1.46	11	0	0	0
GO:0070257	positive regulation of mucus secretion	7	6	0.27	12	0	0	0
GO:0006952	defense response	1246	138	47.89	13	4.20E-029	0	2.39E-025
GO:0031424	keratinization	82	16	3.15	14	0	0	0
GO:0046080	dUTP metabolic process	5	5	0.19	15	0	0	0
GO:0006968	cellular defense response	115	18	4.42	16	0	0	0
GO:0006935	chemotaxis	314	36	12.07	17	0	0	0
GO:0007171	activation of transmembrane receptor pro...	15	7	0.58	18	0	0	0
GO:0045651	positive regulation of macrophage differ...	11	6	0.42	19	0	0	0.01
GO:0045086	positive regulation of interleukin-2 bio...	17	7	0.65	20	0	0	0.01

Notes: All terms were first sorted by 'pval.fis.bonf' (the Bonferroni-corrected p-value for enrichment) and a threshold of $p < 0.05$ was applied. Terms were subsequently sorted by 'pval.elim' for display purposes.
Terms mentioned in the text are in bold, and only the top 20 terms for each type of enrichment are shown.

Table S13. PFAM domain enrichment site-wise and gene-wise positively selected genes

				Mammals mean dNdS								
Pfam ID	Pfam link	Domain name	Notes / description	N sites	N genes	Pos. sites	Neg. sites	Neutral sites	Fraction positive	Fraction negative	Fraction neutral	Mean dN/dS
TOP DOMAINS BY FRACTION OF POSITIVELY SELECTED SITES												
PF03765	PF03765	CRAL/TRIO, n-terminus	Comprises retinal-binding proteins and various transfer proteins	690	9	18	449	223	0.03	0.65	0.32	0.36
PF00031	PF00031	Cystatin	Proteinase inhibitors, play role in protein degradation, bone remodeling, possibly antigen presentation	1404	11	31	816	557	0.02	0.58	0.4	0.41
PF06467	PF06467	MYM-type zinc finger	Zinc finger in proteins associated with chromosomal translocations and myeloproliferative disorders	1594	6	31	909	654	0.02	0.57	0.41	0.42
PF00048	PF00048	IL8	Immune response	1218	17	23	633	562	0.02	0.52	0.46	0.46
PF00957	PF00957	Synaptobrevin	Membrane protein of neuronal synaptic vesicles	600	9	11	294	295	0.02	0.49	0.49	0.41
PF04103	PF04103	CD20-like family	IgE Fc receptor subunit	1649	12	30	845	774	0.02	0.51	0.47	0.46
PF03645	PF03645	Tctex-1	Binds to rhodopsin, possible role in retinitis pigmentosa	596	6	10	375	211	0.02	0.63	0.35	0.59
PF01105	PF01105	Emp24 / GOLD / p24 family	Major membrane components of COPI and COPII coated vesicles	1319	15	21	971	327	0.02	0.74	0.25	0.28
PF05287	PF05287	PMG	Keratin-associated proteins	1024	6	16	203	805	0.02	0.2	0.79	0.74
PF00025	PF00025	ADP-ribosylation factor	Regulators of vesicle biogenesis	908	24	14	565	329	0.02	0.62	0.36	0.38
TOP DOMAINS BY MEAN DN/DS												
PF05287	PF05287	PMG	Keratin-associated proteins	1024	6	16	203	805	0.02	0.2	0.79	0.74
PF03645	PF03645	Tctex-1	Binds to rhodopsin, possible role in retinitis pigmentosa	596	6	10	375	211	0.02	0.63	0.35	0.59
PF00048	PF00048	IL8	Immune response	1218	17	23	633	562	0.02	0.52	0.46	0.46
PF04103	PF04103	CD20		1649	12	30	845	774	0.02	0.51	0.47	0.46
PF00230	PF00230	MIP		1734	10	26	991	717	0.01	0.57	0.41	0.42
PF00095	PF00095	WAP	Milk whey component, protease-inhibitor	564	8	2	309	253	0	0.55	0.45	0.42
PF00711	PF00711	Beta defensin		687	13	7	399	281	0.01	0.58	0.41	0.42
PF06467	PF06467	MYM-type zinc finger		1594	6	31	909	654	0.02	0.57	0.41	0.42
PF01390	PF01390	SEA domain	Sea urchin sperm protein, proteolytic activity	1876	10	16	1012	848	0.01	0.54	0.45	0.41
PF00957	PF00957	Synaptobrevin		600	9	11	294	295	0.02	0.49	0.49	0.41

Notes: Rows were sorted by either mean dN/dS or fraction of positive sites, and the top 10 domains for each set were retained. Those domains showing up in the top 10 on both lists were grayed out. Domains mentioned in the text are in bold.

Table S14. Transcription factor binding sites

JASPAR family	Matrix ID	Min	Max	Mean
ETS class	MF0001	0	13	0.41
bZIP CREB/G-box-like subclass	MF0002	0	7	0.21
REL class	MF0003	0	17	0.33
Nuclear receptor class	MF0004	0	13	0.78
Forkhead class	MF0005	0	13	0.36
bZIP cEBP-like subclass	MF0006	0	11	0.4
bHLH(xip) class	MF0007	0	14	0.58
MADS class	MF0008	0	29	0.42
TRP(MYB) class	MF0009	0	13	0.66
Homeobox class	MF0010	0	21	0.91
HMG class	MF0011	0	14	0.89
TOTAL		**0**	**29**	**0.54**

Table S15. Gene ontology enrichments for human- and primate-accelerated regions

ID	DESCRIPTION	ONTOLOGY	Gene-avg Vert.	Gene-codon Vert.	Codons Vert.	Gene-avg Prim.	Gene-codon Prim.	Codons Prim.	PARS_100kb	PARS_1kb	HARS_100kb	HARS_1kb
GO:0006955	immune response	BP	2.E-36	1.E-08	1.E-228	2.E-15	8.E-07	2.E-102	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005576	extracellular region	CC	3.E-20	1.E+00	6.E-68	8.E-07	1.E+00	1.E-22	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050909	sensory perception of taste	BP	7.E-14	8.E-04	8.E-165	4.E-12	5.E-06	1.E-120	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005125	cytokine activity	MF	9.E-14	1.E+00	1.E-32	4.E-07	1.E+00	7.E-16	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008009	chemokine activity	MF	4.E-10	1.E+00	6.E-19	9.E-01	4.E-02	2.E-15	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031424	keratinization	BP	9.E-10	5.E-02	2.E-200	2.E-01	4.E-05	7.E-136	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005529	sugar binding	MF	1.E-09	1.E+00	1.E-41	5.E-01	1.E+00	1.E-23	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005615	extracellular space	CC	3.E-07	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	2.E-09	4.E-46	1.E+00	1.E+00
GO:0008527	taste receptor activity	MF	4.E-07	2.E-01	1.E-61	1.E-05	7.E-02	1.E-38	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007166	cell surface receptor linked signal transduction	BP	5.E-06	1.E+00	2.E-33	2.E-03	1.E+00	1.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004888	transmembrane receptor activity	MF	7.E-06	1.E+00	2.E-40	1.E-01	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042612	MHC class I protein complex	CC	8.E-06	1.E+00	2.E-122	1.E-07	2.E-09	3.E-44	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006952	defense response	BP	9.E-06	1.E+00	2.E-96	2.E-04	1.E+00	4.E-30	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006954	inflammatory response	BP	1.E-05	5.E-01	5.E-17	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006935	chemotaxis	BP	2.E-05	1.E+00	7.E-26	1.E+00	3.E-03	2.E-02	2.E-91	2.E-144	1.E+00	1.E+00
GO:0019882	antigen processing and presentation	BP	3.E-05	1.E+00	6.E-112	3.E-05	7.E-05	2.E-36	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009615	response to virus	BP	2.E-03	1.E+00	6.E-48	5.E-02	1.E+00	6.E-17	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001533	cornified envelope	CC	3.E-03	1.E-04	4.E-51	3.E-02	1.E-06	4.E-21	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004872	receptor activity	MF	4.E-03	5.E-20	4.E-39	1.E+00	1.E+00	1.E+00	1.E+00	8.E-13	1.E+00	1.E+00
GO:0042742	defense response to bacterium	BP	6.E-03	7.E-01	1.E-18	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016814	hydrolase activity, acting on carbon-nitrogen (but not p	MF	7.E-03	1.E-01	1.E-07	6.E-03	1.E+00	3.E-39	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004522	pancreatic ribonuclease activity	MF	7.E-03	1.E+00	4.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016021	integral to membrane	CC	7.E-03	1.E-11	6.E-13	1.E+00	1.E+00	1.E+00	1.E+00	2.E-16	1.E+00	1.E+00
GO:0006953	acute-phase response	BP	1.E-02	1.E+00	2.E-50	9.E-04	1.E+00	2.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0002504	antigen processing and presentation of peptide or poly	BP	2.E-02	4.E-03	8.E-11	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	2.E-02	2.E-07
GO:0042613	MHC class II protein complex	CC	2.E-02	4.E-03	8.E-11	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	2.E-02	2.E-07
GO:0005126	hematopoietin/interferon-class (D200-domain) cytokin	MF	2.E-02	1.E+00	3.E-38	2.E-02	1.E+00	1.E-12	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030101	natural killer cell activation	BP	2.E-02	1.E+00	2.E-97	2.E-02	1.E+00	7.E-24	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019864	IgG binding	MF	3.E-02	2.E-01	3.E-45	3.E-02	1.E+00	5.E-32	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005882	intermediate filament	CC	6.E-02	7.E-01	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045087	innate immune response	BP	1.E-01	1.E+00	1.E-44	1.E+00	1.E+00	4.E-29	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045410	positive regulation of interleukin-6 biosynthetic proces	BP	2.E-01	1.E+00	3.E-16	1.E+00	1.E+00	4.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009897	external side of plasma membrane	CC	2.E-01	1.E+00	5.E-41	4.E-02	1.E+00	2.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001580	detection of chemical stimulus involved in sensory per	BP	3.E-01	1.E+00	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004866	endopeptidase inhibitor activity	MF	3.E-01	1.E+00	7.E-48	1.E+00	1.E+00	4.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030216	keratinocyte differentiation	BP	4.E-01	7.E-01	4.E-20	1.E+00	4.E-03	5.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005179	hormone activity	MF	5.E-01	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042698	ovulation cycle	BP	5.E-01	1.E+00	1.E-17	5.E-01	1.E-02	3.E-19	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004867	serine-type endopeptidase inhibitor activity	MF	5.E-01	1.E+00	5.E-45	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007267	cell-cell signaling	BP	9.E-01	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004930	G-protein coupled receptor activity	MF	1.E+00	1.E-22	3.E-74	1.E+00	1.E+00	4.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050896	response to stimulus	BP	1.E+00	3.E-28	3.E-43	1.E+00	1.E+00	5.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007186	G-protein coupled receptor protein signaling pathway	BP	1.E+00	2.E-18	5.E-67	1.E+00	1.E+00	4.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016020	membrane	CC	1.E+00	1.E-08	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	2.E-19	1.E+00	1.E+00
GO:0005149	interleukin-1 receptor binding	MF	1.E+00	1.E+00	2.E-15	5.E-02	1.E+00	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001584	rhodopsin-like receptor activity	MF	1.E+00	5.E-21	5.E-36	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004984	olfactory receptor activity	MF	1.E+00	5.E-29	7.E-21	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007608	sensory perception of smell	BP	1.E+00	2.E-28	8.E-16	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004871	signal transducer activity	MF	1.E+00	1.E-11	6.E-23	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005694	chromosome	CC	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	7.E-04	1.E+00	7.E-01	1.E+00	1.E+00
GO:0000775	chromosome, pericentric region	CC	1.E+00	1.E+00	3.E-36	1.E+00	1.E+00	9.E-17	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003950	NAD+ ADP-ribosyltransferase activity	MF	1.E+00	1.E+00	1.E-21	1.E+00	1.E+00	3.E-26	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005198	structural molecule activity	MF	1.E+00	1.E+00	1.E-118	1.E+00	1.E+00	7.E-53	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006281	DNA repair	BP	1.E+00	1.E+00	2.E-38	1.E+00	1.E+00	1.E-26	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006282	regulation of DNA repair	BP	1.E+00	1.E+00	6.E-38	1.E+00	1.E+00	3.E-23	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006471	protein amino acid ADP-ribosylation	BP	1.E+00	1.E+00	8.E-20	1.E+00	1.E+00	7.E-23	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006817	phosphate transport	BP	1.E+00	1.E+00	1.E-30	1.E+00	1.E+00	7.E-21	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006974	response to DNA damage stimulus	BP	1.E+00	1.E+00	5.E-37	1.E+00	1.E+00	1.E-27	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007051	spindle organization and biogenesis	BP	1.E+00	1.E+00	2.E-46	1.E+00	1.E+00	3.E-18	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007098	centrosome cycle	BP	1.E+00	1.E+00	1.E-20	1.E+00	1.E+00	2.E-18	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008656	caspase activator activity	MF	1.E+00	1.E+00	2.E-74	1.E+00	1.E+00	2.E-19	1.E+00	1.E+00	1.E+00	1.E+00
GO:0017114	wide-spectrum protease inhibitor activity	MF	1.E+00	1.E+00	4.E-46	1.E+00	1.E+00	1.E-18	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043159	acrosomal matrix	CC	1.E+00	1.E+00	2.E-77	1.E+00	1.E+00	5.E-19	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045569	TRAIL binding	MF	1.E+00	1.E+00	2.E-16	1.E+00	1.E+00	2.E-18	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042102	positive regulation of T cell proliferation	BP	1.E+00	1.E+00	1.E-21	1.E+00	1.E+00	1.E-14	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006919	caspase activation	BP	1.E+00	1.E+00	2.E-58	1.E+00	1.E+00	1.E-12	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007566	embryo implantation	BP	1.E+00	1.E+00	2.E-12	1.E+00	1.E+00	1.E-12	1.E+00	1.E+00	1.E+00	1.E+00

GO:0008625	induction of apoptosis via death domain receptors	BP	1.E+00	1.E+00	4.E-12	1.E+00	1.E+00	2.E-14	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009048	dosage compensation, by inactivation of X chromosom	BP	1.E+00	1.E+00	1.E-23	1.E+00	1.E+00	1.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045739	positive regulation of DNA repair	BP	1.E+00	1.E+00	6.E-33	1.E+00	1.E+00	5.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006978	DNA damage response, signal transduction by p53 clas	BP	1.E+00	1.E+00	9.E-33	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042759	long-chain fatty acid biosynthetic process	BP	1.E+00	1.E+00	9.E-33	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0046600	negative regulation of centriole replication	BP	1.E+00	1.E+00	9.E-33	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019899	enzyme binding	MF	1.E+00	1.E+00	2.E-41	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005581	collagen	CC	1.E+00	1.E+00	4.E-10	1.E+00	1.E+00	9.E-25	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007218	neuropeptide signaling pathway	BP	1.E+00	1.E+00	3.E-18	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000940	outer kinetochore of condensed chromosome	CC	1.E+00	1.E+00	1.E-15	1.E+00	1.E+00	2.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031436	BRCA1-BARD1 complex	CC	1.E+00	1.E+00	9.E-33	1.E+00	1.E+00	2.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051298	centrosome duplication	BP	1.E+00	1.E+00	5.E-26	1.E+00	1.E+00	3.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006958	complement activation, classical pathway	BP	1.E+00	1.E+00	1.E-10	1.E+00	1.E+00	5.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031398	positive regulation of protein ubiquitination	BP	1.E+00	1.E+00	2.E-28	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019959	interleukin-8 binding	MF	1.E+00	1.E+00	2.E-19	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043120	tumor necrosis factor binding	MF	1.E+00	1.E+00	2.E-19	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004905	interferon-alpha/beta receptor activity	MF	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	8.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016046	detection of fungus	BP	1.E+00	1.E+00	4.E-19	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045362	positive regulation of interleukin-1 biosynthetic proce	BP	1.E+00	1.E+00	4.E-19	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007250	activation of NF-kappaB-inducing kinase activity	BP	1.E+00	1.E+00	8.E-08	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030431	sleep	BP	1.E+00	1.E+00	4.E-32	1.E+00	1.E+00	1.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019966	interleukin-1 binding	MF	1.E+00	1.E+00	6.E-18	1.E+00	1.E+00	1.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042088	T-helper 1 type immune response	BP	1.E+00	1.E+00	4.E-21	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000089	mitotic metaphase	BP	1.E+00	1.E+00	5.E-17	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008320	protein transmembrane transporter activity	MF	1.E+00	1.E+00	4.E-12	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001675	acrosome formation	BP	1.E+00	1.E+00	5.E-35	1.E+00	1.E+00	8.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003674	molecular_function	MF	1.E+00	1.E+00	3.E-12	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030997	regulation of centriole-centriole cohesion	BP	1.E+00	1.E+00	8.E-23	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051382	kinetochore assembly	BP	1.E+00	1.E+00	2.E-16	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007079	mitotic chromosome movement towards spindle pole	BP	1.E+00	1.E+00	1.E-17	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019835	cytolysis	BP	1.E+00	1.E+00	1.E-11	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045576	mast cell activation	BP	1.E+00	1.E+00	4.E-17	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051402	neuron apoptosis	BP	1.E+00	1.E+00	1.E-44	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004865	type 1 serine/threonine specific protein phosphatase i	MF	1.E+00	1.E+00	4.E-22	1.E+00	1.E+00	4.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006957	complement activation, alternative pathway	BP	1.E+00	1.E+00	1.E-22	1.E+00	1.E+00	6.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0046696	lipopolysaccharide receptor complex	CC	1.E+00	1.E+00	4.E-16	1.E+00	1.E+00	6.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008274	gamma-tubulin ring complex	CC	1.E+00	1.E+00	5.E-31	1.E+00	1.E+00	8.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009898	internal side of plasma membrane	CC	1.E+00	1.E+00	2.E-32	1.E+00	1.E+00	1.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007049	cell cycle	BP	1.E+00	1.E+00	1.E-32	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042105	alpha-beta T cell receptor complex	CC	1.E+00	1.E+00	5.E-21	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042923	neuropeptide binding	MF	1.E+00	1.E+00	2.E-30	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050708	regulation of protein secretion	BP	1.E+00	1.E+00	4.E-06	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001530	lipopolysaccharide binding	MF	1.E+00	1.E+00	6.E-15	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007128	meiotic prophase I	BP	1.E+00	1.E+00	2.E-13	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030414	protease inhibitor activity	MF	1.E+00	1.E+00	6.E-14	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005876	spindle microtubule	CC	1.E+00	1.E+00	7.E-09	1.E+00	1.E+00	4.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006959	humoral immune response	BP	1.E+00	1.E+00	4.E-05	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005579	membrane attack complex	CC	1.E+00	1.E+00	1.E-12	1.E+00	1.E+00	4.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007080	mitotic metaphase plate congression	BP	1.E+00	1.E+00	1.E-13	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005813	centrosome	CC	1.E+00	1.E+00	4.E-08	1.E+00	1.E+00	7.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005540	hyaluronic acid binding	MF	1.E+00	1.E+00	3.E-13	1.E+00	1.E+00	9.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042981	regulation of apoptosis	BP	1.E+00	1.E+00	7.E-23	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045368	positive regulation of interleukin-13 biosynthetic proc	BP	1.E+00	1.E+00	2.E-12	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030693	caspase activity	MF	1.E+00	1.E+00	9.E-05	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005730	nucleolus	CC	1.E+00	1.E+00	5.E-06	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007126	meiosis	BP	1.E+00	1.E+00	3.E-36	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005590	collagen type VII	CC	1.E+00	1.E+00	7.E-10	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000776	kinetochore	CC	1.E+00	1.E+00	2.E-20	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005132	interferon-alpha/beta receptor binding	MF	1.E+00	1.E+00	3.E-21	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045840	positive regulation of mitosis	BP	1.E+00	1.E+00	9.E-11	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000281	cytokinesis after mitosis	BP	1.E+00	1.E+00	4.E-11	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008157	protein phosphatase 1 binding	MF	1.E+00	1.E+00	6.E-04	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008630	DNA damage response, signal transduction resulting in	BP	1.E+00	1.E+00	2.E-20	1.E+00	1.E+00	8.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003684	damaged DNA binding	MF	1.E+00	1.E+00	9.E-22	1.E+00	1.E+00	8.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045084	positive regulation of interleukin-12 biosynthetic proc	BP	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	9.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003880	C-terminal protein carboxyl methyltransferase activity	MF	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006481	C-terminal protein amino acid methylation	BP	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045089	positive regulation of innate immune response	BP	1.E+00	1.E+00	9.E-13	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042116	macrophage activation	BP	1.E+00	1.E+00	2.E-09	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000793	condensed chromosome	CC	1.E+00	1.E+00	4.E-11	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019863	IgE binding	MF	1.E+00	1.E+00	3.E-14	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019901	protein kinase binding	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007059	chromosome segregation	BP	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045580	regulation of T cell differentiation	BP	1.E+00	1.E+00	1.E-10	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00

GO:0006290	pyrimidine dimer repair	BP	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015999	eta DNA polymerase activity	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016451	nu DNA polymerase activity	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030690	Noc1p-Noc2p complex	CC	1.E+00	1.E+00	6.E-12	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015631	tubulin binding	MF	1.E+00	1.E+00	6.E-13	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006956	complement activation	BP	1.E+00	1.E+00	8.E-08	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008301	DNA bending activity	MF	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	4.E-15	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030225	macrophage differentiation	BP	1.E+00	1.E+00	5.E-33	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0048306	calcium-dependent protein binding	MF	1.E+00	1.E+00	9.E-07	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000781	chromosome, telomeric region	CC	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001730	2'-5'-oligoadenylate synthetase activity	MF	1.E+00	1.E+00	7.E-04	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004918	interleukin-8 receptor activity	MF	1.E+00	1.E+00	1.E-24	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015711	organic anion transport	BP	1.E+00	1.E+00	1.E-11	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0040001	establishment of mitotic spindle localization	BP	1.E+00	1.E+00	4.E-11	1.E+00	1.E+00	7.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042384	cilium biogenesis	BP	1.E+00	1.E+00	2.E-25	1.E+00	1.E+00	9.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030887	positive regulation of myeloid dendritic cell activation	BP	1.E+00	1.E+00	3.E-09	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019955	cytokine binding	MF	1.E+00	1.E+00	2.E-27	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016410	N-acyltransferase activity	MF	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0047963	glycine N-choloyltransferase activity	MF	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006915	apoptosis	BP	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045132	meiotic chromosome segregation	BP	1.E+00	1.E+00	5.E-04	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015299	solute:hydrogen antiporter activity	MF	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042100	B cell proliferation	BP	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0048305	immunoglobulin secretion	BP	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030139	endocytic vesicle	CC	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005035	death receptor activity	MF	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0018675	(S)-limonene 6-monooxygenase activity	MF	1.E+00	1.E+00	5.E-04	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0018676	(S)-limonene 7-monooxygenase activity	MF	1.E+00	1.E+00	5.E-04	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030271	chymase activity	MF	1.E+00	1.E+00	6.E-04	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030890	positive regulation of B cell proliferation	BP	1.E+00	1.E+00	9.E-06	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045351	interferon type I biosynthetic process	BP	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043515	kinetochore binding	MF	1.E+00	1.E+00	6.E-29	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005597	collagen type XVI	CC	1.E+00	1.E+00	5.E-09	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005594	collagen type IX	CC	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	5.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050906	detection of stimulus involved in sensory perception	BP	1.E+00	1.E+00	7.E-10	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043229	intracellular organelle	CC	1.E+00	1.E+00	8.E-11	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000278	mitotic cell cycle	BP	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006325	establishment and/or maintenance of chromatin archi	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-02	1.E-08	3.E-03	1.E+00	1.E+00
GO:0001656	metanephros development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-60	8.E-82	1.E+00	1.E+00
GO:0001657	ureteric bud development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-69	7.E-87	1.E+00	1.E+00
GO:0003680	AT DNA binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-43	2.E-16	1.E+00	1.E+00
GO:0004716	receptor signaling protein tyrosine kinase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-35	9.E-32	1.E+00	1.E+00
GO:0007156	homophilic cell adhesion	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-52	4.E-69	1.E+00	1.E+00
GO:0007275	multicellular organismal development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-26	3.E-23	1.E+00	1.E+00
GO:0007399	nervous system development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-28	5.E-44	1.E+00	1.E+00
GO:0007411	axon guidance	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-97	5.E-100	1.E+00	1.E+00
GO:0007420	brain development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-29	1.E-48	1.E+00	1.E+00
GO:0008046	axon guidance receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-193	2.E-194	1.E+00	1.E+00
GO:0009986	cell surface	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-69	1.E-105	1.E+00	1.E+00
GO:0017154	semaphorin receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-39	5.E-20	1.E+00	1.E+00
GO:0030154	cell differentiation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-38	3.E-44	1.E+00	1.E+00
GO:0030673	axolemma	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-231	4.E-221	1.E+00	1.E+00
GO:0042802	identical protein binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-46	1.E-83	1.E+00	1.E+00
GO:0050772	positive regulation of axonogenesis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-184	4.E-181	1.E+00	1.E+00
GO:0007155	cell adhesion	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-10	8.E-25	1.E+00	1.E+00
GO:0005021	vascular endothelial growth factor receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-27	8.E-10	1.E+00	1.E+00
GO:0031032	actomyosin structure organization and biogenesis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-12	4.E-08	1.E+00	1.E+00
GO:0004714	transmembrane receptor protein tyrosine kinase activ	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-08	2.E-07	1.E+00	1.E+00
GO:0006487	protein amino acid N-linked glycosylation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-07	4.E-17	1.E+00	1.E+00
GO:0008113	peptide-methionine-(S)-S-oxide reductase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-12	5.E-06	1.E+00	1.E+00
GO:0008093	cytoskeletal adaptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-07	2.E-05	1.E+00	1.E+00
GO:0007417	central nervous system development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	1.E-12	1.E+00	1.E+00
GO:0015247	aminophospholipid transporter activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	9.E-06	1.E+00	1.E+00
GO:0019829	cation-transporting ATPase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	9.E-06	1.E+00	1.E+00
GO:0007169	transmembrane receptor protein tyrosine kinase signa	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	2.E-07	1.E+00	1.E+00
GO:0015204	urea transmembrane transporter activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E-05	1.E+00	1.E+00
GO:0015840	urea transport	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E-05	1.E+00	1.E+00
GO:0008533	astacin activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-08	2.E-03	1.E+00	1.E+00
GO:0005923	tight junction	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-05	2.E-03	1.E+00	1.E+00
GO:0030165	PDZ domain binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E-03	1.E+00	1.E+00
GO:0008510	sodium:bicarbonate symporter activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-03	5.E-04	1.E+00	1.E+00
GO:0004152	dihydroorotate dehydrogenase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	1.E-02	1.E+00	1.E+00
GO:0004158	dihydroorotate oxidase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	1.E-02	1.E+00	1.E+00
GO:0007507	heart development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-05	2.E-02	1.E+00	1.E+00

GO:0007369	gastrulation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-05	2.E-02	1.E+00	1.E+00
GO:0030145	manganese ion binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E-03	1.E+00	1.E+00
GO:0006208	pyrimidine base catabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-05	2.E-02	1.E+00	1.E+00
GO:0006212	uracil catabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-05	2.E-02	1.E+00	1.E+00
GO:0006214	thymidine catabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-05	2.E-02	1.E+00	1.E+00
GO:0017113	dihydropyrimidine dehydrogenase (NADP+) activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-05	2.E-02	1.E+00	1.E+00
GO:0043244	regulation of protein complex disassembly	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-06	2.E-02	1.E+00	1.E+00
GO:0016820	hydrolase activity, acting on acid anhydrides, catalyzin	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	6.E-03	1.E+00	1.E+00
GO:0008373	sialyltransferase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	2.E-04	1.E+00	1.E+00
GO:0047710	bis(5'-adenosyl)-triphosphatase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	5.E-02	1.E+00	1.E+00
GO:0007165	signal transduction	BP	1.E+00	6.E-07	3.E-01	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051301	cell division	BP	1.E+00	1.E+00	5.E-07	1.E+00	1.E+00	6.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005814	centriole	CC	1.E+00	1.E+00	5.E-12	1.E+00	1.E+00	6.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004785	copper, zinc superoxide dismutase activity	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	6.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006337	nucleosome disassembly	BP	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	7.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009642	response to light intensity	BP	1.E+00	1.E+00	5.E-16	1.E+00	1.E+00	7.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005134	interleukin-2 receptor binding	MF	1.E+00	1.E+00	7.E-05	1.E+00	1.E+00	9.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003887	DNA-directed DNA polymerase activity	MF	1.E+00	1.E+00	3.E-08	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006766	vitamin metabolic process	BP	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0035067	negative regulation of histone acetylation	BP	1.E+00	1.E+00	7.E-06	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016290	palmitoyl-CoA hydrolase activity	MF	1.E+00	1.E-01	2.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050850	positive regulation of calcium-mediated signaling	BP	1.E+00	1.E+00	3.E-12	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007338	single fertilization	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042110	T cell activation	BP	1.E+00	1.E+00	3.E-08	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	MF	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	1.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001783	B cell apoptosis	BP	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005201	extracellular matrix structural constituent	MF	1.E+00	1.E+00	7.E-06	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005139	interleukin-7 receptor binding	MF	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030021	extracellular matrix structural constituent conferring c	MF	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045786	negative regulation of cell cycle	BP	1.E+00	1.E+00	4.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-01
GO:0004906	interferon-gamma receptor activity	MF	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004982	N-formyl peptide receptor activity	MF	1.E+00	1.E+00	2.E-03	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000506	glycosylphosphatidylinositol-N-acetylglucosaminyltran	CC	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009893	positive regulation of metabolic process	BP	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylatio	BP	1.E+00	1.E+00	2.E-08	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006260	DNA replication	BP	1.E+00	1.E+00	8.E-09	1.E+00	1.E+00	2.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003696	satellite DNA binding	MF	1.E+00	1.E+00	7.E-10	1.E+00	1.E+00	3.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008624	induction of apoptosis by extracellular signals	BP	1.E+00	1.E+00	7.E-11	1.E+00	1.E+00	3.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030246	carbohydrate binding	MF	1.E+00	1.E+00	4.E-11	1.E+00	1.E+00	3.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050798	activated T cell proliferation	BP	1.E+00	1.E+00	7.E-05	1.E+00	1.E+00	3.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006805	xenobiotic metabolic process	BP	1.E+00	4.E-01	4.E-11	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006359	regulation of transcription from RNA polymerase III pr	BP	1.E+00	1.E+00	9.E-18	1.E+00	1.E+00	4.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045671	negative regulation of osteoclast differentiation	BP	1.E+00	1.E+00	4.E-19	1.E+00	1.E+00	4.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008544	epidermis development	BP	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	4.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042523	positive regulation of tyrosine phosphorylation of Stat	BP	1.E+00	1.E+00	7.E-27	1.E+00	1.E+00	5.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043031	negative regulation of macrophage activation	BP	1.E+00	1.E+00	7.E-27	1.E+00	1.E+00	5.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001781	neutrophil apoptosis	BP	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	6.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005900	oncostatin-M receptor complex	CC	1.E+00	1.E+00	5.E-08	1.E+00	1.E+00	7.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004908	interleukin-1 receptor activity	MF	1.E+00	1.E+00	6.E-09	1.E+00	1.E+00	7.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001669	acrosome	CC	1.E+00	1.E+00	8.E-36	1.E+00	1.E+00	8.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051018	protein kinase A binding	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	8.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015020	glucuronosyltransferase activity	MF	1.E+00	9.E-01	6.E-12	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007130	synaptonemal complex assembly	BP	1.E+00	1.E+00	3.E-08	1.E+00	1.E+00	9.E-01	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004217	cathepsin L activity	MF	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004907	interleukin receptor activity	MF	1.E+00	1.E+00	5.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001562	response to protozoan	BP	1.E+00	1.E+00	1.E-41	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001808	negative regulation of type IV hypersensitivity	BP	1.E+00	1.E+00	1.E-41	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001931	uropod	CC	1.E+00	1.E+00	1.E-23	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004091	carboxylesterase activity	MF	1.E+00	1.E+00	5.E-35	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004694	eukaryotic translation initiation factor 2alpha kinase a	MF	1.E+00	1.E+00	1.E-25	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004896	hematopoietin/interferon-class (D200-domain) cytokir	MF	1.E+00	1.E+00	1.E-17	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005152	interleukin-1 receptor antagonist activity	MF	1.E+00	1.E+00	2.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006968	cellular defense response	BP	1.E+00	1.E+00	2.E-42	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007259	JAK-STAT cascade	BP	1.E+00	1.E+00	6.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008049	male courtship behavior	BP	1.E+00	1.E+00	9.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008889	glycerophosphodiester phosphodiesterase activity	MF	1.E+00	1.E+00	3.E-21	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009056	catabolic process	BP	1.E+00	1.E+00	2.E-28	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009313	oligosaccharide catabolic process	BP	1.E+00	1.E+00	9.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0018149	peptide cross-linking	BP	1.E+00	1.E+00	8.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019953	sexual reproduction	BP	1.E+00	1.E+00	2.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030023	extracellular matrix constituent conferring elasticity	MF	1.E+00	1.E+00	2.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030212	hyaluronan metabolic process	BP	1.E+00	1.E+00	2.E-21	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031295	T cell costimulation	BP	1.E+00	1.E+00	4.E-34	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031323	regulation of cellular metabolic process	BP	1.E+00	1.E+00	9.E-15	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00

GO:0042130	negative regulation of T cell proliferation	BP	1.E+00	1.E+00	5.E-32	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042493	response to drug	BP	1.E+00	1.E+00	9.E-21	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042517	positive regulation of tyrosine phosphorylation of Stat	BP	1.E+00	1.E+00	2.E-20	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042535	positive regulation of tumor necrosis factor biosynthet	BP	1.E+00	1.E+00	1.E-19	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043149	stress fiber formation	BP	1.E+00	1.E+00	3.E-32	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050688	regulation of defense response to virus	BP	1.E+00	1.E+00	1.E-41	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050776	regulation of immune response	BP	1.E+00	1.E+00	4.E-21	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045060	negative thymic T cell selection	BP	1.E+00	1.E+00	2.E-14	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007341	penetration of zona pellucida	BP	1.E+00	1.E+00	3.E-14	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006689	ganglioside catabolic process	BP	1.E+00	1.E+00	4.E-14	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001812	positive regulation of type I hypersensitivity	BP	1.E+00	1.E+00	7.E-14	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019767	IgE receptor activity	MF	1.E+00	1.E+00	7.E-14	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005509	calcium ion binding	MF	1.E+00	1.E+00	1.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007283	spermatogenesis	BP	1.E+00	1.E+00	2.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019185	snRNA-activating protein complex	CC	1.E+00	1.E+00	2.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042795	snRNA transcription from RNA polymerase II promoter	BP	1.E+00	1.E+00	2.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042796	snRNA transcription from RNA polymerase III promote	BP	1.E+00	1.E+00	2.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051383	kinetochore organization and biogenesis	BP	1.E+00	1.E+00	2.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000795	synaptonemal complex	CC	1.E+00	1.E+00	5.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006071	glycerol metabolic process	BP	1.E+00	1.E+00	6.E-13	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042629	mast cell granule	CC	1.E+00	1.E+00	3.E-12	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009301	snRNA transcription	BP	1.E+00	1.E+00	4.E-12	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007585	respiratory gaseous exchange	BP	1.E+00	1.E+00	9.E-12	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008367	bacterial binding	MF	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050905	neuromuscular process	BP	1.E+00	1.E+00	2.E-11	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000783	nuclear telomere cap complex	CC	1.E+00	1.E+00	6.E-11	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0035282	segmentation	BP	1.E+00	1.E+00	6.E-11	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042101	T cell receptor complex	CC	1.E+00	1.E+00	2.E-10	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003691	double-stranded telomeric DNA binding	MF	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0017176	phosphatidylinositol N-acetylglucosaminyltransferase	MF	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043169	cation binding	MF	1.E+00	1.E+00	4.E-10	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030593	neutrophil chemotaxis	BP	1.E+00	1.E+00	6.E-10	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016529	sarcoplasmic reticulum	CC	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007163	establishment and/or maintenance of cell polarity	BP	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0048246	macrophage chemotaxis	BP	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015884	folic acid transport	BP	1.E+00	1.E+00	1.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007131	meiotic recombination	BP	1.E+00	1.E+00	2.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019836	hemolysis by symbiont of host red blood cells	BP	1.E+00	1.E+00	2.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000245	spliceosome assembly	BP	1.E+00	1.E+00	3.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008273	calcium, potassium:sodium antiporter activity	MF	1.E+00	1.E+00	4.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0048247	lymphocyte chemotaxis	BP	1.E+00	1.E+00	4.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001766	membrane raft polarization	BP	1.E+00	1.E+00	4.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006879	cellular iron ion homeostasis	BP	1.E+00	1.E+00	5.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007603	phototransduction, visible light	BP	1.E+00	1.E+00	6.E-09	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004557	alpha-galactosidase activity	MF	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0046479	glycosphingolipid catabolic process	BP	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051001	negative regulation of nitric-oxide synthase activity	BP	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042608	T cell receptor binding	MF	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005815	microtubule organizing center	CC	1.E+00	1.E+00	1.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016494	C-X-C chemokine receptor activity	MF	1.E+00	1.E+00	4.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005764	lysosome	CC	1.E+00	1.E+00	4.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008601	protein phosphatase type 2A regulator activity	MF	1.E+00	1.E+00	5.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004924	oncostatin-M receptor activity	MF	1.E+00	1.E+00	5.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015181	arginine transmembrane transporter activity	MF	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015189	L-lysine transmembrane transporter activity	MF	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015326	cationic amino acid transmembrane transporter activit	MF	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015819	lysine transport	BP	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030345	structural constituent of tooth enamel	MF	1.E+00	1.E+00	7.E-08	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008091	spectrin	CC	1.E+00	1.E+00	1.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045343	regulation of MHC class I biosynthetic process	BP	1.E+00	1.E+00	3.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0046597	negative regulation of virion penetration into host cell	BP	1.E+00	1.E+00	3.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008238	exopeptidase activity	MF	1.E+00	1.E+00	4.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008464	gamma-glutamyl hydrolase activity	MF	1.E+00	1.E+00	4.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006687	glycosphingolipid metabolic process	BP	1.E+00	1.E+00	4.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030833	regulation of actin filament polymerization	BP	1.E+00	1.E+00	6.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005712	chiasma	CC	1.E+00	1.E+00	7.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007144	female meiosis I	BP	1.E+00	1.E+00	7.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045019	negative regulation of nitric oxide biosynthetic process	BP	1.E+00	1.E+00	8.E-07	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007565	female pregnancy	BP	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050681	androgen receptor binding	MF	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001518	voltage-gated sodium channel complex	CC	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030502	negative regulation of bone mineralization	BP	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050716	positive regulation of interleukin-1 secretion	BP	1.E+00	1.E+00	4.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004950	chemokine receptor activity	MF	1.E+00	1.E+00	4.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00

GO:0001946	lymphangiogenesis	BP	1.E+00	1.E+00	6.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042476	odontogenesis	BP	1.E+00	1.E+00	7.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005248	voltage-gated sodium channel activity	MF	1.E+00	1.E+00	7.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015250	water channel activity	MF	1.E+00	1.E+00	7.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009434	microtubule-based flagellum	CC	1.E+00	1.E+00	8.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008559	xenobiotic-transporting ATPase activity	MF	1.E+00	1.E+00	9.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008517	folic acid transporter activity	MF	1.E+00	1.E+00	9.E-06	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004565	beta-galactosidase activity	MF	1.E+00	1.E+00	1.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015026	coreceptor activity	MF	1.E+00	1.E+00	1.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001655	urogenital system development	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030224	monocyte differentiation	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007340	acrosome reaction	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009341	beta-galactosidase complex	CC	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005335	serotonin:sodium symporter activity	MF	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006837	serotonin transport	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015222	serotonin transmembrane transporter activity	MF	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030282	bone mineralization	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030521	androgen receptor signaling pathway	BP	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015809	arginine transport	BP	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006833	water transport	BP	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008324	cation transmembrane transporter activity	MF	1.E+00	1.E+00	3.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007342	fusion of sperm to egg plasma membrane	BP	1.E+00	1.E+00	5.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006637	acyl-CoA metabolic process	BP	1.E+00	1.E+00	5.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005157	macrophage colony stimulating factor receptor bindin	MF	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042488	positive regulation of odontogenesis of dentine-contai	BP	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0018206	peptidyl-methionine modification	BP	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031365	N-terminal protein amino acid modification	BP	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004835	tubulin-tyrosine ligase activity	MF	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016798	hydrolase activity, acting on glycosyl bonds	MF	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005381	iron ion transmembrane transporter activity	MF	1.E+00	1.E+00	7.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006401	RNA catabolic process	BP	1.E+00	1.E+00	8.E-05	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005372	water transporter activity	MF	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004563	beta-N-acetylhexosaminidase activity	MF	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008283	cell proliferation	BP	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043249	erythrocyte maturation	BP	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003956	NAD(P)+-protein-arginine ADP-ribosyltransferase activ	MF	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006298	mismatch repair	BP	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019233	sensory perception of pain	BP	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004385	guanylate kinase activity	MF	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004969	histamine receptor activity	MF	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001820	serotonin secretion	BP	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043306	positive regulation of mast cell degranulation	BP	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045401	positive regulation of interleukin-3 biosynthetic proce	BP	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045425	positive regulation of granulocyte macrophage colony	BP	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050828	regulation of liquid surface tension	BP	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015254	glycerol channel activity	MF	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015793	glycerol transport	BP	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008247	2-acetyl-1-alkylglycerophosphocholine esterase compl	CC	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004869	cysteine protease inhibitor activity	MF	1.E+00	1.E+00	5.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031405	lipoic acid binding	MF	1.E+00	1.E+00	6.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030056	hemidesmosome	CC	1.E+00	1.E+00	7.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045059	positive thymic T cell selection	BP	1.E+00	1.E+00	7.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001948	glycoprotein binding	MF	1.E+00	1.E+00	7.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005477	pyruvate secondary active transmembrane transporte	MF	1.E+00	1.E+00	9.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006848	pyruvate transport	BP	1.E+00	1.E+00	9.E-04	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045078	positive regulation of interferon-gamma biosynthetic p	BP	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006917	induction of apoptosis	BP	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0048155	S100 alpha binding	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051117	ATPase binding	MF	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005775	vacuolar lumen	CC	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0022008	neurogenesis	BP	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030318	melanocyte differentiation	BP	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006280	mutagenesis	BP	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003953	NAD+ nucleosidase activity	MF	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0047704	bile-salt sulfotransferase activity	MF	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004770	sterol carrier protein X-related thiolase activity	MF	1.E+00	1.E+00	5.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016758	transferase activity, transferring hexosyl groups	MF	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030280	structural constituent of epidermis	MF	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050885	neuromuscular process controlling balance	BP	1.E+00	1.E+00	8.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015171	amino acid transmembrane transporter activity	MF	1.E+00	1.E+00	8.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030612	arsenate reductase (thioredoxin) activity	MF	1.E+00	1.E+00	9.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042226	interleukin-6 biosynthetic process	BP	1.E+00	1.E+00	9.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045080	positive regulation of chemokine biosynthetic process	BP	1.E+00	1.E+00	9.E-03	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045085	negative regulation of interleukin-2 biosynthetic proce	BP	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00

GO:0019229	regulation of vasoconstriction	BP	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016176	superoxide-generating NADPH oxidase activator activi	MF	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006506	GPI anchor biosynthetic process	BP	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0009582	detection of abiotic stimulus	BP	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004919	interleukin-9 receptor activity	MF	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050715	positive regulation of cytokine secretion	BP	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004060	arylamine N-acetyltransferase activity	MF	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015198	oligopeptide transporter activity	MF	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050832	defense response to fungus	BP	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045263	proton-transporting ATP synthase complex, coupling f	CC	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006183	GTP biosynthetic process	BP	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051260	protein homooligomerization	BP	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000747	conjugation with cellular fusion	BP	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042289	MHC class II protein binding	MF	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0019861	flagellum	CC	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004964	lutropin-choriogonadotropic hormone receptor activit	MF	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004238	meprin A activity	MF	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043367	CD4-positive, alpha beta T cell differentiation	BP	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0043374	CD8-positive, alpha-beta T cell differentiation	BP	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016712	oxidoreductase activity, acting on paired donors, with	MF	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004574	oligo-1,6-glucosidase activity	MF	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004575	sucrose alpha-glucosidase activity	MF	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015833	peptide transport	BP	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006633	fatty acid biosynthetic process	BP	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007586	digestion	BP	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006525	arginine metabolic process	BP	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005223	intracellular cGMP activated cation channel activity	MF	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006824	cobalt ion transport	BP	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015087	cobalt ion transmembrane transporter activity	MF	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030199	collagen fibril organization	BP	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001772	immunological synapse	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	9.E-02	1.E+00	1.E+00
GO:0005588	collagen type V	CC	1.E+00	1.E+00	5.E-01	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045860	positive regulation of protein kinase activity	BP	1.E+00	1.E+00	6.E-01	1.E+00	1.E+00	2.E-09	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000724	double-strand break repair via homologous recombina	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-19	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005587	collagen type IV	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-33	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042062	long-term strengthening of neuromuscular junction	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-27	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007090	regulation of S phase of mitotic cell cycle	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-14	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016072	rRNA metabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-13	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003697	single-stranded DNA binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-13	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030957	Tat protein binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-13	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042255	ribosome assembly	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-13	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001915	negative regulation of T cell mediated cytotoxicity	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001960	negative regulation of cytokine and chemokine mediat	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050857	positive regulation of antigen receptor-mediated signa	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-11	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004364	glutathione transferase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-10	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005539	glycosaminoglycan binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004126	cytidine deaminase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051209	release of sequestered calcium ion into cytosol	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-08	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045869	negative regulation of retroviral genome replication	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030109	HLA-B specific inhibitory MHC class I receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030529	ribonucleoprotein complex	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000722	telomere maintenance via recombination	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-07	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051607	defense response to virus	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050853	B cell receptor signaling pathway	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004572	mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006642	triacylglycerol mobilization	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003735	structural constituent of ribosome	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007093	mitotic cell cycle checkpoint	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015934	large ribosomal subunit	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050852	T cell receptor signaling pathway	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008037	cell recognition	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-06	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016314	phosphatidylinositol-3,4,5-trisphosphate 3-phosphata	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006376	mRNA splice site selection	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015643	toxin binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030141	secretory granule	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016554	cytidine to uridine editing	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005654	nucleoplasm	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030217	T cell differentiation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007030	Golgi organization and biogenesis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007067	mitosis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-04	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003720	telomerase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005697	telomerase holoenzyme complex	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007004	telomere maintenance via telomerase	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0051726	regulation of cell cycle	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00

GO:0005795	Golgi stack	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005840	ribosome	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0046329	negative regulation of JNK cascade	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016198	axon choice point recognition	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042627	chylomicron	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030546	receptor activator activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008396	oxysterol 7-alpha-hydroxylase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004014	adenosylmethionine decarboxylase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006597	spermine biosynthetic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045861	negative regulation of proteolysis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016311	dephosphorylation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0047497	mitochondrion transport along microtubule	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-03	1.E+00	1.E+00	1.E+00	1.E+00
GO:0045948	positive regulation of translational initiation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006622	protein targeting to lysosome	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0035162	embryonic hemopoiesis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000213	tRNA-intron endonuclease activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0000214	tRNA-intron endonuclease complex	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006777	Mo-molybdopterin cofactor biosynthetic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0001660	fever	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003711	transcription elongation regulator activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0020037	heme binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0030917	midbrain-hindbrain boundary development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0016363	nuclear matrix	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0031575	G1/S transition checkpoint	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0042405	nuclear inclusion body	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0050868	negative regulation of T cell activation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0004277	granzyme A activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006922	cleavage of lamin	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0005792	microsome	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0006885	regulation of pH	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0007286	spermatid development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0008023	transcription elongation factor complex	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	4.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0003896	DNA primase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00	1.E+00	1.E+00
GO:0015012	heparan sulfate proteoglycan biosynthetic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	5.E-02	1.E+00	1.E+00
GO:0030507	spectrin binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-04	6.E-02	1.E+00	1.E+00
GO:0045199	maintenance of epithelial cell polarity	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-04	6.E-02	1.E+00	1.E+00
GO:0019221	cytokine and chemokine mediated signaling pathway	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-05	7.E-02	1.E+00	1.E+00
GO:0016573	histone acetylation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	9.E-04	8.E-02	1.E+00	1.E+00
GO:0006207	'de novo' pyrimidine base biosynthetic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E-01	1.E+00	1.E+00
GO:0004614	phosphoglucomutase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-03	2.E-01	1.E+00	1.E+00
GO:0005020	stem cell factor receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-05	4.E-01	1.E+00	1.E+00
GO:0051539	4 iron, 4 sulfur cluster binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-03	4.E-01	1.E+00	1.E+00
GO:0004968	gonadotropin-releasing hormone receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-03	5.E-01	1.E+00	1.E+00
GO:0005018	platelet-derived growth factor alpha-receptor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-07	7.E-01	1.E+00	1.E+00
GO:0048407	platelet-derived growth factor binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-07	7.E-01	1.E+00	1.E+00
GO:0004610	phosphoacetylglucosamine mutase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-05	7.E-01	1.E+00	1.E+00
GO:0006041	glucosamine metabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-05	7.E-01	1.E+00	1.E+00
GO:0019255	glucose 1-phosphate metabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-05	7.E-01	1.E+00	1.E+00
GO:0019834	phospholipase A2 inhibitor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-10	1.E+00	1.E+00	1.E+00
GO:0008486	diphosphoinositol-polyphosphate diphosphatase activ	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-10	1.E+00	1.E+00	1.E+00
GO:0003727	single-stranded RNA binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-08	1.E+00	1.E+00	1.E+00
GO:0007568	aging	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-08	1.E+00	1.E+00	1.E+00
GO:0047536	2-aminoadipate transaminase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-07	1.E+00	1.E+00	1.E+00
GO:0004473	malate dehydrogenase (oxaloacetate-decarboxylating)	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	1.E+00
GO:0006741	NADP biosynthetic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	1.E+00
GO:0009743	response to carbohydrate stimulus	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-06	1.E+00	1.E+00	1.E+00
GO:0006108	malate metabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-06	1.E+00	1.E+00	1.E+00
GO:0004370	glycerol kinase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-05	1.E+00	1.E+00	1.E+00
GO:0000133	polarisome	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-05	1.E+00	1.E+00	1.E+00
GO:0004700	atypical protein kinase C activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-05	1.E+00	1.E+00	1.E+00
GO:0045216	intercellular junction assembly and maintenance	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-05	1.E+00	1.E+00	1.E+00
GO:0005639	integral to nuclear inner membrane	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-05	1.E+00	1.E+00	1.E+00
GO:0048665	neuron fate specification	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00
GO:0008449	N-acetylglucosamine-6-sulfatase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00
GO:0004470	malic enzyme activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00	1.E+00
GO:0004692	cGMP-dependent protein kinase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	8.E-04	1.E+00	1.E+00	1.E+00
GO:0043325	phosphatidylinositol-3,4-bisphosphate binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00	1.E+00
GO:0050509	N-acetylglucosaminyl-proteoglycan 4-beta-glucuronos	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00
GO:0005547	phosphatidylinositol-3,4,5-triphosphate binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-03	1.E+00	1.E+00	1.E+00
GO:0010001	glial cell differentiation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-03	1.E+00	1.E+00	1.E+00
GO:0045663	positive regulation of myoblast differentiation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00
GO:0016616	oxidoreductase activity, acting on the CH-OH group of	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00
GO:0006072	glycerol-3-phosphate metabolic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00
GO:0004653	polypeptide N-acetylgalactosaminyltransferase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	6.E-03	1.E+00	1.E+00	1.E+00

GO:0008543	fibroblast growth factor receptor signaling pathway	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-02	1.E+00	1.E+00	1.E+00
GO:0030539	male genitalia development	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00	1.E+00
GO:0006024	glycosaminoglycan biosynthetic process	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00	1.E+00
GO:0004859	phospholipase inhibitor activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00	1.E+00
GO:0005487	nucleocytoplasmic transporter activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-01	1.E-02	1.E+00	1.E+00
GO:0004713	protein-tyrosine kinase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-01	6.E-04	1.E+00	1.E+00
GO:0015917	aminophospholipid transport	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-01	2.E-03	1.E+00	1.E+00
GO:0005887	integral to plasma membrane	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-12	1.E+00	1.E+00
GO:0005515	protein binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-09	1.E+00	1.E+00
GO:0006820	anion transport	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	7.E-05	1.E+00	1.E+00
GO:0005834	heterotrimeric G-protein complex	CC	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-04	1.E+00	1.E+00
GO:0018107	peptidyl-threonine phosphorylation	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00
GO:0043508	negative regulation of JNK activity	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E-03	1.E+00	1.E+00
GO:0015380	anion exchanger activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00
GO:0005452	inorganic anion exchanger activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-03	1.E+00	1.E+00
GO:0045749	negative regulation of S phase of mitotic cell cycle	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00
GO:0006904	vesicle docking during exocytosis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-02	1.E+00	1.E+00
GO:0030097	hemopoiesis	BP	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	3.E-02	1.E+00	1.E+00
GO:0004012	phospholipid-translocating ATPase activity	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	5.E-02	1.E+00	1.E+00
GO:0050662	coenzyme binding	MF	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	1.E+00	2.E-01	3.E-03

Supplementary Figures

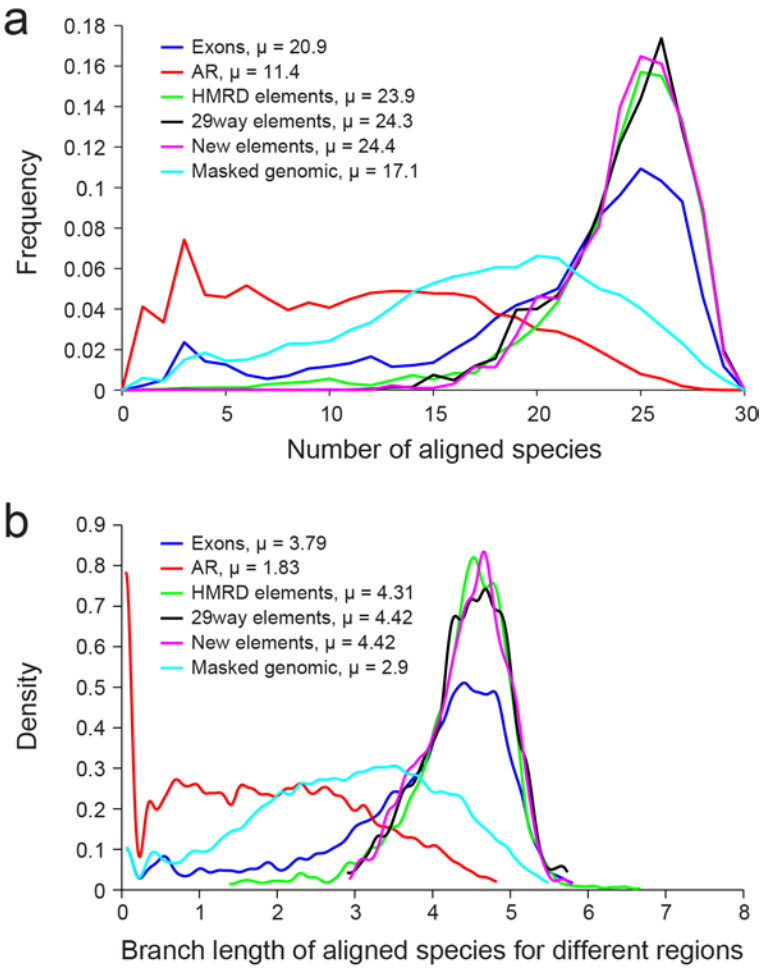


Figure S1 - Evolutionary rate and depth of the 29 mammals multiple alignment in different features in the human genome. a, The number of aligned species for each base in the genome is reported for different features such as neutrally evolving repeats (AR, in red), the whole genome (light blue), exons (dark blue) and non-coding conserved elements (green=top 5% of HMRD elements, black=29mammals elements, purple=newly detected bases). Note that the numbers of aligned species increases with the functional importance of each feature, suggesting that the power is highest over functional elements. **b**, The evolutionary depth for each base in the genome is reported for different features such as neutrally evolving repeats (AR, in red), the whole genome (light blue), exons (dark blue) and non-coding conserved elements (green=top 5% of HMRD elements, black=29mammals elements, purple=newly detected bases). Note that the evolutionary depth increases with the functional importance of each feature, suggesting that the power is highest over functional elements.

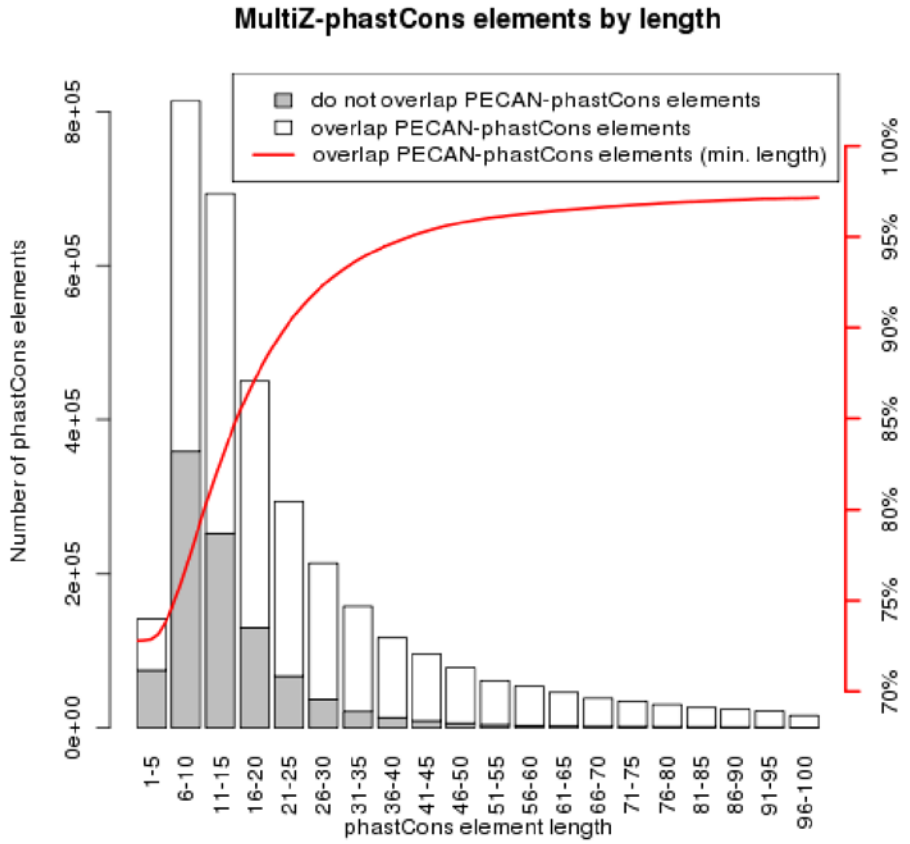
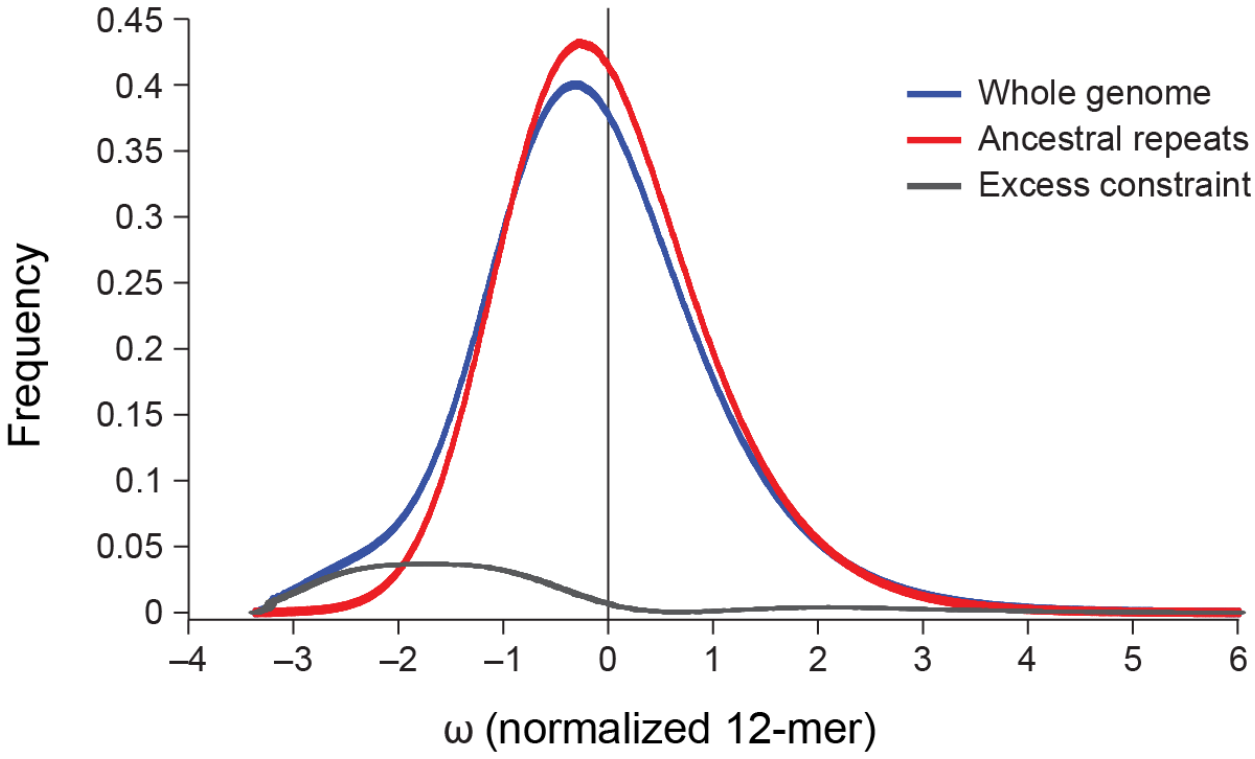
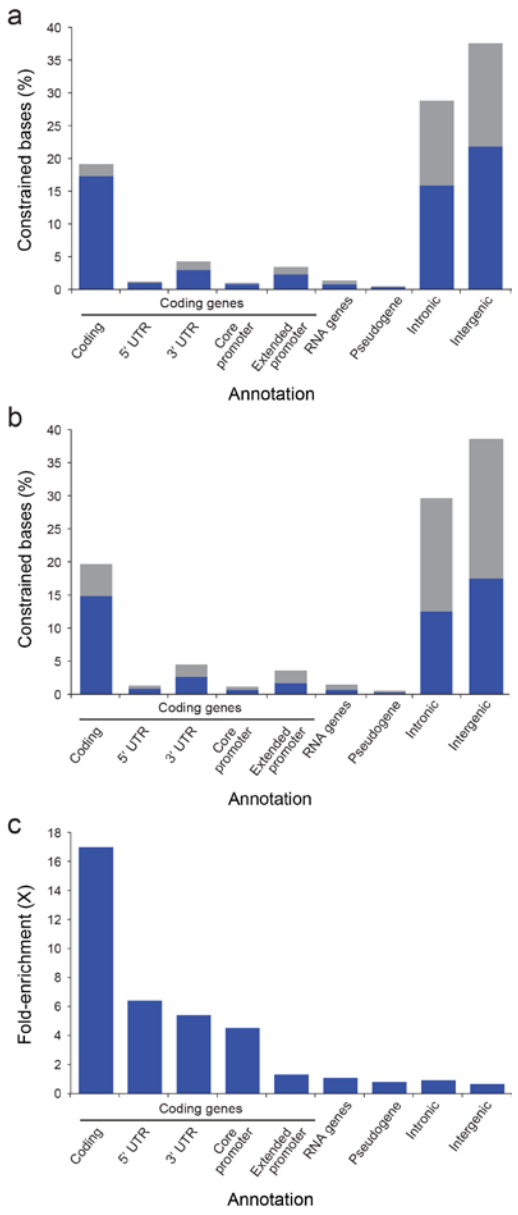


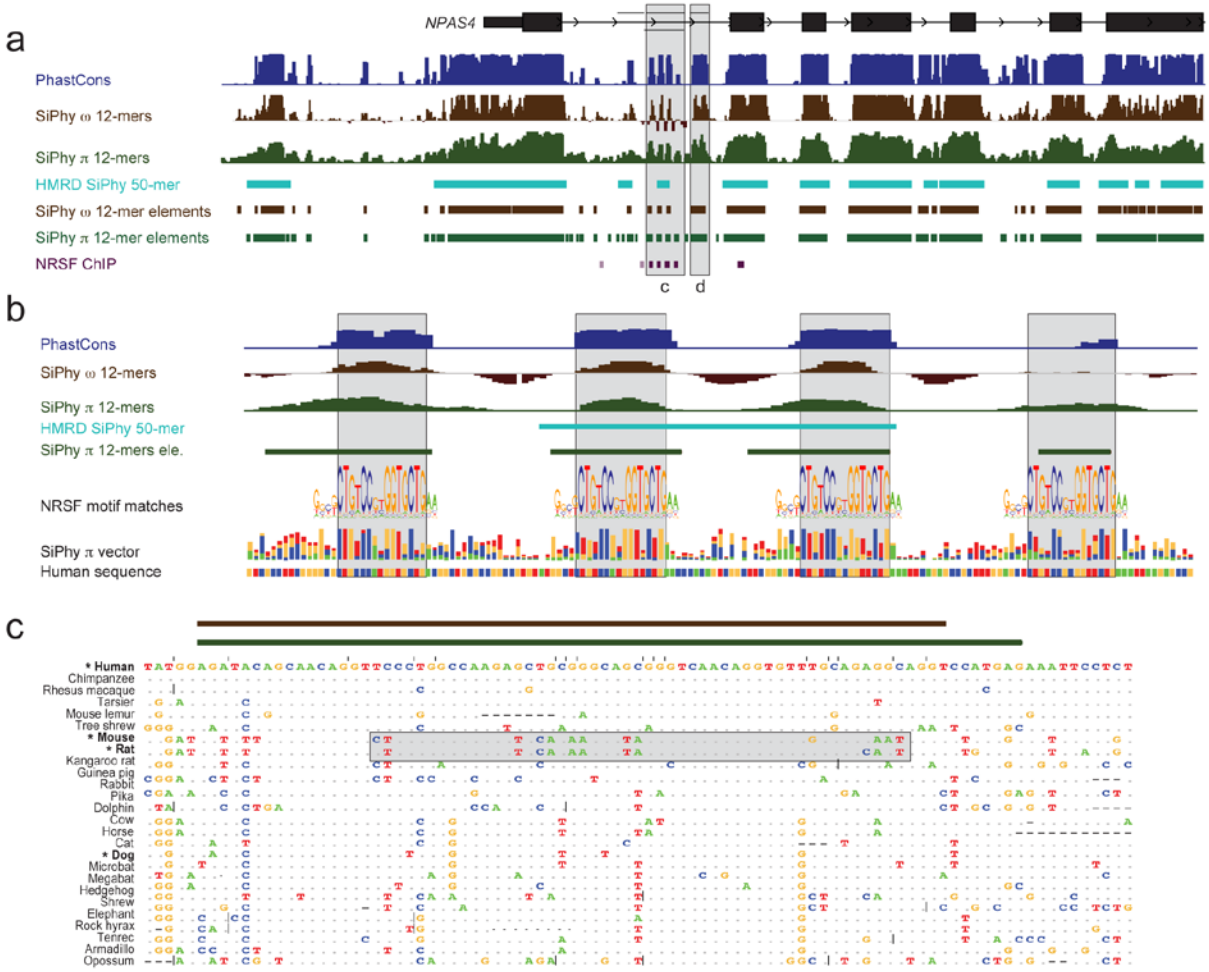
Figure S2 - Comparison between phastCons elements in MultiZ and in PECAN alignments. Histogram of MultiZ-phastCons elements by size, divided into the elements that overlap a PECAN-phastCons element (white bars) and those that do not (grey bars). Also shown in red, the percentage of MultiZ-phastCons elements in agreement with a Pecan-phastCons element as a function of the minimum length of the elements. The agreement between the elements is defined as an overlap of at least 1 nucleotide.



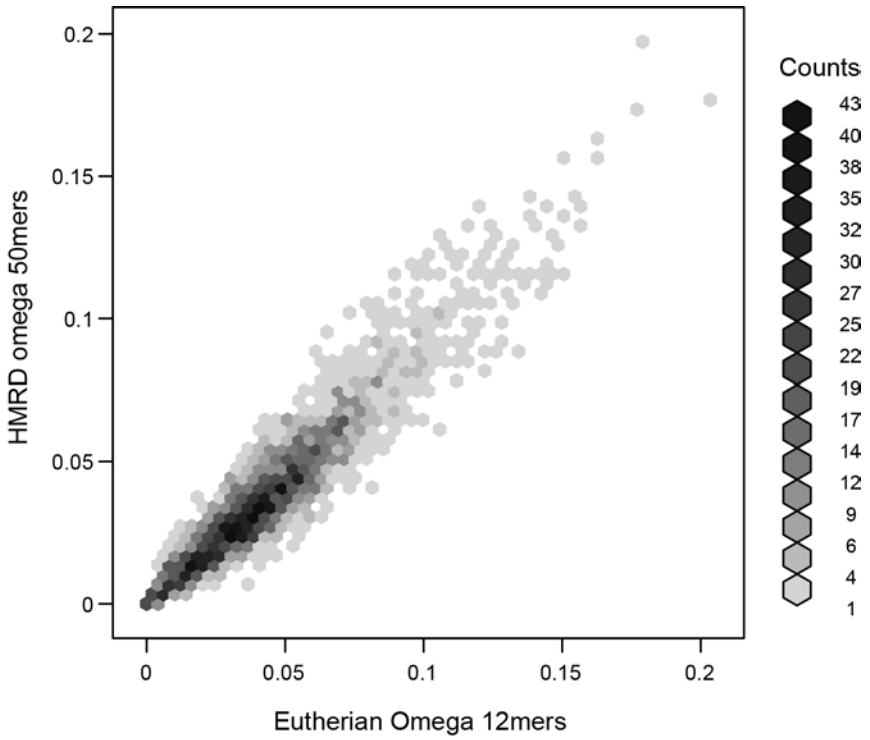
Supplementary Figure S3 - Estimation and detection of constraint. Roughly 5.5% of the genome is estimated to be under constraint using SiPhy-ω with 12-bp windows. The constraint score for ancient repeats is shown in red and the whole genome in blue.



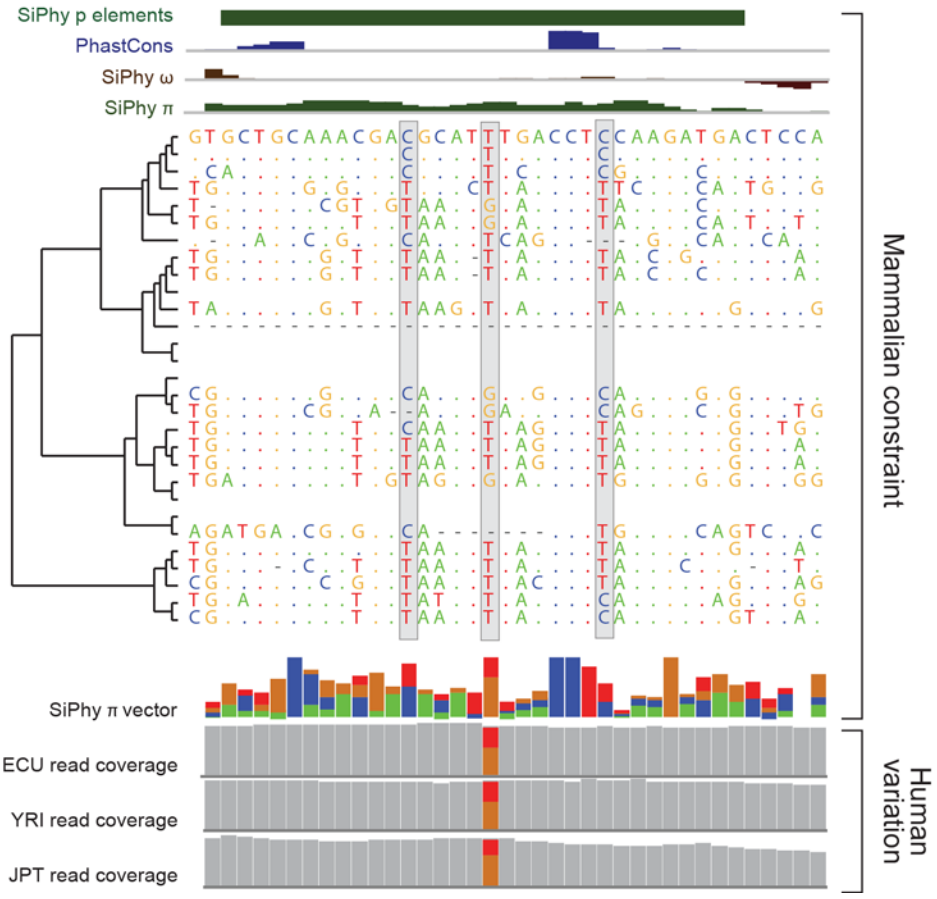
Supplementary Figure S4 - Identification of constrained SiPhy-ω elements. At 10% FDR, 3.6 million constrained SiPhy-ω elements (12-bp windows) can be detected. The largest fraction of constraint can be seen in coding exons, introns and intergenic regions. To account for each constrained base uniquely, the analysis was performed hierarchically as follows: coding exons, 5'-UTRs, 3'-UTRs, promoters, pseudogenes, non-coding RNAs, introns, intergenic. **a,** Distribution of constraint with overlap with HMRD 50 bp + Siepel vertebrate elements shown in blue. **b,** Distribution of constraint with overlap with HMRD elements only shown in blue. Please note the similarity of these data sets. **c,** The 29 mammals constrained bases are particularly enriched in coding transcripts and their promoters. The enrichment was generated by comparing the fraction of constrained bases to the total number of bases in the specific genomic annotation.



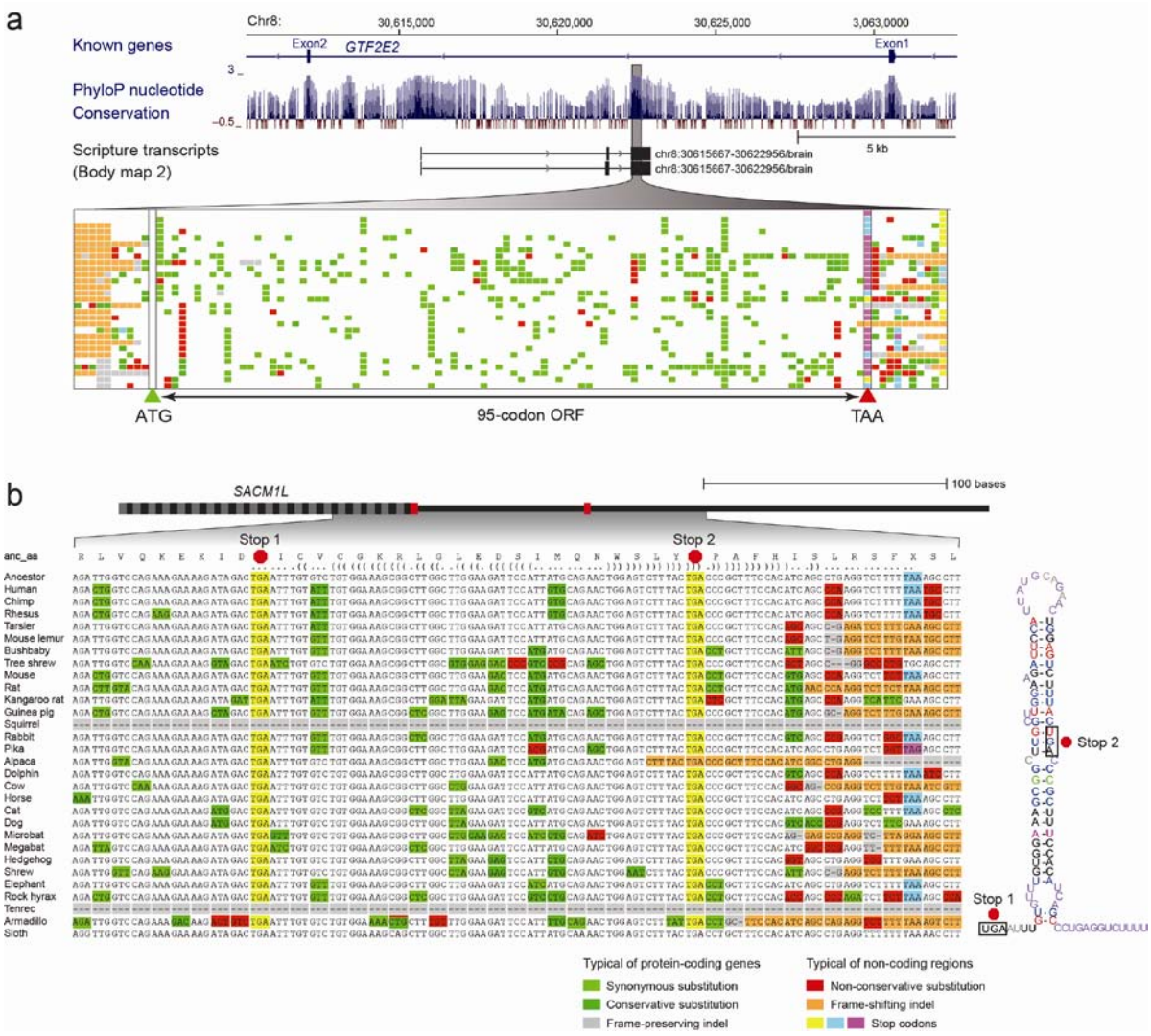
Supplementary Figure S5 - Estimation of fraction of constraint and identification of four NRSF-binding sites in *NPAS4*. The neurological gene *NPAS4* has many constrained elements overlapping introns and the upstream intergenic region. Note that the shaded box c contained only one constrained element using HMRD, while analysis of 29 mammalian sequences reveals four smaller elements. **b,** These four constrained elements in the first intron correspond to binding sites for the NRSF transcription factor, known to regulate neuronal lineages. **c,** Another 70 bp constrained element in the first intron, marked as shaded box d in panel b, was not detected in the HMRD analysis due to unusually high divergence in mouse and rat, but is highly constrained in all other mammals and was therefore detected with sequences from 29 mammals.



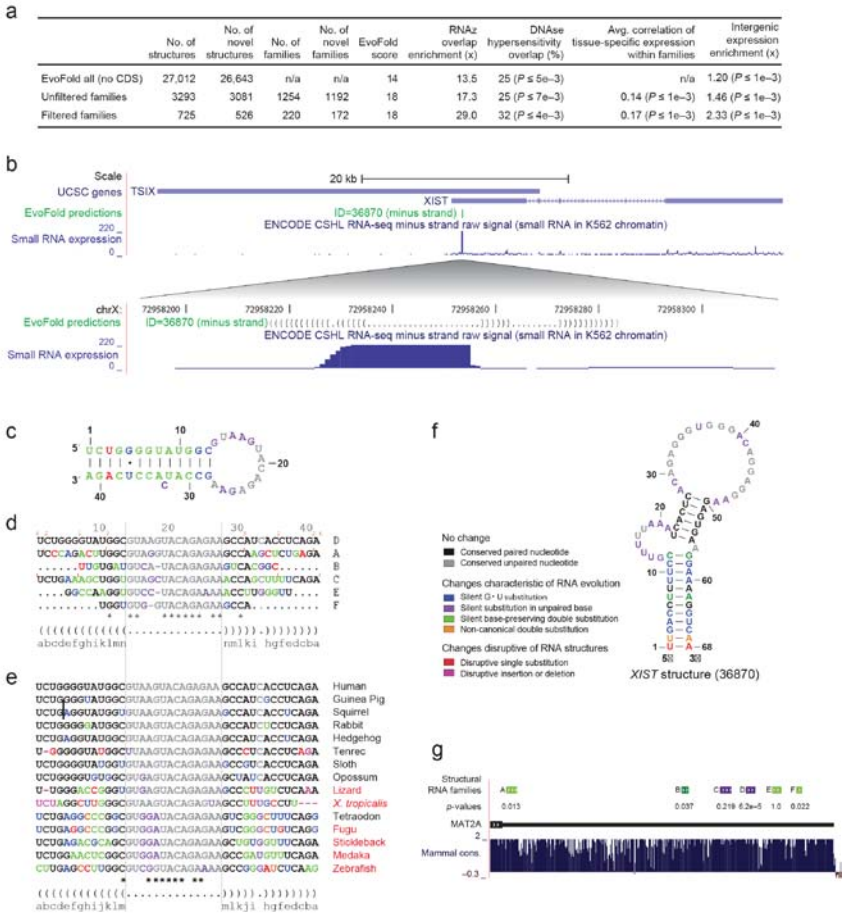
Supplementary Figure S6 - Correlation between element density in 29 mammals and HMRD data sets. The correlation for each megabase in the genome between 29-way eutherian 12mer based element density and HMRD 50mer element density was computed and plotted.



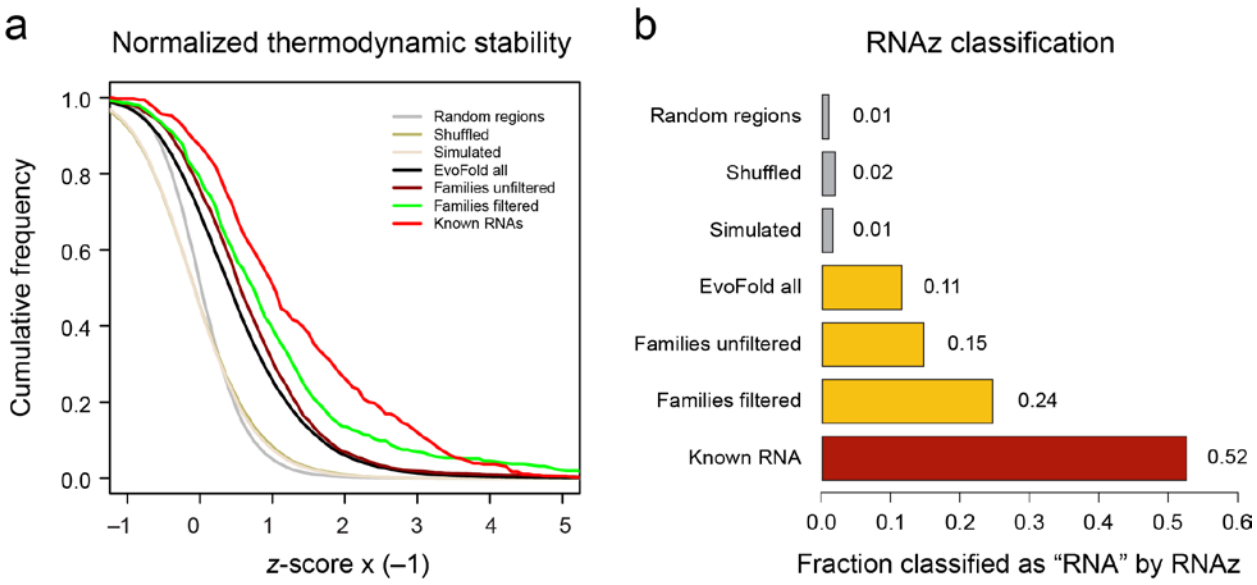
Supplementary Figure S7. Biased nucleotide substitution patterns identifies positions where two bases appear equally constraint and correlating with SNPs in the human population. An example of an intergenic SiPhy-π element (HG18 chr12:1,916,342-1,916,380) detected based on the presence of three 2-fold degenerate constrained bases. Note how these bases (in grey boxes) alternate between bases across the evolutionary tree. One of the degenerate bases matches a SNP present in several human populations, European CEPF (ECU), Yoruban Africans (YRI) and Japanese (JPT).



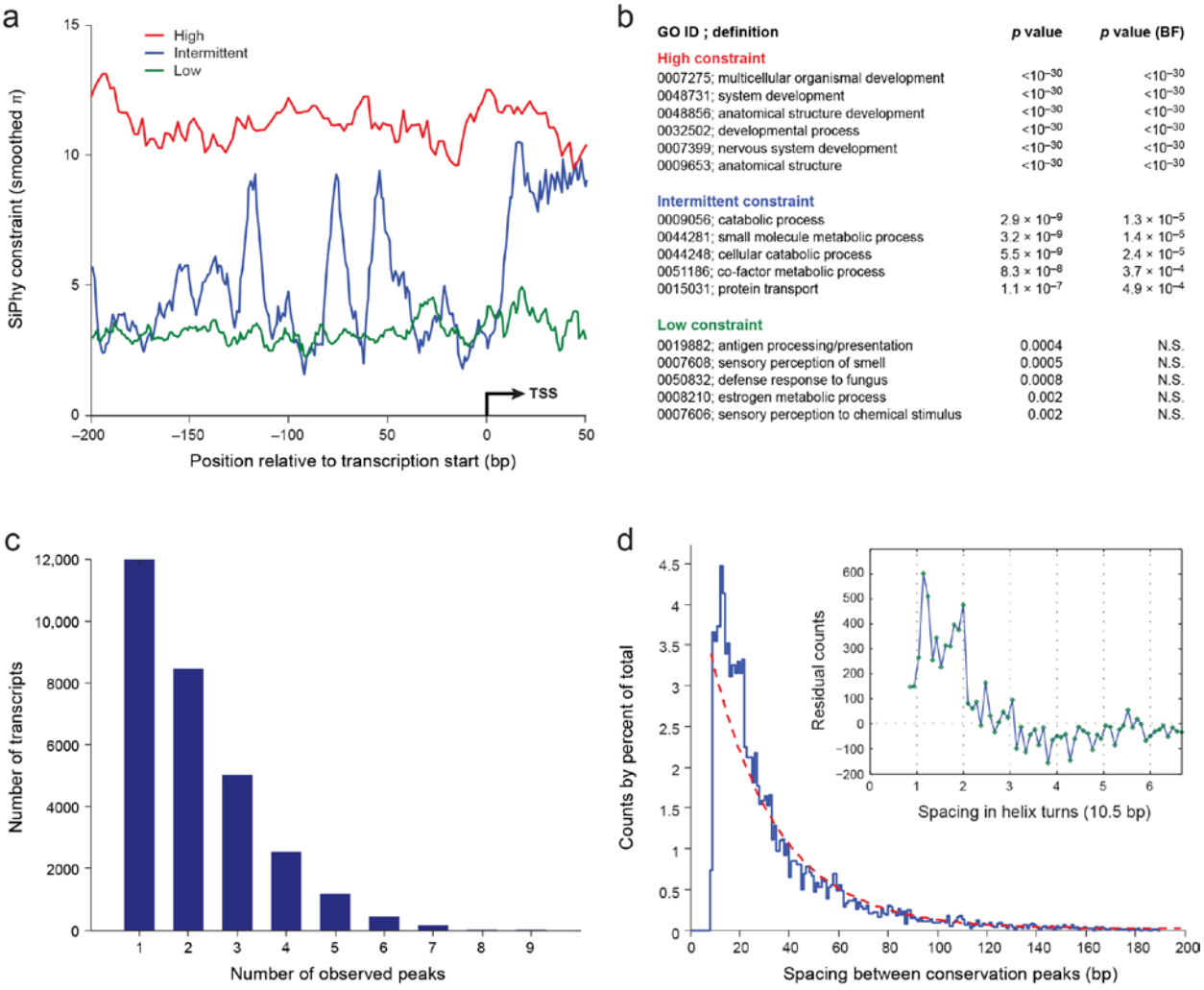
Supplementary Figure S8 - Examination of evolutionary signatures identifies novel genes, synonymous constrained elements, and candidate stop codon readthrough events. a, Protein-coding exon predictions based on evolutionary signatures suggest a new 95-codon protein-coding gene is encoded on the opposite strand of the first intron of *GTF2E2*. The predicted gene is additionally supported by two independent multi-exon transcripts predicted by Scripture based on the Illumina HiSeq Body Map 2[33]. **b,** Evolutionary signatures in the annotated 3' UTR of suppressor of actin 1 (*SACM1L*) suggest conserved stop codon readthrough. The 29 mammals show an overwhelming prevalence of synonymous and conservative substitutions in a short region immediately following the annotated stop codon, ending exactly at the next downstream stop codon, after which conservation markedly degrades. The region following the annotated stop codon contains no computationally-predicted or experimentally-supported splice acceptor sites, but includes a stable, conserved stem loop (shown) similar to the one implicated in readthrough of the Drosophila hdc gene. Parentheses on the alignment denote base pairing of the conserved RNA secondary structure prediction.



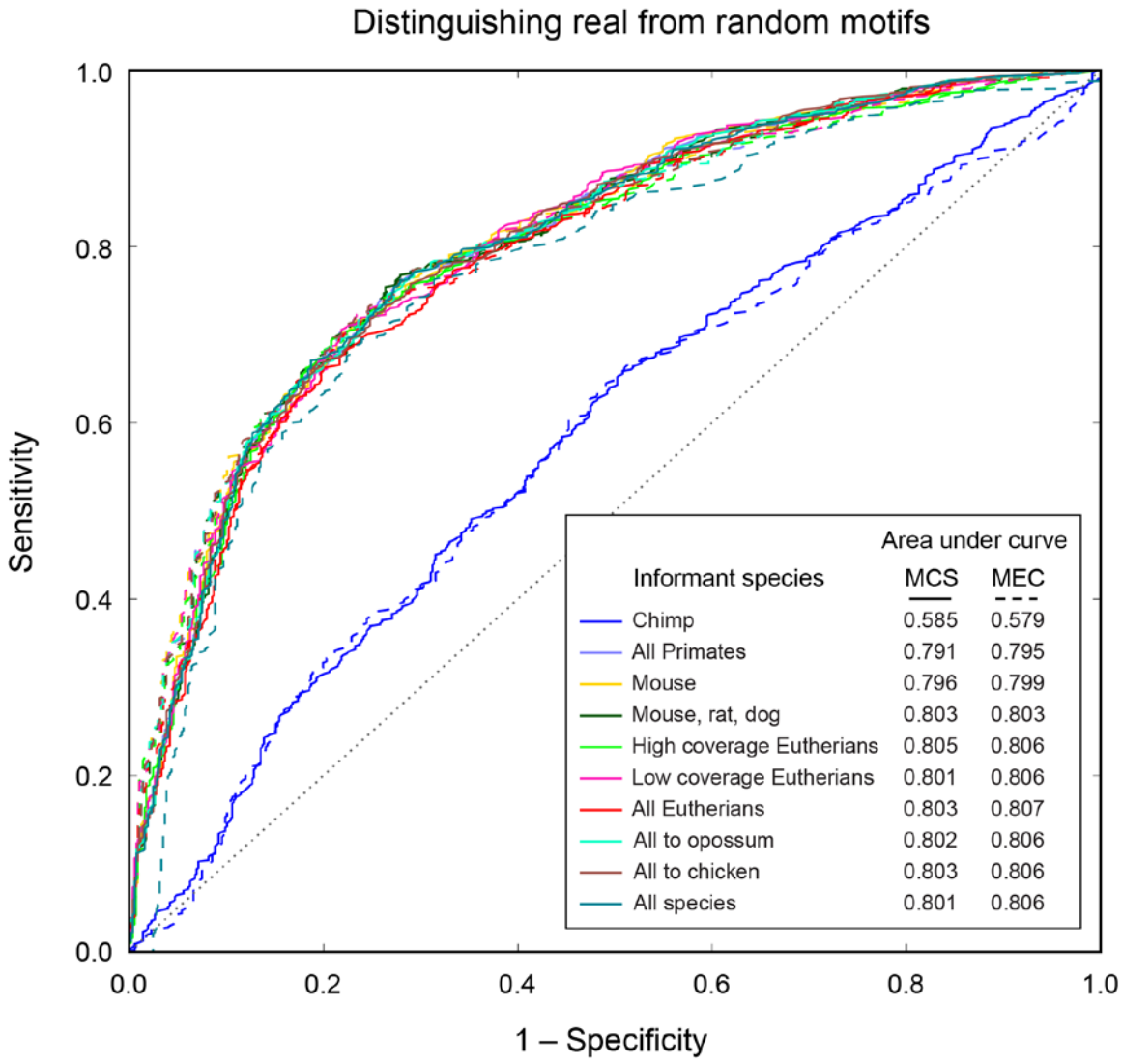
Supplementary Figure S9 - Over 200 families of potential RNA structural elements were identified. **a**, Summary and enrichment statistics for structural RNA predictions sets. **b**, Top: The RNA structure (green) is predicted on the *XIST* strand (purple) and overlaps short RNAs (blue) observed at high abundance in the chromatin cellular compartment. Bottom: base-level resolution showing secondary structure in parenthesis notation (black) and the demarcated expression of short RNAs (blue). **c**, Predicted secondary structure for one of six hairpins (hairpin D) in the 3'UTR of the *MAT2A* gene, responsible for the synthesis of S-adenosylmethionine (SAM), the primary methyl donor in human cells. **d**, The human sequences of all six hairpins were aligned using hairpin D as the reference. Insertions relative to D are shown with orange bars and numbers. Fully conserved positions (*) between the human sequences reveal the same loop region motif. **e** Multiple alignment across vertebrates for hairpin D. **f**, Secondary structure drawing of *XIST* structure with color-coding of substitution evidence (Black= Conserved paired nucleotide, grey= Conserved unpaired nucleotide; blue- Silent G • U_substitution; purple=Silent substitution in unpaired base, green =Silent base preserving substitution, Orange=Non-canonical double substitution, Red=Disruptive single substitution, Pink = Disruptive insertion or deletion). **g**, Family of hairpins in 3'UTR of the *MAT2A* gene, responsible for the synthesis of S-adenosylmethionine (SAM), the primary methyl donor in human cells. Purple=initial family members, dark green=family member after paralog search, light green=additional members found by dedicated additional paralog search, with P-values for substitution evidence in species not used for structure inference.



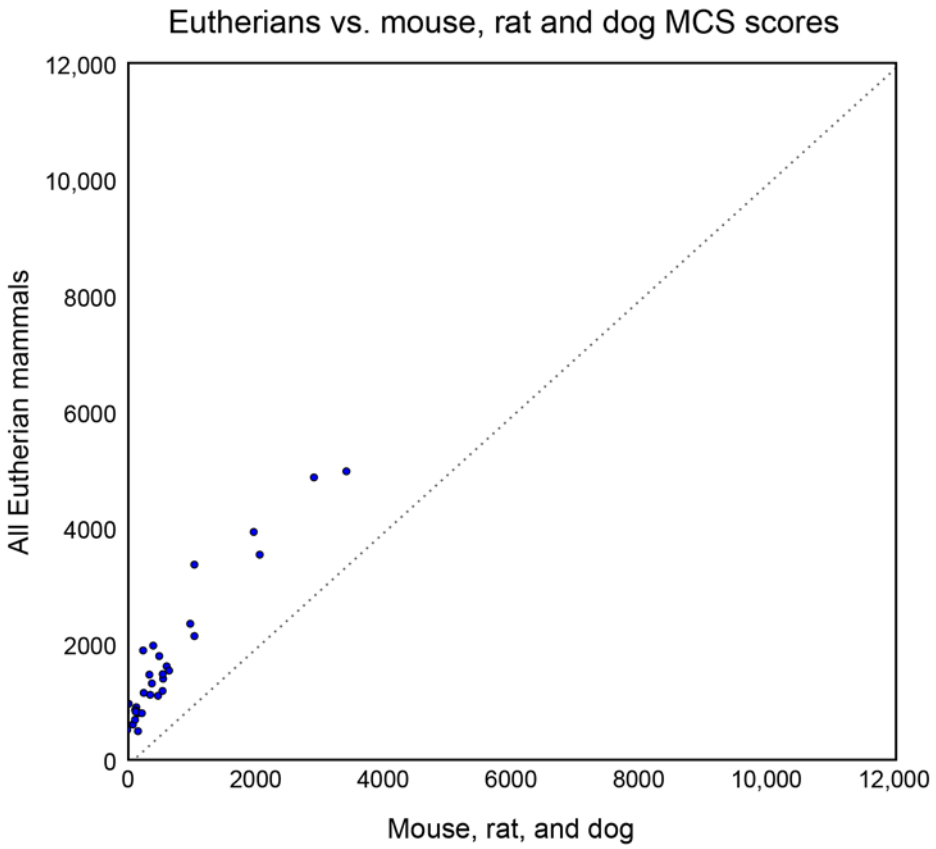
Supplementary Figure S10 - Thermodynamic analysis of EvoFold predictions using RNAz. Left: Cumulative stability z-score distribution for all EvoFold structures structures, structures clustered in families (before and after additional filtering), and positive and negative controls. More negative z-score indicate more stable RNA structures. Right: Fraction of structures predicted as "Functional RNA" by RNAz for the different sets.



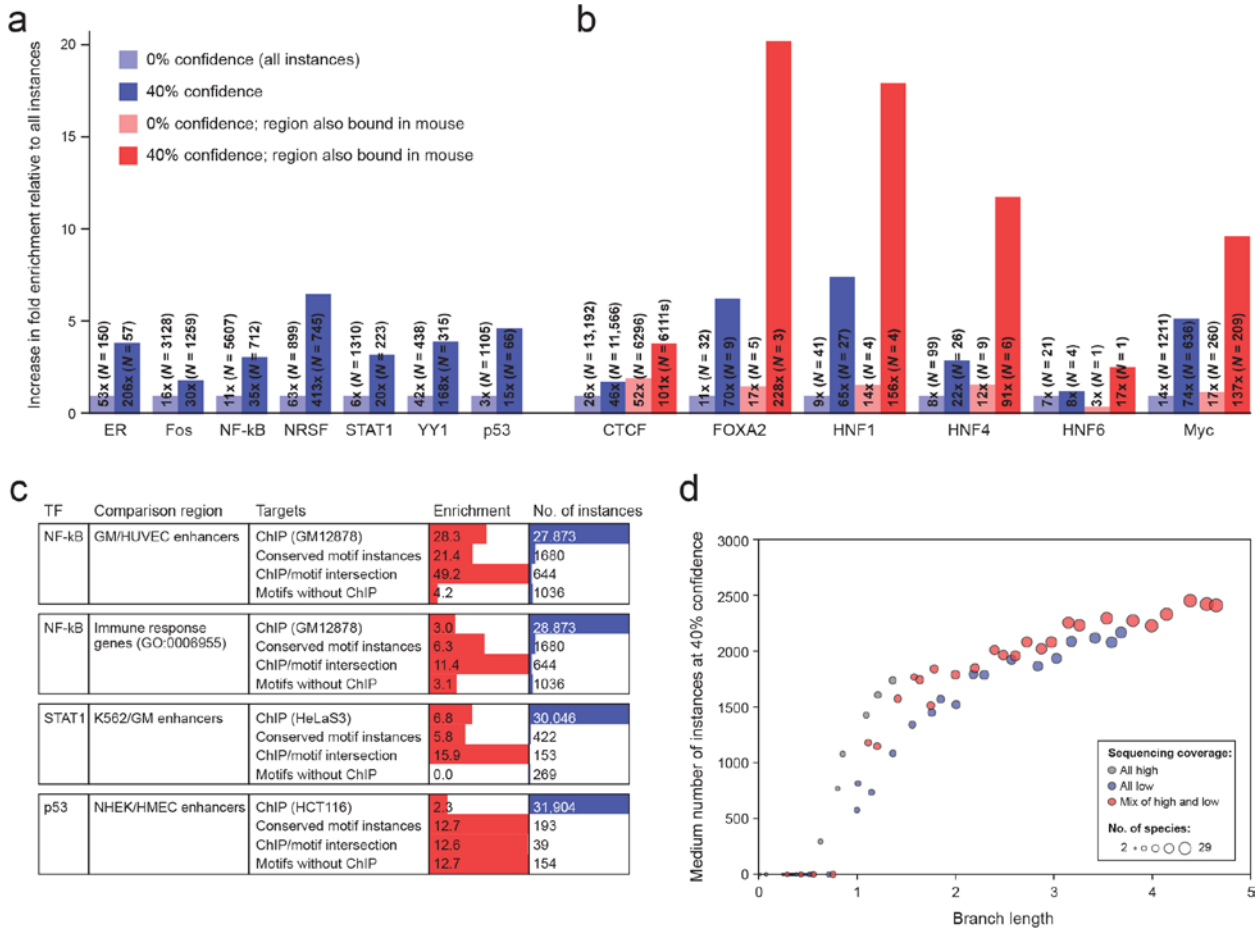
Supplementary Figure S11 - Differing constraint patterns are observed in core promoters. a, Analysis of promoters for 47,945 transcripts identified three patterns of high (red), intermittent (blue) and low (green) constraint. **b,** The different promoter types were enriched for different types of genes, with developmental genes significantly associated with high constraint, basic cell function and metabolic processes associated with intermittent constraint, and low constraint promoter overrepresented for sensory and immune response genes**. c,** The genes with intermittent constraint had between 1-9 peaks of constraint within the 200 bp core promoter. **d,** The spacing between constraint peaks varies between 9 and 200 bp, with a strong enrichment compared to an exponential distribution (cyan line), and local maxima at 12 and 21 bp distance between peaks (inset), corresponding to roughly one and two turns of the helix. Residual counts are obtained by subtracting the shown exponential from the spacing distribution curve.



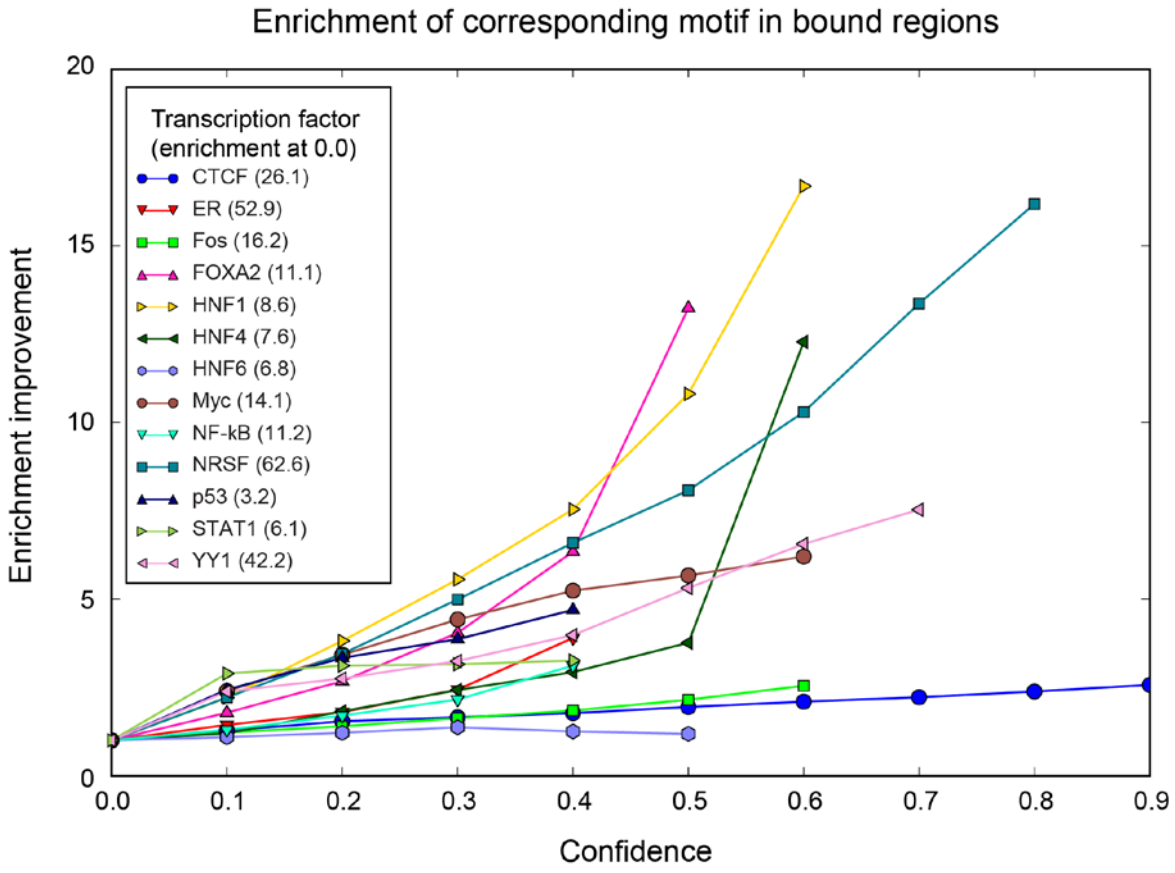
Supplementary Figure S12 - Limited number of species necessary to separate known and random motifs on the basis of conservation. ROC curves comparing different informant species subsets in identifying real motifs (contrasted to motif instances). Two methods are used to score motifs: MCS[54] in solid lines or MEC[55] in dashed lines. All motifs with at least two shuffles (N = 577) in the known motif database were scored genome-wide to show a preference for being conserved at the optimal branch length score (in terms of AUC) for each species subset. Additionally, shuffles of these motifs were scored using the same criterion. Using only mouse, rat, and dog as informant species performs essentially identically to using the entire Eutherian tree in separating the known and shuffled motifs. Indeed, even using just a single informant (mouse), has nearly equivalent performance. The two scoring schemes also distinguish between the two motif sets equally well. This demonstrates that at the number of instances and level of conservation seen for motifs in our database, motif discovery will likely not perform better when using motif conservation methods that employ a statistical conservation signal across the instances found genome-wide.



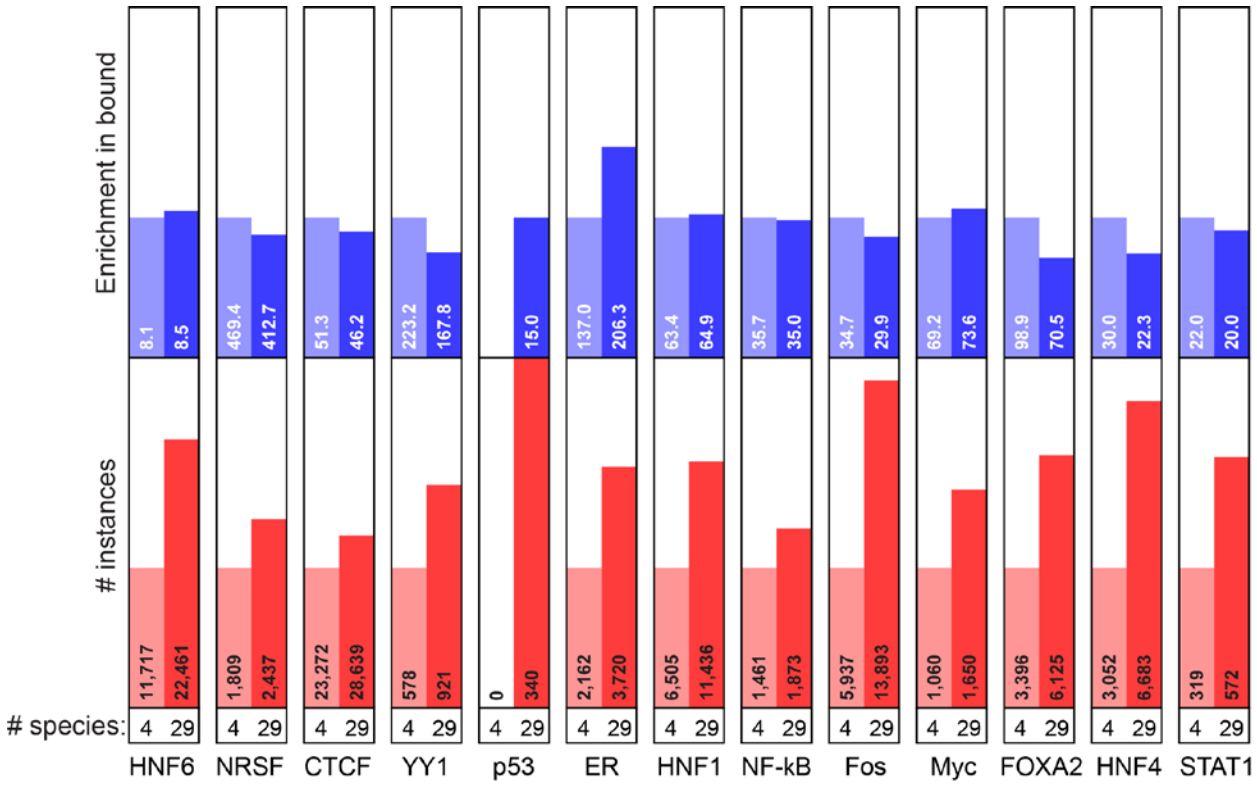
Supplementary Figure S13 - Motif conservation score (MCS) is strongly correlated when using the entire Eutherian tree or only mouse, rat and dog as informant species. A correlation of 0.99 is seen between the MCS scores on known motifs computed using all Eutherian informant species and when only using mouse, rat, and dog as informants. This extreme correlation fails to identify motifs that are better suited to be found with the larger Eutherian clade compared to the three species.



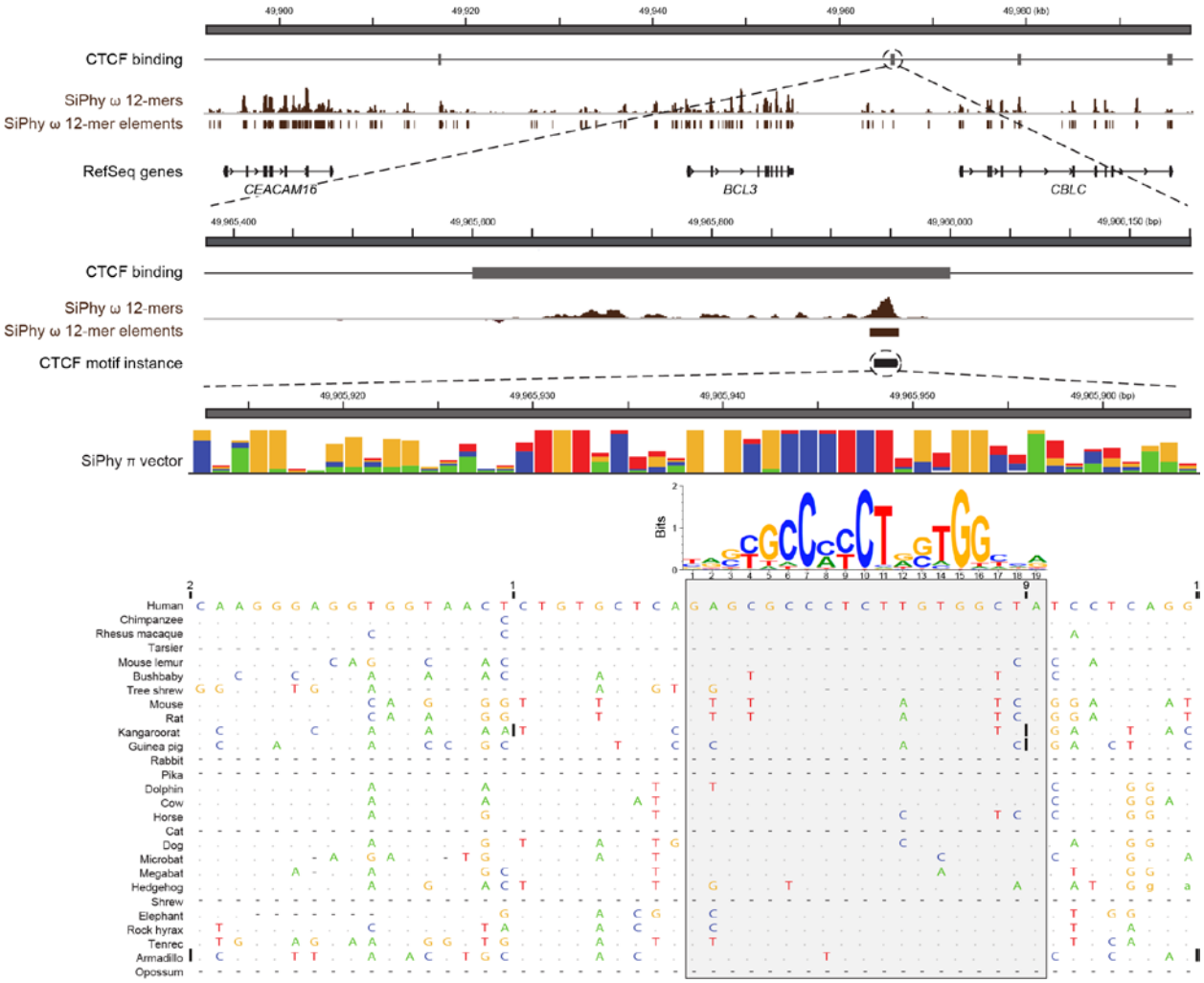
Supplementary Figure S14 - Regulatory motif instances associated with binding and putative functions. a, Enrichment of motifs in published experimental data sets. Known motifs for each factor show an enrichment in experimental data sets, which increases with conservation. **b,** Enrichment further increases for regions that are bound both in human and in the orthologous positions in mouse. **c,** Comparison of ChIP and conserved motif instances in identifying regions and genes likely to be bound by a factor. **d,** Scaling of motif instances using different species subsets. Comparison of high and low coverage species demonstrates the value of having low coverage species.



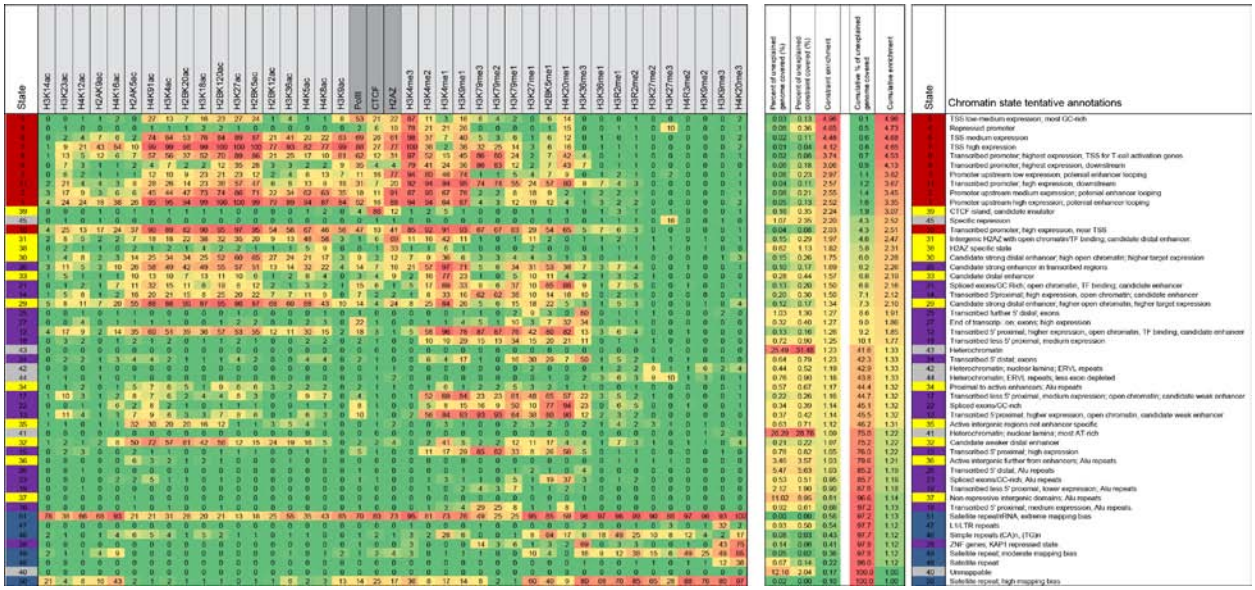
Supplementary Figure S15 - Increase in enrichment of motif instances across several factors. Motif enrichments are divided by enrichment at 0.0 confidence (i.e. all motif instances). Most factors show consistent and substantial increases in enrichment with increasing confidence. Considering only 0.0 and 0.4 confidence values leads to Supplementary Figure S12a.



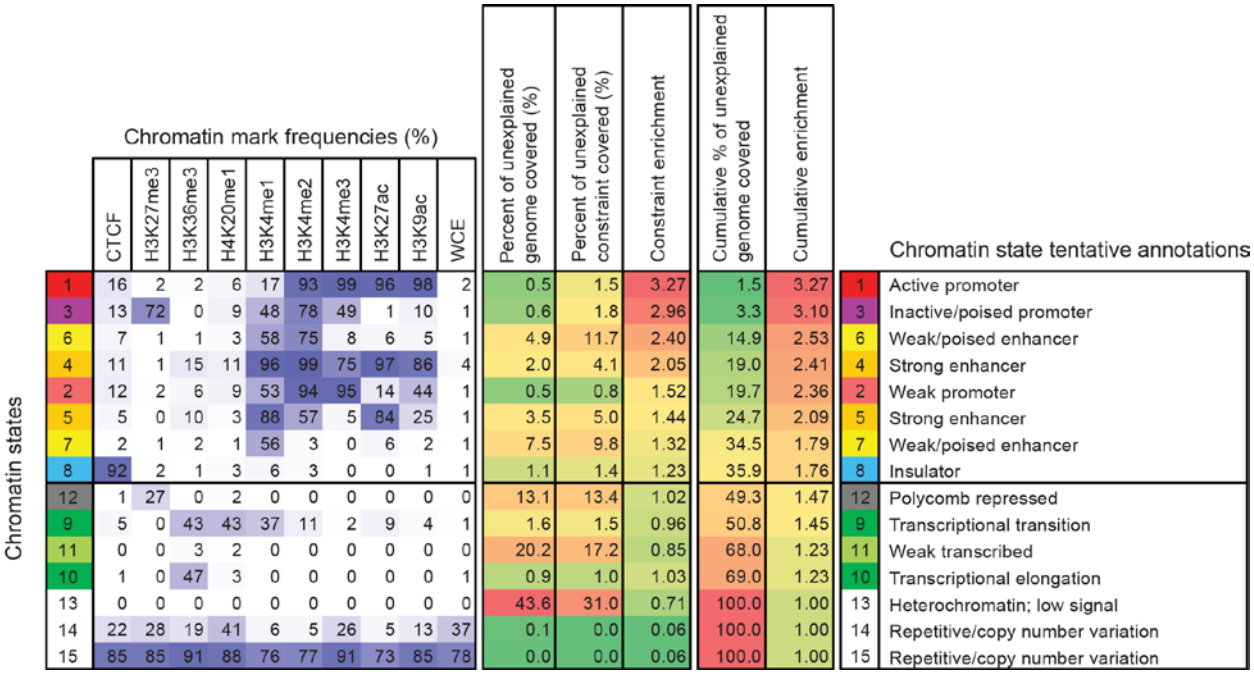
Supplementary Figure S16 - Comparison of number of motif instances and enrichment of motifs at 40% confidence using either 4 species (human, mouse, rat, and dog) or 29 species (all Eutherian mammals). The number of motif instances (shown in red bars; normalized height to 4 species number) always increases when going from 4 species to 29. Conversely, the enrichment (shown in blue bars) does not show a clear preference for either species. This is consistent with the expectation that motif instances be equally good regardless of the species subset used to identify them as long as their confidence level is the same.



Supplementary Figure S17 - Example of a constrained element with a region of CTCF binding between BCL3 and CBLC in the human genome. SiPhy rate indicates the level of constraint in overlapping 12-mers. A close-up of the constrained element shows overlap with a predicted CTCF site.



Supplementary Figure S18- Chromatin state conservation analysis for 41 marks in CD4 T cells. Each row of the table corresponds to a chromatin state[16]. The values in the matrix on the left correspond to the frequency with which the mark is considered detected at a 200 base pair resolution. The first three columns indicate for the non-masked portion of the genome, that is the 'unexplained portion of the genome', the total % of bases in each state, the % of constrained bases, and the enrichment for constrained bases. The states are ordered bases on the enrichment. The next two columns show the cumulative total % of constrained bases and the cumulative enrichment. Candidate annotations for the states from [16] are listed on the right.



Supplementary Figure S19 - Overlap of constraint bases with chromatin states. As much as 36% of unexplained constrained bases overlap chromatin states associated with candidate promoter, enhancer, or insulator states in at least one cell type among nine diverse cell lines. Reported enrichments were calculated after first excluding locations assigned to a higher listed state in one or more cell types.

Cumulative % of "unexplained" constrained bases covered

Chromatin State Tentative Annotations	state	9	8	7	6	5	4	3	2	1	0
Active promoter	1	0.05	0.09	0.14	0.19	0.25	0.32	0.45	0.66	1.51	100.00
Inactive/poised promoter	3	0.06	0.12	0.21	0.32	0.46	0.64	0.89	1.35	3.27	100.00
Weak/poised enhancer	6	0.06	0.13	0.24	0.41	0.67	1.15	2.17	4.92	14.92	100.00
Strong enhancer	4	0.12	0.27	0.52	0.91	1.53	2.55	4.32	8.06	18.98	100.00
Weak promoter	2	0.47	0.80	1.13	1.58	2.23	3.22	4.99	8.75	19.73	100.00
Strong enhancer	5	0.55	0.98	1.50	2.30	3.55	5.23	7.83	12.74	24.72	100.00
Weak/poised enhancer	7	0.67	1.28	2.15	3.44	5.40	8.03	11.89	18.82	34.54	100.00
Insulator	8	1.14	1.94	2.94	4.34	6.40	9.14	13.12	20.15	35.92	100.00
Polycomb repressed	12	1.74	3.27	5.12	7.55	10.94	15.48	21.76	31.48	49.29	100.00
Transcriptional transition	9	2.06	3.78	5.81	8.42	11.96	16.65	23.09	32.96	50.82	100.00
Weak transcribed	11	4.19	8.22	12.73	17.99	24.20	31.33	40.01	51.22	68.05	100.00
Transcriptional elongation	10	9.51	14.10	18.38	23.06	28.49	34.89	42.71	53.06	69.02	100.00
Heterochromatin; low signal	13	99.58	99.93	99.96	99.97	99.97	99.98	99.99	99.99	99.99	100.00
Repetitive/copy number variation	14	99.92	99.97	99.98	99.98	99.99	99.99	99.99	100.00	100.00	100.00
Repetitive/copy number variation	15	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00

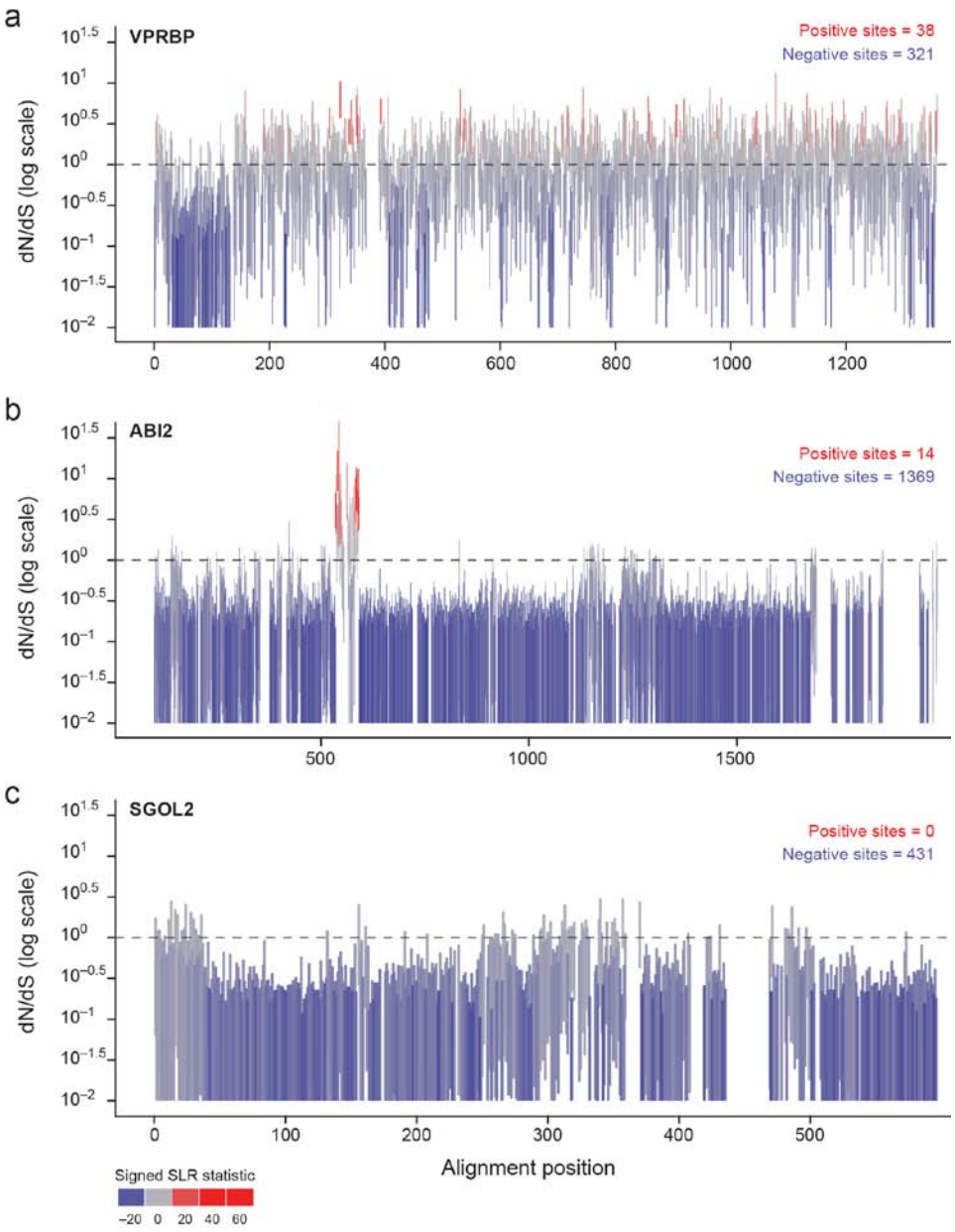
Cumulative % of "unexplained" genome bases covered

Chromatin State Tentative Annotations	state	9	8	7	6	5	4	3	2	1	0
Active promoter	1	0.01	0.02	0.03	0.04	0.05	0.07	0.10	0.15	0.46	100.00
Inactive/poised promoter	3	0.01	0.02	0.04	0.07	0.09	0.14	0.20	0.33	1.06	100.00
Weak/poised enhancer	6	0.01	0.03	0.05	0.09	0.17	0.30	0.61	1.54	5.91	100.00
Strong enhancer	4	0.02	0.06	0.11	0.21	0.37	0.65	1.20	2.57	7.88	100.00
Weak promoter	2	0.13	0.22	0.31	0.43	0.60	0.88	1.46	2.89	8.38	100.00
Strong enhancer	5	0.15	0.26	0.41	0.64	1.03	1.61	2.65	4.93	11.85	100.00
Weak/poised enhancer	7	0.18	0.36	0.63	1.08	1.84	2.97	4.88	8.81	19.31	100.00
Insulator	8	0.38	0.65	1.00	1.52	2.36	3.58	5.60	9.68	20.44	100.00
Polycomb repressed	12	0.55	1.06	1.79	2.94	4.74	7.45	11.68	18.86	33.51	100.00
Transcriptional transition	9	0.68	1.31	2.17	3.45	5.41	8.31	12.76	20.23	35.11	100.00
Weak transcribed	11	2.55	5.46	8.99	13.19	18.16	24.00	31.18	40.54	55.34	100.00
Transcriptional elongation	10	8.18	11.61	14.78	18.27	22.42	27.43	33.76	42.31	56.28	100.00
Heterochromatin; low signal	13	99.31	99.70	99.75	99.78	99.79	99.81	99.83	99.86	99.88	100.00
Repetitive/copy number variation	14	99.80	99.87	99.89	99.90	99.91	99.92	99.93	99.95	99.96	100.00
Repetitive/copy number variation	15	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00	100.00

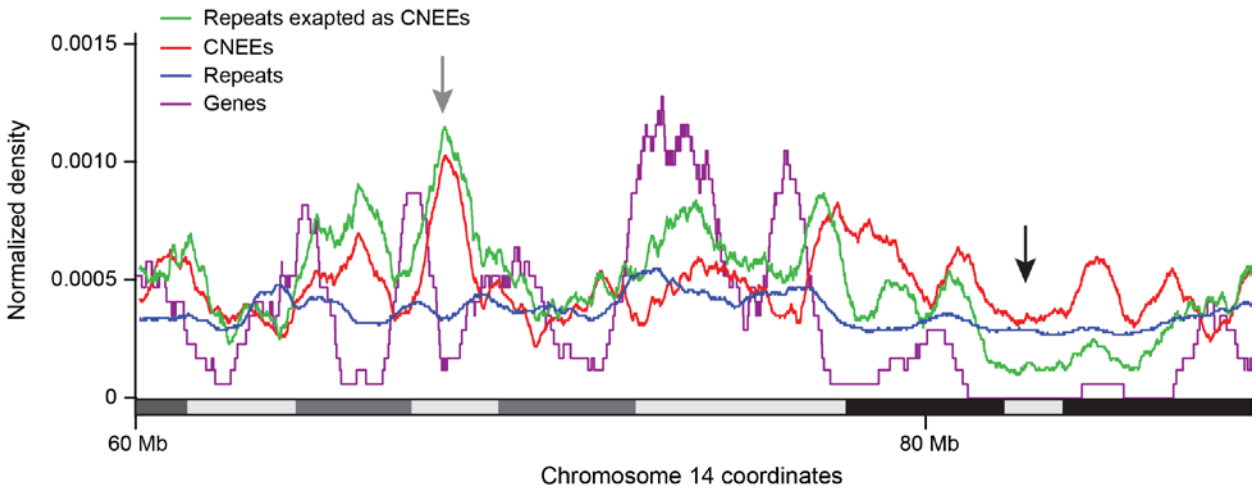
Cumulative enrichments in "unexplained" constrained elements

Chromatin State Tentative Annotations	state	9	8	7	6	5	4	3	2	1	0
Active promoter	1	5.42	5.02	5.00	4.92	4.79	4.62	4.59	4.31	3.27	1.00
Inactive/poised promoter	3	5.59	5.04	5.00	4.93	4.84	4.70	4.49	4.13	3.10	1.00
Weak/poised enhancer	6	5.51	4.92	4.73	4.46	4.07	3.79	3.53	3.20	2.53	1.00
Strong enhancer	4	5.02	4.68	4.53	4.35	4.12	3.89	3.59	3.14	2.41	1.00
Weak promoter	2	3.60	3.63	3.65	3.69	3.71	3.65	3.42	3.03	2.36	1.00
Strong enhancer	5	3.70	3.71	3.68	3.61	3.44	3.24	2.96	2.59	2.09	1.00
Weak/poised enhancer	7	3.73	3.60	3.42	3.18	2.93	2.71	2.44	2.14	1.79	1.00
Insulator	8	2.97	2.98	2.94	2.85	2.71	2.56	2.34	2.08	1.76	1.00
Polycomb repressed	12	3.18	3.09	2.85	2.57	2.31	2.08	1.86	1.67	1.47	1.00
Transcriptional transition	9	3.01	2.89	2.68	2.44	2.21	2.00	1.81	1.63	1.45	1.00
Weak transcribed	11	1.64	1.50	1.42	1.36	1.33	1.31	1.28	1.26	1.23	1.00
Transcriptional elongation	10	1.16	1.21	1.24	1.26	1.27	1.27	1.27	1.25	1.23	1.00
Heterochromatin; low signal	13	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Repetitive/copy number variation	14	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Repetitive/copy number variation	15	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00

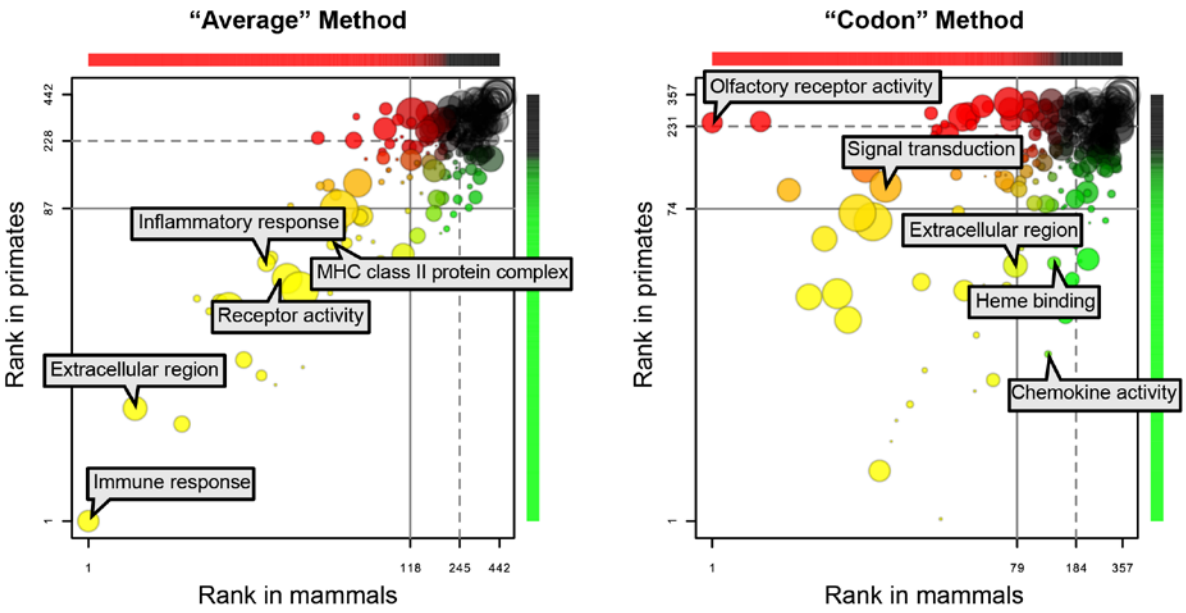
Supplementary Figure S20 - Chromatin state conservation analysis for varying numbers of cell types. The top grid indicates the cumulative total % of constrained bases in the unmasked, that is 'unexplained' portion of the genome, assigned to the state of the row or a higher listed state in that number of cell types of the column or more. The middle table is similar, but for all bases in the 'unexplained' portion of the genome. The last table gives the enrichment for constrained bases, that is the ratio of the values in the first table to the second table.



Supplementary Figure S21 - Positive selection acts uniformly for some genes and in a site-specific fashion for other genes. a, *VPRBP* shows a mixture of negative (purifying) and positive selection along its length, **b,** *ABI2* shows strong purifying selection with negatively-selected sites over most of the sequence and a localized region of positively-selected sites, **c,** *SGOL2* shows only purifying selection with negatively-selected sites over the entire gene. Each vertical bar covers the estimated 95% confidence interval for dN/dS at that site (with values of 0 truncated to 0.01 to accommodate the log scaling), and bars are colored according to a signed version of the SLR statistic for non-neutral evolution: blue for sites under negative selection, gray for sites under neutral evolution, and red for sites under positive selection. A dotted line is shown at neutral evolution (dN/dS=1) for reference, and the number of statistically significant sites under positive and negative selection (FDR<5%) is shown for each gene.



Supplementary Figure S22 - Exaptation of non-coding constrained elements is overrepresented near developmental genes and depleted in the middle of large gene deserts. Repeats exapted as CNEEs follow the density of all CNEEs, and not that of the repeat elements (grey arrow). The normalized density of CNEEs exapted from repeat elements (green) is shown compared to protein coding genes (purple), CNEEs (red), and repeats (blue). Densities are calculated as the number of elements within a 1 Mb window divided by the total number of elements in the genome. The trends in this section of chromosome 14 are representative of the genome as a whole. CNEEs exapted from repeats tend to be depleted in gene deserts larger than 1 Mb (black arrow).



Supplementary Figure S23 - GO enrichments for positively selected genes in primates versus mammals. GO term enrichments were calculated using the distributed positive selection (left) and localized positive selection (right) methods (see Methods). Each bubble represents one GO term, and its size is proportional to the log of the number of times the term was annotated in the gene "universe" (17,709 genes). Colors represent unadjusted p-values for enrichment in primates (red), mammals (green), both (yellow), or neither (black). The horizontal and vertical positions of the bubble correspond to the term's rank in mammals or primates, respectively, plotted on a log scale. Lines on each axis indicate ranks corresponding to p=0.05 (solid) and p=0.5 (dashed). Using the distributed positive selection method, statistical significance of enrichment is highly correlated in primates and mammals, suggesting that similar genes and pathways are under overall selection. In contrast, the localized positive selection method shows greater discordance between primates and mammals, indicating that different sets of genes show signals of selection at the single codon level in the two clades.

Supplemental Figure S24 - Rapid human evolution in the 5' UTR of FGF13. 2xHAR1 is a conserved non-coding element in the 5' UTR of the shortest FGF13 isoform that has evolved rapidly in humans since divergence from chimpanzee. Human-specific substitutions in 2xHAR1 could potentially have altered isoform-specific transcription. *Left:* Unrooted mammal phylogeny for 2xHAR1 with branch lengths proportional to the expected number of substitutions on each lineage, annotated in a bubble on each branch. *Center:* Length of the 2xHAR1 sequence for each species. *Right:* Multiple sequence alignment. Species with very few aligned bases are omitted. Insertions in non-human species are shown as yellow triangles with the number of inserted bases annotated. Human-specific substitutions* are marked in red (fixed differences) or orange (polymorphic substitutions). The five polymorphic sites suggest that the function of 2xHAR1 may still be in the process of diverging from its ancestral state and are potential candidates for BFLS (Borjeson-Forssman-Lehmann syndrome) and other disease associations in humans. Predicted transcription factor binding site turnover events are marked with lines above (losses) or below (gains) the human sequence, with line color denoting the JASPAR family: blue= nuclear receptor, green= bZIP cEBP-like, red= bHLH(zip), purple= HMG. Note that the number of red and orange bases (12) does not match the expected number of substitutions (14), because of insertions and deletions in the alignment that are not displayed.