

## **Supplementary Information for**

### **KDM4 Orchestrates Epigenomic Remodeling of Senescent Cells and Potentiates the Senescence-Associated Secretory Phenotype**

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## Supplementary Methods

### Reagents, plasmids and antibodies.

The pLenti-Puro, pLVX-IRES-Puro and pLKO.1-Puro plasmids were purchased from Addgene. Lentiviral vector pLKO.1-Puro was used to clone small hairpin RNAs (shRNAs): KDM4A shRNA1 (target sequence: GCACCGAGTTTGTCTTGAAAT); KDM4A shRNA2 (target sequence: TTCGAGAGTTCCGCAAGATAG); KDM4A shRNA3 (target sequence: TAGTGAAAGGACGAGCCATTT); KDM4B shRNA1 (target sequence: GCGGCAGACGTATGATGACAT); KDM4B shRNA2 (target sequence: GCGGCATAAGATGACCCTCAT); KDM4B shRNA3 (target sequence: GATGACCTTGAACGCAAATAC). KDM4A and SUV39H1 cDNAs were cloned to pLenti-Puro to generate expression constructs, while KDM4B and HA-SETD2-M cDNAs were cloned to pLVX-IRES-Puro respectively.

Antibodies relevant to this article were from commercial suppliers and used for immunoblotting, immunofluorescence staining, ChIP-seq, ChIP-PCR or immunohistochemistry at optimized concentrations (details listed in Supplementary Table 10).

### *In vitro* cell treatments and senescence appraisal.

Stromal cells were grown until 60%-80% confluent (CTRL) and treated with bleomycin (50 µg/ml, BLEO, MedChemExpress, cat. no. HY-17565), mitoxantrone (1 µM, MIT, Selleck, cat. no. S2485), doxorubicin (2 µM, DOXO, MedChemExpress, cat. no. HY-15142), cisplatin (10 µM, CIS, MedChemExpress, cat. no. HY-17565), carboplatin (20 µM, CARB, MedChemExpress, cat. no. HY-17393), satraplatin (20 µM, SAT, MedChemExpress, cat. no. HY-17576), docetaxel (100 nM, DTX, TOCRIS, cat. no. 4056), paclitaxel (100 nM, PTX, MedChemExpress, cat. no. HY-B0015), vincristine (50 nM, VCR, Selleck, cat. no. S1241) for 12 h. After treatment, the cells were rinsed twice with PBS and allowed to stay for 7-10 d in media.

Oncogenic HRAS<sup>G12V</sup>-transduced cells were selected by puromycin for 3 d and allowed to stay for 7-10 d in media. Alternatively, the cells were allowed to passage consecutively for replicative exhaustion. SA- $\beta$ -Gal staining assay was performed with a commercial kit (Beyotime) to examine cellular senescence. For cell cycle arrest, a single pulse of BrdU (10  $\mu$ M, Yeasen) was performed for 24 h and cells were subject to immunofluorescence staining with an anti-BrdU antibody (1:400 dilution, Cell Signaling, cat no. 5292) before counterstained with DAPI and assessed by fluorescence microscopy. Alternatively, cells were exposed to ML324 (20  $\mu$ M, MedChemExpress, cat. no. HY-12725), Bay 11-7082 (2  $\mu$ M, Selleckchem, cat. no., S2913) or Chaetocin (10 nM, Selleckchem, cat. no. S8068), either alone or alongside other agents for specific assays.

DNA-damage extent was evaluated by immunostaining for  $\gamma$ H2AX (primary dilution 1:500) or p53-BP1 (primary dilution 1:500) foci by following a 4-category counting strategy as formerly reported <sup>1</sup>. Random fields were chosen to show DDR foci, and quantified using CellProfiler (<http://www.cellprofiler.org>). For clonogenic assays, cells were seeded at  $1 \times 10^3$  cells/dish in 10mm dishes for 24 h before treated with chemicals. Cells were fixed with 2% paraformaldehyde 7-10 d post treatment, gently washed with PBS and stained instantly with 10% crystal violet prepared in 50% methanol. Excess dye was removed with PBS, with plates photographed. Colony formation were evaluated by quantifying the number of single colonies per dish.

### **Quantitative RT-PCR.**

Quantitative RT-PCR (qRT-PCR) was performed after RNA extraction using TRIzol (Thermo Fisher). RNA expression was determined with Universal SYBR Green Two-step kit (Yeasen) on a QuantStudio 7 Real-Time PCR System (Thermo). For normalization of human gene expression, *RPL13A* was used as an internal control, and the fold change was calculated using the  $2^{-\Delta\Delta C(t)}$  method for all analyses (primer sequences listed in Supplementary Table 11).

### **Immunoblotting and immunofluorescence.**

Proteins were separated using NuPAGE 4 to 12% Bis-Tris gels and transferred onto nitrocellulose membranes (Life Technologies). The blots were blocked with 5% nonfat dry milk at room temperature for 1 h and incubated overnight at 4°C with desired primary antibodies at concentration per the manufacturer's protocol, followed by incubation with horseradish peroxidase-conjugated secondary antibodies (Santa Cruz) at room temperature for 1 h. The membrane blots were developed with enhanced chemiluminescence (ECL) detection reagent (Millipore) per the manufacturer's protocol and detected through chemiluminescence using ImageQuant LAS 400 Phospho-Imager (GE Healthcare). As a standard protein marker, we used Thermo Fisher Scientific PageRuler Plus Prestained Protein Ladder (no. 26619).

For immunofluorescence staining, cells were cultured in dishes and pre-seeded for at least 24 h on coverslips. Upon brief washing, cells were fixed with 4% paraformaldehyde in PBS for 8 min, blocked with 5% normal goat serum (NGS, Thermo Fisher) for 30 min and incubated with primary antibodies diluted in PBS containing 5% NGS for 2 h at room temperature. Alexa Fluor 488 or 594-conjugated secondary antibodies (Invitrogen, 1:400) were used. Nuclei were stained with Hoechst 33342, with slides mounted with Vectashield medium. Fluorescence imaging was performed on a fluorescence microscope (Nikon Eclipse Ti S). Captured images were analyzed and processed with the Nikon DS-Ri2 fluorescence workstation and processed with NIS-Elements F4.30.01. Alternatively, a confocal microscope (Zeiss LSM 780) was applied to acquire confocal images (antibodies used for this study listed in Supplementary Table 10).

### **Chromatin fractionation and nuclear protein extraction.**

To assess the levels of KDM4 family members at the chromatin-bound fraction, CTRL and BLEO-treated PSC27 cells were cross-linked with 1% formaldehyde for 5 min and quenched with 0.125 M glycine; then, cells were washed thrice



with 1 × PBS, and incubated with buffer A (10 mM HEPES, pH 7.9, 10 mM KCl, 1.5 mM MgCl<sub>2</sub>, 10% glycerol, 0.34 M Sucrose, 1 mM DTT, 0.1% Triton, PMSF, and protease inhibitor mixture) for 10 min at 4 °C. The cell lysates were centrifuged at 1,500 × g for 5 min at 4 °C, with supernatants removed. Pellets were resuspended in buffer B (3 mM EDTA, 0.2 mM EGTA, 1 mM DTT, PMSF, and protease inhibitor mixture) and incubated on ice for 10 min before centrifugation at 1,700 × g for 5 min at 4 °C. To prepare the chromatin-bound fraction, the pellets were incubated for 30 min at 37 °C with buffer A containing 1 mM CaCl<sub>2</sub> and 0.6 unit of MNase and centrifuged at 20,000 × g for 10 min at 4 °C, and the supernatant was collected and subjected to immunoblot analysis. For nuclear protein preparation, a Minute™ Cytoplasmic and Nuclear Extraction Kit (Invent Biotechnologies, Inc. # sc-003) was used by following the manufacturer' procedure.

#### **Stromal cell clonogenic assay.**

PSC27 cells were trypsinized and counted with a hemocytometer. Two milliliters of DMEM full medium containing 500 cells were plated in each well of the six-well plates. The cells were maintained at 37 °C for 7 d to allow colony formation before stained with 0.5% crystal violet (Sigma-Aldrich) in absolute methanol. Colonies per well were counted and numbers were recorded from 3 independent experiments.

#### **Cancer cell phenotype appraisal.**

Epithelial cell proliferation was determined following the MTT procedure (Promega). Migration and invasion were assessed in culture using Transwells (Cultrex 24-well Cell Migration Assay plates) containing a porous (8 μm pore size) membrane uncoated (for the migration assay) or coated (for the invasion assay) with a 0.5 × solution of basement membrane extract and the indicated CM in the bottom portion of the well. After 24 h, migrating or invading cells on the bottom side of the porous membranes were stained and quantified by

absorbance as recommended by the supplier.

### **Histology and immunohistochemistry.**

Mouse tissue specimens were fixed overnight in 10% neutral-buffered formalin and processed for paraffin embedding. Standard staining with hematoxylin/eosin was performed on sections of 5-8  $\mu\text{m}$  thickness processed from each specimen block. For immunohistochemistry, tissue sections were deparaffinized and incubated in citrate buffer at 95 °C for 40 min for antigen retrieval before incubated with the indicated antibodies (for instance, anti-cleaved Caspase 3, 1:1000) overnight at 4 °C. After 3 washes with PBS, tissue sections were incubated with biotinylated anti-mouse IgG (1:200 dilution, Vector Laboratories) for 1 h at room temperature then washed thrice, after which streptavidin-horseradish peroxidase conjugates (Vector Laboratories, CA, USA) were added and the slides incubated for 45 min. DAB solution (Vector Laboratories) was then added and the slides were counterstained with haematoxylin.

### **SILAC sample preparation.**

PSC27 cells were grown to 80% confluence in high glucose (4.5 g/L) DMEM media (with glutamine and sodium pyruvate) containing 10% FBS and 1% penicillin/streptomycin at 37 °C with 95% air and 5% CO<sub>2</sub>. Cells were either labeled with “heavy isotopic lysine” (<sup>13</sup>C-lysine) or “light isotopic lysine” (<sup>12</sup>C-lysine/arginine) using a SILAC protein quantitation kit (Pierce, Thermo) according to manufacturer’s instructions. Briefly, cells in the control group were labeled with L-<sup>13</sup>C<sub>6</sub>-Lysine/L-<sup>13</sup>C<sub>6</sub><sup>15</sup>N<sub>4</sub>-Arginine as “heavy” class, while those in the experimental group were labeled with L-Lysine/L-Arginine as “light” class. In each case, cells were cultured for more than 6 generations before being harvested. At least 1 passage prior to the experiment, incorporation efficiency of the heavy labeled amino acids into proteins was assessed in a pilot experiment, where a small aliquot of intracellular protein was lysed, reduced,

alkylated, and trypsin digested and subjected to mass spectrometric (MS) analysis as described below. Heavy label incorporation into proteins from control (non-senescent) cells was assessed as > 99%.

For the proteomics, 24 h before harvesting, plated cells (approximately  $5 \times 10^8$  in fifteen 150 cm<sup>2</sup> flasks) were washed thrice with fresh FBS-free medium for 10 min at 37°C each. The cells were then incubated in FBS-free medium (12 ml per flask) for 24 h at 37°C. At the end of the culture period, cells showed no evidence of apoptosis. Samples were prepared for MS analysis including removal of phenol red dye by buffer exchange with 50 mM Tris-Cl (pH8.0) (5 washing steps using spin columns at 5000 × g). Samples were denatured with 6M urea, reduced with 20mM DTT (30 min at 37°C), alkylated with 50 mM iodoacetamide (30 min at RT), and digested overnight at 37°C with 1:50 enzyme:substrate ratio (wt/wt) of sequencing grade trypsin (Promega, Madison, WI) as described<sup>2</sup>. Following digestion, samples were acidified with formic acid and desalted using HLB Oasis SPE cartridges (Waters, Milford, MA). Protein/peptide recovery was not specifically assessed, however, the above sample preparation and digestion protocol was thoroughly assessed for reproducibility during previous optimization and reproducibility studies. Hydrophilic Interaction Liquid Chromatography (HILIC) peptide fractionation was performed on a Waters 1525 HPLC system equipped with a 4.6 × 25 mm TSK gel Amide-80 HR 5 mm column (Tosoh Bioscience, South San Francisco, CA). Samples were loaded in 80% solvent B (98% acetonitrile, 0.1% TFA) and eluted with the following gradient: 80% B for 5 min followed by 80% B to 60% B in 40 min, 0% B in 5 min at 0.5 ml/min. Solvent A consisted of 98% HPLC grade water and 0.1% TFA collecting nine fractions.

### **Mass spectrometry.**

Samples were analyzed by reverse-phase HPLC-ESI-MS/MS using an

Eksigent Ultra Plus nano-LC 2D HPLC system (Dublin, CA) connected to a quadrupole time-of-flight TripleTOF 5600 (QqTOF) mass spectrometer (SCIEX). Typically, mass resolution for MS1 scans and corresponding precursor ions was ~35,000 (TripleTOF 5600), while resolution for MS/MS scans and resulting fragmentations (MRM-HR transitions) was ~15,000 ('high sensitivity' product ion scan mode)<sup>3</sup>. Briefly, after injection, peptide mixtures were transferred onto the analytical C18-nanocapillary HPLC column (C18 Acclaim PepMap100, 75 mm I.D. × 15 cm, 3 mm particle size, 100Å pore size, Dionex, Sunnyvale, CA) and eluted at a flow rate of 300 nl/min using stepwise gradients from 5% to 80% solvent B with total runtimes, including mobile phase equilibration, of 90 min. Solvent mobile phase A was 2% acetonitrile/98% of 0.1% formic acid (v/v) in water, and mobile phase B was 98% acetonitrile/2% of 0.1% formic acid (v/v) in water. Data acquisition was performed in data dependent acquisition (DDA) mode on the TripleTOF 5600 to obtain MS/MS spectra for the 30 most abundant precursor ions (50 msec per MS/MS) following each survey MS1 scan (250 msec), yielding a total cycle time of 1.8 s as described<sup>3,4</sup>.

### **Bioinformatics database searches and SILAC quantification.**

MS data were searched using the database search engine ProteinPilot (SCIEX Beta 4.5, revision 1656) with the Paragon algorithm (4.5.0.0, 1654). The search parameters were set as follows: trypsin digestion, cysteine alkylation set to iodoacetamide, SILAC Quantification (Lys-6, Arg-6, no bias correction), and Homo sapiens as species. Trypsin specificity was assumed as C-terminal cleavage at lysine and arginine. Processing parameters were set to "Biological modification" and a thorough ID search effort was used. During the search, Protein Pilot performs an automatic mass recalibration of the datasets based on highly confident peptide spectra. Specifically, a first search iteration was done to select high confidence peptide identifications to recalibrate both the MS and MS/MS data, which was subsequently automatically re-searched. During the iterative steps of re-searching the data, the search parameters were less

stringent, e.g., allowing for additional 'missed cleavages' (with typically not more than 2).

All data files were searched using the SwissProt (2014-01, released January 22, 2014), with a total of 40,464 human 'reviewed' protein sequences searched. A cut-off peptide confidence value of 99 was chosen, and a minimum of 2 identified peptides per protein was required. The Protein Pilot false discovery rate (FDR) analysis tool, the Proteomics System Performance Evaluation Pipeline (PSPEP algorithm) provided a global FDR of 1% and a local FDR at 1% in all cases. For protein quantification comparing samples of senescent (light) *versus* presenescent (heavy) cells a Protein Pilot significance threshold of < 0.05 was required (all database search results and details for peptide identifications and protein quantification are provided in Supplementary Tables 1-3).

### **RNA-seq and data profiling.**

Total RNA samples were obtained from stromal cells. Sample quality was validated by Bioanalyzer 2100 (Agilent), and RNA was subjected to sequencing by Illumina HiSeq X10 with gene expression levels quantified by the software package RSEM (<https://deweylab.github.io/RSEM/>). Briefly, rRNAs in the RNA samples were eliminated using the RiboMinus Eukaryote kit (Qiagen, Valencia, CA, USA), and strand-specific RNA-seq libraries were constructed using the TruSeq Stranded Total RNA preparation kits (Illumina, San Diego, CA, USA) according to the manufacturer's instructions before deep sequencing.

Paired-end transcriptomic reads were mapped to the reference genome (GRCh38/hg38) with reference annotation from Gencode v27 using the Bowtie tool. Duplicate reads were identified using the picard tools (1.98) script mark duplicates (<https://github.com/broadinstitute/picard>) and only non-duplicate reads were retained. Reference splice junctions were provided by a reference transcriptome (Ensembl build 73). FPKM values were calculated using Cufflinks, with differential gene expression called by the Cuffdiff maximum-likelihood

estimate function. Genes of significantly changed expression were defined by a false discovery rate (FDR)-corrected  $P$  value  $< 0.05$ . Only ensembl genes 73 of status “known” and biotype “coding” were used for downstream analysis.

Reads were trimmed using Trim Galore (v0.3.0) ([http://www.bioinformatics.babraham.ac.uk/projects/trim\\_galore/](http://www.bioinformatics.babraham.ac.uk/projects/trim_galore/)) and quality assessed using FastQC (v0.10.0) (<http://www.bioinformatics.bbsrc.ac.uk/projects/fastqc/>). Differentially expressed genes were subsequently analyzed for enrichment of biological themes using the DAVID bioinformatics platform (<https://david.ncifcrf.gov/>), the Ingenuity Pathways Analysis (IPA) program (<http://www.ingenuity.com/index.html>). Raw data were preliminarily analyzed on the free online platform of Majorbio I-Sanger Cloud Platform ([www.i-sanger.com](http://www.i-sanger.com)), and subsequently deposited in the NCBI Gene Expression Omnibus (GEO) database under the accession code GSE128282.

### ***Venn diagrams***

Venn diagrams and associated empirical  $P$ -values were generated using the USeq (v7.1.2) tool IntersectLists<sup>3</sup>. The  $t$ -value used was 22,008, as the total number of genes of status “known” and biotype “coding” in ensembl genes 73. The number of iterations used was 1,000.

### ***RNA-seq heatmaps***

For each gene, the FPKM value was calculated based on aligned reads, using Cufflinks. Z-scores were generated from FPKMs. Hierarchical clustering was performed using the R package heatmap.2 and the `distfun = “pearson”` and `hclustfun = “average”`.

### ***Protein–protein interaction network***

Protein-protein interaction (PPI) analysis was performed with STRING 3.0. The specific proteins meeting the criteria, were imported to NetworkAnalyst (<http://www.networkanalyst.ca>). A minimum interaction network was chosen for further hub and module analysis.

### **Gene set enrichment analysis (GSEA) of RNA-seq data.**

For each differential expression analysis comparison, genes were ranked using “wald statistics” obtained from DESeq2 and GSEA was performed on these ranked lists on all curated gene sets available in MSigDB (<http://software.broadinstitute.org/gsea/msigdb>). DESeq2 independent filtering is based on mean of normalized read counts and filters out genes with very low expression level. The SASP and GSEA signatures were derived as described before <sup>5</sup>.

### **ChIP-seq and ChIP-PCR.**

ChIP experiments were performed as described previously <sup>6</sup> and ChIP-seq libraries were generated using NEBNext Ultra II DNA library preparation kit for Illumina according to the manufacturer’s protocol. Briefly, stromal cells were grown to ~80% confluence before crosslinked in 1% formaldehyde for 10 min at room temperature. Crosslinking was quenched by addition of glycine to a final concentration of 0.15 M for 5 min at room temperature, with crosslinked cells washed with ice-cold PBS, supernatant discarded, pellets flash-frozen in liquid nitrogen and stored at -80 °C. For each sample, 20 million fixed cells were lysed to prepare nuclear extracts. After chromatin shearing by sonication, lysates were incubated overnight at 4°C with protein A Dynabeads (Invitrogen) coupled with 5 µg of antibody. After immunoprecipitation, beads were recovered using a magnet and washed, with DNA eluted, cross-links reverted at 65°C for 4 hours then purified with Qiagen Kit. DNA was quantitated using the Qubit dsDNA HS assay and a Qubit 3.0 Fluorimeter (Invitrogen). For ChIP-seq, 5 ng of purified ChIP DNA were used to generate the sequencing library using the NEBNext ChIP-seq Library Prep Master Mix Set using modified Illumina TruSeq adaptors, and sequenced with Illumina Nova Seq 6000.

ChIP-seq data analyses were performed by DIATRE Biotechnology (Shanghai, China). Adapter sequences of ChIP-seq raw reads are removed by using cutadapt (<https://doi.org/10.14806/ej.17.1.200>). Trimmed reads are

aligned by bowtie2 using default parameters to human genome (hg38). The samtools <sup>7</sup> and picard (<http://broadinstitute.github.io/picard>) were used to sort and remove duplicated reads to avoid PCR bias from the sequencing process. Each group of libraries after the above pre-processing is down-sampled (without replacement) to a fixed number of reads. Peak calling (identification of regions of ChIP-seq enrichment over background) was performed using MACS2 with parameters of “-extsize=146-nomodel”, while the sonicated input served as a control and an initial threshold q-value of 0.01 was used as cutoff. The “broad peak” option is on when identifying binding regions of H3K9me3 and H3K36me3. Visualization of read count data was performed by converting raw bam files to bigwig files using IGV tools <sup>8</sup>. BETA or ChIP seeker was used to analyze expression data and binding data. Basic characteristics and QC of ChIP-seq libraries are available in Supplementary Tables 12-15.

Chromosomal positions were annotated according to the RefSeq database. In our annotation, a TSS region was defined as  $\pm 1$  kb relative to the TSS. For density plots, we generated bigwig files allowing only one read per chromosomal position, eliminating potential spurious spikes. Each remaining read was extended from its 5' end to a total length of 250 bases. Each bigwig file was also scaled to TPM (tags per million) based on the number of unique read positions. For density plots, the regions of  $\pm 5$  kb for all annotated TSSs were divided into 100 equal-sized bins. All peaks with FDR greater than 5% were excluded from further analysis, with uniquely mapped reads used to generate the genome-wide intensity profiles. HOMER was employed to annotate peaks, to calculate overlaps between different peak files, and for motif searches. The genomic features (promoter, TSS, TES, exon, intron, 5' UTR, 3' UTR, and intergenic regions) were defined and calculated using Refseq and HOMER.

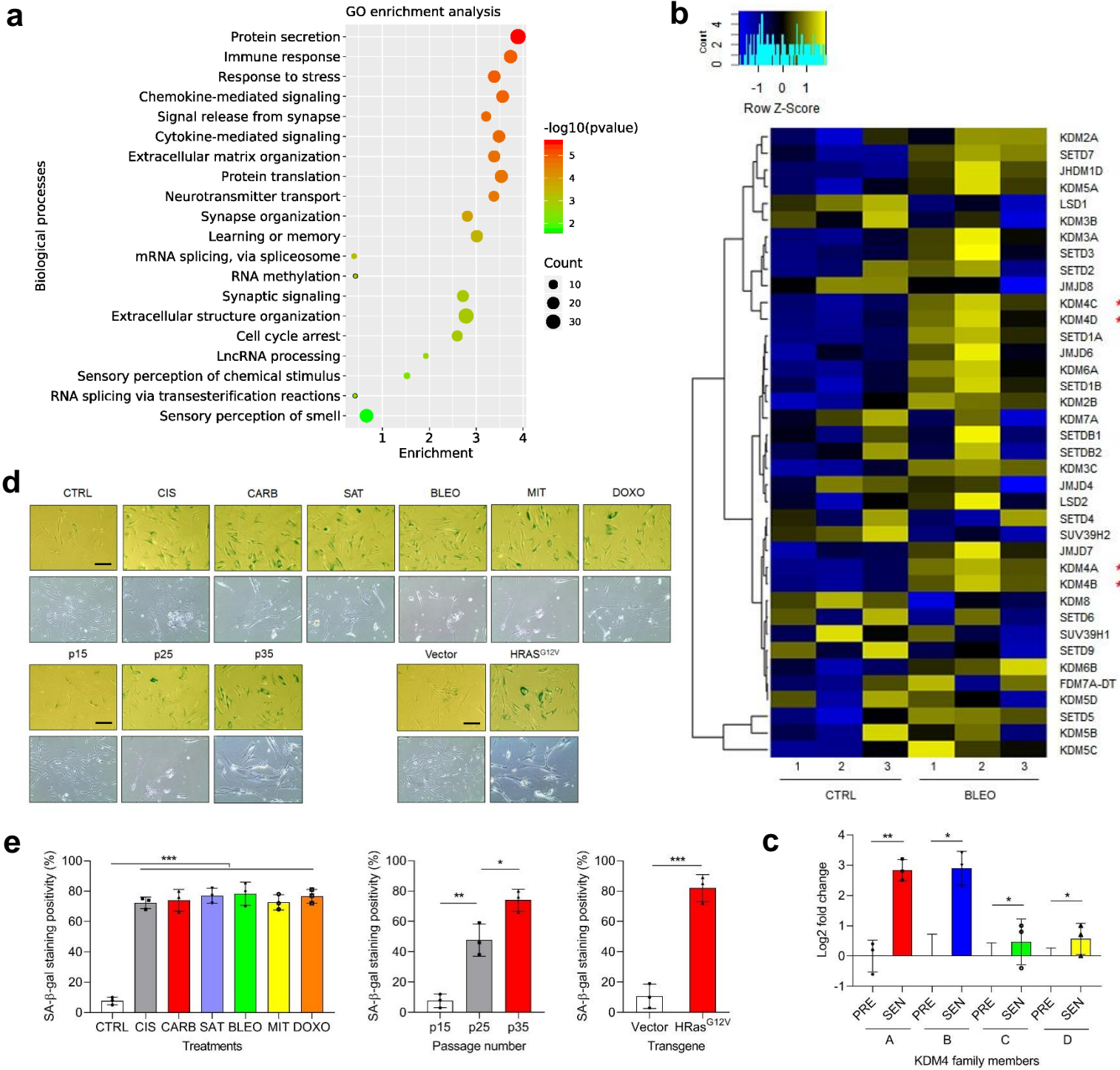
For ChIP-PCR,  $10^7$  cells were used per immunoprecipitation. The protein-chromatin complexes were purified by immunoaffinity captured by magnetic beads (Thermo Fisher Scientific), with the enriched DNA subjected to qPCR.



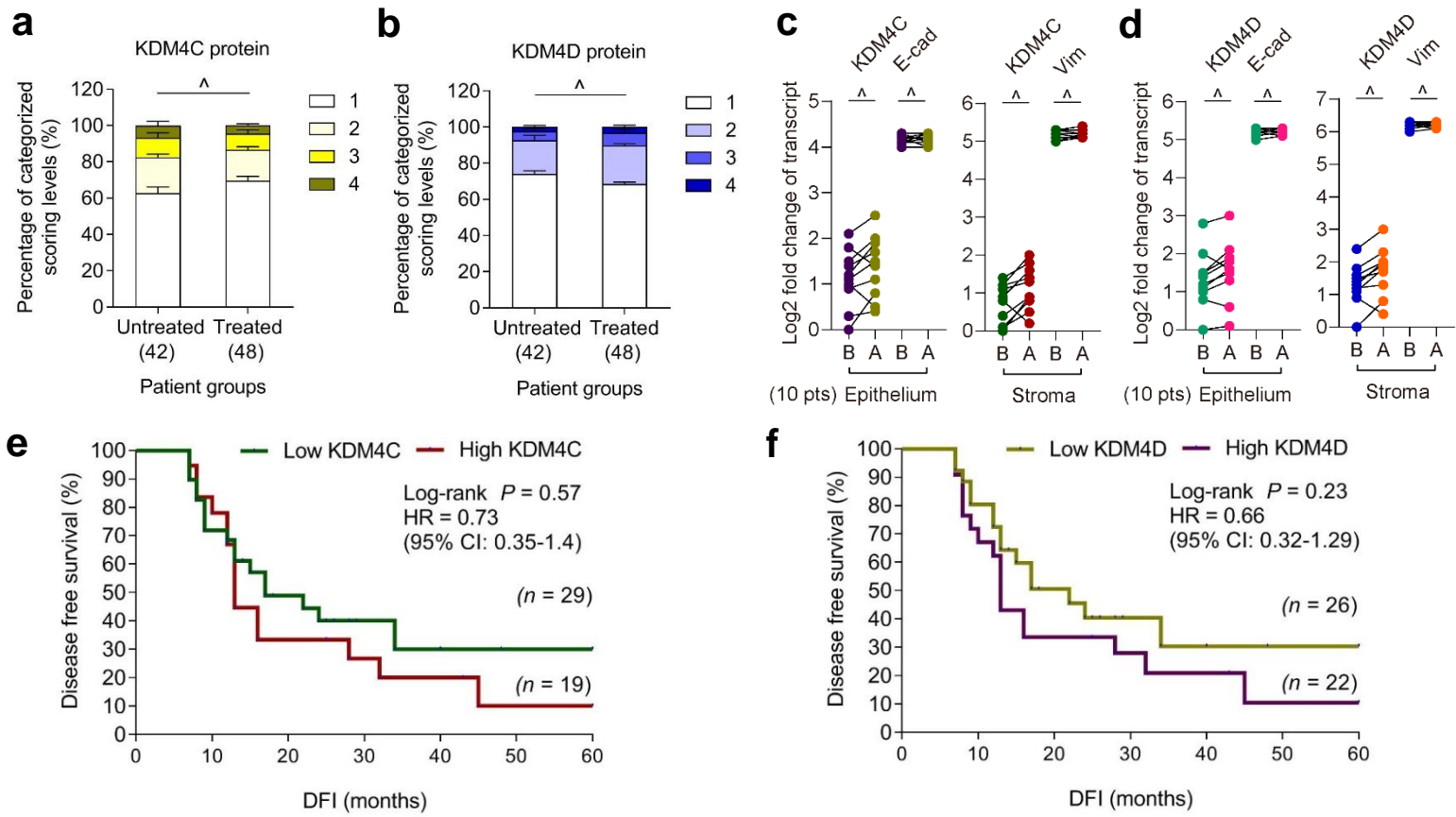
Briefly, immunoprecipitated chromatin complexes were eluted by DTT containing elution Buffer (10 mM DTT, 0.2% SDS in 1 × TE buffer) for 30 min at 37°C and then were further diluted 20-fold in a dilution buffer (10 mM Tris–HCl, pH8.0, 1 mM EDTA, 0.5 M EGTA, 100 mM NaCl, 1% Triton X-100 and protease inhibitor cocktail (Roche)), with DNA in the IP quantified by qPCR assays. The antibody used in ChIP-PCR was anti-KDM4A (abcam, # ab24545), with primers designed to amplify distal promoter regions (within -4kb TSS) of SASP hallmark factors or specified genes (sequences listed in Supplementary Table 16).

## References

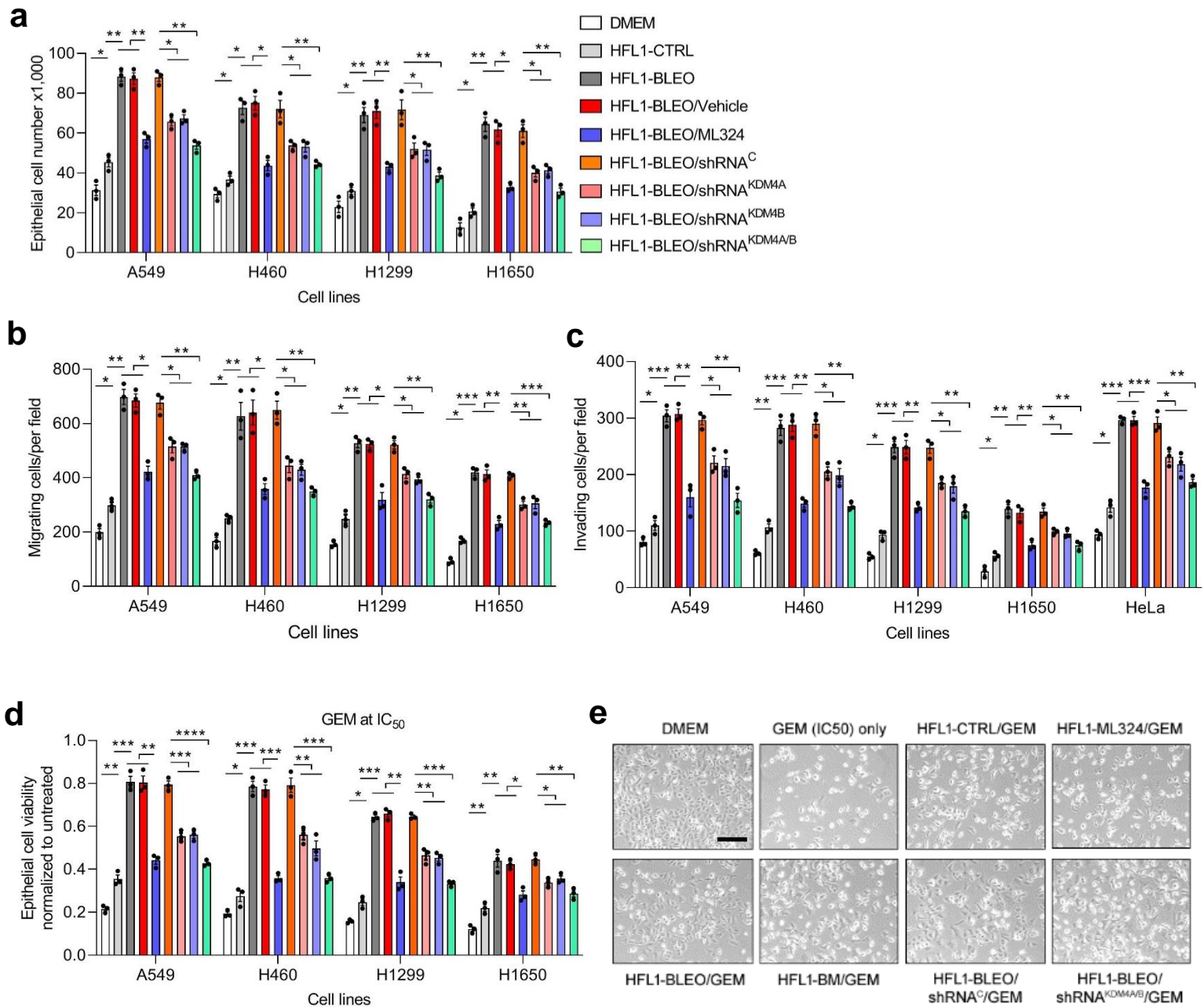
1. Sun, Y. *et al.* Treatment-induced damage to the tumor microenvironment promotes prostate cancer therapy resistance through WNT16B. *Nat Med* **18**, 1359-1368 (2012).
2. Keshishian, H., Addona, T., Burgess, M., Kuhn, E. & Carr, S.A. Quantitative, multiplexed assays for low abundance proteins in plasma by targeted mass spectrometry and stable isotope dilution. *Molecular & cellular proteomics : MCP* **6**, 2212-2229 (2007).
3. Schilling, B. *et al.* Platform-independent and label-free quantitation of proteomic data using MS1 extracted ion chromatograms in skyline: application to protein acetylation and phosphorylation. *Molecular & cellular proteomics : MCP* **11**, 202-214 (2012).
4. Kuhn, M.L. *et al.* Structural, kinetic and proteomic characterization of acetyl phosphate-dependent bacterial protein acetylation. *PLoS one* **9**, e94816 (2014).
5. Zhang, B.Y. *et al.* The senescence-associated secretory phenotype is potentiated by feedforward regulatory mechanisms involving Zscan4 and TAK1. *Nat Commun* **9**, 1723 (2018).
6. Hinohara, K. *et al.* KDM5 Histone Demethylase Activity Links Cellular Transcriptomic Heterogeneity to Therapeutic Resistance. *Cancer cell* **34**, 939-953 e939 (2018).
7. Li, H. *et al.* The Sequence Alignment/Map format and SAMtools. *Bioinformatics* **25**, 2078-2079 (2009).
8. Robinson, J.T., Thorvaldsdottir, H., Wenger, A.M., Zehir, A. & Mesirov, J.P. Variant Review with the Integrative Genomics Viewer. *Cancer research* **77**, e31-e34 (2017).



**Supplementary Fig. 1. Expression of KDM4 family is significantly upregulated in senescent cells in parallel to SASP development.** **a**, GO enrichment profiling of upregulated genes in PSC27 cells upon genotoxicity (bleomycin)-induced senescence. **b**, Heatmap displaying genes correlated with histone methylation and significantly upregulated in senescent cells. CTRL, control. BLEO, bleomycin. Genes are listed by their expression fold change in CTRL *versus* BLEO cells. **c**, Comparative transcript assay of KDM4 subfamily members (A/B/C/D) in presenescent (PRE) *versus* senescent (SEN) stromal cells. Signals were normalized to the PRE samples *per* gene. **d**, Representative SA- $\beta$ -Gal staining images of PSC27 cells upon therapy-induced senescence (TIS), replicative senescence (RS) or oncogene-induced senescence (OIS). Scale bars, 20  $\mu$ m. **e**, Comparative statistics of SA- $\beta$ -Gal staining-based quantification of senescent PSC27 cells. Data organized for cases of TIS, RS or OIS. Data in all bar plots are shown as mean  $\pm$  SD and representative of 3 biological replicates. **c** and **e**, *P* values were determined by two-sided unpaired *t*-test, and adjusted for multiple comparisons. Data in **d** are representative of 3 biological replicates.  $\wedge$ , *P* > 0.05. \*, *P* < 0.05. \*\*, *P* < 0.01.



**Supplementary Fig. 2. *In vivo* expression of KDM4C/D in human prostate cancer patients and corresponding clinical relevance.** **a**, Pathological assessment of stromal KDM4C expression in PCa samples (42 untreated *versus* 48 treated). In each group, patients were pathologically assigned into 4 categories *per* IHC staining intensity of KDM4C in stroma. 1, negative; 2, weak; 3, moderate; 4, strong expression. **b**, Pathological assessment of stromal KDM4D expression in PCa samples (42 untreated *versus* 48 treated). In each group, patients were pathologically assigned into 4 categories *per* IHC staining intensity of KDM4D in tumor stroma. 1, negative; 2, weak; 3, moderate; 4, strong expression. **c**, Comparative analysis of KDM4C expression. Data were organized for epithelial and stromal cells, respectively, after laser capture microdissection (LCM) of either cell lineage followed by quantitative analysis. Each dot represents an individual patient, with the data of “before” and “after” connected to allow direct profiling of KDM4C expression in the same individual patient. Data were normalized to the lowest value of KDM4C *per* cell lineage. **d**, Comparative analysis of KDM4D expression in a strategy similar to that described for (**c**) panel. **e**, Kaplan-Meier analysis of PCa patients. Disease-free survival (DFS) stratified according to KDM4C expression (low, average score < 2, dark green line, n = 29; high, average score ≥ 2, dark red line, n = 19). DFS represents the length of period from the date of PCa diagnosis to the point of first disease relapse. Survival curves generated according to the Kaplan-Meier method, with *P* value calculated using a two-sided log-rank (Mantel-Cox) test. **f**, Kaplan-Meier analysis of PCa patients. DFS stratified according to KDM4D expression (low, average score < 2, Kelly line, n = 26; high, average score ≥ 2, purple line, n = 22). Survival curves generated according to the Kaplan–Meier method as described for (**e**) panel. Data in all bar plots are shown as mean ± SD and representative of 3 biological replicates. **a** and **b**, *P* values were determined by two-way ANOVA with Bonferroni’s post-hoc test. **c** and **d**, *P* values were determined by two-sided unpaired *t*-test. ^, *P* > 0.05.



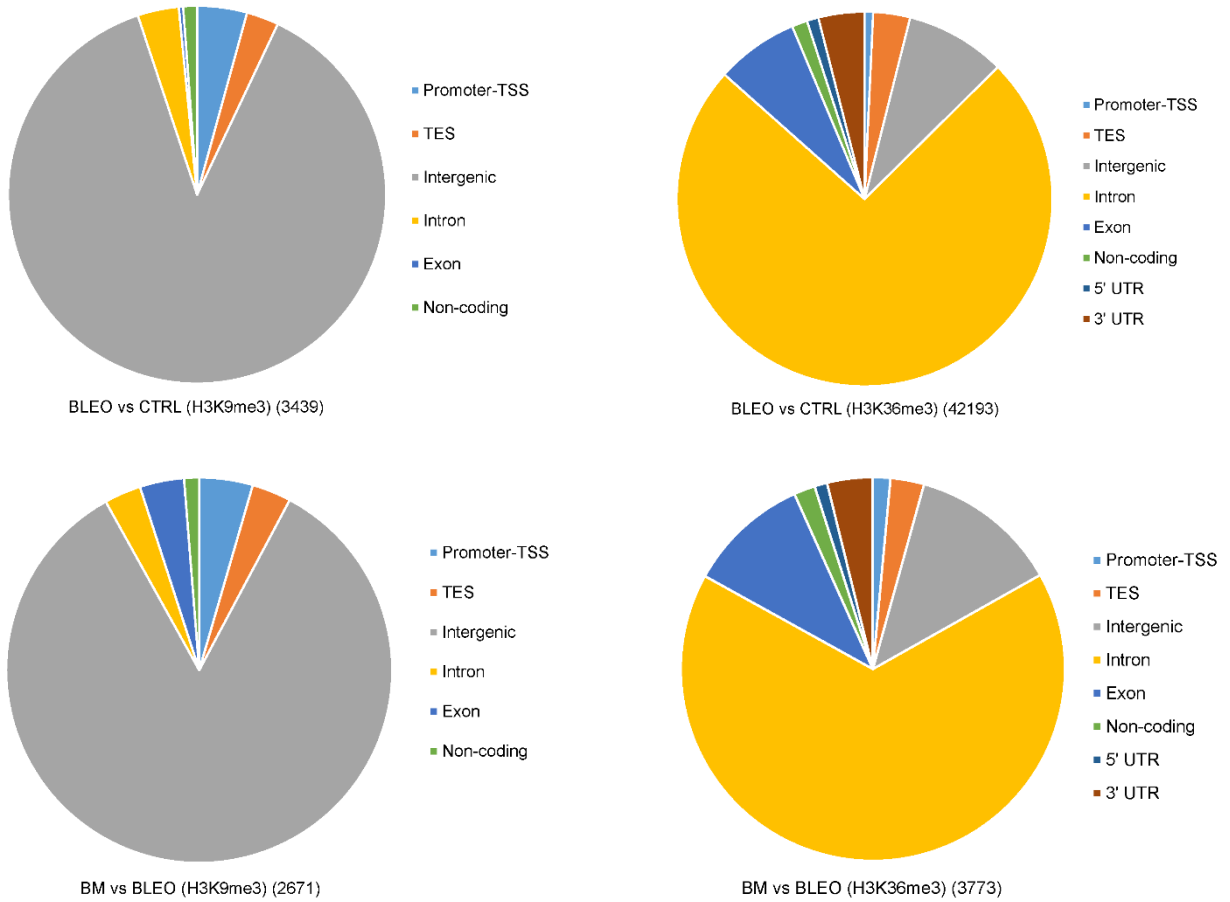
**Supplementary Fig. 3. Targeting KDM4 restrains lung cancer malignancy conferred by senescent fibroblasts.**

**a**, Measurement of *in vitro* proliferation of human lung cancer (LCa) cells after exposure to the conditioned media (CM) of lung fibroblasts (HFL1) treated by BLEO, ML324 or both, or transduced with individual shRNAs to deplete KDM4A/B. DMEM, routine media for LCa cell culture supplemented with 10% FBS. **b**, Assessment of *in vitro* migration of LCa cells after exposure to the CM of lung fibroblasts treated as described in **(a)**. **c**, Evaluation of *in vitro* invasion of LCa cells after exposure to the CM of lung fibroblasts treated as described for **(a)** panel. **d**, Chemoresistance of LCa cells to the chemotherapeutic agent gemcitabine (GEM) provided at the predetermined IC50 value of individual LCa cell lines upon culture with the CM described for **(a)** panel. **e**, Representative images of A549 cells upon treatment with the CM as described in **(a)**. BM, BLEO/ML324. Scale bar, 200  $\mu$ m. Data are shown as mean  $\pm$  SD and representative of 3 independent experiments. **a-d**, *P* values were determined by two-sided unpaired *t*-test, and adjusted for multiple comparisons. Data in **e** are representative of 3 biological replicates.  $\wedge$ ,  $P > 0.05$ . \*,  $P < 0.05$ . \*\*,  $P < 0.01$ . \*\*\*  $P < 0.001$ . \*\*\*\*  $P < 0.0001$ .

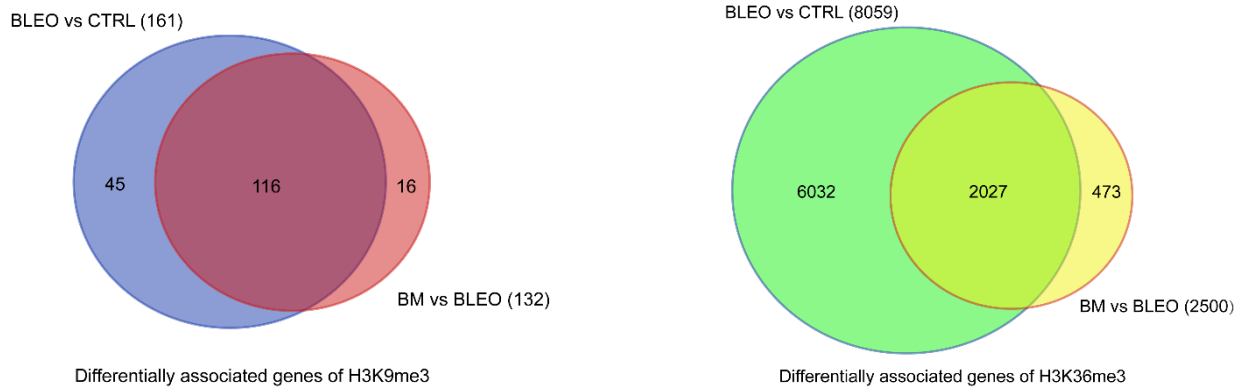
**a**

Sample	Peak distribution and number								
	Promoter-TSS	TES	Intergenic	Intron	Exon	Non-coding	5' UTR	3' UTR	Total
CTRL-H3K9me3	128	220	36661	12212	319	147	5	132	49824
CTRL-H3K36me3	474	2141	5783	58751	3936	1013	93	2520	74711
BLEO-H3K9me3	70	112	14454	3686	266	80	7	101	18776
BLEO-H3K36me3	278	1173	2102	29929	2735	388	42	1523	38170
BM-H3K9me3	328	278	30645	12011	444	215	25	198	44144
BM-H3K36me3	541	2197	4157	65694	3719	1017	84	2526	79935

**b**



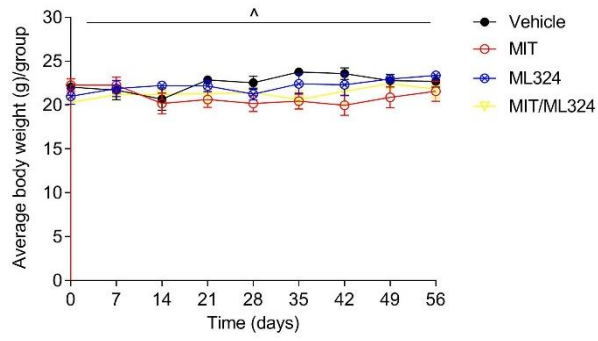
**c**



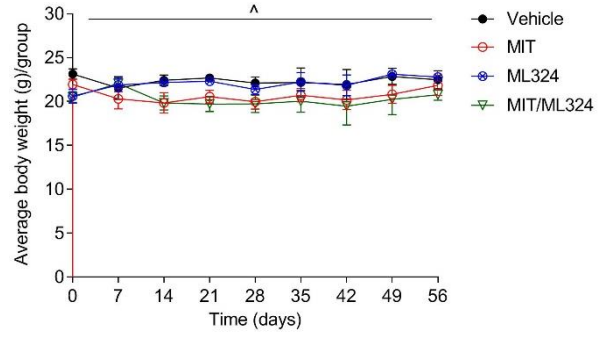


**Supplementary Fig. 4. ChIP-seq mapping of H3K9me3 and H3K36me3 in human stromal cells (PSC27).** **a**, Summary statistics of H3K9me3- and H3K36me3-specific peaks and their distribution across human genome. TSS, transcription start site. TES, transcription end site. BM, BLEO/ML324 co-treatment. **b**, Pie diagrams showing the distribution of differentially mapped H3K9me3 and H3K36me3 peaks between experimental conditions. BLEO vs CTRL, differential peaks of BLEO in contrast to those of CTRL. BM vs BLEO, differential peaks of BM in contrast to those of BLEO. The number of net peaks are indicated *per* comparative analysis. **c**, Venn diagrams displaying the number of genes that have regulatory regions containing binding sites for H3K9me3 or H3K36me3, and differentially mapped between conditions. Left, H3K9me3-associated genes down in 'BLEO vs CTRL' but up in 'BM vs BLEO'. Right, H3K36me3-associated genes up in 'BLEO vs CTRL' but down in 'BM vs BLEO'. The number of genes are shown *per* case.

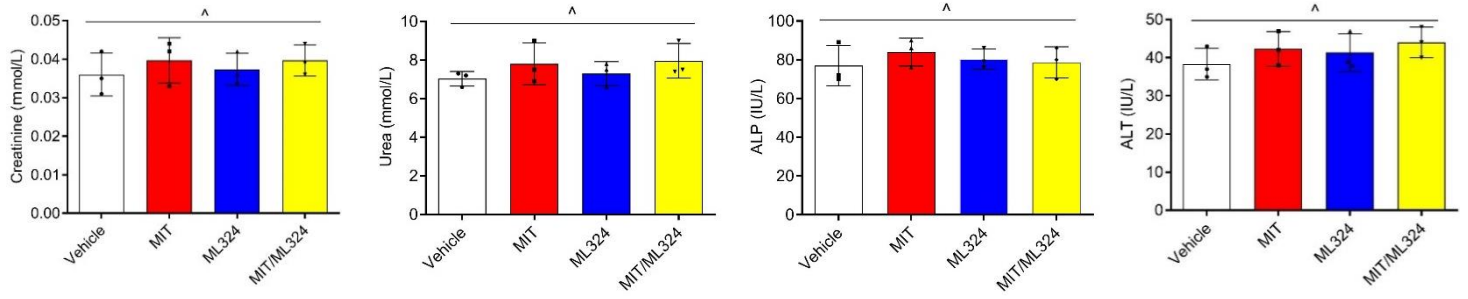
**a**



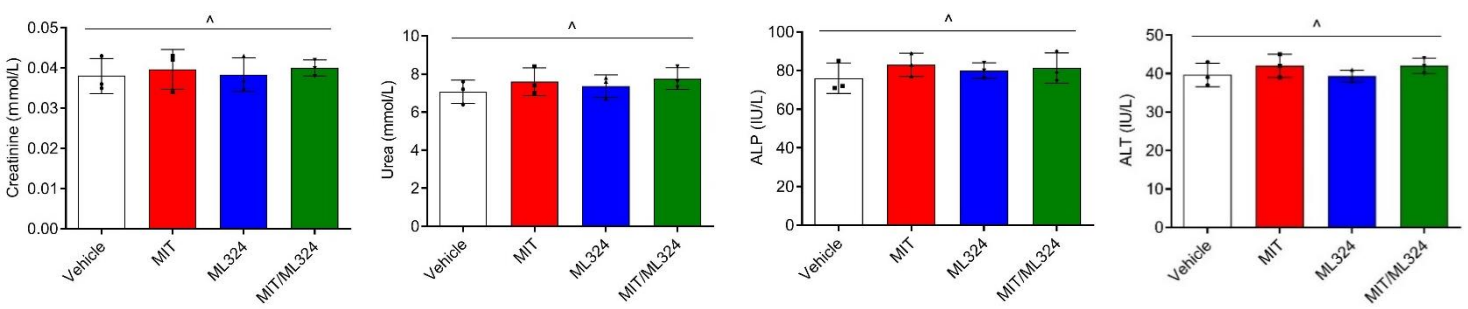
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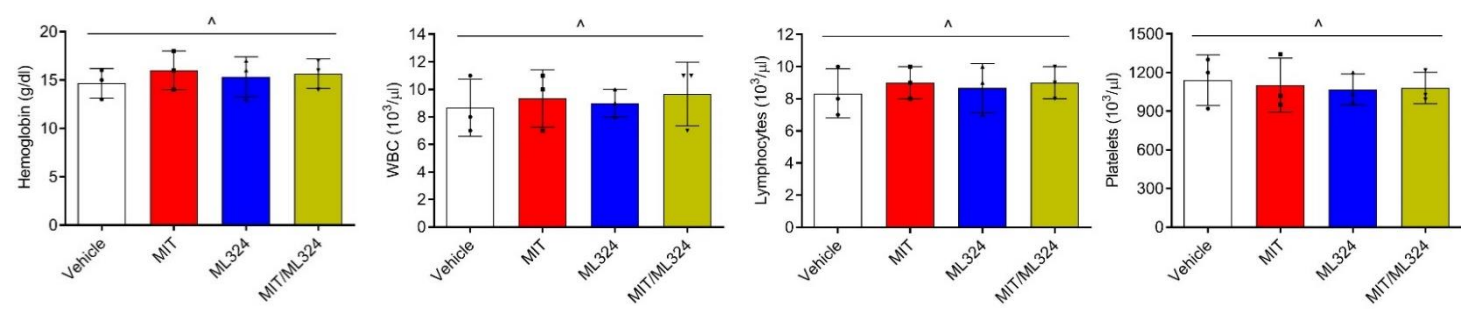
**b**



**d**

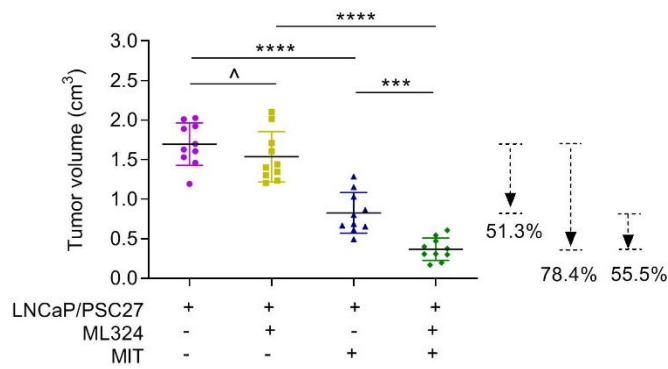


**e**

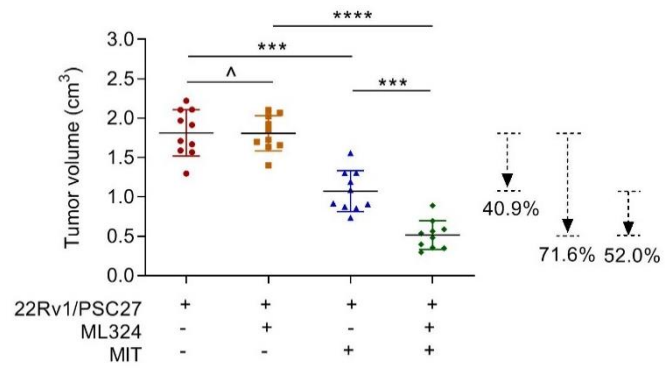


**Supplementary Fig. 5. Pathophysiological evaluation of treatment effects on body weight and functional integrity of key organs.** **a**, Mouse body weight determination performed on a weekly basis for immunodeficient mice. **b**, Serum measurement of creatinine, urea, alkaline phosphatase (ALP), and alanine aminotransferase (ALT) with terminal bleeds (cardiac punctures) taken at the end of therapeutic regimens. **c**, Mouse body weight determination performed on a weekly basis for immunocompetent mice (C57BL/6 strain). **d**, Serum measurement of creatinine, urea, alkaline phosphatase (ALP), and alanine aminotransferase (ALT) with terminal bleeds (cardiac punctures) taken at the end of therapeutic regimens for immunocompetent mice. **e**, Routine analysis of peripheral blood. The circulating levels of hemoglobin, white blood cells, lymphocytes and platelets at the end of each therapeutic regimen were assessed for C57BL/6 mice. Data are shown as mean  $\pm$  SD and representative of 3 independent experiments. MIT, mitoxantrone. WBC, white blood count. For all pathophysiological assays,  $n = 3$  per treatment arm. **a-e**,  $P$  values were determined by two-sided unpaired  $t$ -test, and adjusted for multiple comparisons.  $\wedge$ ,  $P > 0.05$ .

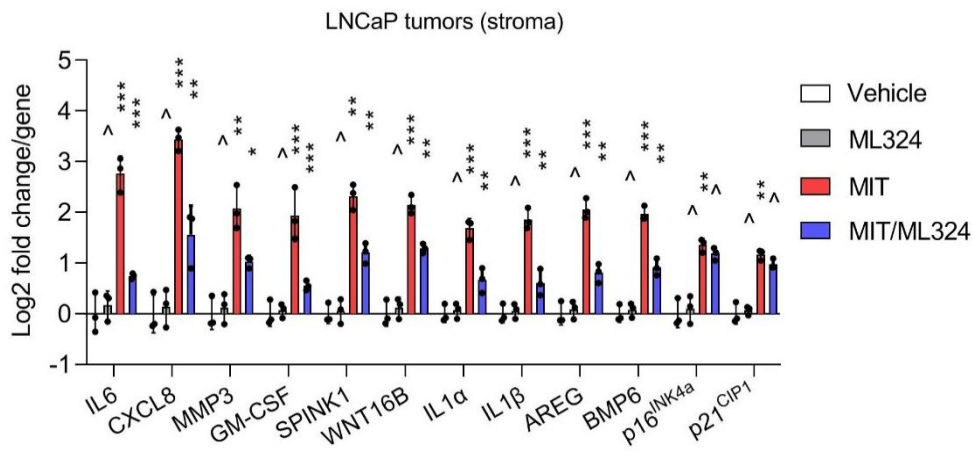
**a**



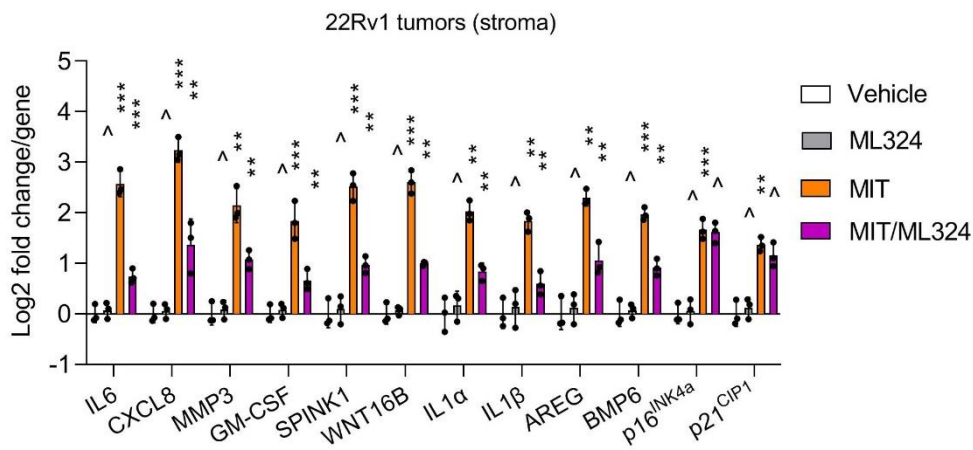
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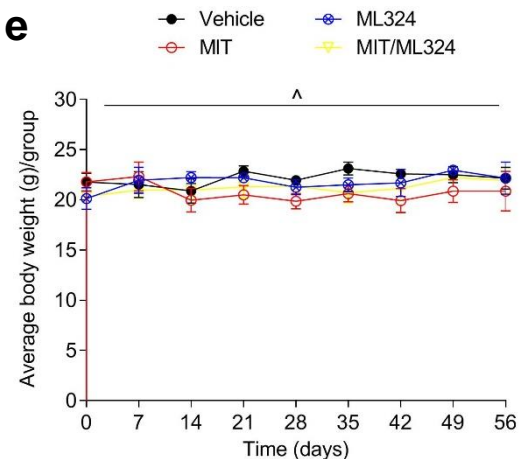
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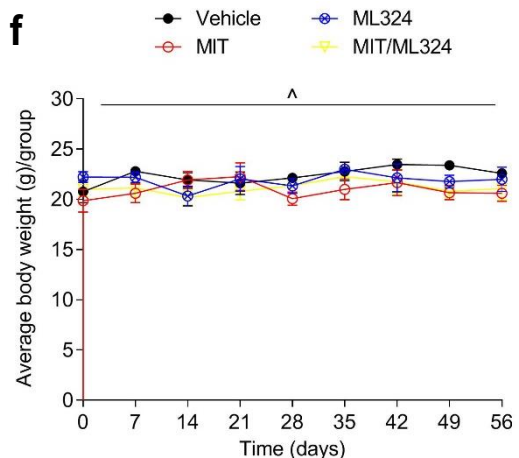
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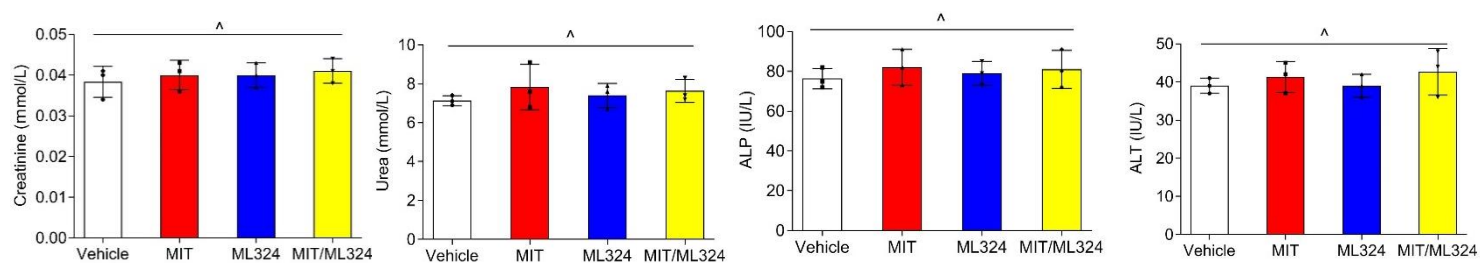
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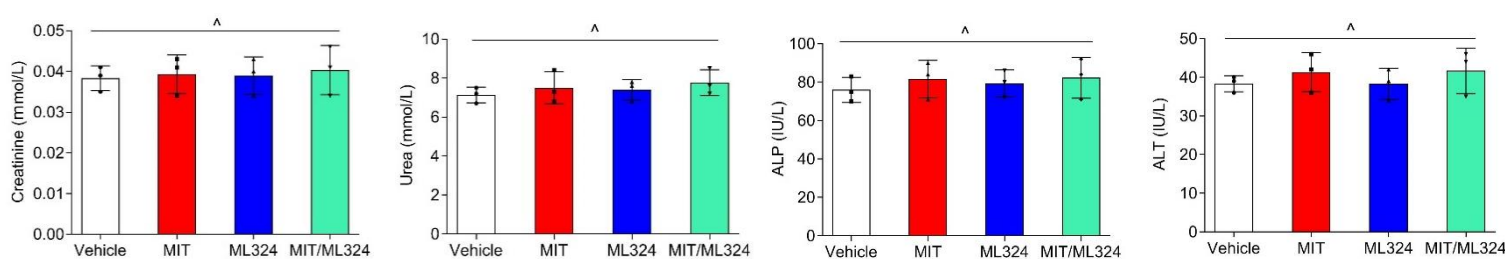
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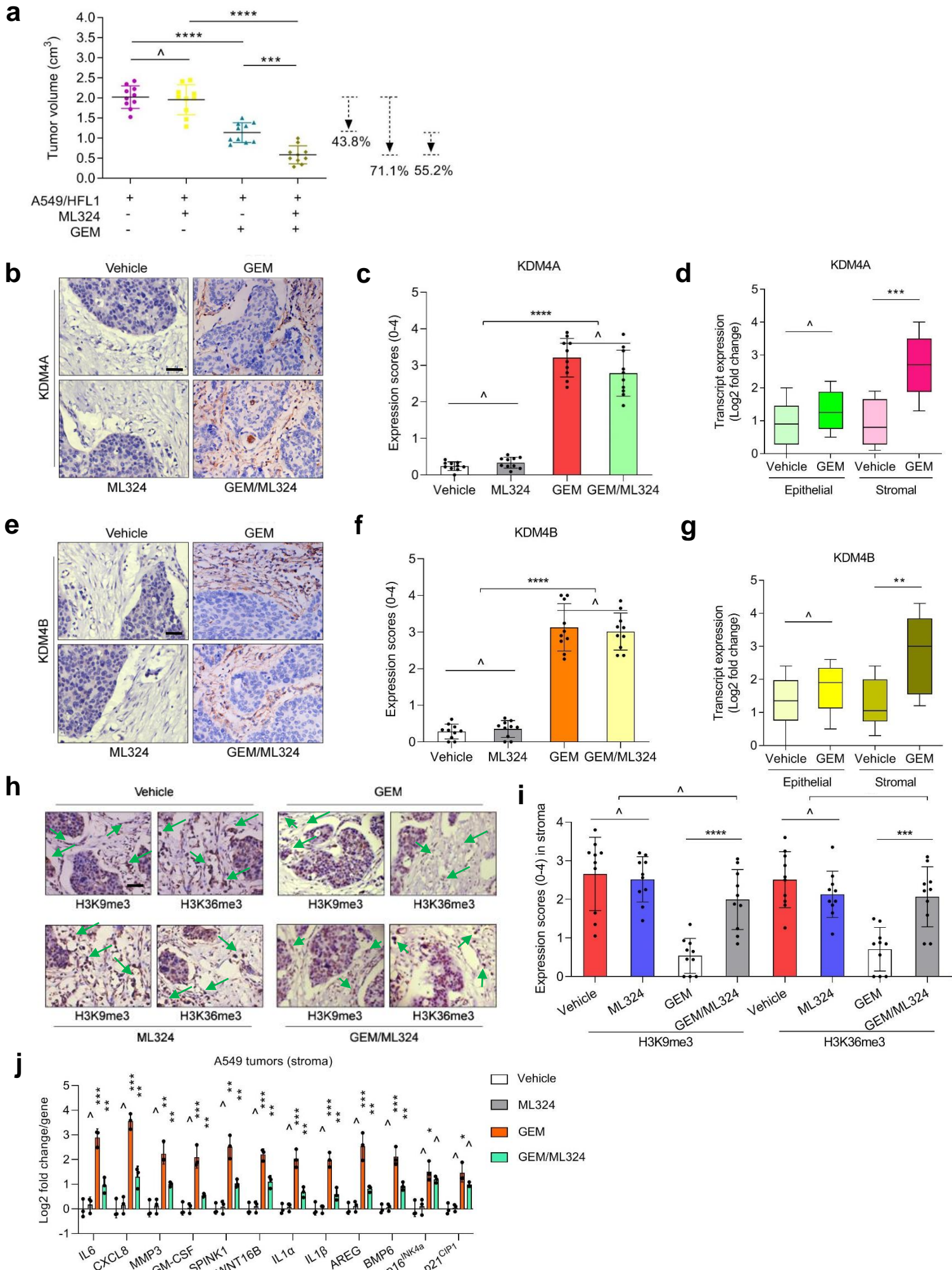
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**h**

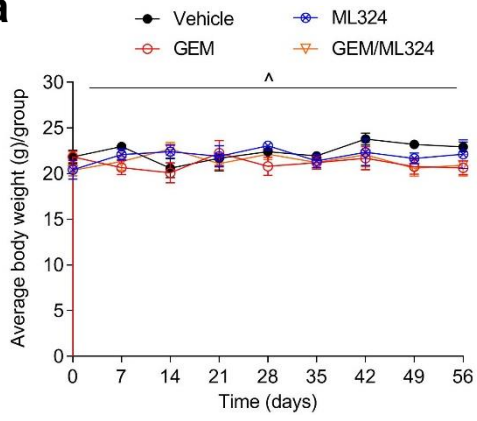
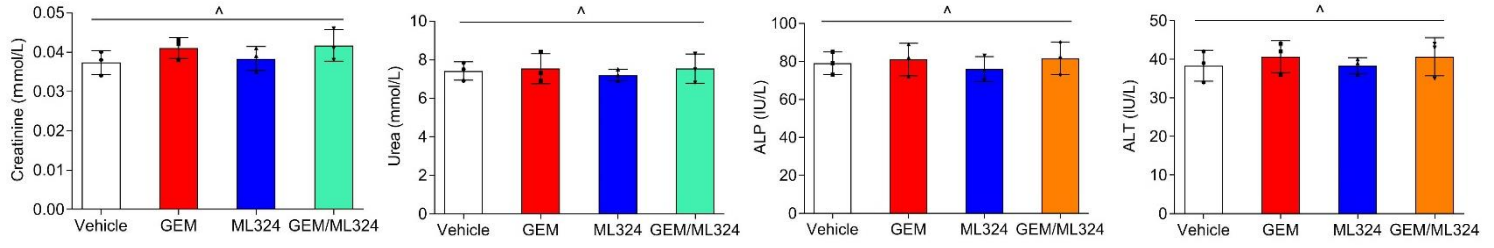


**Supplementary Fig. 6. Tumor measurement, *in vivo* SASP expression, and pathophysiological assessment of animals bearing LNCaP/PSC27 or 22Rv1/PSC27 tumors.** **a**, Comparison of tumor sizes at the end of preclinical treatment. Mice were implanted with androgen receptor (AR)-positive and hormone responsive LNCaP cells that were combined with PSC27 stromal cells, and experienced MIT and/or ML324-involving regimens. **b**, Similar comparison as described in **(a)**, except that 22Rv1 cells were applied as an AR-positive and hormone-refractory PCa line for tumor xenografting. **c**, Quantitative transcript assay of SASP factors and senescence markers expressed in experimental LNCaP/PSC27 mice as described in **(a)**. **d**, Quantitative transcript assay of SASP factors and senescence markers expressed in experimental 22Rv1/PSC27 mice as described in **(b)**. **e**, Body weight measurement of LNCaP/PSC27 mice as described in **(a)**. **f**, Body weight measurement of 22Rv1/PSC27 mice as described in **(b)**. **g**, Serum measurement of creatinine, urea, alkaline phosphatase (ALP), and alanine aminotransferase (ALT) with terminal bleeds (cardiac punctures) taken at the end of therapeutic regimens for LNCaP/PSC27 animals. **h**, Serum analysis of creatinine, urea, alkaline phosphatase (ALP), and alanine aminotransferase (ALT) with terminal bleeds (cardiac punctures) taken at the end of therapeutic regimens for 22Rv1/PSC27 animals. Data are shown as mean  $\pm$  SD and representative of 3 independent experiments. MIT, mitoxantrone. WBC, white blood count. For assays of **(a)**, **(b)**, **(e)** and **(f)**,  $n = 10$  per treatment arm. For tests of **(c)**, **(d)**, **(g)** and **(h)**,  $n = 3$  per group. **a-h**,  $P$  values were determined by two-sided unpaired  $t$ -test, and adjusted for multiple comparisons.  $\wedge$ ,  $P > 0.05$ . \*,  $P < 0.05$ . \*\*,  $P < 0.01$ . \*\*\*  $P < 0.001$ . \*\*\*\*  $P < 0.0001$ .





**Supplementary Fig. 7. Tumor measurement, *in vivo* expression of KDM4A/B, H3K9me3/H3K36me3 and the SASP in animals bearing A549/HFL1 tumors.** **a**, Comparison of tumor sizes at the end of preclinical treatment. Mice were implanted with human lung adenocarcinoma cells (A549) that were combined with HFL1 lung fibroblasts, and experienced gemcitabine (GEM) and/or ML324-mediated regimens. **b**, Pathological examination of KDM4A in lung tumors by IHC staining after mouse dissection. Scale bar, 50  $\mu$ m. **c**, Pathological scoring (in the range of 1-4, averaged from 3 independent readings/animal) of KDM4A expressed in fibroblasts isolated from mouse tumors via LCM. **d**, Comparative analysis of KDM4A expressed in epithelial cancer cells *versus* fibroblasts in tumor foci of animals experiencing different treatments. Cells were acquired from LCM-mediated isolation post tissue process. Signals normalized to the lowest value of cancer epithelial vehicle group. Median, 25th and 75th percentiles, with Turkey whisperm indicated in box-and-whisker plots. **e**, Pathological examination of KDM4B in lung tumors by IHC staining after mouse dissection. Scale bar, 50  $\mu$ m. **f**, Pathological scoring (in the range of 1-4, averaged from 3 independent readings/animal) of KDM4B expressed in fibroblasts isolated from mouse tumors via LCM. **g**, Comparative analysis of KDM4B expressed in epithelial cancer cells and fibroblasts in tumor foci. Cells were acquired from LCM-mediated isolation post tissue process. Signals normalized to the lowest value of cancer epithelial vehicle group. Median, 25th and 75th percentiles, with Turkey whisperm indicated in box-and-whisker plots. **h**, Pathological examination of H3K9me3 and H3K36me3 in lung tumors by IHC staining after mouse dissection. Scale bar, 100  $\mu$ m. Green arrows, representative stromal cells. **i**, Comparative statistics of H3K9me3 and H3K36me3 pathological scores (in a range of 1-4, averaged from 3 independent readings/animal) in lung tumors. **j**, Quantitative transcript assay of SASP factors and senescence markers expressed in experimental A549/HFL1 mice that experienced treatments as described in (**a**). Data are shown as mean  $\pm$  SD and representative of 3 independent experiments. **a**, **c**, **d**, **f**, **g**, **i**, **j**, *P* values were determined by two-sided unpaired *t*-test, and adjusted for multiple comparisons. Data in **b**, **e**, **h** are representative of 3 biological replicates.  $\wedge$ , *P* > 0.05. \*, *P* < 0.05. \*\*, *P* < 0.01. \*\*\* *P* < 0.001. \*\*\*\* *P* < 0.0001. N = 10/group.

**a****b**



**Supplementary Fig. 8. Pathophysiological evaluation of treatment effects on body weight and functional integrity of key organs of A549/HFL1 mice. Related to Fig. 7.** a, Mouse body weight determination performed on a weekly basis for immunodeficient mice carrying A549/HFL1 tumors. b, Serum measurement of creatinine, urea, alkaline phosphatase (ALP), and alanine aminotransferase (ALT) with terminal bleeds (cardiac punctures) taken at the end of therapeutic regimens for A549/HFL1 animals. Data are shown as mean  $\pm$  SD and representative of 3 independent experiments. GEM, gemcitabine. For all assays, n = 3 per treatment arm. **a-b**, *P* values were determined by two-sided unpaired *t*-test, and adjusted for multiple comparisons. <sup>^</sup>, *P* > 0.05.

## Supplementary Information

**Supplementary Table 1. Mass spectrometric profiling of senescent cell proteomics.**

<b>A. MS/MS spectrum database search analysis summary</b>					
Total spectrums	Matched spectrums	Peptides	Unique peptides	Identified proteins	Quantifiable proteins
16495	7694 (46.6%)	4110	3803	732	447

<b>B. Differentially expressed protein summary (Filtered with threshold value of expression fold change and <i>P</i> value &lt; 0.05)</b>					
Compare group	Regulated type	fold change >1.2	fold change >1.3	fold change >1.5	fold change >2
SEN/CTRL	up-regulated	218	194	156	87
	down-regulated	125	106	79	29

Supplementary Information

Supplementary Table 2. Intracellular proteins identified by mass spectrometry.

Protein accession	Gene name	MW [kDa]	Score	Coverage [%]	#Peptides	#PSMs	#Unique peptide	CTRL	SEN	SEN/CTRL Ratio	Subcellular localization	KEGG KO No.	KOG category	KOG NO.	KOG description
P04179	SOD2	24.75	39.431	31.1	5	8	5	8451300	3.25E+08	13.124	mitochondria	K04564	P	KOG0876	Manganese superoxide dismutase
P53007	SLC25A1	34.012	17.126	11.6	3	3	3	6521900	1.06E+08	7.788	plasma membrane	K15100	C	KOG0756	Mitochondrial tricarboxylate/dicarboxylate carrier proteins
P24844	MYL9	19.827	38.661	56.4	11	30	3	19644000	7.47E+08	7.272	mitochondria	K12755	Z	KOG0031	Myosin regulatory light chain, EF-Hand protein superfamily
O00479	HMGN4	9.5388	13.977	16.7	2	3	2	54708000	2.29E+08	5.207	nucleus	K11302			
O00159	MYO1C	121.68	293.12	42.2	34	43	34	2.29E+08	3.93E+09	4.574	cytoplasm	K10356	Z	KOG0164	Myosin class I heavy chain
Q9H4G4	GLIPR2	17.218	20.284	37	3	3	3	22738000	1.3E+08	4.032	cytoplasm		S	KOG3017	Defense-related protein containing SCP domain
P25705	ATP5F1A	59.75	152.64	38	15	19	15	1.33E+08	1.5E+09	3.877	mitochondria	K02132	C	KOG1353	F0F1-type ATP synthase, alpha subunit
P80723	BASP1	22.693	88.605	75.3	11	15	11	1.93E+08	1.47E+09	3.766	nucleus	K17272			
P08582	MELTF	80.214	138.98	40.4	16	22	16	54881000	1.22E+09	3.725	extracellular	K06569			
Q8NBQ5	HSD17B11	32.935	93.938	45	10	14	10	57261000	5.51E+08	3.637	endoplasmic reticulum		Q	KOG1201	Hydroxysteroid 17-beta dehydrogenase 11
P48047	ATP5O	23.277	22.969	17.4	3	4	3	19552000	1.1E+08	3.591	mitochondria	K02137	C	KOG1662	Mitochondrial F1F0-ATP synthase, subunit OSCP/ATP5
P21589	NT5E	63.367	103.23	38.7	14	19	14	99343000	8.05E+08	3.55	peroxisome	K19970	F	KOG4419	5' nucleotidase
P27824	CANX	67.567	24.663	12.3	4	5	4	15641000	1.22E+08	3.534	endoplasmic reticulum	K08054	O	KOG0675	Calnexin
P02545	LMNA	74.139	176.93	45.2	20	23	20	88713000	9.26E+08	3.529	nucleus	K12641	DY	KOG0977	Nuclear envelope protein lamin, intermediate filament superfamily
P52926	HMGA2	11.832	31.678	40.4	3	5	3	16460000	1.07E+08	3.524	nucleus	K09283			
Q56VL3	OCIAD2	16.953	36.745	43.5	5	5	5	19218000	2.44E+08	3.498	extracellular				
P06576	ATP5F1B	56.559	248.4	68.8	22	33	22	4.87E+08	4.34E+09	3.378	mitochondria	K02133	C	KOG1350	F0F1-type ATP synthase, beta subunit
P30838	ALDH3A1	50.394	58.004	24.3	7	10	7	1.01E+08	3.29E+08	3.296	mitochondria	K00129	C	KOG2456	Aldehyde dehydrogenase
P56385	ATP5ME	7.9331	23.651	52.2	4	4	4	9839500	1.13E+08	3.254	mitochondria	K02129	C	KOG4326	Mitochondrial F1F0-ATP synthase, subunit e
Q96N66	MBOAT7	52.764	28.204	10.8	3	3	3	12169000	1.16E+08	3.244	plasma membrane	K13516	S	KOG2706	Predicted membrane protein
P09493	TPM1	32.708	323.31	53.2	27	37	9	9.32E+08	9.19E+09	3.19	cytoplasm	K10373			
P09525	ANXA4	35.882	72.36	28.8	7	7	7	54065000	4.89E+08	3.18	cytoplasm	K17093	U	KOG0819	Annexin
P47755	CAPZA2	32.949	35.751	30.4	5	6	4	40361000	2.26E+08	3.176	cytoplasm	K10364	Z	KOG0836	F-actin capping protein, alpha subunit
P07858	CTSB	37.821	45.797	25.1	5	6	5	16233000	1.97E+08	3.153	extracellular	K01363	O	KOG1543	Cysteine proteinase Cathepsin L
P67936	TPM4	28.521	119.29	66.1	21	19	10	1.74E+08	1.72E+09	3.068	cytoplasm	K10375			
P04792	HSPB1	22.782	56.634	57.6	8	12	8	76335000	7.93E+08	3.047	nucleus	K04455	O	KOG3591	Alpha crystallins
Q16795	NDUFA9	42.509	31.695	17	5	5	5	18465000	1.28E+08	3.003	mitochondria	K03953	C	KOG2865	NADH:ubiquinone oxidoreductase, NDUFA9/39kDa subunit
Q9UM54	MYO6	149.69	116.21	20.4	15	18	15	36694000	8.46E+08	2.984	cytoplasm	K10358	Z	KOG0163	Myosin class VI heavy chain
P60903	S100A10	11.203	17.953	35.1	2	5	2	61356000	5.37E+08	2.952	cytoplasm	K17274			
Q9Y608	LRRFIP2	82.17	18.271	6.8	2	3	2	10794000	1.41E+08	2.924	nucleus		R	KOG2010	Double stranded RNA binding protein
Q6NZI2	CAVIN1	43.476	68.981	24.4	6	8	6	20151000	1.7E+08	2.922	nucleus	K19387			
P06753	TPM3	32.95	77.878	46.3	24	28	7	1.5E+08	1.41E+09	2.875	cytoplasm	K09290	Z	KOG1003	Actin filament-coating protein tropomyosin
Q9Y4I1	MYO5A	215.4	149	15	19	22	19	86320000	7.27E+08	2.853	cytoplasm	K10357	Z	KOG0161	Myosin class II heavy chain
Q9P0K7	RAI14	110.04	323.31	50.3	34	45	34	3.51E+08	2.35E+09	2.767	nucleus				
P39656	DDOST	50.8	46.385	20.6	6	6	6	24268000	2.9E+08	2.724	plasma membrane	K12670	O	KOG2754	Oligosaccharyltransferase, beta subunit
P56134	ATP5J2	10.918	16.065	25.5	2	2	2	9911200	1.17E+08	2.709	cytoplasm	K02130	C	KOG4092	Mitochondrial F1F0-ATP synthase, subunit f
Q14257	RCN2	36.876	11.758	11	2	2	2	10436000	44429000	2.703	extracellular		TU	KOG4223	Reticulocalbin, calumenin, DNA supercoiling factor, and related
Q15165	PON2	39.38	42.55	35	5	5	5	12239000	1.7E+08	2.7	extracellular	K01045			Ca <sup>2+</sup> -binding proteins of the CREC family (EF-Hand protein superfamily)
P13987	CD59	14.177	38.046	25.8	5	7	5	31798000	2.08E+08	2.678	extracellular	K04008			
P51608	MECP2	52.44	67.069	24.7	9	10	9	40833000	3.08E+08	2.665	nucleus	K11588	KB	KOG4161	Methyl-CpG binding transcription regulators
P23141	CES1	62.52	35.558	12.3	5	7	5	13822000	1.78E+08	2.661	extracellular	K01044	R	KOG1516	Carboxylesterase and related proteins
Q6WCQ1	MPRIP	116.53	323.31	40.7	32	40	32	5.72E+08	2.44E+09	2.643	nucleus		Z	KOG4807	F-actin binding protein, regulates actin cytoskeletal organization
P36957	DLST	48.755	39.504	18.1	5	5	5	20952000	1.17E+08	2.621	mitochondria	K00658	C	KOG0559	Dihydrolipoamide succinyltransferase (2-oxoglutarate dehydrogenase, E2 subunit)
P04843	RPN1	68.569	41.954	14.7	6	6	6	18973000	1.15E+08	2.613	endoplasmic reticulum	K12666	O	KOG2291	Oligosaccharyltransferase, alpha subunit (ribophorin I)
P10301	RRAS	23.48	29.383	28.4	4	4	4	16909000	1.31E+08	2.584	nucleus	K07829	R	KOG0395	Ras-related GTPase

P18206	VCL	123.8	32.739	8.9	5	5	5	11979000	1.14E+08	2.561	cytoplasm	K05700	W	KOG3681	Alpha-catenin
P11233	RALA	23.567	28.725	25.2	4	4	4	6799500	87280000	2.553	cytoplasm	K07834	R	KOG0395	Ras-related GTPase
Q13045	FLII	144.75	32.266	5.1	5	5	5	12253000	86182000	2.544	cytoplasm		Z	KOG0444	Cytoskeletal regulator Flightless-I (contains leucine-rich and gelsolin repeats)
O60506	SYNCRIP	69.602	53.512	22.2	8	9	6	82070000	2.82E+08	2.535	nucleus	K13160	A	KOG0117	Heterogeneous nuclear ribonucleoprotein R (RRM superfamily)
P21333	FLNA	280.74	323.31	36.4	56	75	54	7.97E+08	4.37E+09	2.534	cytoplasm	K04437	Z	KOG0518	Actin-binding cytoskeleton protein, filamin
O75368	SH3BGRL	12.774	47.672	60.5	5	7	5	44555000	2.6E+08	2.512	mitochondria		S	KOG4023	Uncharacterized conserved protein
P09936	UCHL1	24.824	47.314	32.3	4	5	4	37857000	2.45E+08	2.473	cytoplasm	K05611	O	KOG1415	Ubiquitin C-terminal hydrolase UCHL1
Q9P0M6	H2AFY2	40.058	92.939	52.2	13	16	11	75946000	3.21E+08	2.443	mitochondria	K11251	BK	KOG2633	Hismacro and SEC14 domain-containing proteins
Q9H9B4	SFXN1	35.619	7.1511	12.1	2	3	1	13476000	49510000	2.398	cytoplasm		R	KOG3767	Sideroflexin
O15231	ZNF185	73.525	33.738	10.4	5	5	5	15110000	1.46E+08	2.389	cytoplasm,nucleus				
O00151	PDLIM1	36.071	53.529	46.5	7	7	7	4.29E+08	2.26E+08	2.379	cytoplasm		TZ	KOG1703	Adaptor protein Enigma and related PDZ-LIM proteins
P21980	TGM2	77.328	35.084	13.4	5	5	5	18150000	91747000	2.352	cytoplasm	K05625			
O75947	ATP5H	18.491	25.399	37.3	4	5	4	20152000	2.08E+08	2.344	cytoplasm	K02138	C	KOG3366	Mitochondrial F1F0-ATP synthase, subunit d/ATP7
P46821	MAP1B	270.63	20.901	1.7	3	3	3	10930000	62882000	2.328	nucleus	K10429	Z	KOG3592	Microtubule-associated proteins
P42330	AKR1C3	36.853	71.259	45.8	9	9	6	42453000	2.33E+08	2.322	cytoplasm	K04119	R	KOG1577	Aldo/keto reductase family proteins
P63000	RAC1	21.45	29.252	25	4	7	4	38019000	2.81E+08	2.303	cytoplasm	K04392			
O43795	MYO1B	131.98	299.66	36.4	32	46	32	3.26E+09	3.91E+09	2.3	cytoplasm	K10356	Z	KOG0164	Myosin class I heavy chain
O75369	FLNB	278.16	153.87	14.3	23	23	21	1.7E+08	4.45E+08	2.289	cytoplasm,nucleus	K04437	Z	KOG0518	Actin-binding cytoskeleton protein, filamin
Q13838	DDX39B	48.991	61.277	29.9	9	11	9	57869000	4.2E+08	2.279	cytoplasm,nucleus	K12812	A	KOG0329	ATP-dependent RNA helicase
P27105	STOM	31.73	85.013	42	7	11	7	1.52E+08	1.17E+09	2.268	cytoplasm	K17286	C	KOG2621	Prohibitins and stomatins of the PID superfamily
P04899	GNAI2	40.45	54.268	27.6	7	8	4	99363000	4.2E+08	2.261	cytoplasm	K04630	DT	KOG0082	G-protein alpha subunit (small G protein superfamily)
Q9BWM7	SFXN3	35.503	19.391	12.8	3	3	2	23716000	1.33E+08	2.253	cytoplasm		R	KOG3767	Sideroflexin
Q16881	TXNRD1	70.905	19.137	5.9	2	2	2	12954000	70308000	2.238	cytoplasm	K22182	O	KOG4716	Thioredoxin reductase
P14923	JUP	81.744	56.36	17.7	7	8	7	33753000	2.4E+08	2.229	cytoplasm	K10056	TZ	KOG4203	Armadillo/beta-Catenin/plakoglobin
P14866	HNRNPL	64.132	73.749	28.5	8	9	8	72239000	4.14E+08	2.2	nucleus	K13159	A	KOG1456	Heterogeneous nuclear ribonucleoprotein L (contains RRM repeats)
P62873	GNB1	37.377	68.028	32.9	7	9	4	51229000	3.13E+08	2.189	cytoplasm	K04536	R	KOG0286	G-protein beta subunit
O75489	NDUFS3	30.241	50.015	31.1	6	6	6	27136000	90619000	2.178	mitochondria	K03936	C	KOG1713	NADH-ubiquinone oxidoreductase, NDUFS3/30 kDa subunit
P15121	AKR1B1	35.853	96.443	55.1	11	15	11	2.89E+08	1.63E+09	2.175	cytoplasm	K00011	R	KOG1577	Aldo/keto reductase family proteins
Q9UBI6	GNG12	8.0061	21.612	56.9	3	3	3	52453000	3.5E+08	2.155	nucleus	K04347	T	KOG4119	G protein gamma subunit
P10620	MGST1	17.598	38.185	20	4	6	4	68874000	4.38E+08	2.145	cytoplasm,nucleus	K00799			
P35580	MYH10	229	323.31	38.8	72	109	40	8.41E+08	5.69E+09	2.132	cytoplasm	K10352	Z	KOG0161	Myosin class II heavy chain
P37802	TAGLN2	22.391	71.639	52.3	9	10	9	1.18E+08	6.42E+08	2.127	cytoplasm,nucleus	K20526	Z	KOG2046	Calponin
P40199	CEACAM6	37.194	17.137	5.8	2	3	2	12938000	40194000	2.11	extracellular	K06499			
Q09666	AHNAK	629.09	120.14	12.9	18	21	18	2.08E+08	6.63E+08	2.109	nucleus				
Q13813	SPTAN1	284.54	62.961	5.4	7	7	7	46211000	1.39E+08	2.081	nucleus	K06114	Z	KOG0035	Ca <sup>2+</sup> -binding actin-bundling protein (actinin), alpha chain
Q6NUK1	SLC25A24	53.354	37.688	16.4	6	6	6	26640000	1.54E+08	2.06	cytoplasm	K14684	F	KOG0036	Predicted mitochondrial carrier protein
P26038	MSN	67.819	32.027	10.2	5	5	5	13531000	1.09E+08	2.052	cytoplasm	K05763	R	KOG3529	Radixin, moesin and related proteins of the ERM family
P51970	NDUFA8	20.105	24.495	30.2	3	4	3	70760000	1.43E+08	2.052	extracellular	K03952	C	KOG3458	NADH:ubiquinone oxidoreductase, NDUFA8/PGIV/19 kDa subunit
Q9NYL9	TMOD3	39.594	177.16	75	20	30	19	5.01E+08	3.33E+09	2.04	cytoplasm	K10370	Z	KOG3735	Tropomodulin and leiomodulin
Q07065	CKAP4	66.022	80.037	23.8	10	11	10	2.63E+08	3.76E+08	2.019	plasma membrane	K13999			
Q969G5	CAVIN3	27.701	14.168	7.7	2	2	2	9055800	40254000	2.011	extracellular				
O60675	MAFK	17.523	21.419	24.4	3	3	3	23843000	97765000	2.009	nucleus	K09037			
P0DMV9	HSPA1B	70.051	66.554	27.3	10	14	6	1.27E+08	4.33E+08	1.996	cytoplasm	K03283			
O43390	HNRNPR	70.942	35.432	15.8	7	9	5	45012000	2.25E+08	1.992	nucleus	K13161	A	KOG0117	Heterogeneous nuclear ribonucleoprotein R (RRM superfamily)
Q16719	KYNU	52.351	38.241	19.1	6	8	6	34369000	1.44E+08	1.982	cytoplasm	K01556	E	KOG3846	L-kynurenine hydrolase
P49411	TUFM	49.541	32.492	15.5	5	5	5	14538000	1.06E+08	1.97	mitochondria	K02358	J	KOG0460	Mitochondrial translation elongation factor Tu
P14649	MYL6B	22.764	42.857	49	7	11	5	57876000	2.48E+08	1.951	cytoplasm	K12751	Z	KOG0030	Myosin essential light chain, EF-Hand protein superfamily
Q13435	SF3B2	100.23	58.085	15.5	9	9	9	42298000	2.72E+08	1.944	nucleus	K12829	A	KOG2330	Splicing factor 3b, subunit 2
Q9Y5S9	RBM8A	19.889	12.701	33.3	2	2	2	9105600	84319000	1.944	nucleus	K12876	R	KOG0130	RNA-binding protein RBM8/Tsunagi (RRM superfamily)
P07099	EPHX1	52.948	15.98	8.4	2	2	2	20502000	1.22E+08	1.922	endoplasmic reticulum	K01253	R	KOG2565	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
P11413	G6PD	59.256	91.487	31.5	11	13	11	82504000	3.68E+08	1.909	cytoplasm	K00036	G	KOG0563	Glucose-6-phosphate 1-dehydrogenase



P38117	ETFB	27.843	21.789	17.6	4	4	4	37310000	53308000	1.559	cytoplasm	K03521	C	KOG3180	Electron transfer flavoprotein, beta subunit
P52272	HNRNPM	77.515	48.747	12.3	6	6	6	63160000	1.89E+08	1.556	cytoplasm	K12887	A	KOG4212	RNA-binding protein hnRNP-M
Q06830	PRDX1	22.11	85.37	60.3	10	12	10	3.35E+08	9.59E+08	1.555	cytoplasm	K13279	O	KOG0852	Alkyl hydroperoxide reductase, thiol specific antioxidant and related enzymes
O15511	ARPC5	16.32	21.356	43.7	3	5	3	63159000	2.99E+08	1.547	cytoplasm	K05754	Z	KOG3380	Actin-related protein Arp2/3 complex, subunit ARPC5
P60981	DSTN	18.506	11.586	17	2	3	2	27428000	88172000	1.54	mitochondria	K10363	Z	KOG1735	Actin depolymerizing factor
P07355	ANXA2	38.604	283.3	75.5	27	40	27	1.66E+09	9.76E+09	1.519	cytoplasm	K17092	U	KOG0819	Annexin
P62306	SNRPF	9.7251	22.789	48.8	3	4	3	19331000	47349000	1.516	cytoplasm	K11098	A	KOG3482	Small nuclear ribonucleoprotein (snRNP) SMF
P05114	HMGNI	10.659	30.051	45	4	4	4	5544900	12703000	1.515	nucleus	K11299			
Q96QD9	FYTDD1	35.818	19.718	12.6	3	3	3	16487000	78063000	1.511	mitochondria				
O60701	UGDH	55.023	46.08	19.6	7	9	7	1.13E+08	2.81E+08	1.498	cytoplasm	K00012	GT	KOG2666	UDP-glucose/GDP-mannose dehydrogenase
P63104	YWHAZ	27.745	108.55	44.5	11	13	10	2.87E+08	1.1E+09	1.496	cytoplasm	K16197	O	KOG0841	Multifunctional chaperone (14-3-3 family)
P08574	CYC1	35.422	13.149	8.6	2	2	2	13849000	41576000	1.474	mitochondria	K00413	C	KOG3052	Cytochrome c1
P09651	HNRNPA1	38.746	127.64	34.7	11	17	11	2.72E+08	9.67E+08	1.47	nucleus	K12741	R	KOG0118	FOG: RRM domain
Q8IY81	FTSJ3	96.557	22.156	7.6	3	3	3	22601000	1.14E+08	1.469	nucleus	K14857	AR	KOG1098	Putative SAM-dependent rRNA methyltransferase SPB1
P07339	CTSD	44.552	37.804	15	5	5	5	1.06E+08	2.59E+08	1.462	extracellular	K01379	O	KOG1339	Aspartyl protease
P26641	EEF1G	50.118	11.457	5.5	2	2	2	10197000	23763000	1.456	cytoplasm	K03233	J	KOG1627	Translation elongation factor EF-1 gamma
Q00839	HNRNPU	90.583	107.12	26.5	14	15	14	2.3E+08	8.32E+08	1.456	nucleus	K12888			
P68371	TUBB4B	49.83	135.95	44.5	14	23	2	4.94E+08	1.8E+09	1.453	cytoplasm,nucleus	K07375	Z	KOG1375	Beta tubulin
P18859	ATP5J	12.587	19.801	44.4	3	3	3	24042000	94681000	1.45	mitochondria	K02131	C	KOG4634	Mitochondrial F1F0-ATP synthase, subunit Cf6 (coupling factor 6)
Q9ULV4	CORO1C	53.248	45.91	20.9	6	7	6	1.12E+08	4.5E+08	1.443	mitochondria	K13886	Z	KOG0303	Actin-binding protein Coronin, contains WD40 repeats
P61421	ATP6V0D1	40.329	20.734	17.7	3	4	3	16904000	1.32E+08	1.438	cytoskeleton	K02146	C	KOG2957	Vacuolar H+-ATPase V0 sector, subunit d
P22695	UQCRC2	48.442	105.97	34.4	11	14	11	1.46E+08	3.94E+08	1.434	mitochondria	K00415	C	KOG2583	Ubiquinol cytochrome c reductase, subunit QCR2
P63096	GNAI1	40.361	32.294	24.3	6	9	3	25292000	1.71E+08	1.434	cytoplasm	K04630	DT	KOG0082	G-protein alpha subunit (small G protein superfamily)
P40926	MDH2	35.503	65.044	37.6	8	8	8	1.01E+08	3.26E+08	1.431	mitochondria	K00026	C	KOG1494	NAD-dependent malate dehydrogenase
Q9UJS0	SLC25A13	74.175	43.396	12.4	6	7	6	36183000	1.48E+08	1.424	cytoplasm	K15105	C	KOG0751	Mitochondrial aspartate/glutamate carrier protein Aralar/Citrin
P0DP25	CALM3	16.837	169.78	74.5	14	32	14	1.91E+09	9.01E+09	1.423	cytoplasm,nucleus	K02183			(contains EF-hand Ca2+-binding domains)
O95758	PTBP3	59.689	43.225	17.6	7	7	4	13066000	84000000	1.419	cytoskeleton	K17844	A	KOG1190	Polypyrimidine tract-binding protein
P29401	TKT	67.877	137.46	46.4	15	20	15	4.37E+08	1.27E+09	1.412	cytoplasm	K00615	G	KOG0523	Transketolase
Q15050	RRS1	41.193	19.557	12.1	3	4	3	30183000	98726000	1.411	nucleus	K14852	J	KOG1765	Regulator of ribosome synthesis
P82979	SARNP	23.671	38.586	22.4	4	4	4	1.22E+08	2E+08	1.409	nucleus	K18732	D	KOG4259	Putative nucleic acid-binding protein Hcc-1/proliferation associated
P05141	SLC25A5	32.852	96.017	39.9	13	16	6	2.59E+08	8.99E+08	1.396	cytoplasm	K05863	C	KOG0749	Mitochondrial ADP/ATP carrier proteins
P62241	RPS8	24.205	57.806	42.3	7	8	7	1.05E+08	2.9E+08	1.396	nucleus	K02995	J	KOG3283	40S ribosomal protein S8
P10599	TXN	11.737	29.269	41	4	5	4	90494000	4.21E+08	1.38	extracellular	K03671	O	KOG0907	Thioredoxin
Q10588	BST1	35.724	16.501	6.9	2	2	2	17279000	61227000	1.378	extracellular	K18152			
P08579	SNRPB2	25.486	37.056	28	5	5	3	81171000	1.05E+08	1.377	nucleus	K11094	A	KOG4206	Spliceosomal protein snRNP-U1A/U2B
Q9Y4Z0	LSM4	15.35	14.511	11.5	2	2	2	23048000	50035000	1.375	cytoplasm,nucleus	K12623	A	KOG3293	Small nuclear ribonucleoprotein (snRNP)
P16070	CD44	81.537	27.406	5.1	3	3	3	65026000	1.7E+08	1.368	extracellular,plasma r	K06256			
P37837	TALDO1	37.54	11.011	7.4	2	2	2	10443000	34823000	1.367	mitochondria	K00616	G	KOG2772	Transaldolase
P62308	SNRPG	8.496	13.777	25	2	2	2	27941000	78527000	1.355	cytoplasm	K11099	A	KOG1780	Small Nuclear ribonucleoprotein G
O95831	AIFM1	66.9	20.785	8.8	3	3	3	11579000	46268000	1.338	mitochondria	K04727	T	KOG1346	Programmed cell death 8 (apoptosis-inducing factor)
Q15365	PCBP1	37.497	15.178	10.7	3	4	2	27243000	63739000	1.337	cytoskeleton	K12889	AR	KOG2190	PolyC-binding proteins alphaCP-1 and related KH domain proteins
P15144	ANPEP	109.54	22.262	7.1	3	3	3	27947000	82277000	1.328	endoplasmic reticulum	K11140	EO	KOG1046	Puromycin-sensitive aminopeptidase and related aminopeptidases
Q9Y3Y2	CHTOP	26.396	60.395	29.8	6	7	6	1.61E+08	4.72E+08	1.327	mitochondria				
P12236	SLC25A6	32.866	41.928	43.6	12	16	4	1.33E+08	4.68E+08	1.326	cytoplasm	K05863	C	KOG0749	Mitochondrial ADP/ATP carrier proteins
Q12965	MYO1E	127.06	75.718	13.2	10	10	10	1.04E+08	3.35E+08	1.325	cytoplasm	K10356	Z	KOG0164	Myosin class I heavy chain
P60953	CDC42	21.258	33.308	34.6	4	4	4	44736000	2.53E+08	1.319	cytoplasm	K04393	R	KOG0393	Ras-related small GTPase, Rho type
P23284	PPIB	23.742	59.35	34.3	7	10	7	99955000	3.67E+08	1.315	extracellular	K03768	O	KOG0880	Peptidyl-prolyl cis-trans isomerase
P83916	CBX1	21.418	24.182	24.9	4	5	3	21373000	46752000	1.298	nucleus	K11585			
P05556	ITGB1	88.414	51.146	15.3	7	8	7	82078000	2.87E+08	1.295	extracellular	K05719	TW	KOG1226	Integrin beta subunit (N-terminal portion of extracellular region)
P00441	SOD1	15.936	43.508	53.9	3	4	3	1.69E+08	6.67E+08	1.292	cytoplasm	K04565	P	KOG0441	Cu2+/Zn2+ superoxide dismutase SOD1
P11021	HSPA5	72.332	100.64	29.8	13	14	13	1.41E+08	3.36E+08	1.291	endoplasmic reticulum	K09490	O	KOG0101	Molecular chaperones HSP70/HSC70, HSP70 superfamily

P59998	ARPC4	19.667	49.465	39.9	6	7	6	86038000	2.39E+08	1.286	mitochondria	K05755	Z	KOG1876	Actin-related protein Arp2/3 complex, subunit ARPC4
P62820	RAB1A	22.677	21.346	22.9	3	3	2	49001000	1.12E+08	1.285	cytoplasm	K07874	TU	KOG0084	GTPase Rab1/YPT1, small G protein superfamily
P30043	BLVRB	22.119	22.664	25.7	3	3	3	19638000	72070000	1.284	cytoplasm	K05901			
P60174	TPI1	30.791	82.503	48.3	9	12	9	2.63E+08	7.77E+08	1.284	cytoplasm	K01803	G	KOG1643	Triosephosphate isomerase
P49755	TMED10	24.976	17.095	11.9	2	3	2	65658000	1.34E+08	1.278	extracellular	K20352	U	KOG1691	emp24/gp25L/p24 family of membrane trafficking proteins
Q04837	SSBP1	17.259	32.785	32.4	3	4	3	36110000	1.42E+08	1.278	nucleus	K03111	L	KOG1653	Single-stranded DNA-binding protein
P27348	YWHAQ	27.764	45.7	30.6	6	7	5	68082000	2.87E+08	1.277	cytoplasm	K16197	O	KOG0841	Multifunctional chaperone (14-3-3 family)
P20674	COX5A	16.762	30.699	26	4	9	4	1.34E+08	4.27E+08	1.267	mitochondria	K02264	C	KOG4077	Cytochrome c oxidase, subunit Va/COX6
Q9NZI8	IGF2BP1	63.48	34.163	10.6	4	5	3	46592000	1.15E+08	1.26	cytoplasm	K17391	AR	KOG2193	IGF-II mRNA-binding protein IMP, contains RRM and KH domains
O15145	ARPC3	20.546	14.718	20.8	2	2	2	31039000	86242000	1.254	cytoplasm	K05756	Z	KOG3155	Actin-related protein Arp2/3 complex, subunit ARPC3
Q99536	VAT1	41.92	29.445	16	4	4	4	12017000	73587000	1.249	cytoplasm		CR	KOG1198	Zinc-binding oxidoreductase
Q9Y3A2	UTP11	30.446	15.097	13.4	2	2	2	19442000	60785000	1.249	nucleus	K14769	S	KOG3237	Uncharacterized conserved protein
P04075	ALDOA	39.42	82.281	47.8	10	13	8	1.99E+08	4.83E+08	1.239	cytoplasm	K01623	G	KOG1557	Fructose-biphosphate aldolase
P04844	RPN2	69.283	71.392	29	8	9	8	58636000	5.4E+08	1.234	extracellular	K12667	O	KOG2447	Oligosaccharyltransferase, delta subunit (ribophorin II)
P22392	NME2	17.298	48.122	48	5	7	3	74551000	1.54E+08	1.234	cytoplasm	K00940	F	KOG0888	Nucleoside diphosphate kinase
P52907	CAPZA1	32.922	50.431	28	5	6	4	73449000	3.38E+08	1.234	cytoplasm	K10364	Z	KOG0836	F-actin capping protein, alpha subunit
P61981	YWHAG	28.302	49.691	42.9	8	10	6	72331000	5.13E+08	1.225	cytoplasm	K16198	O	KOG0841	Multifunctional chaperone (14-3-3 family)
Q15084	PDIA6	48.121	24.755	14.1	3	3	3	12260000	38116000	1.225	extracellular	K09584	O	KOG0191	Thioredoxin/protein disulfide isomerase
P68363	TUBA1B	50.151	175.57	62.7	19	29	0	8.13E+08	2.85E+09	1.221	cytoskeleton	K07374	Z	KOG1376	Alpha tubulin
P31943	HNRNPH1	49.229	32.803	14.9	4	4	4	28193000	78899000	1.209	nucleus	K12898	A	KOG4211	Splicing factor hnRNP-F and related RNA-binding proteins
P68032	ACTC1	42.019	43.304	44.8	19	50	3	99415000	4.12E+08	1.194	cytoskeleton	K12314	Z	KOG0676	Actin and related proteins
P38159	RBMX	42.331	37.335	15.9	5	6	5	65070000	2.34E+08	1.182	nucleus	K12885			
Q15428	SF3A2	49.255	28.014	9.5	3	4	3	46945000	1.42E+08	1.175	cytoplasm	K12826	A	KOG0227	Splicing factor 3a, subunit 2
Q14978	NOLC1	73.602	81.159	15.5	10	18	10	5.2E+08	1.16E+09	1.173	nucleus		Y	KOG2992	Nucleolar GTPase/ATPase p130
P62937	PPIA	18.012	86.457	58.2	9	14	9	3.04E+08	8.89E+08	1.169	cytoplasm	K03767	O	KOG0865	Cyclophilin type peptidyl-prolyl cis-trans isomerase
O00567	NOP56	66.049	77.556	26.1	10	12	10	89590000	2.55E+08	1.166	nucleus	K14564	AJ	KOG2572	Ribosome biogenesis protein - Nop58p/Nop5p
P61604	HSPE1	10.932	37.551	52	5	6	5	1.35E+08	3.03E+08	1.164	mitochondria	K04078	O	KOG1641	Mitochondrial chaperonin
Q14764	MVP	99.326	51.658	15.5	7	7	7	27365000	1.75E+08	1.16	cytoplasm	K17266			
P07919	UQCRH	10.739	23.867	19.8	1	3	1	46412000	82857000	1.159	extracellular	K00416	C	KOG4763	Ubiquinol-cytochrome c reductase hinge protein
Q9NX24	NHP2	17.201	49.201	68.6	5	7	5	2.37E+08	8.13E+08	1.155	cytoplasm	K11129	A	KOG3167	Box H/ACA snoRNP component, involved in ribosomal RNA pseudouridylation
P62314	SNRPD1	13.281	30.049	54.6	4	5	4	1.11E+08	2.86E+08	1.149	nucleus	K11087	A	KOG3428	Small nuclear ribonucleoprotein SMD1 and related snRNPs
Q9Y6C9	MTCH2	33.331	47.901	32	6	8	6	1.71E+08	6.16E+08	1.147	extracellular	K17885	R	KOG2745	Mitochondrial carrier protein
P43243	MATR3	94.622	55.917	12.9	6	6	6	1.63E+08	4.5E+08	1.144	nucleus	K13213			
P38646	HSPA9	73.68	131.03	29.5	15	16	15	2.34E+08	5.83E+08	1.136	mitochondria	K04043	O	KOG0102	Molecular chaperones mortalin/PBP74/GRP75, HSP70 superfamily
P62316	SNRPD2	13.527	51.649	67.8	8	8	8	1.03E+08	2.66E+08	1.136	cytoplasm	K11096	A	KOG3459	Small nuclear ribonucleoprotein (snRNP) Sm core protein
P22626	HNRNPA2B	37.429	143.87	55.5	17	25	17	4.85E+08	1.54E+09	1.131	nucleus	K13158	R	KOG0118	FOG: RRM domain
P54289	CACNA2D1	124.57	37.792	7.9	6	6	6	22916000	1.12E+08	1.121	plasma membrane	K04859	PT	KOG2353	L-type voltage-dependent Ca <sup>2+</sup> channel, alpha2/delta subunit
P62879	GNB2	37.331	11.35	19.1	4	6	1	21775000	68770000	1.121	cytoplasm	K04537	R	KOG0286	G-protein beta subunit
P53999	SUB1	14.395	29.265	37	4	4	4	64254000	1.45E+08	1.12	nucleus		K	KOG2712	Transcriptional coactivator
P38919	EIF4A3	46.871	33.937	18.2	5	5	4	57083000	1.68E+08	1.116	nucleus	K13025	J	KOG0327	Translation initiation factor 4F, helicase subunit (eIF-4A) and related helicases
P31949	S100A11	11.74	19.958	45.7	2	3	2	1.51E+08	8.2E+08	1.114	cytoplasm				
P22087	FBL	33.784	157.07	58.6	14	28	13	1.68E+09	6.15E+09	1.109	nucleus	K14563	A	KOG1596	Fibrillarin and related nucleolar RNA-binding proteins
O75955	FLOT1	47.355	100.79	33.7	10	14	10	2.01E+08	4.76E+08	1.107	cytoplasm	K07192	UZ	KOG2668	Flotillins
P62753	RPS6	28.68	40.198	22.9	5	5	5	61555000	1.08E+08	1.107	cytoplasm	K02991	J	KOG1646	40S ribosomal protein S6
Q14254	FLOT2	47.064	104.2	34.8	11	14	11	2.27E+08	6.18E+08	1.105	cytoplasm	K07192	UZ	KOG2668	Flotillins
Q9NS69	TOMM22	15.521	42.084	66.2	5	6	5	88148000	1.97E+08	1.096	cytoplasm	K17769	U	KOG4111	Translocase of outer mitochondrial membrane complex, subunit TOM22
Q5SSJ5	HP1BP3	61.206	25.639	7.6	4	4	4	11907000	54544000	1.095	nucleus		B	KOG4012	Histone H1
P04083	ANXA1	38.714	175.13	60.4	17	24	17	6.82E+08	1.99E+09	1.091	cytoplasm	K17091	U	KOG0819	Annexin
P46087	NOP2	89.301	23.223	4.7	3	4	3	26268000	59835000	1.09	nucleus	K14835	A	KOG1122	tRNA and rRNA cytosine-C5-methylase (nucleolar protein NOL1/NOP2)
Q02543	RPL18A	20.762	22.969	16.5	3	3	3	26262000	50653000	1.089	nucleus	K02882	J	KOG0829	60S ribosomal protein L18A
Q9H1E3	NUCKS1	27.296	21.183	17.7	3	5	3	16198000	37669000	1.088	nucleus				



P55769	SNU13	14.173	78.825	68.8	9	12	9	5.35E+08	2.3E+09	1.084	cytoplasm	K12845	AJ	KOG3387	60S ribosomal protein 15.5kD/SNU13, NHP2/L7A family
P14406	COX7A2	9.3959	16.479	27.7	2	2	2	67689000	2.08E+08	1.08	mitochondria	K02270			(includes ribonuclease P subunit p38), involved in splicing
P10809	HSPD1	61.054	116.04	33	15	18	15	3.57E+08	7.7E+08	1.077	mitochondria	K04077	O	KOG0356	Mitochondrial chaperonin, Cpn60/Hsp60p
P07195	LDHB	36.638	75.239	38.6	10	13	9	2.05E+08	5.79E+08	1.076	cytoplasm	K00016	C	KOG1495	Lactate dehydrogenase
P07437	TUBB	49.67	42.713	41.2	13	21	3	1.08E+08	4.59E+08	1.072	cytoplasm,nucleus	K07375	Z	KOG1375	Beta tubulin
P14625	HSP90B1	92.468	50.801	16.4	8	8	7	53330000	2.29E+08	1.07	endoplasmic reticulum	K09487	O	KOG0020	Endoplasmic reticulum glucose-regulated protein (GRP94/endoplasmic)
Q96AE4	FUBP1	67.56	23.382	5.3	3	4	3	16929000	32690000	1.069	cytoplasm	K13210	A	KOG1676	K-homology type RNA binding proteins
Q12906	ILF3	95.337	104.35	23.2	12	15	12	3.75E+08	9.15E+08	1.066	nucleus	K13090	R	KOG3792	Transcription factor NFAT, subunit NF90
P14854	COX6B1	10.192	21.178	47.7	3	4	3	70423000	2.04E+08	1.058	extracellular	K02267	C	KOG3057	Cytochrome c oxidase, subunit VIb/COX12
Q05639	EEF1A2	50.47	15.094	41	11	16	2	56349000	1.9E+08	1.048	cytoplasm	K03231	J	KOG0052	Translation elongation factor EF-1 alpha/Tu
P24534	EEF1B2	24.763	12.633	22.2	2	2	2	15912000	39326000	1.046	nucleus	K03232	K	KOG1668	Elongation factor 1 beta/delta chain
P84090	ERH	12.259	32.627	64.4	4	4	4	1.13E+08	3.98E+08	1.043	cytoplasm		R	KOG1766	Enhancer of rudimentary
P62826	RAN	24.423	79.21	43.1	9	12	9	2.2E+08	6.14E+08	1.041	cytoplasm	K07936	U	KOG0096	GTPase Ran/TC4/GSP1 (nuclear protein transport pathway), small G protein
Q92522	H1FX	22.487	5.5407	5.6	1	2	1	1.28E+08	2.47E+09	1.034	nucleus	K11275	B	KOG4012	Histone H1
P62258	YWHAE	29.174	56.839	35.3	8	8	7	1.07E+08	3.27E+08	1.033	cytoplasm	K06630	O	KOG0841	Multifunctional chaperone (14-3-3 family)
P11142	HSPA8	70.897	177.54	42.1	19	25	14	9.59E+08	1.8E+09	1.031	cytoplasm	K03283	O	KOG0101	Molecular chaperones HSP70/HSC70, HSP70 superfamily
Q9Y2R4	DDX52	67.497	12.764	4.5	2	4	2	18669000	30965000	1.028	nucleus	K14779	A	KOG0344	ATP-dependent RNA helicase
Q8N3V7	SYNPO	99.462	22.52	5	3	3	3	20215000	43332000	1.024	nucleus	K21112			
Q9BZE4	GTPBP4	73.964	11.716	5.5	2	2	2	20259000	43118000	1.022	cytoplasm	K06943	R	KOG1490	GTP-binding protein CRFG/NOG1 (ODN superfamily)
P00338	LDHA	36.688	87.39	58.7	12	13	11	2.07E+08	4.46E+08	1.014	cytoplasm	K00016	C	KOG1495	Lactate dehydrogenase
Q969Q0	RPL36AL	12.469	12.836	16	2	2	2	28577000	49748000	1.012	extracellular	K02929	J	KOG3464	60S ribosomal protein L44
P54727	RAD23B	43.171	11.76	5.9	2	2	2	14483000	21159000	1.01	cytoplasm	K10839	L	KOG0011	Nucleotide excision repair factor NEF2, RAD23 component
P67809	YBX1	35.924	31.287	20.4	3	3	2	49915000	77928000	1.007	nucleus	K09276	J	KOG3070	Predicted RNA-binding protein containing PIN domain
P13073	COX4I1	19.576	32.266	26	4	4	4	1.28E+08	3.7E+08	1.003	mitochondria	K02263	C	KOG4075	Cytochrome c oxidase, subunit IV/COX5b
Q96A72	MAGOHB	17.276	23.805	29.7	3	4	3	94435000	87526000		1 cytoplasm	K12877	A	KOG3392	Exon-exon junction complex, Magoh component
O14950	MYL12B	19.779	5.634	83.7	15	51	1	1.73E+08	1.29E+09	0.999	mitochondria	K12757	Z	KOG0031	Myosin regulatory light chain, EF-Hand protein superfamily
P46782	RPS5	22.876	25.987	30.9	3	6	3	1.28E+08	3.48E+08	0.992	cytoplasm	K02989	J	KOG3291	Ribosomal protein S7
Q15061	WDR43	74.89	11.627	5.3	2	2	2	18118000	51542000	0.983	cytoplasm	K14546	R	KOG4547	WD40 repeat-containing protein
P62701	RPS4X	29.597	72.339	37.3	9	10	9	2.4E+08	4.93E+08	0.968	cytoplasm	K02987	J	KOG0378	40S ribosomal protein S4
P51858	HDGF	26.788	101.39	51.2	10	14	10	6.04E+08	9.68E+08	0.962	nucleus	K16641			
Q1KMD3	HNRNPUL2	85.104	45.15	15.4	6	6	6	2.61E+09	1.86E+08	0.957	nucleus				
P36873	PPP1CC	36.983	36.626	23.2	5	5	5	22655000	87564000	0.954	cytoplasm	K06269			
O75569	PRKRA	34.404	31.566	18.2	4	4	4	56338000	1.37E+08	0.953	cytoplasm		UK	KOG3732	Staufen and related double-stranded-RNA-binding proteins
P08195	SLC3A2	67.993	42.579	13.3	5	5	5	64992000	1.09E+08	0.951	endoplasmic reticulum	K06519	G	KOG0471	Alpha-amylase
P14678	SNRPB	24.61	49.941	21.7	7	9	7	1.55E+08	3.59E+08	0.95	cytoplasm	K11086	K	KOG3168	U1 snRNP component
P09382	LGALS1	14.716	65.318	60.7	7	9	7	2.77E+08	9.05E+08	0.947	extracellular	K06830	W	KOG3587	Galectin, galactose-binding lectin
P36578	RPL4	47.697	49.215	20.6	6	7	6	2.33E+08	5.65E+08	0.944	cytoplasm	K02930	A	KOG1475	Ribosomal protein RPL1/RPL2/RL4L4
P18669	PGAM1	28.804	29.875	32.7	4	5	4	1.25E+08	2.47E+08	0.941	cytoplasm	K01834	G	KOG0235	Phosphoglycerate mutase
P23528	CFL1	18.502	92.828	71.1	11	16	8	6.03E+08	1.75E+09	0.941	mitochondria	K05765	Z	KOG1735	Actin depolymerizing factor
P30050	RPL12	17.818	56.55	49.7	6	6	6	1.31E+08	3.33E+08	0.935	cytoplasm	K02870	J	KOG0886	40S ribosomal protein S2
P62910	RPL32	15.86	32.515	33.3	4	6	4	41599000	70131000	0.935	cytoplasm	K02912	J	KOG0878	60S ribosomal protein L32
P41208	CETN2	19.738	15.793	17.4	2	3	2	22533000	47340000	0.933	nucleus	K10840	ZD	KOG0028	Ca <sup>2+</sup> -binding protein (centrin/caltractin), EF-Hand superfamily protein
Q99848	EBNA1BP2	34.852	44.547	22.2	5	8	5	1.56E+08	3.33E+08	0.933	nucleus	K14823	A	KOG3080	Nucleolar protein-like/EBNA1-binding protein
Q9Y277	VDAC3	30.658	84.84	45.2	9	13	9	1.88E+08	4.46E+08	0.933	cytoplasm	K15041	P	KOG3126	Porin/voltage-dependent anion-selective channel protein
Q9NY12	GAR1	22.348	39.287	27.2	6	7	6	2.28E+08	6.74E+08	0.93	cytoplasm	K11128	J	KOG3262	H/ACA small nucleolar RNP component GAR1
Q9UJZ1	STOML2	38.534	79.115	37.1	8	12	8	1.66E+08	3.87E+08	0.93	mitochondria		C	KOG2620	Prohibitins and stomatins of the PID superfamily
P62913	RPL11	20.252	28.274	19.7	3	3	3	58378000	1.04E+08	0.924	cytoplasm	K02868	J	KOG0397	60S ribosomal protein L11
P18077	RPL35A	12.538	12.206	14.5	2	2	2	30936000	45372000	0.921	cytoplasm	K02917	J	KOG0887	60S ribosomal protein L35A/L37
P27635	RPL10	24.604	20.039	23.8	3	4	3	60694000	1.39E+08	0.92	cytoplasm	K02866	J	KOG0857	60s ribosomal protein L10
O43169	CYB5B	16.332	16.541	23.3	1	2	1	69509000	2.15E+08	0.917	peroxisome		C	KOG0537	Cytochrome b5
P11940	PABPC1	70.67	15.494	6.3	2	2	2	24395000	44159000	0.917	nucleus	K13126	AJ	KOG0123	Polyadenylate-binding protein (RRM superfamily)



O43707	ACTN4	104.85	323.31	71.2	48	80	33	3.96E+09	1.17E+10	0.915	cytoplasm	K05699	Z	KOG0035	Ca <sup>2+</sup> -binding actin-bundling protein (actinin), alpha chain
P50395	GDI2	50.663	15.426	4.5	2	3	2	53585000	88082000	0.913	endoplasmic reticulum	K17255	O	KOG1439	RAB proteins geranylgeranyltransferase component A (RAB escort protein)
P52209	PGD	53.139	31.17	13.7	5	6	5	53902000	1.39E+08	0.913	cytoplasm,nucleus	K00033	G	KOG2653	6-phosphogluconate dehydrogenase
Q16891	IMMT	83.677	211.6	43.3	24	32	24	8.46E+08	1.83E+09	0.903	mitochondria	K17785	M	KOG1854	Mitochondrial inner membrane protein (mitofilin)
Q9Y512	SAMM50	51.976	51.727	16.6	6	6	6	1.05E+08	1.59E+08	0.898	cytoplasm	K07277	R	KOG2602	Predicted cell surface protein homologous to bacterial outer membrane proteins
P17676	CEBPB	36.105	38.469	19.1	4	5	4	35107000	74370000	0.895	nucleus	K10048			
P62318	SNRPD3	13.916	51.628	53.2	5	8	5	2.81E+08	6.62E+08	0.892	cytoplasm	K11088	A	KOG3172	Small nuclear ribonucleoprotein Sm D3
Q9NR30	DDX21	87.343	11.949	4.2	2	2	2	17984000	41203000	0.888	cytoplasm,nucleus	K16911	A	KOG0331	ATP-dependent RNA helicase
P13639	EEF2	95.337	39.816	13.6	6	7	6	46310000	97633000	0.886	cytoplasm	K03234	J	KOG0469	Elongation factor 2
P46783	RPS10	18.898	48.493	38.2	5	10	5	2.29E+08	2.15E+09	0.886	nucleus	K02947	J	KOG3344	40s ribosomal protein s10
P18754	RCC1	44.969	115.39	50.8	11	14	11	3.86E+08	8.69E+08	0.882	nucleus	K11493			
Q9NVP1	DDX18	75.406	24.057	6.3	3	3	3	45458000	76925000	0.879	nucleus	K13179	A	KOG0342	ATP-dependent RNA helicase pitchoune
Q15287	RNPS1	34.208	48.054	23.3	5	8	5	1.43E+08	3.32E+08	0.875	nucleus	K14325	A	KOG4209	Splicing factor RNPS1, SR protein superfamily
P25398	RPS12	14.515	25.109	34.1	3	5	3	49025000	71815000	0.874	cytoplasm	K02951	J	KOG3406	40S ribosomal protein S12
P40429	RPL13A	23.577	19.102	14.8	3	3	3	29247000	57904000	0.869	cytoplasm	K02872	J	KOG3204	60S ribosomal protein L13a
P14618	PKM	57.936	294.48	72.5	27	40	27	1.68E+09	4.14E+09	0.867	cytoplasm	K00873	G	KOG2323	Pyruvate kinase
P55072	VCP	89.321	27.984	7.4	4	5	4	46812000	81607000	0.847	cytoplasm,nucleus	K13525	O	KOG0730	AAA+-type ATPase
P06733	ENO1	47.168	186.92	53.5	15	22	15	5.24E+08	1.22E+09	0.845	cytoplasm	K01689	G	KOG2670	Enolase
P07237	P4HB	57.116	21.837	8.5	4	4	4	29359000	83374000	0.838	extracellular	K09580	O	KOG0190	Protein disulfide isomerase (prolyl 4-hydroxylase beta subunit)
O75367	H2AFY	39.617	183.62	68.8	17	28	15	9.41E+08	2.56E+09	0.836	mitochondria	K11251	BK	KOG2633	Hismacro and SEC14 domain-containing proteins
Q00688	FKBP3	25.177	23.618	16.5	3	3	3	14188000	25173000	0.836	cytoplasm	K09570	O	KOG0544	FKBP-type peptidyl-prolyl cis-trans isomerase
P63261	ACTG1	41.792	323.31	95.5	38	130	2	1.18E+10	6.32E+10	0.834	cytoskeleton	K05692	Z	KOG0676	Actin and related proteins
P09972	ALDOC	39.455	18.737	16.8	4	6	2	86404000	2.53E+08	0.832	cytoplasm	K01623	G	KOG1557	Fructose-biphosphate aldolase
Q96C19	EFHD2	26.697	84.193	43.3	11	12	11	3.51E+08	9.06E+08	0.829	cytoplasm		R	KOG0041	Predicted Ca <sup>2+</sup> -binding protein, EF-Hand protein superfamily
P31930	UQCRC1	52.645	37.454	12.5	4	5	4	82151000	3.28E+08	0.821	mitochondria	K00414	O	KOG0960	Mitochondrial processing peptidase, beta subunit, and related enzymes
P07900	HSP90AA1	84.659	35.3	16	10	13	4	41650000	78295000	0.82	cytoplasm	K04079	O	KOG0020	Endoplasmic reticulum glucose-regulated protein (GRP94/endoplasmic)
Q6DKI1	RPL7L1	28.661	38.509	31.3	6	6	6	1.08E+08	2.08E+08	0.815	cytoplasm		J	KOG3184	60S ribosomal protein L7
P08238	HSP90AB1	83.263	106.07	25	14	16	6	2.42E+08	3.57E+08	0.814	cytoplasm	K04079	O	KOG0020	Endoplasmic reticulum glucose-regulated protein (GRP94/endoplasmic)
Q99729	HNRNPAB	36.224	22.316	12.7	3	4	3	61885000	99963000	0.812	nucleus	K13044	R	KOG0118	FOG: RRM domain
P28331	NDUFS1	79.467	36.535	13.6	5	5	5	42678000	1.37E+08	0.81	mitochondria	K03934	C	KOG2282	NADH-ubiquinone oxidoreductase, NDUFS1/75 kDa subunit
Q15149	PLEC	531.78	323.31	29.7	100	118	100	2.25E+09	4.12E+09	0.807	cytoplasm,nucleus	K10388	J	KOG3344	40s ribosomal protein s10
P56182	RRP1	52.839	26.155	13.7	4	4	4	38706000	92684000	0.804	nucleus	K14849	A	KOG3911	Nucleolar protein NOP52/RRP1
Q00059	TFAM	29.096	66.881	30.9	8	13	8	5.17E+08	8.46E+08	0.798	mitochondria	K11830	R	KOG0381	HMG box-containing protein
Q15427	SF3B4	44.385	17.566	11.1	2	3	2	1.01E+08	2.84E+08	0.795	nucleus	K12831	A	KOG0131	Splicing factor 3b, subunit 4
Q86V81	ALYREF	26.888	108.35	49.4	11	15	11	6.28E+08	1.66E+09	0.792	cytoplasm	K12881	A	KOG0533	RRM motif-containing protein
P45880	VDAC2	31.566	142.4	60.9	14	22	14	5.72E+08	1.22E+09	0.788	cytoplasm	K15040	P	KOG3126	Porin/voltage-dependent anion-selective channel protein
Q7Z406	MYH14	227.87	37.842	8.1	16	26	5	1.67E+08	2E+09	0.788	nucleus	K10352	Z	KOG0161	Myosin class II heavy chain
P05388	RPLP0	34.273	26.453	20.8	4	4	4	68020000	1.36E+08	0.78	cytoplasm,nucleus	K02941	J	KOG0815	60S acidic ribosomal protein P0
Q07021	C1QBP	31.362	23.571	21.6	3	3	3	32473000	1.04E+08	0.778	mitochondria	K15414	V	KOG4024	Complement component 1, Q subcomponent binding protein
P21796	VDAC1	30.772	176.48	79.2	16	29	16	1.01E+09	2.48E+09	0.77	cytoplasm	K05862	P	KOG3126	Porin/voltage-dependent anion-selective channel protein
P39023	RPL3	46.108	18.71	14.4	3	3	3	39271000	1.08E+08	0.77	cytoplasm	K02925	J	KOG0746	60S ribosomal protein L3 and related proteins
P60660	MYL6	16.93	135.52	81.5	12	37	10	2.94E+09	1.82E+10	0.767	cytoplasm	K12751	Z	KOG0030	Myosin essential light chain, EF-Hand protein superfamily
P15880	RPS2	31.324	78.112	42.7	10	11	10	2.5E+08	4.63E+08	0.76	cytoplasm	K02981	J	KOG0877	40S ribosomal protein S2/30S ribosomal protein S5
P15559	NQO1	30.867	38.08	22.6	4	6	4	1.7E+08	3.5E+08	0.759	cytoplasm	K00355			
P36542	ATP5F1C	32.996	12.471	6	2	2	2	20420000	31931000	0.757	mitochondria	K02136	C	KOG1531	F0F1-type ATP synthase, gamma subunit
P62424	RPL7A	29.995	84.3	37.6	10	11	10	2.38E+08	3.96E+08	0.757	cytoplasm	K02936	J	KOG3166	60S ribosomal protein L7A
P05204	HMG2	9.3926	27.167	16.7	4	6	4	56696000	69429000	0.756	nucleus	K11300			
Q8TDN6	BRX1	41.401	61.244	30.6	8	11	8	1.79E+08	4.4E+08	0.754	nucleus	K14820	J	KOG2971	RNA-binding protein required for biogenesis of the ribosomal 60S subunit
Q9Y2X3	NOP58	59.578	122.37	36.1	13	18	13	3.39E+08	6.82E+08	0.753	cytoplasm	K14565	AJ	KOG2572	Ribosome biogenesis protein - Nop58p/Nop5p
Q9Y221	NIP7	20.462	22.283	29.4	3	3	3	46442000	69574000	0.752	cytoplasm	K07565	J	KOG3492	Ribosome biogenesis protein NIP7
P04406	GAPDH	36.053	139.2	68.7	15	28	15	1.03E+09	2.3E+09	0.74	cytoplasm	K00134	G	KOG0657	Glyceraldehyde 3-phosphate dehydrogenase

P61353	RPL27	15.798	31.496	36	4	5	4	1.35E+08	2.7E+08	0.737	mitochondria	K02901	J	KOG3418	60S ribosomal protein L27
O00422	SAP18	17.561	71.412	62.1	9	12	9	3.05E+08	5.32E+08	0.722	nucleus	K14324	K	KOG3391	Transcriptional co-repressor component
P56537	EIF6	26.599	27.552	17.1	2	3	2	72516000	1.24E+08	0.717	cytoplasm,nucleus	K03264	J	KOG3185	Translation initiation factor 6 (eIF-6)
O76021	RSL1D1	54.972	134.21	30	15	20	15	7.98E+08	1.65E+09	0.714	nucleus	K14775	S	KOG1685	Uncharacterized conserved protein
P23396	RPS3	26.688	125.98	67.5	16	18	16	5.34E+08	9.96E+08	0.711	cytoplasm	K02985	J	KOG3181	40S ribosomal protein S3
Q5JTH9	RRP12	143.7	23.91	3.9	4	4	4	34147000	37577000	0.71	nucleus	K14794	S	KOG1248	Uncharacterized conserved protein
Q15397	PUM3	73.584	40.877	13.1	5	5	5	1.07E+08	2.28E+08	0.709	nucleus	K14844	J	KOG2050	Puf family RNA-binding protein
Q9BYG3	NIFK	34.222	48.093	27.3	5	5	5	88678000	1.41E+08	0.708	nucleus	K14838	R	KOG4208	Nucleolar RNA-binding protein NIFK
P46779	RPL28	15.747	17.872	18.2	3	3	3	22805000	45762000	0.701	mitochondria	K02903	J	KOG3412	60S ribosomal protein L28
P06703	S100A6	10.18	35.47	74.4	5	7	5	5.37E+08	1.11E+09	0.697	cytoplasm				
P18621	RPL17	21.397	25.202	23.9	3	5	3	95331000	1.43E+08	0.693	cytoplasm	K02880	J	KOG3353	60S ribosomal protein L22
Q02878	RPL6	32.728	81.771	37.2	11	16	11	2.96E+08	4.13E+08	0.693	cytoplasm	K02934	J	KOG1694	60s ribosomal protein L6
Q12905	ILF2	43.062	174.06	65.6	17	25	17	1.44E+09	3.32E+09	0.689	cytoplasm	K13089	K	KOG3793	Transcription factor NFAT, subunit NF45
P62280	RPS11	18.431	49.374	39.2	6	8	6	1.97E+08	3.53E+08	0.684	cytoplasm	K02949	J	KOG1728	40S ribosomal protein S11
P62888	RPL30	12.784	42.476	59.1	5	6	5	1.13E+08	1.62E+08	0.678	cytoplasm	K02908	J	KOG2988	60S ribosomal protein L30
Q9UNX3	RPL26L1	17.256	25.098	22.8	4	4	4	90882000	1.21E+08	0.674	nucleus	K02898	J	KOG3401	60S ribosomal protein L26
P55209	NAPIL1	45.374	21.934	11.8	3	3	3	61753000	64006000	0.67	cytoplasm,nucleus	K11279	BD	KOG1507	Nucleosome assembly protein NAP-1
P62906	RPL10A	24.831	53.658	31.3	6	10	6	2.77E+08	4.28E+08	0.665	cytoplasm,nucleus	K02865	J	KOG1570	60S ribosomal protein L10A
Q9UKM9	RALY	32.463	93.93	35.9	10	13	10	8.7E+08	1.77E+09	0.663	nucleus	K12895	R	KOG0118	FOG: RRM domain
P12956	XRCC6	69.842	12.043	3.3	2	2	2	17643000	19575000	0.661	cytoplasm	K10884	L	KOG2327	DNA-binding subunit of a DNA-dependent protein kinase (Ku70 autoantigen)
P00403	MT-CO2	25.565	38.93	36.1	6	6	6	1.62E+08	4.85E+08	0.657	plasma membrane	K02261	C	KOG4767	Cytochrome c oxidase, subunit II, and related proteins
P62269	RPS18	17.718	60.012	39.5	8	9	8	3.41E+08	6.87E+08	0.655	cytoplasm	K02964	J	KOG3311	Ribosomal protein S18
P09661	SNRPA1	28.415	59.861	25.5	5	9	5	91111000	2.69E+08	0.651	cytoplasm,nucleus	K11092	A	KOG1644	U2-associated snRNP A' protein
P63167	DYNLL1	10.366	21.284	37.1	2	4	1	61457000	1.12E+08	0.651	cytoplasm	K10418	Z	KOG3430	Dynein light chain type 1
Q9NR12	PDLIM7	49.844	27.028	17.9	4	4	4	86490000	1.08E+08	0.649	nucleus		TZ	KOG1703	Adaptor protein Enigma and related PDZ-LIM proteins
Q07020	RPL18	21.634	36.453	25	4	4	4	1.55E+08	3.12E+08	0.646	cytoplasm	K02883	J	KOG1714	60s ribosomal protein L18
Q9Y265	RUVBL1	50.227	20.391	11.6	3	4	3	44830000	55353000	0.628	cytoplasm	K04499	L	KOG1942	DNA helicase, TBP-interacting protein
P18124	RPL7	29.225	42.776	28.6	6	7	6	2.75E+08	3.73E+08	0.625	cytoplasm	K02937	J	KOG3184	60S ribosomal protein L7
P19105	MYL12A	19.794	179.35	84.2	15	50	1	3.05E+09	2.09E+10	0.625	mitochondria	K12757	Z	KOG0031	Myosin regulatory light chain, EF-Hand protein superfamily
Q9UKD2	MRTO4	27.56	12.488	9.6	2	3	2	57565000	74974000	0.623	nucleus	K14815	A	KOG0816	Protein involved in mRNA turnover
Q71UM5	RPS27L	9.4771	6.5039	15.5	1	2	1	60770000	88218000	0.622	extracellular	K02978	J	KOG1779	40s ribosomal protein S27
P63241	EIF5A	16.832	57.264	51.3	6	8	6	1.28E+08	1.85E+08	0.621	cytoplasm	K03263	J	KOG3271	Translation initiation factor 5A (eIF-5A)
O96008	TOMM40	37.893	85.027	53.7	9	13	9	4.5E+08	7.87E+08	0.62	nucleus	K11518	U	KOG3296	Translocase of outer mitochondrial membrane complex, subunit TOM40
P06748	NPM1	32.575	144.37	46.9	12	29	12	3.07E+09	5.91E+09	0.618	nucleus	K11276			
P31946	YWHAB	28.082	22.27	22.8	4	4	2	57969000	57058000	0.618	cytoplasm	K16197	O	KOG0841	Multifunctional chaperone (14-3-3 family)
P08708	RPS17	15.55	24.623	40	3	6	3	2.92E+08	4.32E+08	0.615	cytoplasm	K02962	J	KOG0187	40S ribosomal protein S17
P49207	RPL34	13.293	12.89	12.8	2	2	2	44205000	58632000	0.614	nucleus	K02915	J	KOG1790	60s ribosomal protein L34
P62841	RPS15	17.04	38.447	55.2	4	8	4	3.17E+08	6.08E+08	0.612	cytoplasm	K02958	J	KOG0898	40S ribosomal protein S15
P26447	S100A4	11.728	12.93	18.8	2	2	2	93639000	1.8E+08	0.61	extracellular				
P62277	RPS13	17.222	51.239	39.1	7	9	7	5.5E+08	1.2E+09	0.604	cytoplasm	K02953	J	KOG0400	40S ribosomal protein S13
Q9H7B2	RPF2	35.582	42.586	21.9	6	8	6	1.4E+08	2.08E+08	0.603	nucleus	K14847	J	KOG3031	Protein required for biogenesis of the ribosomal 60S subunit
P62854	RPS26	13.015	15.56	23.5	2	3	2	48127000	1E+08	0.602	cytoplasm		J	KOG1768	40s ribosomal protein S26
Q13765	NACA	23.384	20.383	13	2	2	2	24197000	28341000	0.602	cytoplasm	K03626	K	KOG2239	Transcription factor containing NAC and TS-N domains
P62829	RPL23	14.865	44.385	40	5	6	5	2.54E+08	3.93E+08	0.599	cytoplasm	K02894	J	KOG0901	60S ribosomal protein L14/L17/L23
P42766	RPL35	14.551	25.603	26	3	4	3	1.54E+08	1.98E+08	0.598	cytoplasm	K02918	J	KOG3436	60S ribosomal protein L35
P46781	RPS9	22.591	44.901	26.8	7	8	7	1.33E+08	2.24E+08	0.593	cytoplasm	K02997	J	KOG3301	Ribosomal protein S4
P39019	RPS19	16.06	55.907	38.6	8	9	8	2.98E+08	5.26E+08	0.588	cytoplasm	K02966	J	KOG3411	40S ribosomal protein S19
P83731	RPL24	17.779	13.67	13.4	2	2	2	61961000	82579000	0.587	cytoplasm	K02896	J	KOG1722	60s ribosomal protein L24
Q15366	PCBP2	38.58	73.114	40.5	8	12	7	4.08E+08	6.04E+08	0.577	cytoskeleton	K13162	AR	KOG2190	PolyC-binding proteins alphaCP-1 and related KH domain proteins
P19338	NCL	76.613	125.15	22.4	12	18	12	7.46E+08	1.24E+09	0.574	nucleus	K11294			
Q14974	KPNB1	97.169	12.635	2.7	2	2	2	24081000	32380000	0.574	cytoplasm	K14293	YU	KOG1241	Karyopherin (importin) beta 1

Q9H6F5	CCDC86	40.235	22.937	14.7	4	4	4	42139000	52210000	0.574	nucleus	K14822	R	KOG4538	Predicted coiled-coil protein
P05387	RPLP2	11.665	34.534	55.7	3	5	3	2.14E+08	3.2E+08	0.571	mitochondria	K02943	J	KOG3449	60S acidic ribosomal protein P2
P84243	H3F3A	15.328	26.518	61.8	12	32	2	2.33E+09	5.39E+09	0.567	nucleus	K11253	B	KOG1745	Histones H3 and H4
O75475	PSIP1	60.103	84.796	19.8	8	14	8	5.52E+08	7.73E+08	0.562	nucleus		K	KOG1904	Transcription coactivator
P62750	RPL23A	17.695	52.689	43.6	7	8	7	5.71E+08	8.69E+08	0.56	cytoplasm	K02893	J	KOG1751	60s ribosomal protein L23
O75531	BANF1	10.058	59.517	70.8	7	14	7	2.79E+09	5.27E+09	0.556	extracellular	K21870	BL	KOG4233	DNA-bridging protein BAF
P62861	FAU	6.6478	13.507	18.6	2	2	2	83690000	1.29E+08	0.556	nucleus	K02983	JO	KOG0009	Ubiquitin-like/40S ribosomal S30 protein fusion
Q9Y3U8	RPL36	12.254	21.984	21	3	3	3	1.07E+08	1.59E+08	0.556	nucleus	K02920	J	KOG3452	60S ribosomal protein L36
P05386	RPLP1	11.514	13.495	51.8	2	2	2	1.49E+08	2.32E+08	0.549	mitochondria	K02942	J	KOG1762	60s acidic ribosomal protein P1
O14880	MGST3	16.516	60.521	53.3	6	8	6	2.27E+08	1.09E+09	0.533	extracellular	K00799			
P17096	HMGA1	11.676	45.363	23.4	4	7	4	3.18E+08	6.19E+08	0.533	nucleus	K09282			
P46776	RPL27A	16.561	26.317	22.3	4	4	4	1.45E+08	1.4E+08	0.528	cytoplasm	K02900	J	KOG1742	60s ribosomal protein L15/L27
P68104	EEF1A1	50.14	166.43	52.2	17	29	8	1.61E+09	2.65E+09	0.526	cytoplasm	K03231	J	KOG0052	Translation elongation factor EF-1 alpha/Tu
P62899	RPL31	14.463	21.781	24.8	3	4	3	3.06E+08	4.24E+08	0.518	cytoplasm	K02910	J	KOG0893	60S ribosomal protein L31
P61247	RPS3A	29.945	61.179	34.5	8	10	8	2.94E+08	3.69E+08	0.511	nucleus	K02984	J	KOG1628	40S ribosomal protein S3A
P46778	RPL21	18.565	15.276	16.2	2	2	2	66782000	69890000	0.504	nucleus	K02889	J	KOG1732	60S ribosomal protein L21
P62081	RPS7	22.127	60.573	52.1	8	11	8	6.25E+08	9.42E+08	0.499	cytoplasm	K02993	J	KOG3320	40S ribosomal protein S7
Q92979	EMG1	26.72	18.191	18	3	3	3	62994000	62197000	0.496	nucleus	K14568			
P45973	CBX5	22.225	21.197	30.9	4	6	3	1.21E+08	99991000	0.48	nucleus	K11587			
P62266	RPS23	15.807	21.79	27.3	3	3	3	1.02E+08	1.63E+08	0.478	cytoplasm	K02973	J	KOG1749	40S ribosomal protein S23
P62249	RPS16	16.445	31.819	26.7	4	5	4	2.13E+08	3.16E+08	0.477	cytoplasm	K02960	J	KOG1753	40S ribosomal protein S16
P60866	RPS20	13.373	24.91	22.7	3	6	3	4.49E+08	6.5E+08	0.471	cytoplasm	K02969	J	KOG0900	40S ribosomal protein S20
P62917	RPL8	28.024	12.285	10.5	2	2	2	17638000	20150000	0.464	cytoplasm	K02938	J	KOG2309	60s ribosomal protein L2/L8
P35268	RPL22	14.787	23.328	30.5	2	2	2	2.33E+08	4.18E+08	0.459	nucleus	K02891	J	KOG3434	60S ribosomal protein L22
P62847	RPS24	15.423	18.4	20.3	2	2	2	1.89E+08	3.15E+08	0.456	cytoplasm	K02974	J	KOG3424	40S ribosomal protein S24
P26373	RPL13	24.261	22.164	11.4	2	3	2	1.42E+08	4.25E+08	0.446	cytoplasm	K02873	J	KOG3295	60S Ribosomal protein L13
P07910	HNRNPC	33.67	153.89	50.7	17	34	17	3.5E+09	7.76E+09	0.441	nucleus	K12884	R	KOG0118	FOG: RRM domain
P62979	RPS27A	17.965	55.233	42.3	6	14	6	7.7E+08	1.55E+09	0.44	extracellular	K02977	J	KOG0004	Ubiquitin/40S ribosomal protein S27a fusion
P62851	RPS25	13.742	21.177	22.4	3	3	3	90047000	90490000	0.434	nucleus	K02975	J	KOG1767	40S ribosomal protein S25
P57053	H2BFS	13.944	110.97	60.3	12	62	6	1.35E+10	1.44E+10	0.421	nucleus		B	KOG1744	Histone H2B
P26599	PTBP1	57.221	220.5	64.2	21	33	18	2.72E+09	4.72E+09	0.411	cytoplasm,nucleus	K13218	A	KOG1190	Polypyrimidine tract-binding protein
P62805	HIST1H4A	11.367	271.06	86.4	27	70	27	2.16E+10	2.32E+10	0.344	nucleus	K11254	B	KOG3467	Histone H4
P35659	DEK	42.674	16.472	6.7	2	2	2	70443000	47831000	0.331	nucleus	K17046	B	KOG2266	Chromatin-associated protein Dek and related proteins
Q13185	CBX3	20.811	43.747	45.9	5	6	3	4.77E+08	6.11E+08	0.331	nucleus	K11586	B	KOG1911	Heterochromatin-associated protein HP1 and related CHROMO domain proteins
P09429	HMGB1	24.893	53.2	39.1	7	8	5	3.32E+08	1.89E+08	0.297	nucleus	K10802	R	KOG0381	HMG box-containing protein
Q71DI3	HIST2H3A	15.388	114.43	72.1	14	39	3	2.17E+10	2.3E+10	0.276	nucleus	K11253	B	KOG1745	Histones H3 and H4
P62244	RPS15A	14.839	23.841	29.2	4	4	4	1.77E+08	2.36E+08	0.264	cytoplasm	K02957	J	KOG1754	40S ribosomal protein S15/S22
O15347	HMGB3	22.98	14.08	14.5	2	3	2	1.31E+08	56663000	0.242	nucleus	K11296	R	KOG0381	HMG box-containing protein
P68431	HIST1H3A	15.404	34.78	72.1	14	36	3	6.68E+09	6.98E+09	0.225	nucleus	K11253	B	KOG1745	Histones H3 and H4
Q71UI9	H2AFV	13.509	50.682	53.9	6	16	4	2.26E+09	6.77E+09	0.201	nucleus	K11251	B	KOG1757	Histone 2A
Q16777	HIST2H2AC	13.988	87.492	58.1	8	37	1	5.48E+09	6.18E+09	0.17	nucleus	K11251	B	KOG1756	Histone 2A
P16401	HIST1H1B	22.58	45.529	25.2	7	19	6	4.31E+08	2.27E+08	0.168	nucleus	K11275	B	KOG4012	Histone H1
P68366	TUBA4A	49.924	20.498	54	17	28	3	3.6E+08	1.84E+08	0.165	cytoskeleton	K07374	Z	KOG1376	Alpha tubulin
Q16778	HIST2H2BE	13.92	25.117	54.8	9	55	1	2.35E+09	2.8E+09	0.15	nucleus	K11252	B	KOG1744	Histone H2B
P16403	HIST1H1C	21.364	70.975	28.6	9	22	8	2.44E+09	1.11E+09	0.107	nucleus	K11275	B	KOG4012	Histone H1
A6NHQ2	FBLL1	34.803	13.4	6.9	3	5	2	1.28E+08	4.59E+08		nucleus	K14563			
A6NMZ7	COL6A6	247.17	5.6244	0.3	1	2	1	8863100	32431000		endoplasmic reticulum	K06238	W	KOG3544	Collagens (type IV and type XIII), and related proteins
O00299	CLIC1	26.922	6.2216	9.1	1	1	1	0	14455000		cytoplasm	K05021			
O00425	IGF2BP3	63.704	5.7634	4.7	2	2	1	7740500	25114000		cytoplasm	K13197	AR	KOG2193	IGF-II mRNA-binding protein IMP, contains RRM and KH domains
O00764	PDXK	35.102	7.3517	6.7	1	1	1	0	15943000		cytoplasm	K00868	H	KOG2599	Pyridoxal/pyridoxine/pyridoxamine kinase
O14548	COX7A2L	12.615	7.4336	11.4	1	1	1	26040000	8935100		cytoplasm	K02270			

O14561	NDUFAB1	17.417	6.665	9.6	1	1	1	19076000	42846000	mitochondria	K03955	CIQ	KOG1748 Acyl carrier protein/NADH-ubiquinone oxidoreductase
O14949	UQCRQ	9.9062	19.184	24.4	2	2	2	16497000	33371000	mitochondria	K00418	C	KOG4116 Ubiquinol cytochrome c reductase, subunit QCR8
O14974	PPP1R12A	115.28	18.455	3.5	2	3	2	1496200	40535000	nucleus	K06270	OT	KOG0505 Myosin phosphatase, regulatory subunit
O14979	HNRNPDL	46.437	9.3153	5.7	2	2	1	7332800	26663000	nucleus	K13044		
O15143	ARPC1B	40.949	6.4187	2.7	1	1	1	0	6607200	cytoplasm	K05757	Z	KOG1523 Actin-related protein Arp2/3 complex, subunit ARPC1/p41-ARC
O15144	ARPC2	34.333	5.7582	3.7	1	1	1	0	8704700	cytoplasm	K05758	Z	KOG2826 Actin-related protein Arp2/3 complex, subunit ARPC2
O15514	POLR2D	16.311	8.7078	14.1	1	1	1	8240600	41519000	cytoplasm	K03012	K	KOG2351 RNA polymerase II, fourth largest subunit
O15523	DDX3Y	73.153	8.749	2.6	1	1	1	0	8379300	nucleus	K17642	A	KOG0335 ATP-dependent RNA helicase
O43143	DHX15	90.932	5.6074	1.5	1	1	1	0	15867000	nucleus	K12820	A	KOG0925 mRNA splicing factor ATP-dependent RNA helicase
O43159	RRP8	50.714	9.3315	3.5	1	1	1	0	0	nucleus	K14850	A	KOG3045 Predicted RNA methylase involved in rRNA processing
O43504	LAMTOR5	9.6138	14.13	15.4	1	1	1	0	15379000	cytoskeleton	K16344		
O43570	CA12	39.45	15.077	9.9	2	2	2	5477700	56606000	extracellular	K01672	R	KOG0382 Carbonic anhydrase
O43678	NDUFA2	10.921	5.7938	21.2	1	1	1	5403700	13281000	mitochondria	K03946	C	KOG3446 NADH:ubiquinone oxidoreductase NDUFA2/B8 subunit
O43852	CALU	37.106	6.8954	6	1	1	1	3746800	14911000	extracellular		TU	KOG4223 Reticulocalbin, calumenin, DNA supercoiling factor
O60664	PLIN3	47.074	10.538	3.7	1	1	1	17069000	26341000	cytoplasm	K20287		of the CREC family (EF-Hand protein superfamily)
O60784	TOM1	53.818	6.8881	3.5	1	1	1	0	24041000	cytoplasm		U	KOG1087 Cytosolic sorting protein GGA2/TOM1
O60828	PQBP1	30.472	12.519	13.2	2	2	2	0	28920000	nucleus	K12865	K	KOG3427 Polyglutamine tract-binding protein PQBP-1
O75251	NDUFS7	23.563	11.116	6.6	1	1	1	6197300	23206000	mitochondria	K03940	C	KOG1687 NADH-ubiquinone oxidoreductase, NUFS7/PSST/20 kDa subunit
O75306	NDUFS2	52.545	5.6926	1.5	1	1	1	0	4280500	mitochondria	K03935	C	KOG2870 NADH:ubiquinone oxidoreductase, NDUFS2/49 kDa subunit
O75396	SEC22B	24.593	7.6914	6.5	1	1	1	3243400	24880000	endoplasmic reticulum	K08517		
O75431	MTX2	29.763	11.571	8.4	1	2	1	52956000	1.37E+08	cytoplasm	K17776	MU	KOG3027 Mitochondrial outer membrane protein Metaxin 2, Metaxin 1-binding protein
O75533	SF3B1	145.83	17.897	2.4	2	2	2	7789400	37550000	plasma membrane	K12828	A	KOG0213 Splicing factor 3b, subunit 1
O75683	SURF6	41.45	5.4869	1.9	1	1	1	0	0	nucleus		S	KOG2885 Uncharacterized conserved protein
O75874	IDH1	46.659	12.158	4.8	2	2	2	4102100	36785000	cytoplasm	K00031	C	KOG1526 NADP-dependent isocitrate dehydrogenase
O75880	SCO1	33.814	6.1446	5.3	1	1	1	9553500	40285000	mitochondria	K07152	C	KOG2792 Putative cytochrome C oxidase assembly protein
O75940	SMNDC1	26.711	15.222	13	2	3	2	6937200	22542000	nucleus	K12839	A	KOG3026 Splicing factor SPF30
O94826	TOMM70	67.454	12.805	5.8	2	2	2	10158000	64091000	endoplasmic reticulum	K17768	U	KOG0547 Translocase of outer mitochondrial membrane complex, subunit TOM70/TOM72
O94889	KLHL18	63.638	5.5906	1.2	1	1	1	20703000	2E+08	nucleus	K10455	TR	KOG4441 Proteins containing BTB/POZ and Kelch domains
O94973	AP2A2	103.96	11.892	2.6	2	2	1	2567400	12611000	cytoplasm	K11824	U	KOG1077 Vesicle coat complex AP-2, alpha subunit
O95182	NDUFA7	12.551	6.7433	15.9	1	1	1	13278000	41743000	mitochondria	K03951	C	KOG4630 NADH:ubiquinone oxidoreductase, NDUFA7/B14.5A subunit
O95425	SVIL	247.74	34.27	3.4	4	4	4	3083000	66999000	nucleus	K10369	Z	KOG0445 Actin regulatory protein supervillin (gelsolin/villin family)
O95613	PCNT	378.03	-2	0.4	1	1	1	0	0	nucleus	K16481		
O95782	AP2A1	107.54	6.3704	3.9	2	2	1	3958200	38005000	cytoplasm	K11824	U	KOG1077 Vesicle coat complex AP-2, alpha subunit
O95793	STAU1	63.182	11.882	4.5	2	2	2	12110000	23381000	nucleus	K17597	UK	KOG3732 Staufen and related double-stranded-RNA-binding proteins
O95816	BAG2	23.772	5.4999	10.4	1	1	1	3141000	13503000	cytoplasm	K09556	O	KOG3633 BAG family molecular chaperone regulator 2
P00387	CYB5R3	34.234	17.366	14.3	3	3	3	0	49408000	extracellular	K00326	HC	KOG0534 NADH-cytochrome b-5 reductase
P00450	CP	122.2	5.9239	1.6	1	1	1	0	17352000	endoplasmic reticulum	K13624	Q	KOG1263 Multicopper oxidases
P01116	KRAS	21.656	7.7576	13.2	1	1	1	15914000	39660000	cytoplasm	K07827	R	KOG0395 Ras-related GTPase
P02792	FTL	20.019	9.622	9.1	1	1	1	16635000	15554000	cytoplasm	K13625		
P02794	FTH1	21.225	6.2798	8.2	1	1	1	7740200	10069000	cytoplasm	K00522	P	KOG2332 Ferritin
P04080	CSTB	11.139	9.9269	21.4	1	2	1	0	14073000	cytoplasm	K13907		
P04156	PRNP	27.661	9.9192	4.7	1	1	1	11905000	38649000	extracellular	K05634		
P04259	KRT6B	60.066	12.221	13.1	10	0	0	0	77065000	nucleus	K07605		
P04632	CAPNS1	28.315	32.99	19.4	3	3	3	11330000	70495000	cytoplasm	K08583	T	KOG0037 Ca <sup>2+</sup> -binding protein, EF-Hand protein superfamily
P05976	MYL1	21.145	20.768	8.2	2	7	2	0	0	cytoplasm	K05738	Z	KOG0030 Myosin essential light chain, EF-Hand protein superfamily
P06454	PTMA	12.203	6.9758	12.6	1	1	1	9756100	8035600	cytoplasm	K13784		
P07948	LYN	58.573	5.4748	4.3	2	2	1	0	0	cytoplasm,nucleus	K05854	T	KOG0197 Tyrosine kinases
P08865	RPSA	32.854	26.808	23.1	3	3	3	8428400	42520000	cytoplasm	K02998	J	KOG0830 40S ribosomal protein SA (P40)/Laminin receptor 1
P09622	DLD	54.177	7.496	3.7	1	1	1	6189300	44160000	mitochondria	K00382	C	KOG1335 Dihydrolipoamide dehydrogenase
P0DP13	CENPVL2	29.887	6.8835	2.9	1	1	1	9927200	40970000	mitochondria			
P10515	DLAT	68.996	5.861	2.6	1	1	1	0	0	mitochondria	K00627	C	KOG0557 Dihydrolipoamide acetyltransferase

P11217	PYGM	97.091	11.054	3.4	2	2	2	3901300	32647000	cytoplasm	K00688	G	KOG2099 Glycogen phosphorylase
P12235	SLC25A4	33.064	6.7433	31.9	8	10	1	2799000	15242000	mitochondria	K05863	C	KOG0749 Mitochondrial ADP/ATP carrier proteins
P12931	SRC	59.834	13.226	5.2	2	2	1	6490200	57499000	cytoplasm	K05704	T	KOG0197 Tyrosine kinases
P13010	XRCC5	82.704	9.5646	2.2	1	1	1	18904000	23683000	cytoplasm	K10885	L	KOG2326 DNA-binding subunit of a DNA-dependent protein kinase (Ku80 autoantigen)
P13473	LAMP2	44.96	17.701	4.9	2	2	2	5613100	53356000	extracellular	K06528		
P14174	MIF	12.476	6.4327	7.8	1	1	1	9031500	1.17E+08	cytoplasm,nucleus	K07253	V	KOG1759 Macrophage migration inhibitory factor
P14550	AKR1A1	36.573	7.7634	3.1	1	1	1	12381000	88726000	cytoplasm	K00002	R	KOG1577 Aldo/keto reductase family proteins
P15531	NME1	17.149	7.425	31.6	3	3	1	18359000	39178000	cytoplasm	K00940	F	KOG0888 Nucleoside diphosphate kinase
P15954	COX7C	7.2454	6.3913	27	1	1	1	23051000	63299000	mitochondria	K02272	C	KOG4527 Cytochrome c oxidase, subunit VIIc/COX8
P16104	H2AFX	15.144	7.5736	52.4	6	19	0	0	0	nucleus	K11251	B	KOG1756 Histone 2A
P16989	YBX3	40.089	13.295	9.7	2	2	1	13092000	17262000	nucleus	K06099	J	KOG3070 Predicted RNA-binding protein containing PIN domain
P17066	HSPA6	71.027	9.0598	11.7	6	9	1	47196000	1.16E+08	cytoplasm	K03283	O	KOG0101 Molecular chaperones HSP70/HSC70, HSP70 superfamily
P17480	UBTF	89.405	14.708	4.1	2	3	2	19316000	28691000	nucleus	K09273	R	KOG0381 HMG box-containing protein
P17844	DDX5	69.147	7.0362	2	1	1	1	3239200	8602000	nucleus	K12823	A	KOG0331 ATP-dependent RNA helicase
P17931	LGALS3	26.152	6.1018	6	1	1	1	0	0	cytoplasm,nucleus	K06831	W	KOG3587 Galectin, galactose-binding lectin
P18085	ARF4	20.511	33.278	16.7	2	2	1	14266000	67340000	cytoplasm	K07939	U	KOG0070 GTP-binding ADP-ribosylation factor Arf1
P19404	NDUFV2	27.391	6.2706	5.2	1	1	1	7539100	27798000	mitochondria	K03943	C	KOG3196 NADH:ubiquinone oxidoreductase, NDUFV2/24 kD subunit
P19525	EIF2AK2	62.094	6.3859	2.2	1	1	1	0	19915000	cytoplasm	K16195	J	KOG1033 eIF-2alpha kinase PEK/EIF2AK3
P21291	CSRP1	20.567	16.763	16.6	2	2	2	0	20787000	nucleus	K09377		
P23497	SP100	100.42	6.9185	2.2	2	2	1	0	5457100	nucleus	K15413	O	KOG2177 Predicted E3 ubiquitin ligase
P24539	ATP5F1	28.908	7.529	4.7	1	1	1	2932800	20836000	mitochondria	K02127		
P25787	PSMA2	25.898	7.4953	6	1	2	1	6262800	12291000	cytoplasm	K02726	O	KOG0181 20S proteasome, regulatory subunit alpha type PSMA2/PRE8
P27449	ATP6V0C	15.736	5.8043	11.6	1	1	1	7629700	28872000	plasma membrane	K02155	C	KOG0232 Vacuolar H+-ATPase V0 sector, subunits c/c'
P27816	MAP4	121	17.429	6.5	3	3	3	6617700	45590000	nucleus	K10431		
P28066	PSMA5	26.411	6.9936	5	1	1	1	8327000	11158000	cytoplasm	K02729	O	KOG0176 20S proteasome, regulatory subunit alpha type PSMA5/PUP2
P28289	TMOD1	40.569	18.487	15	4	4	3	12675000	63133000	cytoplasm	K10370	Z	KOG3735 Tropomodulin and leiomodulin
P29692	EEF1D	31.121	19.271	8.5	1	1	1	8186300	21900000	cytoplasm	K15410	K	KOG1668 Elongation factor 1 beta/delta chain
P29966	MARCKS	31.554	5.5636	5.4	1	1	1	1372200	6158400	nucleus	K12561		
P30041	PRDX6	25.035	10.178	7.6	1	2	1	0	42061000	mitochondria	K11188	O	KOG0854 Alkyl hydroperoxide reductase, thiol specific antioxidant and related enzymes
P30048	PRDX3	27.692	9.6957	5.5	1	1	1	5081600	17652000	mitochondria	K20011	O	KOG0852 Alkyl hydroperoxide reductase, thiol specific antioxidant and related enzymes
P30049	ATP5F1D	17.49	6.259	8.3	1	1	1	1980600	34064000	mitochondria	K02134	C	KOG1758 Mitochondrial F1F0-ATP synthase, subunit delta/ATP16
P30086	PEBP1	21.057	11.763	27.8	2	2	2	1853800	29433000	cytoplasm		R	KOG3346 Phosphatidylethanolamine binding protein
P30153	PPP2R1A	65.308	18.219	7	3	3	3	12909000	22634000	cytoplasm	K03456	T	KOG0211 Protein phosphatase 2A regulatory subunit A and related proteins
P31689	DNAJA1	44.868	6.1034	6.3	1	1	1	0	11114000	cytoplasm	K09502	O	KOG0712 Molecular chaperone (DnaJ superfamily)
P31942	HNRNPH3	36.926	6.3913	4	1	1	1	3575000	10546000	cytoplasm	K12898	A	KOG4211 Splicing factor hnRNP-F and related RNA-binding proteins
P31947	SFN	27.774	12.352	20.6	3	3	2	9397600	40503000	cytoplasm,nucleus	K06644	O	KOG0841 Multifunctional chaperone (14-3-3 family)
P32969	RPL9	21.863	17.691	38.5	3	3	3	10233000	40700000	cytoplasm	K02940	J	KOG3255 60S ribosomal protein L9
P34932	HSPA4	94.33	14.049	3.9	2	2	2	7851300	32912000	cytoplasm	K09489	O	KOG0103 Molecular chaperones HSP105/HSP110/SSE1, HSP70 superfamily
P35221	CTNNA1	100.07	5.5057	1.4	1	1	1	4134500	11142000	nucleus	K05691	W	KOG3681 Alpha-catenin
P35754	GLRX	11.776	10.667	39.6	2	2	2	0	47555000	cytoplasm	K03676	O	KOG1752 Glutaredoxin and related proteins
P36543	ATP6V1E1	26.145	7.1745	6.2	1	1	1	0	0	cytoplasm	K02150	C	KOG1664 Vacuolar H+-ATPase V1 sector, subunit E
P37108	SRP14	14.57	14.274	10.3	1	1	1	80715000	96060000	cytoplasm	K03104	U	KOG1761 Signal recognition particle, subunit Srp14
P40261	NNMT	29.574	6.7658	7.2	1	1	1	48815000	58823000	cytoplasm	K00541		
P40925	MDH1	36.426	10.518	5.1	1	1	1	4149900	19134000	cytoplasm	K00025	C	KOG1496 Malate dehydrogenase
P40939	HADHA	82.999	8.1466	2.8	1	1	1	0	8626500	mitochondria	K07515	I	KOG1683 Hydroxyacyl-CoA dehydrogenase/enoyl-CoA hydratase
P41223	BUD31	17	5.9224	5.6	1	1	1	0	15367000	extracellular	K12873	K	KOG3404 G10 protein/predicted nuclear transcription regulator
P42167	TMPO	50.67	9.4494	2.6	1	1	1	10621000	9145500	cytoplasm			
P42704	LRPPRC	157.9	18.324	2.4	3	3	3	7661400	18666000	mitochondria	K17964	A	KOG4318 Bicoid mRNA stability factor
P43307	SSR1	32.235	9.1812	5.2	1	1	1	31455000	71071000	endoplasmic reticulum	K13249	U	KOG1631 Translocon-associated complex TRAP, alpha subunit
P46777	RPL5	34.362	11.266	10.4	2	2	2	88553	32137000	nucleus	K02932	J	KOG0875 60S ribosomal protein L5
P47914	RPL29	17.752	9.2572	9.4	1	1	1	62899000	83623000	nucleus	K02905	J	KOG3504 60S ribosomal protein L29

P49458	SRP9	10.112	9.0865	12.8	1	1	1	28588000	28095000	cytoplasm	K03109	U	KOG3465	Signal recognition particle, subunit Srp9
P49821	NDUFV1	50.817	12.5	4.7	2	3	2	5127600	17039000	mitochondria	K03942	C	KOG2658	NADH:ubiquinone oxidoreductase, NDUFV1/51kDa subunit
P50238	CRIP1	8.5328	5.7614	36.4	1	1	1	3685900	22691000	nucleus		TZ	KOG1700	Regulatory protein MLP and related LIM proteins
P50914	RPL14	23.432	15.847	10.2	2	2	2	13057000	44241000	mitochondria	K02875	J	KOG3421	60S ribosomal protein L14
P50990	CCT8	59.62	5.5967	2.2	1	1	1	7544000	8919100	cytoplasm	K09500	O	KOG0362	Chaperonin complex component, TCP-1 theta subunit (CCT8)
P51148	RAB5C	23.482	5.5558	6.5	1	1	1	0	32160000	cytoplasm	K07889	U	KOG0092	GTPase Rab5/YPT51 and related small G protein superfamily GTPases
P51571	SSR4	18.998	8.4155	6.4	1	1	1	5025600	23569000	plasma membrane	K04571	U	KOG4088	Translocon-associated complex TRAP, delta subunit
P51572	BCAP31	27.991	13.625	7.3	2	2	2	5162900	26827000	endoplasmic reticulum	K14009	V	KOG1962	B-cell receptor-associated protein and related proteins
P52292	KPNA2	57.861	7.8933	2.8	1	1	1	6840100	11673000	cytoplasm,nucleus	K15043	U	KOG0166	Karyopherin (importin) alpha
P52597	HNRNPF	45.671	12.146	15.7	2	2	2	5163300	61309000	cytoplasm	K12898	A	KOG4211	Splicing factor hnRNP-F and related RNA-binding proteins
P52815	MRPL12	21.348	11.69	11.6	2	2	2	0	0	mitochondria	K02935	J	KOG1715	Mitochondrial/chloroplast ribosomal protein L12
P53396	ACLY	120.84	5.6466	1.3	1	1	1	0	0	cytoplasm	K01648	C	KOG1254	ATP-citrate lyase
P53567	CEBPG	16.408	6.3625	20.7	1	1	1	0	0	nucleus	K10049			
P54652	HSPA2	70.02	7.8145	12.5	6	6	1	11149000	18344000	cytoplasm	K03283	O	KOG0101	Molecular chaperones HSP70/HSC70, HSP70 superfamily
P54855	UGT2B15	61.036	6.1825	1.3	1	1	1	67849000	2.55E+08	peroxisome	K00699	GC	KOG1192	UDP-glucuronosyl and UDP-glucosyl transferase
P55084	HADHB	51.294	5.9778	5.5	1	1	1	0	67202000	nucleus	K07509	I	KOG1392	Acetyl-CoA acetyltransferase
P60228	EIF3E	52.22	6.771	2.9	1	1	1	0	0	cytoplasm	K03250	J	KOG2758	Translation initiation factor 3, subunit e (eIF-3e)
P60602	ROMO1	8.1828	11.904	21.5	1	1	1	13480000	33517000	extracellular		S	KOG4096	Uncharacterized conserved protein
P60709	ACTB	41.736	15.56	95.5	37	129	1	0	0	cytoskeleton	K05692	Z	KOG0676	Actin and related proteins
P61026	RAB10	22.541	8.4155	11	2	2	1	11795000	36198000	cytoplasm	K07903	TU	KOG0078	GTP-binding protein SEC4, small G protein superfamily
P61225	RAP2B	20.504	6.0578	6.6	1	1	1	0	11994000	cytoplasm	K07838	R	KOG0395	Ras-related GTPase
P61513	RPL37A	10.275	7.9589	19.6	1	1	1	12424000	13074000	extracellular	K02921	J	KOG0402	60S ribosomal protein L37
P61586	RHOA	21.768	5.5395	6.2	1	1	1	2490000	6892600	cytoplasm	K04513	R	KOG0393	Ras-related small GTPase, Rho type
P62263	RPS14	16.273	12.951	13.9	2	2	2	8468600	13448000	cytoplasm	K02955	J	KOG0407	40S ribosomal protein S14
P62273	RPS29	6.6767	5.4488	14.3	1	1	1	9848100	21171000	extracellular	K02980	J	KOG3506	40S ribosomal protein S29
P62304	SNRPE	10.803	14.313	40.2	2	2	2	1.16E+08	2.77E+08	mitochondria	K11097	A	KOG1774	Small nuclear ribonucleoprotein E
P62328	TMSB4X	5.0526	5.7749	31.8	1	1	1	6968900	29006000	nucleus	K05764	N	KOG4794	Thymosin beta
P62834	RAP1A	20.987	6.8051	5.4	1	1	1	2849400	18419000	cytoplasm	K04353	R	KOG0395	Ras-related GTPase
P62857	RPS28	7.8409	9.8793	17.4	1	2	1	34313000	69242000	mitochondria	K02979	J	KOG3502	40S ribosomal protein S28
P62942	FKBP1A	11.951	14.963	28.7	2	2	2	2785200	32668000	cytoplasm	K09568	O	KOG0544	FKBP-type peptidyl-prolyl cis-trans isomerase
P62995	TRA2B	33.665	6.9499	5.6	1	1	1	5514300	13524000	nucleus	K12897			
P63092	GNAS	45.664	10.791	9.4	3	3	2	2889400	21121000	cytoplasm	K04632	T	KOG0099	G protein subunit Galphas, small G protein superfamily
P63173	RPL38	8.2178	12.651	18.6	1	1	1	61710000	88103000	nucleus	K02923	J	KOG3499	60S ribosomal protein L38
P63313	TMSB10	5.0256	8.543	31.8	1	1	1	61494000	1.11E+08	cytoplasm	K13785	N	KOG4794	Thymosin beta
P67812	SEC11A	20.625	9.0012	6.7	1	1	1	0	0	cytoplasm	K13280	U	KOG3342	Signal peptidase I
P78417	GSTO1	27.566	5.8036	3.3	1	1	1	0	0	cytoplasm	K00799	O	KOG0406	Glutathione S-transferase
P84077	ARF1	20.697	7.3522	21	2	2	1	0	17636000	cytoplasm	K07937	U	KOG0070	GTP-binding ADP-ribosylation factor Arf1
P84098	RPL19	23.466	11.447	8.7	1	1	1	0	0	cytoplasm	K02885	J	KOG1696	60s ribosomal protein L19
P84103	SRSF3	19.329	6.3039	12.8	1	1	1	0	28029000	nucleus	K12892	A	KOG0107	Alternative splicing factor SRp20/9G8 (RRM superfamily)
P98187	CYP4F8	59.994	5.7738	1.5	1	1	1	0	0	plasma membrane	K17728			
Q01082	SPTBN1	274.61	34.147	2.8	5	5	5	5241600	27824000	cytoplasm	K06115	Z	KOG0035	Ca2+-binding actin-bundling protein (actinin), alpha chain
Q01469	FABP5	15.164	22.266	25.9	2	2	2	1.89E+08	77514000	extracellular	K08754	I	KOG4015	Fatty acid-binding protein FABP
Q01518	CAP1	51.901	5.6686	2.7	1	2	1	0	0	cytoplasm	K17261	ZT	KOG2675	Adenylate cyclase-associated protein (CAP/Srv2p)
Q01995	TAGLN	22.611	19.333	17.4	3	3	3	1352200	87694000	cytoplasm	K20526	Z	KOG2046	Calponin
Q03701	CEBPZ	120.97	5.7113	2.1	1	1	1	0	0	nucleus	K14832	JK	KOG2038	CAATT-binding transcription factor/60S ribosomal subunit biogenesis protein
Q05682	CALD1	93.23	6.7682	2.3	1	1	1	5371700	40718000	nucleus	K12327			
Q06323	PSME1	28.723	18.841	12	3	3	3	7276200	54218000	nucleus	K06696	O	KOG4470	Proteasome activator subunit
Q07666	KHDRBS1	48.227	5.9412	6.5	1	1	1	15118000	80492000	cytoplasm	K13198	A	KOG1588	RNA-binding protein Sam68 and related KH domain proteins
Q08211	DHX9	140.96	13.825	2.8	2	2	2	8517900	69707000	nucleus	K13184	A	KOG0920	ATP-dependent RNA helicase A
Q12797	ASPH	85.862	8.0841	2.4	1	1	1	9173100	22070000	plasma membrane	K00476	O	KOG3696	Aspartyl beta-hydroxylase
Q12860	CNTN1	113.32	11.369	2.8	2	2	2	0	10733000	plasma membrane	K06759	T	KOG3513	Neural cell adhesion molecule L1

Q13011	ECH1	35.816	7.2928	6.7	1	1	1	0	32763000	mitochondria	K12663	I	KOG1681	Enoyl-CoA isomerase
Q13423	NNT	113.89	23.343	5.9	4	4	4	0	52574000	plasma membrane	K00323			
Q13478	IL18R1	62.303	6.4925	1.3	1	1	1	7134500	28674000	peroxisome	K05173			
Q13492	PICALM	70.754	12.388	8.1	2	2	2	7122700	63954000	nucleus	K20044	TU	KOG0251	Clathrin assembly protein AP180 and related proteins, contain ENTH domain
Q13601	KRR1	43.664	14.695	7.3	1	1	1	3981300	17204000	nucleus	K06961	JD	KOG2874	rRNA processing protein
Q13617	CUL2	86.982	5.8013	1.2	1	1	1	34062000	2.99E+08	cytoplasm	K03870	O	KOG2284	E3 ubiquitin ligase, Cullin 2 component
Q13895	BYSL	49.601	5.7002	3	1	1	1	0	0	cytoplasm	K14797	W	KOG3871	Cell adhesion complex protein bystin
Q14126	DSG2	122.29	9.9498	2.1	1	1	1	6665900	26805000	plasma membrane	K07597	S	KOG3594	FOG: Cadherin repeats
Q14573	ITPR3	304.1	11.896	1.2	2	2	2	5187700	30066000	plasma membrane	K04960	T	KOG3533	Inositol 1,4,5-trisphosphate receptor
Q14847	LASP1	29.717	6.2428	5	1	1	1	24887000	51365000	nucleus		Z	KOG1702	Nebulin repeat protein
Q14914	PTGR1	35.869	11.436	7	1	1	1	10108000	43854000	cytoplasm	K13948	R	KOG1196	Predicted NAD-dependent oxidoreductase
Q15005	SPCS2	25.003	10.968	8.4	1	1	1	4438600	38679000	plasma membrane	K12947	U	KOG4072	Signal peptidase complex, subunit SPC25
Q15019	SEPT2	41.487	5.4982	6.4	1	1	1	0	0	cytoplasm	K16942	DZU	KOG2655	Septin family protein (P-loop GTPase)
Q15181	PPA1	32.66	5.8487	5.5	1	1	1	4432800	23881000	cytoplasm	K01507	C	KOG1626	Inorganic pyrophosphatase/Nucleosome remodeling factor, subunit NURF38
Q15363	TMED2	22.761	18.166	24.9	3	3	3	0	1.37E+08	extracellular	K20347	U	KOG1692	Putative cargo transport protein EMP24 (p24 protein family)
Q15388	TOMM20	16.298	9.0043	13.8	1	1	1	11250000	30756000	extracellular	K17770	U	KOG4056	Translocase of outer mitochondrial membrane complex, subunit TOM20
Q15637	SF1	68.329	5.8963	3.3	1	1	1	17632000	15211000	nucleus	K13095	A	KOG0119	Splicing factor 1/branch point binding protein (RRM superfamily)
Q15836	VAMP3	11.309	8.0807	24	1	1	1	3027900	14594000	plasma membrane	K13505	U	KOG0860	Synaptobrevin/VAMP-like protein
Q16352	INA	55.39	17.4	6	3	3	2	6064500	41792000	nucleus	K07608			
Q16555	DPYSL2	62.293	8.5422	3.5	1	1	1	9338300	37294000	cytoplasm,nucleus	K07528	F	KOG2584	Dihydroorotase and related enzymes
Q3ZCM7	TUBB8	49.775	6.568	18.5	6	9	1	28679000	70993000	cytoplasm	K07375	Z	KOG1375	Beta tubulin
Q53GQ0	HSD17B12	34.324	6.6243	4.8	1	1	1	0	27252000	cytoplasm	K10251	I	KOG1014	17 beta-hydroxysteroid dehydrogenase type 3, HSD17B3
Q58FF8	HSP90AB2P	44.348	9.9593	12.1	4	5	1	7454500	24015000	cytoplasm	K04079			
Q5GLZ8	HERC4	118.56	5.9429	1.1	1	1	1	0	0	nucleus	K10615	O	KOG0941	E3 ubiquitin protein ligase
Q5M775	SPECC1	118.58	7.8801	1.2	1	1	1	0	51071000	nucleus		R	KOG4678	FOG: Calponin homology domain
Q5RI15	COX20	13.291	9.5323	19.5	1	1	1	0	24102000	cytoplasm	K18184			
Q5T2N8	ATAD3C	46.379	6.2077	3.4	1	1	1	3982500	17031000	cytoplasm		O	KOG0742	AAA+-type ATPase
Q5TGY3	AHDC1	168.35	-2	0.4	1	1	1	0	0	nucleus	K22592			
Q5TGZ0	MINOS1	8.8081	5.5134	41	1	1	1	0	0	mitochondria	K17784	S	KOG4604	Uncharacterized conserved protein
Q5UIP0	RIF1	274.46	5.6115	0.3	1	1	1	0	0	cytoplasm	K11138			
Q6PIJ6	FBXO38	133.94	5.5397	0.8	1	1	1	31275000	36486000	nucleus	K10313			
Q6R327	RICTOR	192.22	-2	0.6	1	1	1	0	0	nucleus	K08267	D	KOG3694	Protein required for meiosis
Q6UW68	TMEM205	21.198	14.074	6.9	1	1	1	6643700	31303000	extracellular		S	KOG2886	Uncharacterized conserved protein
Q71U36	TUBA1A	50.135	12.117	59.9	18	28	1	0	0	cytoskeleton	K07374	Z	KOG1376	Alpha tubulin
Q7Z434	MAVS	56.527	5.6769	4.3	1	1	1	0	0	cytoplasm	K12648			
Q7Z6B0	CCDC91	49.971	6.3999	2	1	1	1	0	0	cytoplasm				
Q7Z6I8	C5orf24	20.132	6.5904	11.2	1	1	1	12990000	20774000	nucleus				
Q7Z7K0	CMC1	12.49	6.0891	9.4	1	1	1	3305100	16535000	extracellular	K18171	S	KOG4624	Uncharacterized conserved protein
Q86U42	PABPN1	32.749	8.1029	9.2	1	1	1	0	36300000	nucleus	K14396	A	KOG4209	Splicing factor RNPS1, SR protein superfamily
Q86VV8	RTTN	248.63	6.4476	0.3	1	1	1	0	0	plasma membrane	K16484			
Q86XN8	MEX3D	64.882	6.1853	1.1	1	1	1	23343000	29115000	cytoplasm,nucleus	K15686	R	KOG2113	Predicted RNA binding protein, contains KH domain
Q86Y39	NDUFA11	14.852	7.763	10.6	1	1	1	5290400	25968000	mitochondria	K03956			
Q8IUE6	HIST2H2AB	13.995	6.7166	57.7	5	11	1	2.01E+08	1.68E+08	nucleus	K11251	B	KOG1756	Histone 2A
Q8IVF2	AHNAK2	616.62	13.338	5.2	2	2	2	1453600	76244000	nucleus				
Q8N257	HIST3H2BB	13.908	6.2488	50.8	8	53	1	6876600	5978800	nucleus	K11252	B	KOG1744	Histone H2B
Q8N283	ANKRD35	109.96	6.71	0.8	1	1	1	4123600	39366000	mitochondria				
Q8N2U0	TMEM256	11.741	8.4805	24.8	1	1	1	11093000	56113000	mitochondria		S	KOG3472	Predicted small membrane protein
Q8N3E9	PLCD3	89.257	10.162	2.9	1	1	1	5049500	31490000	mitochondria	K05857	T	KOG0169	Phosphoinositide-specific phospholipase C
Q8N4H5	TOMM5	6.0352	6.8738	19.6	1	1	1	8737100	14948000	cytoplasm	K17773			
Q8N8Y2	ATP6V0D2	40.426	11.358	5.1	1	1	1	3995900	19494000	cytoplasm	K02146	C	KOG2957	Vacuolar H+-ATPase V0 sector, subunit d
Q8NAV1	PRPF38A	37.476	5.7403	3.8	1	1	1	0	13461000	nucleus	K12849	S	KOG2889	Predicted PRP38-like splicing factor



Q8ND76	CCNY	39.336	5.8103	4.4	1	1	1	0	16965000	nucleus		R	KOG1675	Predicted cyclin
Q8NE86	MCU	39.866	10.867	5.4	1	1	1	13576000	45060000	mitochondria	K20858	R	KOG2966	Uncharacterized conserved protein
Q8WTT2	NOC3L	92.547	13.589	4.4	2	2	2	9971800	40562000	nucleus	K14834	JU	KOG2153	Protein involved in the nuclear export of pre-ribosomes
Q8WWI1	LMO7	192.69	9.0215	0.8	1	1	1	21694000	9338000	nucleus	K06084	TZR	KOG1704	FOG: LIM domain
Q8WXE9	STON2	101.16	7.198	1	1	1	1	17216000	1.33E+08	plasma membrane	K20067	U	KOG2677	Stoned B synaptic vesicle biogenesis protein
Q8WZ42	TTN	3816	5.516	0	1	1	1	0	24624000		K12567	Z	KOG0613	Projectin/twitchin and related proteins
Q92614	MYO18A	233.11	17.6	1.9	2	2	2	2518800	29474000	nucleus	K10362	Z	KOG0161	Myosin class II heavy chain
Q96A26	FAM162A	17.342	6.5455	13	1	1	1	0	15158000	plasma membrane				
Q96AG4	LRRC59	34.93	5.876	3.9	1	2	1	21430000	24854000	cytoplasm,peroxisome		S	KOG0473	Leucine-rich repeat protein
Q96AY2	EME1	63.251	5.5701	1.6	1	1	1	0	2.56E+08	nucleus	K10882			
Q96B49	TOMM6	8.0019	7.1713	18.9	1	1	1	0	0	cytoplasm,nucleus	K17772			
Q96CS3	FAF2	52.623	16.557	10.1	2	2	2	9925200	53915000	cytoplasm	K18726	T	KOG1363	Predicted regulator of the ubiquitin pathway (contains UAS and UBX domains)
Q96CW1	AP2M1	49.654	5.7793	3.7	1	1	1	0	6015300	cytoplasm	K11826	U	KOG0937	Adaptor complexes medium subunit family
Q96DI7	SNRNP40	39.31	17.086	8.4	1	1	1	5436800	39994000	nucleus	K12857	A	KOG0265	U5 snRNP-specific protein-like factor and related proteins
Q96EU6	RRP36	29.823	5.5604	5.8	1	1	1	0	0	nucleus	K14795	S	KOG3190	Uncharacterized conserved protein
Q96FJ2	DYNLL2	10.35	7.7422	37.1	2	3	1	0	18194000	cytoplasm	K10418	Z	KOG3430	Dynein light chain type 1
Q96IX5	USMG5	6.4575	7.9504	25.9	1	1	1	8224600	38931000	cytoplasm	K18194			
Q96LW4	PRIMPOL	64.411	5.5479	2.1	1	1	1	0	0	cytoplasm,nucleus	K22761			
Q96S97	MYADM	35.273	11.327	7.1	1	1	1	23897000	94638000	plasma membrane		V	KOG4788	Members of chemokine-like factor super family and related proteins
Q96ST3	SIN3A	145.17	5.6198	1	1	1	1	0	0	nucleus	K11644	B	KOG4204	Histone deacetylase complex, SIN3 component
Q99439	CNN2	33.697	7.0667	5.2	1	1	1	0	0	cytoplasm		Z	KOG2046	Calponin
Q99497	PARK7	19.891	6.1061	13.8	1	1	1	0	0	cytoplasm	K05687	RV	KOG2764	Putative transcriptional regulator DJ-1
Q99640	PKMYT1	54.521	5.6913	1.8	1	1	1	1.94E+09	2.39E+09	nucleus	K06633	D	KOG0601	Cyclin-dependent kinase WEE1
Q99878	HIST1H2AJ	13.936	10.603	58.6	8	37	0	0	0	nucleus	K11251	B	KOG1756	Histone 2A
Q9BPU6	DPYSL5	61.421	6.1601	1.2	1	2	1	6.27E+08	7.39E+08	cytoplasm	K07529	F	KOG2584	Dihydroorotase and related enzymes
Q9BQE3	TUBA1C	49.895	11.763	56.3	17	24	1	40820000	65044000	cytoskeleton	K07374	Z	KOG1376	Alpha tubulin
Q9BRT6	LLPH	15.225	7.468	12.4	1	1	1	11444000	11424000	nucleus		S	KOG4811	Uncharacterized conserved protein
Q9BTV4	TMEM43	44.875	19.897	7.5	3	3	3	2836700	16768000	plasma membrane				
Q9BUF5	TUBB6	49.857	6.74	16.4	7	10	1	0	6710500	cytoplasm,nucleus	K07375	Z	KOG1375	Beta tubulin
Q9BVA1	TUBB2B	49.953	7.6727	29.2	10	17	1	6663000	21205000	cytoplasm	K07375	Z	KOG1375	Beta tubulin
Q9BVI4	NOC4L	58.467	6.9148	4.1	1	1	1	16125000	24721000	cytoplasm	K14771	J	KOG2154	Predicted nucleolar protein involved in ribosome biogenesis
Q9BVJ6	UTP14A	87.977	10.913	3	2	2	2	0	0	nucleus	K14567	S	KOG2172	Uncharacterized conserved protein
Q9BVK6	TMED9	27.277	19.201	8.9	2	2	2	4324000	23939000	peroxisome	K20346	U	KOG1690	emp24/gp25L/p24 family of membrane trafficking proteins
Q9BW72	HIGD2A	11.528	9.03	23.6	1	1	1	21147000	63616000	cytoplasm,mitochondria		R	KOG4431	Uncharacterized protein, induced by hypoxia
Q9BWJ5	SF3B5	10.135	11.428	27.9	2	2	2	3381200	16432000	extracellular	K12832	S	KOG3485	Uncharacterized conserved protein
Q9BXY0	MAK16	35.368	5.7458	6.3	1	1	1	4782900	17969000	nucleus	K14831	A	KOG3064	RNA-binding nuclear protein (MAK16) containing a distinct C4 Zn-finger
Q9BZI7	UPF3B	57.761	-2	1.9	1	1	1	0	0	cytoplasm,nucleus	K14328	A	KOG1295	Nonsense-mediated decay protein Upf3
Q9BZZ5	API5	59.004	19.212	3.4	1	1	1	19785000	58117000	cytoplasm		T	KOG2213	Apoptosis inhibitor 5/fibroblast growth factor 2-interacting factor 2
Q9C002	NMES1	9.6172	13.611	32.5	2	2	2	0	0	extracellular				
Q9C005	DPY30	11.25	17.119	36.4	2	2	2	32286000	80674000	cytoplasm	K14965	K	KOG4109	Histone H3 (Lys4) methyltransferase complex, subunit CPS25/DPY-30
Q9H061	TMEM126A	21.527	5.5456	10.3	1	1	1	3464600	17546000	cytoplasm	K18157			
Q9H307	PNN	81.627	8.5561	2.4	1	1	1	4483000	26169000	nucleus	K13114	Z	KOG3756	Pinin (desmosome-associated protein)
Q9H8H0	NOL11	81.123	7.5053	1.9	1	1	1	10165000	34734000	cytoplasm				
Q9HAW7	UGT1A7	59.818	5.8913	2.3	1	1	1	0	0	plasma membrane	K00699	GC	KOG1192	UDP-glucuronosyl and UDP-glucosyl transferase
Q9HBG6	IFT122	141.82	10.434	1.5	2	2	2	26461000	2507200	cytoplasm	K19656	R	KOG1538	Uncharacterized conserved protein WDR10, contains WD40 repeats
Q9HDC9	APMAP	46.48	6.7424	6.5	1	1	1	11600000	44347000	plasma membrane	K21407	R	KOG1520	Predicted alkaloid synthase/Surface mucin Hemomucin
Q9NPE3	NOP10	7.7059	12.458	20.3	1	1	1	44365000	1.7E+08	cytoplasm	K11130	A	KOG3503	H/ACA snoRNP complex, subunit NOP10
Q9NPG4	PCDH12	128.99	5.6904	0.8	1	1	1	37543000	0	endoplasmic reticulum	K16499	S	KOG3594	FOG: Cadherin repeats
Q9NQC3	RTN4	129.93	11.755	4.9	2	2	2	2.46E+08	2.87E+08	plasma membrane	K20720	U	KOG1792	Reticulon
Q9NQG5	RPRD1B	36.899	12.844	7.4	2	2	2	4327400	14111000	nucleus	K15559	A	KOG2669	Regulator of nuclear mRNA
Q9NSI2	FAM207A	25.456	5.9571	6.1	1	1	1	0	0	nucleus				



Q9NX40	OCIAD1	27.626	12.761	18.8	2	2	2	7684700	47680000	nucleus			
Q9NY93	DDX56	61.589	9.3496	2.7	1	1	1	7122800	11793000	nucleus	K14810	A	KOG0346 RNA helicase
Q9NZ45	CISD1	12.199	5.9327	12	1	1	1	0	14742000	extracellular		R	KOG3461 CDGSH-type Zn-finger containing protein
Q9NZN4	EHD2	61.161	20.895	10.3	3	3	3	5540300	80564000	cytoplasm	K12469	TU	KOG1954 Endocytosis/signaling protein EHD1
Q9P035	HACD3	43.159	6.1709	6.1	1	1	1	3325100	47841000	cytoplasm	K10703	R	KOG3187 Protein tyrosine phosphatase-like protein PTPLA (contains Pro)
Q9P0J0	NDUFA13	16.698	18.473	16	2	2	2	7295600	37105000	cytoplasm	K11353	CD	KOG3300 NADH:ubiquinone oxidoreductase, B16.6 subunit/cell death-regulatory protein
Q9P2E9	RRBP1	152.45	5.6389	1.2	1	1	1	0	0	endoplasmic reticulum	K14000		
Q9UBD6	RHCG	53.178	23.575	9.2	2	3	2	3858700	70541000	plasma membrane	K06580	UR	KOG3796 Ammonium transporter RHBG
Q9UDW1	UQCR10	7.3084	7.2677	27	1	1	1	4543400	12839000	mitochondria	K00419	C	KOG3494 Ubiquinol cytochrome c oxidoreductase, subunit QCR9
Q9UJC5	SH3BGRL2	12.326	5.5437	12.1	1	1	1	0	21047000	cytoplasm		S	KOG4023 Uncharacterized conserved protein
Q9UM00	TMCO1	21.175	8.3169	8	1	1	1	7150400	45256000	extracellular	K21891	S	KOG3312 Predicted membrane protein
Q9UMY1	NOL7	29.426	6.7256	5.4	1	1	1	15385000	21291000	nucleus			
Q9UQ80	PA2G4	43.786	6.1233	5.8	1	1	1	11917000	13548000	nucleus		R	KOG2776 Metallopeptidase
Q9Y224	RTRAF	28.068	14.607	13.9	2	2	2	18730000	57139000	cytoplasm	K15433	R	KOG4380 Carnitine deficiency associated protein
Q9Y241	HIGD1A	10.143	7.1218	19.4	1	1	1	0	15337000	cytoplasm		R	KOG4431 Uncharacterized protein, induced by hypoxia
Q9Y281	CFL2	18.736	10.625	39.2	5	8	2	7478900	33080000	mitochondria	K05765	Z	KOG1735 Actin depolymerizing factor
Q9Y295	DRG1	40.542	5.5475	3	1	1	1	0	0	cytoplasm		T	KOG1487 GTP-binding protein DRG1 (ODN superfamily)
Q9Y333	LSM2	10.834	13.51	28.4	2	3	2	14493000	76749000	cytoplasm	K12621	A	KOG3448 Predicted snRNP core protein
Q9Y3B3	TMED7	25.171	7.7208	5.8	1	1	1	0	18200000	mitochondria	K20349	U	KOG1693 emp24/gp25L/p24 family of membrane trafficking proteins
Q9Y3B4	SF3B6	14.585	5.5693	11.2	1	1	1	14344000	36025000	nucleus	K12833	R	KOG0114 Predicted RNA-binding protein (RRM superfamily)
Q9Y3B9	RRP15	31.484	5.5586	3.9	1	1	1	0	0	nucleus		S	KOG2974 Uncharacterized conserved protein
Q9Y3C1	NOP16	21.188	6.2276	3.9	1	1	1	8380600	12981000	nucleus		S	KOG4706 Uncharacterized conserved protein
Q9Y3T9	NOC2L	84.918	8.1003	2.1	1	1	1	2564200	15010000	nucleus	K14833	J	KOG2256 Predicted protein involved in nuclear export of pre-ribosomes
Q9Y5J1	UTP18	62.003	6.0631	3.1	1	1	1	0	11635000	nucleus	K14553	R	KOG2055 WD40 repeat protein

Supplementary Information

Supplementary Table 3. A representative list of proteins subject to remarkable methylation or demethylation in senescent cells.

**A. Differentially modified sites summary (Filtered with threshold value of expression fold change, dimethylation)**

Compare group	Regulated type	Fold change >1.2	Fold change >1.3	Fold change >1.5	Fold change >2
SEN/CTRL	up-regulated	(0)	(0)	(0)	(0)
	down-regulated	1 (1)	1 (1)	1 (1)	(0)

Protein accession	Position	Amino acid	Protein description	Gene name	Localization probability	PEP	Score	Modified sequence	Charge	Mass error (ppm)	MS/MS Count	CTRL	SEN	SEN/CTRL Ratio
Q71DI3	<b>36</b>	<b>K</b>	<b>Histone H3.2</b>	HIST2H3A	0.837398	0.0267953	64.22	KSAPATGGVK(0.837)K(0.16:4		-2.4441	1	5175500	15592000	<b>0.554</b>

**B. Differentially modified sites summary (Filtered with threshold value of expression fold change, trimethylation)**

Compare group	Regulated type	Fold change >1.2	Fold change >1.3	Fold change >1.5	Fold change >2
BLEO/CTRL	up-regulated	1 (1)	1 (1)	1 (1)	(0)
	down-regulated	3 (2)	3 (2)	2 (2)	(0)

Protein accession	Position	Amino acid	Protein description	Gene name	Localization probability	PEP	Score	Modified sequence	Charge	Mass error (ppm)	MS/MS Count	CTRL	SEN	SEN/CTRL Ratio
P05141	52	K	ADP/ATP translocase 2	SLC25A5	1	0.001817	129	QYK(1)GIIDCVVR	2	-0.78278	2	42366000	1.75E+08	1.66
P0DP25	116	K	Calmodulin-3	CALM3	1	4.783E-18	231.9	HVMTNLGEK(1)LTDEEVDEI3		-0.4112	11	1.54E+09	7.47E+09	0.863
P68104	318	K	Elongation factor 1-alpha 1	EEF1A1	1	0.0643065	63.82	NVSVK(1)DVR	2	-0.84943	1	36018000	46913000	0.526
P68104	79	K	Elongation factor 1-alpha 1	EEF1A1	1	8.348E-07	141	GITIDISLWK(1)FETSK	3	-0.05163	2	46087000	54182000	0.701
Q71DI3	<b>27</b>	<b>K</b>	<b>Histone H3.2</b>	HIST2H3A	0.999996	0.0267953	64.22	K(1)SAPATGGVKKPHR	4	-2.4441	1	5175500	15592000	<b>0.554</b>
Q9HBG6	711	K	Intraflagellar transport protein 122 homolog IFT122		1	0.0500242	78.52	FHEAAK(1)LYK	2	0.015077	1	0	1.32E+08	

## Supplementary Information

**Supplementary Table 4. A representative list of human genes associated with ChIP-seq identified H3K9me3 peaks differentially mapped between experimental conditions of stromal cells.**

Category name	Number of peaks	Gene names (as output elements)
Overlapping between 'BLEO vs CTRL down' and 'BM vs BLEO up'	116	FAM230E OR11H12 ROCK1 MMP1 POTEA USP17L20 TPTE MIR6724-1 ART1 CHEK2P2 MMP3 FAM230F CXCL8 FRG2 IL7 RNA28SN3 LSP1P5 LOC390705 KCNE1B ACTR3BP2 MIR6724-3 MTRNR2L9 RNA28SN5 EPHA3 MIR10396A ZXDA NID1 FRG1DP MMP10 DEFB115 SFRP2 MIR4477A PROS1 SPINK1 ASNRP1 MMP12 LOC650226 AREG RNA5-8SN5 HCN1 LOC101929512 HAVCR1P1 CWH43 LINC00960 MMP8 LOC105379477 EMB EMBP1 CCNYL3 CCT8L2 ROCK1P1 FAM230C FRG1FP ZNF733P MIR5195 OTOAP1 OR11H1 ALG10B ZNF716 REXO1L2P LOC102724904 ACTR3BP5 LINC00999 ZNF707 MMEL1 FRG2B BAGE OR4C46 PLCH2 RNU2-1 LINC02218 LOC284240 CXCL1 LOC102723769 LOC100132249 LOC646813 MIR6724-2 ANKRD26P1 ACTN2 LSP1P4 SPIN4 IZUMO1R FRG1CP SLC6A10P RHOA LOC644669 BMS1P14 FRG1EP WNT16 ALG10 LOC102724159 FRG1BP USP17L6P SPRY3 DUX4 RNA5-8SN4 SNHG27 LOC100506585 MTRNR2L1 H3.Y GYG2P1 TEKT4P2 ANKRD30BP2 IL1B BMS1P22 LINC01667 LINC02167 FRG2EP RNA45SN3 MIR663AHG CSF2 MIR4477B DCUN1D4 MIR9901 ARHGEF18 ZNF565
Unique to 'BLEO vs CTRL down'	45	LOC101929572 LOC102724843 CDKN2A-DT DOCK1 LOC102724580 RNA5S2 LOC112267871 SNORD164 LOC105369266 LOC100133920 RNA5S11 LINC01945 TTC34 LOC100134317 DHX32 USP17L24 ACAP2 UNCX FAM90A7P FAM72C RN7SL1 CDKN1A NKX1-1 USP17L15 FANK1 MIR4273 RNA5S16 RNA5S6 ZNF717 BAGE2 ZNF875 HGH1 ELOA3 MLLT10P1 MIR6724-4 RNA5S4 ZNF561 LOC286083 ABR MIR3648-1 DLEC1 FRG1HP DUSP5P1 C7orf33 SPATA31A5
Unique to 'BM vs BLEO up'	16	USP17L28 FRG1JP BAGE3 RNA28SN2 RNA28SN1 RNA5-8SN3 RNA5S14 MIR3648-2 SNAR-C3 ELOA3D

		RNA5S3 SPATA31A7 USP17L11 UBBP4 LINC01163 LINC01596
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## Supplementary Information

**Supplementary Table 5. A representative list of human genes associated with ChIP-seq identified H3K36me3 peaks differentially mapped between experimental conditions of stromal cells.**

Category name	Number of peaks	Gene names (as output elements)
Overlapping between 'BLEO vs CTRL up' and 'BM vs BLEO down'	2027	TRAF3IP2-AS1 ZNF799 OR2K2 LMAN1 MIR6886 CHRNA10 ZAR1L PARN SOD2 MIER1 MIR4511 EVC SCYL3 NAT10 LINC02601 DHRS11 TAOK3 BAZ1B TERF2IP CD160 PHF20 COL1A1 RAB33B ZNF83 CEP350 MIR1228 SNORD98 VWA5A ABR LINC00597 POLR2B GPN2 GCC2 WBP4 KIAA0100 SETDB1 RUVBL1-AS1 PTP4A2 BDKRB1 SEC14L1 CHFR SF3B6 NIPSNAP3B ELAC2 GTF2IP20 RICTOR ZNF687 COX7A2 KDM4B UBN2 LINC01450 WASHC5 MRM3 COMMD5 OSBP WASHC3 ZNF350 AHI1 EIF4A3 PRPF3 PXN-AS1 CAMSAP1 MIR6889 SNORA58B MIR628 EXOC1 TTC13 VRK2 FARSA-AS1 ZNF568 TTC3 TMEM248 ANKRD26 SCR1 PFN1P2 FAM161A PIGG JAK2 RNU6-2 CASP1 LINC01619 RAB11FIP4 TALDO1 EHD2 YTHDC2 XXYLT1 NPIP5 SAFB2 MIR6868 CCAR2 CALCOCO2 ZNF551 HBQ1 GEMIN6 LINC-PINT BSDC1 MIR1182 ZNF480 LOC102723582 PROS1 PSMB8 ZBTB41 AHCTF1 PCNX2 WDR26 TOMM22 SOCS3 SOX15 EPN1 GAL RDH11 KIF1B SPHAR ALAS1 DUSP10 FBXO7 STH ZC3H14 SNORA68 ZNF287 ZFYVE9 HSD17B13 FBRS GRAMD1C GSR SCGB1C2 SIGLEC15 HEATR5A MIR4498 CFAP36 GUSBP5 SLC35F5 EMB SRP14 LINC01587 MIR6780B UBN1 CTNNA1 MIR765 KRTCAP3 SPDYE10P C19orf18 ZNF16 RFT1 TACC1 ARL17B UBE2CP5 MDM2 GNAI1 VPS4B SLC25A4 CYB5B FARP2 ZFP36L1 GPR161 ZNF10 HOXB-AS1 LOC100506321 NEO1 TARS2 ZNF624 AGL SH3D21 DEGS1 TCTEX1D4 CMTR1 TXNRD1 FUT11 ABHD8 ZNF121 MTHFD1L SYT11 ZNF585A TARDBP LRP1-AS CHMP1A ZNF160 LRSAM1 ADAR DHX29 NSFL1C XRN1 SNX22 CROCCP2 SDC3 RPUSD2 MIR1226 ZSCAN31 RSPH10B ZNF559-ZNF177 MIR4430 POLR2J3 POU5F1P4 SNORD164 ZNF594 SLC41A1 LY6G5B ZMYM2 PCOTH MRPS21 ITCH GTF2H2C MIR12119 PIK3R1 STAMPB MIR555 SNORA90 ELMOD3 OIP5-AS1 NEK9 ADNP BTD ZNF570 ZNF847P MIR6081 ACBD3-AS1 SORBS3 SNORD62A UBAP2 NBPF14 SBDSP1 C11orf65 MIR4714 HMGXB3 TPR ZSCAN20 LOC105371998 MCPH1 ZNF57 CHCHD2 RHOBTB1 SLC4A4 SUMO1P3 AP2A2 DDX56 MRPS18B ZNF682 IL1R1 STIM2-AS1 NR1D1 ARID1A RPL23AP82 UQCRH SAV1 ZNF445 LOC154761 SNORA14B LBR MIR1255B2 MMS19 KDM4A-AS1 ZNF485 MIR4785 LOC100289580 LOC101927018 SLTM NID1 KIF7 NBEAL1 SMARCC2 POLI ZNF248 IRF2BP2 ZNF230 C5orf24 RNF41 THOC5 MUSK LOC102724904 ZNF347 STRADB ARHGAP17 OR4C46 LOC646813 LINC00260 SMAD3

MIR597 YARS2 RMC1 ZNF669 CDK12 CHMP5 ZNF43 SKP1 ZBTB38  
FYCO1 RAPH1 MIR558 ZFP37 ZNF154 ACBD5 TIPARP VEGFA IPO8  
PHC3 TNFRSF11B EXO5 ZNF117 GPCPD1 PIGV EMBP1 DYNC1LI2  
RSKR ERMP1 SCD5 LSG1 CBR4 MIR7161 MIR574 CDR2 ZNF778  
SRP68 ARPC5 NPIP11 UBR5 ZNF20 ANXA6 SNORD13H PPHLN1  
CNTF STC1 STOM CPSF3 MIR548A3 GBAT2 ARPP19 BOLA2 RNF19B  
MPI SDHAP1 FAM229B ARMH3 TCTN1 MIR6766 MPZL1 SPIN4 VPS11  
MTCH1 CDC26 LAMTOR5-AS1 ZNF32-AS1 PPIB SCARNA11 GOLGA5  
ATP5MC2 IL6R-AS1 PYGO2 PPP1R10 TOM1 SLC26A11 RIOK3  
NSUN5P1 PPP1R12C MRPS26 PRICKLE2-AS3 NPIP3 UBE2B  
SNORD141B ARRDC4 TRAPPC10 SERPIND1 ZNF184 ZNF267 TXNIP  
ZNF260 SEC31A POLR2D HNRNPC FXR1 ZNF461 TH2LCRR  
PRPF40A RGS2 LOC101927604 IVNS1ABP MIR125B1 MIR6735  
ACTR3BP2 EPHA3 RBM12 MOV10 DEDD TMEM9 ZNF174 LEAP2  
SLU7 ANAPC11 UBR5-AS1 MIR6827 DNAJA2 PPIAP30 CCNL1 GDAP2  
MIR1231 ZNF491 COX6B1 LOC102723769 RNFT1 B3GNT4 SNX27  
DENND10 SLC16A6 HIBCH UTS2 DNMBP SEC24C LOC101929599  
RUSC1 DHX57 FAM177B ZNF226 ZNF773 APH1A COX18 TP53INP1  
MIR26A2 BAZ2A SECISBP2L DDX6 AP3M1 AKAP9 NGLY1 HLTF-AS1  
RBM22 TRIM38 CORIN TMCC1 SMG5 CYCSP52 NIT1 MIR3651  
FRG1CP DUT ZNF34 CDC73 GSTM3 EIF3L PMS2P5 NPIP13 RIT1  
RAB13 KIAA1614 MIR3162 TUBG2 PSMD1 CDC123 AMN ZNF700  
HAVCR1P1 TTC23L MIR6738 ZNF607 ZNF733P RAB11A SNX1  
MIR5191 MIR3175 ZFR MIR6852 MFSD4B TTC23 TRIM39-RPP21  
SMA4 OVCH1 MYPOP MIR6511B2 UCHL5 AIM2 SHC4 RARS ZFP69  
COX4I1 DTWD1 ARID4B SETX ZNF326 ZNF8-ERV3-1 IFT57  
LOC105379183 LMNA ZNF250 ZNF12 SNED1 ST7 PDHB MIR1343  
MIR4799 AP4E1 RASA3 PGD WAC ZNF816 MTMR11 SUOX STXBP3  
EIF3G UPK3BL1 SLC18B1 SUSD1 MIR553 PRUNE1 PRKAG1 MDM4  
NBPF15 ZNF200 LIMS3-LOC440895 CBR1 SNORD151 ZNF638  
VPS33A TFIP11 MIR3662 MIR4759 BTG3-AS1 SNORD13F MINDY1  
ZNF181 PIKFYVE PI4KB OAZ2 SNORA70G HSD11B2 CACTIN USE1  
CAND1 COL4A2-AS2 CDK11A COL9A2 PALLD GNAS MIR4757  
GOLGA3 BBS7 ZNF345 RTF1 WDR59 EVI2A INE1 TPI1 ZNF484 RIN2  
LOC100288069 HYOU1 ZNF25 ZSCAN16 STARD13 NPTN-IT1 SBNO2  
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RGL1 APPBP2 USP19 KDM5A ZNF467 MYOCOS CFAP298 NUP88  
DHX16 ARL2BP HSPA8 ABCC11 ZNF432 FUBP1 AAMDC NOTCH2NLC  
ZNF583 ATP1A1 ZNF805 IFI16 CLTCL1 ZNF891 SEC63 TOR1AIP1  
CEBPD SVEP1 GANAB C1orf198 BMP8A ZNF254 PSMC4 SGK1  
ZNF271P RARS2 LRBA NFKBIZ PPOX ZNF439 PLIN3 ATG7 HYPK  
MCFD2 TRPA1 FAM81B CBX1 SPIDR UBE2D3 MIR579 ZNF561  
RUNX1T1 EAF1 CTSK TRIM35 ZFP90 SLC30A7 S100B LINC01000  
ZNF565 NACA GLOD4 ZNF790 SPATA9 TEX10 TNFRSF19 HIF1A-AS2

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GNA13 ARL8A NEK10 STAT1 PEX11B IRF2BPL PROCA1 BBX  
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DTX2 RABIF DYRK3 RBM34 CDRT1 ZNF528 ZNF44 MTFR2 ZNF555  
SASH1 LOC100506076 ALG10B CDC14B ANGPT1 LSM14B HECTD1  
ELOA SNORA94 RPS6 TBCE TTC36 MAPK1 GADD45A MASC RNA  
DHX8 UBE3B SPDYE8P IKBKB LINC02167 TRIM66 ZNF132 USF3  
UBE2Q1-AS1 POLDIP2 VPS37A NISCH LRRC37B CCNT1 TNKS1BP1  
SNORA3B ZFYVE28 PIK3R2 AKR1B1 PSMB4 GSDMB PMPCB NID2  
ZNF616 EXTL2 CNIH4 POP1 RNF24 SETD1B ZNF606 SSR1 NFS1  
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APH1B USP36 CTNND1 NUDCD3 NUP50-DT GUSBP9 PITRM1 USO1  
RUFY3 LDB1 ABCC1 LINC01341 FCER1G LOC101928000 TPST1  
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CDC25C RCOR3 CPSF7 ARID5B SPTAN1 ACTR1A SCARNA26A PPIG  
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THOC1 INTS10 ZNF124 SPRED1 ZNF217 ZNF101 ACO1 RNVI1-19  
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AS1 CFHR3 SF3B4 ZNF222 COL10A1 WDR55 NBPF9 CACNA1C-AS2  
ELL2 RIPOR2 IGFBP4 HLX-AS1 ZNFX1 B3GALNT2 CLNS1A MIR378H  
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MYBPHL FMN2 VDAC2 VHL SNORD8 SPART PLSCR3 TOP1  
KRTCAP2 DPY30 MIR4677 BTG2 ABCC6 LRRC41 C12orf66  
LOC101927151 C2orf49 ANAPC4 COX15 FBH1 SRPK1 ARL6IP1  
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VGLL3 TRAF5 KLF3-AS1 MARF1 SRSF11 PXDN ZNF35 VIM-AS1  
COG1 IRS1 ZSCAN32 PCDH18 MIR3117 LOC100507346 KDM2A  
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SLC3A1 PIGF LOC100130111 YIPF2 PSMF1 NRF1 MICALL1 DUS4L  
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TRIM24 PABPN1 CC2D1B ZNF695 ABCD3 MSC-AS1 ZNF84 CITED2  
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BLMH TXLNG FAM171B PRPH2 RPS10 PSMB7 SNORD90 MMP14  
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ZNF2 NFKBIA PSMA6 CRTCL1 ZNF823 KCTD3 NXPE3 LINC00616  
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NAPG ZNF513 SLC66A3 MDH1 RPL7L1 KATNAL1 PAQR6 VCAN-AS1  
LOC644189 OSMR VWA8 LOC647070 ZNF175 SLC40A1 NCF2 HUS1B  
FAM133B NIPSNAP1 PI4K2A MED8 SNRPA C9orf163 ETS2 PRMT2



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MAN1C1 MIR1302-5 PDK2 NEK1 DUSP1 DDAH2 STX7 SLC45A2 MRC2  
SETD5 MYO18A MTSS2 ATM PRRC2C ZNF134 HHIPL2 TTC3-AS1  
TMEM183A TMEM106A FCHSD2 MIR6506 ZNF195 DHX34 CELF3  
NUMBL H2AFX SNORA77 GOSR1 RAB7B SPCS1 KDEL3 LRRC73  
IER3-AS1 TMED10P1 DYNLRB1 MAP4K5 EXOSC8 ARHGAP23  
MIR6736 MCL1 PRNP SNORD71 RSPH6A LOC613038 KRBA2 ZNF335  
CPT2 LIMS4 ATP5PF MVP ZC3H18 SF1 RNF213 NCKAP1 CLK1 XPR1  
ZNF333 DUSP11 LSP1P5 LOC101927989 KREMEN2 SNORA55  
LINC01072 CDK9 CD59 ARHGAP18 POMP AHSA1 TIMM9 ORC2  
CERS5 LOC100289561 SNORD15B PABPC1L UBE2C MIR3675  
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MRPS5 NEMF ZNF841 ERVFRD-1 PDZK1P1 SNORA70B KLHL12  
SF3B1 OR11H1 PSMA7 LINC00342 TUBG1 WASHC2A PPP4R3A  
MXD3 IKBKE RNVU1-15 FAM98C EP300-AS1 MIR6885 IBTK BIRC6-  
AS2 ST14 MLF2 NRADDP MIR6740 SUPT20H C1orf189 ZFP64 SOCS2  
TMEM242 LOC646471 MBIP COPB1 COQ8B SMG6 CIZ1 NFX1 MBD3  
LOC100505549 MMD POLR2J2 CDV3 TOR1AIP2 DAP RRM2B GNPAT  
WDR18 LOC100131315 CAMKK2 TBC1D2 ZNF77 EIF3K ZNF28 POP5  
PTP4A1 CARF LOC440300 ZNF613 SNORD13G ZNF490 BMS1P20  
SERPINC1 F3 ZNF37A ZNF266 MIEF2 APOA1 KPNB1 FOXO3 IFT20  
RFX7 SUPT7L CSF1R TMEM101 RBM43 DDX3X SESN2 HNRNPL  
EPB41L5 SH2D5 HDC OCA2 RPS6KC1 TNFRSF10D SMARCE1  
STK17B LINC01964 LOC105379331 PATL1 RANGAP1 KCNJ2 ZNF684  
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LRRC37A4P HMGN1 ZNF718 ABCC5-AS1 PCYT2 TSC22D1 CLCC1  
ACSL3 IMPDH2 INTS6 ZFP14 ZNF660-ZNF197 ALKBH2 SNORA100  
SLC27A3 CEP170 MSH6 HECTD2 PTK2 RNF217 USP3-AS1 PLIN2  
NFKB2 FZD9 ZNF75A ZNF605 MIR1278 CELF1 EDRF1 POGZ NBPF19  
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RGPD5 FENDRR CDC6 ATP5PD VSIG10L ZNF320 BRD8 MIR5706  
SPG11 KCNJ13 COP1 KRT8P41 LACTB2 VAMP4 MIR6851 DDX24  
NEK6 C6orf62 SOWAHB GUSBP1 FTH1 WWC2-AS1 SNORD53B  
TIMM17A ZNF354C NSD1 LARGE2 GLDN MIR7-1 LRRC42 RBM26  
CYB561 ANTXR1 CRCP ZNF177 ZNF442 ZNF627 WIPI2 SVIL-AS1  
ZNF468 BAG3 LAMC1-AS1 PSMD2 PLEKHO2 BCAS2 APTX SNRPG  
ZNF514 ZKSCAN1 HSD17B7 ZNF354A SELENOS MDH2 BCL6  
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TBCEL LOC100192426 AMFR SNORA59A DKK3 PDCL DMXL2  
SCARNA26B NAE1 SNORD23 LOC105377102 MEX3A ZNF268 MYLK  
ARL4D GPBAR1 SLC25A17 ARHGEF28 AGAP6 GTF3C2-AS1 PDLIM4  
NPIPA8 ZNF880 MIR711 ZNF426 LOC400710 PHF2 ACTL7A TMBIM6  
DNAJC21 PDE7A ARSG ZNF483 LMBR1L RALGPS2 LINC01926  
SLC35D1 PSMD4 ERLIN1 MRPL27 RBPMS-AS1 ZNF26 CDK11B SNF8  
STX10 ZNF143 TIPRL LOC100287049 STK19 IGF2BP2-AS1 TGIF1  
TP53 ZFAND5 RAPGEF2 PSMC5 ZNF564 SNORA86 ZNF782 GPR25  
ATP6V0A1 MIR1256 ZNF615 DNAH3 ALG5 S100PBP SNORD94  
TCTEX1D1 ZMAT2 DLC1 MXD1 NUAKE2 PMS2P3 MANBA ZNF671  
UBFD1 ELP2 MIR663AHG ZNF418 KLHL11 MIR2110 ORC4 GYG1  
ZNF91 GAPDH GPX1 PRPF40B SNAPC3 B4GALT5 TRMT1L VNN2  
CALM1 GPS2 RUFY2 HSPB9 TP53BP2 ZNF850 ZNF440 TMEM81 C9  
MRNIP RRN3 SLC5A11 MEF2D MYO1B ANKRA2 LINC01820 ZNF189  
C1R TICAM1 ZFP28 LOC284454 DOCK4-AS1 TRIM22 TSC22D1-AS1  
MRPS14 MRI1 TGM2 BASP1 ZNF202 MIR6769A ZNF197 ZNF274 ATF3  
UCHL1 APOL6 ZNF397 SYT2 DDX47 ATP8B2 DPP4 PSMC2 EXOC6B  
C5orf15 ARNT ZNF596 SEMA3A EIF4EBP3 ACBD6 YEATS2 JTB  
GMCL1 MGAT5 RAP1GAP MEF2A ZNF836 TBX2 COL21A1 RAI14  
CLP1 ZNF716 LOC114483834 BNIP2 CASC3 PPP2R1B TANC1  
LOC644669 ZNF527 TTBK2 NRAS ABHD15 FAM133CP LINC01465  
TRAPPC2B ACTR6 SNORA50A ZNF585B NBPF1 SLC2A8 SNRPE  
LRIG3 MTFMT PRKAB2 AFF4 RSRP1 SNX4 COPS2 ZNF221 PIP5K1A  
PRKAR1A ATG5 RAD52 ETV4 ZFP30 BMS1P14 RAB11FIP3 MIR4743  
GNG4 RGCC SLC6A13 KANSL1 CRIM1 ZNF546 GABARAPL1  
ANGPTL8 BMP4 POTEA AHSA2P RNF115 GBA PNRC1 TRIB1 CD46  
TYSND1 DEF6 SEC22B CDKL2 POLR3C FBN1 ZNF621 TBL2 ATP5ME  
TXLNA DIPK2B PRR1 STAG3L3 SNORD163 KPNA1 FAM149B1 CLTC  
SRP9 SMYD2 ZNF761 FRG1EP ECI2 CORO6 MED23 INTS3 ZNF558  
TRPM4 FAM227B NMRAL1 EEF1AKNMT GPR89B CLOCK LOC91370  
PSMA4 ROCK1 SCARNA3 ZNF45 ZNF610 ZNF329 ZDHHC18 VEZF1  
SPDYE11 LINC01555 ZNF394 EFCAB10 PPP1R12B SACS FOXO3B  
LAYN PLK2 PRMT5-AS1 OPTN SP100 GORAB-AS1 ZNF283 SBF2  
ZNF699 MBD6 C17orf64 RTTN STX12 ZNF322 PTGR1 ZNF69  
CCDC144CP HSPA5 ZKSCAN5 ACAT2 ZMYM4-AS1 MICB LINC01096  
PPIF CPNE3 ABCF3 CTSL FOXF1 PRPF18 TMCO1 PAPSS1 NBPF26  
EID3 FLJ31356 MIR194-1 ZNF569 MED28 ADSL BAP1 TMEM161A  
ERP44 ZNF180 NDUFAF5 LOC100128494 PA2G4 LOC100190986 RILP  
MIR29C SDHC B4GALT3 MAP1B ATAT1 GGNBP2 MIR6870 PRPF38A  
OXNAD1 RNF40 IFT81 LOC100289511 NT5C2 NUCB1-AS1 TSACC  
DNAJB12 SCAND2P MIR4273 ARFGEF1 NOLC1 TKFC MIR6894  
QSOX1 PKDCC FOXP1 RGMA SERINC1 PEX19 PSMD7 PPP1R3C

		<p>TTC17 C3orf35 ZNF736 ZNF791 LOC729867 CERS2 TXN MIR570HG          BECN1 ATP6V1D PTGS1 ADPGK-AS1 ZNF112 ZNF436 SNRNP27          LOC100132215 HGSNAT KIAA0754 VPS13C GCC2-AS1 TULP3          OTOAP1 ATP2A2 MIR3126 STRN UEVLD ZNF845 ZGPAT BAX NCOA4          SMARCAL1 PRMT7 DNAH5 PGPEP1 RNF6 ZNF383 S100A13 WDR66          RETREG1 DNAJC13 VPS13B LOC645513 DCLRE1C XPO5</p>
<p>Unique to          'BLEO vs          CTRL up'</p>	<p>6032</p>	<p>MSRB1 FSTL1 CLMP AACS ELMO2 PNMA1 SLMAP FAM219A          SAMD4A TMEM216 ERCC5 APBB2 GARS-DT PDCL3 DECR1 SALL1          IRAK1 ESYT1 MIRLET7G CHD8 SUMO1 GP1BA TMC4 UQCR11          LINC01279 EP300 CRNKL1 RNVU1-14 DTNBP1 COPRS EFCAB9          CYTH1 CHD9 TOB2 INIP NINL MAP3K3 GRM2 CAPS OSBPL8 LONP1          SLC25A52 LOC102723566 CHD1 WDR34 LHB ADNP-AS1 MINAR2          STK25 SNORA80D MIR611 NOXO1 HIGD1B ABCD4 LOC105372383          MIR331 MIR6807 SLC25A46 GTPBP1 MIR6746 ZNF212 ACBD3 PRDM2          MIR630 PDCD4 CST7 NUP42 CIAO1 LTBP4 SIRT6 MIR3121 C2CD3          ZDHHC6 NEFH PGBD5 EXOSC7 RFXAP RNF4 EMC1 HDAC7 ALG2          GRB2 TPM3 FPGT GDF10 LOC102724843 LOC101927178 PLXNA1          PMF1 CRELD2 CD82 PMM1 GCLM INTS1 BIN3-IT1 LOC100287497          GMPPA OGFR-AS1 EMILIN1 THADA PIK3CB PRORP CDCA4 C9orf16          MIR11401 MTMR14 USP42 TMEM59 LOC729603 SNX6 DDX18          BORCS8-MEF2B TMEM104 POMT1 CAPN1 DDHD2 MRLN LAGE3          LOC101929464 UNC13B TTLL4 ZBED1 ANKRD49 METTL21A SARS          CACNB1 MAN2B1 OFD1 PDP1 AHCYL2 GPHB5 PEX16 HABP4          MIR548AU UFL1 RP9 TMEM11 LOC100129617 MIR5004 LOC400541          IPO13 PCCB UNG MIR6509 GSTP1 DCUN1D5 LTBR HDHD2 IGDCC3          ANKLE2 NBPF3 DOCK11 RPRD1B CHMP7 REM2 DNHD1 OVCA2          ASAH1 FKBP4 NADSYN1 OSGEP HK3 PSMD5 RSU1 E4F1 ACO2          RPS21 WAPL IFITM10 MIR5010 HDAC3 SNORA54 KRCC1 RPL13AP3          HUS1 UIMC1 GOT2 ZNF667 ACOT2 KIN ETFA SNORD65C AHRR          PDAP1 POLRMT MIA2 EIF4E2 NENF ZNF324 ENTPD7 CASC4          LOC100506083 TSTD3 AKIRIN1 RDX DNAJC9 ITSN1 EHP1L1 DCTN1          CAMK2B TNKS2 TMEM241 MRTO4 C1QBP NDUFB8 GRHL1 NDUFAF8          STOML3 R3HDM2 SLC2A10 TMED7 CENPL MIR2054 HCRTR1 VWCE          SNORA110 DDI2 GPATCH8 TANC2 ZNF511 ZMYM5 ZNF586          ADAMTS19-AS1 CPD TANK TEX53 PROSER3 DNAJB4 LIMD2          LOC101928371 TMEM189 SVOPL TACR2 NUP85 LOC100130744          GPR135 TM9SF4 ZNF264 RAB5A PRRT1 SUSD6 ABCG8 ICA1L          IFNAR1 TCTA LINC00680-GUSBP4 KMT5A SQLE MIR6129 GLIPR2          FAM49A PLRG1 SPG7 NUP133 ILF3-DT INPP5B PPID MIR3150A          UBE2J1 ELF1 LINC01291 ERMARD ICE1 LOC100506271 NCK2 OXA1L          LOC100506472 CLDN10 MIR4726 MEX3D KIAA0232 NFAT5 FBXO3          MSS51 GPR157 PEF1 FAM199X ZNF750 ALG9 MCM5 NOL4L BTBD10          BAIAP3 ANKRD40 LPP-AS1 SLC48A1 CDK16 HRAS ARSK CPNE9          NDUFAF1 PLAC8L1 TEKT2 MAP3K6 MIR943 SRRD SOCS4 PPP6R2</p>

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UNKL POP4 ZNF839 CCNA2 LOC285638 TMEM132A DACT3-AS1  
CGRRF1 ISCA1 RPAP1 GATD3A LOC101241902 NIPA2 MFSD14B  
SNORA115 SLC35A1 RAVER1 TSTD1 SNORA92 AUH SLC25A39  
EIF3H PLA2G10 MRPL37 LOC100996437 SNORA15B-2  
LOC105374952 PSMA5 RESF1 AMPD3 PIAS1 HMGXB4 RBMXL1  
CRTAP DDX50 LOC148696 TK2 STYXL1 TRIM16 A1BG-AS1 MIR6726  
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SLC25A24 MRPL22 SLC25A15 KLHDC1 TDP1 TCTN3 DNAJB11 GBA2  
NDUFB3 LINC02542 SPATA24 PTC2 USP38 CABP7 ITGA10 MAGEF1  
NDE1 MIR6752 SCARNA22 FH PTPN23 DGCR8 DNAJB13 PAQR7  
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EIF4E TCHP IMPG2 SLC29A4 TRAF6 TELO2 PNPLA3 LOC102723885  
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IFT172 ST7L CBX4 FOXN3 MIR6721 LCLAT1 MIR3164 LHX4-AS1  
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GALR3 AKT2 ZDHHC3 MIR6761 NDRG1 SESN1 LINC02623 GBE1  
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OAS2 SEC61G TRIM11 CAPN11 C1RL-AS1 TMEM50B ATXN7L3  
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CCNE2 MBTD1 CWC22 USP33 NRDC FAM184A C15orf39 ERBIN  
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GUF1 LOC107985911 NUDT16L1 MED21 MIR4294 FBXL17 LINC01018  
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NUMB TNIP1 TM9SF2 PSKH1 LINC01743 TOX2 RHOG MED15  
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ZFYVE16 LOC100287944 POLE MAPK11 TBC1D22A MIR6859-2 DET1  
FECH ZNF532 RAP2A TP53TG1 LAMTOR4 FBLN7 C16orf58 NOL7  
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MAN2B2 ARL6IP4 CCDC157 CHP1 ZCCHC2 CLIP3 MAP4K2 ACAP2  
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CSNK1G2-AS1 LRRN4CL KIAA1586 SLC2A4RG MPHOSPH9 CLEC2D  
TENT4A IMPA1 SH3BP1 NPM3 B3GNTL1 ARPC5L ERMN MBP  
TANGO6 C20orf194 TNRC6C-AS1 MIR6770-1 ZMIZ2 MPEP1 C22orf39  
SEC24B-AS1 TCF20 KLHL20 STAG3L2 SRM MIR199A1 MPC1L SSH3

LDLRAD1 SARNP PER1 TIMM50 SELENON MIR4800 KLC2  
SMARCAD1 FNDC3B MICAL1 BLZF1 SUZ12P1 AREL1 PPP1R21  
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BMP2K NFU1 STT3A-AS1 SFXN5 SETD4 DYNLT3 FKBP11 BAIAP2-DT  
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PTPRCAP IL12RB1 HIVEP1 HSPB6 ARV1 IER2 MIR26B COX5A MRPL4  
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SLC39A14 RTL1 GPR137B NFATC4 TOP3B TMEM60 MIR933  
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CHD3 BCAP31 SLC25A44 PP7080 ESYT3 GSN-AS1 WHAMMP2  
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EHMT2 NDUFAF6 LINC02603 COA5 WTIP HACE1 C3orf20 ATG4B  
SNU13 GPR22 WDR5B GRIN2C LOC100128079 DMPK POC5 LPXN  
IDNK RPS13 NPPA-AS1 FADS2 PDZD9 ATP2C1 RCC2 TMEM230  
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NLGN2 ZNF566 PDRG1 SSR3 CC2D1A PPP4R3B STRADA PLAGL1  
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ANKS1B FLJ45513 HIST1H2BN RAPGEF1 AKAP10 DLG4 RPAP3  
EFCAB14 PLEKHA3 TCP11L1 CWF19L1 GPKOW LOC100507547  
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LOC101409256 INPP1 DENND4A PCNX4 NFKBID NDUFB5 TMEM214  
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FBXW9 HK1 SLIRP WDR4 VPS33B NPIPA1 HEXB MRPL35 SNORA77B  
MIR6820 C5orf34 ARHGEF18 TRMT13 ITM2C EREG MIR30C2 SUMF2  
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CINP PPP1R26 PFKM SGMS1 NEXN-AS1 PRPSAP1 GRAMD4  
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BCL2L13 GNB2 TMEM63B CCDC130 MIR626 LEMD3 LINC01988 CPQ  
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UBAP1L SNORA22C CCDC142 RNF165 ZMYM3 CREBL2 SNORD125  
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ARHGEF11 ZNF529-AS1 PIK3R4 LINC01497 NDUFV3 ZDHHC11  
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SDAD1P1 ZNF619 ELP5 TOMM6 HGD C17orf58 SERPINE2 AARSD1  
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NUP160 USP21 C5orf66-AS1 NAXD ORMDL2 SERPINB1 GGT7 TUT7  
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NPEPL1 ZNF451-AS1 TUBB6 LATS1 SPOCK2 FGF2 ZSCAN25  
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SIL1 MIR5588 ASB6 SNORD112 EFNB2 PCM1 TSG101 NOB1 ATRIP  
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ISM2 SNRPN LOC102724804 GCFC2 COQ8A PLEC VWA7 NCAPD2  
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SAP30BP PRMT3 MEAF6 DOP1A SNORD14A TMEM92-AS1 KIF13B  
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ORAI2 WWTR1 DDX60L CIB1 TSSK1B ZNF680 MDN1 CLDN20  
TNFAIP2 ADPRM LINC00668 ZNF575 KCTD7 MCM3AP MYO1F  
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NDUFA3 CANX DESI2 LOC107985946 UGP2 ANKIB1 FRZB CATSPER2  
CUEDC1 STARD9 PPM1F RP9P ZFH3X3 NDUFA9 CTPS2 PGBD2  
AURKC SCRIB ORM2 MIR6071 CUX1 GPX3 UNC119 SNORD134 TBCK  
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CTSH PAF1 TTC9C ZNF592 ZNF579 MIR6511A4 MIR6848 PPFIA4  
DCTD CNIH3 MAP4K4 GPRACR THSD4 FEZ2 DLAT CDC5L TBCD  
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ALDH9A1 ZNF600 MIR6788 ZNF678 PKD2L2 URM1 C2orf66 LRIG2  
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WNT8B ATP5MC1 SNORA119 ARHGAP39 SERPINB9 GLE1 DHRS7  
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ITGB1BP2 METTL2B ALDH18A1 PRICKLE2-AS2 TMEM191C DNAJC5  
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ACTC1 INO80D SNORD114-6 TMEM87B AFAP1L1 MIR6513 ENDOG  
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C12orf4 NTAN1 SNORD114-27 MOB4 SLC35A5 LEMD2 IGFBP7-AS1  
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SPDYE5 ACTG1P20 ZNF7 SERTAD2 ZNF672 YWHAZ ANKRD52  
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CHAMP1 KLHL10 MIR3160-1 GNRH1 SNORA38B MIR6732 ERCC1  
HARS CREBBP BVES PARK7 COQ5 NOP10 IFT43 RABGEF1  
MAP1LC3B MEMO1 DCLK2 NAPB SIGLEC16 ZNF827 LMAN2L DPP7  
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DNMT3A MIR1204 NCKAP5L AP2B1 LINC00324 SMCHD1 BMP2  
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IRAK1BP1 GGT1 SNORD124 LINC02362 MIR6836 WDTC1 HAS3 TET2-  
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BRPF1 ATP9A FNIP2 GJD4 RNF216 TMEM70 SBF1 KAT14 C1orf50  
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COPE IQCE HS1BP3-IT1 FBXW10 YRDC BLVRA MIR1273C KDF1  
BTN2A2 FRG1 NIPSNAP2 ADAMTS15 ARHGAP1 SPRY4-AS1 FCHO1  
PGAP1 FSCN1 ANKRD36C BNIP1 MIR6084 RELCH MIR6891 TYW5  
PLCD1 SRD5A1 NDUFV1 TASOR UFSP2 ZNF56 ATP1A1-AS1 ZNF142  
ANKHD1 LARS2-AS1 BRD7 RNU6ATAC DTYMK TAX1BP3 MARK2



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CEMP1 E2F7 LIN7B VCP THEMIS2 ICAM2 FAS-AS1 RALB SNORD62B  
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LINC00265 LOC105370802 PAPLN ARF3 EFCAB13 MIR4640 TM2D1  
SLC5A2 ELP1 SELENOO SNORA11F TTC21B-AS1 MRPL16 RHBDD3  
LCMT1-AS2 LPCAT3 ABLIM3 C2orf42 LINC01433 CALHM6 LTC4S  
EEF1AKMT2 PSMC3 SMARCA2 CABLES1 TUBGCP6 SPATA33 BRF2  
BLOC1S6 STAC3 TM4SF19-TCTEX1D2 CLUAP1 HRAT5 FANCE GMPS  
SPAG7 NPS TACO1 SYNPO SNRNP40 UBE3C PDSS2 MIR1285-1  
DCTN5 HKDC1 PSME3 PHF10 MIR1307 NME3 CHN1 MIR1205 LARP4B  
EMILIN3 GATAD2B RTF2 UAP1 MIR4722 ATIC ADAM15 ATOH7  
PRSS53 SCAF11 DLEU1 ZMYM6 KBTBD11-OT1 C20orf204 PXX FLNA  
MIR6744 LRPAP1 G6PC3 RAB5IF LRRC14 METTL21C GORASP1  
FCHO2 NDUFS7 FBXW4P1 ABCB8 SCARNA5 LOC102724034 SRF  
C2orf74 SIN3B TRIM8 SEMA3C LOC606724 MIR7108 FBXO10 PDGFC  
CLIP1-AS1 PEPD PHF21A CNST ERCC2 SMIM18 TRMU CCDC9  
LINC00940 HCLS1 MIR1972-1 CSF2 SLC2A11 GRIP2 RAB8A PCIF1  
PIK3IP1 SLC39A6 SNRPD2 LINC01806 AQP7

<p>Unique to 'BM vs BLEO down'</p>	<p>473</p>	<p>MMP2 BRIX1 TMSB10 CCNI SMYD3 EIF1 RASA4B TAF12 MIR7705  FUS BTF3 MIR637 SNORD14D LINC00475 OSER1 PAWR NCF1  ZNF614 GRPEL2 HSCB MIR4750 LINC00641 WSB1 SNORA63B ZNF3  GRID1 ANXA2 C4B SNORD72 HNRNPH1 PPP1R15A LINC01554 AXL  SPDYE18 WASH7P MFGE8 EPC2 SNX18 LOC100506282 ERFE  LGALS3 TAGLN3 SSB SLC3A2 MIR22 FRG1JP RPL35A PTRH2  SNORA33 TPM1-AS CAV2 RPL31 KDEL2 AGL2 EIF3CL HLA-C  SNORD79 SNORA73B FBXO39 THUMPD3-AS1 LBH RPS16 ZBTB46  RBAK LINC01054 SMAD6 MAP4 SNORD83A MEX3B SFPQ INTU IDI2-  AS1 SNORD156 SNORA40 MIR181B1 SLC12A2 KLF6 COL6A2 HLA-A  LDHA ZSCAN29 CAP1 TMED2 RPL6 NUP50 RPL36AL DUSP6 ZNF460  MIR6859-4 SLC25A6 RPL18 CDKN2AIP SNORD68 NR2F1-AS1  LRRC59 DRAP1 SNORD10 OGA SNORA65 LINC01578 LINC01426  INHBA-AS1 TRPS1 RNU1-3 CDKL1 GARS ACTN4 COX7A2L UBB  KPNA2 TRA2B MYL12A HNRNPR LOC646652 PHLDA1 PHF1 FN1  ZFP36 ITGB1 TUBA1A MST1P2 MIR6743 CNOT7 DMTF1 XPOT CWH43  RPS24 RPL24 ARID2 TNRC6B LOC100506142 RPLP0 HNRNPA2B1  SDHAF2 TSC22D2 LINC02283 RPL34 STAR TUBA1C SNORA64  RNPS1 ANKRD13A CCN1 SNORA31 BRD2 TPM2 MIR6779 ADM  MARK2P9 NAT1 ACTG1 SRRM2 LOC101928461 HNRNPA1 MIR29A  PHF23 SMNDC1 LINC01184 JPT1 DNAJB1 SULT1A4 SNORD59B  YWHAE SLC2A3 KIF5B SMLR1 LPGAT1-AS1 FLNC LRRC66 CDC37L1  CCN2 WARS LPCAT2 MIR6515 AP5M1 TTC32 MIDN LINC01767  PGM5P2 ATP5F1A CSNK1D MIR6759 ALDOA PSMC1 CCNO NIP7  SERPINH1 PNRC2 GPR37 TPM4 UGDH ADAMTS1 SNORD173 ZNF302  CALU RHOB MIR4482 SIX4 SNORD36C MIR10393 TTLL3 WTAP  SNORA28 ILKAP HNRNPA3 PDZK1 MIR5047 HSD17B8 YBX3 MIR6797  BCL3 SNORD12 ZNF385A TGFBI ZBTB49 CLDN18 SNORD63  LINC01004 CD44 RPL19 SNORD37 SMG1P6 TUBB SNORA19 SNX19  ZNF655 AHNAK HP09053 AHR RBBP6 MAGOHB SOX9 SNORD35B  SNORD11 SET CLMAT3 AGER MICA KCNV2 SNORD114-10 MIR6895  ERH MYC GASAL1 SRSF3 SNORD96A GRAMD2A SEC61A1 MIR3129  ASH1L-AS1 MIR3605 ZNF544 PDE5A CMAS RPL9 DDX11L2 NABP1  DDX17 SNORD82 CBX3 FRG1FP TMEM50A CFDP1 HMGCS1 DCN  SUCLG2 ACTN1 SNORA71B COL1A2 LOC101929130 HMGB1 SEC24D  NUFIP2 MTA2 RNU6-1 IRF1 ZSCAN5A PDLIM7 MXRA8 CSTF3  A3GALT2 CCT2 RNF145 SNRPF SNORD111 RUNX1 SEPTIN7P2  SNORD69 EIF2S3 RIF1 UQCRB SNORD14B SNORA53 SLC38A2 IL34  MIR4804 NDFIP2-AS1 SLC4A7 MTNR1A PSME1 SLC7A2 OPN1SW  ZNF155 SNX29P2 KLF7 TAF13 MIR6819 LIX1L-AS1 HNRNPD  NECTIN3 PLAG1 MIR6747 SNORA66 SNORD97 PCBP2-OT1 PIP4P2  TM2D2 IL6ST SETDB2 MIR6501 RELA MIR1244-4 GDI2 XBP1  ADAMTSL4-AS1 ACTB MAP3K20-AS1 BSCL2 C19orf24 HIPK2 ABCA7  ZC3H10 COL6A3 SLFN5 SPDYE2 GP5 STC2 LPAR1 SNORA22B</p>
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	SERBP1 JUN PNN POLR3D MLLT10P1 SNORD33 UBC ATP5MC3 BTN2A1 ZSCAN9 ARF6 RPL35 SNORA21B RPLP1 MIR4647 TMEM99 TRAM1 SNORD66 GPD1 NPM1 CCT8 TAF10 H3F3B ARPC3 AHCYL1 CDH24 GPATCH11 NET1 SURF4 RPL17 PRKACB MIR4426 ELL3 NUFIP1 SAMD5 MIR6875 RPH3A NAP1L1 DUSP12 EXT1 TMCO1-AS1 MYL12B PRAG1 ROMO1 ZNF691 MAML1 NAAA CFL1 NOP53 GBP1 SULT1A3 TRA2A DDX10 RDH14 SEC62 SBDS SNORD117 GTF2I TUBB4B MRPL42 ECT2L ZNF207 MIR4668 LINC01001 SNORD42A RPS9 MIR198 HGF RNF25 PLAU ANXA1 SQSTM1 SEPTIN11 HLA-E SWAP70 ATP13A3 SNORD1A RPS4X SLC1A5 SNORD30 VTRNA2-1 TUBA1B MIR2355 LIMA1 LOC100505502 BMS1P4-AGAP5 BZW1 MIR3606 MIR6728 SNORA27 SNORD73A MIR12128 HNRNPUL1 LOC100287467 PPIA S100A6 ABHD17C S100A11 LAMC1 RAN PHLDB1 PHF5A SERTAD3 ARHGAP9 LAMB1 JMJD6 SNORD119 SMARCD2 ZNF23 ARRDC3 SNORD38D TRABD2A SRSF1 MICAL2 WASIR1 ZNF584 GTDC1 SNORD18C ST6GALNAC6 STAT2 EWSR1 RPS7 CNP WASH3P ZNF330 KLF10 DCP1B RPS14 SNAI2 ZNF562 MAT2A USP3 RPS27 CTSC
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Supplementary Information

Supplementary Table 6. Genome-wide profiling of differential peaks between proliferating and senescent cells (ChIP-seq for H3K9me3).

geneID	baseMea	log2Fold	lfcSE	stat	pvalue	padj	Chr	Start	End	Strai	Peak	Focus	Annotati	Detailed	Distance	Nearest F	Entrez ID	Nearest L	Nearest F	Nearest E	Gene	Nar	Gene Ali	Gene Des	Gene Type
chr13-182	227.8114	-2.42336	0.203217	-11.925	8.77E-33	3.00E-29	chr13	18211746	18212407	+	0	NA	intron (HSATI)	Sat	16779	NR_027278	26080	Hs.448582	NR_027278	ENSG000004	FAM230C	LINC00281	family	wincRNA	
chr21-792	1231.017	-1.52941	0.143729	-10.6409	1.92E-26	3.29E-23	chr21	7926271	7926544	+	0	NA	Intergeni	(ATGCATTC)	-96775	NM_001365	1.03E+08	NM_001333	ENSG000004	KCNE1B	-	-	potassium	protein-coding	
chr16-345	603.1495	-1.61484	0.15471	-10.4378	1.67E-25	1.90E-22	chr16	34592589	34596135	+	0	NA	Intergeni	(ATGCATTC)	-212882	NR_158155	1.03E+08	Hs.69271CNR_158158	CCNYL3	-	-	-	-	cyclin Y	pseudo
chr3-9347	22612.98	-1.24721	0.125957	-9.90185	4.09E-23	3.50E-20	chr3	93470428	93470734	+	0	NA	Intergeni	SAR Satel	503500	NM_001314	5627	Hs.64016	NM_000313	ENSG000004	PROS1	PROS PS21	protein	Sprotein-coding	
chr16-463	2232.028	-1.22852	0.128709	-9.54497	1.36E-21	9.33E-19	chr16	46394225	46395185	+	0	NA	Intergeni	Intergeni	174392	NR_026556	124149	Hs.97414	NM_001004299	ANKRD26P1	-	-	ankyrin	rpseudo	
chr4-739C	101.9806	-1.23316	0.275132	-9.18423	1.64E-21	3.73E-18	chr4	73906089	73906784	+	0	NA	Intergeni	LIP3A LIP	37043	NM_001511	2919	Hs.789	NM_001511	ENSG000004	CXCL1	FSP GRO1	C-X-C	motprotein-coding	
chr16-345	1126.969	-1.26028	0.134457	-9.37314	7.04E-21	4.02E-18	chr16	34581388	34583833	+	0	NA	Intergeni	Intergeni	-201130	NR_158155	1.03E+08	Hs.69271CNR_158158	CCNYL3	-	-	-	-	cyclin Y	pseudo
chr16-463	1488.808	-1.21876	0.13058	-9.33342	1.03E-20	5.02E-18	chr16	46385254	46391433	+	0	NA	Intergeni	Intergeni	180754	NR_026556	124149	Hs.97414	NM_001004299	ANKRD26P1	-	-	ankyrin	rpseudo	
chr1-1431	597.6095	-1.34679	0.148916	-9.04399	1.51E-19	6.47E-17	chr1	1431519	1431519	+	0	NA	Intergeni	Intergeni	228599	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr16-345	1040.462	-1.20918	0.134867	-8.96572	3.08E-19	1.17E-16	chr16	34576184	34576656	+	0	NA	Intergeni	(AATGGAC)	-194940	NR_158155	1.03E+08	Hs.69271CNR_158158	CCNYL3	-	-	-	-	cyclin Y	pseudo
chr4-74597144	7455	-1.27643	0.269065	-6.99583	3.27E-17	4.49E-15	chr4	74597145	74598143	+	0	NA	Intergeni	THE1B-int	152508	NM_001657	374	Hs.270832	NM_001657	ENSG000004	AREG	AR AREGB	amphireg	protein-coding	
chr16-463	1910.513	-1.32509	0.157651	-8.40519	4.27E-17	1.46E-14	chr16	46398315	46401608	+	0	NA	Intergeni	Intergeni	169136	NR_026556	124149	Hs.97414	NM_001004299	ANKRD26P1	-	-	ankyrin	rpseudo	
chr1-1432	673.684	-1.21507	0.144887	-8.38637	5.01E-17	1.56E-14	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	220709	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr22-187	102.7861	-2.35172	0.285252	-8.24436	1.66E-16	4.74E-14	chr22	18730441	18730694	+	0	NA	Intergeni	AluSc8 SI	-3347	NR_136561	642643	NR_136561	ENSG000004	FAM230E	LINC01662	family	wincRNA		
chr4-497	1159.323	-1.15338	0.142329	-8.10364	5.33E-16	1.41E-13	chr4	49709331	49711815	+	0	NA	Intergeni	SAR Satel	723931	NM_00128E	80157	Hs.479703	NM_025087	ENSG000004	CWH43	CWH43-C Fcell	wall	protein-coding	
chr10-133	502.6286	-1.22932	0.152712	-8.0499	8.29E-16	2.03E-13	chr10	1330000	1330000	+	0	NA	Intergeni	BSR Beta	-61888	NM_00108C	441581	Hs.690471	NM_00108C	ENSG000004	FRG2B	-	-	FSHD	regiprotein-coding
chr22-188	76.47112	-2.50137	0.314582	-7.95142	1.84E-15	4.21E-13	chr22	18896187	18896559	+	0	NA	Intergeni	AluSc8 SI	-1942	NR_136571	1.01E+08	Hs.631668	NR_136571	FAM230F	LINC01662	family	wincRNA		
chr4-7461	97.86165	-1.65222	0.282437	-6.18557	7.86E-15	7.29E-13	chr4	74616713	74616924	+	0	NA	Intergeni	AluY6 SI	171682	NM_001657	374	Hs.270832	NM_001657	ENSG000004	AREG	AR AREGB	amphireg	protein-coding	
chr1-1432	1022.495	-1.04798	0.138802	-7.55019	4.35E-14	9.31E-12	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	205027	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr1-1251	3170.92	-0.97622	0.130246	-7.4952	6.62E-14	1.33E-11	chr1	1251000	1251000	+	0	NA	Intergeni	Intergeni	3662018	NR_00395E	647121	Hs.697682	NR_00395E	ENSG000004	EMBP1	-	-	embigin	rpseudo
chr5-495	313.0752	-1.30045	0.174025	-7.47277	7.85E-14	1.49E-11	chr5	49599496	49603043	+	0	NA	Intergeni	(TGGAA)n	840019	NM_19844E	133418	Hs.561411	NM_19844E	ENSG000004	EMB	GP70	embigin	protein-coding	
chr1-1432	807.1749	-1.10926	0.14857	-7.46625	8.25E-14	1.49E-11	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	190845	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr16-345	421.4881	-1.1773	0.158978	-7.40547	1.31E-13	2.24E-11	chr16	34571575	34574186	+	0	NA	Intergeni	(GAATG)n	-191400	NR_158155	1.03E+08	Hs.69271CNR_158158	CCNYL3	-	-	-	-	cyclin Y	pseudo
chr1-1432	710.6941	-1.05878	0.143971	-7.35417	1.92E-13	3.13E-11	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	172643	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr18-103	672.0041	-1.05243	0.147814	-7.11999	1.08E-12	1.38E-10	chr18	1030000	111007	+	0	NA	Intergeni	promoter-promoter	-181	NR_03377C	727758	Hs.585842	NR_03377C	ENSG000004	ROCK1P1	ROCK1P	Rho	assoc	protein-coding
chr22-126	256.5703	-1.29617	0.182934	-7.08544	1.39E-12	2.06E-10	chr22	12691987	12692697	+	0	NA	Intergeni	BSR Beta	794936	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC102722	-	-	uncharact	ncRNA	
chr1-1432	677.3255	-1.01271	0.143639	-7.05036	1.78E-12	2.55E-10	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	168326	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr4-744	35.38616	-2.42017	0.414143	-6.97563	1.90E-12	4.55E-10	chr4	74498802	74499010	+	0	NA	Intergeni	LIM2 LINE	53770	NM_001657	374	Hs.270832	NM_001657	ENSG000004	AREG	AR AREGB	amphireg	protein-coding	
chr21-842	103.687	-1.79766	0.258068	-6.96584	3.26E-12	4.47E-10	chr21	8420098	8421999	+	0	NA	Intergeni	Intergeni	-11482	NR_12871E	1.04E+08	NR_12871E	ENSG000004	MIR6724-2	hsa-mir-6	microRNA	ncRNA		
chr1-1432	620.0777	-1.01644	0.147537	-6.88943	5.60E-12	7.38E-10	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	175343	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr4-1901	504.1323	-1.04921	0.152753	-6.87679	6.12E-12	7.52E-10	chr4	1901000	1901000	+	0	NA	Intergeni	(BSR Beta)	4904	NR_137167	1E+08	Hs.728745	NM_00120E	ENSG000004	DUX4	DUX4L	double	hcprotein-coding	
chr19-745	93.07395	-1.84056	0.267669	-6.87626	6.14E-12	7.52E-10	chr19	7450655	7451110	+	0	NA	Intergeni	(intron)	11194	NM_00113C	23370	Hs.465761	NM_01531E	ENSG000004	ARHGFE18	P114-Rho	Rho/Rac	gprotein-coding	
chr14-495	71.36606	-0.94801	0.1464575	-6.71922	1.83E-11	2.16E-09	chr14	49586559	49586837	+	0	NA	Intergeni	promoter-promoter	118	NR_00271E	6029	NR_00271E	ENSG000004	CN75L1	7L1a 7SL	RNA	comp	ncRNA	
chr16-345	474.8951	-1.0646	0.160309	-6.64092	3.12E-11	3.56E-09	chr16	34584692	34588632	+	0	NA	Intergeni	Intergeni	-205182	NR_158155	1.03E+08	Hs.69271CNR_158158	CCNYL3	-	-	-	-	cyclin Y	pseudo
chrY-113C	178.6599	-1.34674	0.204912	-6.57227	4.96E-11	5.48E-09	chrY	11308792	11309745	+	0	NA	Intergeni	BSR Beta	1112322	NR_033667	352887	Hs.546221	NR_033667	ENSG000004	GYG2P1	GYG2P	glycogen	pseudo	
chr21-841	86.847	-1.77608	0.274038	-6.48114	9.10E-11	9.75E-09	chr21	8417703	8418926	+	0	NA	Intergeni	Intergeni	-14216	NR_12871E	1.04E+08	NR_12871E	ENSG000004	MIR6724-2	hsa-mir-6	microRNA	ncRNA		
chr7-1581	29.59405	-3.86084	0.597263	-6.46423	1.02E-10	1.06E-08	chr7	1581000	1581000	+	0	NA	Intergeni	(intron)	293551	NR_03896E	1.01E+08	Hs.66126E	NR_03896E	LOC10050E	-	-	uncharact	ncRNA	
chr10-388	123.6202	-1.4721	0.234121	-6.28778	3.22E-10	3.25E-08	chr10	38814069	38814273	+	0	NA	Intergeni	(TTCCA)n	117575	NR_04500C	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo	
chr4-1901	294.6036	-1.11777	0.179157	-6.22232	4.90E-10	4.80E-08	chr4	1901000	1901000	+	0	NA	Intergeni	(BSR Beta)	7358	NR_137167	1E+08	Hs.728745	NM_00120E	ENSG000004	DUX4	DUX4L	double	hcprotein-coding	
chr1-1432	412.6005	-1.12477	0.179445	-6.20119	5.60E-10	5.33E-08	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	183664	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr21-838	95.94166	-1.61222	0.262226	-6.14822	7.84E-10	7.26E-08	chr21	8388083	8391544	+	0	NA	Intergeni	non-codir	778	NR_146151	1.1E+08	NR_146151	RNA45SN3	-	-	RNA,	45S	rRNA	
chr1-1432	219.2181	-1.21601	0.199889	-6.08342	1.18E-09	1.06E-07	chr1	1432008	1432008	+	0	NA	Intergeni	Intergeni	236316	NR_027354	645166	Hs.744182	NR_027354	LSP1P5	-	-	LSP1	psetpseudo	
chr21-841	98.1																								



chr4-4925 64.01477	-1.19455	0.300648	-3.97325	7.09E-05	0.00227	chr4	49295581	49297505 +	0 NA	Intergeni (GAAG)n S	309901 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr10-418 45.55059	-1.37738	0.350991	-3.92426	8.70E-05	0.00276	chr10	41858236	41860105 +	0 NA	Intergeni (ATGGA)n	508875 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chr22-126 45.98197	-1.41137	0.360929	-3.91038	9.22E-05	0.002896	chr22	12693713	12693966 +	0 NA	IntergeniCpG	796433 NR_110761	1.03E+08 Hs. 65292ENR_110761	LOC102722-		uncharactncRNA
chr10-133 33.24204	-1.61292	0.414828	-3.88816	0.000101	0.003146	chr10	1.34E+08	1.34E+08 +	0 NA	IntergeniCpG	-126725 NM_00108C	441581 Hs. 690471NM_00108C	ENSG00000FRG2B	-	FSHD regiprotein-coding
chr21-106 47.03399	-1.34274	0.345538	-3.88595	0.000102	0.003146	chr21	10692087	10693085 +	0 NA	Intergeni (TTCCA)n	171072 NM_19926C	7179 Hs. 12298ENM_19925E	ENSG00000TPT	CT44 PTEN	transmemprotein-coding
chr21-932 25.83842	-1.83108	0.473456	-3.86747	0.00011	0.003364	chr21	9324988	9325365 +	0 NA	IntergeniCpG	-195415 NR_038327	1E+08 Hs. 487562NM_17494E	ENSG00000TEKT4P2	MAFIPL TE	tektin 4 pseudo
chr10-406 320.9418	-0.65192	0.170309	-3.82783	0.000129	0.003919	chr10	40593342	40593686 +	0 NA	IntergeniALR/Alphe	1774531 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chr1-2366 89.63159	-0.99674	0.260536	-3.82572	0.00013	0.003919	chr1	2.36E+08	2.36E+08 +	0 NA	IntergeniLITR10A L	-32161 NR_002508	4811 Hs. 356624NM_002508	ENSG00000CNID1	NID	nidogen lprotein-coding
chr21-825 56.66185	-1.20476	0.316883	-3.80191	0.000144	0.004278	chr21	8253472	8260776 +	0 NA	TTS (NR_ITTS (NR_	343 NR_14612C	1.1E+08 Hs. NR_146120	RNA5-8SN4RN5-8S1 FRNA, 5.8S	rRNA	
chr21-122 42.62947	-1.37965	0.364327	-3.78684	0.000153	0.004506	chr1	12036276	12036506 +	0 NA	IntergeniALR/Alphe	-1001775 NR_02691E	149992 Hs. 55864ENM_153773	ANKRD30BF	C21orf99	ankyrin rpseudo
chr1-1235 449.9485	-0.58834	0.15613	-3.76826	0.000164	0.004766	chr1	1.24E+08	1.24E+08 +	0 NA	IntergeniALR/Alphe	2407212 NR_00395E	647121 Hs. 69768ENR_00395E	ENSG00000EMB1P1	-	embigin rpseudo
chr9-429 22.20424	-1.91983	0.509499	-3.76808	0.000165	0.004766	chr9	42900239	42900554 +	0 NA	IntergeniIntergeni	111996 NR_131213	1.06E+08 Hs. NR_131213	XLOC_007E-		uncharactncRNA
chr13-176 69.80037	-1.112	0.295234	-3.76651	0.000166	0.004766	chr13	17950249	17950597 +	0 NA	IntergeniALR/Alphe	-244874 NR_02727E	26080 Hs. 44858ENR_02727E	ENSG00000FAM230C	LINC00281	family wincRNA
chr17-233 1001.062	-0.52158	0.138561	-3.76428	0.000167	0.004769	chr17	23302163	23301667 +	0 NA	IntergeniALR/Alphe	493334 NM_00119C	1E+08 Hs. 74018ENM_00119C	ENSG00000CMTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr7-5637 35.94944	-1.48587	0.396156	-3.75071	0.000176	0.004993	chr7	56370528	56374724 +	0 NA	IntergeniIntergeni	75749 NR_02942C	650226 Hs. 448401NR_029420	LOC65022E-		ankyrin rpseudo
chr1-228E 22.723	-1.8865	0.503303	-3.74824	0.000178	0.005001	chr1	2.29E+08	2.29E+08 +	0 NA	promoter-promoter-	-277 NR_02337E	1E+08 Hs. NR_02337E	ENSG00000RNA5S16	RN5S16	RNA, 5S rRNA
chr4-4963 33.43406	-1.52301	0.40852	-3.72812	0.000193	0.005373	chr4	49651362	49653432 +	0 NA	Intergeni (GAATG)n	665755 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr20-310 53.724	-1.2075	0.324095	-3.72577	0.000195	0.00538	chr20	31051831	31069369 +	0 NA	Intergeni (GAAT)n	-197064 NM_001037	245929 Hs. 580793NM_001037	ENSG00000DEFB115	DEFB-15	defensin protein-coding
chr4-493 33.94226	-1.49804	0.404442	-3.70396	0.000212	0.005818	chr4	49303452	49304069 +	0 NA	IntergeniIntergeni	317118 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr14-177 183.8708	-0.75382	0.203884	-3.69729	0.000218	0.005925	chr14	17292720	17293026 +	0 NA	IntergeniALR/Alphe	-1308244 NM_00101E	440153 Hs. 53488ENM_00101E	ENSG00000COR11H12	-	olfactoryprotein-coding
chr22-102 21.73442	-1.87763	0.513214	-3.65857	0.000254	0.006842	chr22	10729225	10729256 +	0 NA	Intergeni (TCCATTC	232149 NR_13232C	1.03E+08 Hs. NR_132320	FRG1FP	-	FSHD regiprotein-coding
chr22-116 60.30936	-1.18666	0.306264	-3.65261	0.00026	0.006948	chr22	11697905	11700168 +	0 NA	IntergeniMER5A DN	-198370 NR_110761	1.03E+08 Hs. 65292ENR_110761	LOC102722-		uncharactncRNA
chr10-418 34.70703	-1.452	0.398251	-3.64593	0.000266	0.007076	chr10	41877707	41877984 +	0 NA	Intergeni (ATGGA)n	490200 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chrY-1131 57.67989	-1.12304	0.312531	-3.59337	0.000326	0.008603	chrY	11316867	11321091 +	0 NA	IntergeniBSR/Beta	1102611 NR_033667	352887 Hs. 546221NR_033667	ENSG00000GYG2P	GYG2P	glycogenin pseudo
chr10-405 398.1717	-0.5897	0.164556	-3.58355	0.000339	0.008864	chr10	40980947	40981362 +	0 NA	IntergeniALR/Alphe	1386891 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chr10-418 49.37627	-1.19438	0.335123	-3.564	0.000365	0.00948	chr10	41861599	41861892 +	0 NA	Intergeni (ATG)n	506300 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chr2-105 26.19522	-1.64527	0.463154	-3.55231	0.000382	0.009833	chr2	10936135	10936593 +	0 NA	IntergeniAluJo S	25165 NR_13232C	1.03E+08 Hs. NR_132320	FRG1FP	-	FSHD regiprotein-coding
chr10-418 33.30435	-1.41821	0.405203	-3.49999	0.000465	0.011896	chr10	41898663	41900578 +	0 NA	Intergeni (AATGG)n	468425 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chr10-132 26.93271	-1.58471	0.453364	-3.49546	0.000473	0.011954	chr10	1.34E+08	1.34E+08 +	0 NA	IntergeniCpG	-40706 NM_00108C	441581 Hs. 690471NM_00108C	ENSG00000FRG2B	-	FSHD regiprotein-coding
chr10-418 51.1034	-1.15144	0.329478	-3.49474	0.000475	0.011954	chr10	41845577	41846553 +	0 NA	IntergeniIntergeni	521980 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000CLOC44166E-		zinc fingpseudo
chr4-493 32.06976	-1.43394	0.412401	-3.47705	0.000507	0.012678	chr4	49306056	49309600 +	0 NA	IntergeniIntergeni	321186 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr21-12 38.42528	-1.31348	0.379401	-3.46198	0.000536	0.013312	chr21	12066830	12067106 +	0 NA	IntergeniALR/Alphe	-971198 NR_02691E	149992 Hs. 55864ENM_153773	ANKRD30BF	C21orf99	ankyrin rpseudo
chr4-4914 40.37566	-1.27379	0.368259	-3.45896	0.000542	0.013366	chr4	49143929	49144773 +	0 NA	Intergeni (TCCAT)n	157709 NR_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr17-231 748.6793	-0.50117	0.145189	-3.45185	0.000557	0.013624	chr17	23190216	23190599 +	0 NA	IntergeniALR/Alphe	667296 NM_00119C	1E+08 Hs. 74018ENM_00119C	ENSG00000CMTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr22-165 50.39314	-1.14632	0.332543	-3.44715	0.000567	0.013766	chr22	16352695	16352954 +	0 NA	Intergeni (GGAAT)n	239986 NR_01440E	150160 Hs. 128342NM_01440E	ENSG00000CCT8L2	CESK1	chaperonin protein-coding
chr13-164 75.2502	-0.96694	0.282327	-3.4249	0.000615	0.014839	chr13	16499326	16499635 +	0 NA	IntergeniALR/Alphe	-1695817 NR_02727E	26080 Hs. 44858ENR_02727E	ENSG00000FAM230C	LINC00281	family wincRNA
chr21-881 16.97588	-1.99783	0.584345	-3.41893	0.000629	0.01497	chr21	8814228	8814581 +	0 NA	IntergeniGSATII Se	-172595 NR_037421	1.01E+08 Hs. NR_037421	ENSG00000MIR3648-1	MIR3648	microRNA ncRNA
chr4-4932 52.76493	-1.11004	0.324695	-3.41871	0.000629	0.01497	chr4	49326006	49327442 +	0 NA	IntergeniLIPAI10 L	340082 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr20-310 49.90556	-1.13824	0.334005	-3.40785	0.000655	0.01547	chr20	31070765	31075914 +	0 NA	Intergeni (GGAAT)n	-184325 NM_001037	245929 Hs. 580793NM_001037	ENSG00000DEFB115	DEFB-15	defensin protein-coding
chr21-896 47.50432	-1.16757	0.343895	-3.39514	0.000686	0.016096	chr21	8986973	8988653 +	0 NA	TTS (NR_CTTS (NR_C	196 NR_16210E	1.13E+08 Hs. NR_162105	MIR10396F-		microRNA ncRNA
chr1-228E 20.46645	-1.77461	0.523131	-3.39228	0.000693	0.016155	chr1	2.29E+08	2.29E+08 +	0 NA	TTS (NR_CTTS (NR_C	575 NR_02336E	1E+08 Hs. NR_02336E	ENSG00000RNA5S4	RN5S4	RNA, 5S rRNA
chr17-267 30.98879	-1.41663	0.41887	-3.38202	0.00072	0.016559	chr17	26797006	26799208 +	0 NA	IntergeniIntergeni	291777 NR_13567E	1.05E+08 Hs. 64991ENR_135673	LOC105371-		uncharactncRNA
chr1-228E 22.24987	-1.68836	0.499252	-3.38178	0.00072	0.016559	chr1	2.29E+08	2.29E+08 +	0 NA	TTS (NR_CTTS (NR_C	796 NR_02336E	1E+08 Hs. NR_02336E	ENSG00000RNA5S6	RN5S6	RNA, 5S rRNA
chr1-228E 20.96909	-1.73411	0.51499	-3.36726	0.000759	0.01734	chr1	2.29E+08	2.29E+08 +	0 NA	IntergeniCpG	-3604 NR_03796E	58480 Hs. 647774NM_02120E	ENSG00000CRHOU	ARHU CDC4	ras homolprotein-coding
chr6-5964 168.2998	-0.69591	0.207273	-3.35747	0.000789	0.017774	chr6	59640040	59640423 +	0 NA	IntergeniALR/Alphe	-1678785 NR_13299E	1.07E+08 Hs. 56153ENR_125727	ENSG00000LINC0068C-		long intencRNA
chr13-171 44.19967	-1.20452	0.358832	-3.35677	0.000789	0.017774	chr13	17119617	17119840 +	0 NA	IntergeniALR/Alphe	-1075569 NR_02727E	26080 Hs. 44858ENR_02727E	ENSG00000FAM230C	LINC00281	family wincRNA
chr4-491 37.51407	-1.2755	0.380748	-3.34998	0.000808	0.018097	chr4	49152261	49156344 +	0 NA	Intergeni (TCCAT)n	167660 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr10-385 38.55994	-1.25343	0.375962	-3.33394	0.000856	0.019049	chr10	38526837	38529774 +	0 NA	IntergeniIntergeni	100159 NR_024497	399744 Hs. 497951NM_001013665	LINC0099E-		long intencRNA
chr4-4911 33.45018	-1.33558	0.402294	-3.31992	0.0009	0.019903	chr4	49112262	49113662 +	0 NA	Intergeni (TCCAT)n	162320 NM_00128E	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C	Fcell wallprotein-coding
chr5-487 466.7656	-0.51509	0.155488	-3.31271	0.000924	0.020291	chr5	48732007	48732479 +	0 NA	IntergeniALR/Alphe	1709445 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr19-265 491.9488	-0.50739	0.153392	-3.30783	0.00094	0.02046	chr19	26331538	26331990 +	0 NA	IntergeniALR/Alphe	-1461667 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG00000CLOC101927-		uncharactncRNA
chr21-111 35.35721	-1.32152	0.399633	-3.30684	0.000944	0.02046										



chr19-362 16.67251	-1.66343	0.570657	-2.91493	0.003558	0.052993	chr19	36268738	36278848	+	0 NA	IntergeniSST1 Sate	-27865	NM_00136E	147929	Hs.59633E	NM_152477	ENSG00000	ZNF565	-	zinc_fingprotein-coding	
chr9-435 25.79997	-1.32583	0.455441	-2.9111	0.003602	0.053416	chr9	43509542	43509888	+	0 NA	IntergeniALR Alphe	383549	NR_160666	1.03E+08	NR_160669	LOC102724-				methylenepseudo	
chr2-161 29.68072	-1.22766	0.422029	-2.90896	0.003626	0.053551	chr2	1.61E+08	1.61E+08	+	0 NA	IntergeniIntergeni	-25972	NR_110592	1.02E+08	Hs.66648E	NR_110593	LOC101925-			uncharactncRNA	
chr10-41 26.41948	-1.30099	0.447745	-2.90566	0.003665	0.053887	chr10	41784567	41876859	+	0 NA	Intergeni(ATGGA)n	492332	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E-			zinc_fingpseudo
chr9-4351 32.96925	-1.1656	0.401595	-2.90244	0.003703	0.054212	chr9	43511915	43512232	+	0 NA	IntergeniALR Alphe	385907	NR_160666	1.03E+08	NR_160669	LOC102724-				methylenepseudo	
chr14-16 26.82694	-1.28748	0.444474	-2.89663	0.003772	0.05499	chr14	16888632	16888984	+	0 NA	IntergeniALR Alphe	-1712309	NM_001013	440153	Hs.53488C	NM_001013	ENSG00000	COR11H12	-		olfactoryprotein-coding
chr13-18 67.62166	-0.8588	0.297032	-2.89128	0.003837	0.055699	chr13	18002268	18002536	+	0 NA	IntergeniALR Alphe	-192895	NR_02727E	26080	Hs.44858E	NR_02727E	ENSG00000	FAM230C	LINC00281	family_wincRNA	
chr19-362 17.17514	-1.61907	0.560514	-2.88855	0.00387	0.055946	chr19	36279928	36286502	+	0 NA	IntergeniSST1 Sate	-28128	NR_02938E	1E+08	Hs.46655C	NR_02938E	LOC100134-				uncharactncRNA
chr5-479 159.2965	-0.608	0.210807	-2.88417	0.003925	0.056493	chr5	47907355	47907619	+	0 NA	IntergeniALR Alphe	-2211107	NM_021072	348980	Hs.35317E	NM_021072	ENSG00000	HCN1	BCNG-1 BChyperpolaprotein-coding		
chr5-496 180.1123	-0.59529	0.206568	-2.88181	0.003954	0.056511	chr5	49625442	49627096	+	0 NA	IntergeniALR Alphe	815019	NM_19844E	133418	Hs.561411	NM_19844E	ENSG00000	EMB	GP70	embigin_protein-coding	
chr13-16 57.9298	-0.89914	0.312045	-2.88143	0.003959	0.056511	chr13	16607704	16608088	+	0 NA	IntergeniALR Alphe	-1587401	NR_02727E	26080	Hs.44858E	NR_02727E	ENSG00000	FAM230C	LINC00281	family_wincRNA	
chr19-264 54.22713	-0.92653	0.322225	-2.87542	0.004035	0.057359	chr19	26412824	26413045	+	0 NA	IntergeniALR Alphe	-1380497	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-			uncharactncRNA
chr10-42 41.7833	-1.03021	0.358773	-2.87147	0.004086	0.057841	chr10	42104468	42105022	+	0 NA	IntergeniIntergeni	263300	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E-			zinc_fingpseudo
chr22-13 59.52734	-0.90347	0.315372	-2.86478	0.004173	0.058765	chr22	13863488	13863747	+	0 NA	IntergeniALR Alphe	-1664542	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG00000	COR11H1	OR11H12 Colfactoryprotein-coding		
chr19-26 95.97198	-0.71891	0.251078	-2.86329	0.004193	0.058765	chr19	26097581	26097873	+	0 NA	IntergeniALR Alphe	-1695704	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-			uncharactncRNA
chr10-41 28.87529	-1.22586	0.42824	-2.86255	0.004202	0.058765	chr10	41854079	41857383	+	0 NA	IntergeniIntergeni	512314	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E-			zinc_fingpseudo
chrY-568 23.28845	-1.40476	0.492079	-2.85475	0.004307	0.059984	chrY	56842214	56842455	+	0 NA	IntergeniBSR Beta	-11921	NM_00584C	10251	Hs.381912	NM_00584C	ENSG00000	SPRY3	spry-3	sprouty_Fprotein-coding	
chr10-40 227.0854	-0.53057	0.186169	-2.84993	0.004373	0.060654	chr10	40892033	40892746	+	0 NA	IntergeniALR Alphe	1475656	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E-			zinc_fingpseudo
chr1-121 213.1768	-0.55061	0.193445	-2.84631	0.004423	0.0611	chr1	1.22E+08	1.22E+08	+	0 NA	IntergeniALR Alphe	248539	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000	EMB1P	-	embigin_pseudo	
chr21-75 16.39419	-1.63102	0.573489	-2.84403	0.004455	0.061291	chr21	7931792	7932803	+	0 NA	Intergeni(ATTCAT	-102665	NM_00136E	1.03E+08	NM_00133C	ENSG00000	KCNE1B	-		potassiumprotein-coding	
chr19-29 61.58127	-0.88605	0.312075	-2.83923	0.004522	0.061864	chr19	25339247	25339455	+	0 NA	IntergeniALR Alphe	-1175904	NR_00360E	1E+08	Hs.149312	NR_00360E	ENSG00000	HAVCR1P1	-	hepatitispseudo	
chr22-14 62.29264	-0.88894	0.31317	-2.83852	0.004532	0.061864	chr22	14355616	14355877	+	0 NA	IntergeniALR Alphe	-1172413	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG00000	COR11H1	OR11H12 Colfactoryprotein-coding		
chr10-40 32.64753	-1.14585	0.403863	-2.83723	0.004551	0.061867	chr10	40024602	40024927	+	0 NA	IntergeniALR Alphe	1328168	NR_04500C	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr21-11 22.90441	-1.37035	0.485155	-2.82456	0.004735	0.064089	chr21	11537490	11537775	+	0 NA	IntergeniALR Alphe	1016118	NR_19926C	7179	Hs.12298E	NM_19925E	ENSG00000	TPTE	CT44 PTEN	transmemprotein-coding	
chr17-26 16.98363	-1.59366	0.564673	-2.82228	0.004768	0.064089	chr17	26947666	26947976	+	0 NA	IntergeniMER5A L	141420	NR_13567E	1.05E+08	Hs.64991E	NR_135673	LOC105371-			uncharactncRNA	
chr21-11 47.21149	-0.95561	0.338609	-2.82216	0.00477	0.064089	chr21	11499681	11499932	+	0 NA	IntergeniALR Alphe	978292	NR_19926C	7179	Hs.12298E	NM_19925E	ENSG00000	TPTE	CT44 PTEN	transmemprotein-coding	
chr21-12 20.93901	-1.42202	0.5042	-2.82034	0.004797	0.064166	chr21	12801182	12801512	+	0 NA	IntergeniALR Alphe	-22801182	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30B	C21orf99	ankyrin_pseudo		
chr4-13 17.1379	-1.68422	0.597396	-2.81927	0.004813	0.064166	chr4	1.32E+08	1.32E+08	+	0 NA	IntergeniCpG	-13960	NR_12588E	1.02E+08	Hs.507924	NR_125883	SNHG27	-		small_nucncRNA	
chr13-17 35.27973	-1.10143	0.391421	-2.81394	0.004894	0.064986	chr13	17079667	17080696	+	0 NA	IntergeniALR Alphe	-1115116	NR_02727E	26080	Hs.44858E	NR_02727E	ENSG00000	FAM230C	LINC00281	family_wincRNA	
chr14-18 70.49211	-0.79774	0.284066	-2.80828	0.004981	0.065883	chr14	18072507	18072967	+	0 NA	IntergeniALR Alphe	-528410	NM_001013	440153	Hs.53488C	NM_001013	ENSG00000	COR11H12	-	olfactoryprotein-coding	
chr21-91 19.74782	-1.45075	0.51767	-2.80245	0.005072	0.066579	chr21	9109383	9110148	+	0 NA	intron (AluSx1) S	19996	NR_03832E	1E+08	Hs.48756E	NM_17494E	ENSG00000	TEKT4P2	MAFIPL Tektin 4_pseudo		
chr4-496 36.22268	-1.07491	0.383564	-2.80242	0.005072	0.066579	chr4	49637971	49638186	+	0 NA	Intergeni(GAATG)n	615436	NM_00128E	80157	Hs.47970E	NM_02508E	ENSG00000	CWH43	CWH43-C Fcell	wallprotein-coding	
chr21-11 33.38502	-1.11451	0.398887	-2.79404	0.005205	0.067716	chr21	1100437	11004626	+	0 NA	IntergeniALR Alphe	1100437	NM_19926C	7179	Hs.12298E	NM_19925E	ENSG00000	TPTE	CT44 PTEN	transmemprotein-coding	
chr10-13 15.63495	-1.64593	0.589244	-2.79328	0.005218	0.067716	chr10	1.34E+08	1.34E+08	+	0 NA	IntergeniCpG	-50567	NM_00108C	441581	Hs.690471	NM_00108C	ENSG00000	FRG2B	-	FSHD	regiprotein-coding
chr21-88 18.61235	-1.5084	0.540014	-2.79326	0.005218	0.067716	chr21	8815569	8815818	+	0 NA	IntergeniTAR1 Sate	-171306	NR_037421	1.01E+08	NR_037421	ENSG00000	MIR3648	-MIR3648	hmicroRNA	ncRNA	
chr14-16 52.63131	-0.90228	0.323386	-2.79009	0.005269	0.068123	chr14	16898852	16899735	+	0 NA	IntergeniALR Alphe	-170824	NM_001013	440153	Hs.53488C	NM_001013	ENSG00000	COR11H12	-	olfactoryprotein-coding	
chr19-36 15.59155	-1.64254	0.589286	-2.78734	0.005314	0.06823	chr19	36287580	36291565	+	0 NA	IntergeniSST1 Sate	-21771	NR_02938E	1E+08	Hs.46655C	NR_02938E	LOC100134-			uncharactncRNA	
chr22-13 17.9427	-1.51681	0.544217	-2.78715	0.005317	0.06823	chr22	13905821	13906059	+	0 NA	IntergeniALR Alphe	-1622219	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG00000	COR11H1	OR11H12 Colfactoryprotein-coding		
chr1-12 4 39.1622	-1.024	0.369214	-2.77344	0.005547	0.070906	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR Alphe	2872660	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000	EMB1P	-	embigin_pseudo	
chr22-12 20.20705	-1.4178	0.511667	-2.77094	0.005589	0.071188	chr22	12171048	12172275	+	0 NA	IntergeniACR01 Sat	274255	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272E-			uncharactncRNA	
chr10-41 23.4655	-1.30978	0.47346	-2.76664	0.005668	0.07192	chr10	41903057	41907879	+	0 NA	Intergeni(AATGG)n	462577	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E-			zinc_fingpseudo
chr4-190 20.70689	-1.39354	0.504288	-2.76338	0.005721	0.072321	chr4	1.9E+08	1.9E+08	+	0 NA	IntergeniCpG	6284	NM_00129E	1E+08	Hs.47824E	NM_00129E	ENSG00000	DUX4	DUX4L	double_hcprotein-coding	
chr21-92 36.94126	-1.04538	0.379619	-2.75375	0.005892	0.074208	chr21	9255137	9260549	+	0 NA	IntergeniMER5A DN	-128082	NR_03832E	1E+08	Hs.48756E	NM_17494E	ENSG00000	TEKT4P2	MAFIPL Tektin 4_pseudo		
chr19-27 227.2699	-0.56218	0.204411	-2.75023	0.005955	0.074735	chr19	27183517	27183747	+	0 NA	IntergeniALR Alphe	-609799	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-			uncharactncRNA
chr22-11 21.29633	-1.37164	0.498959	-2.74901	0.005978	0.074742	chr22	11895531	11897831	+	0 NA	promoter-promoter-	-725	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272E-			uncharactncRNA	
chr21-79 16.7081	-1.55602	0.566772	-2.7454	0.006044	0.075293	chr21	7915922	7917997	+	0 NA	Intergeni(ATTCAT	-87327	NM_00136E	1.03E+08	NM_00133C	ENSG00000	KCNE1B	-		potassiumprotein-coding	
chr21-11 47.44803	-0.94875	0.345825	-2.74345	0.006068	0.075467																

chr13-172.61.93852	-0.76593	0.302883	-2.52879	0.011446	0.110997	chr13	17258381	17258636	+	0	NA	IntergeniALR/Alphe	-936789	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family	wincRNA	
chr1-1231.155.2765	-0.54415	0.215246	-2.52803	0.01147	0.110997	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1582448	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMB1	-	embigin	fpseudo	
chr5-4886.123.263	-0.59153	0.234135	-2.52645	0.011522	0.110997	chr5	48860473	48860835	+	0	NA	IntergeniALR/Alphe	1580634	NM_198445	133418	Hs.561411NM_198445	ENSG00000CMB	GP70	embigin	protein-coding	
chr22-16.20.37736	-0.27996	0.506694	-2.52609	0.011534	0.110997	chr22	16315702	16315901	+	0	NA	IntergeniIntergeni	277009	NM_014406	150160	Hs.128342NM_014406	ENSG00000CCT8L2	CESK1	chaperonin	protein-coding	
chr19-265.21.34698	-1.25218	0.496236	-2.52335	0.011624	0.110992	chr19	26519327	26519546	+	0	NA	IntergeniALR/Alphe	-1273995	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000LOC101927-	-	uncharactncRNA		
chr19-271.35.07828	-0.98562	0.390636	-2.52311	0.011632	0.110992	chr19	27178394	27178608	+	0	NA	IntergeniALR/Alphe	-614930	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000LOC101927-	-	uncharactncRNA		
chr21-10.15.78356	-1.45303	0.57595	-2.52284	0.011641	0.110992	chr21	10388640	10388839	+	0	NA	IntergeniAluSg7 S1	-24781	NM_001187	574	Hs.545785NM_001187	BAGE	BAGE1 CT2B	melanin	protein-coding	
chr4-491.21.8524	-1.2261	0.486767	-2.51887	0.011773	0.110992	chr4	49135908	49137930	+	0	NA	Intergeni(TCCAT)n	150277	NM_00128E	80157	Hs.479703NM_025087	ENSG00000CWH43	CWH43-C F	cell	wall	protein-coding
chr9-435.24.02157	-1.18146	0.469089	-2.51862	0.011781	0.111514	chr9	43562303	43562611	+	0	NA	IntergeniALR/Alphe	436291	NR_16066E	1.03E+08	NR_160669	LOC102724-	-	methylencpseudo		
chr1-124.43.8041	-0.46314	0.183939	-2.51791	0.011805	0.111514	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2790644	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMB1	-	embigin	fpseudo	
chr1-124.43.88458	-0.88624	0.35211	-2.51694	0.011838	0.111514	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3142981	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMB1	-	embigin	fpseudo	
chr13-16.24.77129	-1.16575	0.463215	-2.51664	0.011848	0.111514	chr13	16672847	16673127	+	0	NA	IntergeniALR/Alphe	-1522310	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family	wincRNA	
chr21-104.15.78635	-1.44752	0.575659	-2.51454	0.011919	0.111663	chr21	10453016	10424825	+	0	NA	intron (AluY SINE	10388	NM_18248E	85319	Hs.545785NM_18248E	BAGE2	CT2.2	BAGE	famiprotein-coding	
chr5-485.138.9615	-0.56382	0.22245	-2.51424	0.011929	0.111663	chr5	48529166	48590520	+	0	NA	IntergeniALR/Alphe	1851320	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin	protein-coding	
chr5-476.224.1711	-0.47946	0.190817	-2.51264	0.011983	0.111865	chr5	47648570	47648811	+	0	NA	IntergeniALR/Alphe	-1952310	NM_02107E	348980	Hs.35317E NM_02107E	ENSG00000HCN1	BCNG-1 B	hyperpolaprotein-coding		
chr22-147.55.88976	-0.79051	0.314969	-2.50982	0.012079	0.112399	chr22	14745789	14746123	+	0	NA	IntergeniALR/Alphe	-782203	NM_00100E	81061	Hs.55470E NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactory	protein-coding	
chr1-127.139.1094	-0.54624	0.21777	-2.50833	0.01213	0.112399	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2264899	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMB1	-	embigin	fpseudo	
chr17-268.1048.386	-0.39567	0.157757	-2.50808	0.012139	0.112399	chr17	26880902	26885958	+	0	NA	IntergeniALR/Alphe	205811	NR_13567E	1.05E+08	Hs.64991E NR_13567E	LOC105371-	-	uncharactncRNA		
chr13-17.24.59768	-1.15648	0.461894	-2.50378	0.012288	0.113444	chr13	17981163	17981571	+	0	NA	IntergeniALR/Alphe	-213930	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family	wincRNA	
chr21-91.25.75485	-1.13118	0.451948	-2.5029	0.012318	0.113444	chr21	9167848	9168578	+	0	NA	IntergeniIntergeni	-38452	NR_038327	1E+08	Hs.487562NM_17494E	ENSG00000TEKT4P2	MAFIPL T	tektin	4	pseudo
chr10-41.27.20539	-1.09988	0.441017	-2.49396	0.012633	0.115968	chr10	41901705	41902012	+	0	NA	Intergeni(AATGG)n	466187	NR_02438C	441666	Hs.25572E NR_02438C	ENSG00000LOC44166E-	-	zinc	finger	
chr20-27.43.19602	-0.87685	0.351817	-2.49234	0.012691	0.115968	chr20	27054504	27055659	+	0	NA	IntergeniALR/Alphe	-845848	NR_04009E	284801	Hs.37069E NR_04009E	ENSG00000MIR663AHC	MIR663A	lncRNA		
chr17-247.334.8753	-0.41538	0.166667	-2.49225	0.012693	0.115968	chr17	24740194	24740464	+	0	NA	IntergeniALR/Alphe	2217218	NM_00119C	1E+08	Hs.74018E NM_00119C	ENSG00000MTRNR2L1	HN1	MT-RNR2	lprotein-coding	
chr6-593.90.08121	-0.63984	0.25714	-2.4883	0.012836	0.116955	chr6	59385445	59386412	+	0	NA	IntergeniALR/Alphe	-1424482	NR_13299E	1.07E+08	Hs.56153E NR_12572E	ENSG00000LINC0068C-	-	long	intencRNA	
chr14-16.28.29366	-1.08404	0.436266	-2.48481	0.012962	0.117795	chr14	16982284	16982946	+	0	NA	IntergeniALR/Alphe	-1618502	NM_00101E	440153	Hs.53488E NM_00101E	ENSG00000OR11H12	OR11H12 C	olfactory	protein-coding	
chr9-434.16.80495	-1.39248	0.56107	-2.48183	0.013071	0.118468	chr9	43495809	43496223	+	0	NA	IntergeniALR/Alphe	369850	NR_16066E	1.03E+08	NR_160669	LOC102724-	-	methylencpseudo		
chr21-11.50.69147	-0.81166	0.327252	-2.48024	0.013129	0.118567	chr21	11641143	11642052	+	0	NA	IntergeniALR/Alphe	1120083	NM_19926C	7179	Hs.12298E NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem	protein-coding	
chr21-124.41.57683	-0.89442	0.360762	-2.47925	0.013166	0.118567	chr21	12404628	12404945	+	0	NA	IntergeniALR/Alphe	-633380	NR_02691E	149992	Hs.55864E NM_153773	ANKRD30BF	C21orf99	ankyrin	fpseudo	
chr14-17.37.44612	-0.92849	0.374584	-2.47871	0.013186	0.118567	chr14	17241846	17242129	+	0	NA	IntergeniALR/Alphe	-1359130	NM_00101E	440153	Hs.53488E NM_00101E	ENSG00000OR11H12	OR11H12 C	olfactory	protein-coding	
chr10-38.20.05007	-1.25726	0.507606	-2.47683	0.013255	0.118882	chr10	39918348	39921148	+	0	NA	Intergeni(GAATG)n	223152	NR_04500C	349746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr4-492.38.44859	-0.91545	0.369998	-2.4742	0.013353	0.119149	chr4	49286447	49287455	+	0	NA	IntergeniIntergeni	300309	NM_00128E	80157	Hs.47970E NM_025087	ENSG00000CWH43	CWH43-C F	cell	wall	protein-coding
chr21-11.22.92834	-1.18154	0.477713	-2.47332	0.013386	0.119149	chr21	11373327	11373542	+	0	NA	IntergeniALR/Alphe	851920	NM_19926C	7179	Hs.12298E NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem	protein-coding	
chr5-488.143.6209	-0.53686	0.217068	-2.47324	0.01339	0.119149	chr5	48840395	48840679	+	0	NA	IntergeniALR/Alphe	1600751	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin	protein-coding	
chr14-17.29.84495	-1.04767	0.42399	-2.47097	0.013475	0.119597	chr14	17097306	17097521	+	0	NA	IntergeniALR/Alphe	-1503704	NM_00101E	440153	Hs.53488E NM_00101E	ENSG00000OR11H12	OR11H12 C	olfactory	protein-coding	
chr22-14.42.25987	-0.93332	0.378357	-2.46677	0.013634	0.119812	chr22	14174790	14175005	+	0	NA	IntergeniALR/Alphe	-1353262	NM_00100E	81061	Hs.55470E NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactory	protein-coding	
chr21-12.56.11408	-0.77159	0.314253	-2.46676	0.013634	0.119812	chr21	12879543	12879870	+	0	NA	IntergeniALR/Alphe	-1584600	NR_02691E	149992	Hs.55864E NM_153773	ANKRD30BF	C21orf99	ankyrin	fpseudo	
chr13-16.47.96632	-0.86298	0.349846	-2.46675	0.013634	0.119812	chr13	16736413	16736664	+	0	NA	IntergeniALR/Alphe	-1458759	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family	wincRNA	
chr21-88.20.52542	-1.24065	0.502971	-2.46664	0.013639	0.119812	chr21	8876436	8878232	+	0	NA	IntergeniAluSg2 S1	-109665	NR_037421	1.01E+08	NR_037421	ENSG00000MIR3648-1	MIR3648	microRNA	ncRNA	
chr1-1237.81.56717	-0.65728	0.266776	-2.46381	0.013747	0.120442	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2271259	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMB1	-	embigin	fpseudo	
chr21-98.17.21798	-1.35809	0.551414	-2.46292	0.013781	0.120442	chr21	9818829	9821819	+	0	NA	intron (SST1 Sate	737	NR_038377	441058	Hs.13053E NR_038377	LINC01667-	-	long	intencRNA	
chr14-16.21.09594	-1.21798	0.495131	-2.45991	0.013897	0.121151	chr14	16961410	16961803	+	0	NA	IntergeniALR/Alphe	-1639511	NM_00101E	440153	Hs.53488E NM_00101E	ENSG00000OR11H12	OR11H12 C	olfactory	protein-coding	
chr10-41.25.36245	-1.10903	0.451132	-2.45833	0.013958	0.121374	chr10	41885191	41886626	+	0	NA	Intergeni(ATGGA)n	482137	NR_02438C	441666	Hs.25572E NR_02438C	ENSG00000LOC44166E-	-	zinc	finger	
chr13-17.32.10925	-0.98841	0.402832	-2.45365	0.014142	0.122393	chr13	17304012	17305676	+	0	NA	IntergeniALR/Alphe	-890453	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family	wincRNA	
chr9-434.24.28371	-1.14904	0.468397	-2.45313	0.014162	0.122393	chr9	43488105	43488308	+	0	NA	IntergeniALR/Alphe	362040	NR_16066E	1.03E+08	NR_160669	LOC102724-	-	methylencpseudo		
chr21-11.25.8415	-1.10146	0.449118	-2.45249	0.014187	0.122393	chr21	11505322	11505800	+	0	NA	IntergeniALR/Alphe	983937	NM_19926C	7179	Hs.12298E NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem	protein-coding	
chrY-112.25.84059	-1.09591	0.447	-2.4517	0.014218	0.122393	chrY	11297479	11297696	+	0	NA	Intergeni(ATTC)n	1124003	NR_033667	352887	Hs.546221NR_033667	ENSG00000GYG2P1	GYG2P	glycoenipseudo		



chr14-181 53.43836	-0.74438	0.322269	-2.30981	0.020899	0.150246	chr14	18137208	18137572	+	0 NA	IntergeniALR/Alphe	-463727 NM_001013	440153 Hs. 53488CNM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding
chr19-265 134.3893	-0.51151	0.221485	-2.30945	0.020919	0.150246	chr19	26528930	26529948	+	0 NA	IntergeniALR/Alphe	-1263992 NR_146732	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	-	uncharacterncRNA
chr4-494f 17.18568	-1.26317	0.547628	-2.30662	0.021076	0.151058	chr4	49489903	49492553	+	0 NA	IntergeniL1MA5 LI	504586 NM_00128f	80157 Hs. 479703NM_025087	ENSG00000CWH43	CWH43-C F	cell wallprotein-coding
chr1-123f 63.62119	-0.68611	0.298149	-2.30125	0.021378	0.152902	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2372290 NR_00395f	647121 Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr14-17f 27.22238	-0.99922	0.435575	-2.29402	0.02179	0.155523	chr14	17236303	17237784	+	0 NA	IntergeniALR/Alphe	-1364700 NR_001013	440153 Hs. 53488CNM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding
chr21-104 17.71281	-1.23231	0.537543	-2.29249	0.021877	0.155825	chr21	10467639	10468213	+	0 NA	intron (MIR SINE	-53588 NM_19925f	7179 Hs. 12298fNM_19925f	ENSG00000TPTE	CT44 PTEN	transmemt protein-coding
chr13-17f 38.92561	-0.85763	0.374491	-2.29013	0.022014	0.156473	chr13	17330020	17330328	+	0 NA	IntergeniALR/Alphe	-865123 NR_02727f	26080 Hs. 44858fNR_02727f	ENSG00000FAM230C	LINC00281	family wincRNA
chr8-4584 58.2186	-0.70695	0.308917	-2.28849	0.022109	0.156823	chr8	45840477	45840759	+	0 NA	IntergeniALR/Alphe	775203 NR_146077	389652 NR_146077	ENSG00000ASNSP1	ASNSL1	asparagipseudo
chr22-107 18.21265	-1.21118	0.530098	-2.28482	0.022323	0.158017	chr22	10736306	10739779	+	0 NA	IntergeniL2 LINE I	223487 NR_13232C	1.03E+08 NR_132320	FRG1FP	-	FSHD regipseudo
chr21-11f 22.97341	-1.08443	0.475831	-2.27902	0.022666	0.16011	chr21	11528066	11528737	+	0 NA	IntergeniALR/Alphe	1006884 NM_19926C	7179 Hs. 12298fNM_19925f	ENSG00000TPTE	CT44 PTEN	transmemt protein-coding
chr22-11f 36.64403	-0.86924	0.381772	-2.27685	0.022795	0.160694	chr22	11898762	11899230	+	0 NA	intron (intron (	1590 NR_110761	1.03E+08 Hs. 65292fNR_110761	LOC10272f-	-	uncharacterncRNA
chr5-489f 138.1332	-0.50082	0.22042	-2.27211	0.02308	0.162363	chr5	48929400	48930438	+	0 NA	IntergeniALR/Alphe	1511369 NM_19844f	133418 Hs. 561411NM_19844f	ENSG00000EMB	GP70	embigin protein-coding
chr13-16f 27.22937	-0.99287	0.439469	-2.25926	0.023867	0.162711	chr13	16859959	16860687	+	0 NA	IntergeniALR/Alphe	-1334974 NR_02727f	26080 Hs. 44858fNR_02727f	ENSG00000FAM230C	LINC00281	family wincRNA
chr20-274 61.97188	-0.67998	0.30099	-2.25914	0.023875	0.162721	chr20	27425468	27426193	+	0 NA	IntergeniALR/Alphe	1176835 NR_13231f	1E+08 Hs. 529357NR_13231f	ENSG00000FRG1CP	-	FSHD regipseudo
chr21-91f 23.1092	-1.08463	0.481007	-2.25491	0.024139	0.168777	chr21	9128188	9128456	+	0 NA	intron (MLTIH LTF	1439 NR_03832f	1E+08 Hs. 487562NM_17494f	ENSG00000TEKT4P2	MAFIPL T	tektin 4 pseudo
chr21-12f 26.48625	-0.99092	0.440143	-2.25136	0.024363	0.169691	chr21	12095898	12097528	+	0 NA	IntergeniALR/Alphe	-941453 NR_02691f	149992 Hs. 55864fNM_153773	ANKRD30BF	C21orf99	ankyrin rpseudo
chr17-26f 19.19621	-1.1623	0.516288	-2.25126	0.024369	0.169691	chr17	26936136	26940956	+	0 NA	Intergeni(GAATG)n	140563 NR_13567f	1.05E+08 Hs. 64991fNR_135673	LOC105371-	-	uncharacterncRNA
chr22-14f 19.62537	-1.14925	0.512096	-2.24421	0.024819	0.171621	chr22	14376663	14380022	+	0 NA	IntergeniALR/Alphe	-1149927 NM_00100f	81061 Hs. 55470fNM_00100f	ENSG00000COR11H1	OR11H12 C	olfactoryprotein-coding
chr22-13f 19.62258	-1.15363	0.514082	-2.24406	0.024828	0.171621	chr22	13323846	13324518	+	0 NA	IntergeniALR/Alphe	1426776 NR_110761	1.03E+08 Hs. 65292fNR_110761	LOC10272f-	-	uncharacterncRNA
chr9-440f 19.17451	-1.16082	0.517638	-2.24253	0.024927	0.171621	chr9	44028506	44028793	+	0 NA	IntergeniALR/Alphe	902483 NR_16066f	1.03E+08 NR_160669	LOC102724-	-	methylenepseudo
chr21-93f 20.69573	-1.11287	0.496477	-2.24154	0.024991	0.171621	chr21	9370768	9376997	+	0 NA	IntergeniIntergeni	169148 NR_135512	1.05E+08 Hs. 46232fNR_135512	LOC105372-	-	nuclear rpseudo
chr21-91f 16.42923	-1.2544	0.559616	-2.24153	0.024992	0.171621	chr21	9111026	9114970	+	0 NA	intron (LIMB2 LI	16763 NR_03832f	1E+08 Hs. 487562NM_17494f	ENSG00000TEKT4P2	MAFIPL T	tektin 4 pseudo
chr20-28f 48.66426	-0.74914	0.334221	-2.24146	0.024996	0.171621	chr20	28077682	28077914	+	0 NA	IntergeniALR/Alphe	524867 NR_13231f	1E+08 Hs. 529357NR_13231f	ENSG00000FRG1CP	-	FSHD regipseudo
chr20-28f 51.17184	-0.73327	0.327141	-2.24145	0.024997	0.171621	chr20	28022754	28023142	+	0 NA	IntergeniALR/Alphe	579717 NR_13231f	1E+08 Hs. 529357NR_13231f	ENSG00000FRG1CP	-	FSHD regipseudo
chr5-484f 65.71182	-0.65161	0.291114	-2.23834	0.025199	0.172661	chr5	48449574	48449824	+	0 NA	IntergeniALR/Alphe	1991589 NM_19844f	133418 Hs. 561411NM_19844f	ENSG00000EMB	GP70	embigin protein-coding
chr22-14f 44.96276	-0.7859	0.351249	-2.23744	0.025258	0.17272	chr22	14941654	14942053	+	0 NA	IntergeniALR/Alphe	-586306 NM_00100f	81061 Hs. 55470fNM_00100f	ENSG00000COR11H1	OR11H12 C	olfactoryprotein-coding
chr4-504f 33.17353	-0.89283	0.399591	-2.23436	0.025459	0.173467	chr4	50472252	50472624	+	0 NA	IntergeniALR/Alphe	-1370562 NM_001511f	23142 Hs. 60538fNM_001511f	ENSG00000DCUN1D4	-	defectiveprotein-coding
chr18-20f 20.64675	-1.11841	0.500558	-2.23423	0.025468	0.173467	chr18	20732904	20733200	+	0 NA	IntergeniALR/Alphe	378761 NM_00540f	6093 Hs. 306307NM_00540f	ENSG00000ROCK1	P160ROCK	Rho assocprotein-coding
chr13-17f 18.05516	-1.20993	0.541817	-2.2331	0.025543	0.173628	chr13	17492058	17492303	+	0 NA	IntergeniALR/Alphe	-703117 NR_02727f	26080 Hs. 44858fNR_02727f	ENSG00000FAM230C	LINC00281	family wincRNA
chr21-11f 21.17108	-1.1008	0.493137	-2.23224	0.025599	0.173668	chr21	11516807	11517437	+	0 NA	IntergeniALR/Alphe	995608 NR_19926C	7179 Hs. 12298fNM_19925f	ENSG00000TPTE	CT44 PTEN	transmemt protein-coding
chr6-589f 174.7492	-0.44766	0.200775	-2.22965	0.025771	0.173942	chr6	58924121	58925151	+	0 NA	IntergeniALR/Alphe	-963190 NR_13299f	1.07E+08 Hs. 56153fNR_12572f	ENSG00000LINC0068C-	-	long intencRNA
chr9-435f 20.24487	-1.12284	0.503744	-2.229	0.025814	0.173942	chr9	43521822	43522199	+	0 NA	IntergeniALR/Alphe	395844 NR_16066f	1.03E+08 NR_160669	LOC102724-	-	methylenepseudo
chr22-107f 21.71991	-1.0815	0.4852	-2.22897	0.025816	0.173942	chr22	10753451	10754566	+	0 NA	IntergeniIntergeni	207576 NR_13232C	1.03E+08 NR_132320	FRG1FP	-	FSHD regipseudo
chr15-18f 16.88567	-1.22761	0.55089	-2.22842	0.025852	0.173942	chr15	18540956	18541260	+	0 NA	IntergeniALR/Alphe	-1741636 NR_03883f	646096 Hs. 44878fNR_03883f	ENSG00000CHEK2P2	-	checkpoirpseudo
chr5-485f 29.95011	-0.92417	0.414924	-2.22734	0.025925	0.173942	chr5	48529008	48529213	+	0 NA	IntergeniALR/Alphe	1912178 NM_19844f	133418 Hs. 561411NM_19844f	ENSG00000EMB	GP70	embigin protein-coding
chr19-25f 149.2027	-0.49798	0.223675	-2.22634	0.025991	0.173942	chr19	25506889	25507124	+	0 NA	IntergeniALR/Alphe	-1343559 NR_00360f	1E+08 Hs. 149312NR_00360f	ENSG00000HAVCR1P1	-	hepatitispseudo
chr14-18f 40.66897	-0.80865	0.363229	-2.22629	0.025995	0.173942	chr14	18007663	18007927	+	0 NA	IntergeniALR/Alphe	-593322 NM_00101f	440153 Hs. 53488CNM_00101f	ENSG00000COR11H12	-	olfactoryprotein-coding
chr10-41f 16.88846	-1.22258	0.549678	-2.22418	0.026137	0.17407	chr10	44870822	44871330	+	0 NA	Intergeni(ATGGA)n	499591 NR_02438f	441666 Hs. 25572fNR_02438f	ENSG00000LOC44166f-	-	zinc fingpseudo
chr14-16f 25.84504	-0.66535	0.299377	-2.22425	0.026215	0.17407	chr14	16611108	16613420	+	0 NA	IntergeniALR/Alphe	-1989897 NM_00101f	440153 Hs. 53488CNM_00101f	ENSG00000COR11H12	-	olfactoryprotein-coding
chr21-114f 61.65574	-0.66535	0.299377	-2.22425	0.026253	0.17407	chr21	11472272	11472662	+	0 NA	IntergeniALR/Alphe	950953 NM_19926C	7179 Hs. 12298fNM_19925f	ENSG00000TPTE	CT44 PTEN	transmemt protein-coding
chr22-14f 22.2254	-1.06442	0.479156	-2.22145	0.02632	0.17407	chr22	14948496	14948970	+	0 NA	IntergeniALR/Alphe	-579426 NM_00100f	81061 Hs. 55470fNM_00100f	ENSG00000COR11H1	OR11H12 C	olfactoryprotein-coding
chr10-41f 35.88757	-0.85739	0.385982	-2.22131	0.02633	0.17407	chr10	11410176	11410395	+	0 NA	IntergeniALR/Alphe	-1241076 NR_02438f	441666 Hs. 25572fNR_02438f	ENSG00000LOC44166f-	-	zinc fingpseudo
chr22-13f 29.04281	-0.93666	0.421762	-2.22083	0.026362	0.17407	chr22	13373646	13373936	+	0 NA	IntergeniALR/Alphe	1476385 NR_110761	1.03E+08 Hs. 65292fNR_110761	LOC10272f-	-	uncharacterncRNA
chr14-18f 21.70099	-1.0763	0.484662	-2.22072	0.02637	0.17407	chr14	18141181	18141766	+	0 NA	IntergeniALR/Alphe	-459644 NM_00101f	440153 Hs. 53488CNM_00101f	ENSG00000COR11H12	-	olfactoryprotein-coding
chr22-14f 17.41	-1.20241	0.541643	-2.21993	0.026423	0.174089	chr22	14983930	14984689	+	0 NA	IntergeniALR/Alphe	-543850 NM_00100f	81061 Hs. 55470fNM_00100f	ENSG00000COR11H1	OR11H12 C	olfactoryprotein-coding
chr5-479f 78.57587	-0.59906	0.270239	-2.21679	0.026637	0.175162	chr5	47961076	47984100	+	0 NA	IntergeniALR/Alphe	-2286208 NM_02107f	348980 Hs. 35317fNM_02107f	ENSG00000HCN1	BCNG-1 B	hyperpoleprotein-coding
chr10-41f 35.70559	-0.85777	0.387168	-2.2155	0.026726	0.175248	chr10	41502836	41503108	+	0 NA	IntergeniALR/Alphe	865073 NR_02438f	441666 Hs. 25572fNR_02438f	ENSG00000LOC44166f-	-	zinc fingpseudo
chr19-26f 147.3858	-0.47258	0.213346	-2.21511	0.026753	0.175248	chr19	26439881	26440183	+	0 NA	IntergeniALR/Alphe	-1353399 NR_146732	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	-	uncharacterncRNA
chr8-120f 16.99696	-1.23088	0.555958	-2.21398	0.02683	0.175419	chr8	12606347	12606872	+	0 NA	intron (intron (	96148 NR_11194f	286083 Hs. 382131NR_03389f	ENSG00000LOC28608f-	-	uncharacterncRNA
chr21-12f 32.43598	-0.88387	0.399917	-2.21013	0.027096	0.176401	chr21	12168528	12170203	+	0 NA	IntergeniALR/Alphe	-868801 NR_02691f	149992 Hs. 55864fNM_153773	ANKRD30BF	C21orf99	ankyrin rpseudo
chr14-16f 21.10877	-1.09275	0.494547	-2													

chr7-5875	239.5871	-0.38882	0.183538	-2.11848	0.034134	0.194285	chr7	58797682	58798052	+	0	NA	IntergeniALR/Alphe	1347690	NM_001155	441234	Hs.533121NM_001155	ENSG000003ZNF716	-	zinc_fingprotein-coding	
chr20-266	26.9293	-0.92789	0.438056	-2.11819	0.034159	0.194285	chr20	26682528	26683157	+	0	NA	IntergeniALR/Alphe	-473609	NR_040095	284801	Hs.370695NR_040095	ENSG000003MIR663AHC	-	MIR663A lncRNA	
chr13-165	23.81338	-0.98499	0.465035	-2.1181	0.034167	0.194285	chr13	16563719	16563999	+	0	NA	IntergeniALR/Alphe	-1631438	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr19-166	66.1282	-0.62074	0.293089	-2.11793	0.034181	0.194285	chr19	26049087	26049338	+	0	NA	IntergeniALR/Alphe	-1744219	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-		uncharactncRNA	
chr14-174	24.31322	-0.97516	0.460518	-2.11753	0.034215	0.194285	chr14	17709765	17709966	+	0	NA	IntergeniALR/Alphe	-891252	NM_001013	440153	Hs.534888NM_001013	ENSG000003OR11H12	-	olfactoryprotein-coding	
chr21-104	18.63679	-1.10404	0.521491	-2.11709	0.034252	0.194285	chr21	10429411	10432892	+	0	NA	intron (AluSq2)S1	17619	NM_182482	85319	Hs.545785NM_182482	BAGE2	CT2.2	BAGE_famiprotein-coding	
chr21-114	42.39555	-0.75118	0.355143	-2.11515	0.034417	0.194899	chr21	11493506	11493852	+	0	NA	IntergeniALR/Alphe	972165	NM_199266	7179	Hs.122988NM_199265	ENSG000003TPTE	CT44 PTEN	transmemtprotein-coding	
chr1-1236	26.91318	-0.92052	0.435454	-2.11393	0.034522	0.195167	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2292340	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMBP1	-	embigin_pseudo	
chr13-171	38.39124	-0.77903	0.369094	-2.11066	0.034801	0.196216	chr13	17173198	17174274	+	0	NA	IntergeniALR/Alphe	-1021561	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr22-145	43.40918	-0.73617	0.348824	-2.11043	0.034822	0.196216	chr22	14392811	14393034	+	0	NA	IntergeniALR/Alphe	-1135237	NM_001005	81061	Hs.554706NM_001005	ENSG000003OR11H1	OR11H12	Colfactoryprotein-coding	
chr1-1245	71.02922	-0.59304	0.281459	-2.10702	0.035116	0.197059	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	2995393	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMBP1	-	embigin_pseudo	
chr13-178	19.03756	-1.1202	0.531656	-2.107	0.035118	0.197059	chr13	17855578	17856028	+	0	NA	IntergeniALR/Alphe	-339494	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr3-924	23.84841	-0.9985	0.474011	-2.10649	0.035162	0.197059	chr3	92448223	92448696	+	0	NA	IntergeniALR/Alphe	1525622	NM_001314	5627	Hs.64016	NM_000313	ENSG000003PROS1	PROS PS21	protein_Sprotein-coding
chr3-915	33.66495	-0.86341	0.409968	-2.10603	0.035202	0.197059	chr3	91552654	91553217	+	0	NA	IntergeniALR/Alphe	1242146	NM_001314	5627	Hs.64016	NM_000313	ENSG000003PROS1	PROS PS21	protein_Sprotein-coding
chr14-18	30.8496	-0.86244	0.409693	-2.10508	0.035285	0.197202	chr14	18049613	18050998	+	0	NA	IntergeniALR/Alphe	-550812	NM_001013	440153	Hs.534888NM_001013	ENSG000003OR11H12	-	olfactoryprotein-coding	
chr13-164	39.85294	-0.76369	0.36294	-2.10418	0.035363	0.197319	chr13	16485731	16487008	+	0	NA	IntergeniALR/Alphe	-1708928	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr14-16	18.54719	-1.10252	0.524831	-2.10071	0.035667	0.198182	chr14	16699638	16699884	+	0	NA	IntergeniALR/Alphe	-1901356	NM_001013	440153	Hs.534888NM_001013	ENSG000003OR11H12	-	olfactoryprotein-coding	
chr5-488	36.36738	-0.79455	0.378262	-2.10053	0.035682	0.198182	chr5	48867704	48868028	+	0	NA	IntergeniALR/Alphe	1573422	NM_198445	133418	Hs.561411NM_198445	ENSG000003EMB	GP70	embigin_protein-coding	
chr22-141	27.29615	-0.91695	0.436556	-2.10043	0.035691	0.198182	chr22	14117129	14118594	+	0	NA	IntergeniALR/Alphe	-1410298	NM_001005	81061	Hs.554706NM_001005	ENSG000003OR11H1	OR11H12	Colfactoryprotein-coding	
chr22-136	18.6991	-1.11336	0.530467	-2.09883	0.035832	0.198262	chr19	25072928	25073166	+	0	NA	IntergeniALR/Alphe	-909600	NR_003603	1E+08	Hs.149312NR_003603	ENSG000003HAVCRIP1	-	hepatitis_pseudo	
chr22-134	43.84392	-0.73164	0.34865	-2.09949	0.035862	0.198262	chr22	13650829	13651070	+	0	NA	IntergeniALR/Alphe	1753543	NR_110761	1.03E+08	Hs.652929NR_110761	LOC102722-		uncharactncRNA	
chr13-176	30.32248	-0.87276	0.415938	-2.09829	0.035879	0.198262	chr13	17659737	17660072	+	0	NA	IntergeniALR/Alphe	-535393	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr12-365	25.8456	-0.93616	0.446656	-2.09594	0.036088	0.199094	chr12	36335879	36336119	+	0	NA	IntergeniALR/Alphe	-1980775	NM_001308	144245	Hs.259305NM_001013	ENSG000003ALG10	ALG10 KCFALG10	alpprotein-coding	
chr16-367	17.99837	-1.12591	0.537984	-2.09283	0.036364	0.200296	chr16	36909729	36909965	+	0	NA	IntergeniALR/Alphe	1163295	NR_003398	400533	Hs.499133NR_003398	ENSG000003LINC02167-		long_intencRNA	
chr13-165	20.59554	-1.03786	0.496208	-2.09157	0.036477	0.200594	chr13	16513501	16516676	+	0	NA	IntergeniALR/Alphe	-1680209	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr13-172	35.00364	-0.80662	0.38646	-2.08721	0.036869	0.202427	chr13	17202265	17202571	+	0	NA	IntergeniALR/Alphe	-992879	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr22-118	20.70963	-1.03665	0.497751	-2.08267	0.037281	0.20406	chr22	11883134	11884175	+	0	NA	IntergeniIntergeni	-13751	NR_110761	1.03E+08	Hs.652929NR_110761	LOC102722-		uncharactncRNA	
chr19-265	83.35003	-0.55237	0.265226	-2.08262	0.037286	0.20406	chr19	26951168	26951397	+	0	NA	IntergeniALR/Alphe	-842149	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-		uncharactncRNA	
chr2-898	15.85368	-1.17518	0.565143	-2.07943	0.037578	0.204644	chr2	89832331	89834070	+	0	NA	Intergeni(ATTC)Cn	-195296	NR_136323	1.02E+08	Hs.578075NR_136329	LOC101927-		lysine_mepseudo	
chr21-93	22.12234	-0.99509	0.478583	-2.07925	0.037594	0.204644	chr21	9363212	9369930	+	0	NA	IntergeniIntergeni	-176459	NR_135512	1.05E+08	Hs.462323NR_135512	LOC105375-		nuclear_ipseudo	
chr10-401	134.2779	-0.45663	0.219646	-2.07892	0.037625	0.204644	chr10	40135042	40135926	+	0	NA	IntergeniALR/Alphe	1438888	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	ppseudo
chr20-274	15.8264	-1.18416	0.569674	-2.07866	0.037649	0.204644	chr20	27421924	27422179	+	0	NA	IntergeniALR/Alphe	1180614	NR_132315	1E+08	Hs.529357NR_132315	ENSG000003FRG1CP	-	FSHD	regipseudo
chr21-122	53.16117	-0.66566	0.320279	-2.0782	0.037691	0.204644	chr21	12245149	12245414	+	0	NA	IntergeniALR/Alphe	-1792885	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin_ipseudo	
chr22-14	21.57631	-1.00772	0.485071	-2.07748	0.037758	0.20468	chr22	14009075	14009812	+	0	NA	IntergeniALR/Alphe	-1518716	NM_001005	81061	Hs.554706NM_001005	ENSG000003OR11H1	OR11H12	Colfactoryprotein-coding	
chr1-1241	135.483	-0.45788	0.22065	-2.07514	0.037974	0.205526	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2604873	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMBP1	-	embigin_ipseudo	
chr8-8578	16.33182	-1.15203	0.5563	-2.07089	0.038369	0.207127	chr8	85789728	85795306	+	0	NA	IntergeniIntergeni	-1149	NR_003594	1E+08	Hs.535055NR_003594	REX01L2P	-	REX01	likpseudo
chr12-355	16.35074	-1.15895	0.559702	-2.07066	0.03839	0.207127	chr12	35503210	35503799	+	0	NA	IntergeniALR/Alphe	1481008	NM_032834	84920	Hs.102971NM_032834	ENSG000003ALG10	ALG10A DIALG10	alpprotein-coding	
chr5-4917	37.97045	-0.77359	0.373966	-2.06861	0.038583	0.207259	chr5	49173292	49173501	+	0	NA	IntergeniALR/Alphe	1267892	NM_198445	133418	Hs.561411NM_198445	ENSG000003EMB	GP70	embigin_protein-coding	
chr22-141	23.17101	-0.96914	0.468519	-2.06852	0.038592	0.207259	chr22	14172209	14172480	+	0	NA	IntergeniALR/Alphe	-1157515	NM_001005	81061	Hs.554706NM_001005	ENSG000003OR11H1	OR11H12	Colfactoryprotein-coding	
chr14-173	21.5791	-1.00384	0.485449	-2.06786	0.038653	0.207259	chr14	17379948	17380930	+	0	NA	IntergeniALR/Alphe	-1220678	NM_001013	440153	Hs.534888NM_001013	ENSG000003OR11H12	-	olfactoryprotein-coding	
chr7-580	23.64915	-0.95812	0.46335	-2.06782	0.038657	0.207259	chr7	58067483	58067724	+	0	NA	IntergeniIntergeni	617426	NM_001155	441234	Hs.533121NM_001155	ENSG000003ZNF716	-	zinc_fingprotein-coding	
chr1-1235	118.7895	-0.48748	0.236253	-2.0634	0.039075	0.209019	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2429015	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMBP1	-	embigin_ipseudo	
chr13-165	25.15146	-0.92799	0.450112	-2.06169	0.039237	0.209019	chr13	16930416	16930780	+	0	NA	IntergeniALR/Alphe	-1264699	NR_027278	26080	Hs.448582NR_027278	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr10-418	24.19239	-0.95125	0.461546	-2.061	0.039303	0.209019	chr10	41843480	41844321	+	0	NA	IntergeniIntergeni	521415	NR_02438C	441666	Hs.255725NR_02438C	ENSG000003LOC441666-		zinc_fingpseudo	
chr17-265	71.06039	-0.58684	0.284814	-2.06044	0.039357	0.209019	chr17	26398434	26398681	+	0	NA	IntergeniALR/Alphe	690684	NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371-		uncharactncRNA	
chr22-141	25.60511	-0.92086	0.447001	-2.06008	0.03939	0.209019	chr22	14146208	14146635	+	0	NA	IntergeniALR/Alphe	-1381738	NM_001005	81061	Hs.554706NM_001005	ENSG000003OR11H1	OR11H12	Colfactoryprotein-coding	
chr5-494	249.8001	-0.38695	0.187847	-2.0599	0.039408	0.209019	chr5	49423219	49423481	+	0	NA	IntergeniALR/Alphe	1017938	NM_198445	133418	Hs.561411NM_198445	ENSG000003EMB	GP70	embigin_protein-coding	
chr21-115	15.78858	-1.16989	0.568124	-2.05922	0.039473	0.209019	chr21	11500999	11501215	+	0	NA	IntergeniALR/Alphe	979593	NM_199266	7179	Hs.122988NM_199265	ENSG000003TPTE	CT44 PTEN	transmemtprotein-coding	
chr22-145	54.31945	-0.65974	0.320441	-2.05885	0.039508	0.209019	chr22	14520915	14521648	+	0	NA	IntergeniALR/Alphe	-1006878	NM_001005	81061	Hs.554706NM_001005	ENSG000003OR11H1	OR11H12	Colfactoryprotein-coding	
chr1-1241	26.15394	-0.90887	0.441707	-2.05763	0.039626	0.209019	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2669980	NR_003955	647121					



chrY-5684 33.32487	-0.78491	0.393518	-1.99459	0.046088	0.218486	chrY	56845355	56845583	+	0	NA	IntergeniBSR/Beta	-108786	NM_00584C	10251	Hs.381912NM_00584C	ENSG00000SPRY3	spry-3	sprouty Fprotein-coding
chr6-5875 56.79751	-0.62257	0.31216	-1.99441	0.046108	0.218486	chr6	58791973	58793794	+	0	NA	IntergeniALR/Alphe	-831437	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG00000LINC0068C-		long intencRNA
chr6-5908 34.33014	-0.77241	0.38759	-1.99285	0.046278	0.218542	chr6	59082994	59083312	+	0	NA	IntergeniALR/Alphe	-121707	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG00000LINC0068C-		long intencRNA
chr20-275 25.87562	-0.88479	0.443992	-1.99228	0.046284	0.218542	chr20	27943250	27943667	+	0	NA	IntergeniALR/Alphe	659207	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000FRG1CP		FSHD regipseudo
chr22-135 21.2301	-0.9791	0.491383	-1.99255	0.046311	0.218542	chr22	16798333	16798966	+	0	NA	IntergeniALR/Alphe	16798333	NR_110761	1.03E+08	Hs.652929NR_110761	ENSG00000LOC102722-		uncharactcrRNA
chr1-123 27.32895	-0.86554	0.43542	-1.98783	0.046831	0.22069	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2160206	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr18-157 27.92676	-0.85148	0.429598	-1.98205	0.047474	0.22298	chr18	15779200	15779533	+	0	NA	IntergeniALR/Alphe	-453447	NR_027417	644669	Hs.579474NR_027417	ENSG00000LOC64466E-		ankyrin rpseudo
chr13-18 20.92177	-1.01393	0.511697	-1.9815	0.047535	0.22298	chr13	18013269	18013468	+	0	NA	IntergeniALR/Alphe	-181929	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr22-107 24.26201	-0.90848	0.458488	-1.98148	0.047538	0.22298	chr22	10731200	10731758	+	0	NA	IntergeniAluS26 S1	230050	NR_13232C	1.03E+08	NR_132320	FRG1FP		FSHD regipseudo
chr5-4795 53.81737	-0.62975	0.317954	-1.98064	0.047631	0.22298	chr5	47952841	47953439	+	0	NA	IntergeniALR/Alphe	-2256760	NM_021072	348980	Hs.353176NM_021072	ENSG00000HCN1	BCNG-1 B	hyperpoleprotein-coding
chr14-17 27.76927	-0.85	0.429178	-1.98053	0.047644	0.22298	chr14	17523753	17526511	+	0	NA	IntergeniALR/Alphe	-1075985	NM_001012	440153	Hs.53488CNM_001012	ENSG00000OR11H12		olfactoryprotein-coding
chr1-124 71.70774	-0.55744	0.281648	-1.9792	0.047794	0.22298	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2486277	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr10-404 109.6909	-0.47539	0.240236	-1.97884	0.047834	0.22298	chr10	40412639	40414674	+	0	NA	IntergeniALR/Alphe	1717060	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr9-412 16.50995	-1.093	0.552349	-1.97881	0.047837	0.22298	chr9	41243497	41243696	+	0	NA	IntergeniMER103C I	-9761	NR_03968E	1.01E+08	NR_03968E	ENSG00000MIR4477B		microRNA ncRNA
chr4-494 17.05319	-1.07861	0.54538	-1.97773	0.04796	0.223247	chr4	49493662	49495077	+	0	NA	IntergeniLIMB8 L1N	507727	NM_00128E	80157	Hs.479703NM_025087	ENSG00000CWH43	CWH43-C F	cell wallprotein-coding
chr10-385 15.96112	-1.11897	0.566173	-1.97637	0.048112	0.223421	chr10	38911736	38913293	+	0	NA	Intergeni(GAGTG)n	215918	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chrY-121 22.42013	-0.94576	0.478907	-1.97484	0.048286	0.223421	chrY	11283847	11284474	+	0	NA	IntergeniLIPA4 L1N	1137430	NR_033667	532887	Hs.546221NR_033667	ENSG00000GYG2P1	GYG2P	glycogenin pseudo
chr20-29 17.00979	-1.07258	0.545441	-1.97465	0.048308	0.223421	chr20	29121882	29123726	+	0	NA	IntergeniIntergeni	42414	NR_13231E	1.03E+08	NR_132316	FRG1DP		FSHD regipseudo
chr13-17 30.75498	-0.80871	0.409565	-1.97456	0.048318	0.223421	chr13	17827645	17828325	+	0	NA	IntergeniALR/Alphe	-367312	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr22-137 43.59562	-0.68741	0.348141	-1.97452	0.048323	0.223421	chr22	13727052	13727418	+	0	NA	IntergeniALR/Alphe	-1800924	NM_00100E	81061	Hs.554706NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactoryprotein-coding
chr6-5974 43.04958	-0.68976	0.34959	-1.97305	0.04849	0.223892	chr6	59747781	59748798	+	0	NA	IntergeniALR/Alphe	-1786843	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG00000LINC0068C-		long intencRNA
chr14-17 28.77453	-0.83269	0.422526	-1.97073	0.048755	0.224518	chr14	17209945	17210203	+	0	NA	IntergeniALR/Alphe	-1391043	NM_001012	440153	Hs.53488CNM_001012	ENSG00000OR11H12		olfactoryprotein-coding
chrY-5684 17.53412	-1.0555	0.535595	-1.97071	0.048757	0.224518	chrY	56846906	56849346	+	0	NA	IntergeniBSR/Beta	-106129	NM_00584C	10251	Hs.381912NM_00584C	ENSG00000SPRY3	spry-3	sprouty Fprotein-coding
chr4-5034 17.01258	-1.07037	0.543985	-1.96765	0.049108	0.22583	chr4	50348853	50349436	+	0	NA	IntergeniALR/Alphe	1362507	NM_00128E	80157	Hs.479703NM_025087	ENSG00000CWH43	CWH43-C F	cell wallprotein-coding
chr1-122 98.24792	-0.4904	0.249315	-1.96699	0.049184	0.225876	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1126278	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr14-18 23.33301	-0.92206	0.46896	-1.96618	0.049278	0.226005	chr14	18075407	18075871	+	0	NA	IntergeniALR/Alphe	-525478	NM_001012	440153	Hs.53488CNM_001012	ENSG00000OR11H12		olfactoryprotein-coding
chr22-14 18.84777	-1.03658	0.527609	-1.96468	0.049452	0.226499	chr22	14452605	14442928	+	0	NA	IntergeniALR/Alphe	-1085393	NM_00100E	81061	Hs.554706NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactoryprotein-coding
chr1-121 86.91067	-0.51254	0.260982	-1.96387	0.049545	0.226624	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	231292	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr21-11 22.18917	-0.95152	0.484768	-1.96284	0.049664	0.226867	chr21	11247493	11247764	+	0	NA	IntergeniLIPA4 L1N	726114	NM_19926C	7179	Hs.122988NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem protein-coding
chrY-5687 18.53659	-1.02085	0.520814	-1.96012	0.049982	0.228015	chrY	56876321	56880471	+	0	NA	IntergeniMT1E1A I	-75874	NM_00584C	10251	Hs.381912NM_00584C	ENSG00000SPRY3	spry-3	sprouty Fprotein-coding
chr5-483 39.58573	-0.71204	0.363608	-1.95826	0.0502	0.228408	chr5	48304649	48304918	+	0	NA	IntergeniALR/Alphe	2136505	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr1-124 54.00113	-0.63106	0.322259	-1.95824	0.050202	0.228408	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2918763	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr6-584 100.3648	-0.48281	0.246692	-1.95715	0.050329	0.228685	chr6	58450057	58450907	+	0	NA	IntergeniALR/Alphe	-489036	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG00000LINC0068C-		long intencRNA
chr21-11 17.5614	-1.04761	0.536051	-1.95431	0.050665	0.229262	chr21	11187952	11188312	+	0	NA	IntergeniALR/Alphe	666618	NM_19926C	7179	Hs.122988NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem protein-coding
chr9-628 16.93911	-1.08035	0.552812	-1.95427	0.050669	0.229262	chr9	62833530	62833816	+	0	NA	TTS (NR_1TTS) (NR_1)	4673	NR_135128	1E+08	Hs.536982NR_135128	LOC100132-		uncharactcrRNA
chr19-24 84.9575	-0.51169	0.261868	-1.95399	0.050702	0.229262	chr19	24891472	24891808	+	0	NA	IntergeniALR/Alphe	-728193	NR_003602	440153	Hs.53488CNM_001012	ENSG00000HAVCR1P1		hepatitis pseudo
chr14-17 52.64129	-0.62834	0.321596	-1.95381	0.050724	0.229262	chr14	17640155	17640866	+	0	NA	IntergeniALR/Alphe	-960607	NM_001012	440153	Hs.53488CNM_001012	ENSG00000OR11H12		olfactoryprotein-coding
chr14-17 19.51458	-0.9928	0.50884	-1.95111	0.051045	0.230106	chr14	17183616	17185169	+	0	NA	IntergeniALR/Alphe	-416725	NM_001012	440153	Hs.53488CNM_001012	ENSG00000OR11H12		olfactoryprotein-coding
chr21-91 19.51458	-0.9928	0.50884	-1.95111	0.051045	0.230106	chr21	9130908	9131420	+	0	NA	IntergeniMER66A L1	-14203	NR_038327	284801	Hs.370695NR_04009E	ENSG00000MIR663AHC-		MIR663A lncRNA
chr20-26 104.6813	-0.47576	0.244066	-1.94933	0.051257	0.230528	chr20	26601669	26608003	+	0	NA	IntergeniALR/Alphe	-395603	NR_04009E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr21-11 20.03891	-0.97787	0.50168	-1.94919	0.051273	0.230528	chr21	11563639	11564968	+	0	NA	IntergeniALR/Alphe	1042654	NM_19926C	7179	Hs.122988NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem protein-coding
chr18-18 50.10086	-0.64553	0.330859	-1.94804	0.05141	0.230561	chr18	18084962	18085268	+	0	NA	IntergeniALR/Alphe	-2759196	NR_027417	644669	Hs.579474NR_027417	ENSG00000LOC64466E-		ankyrin rpseudo
chr22-137 46.45391	-0.66512	0.341499	-1.94765	0.051456	0.230561	chr22	13739462	13739750	+	0	NA	IntergeniALR/Alphe	-1788553	NM_00100E	81061	Hs.554706NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactoryprotein-coding
chr5-496 113.7347	-0.47028	0.241487	-1.94744	0.051482	0.230561	chr5	49609993	49610315	+	0	NA	IntergeniALR/Alphe	831134	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr22-14 24.42787	-0.89959	0.462116	-1.94667	0.051575	0.230673	chr22	14939638	14939982	+	0	NA	IntergeniALR/Alphe	-588349	NM_00100E	81061	Hs.554706NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactoryprotein-coding
chr1-124 76.20687	-0.53318	0.274039	-1.94563	0.051699	0.230926	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3062382	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMBPI		embigin fpseudo
chr21-12 17.49351	-1.04749	0.538713	-1.94442	0.051845	0.231276	chr21	12304128	12304402	+	0	NA	IntergeniALR/Alphe	-733901	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin rpseudo
chr5-492 58.16465	-0.60581	0.31187	-1.																

chr14-165	18.69302	-0.97021	0.519092	-1.86905	0.061616	0.249486	chr14	16577842	16578052	+	0	NA	IntergeniALR/Alphe	-2023170	NM_001013	440153	Hs.53488CNM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding	
chr21-918	20.76028	-0.92591	0.495507	-1.86862	0.061676	0.249486	chr21	9185036	9185285	+	0	NA	IntergeniLIP4 LII	-55399	NR_038327	1E+08	Hs.487562NM_174948	ENSG00000TEKT4P2	MAFIPL Tf	tektin 4 pseudo	
chr13-165	15.66669	-1.06882	0.572038	-1.86844	0.061701	0.249486	chr13	16938603	16938804	+	0	NA	IntergeniALR/Alphe	-1256594	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA	
chr9-437	21.76554	-0.8992	0.481355	-1.86807	0.061752	0.249486	chr9	43767179	43767781	+	0	NA	IntergeniALR/Alphe	641314	NR_160666	1.03E+08	NR_160669	LOC102724-		methylenepseudo	
chr21-126	30.67091	-0.76709	0.410976	-1.86651	0.061971	0.249516	chr21	12692224	12692900	+	0	NA	IntergeniALR/Alphe	249516	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr20-276	21.79003	-0.89674	0.480688	-1.86552	0.062108	0.249516	chr20	27688376	27688907	+	0	NA	IntergeniALR/Alphe	914024	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo	
chr17-255	45.15023	-0.29423	0.157781	-1.8648	0.062209	0.249516	chr17	25389805	25390063	+	0	NA	IntergeniALR/Alphe	1699307	NR_13567E	1.05E+08	Hs.649918NR_135673	LOC105371-		uncharactncRNA	
chr22-135	20.21982	-0.92914	0.498281	-1.8647	0.062224	0.249516	chr22	13516597	13519725	+	0	NA	IntergeniALR/Alphe	1620755	NR_110761	1.03E+08	Hs.652929NR_110761	LOC102722-		uncharactncRNA	
chr21-128	20.32833	-0.93637	0.502176	-1.86463	0.062233	0.249516	chr21	12877811	12878085	+	0	NA	IntergeniALR/Alphe	-160218	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr1-124	64.61194	-0.54755	0.293688	-1.86438	0.062269	0.249516	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2964628	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1P	-	embigin ipseudo	
chr20-274	17.69333	-0.96561	0.534592	-1.86407	0.062313	0.249516	chr20	27406136	27407637	+	0	NA	IntergeniALR/Alphe	1195779	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo	
chr13-175	31.65447	-0.75319	0.404193	-1.86344	0.0624	0.249516	chr13	17927311	17928745	+	0	NA	IntergeniALR/Alphe	-267269	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA	
chr7-601	21.72213	-0.89652	0.481145	-1.86333	0.06242	0.249516	chr7	60106584	60106948	+	0	NA	IntergeniALR/Alphe	16016584	NR_00115E	441234	Hs.533121NM_00115E	ENSG00000ZNF716	-	zinc fingprotein-coding	
chr5-4754	152.5734	-0.3916	0.210227	-1.86277	0.062495	0.249516	chr5	47541711	47547678	+	0	NA	IntergeniALR/Alphe	-851164	NM_02107E	348980	Hs.353176NM_02107E	ENSG00000HCN1	BCNG-1 B	hyperpolprotein-coding	
chr21-122	28.19062	-0.79267	0.425733	-1.86189	0.062619	0.249516	chr21	12266066	12268779	+	0	NA	IntergeniALR/Alphe	-770744	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr11-51	22.72461	-0.87606	0.470667	-1.86132	0.062699	0.249516	chr11	51575722	51576079	+	0	NA	IntergeniALR/Alphe	1166753	NR_024504	646813	Hs.684175NR_024504	LOC64681-		DExH-box pseudo	
chr5-484	23.7215	-0.86447	0.464582	-1.86075	0.062779	0.249516	chr5	48485068	48485425	+	0	NA	IntergeniALR/Alphe	1956042	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding	
chr19-251	117.0684	-0.43875	0.235798	-1.86069	0.062788	0.249516	chr19	25143539	25143786	+	0	NA	IntergeniALR/Alphe	-980215	NR_00360E	1E+08	Hs.149312NR_00360E	ENSG00000HAVCR1P1	-	hepatitispsudo	
chr9-4384	23.72708	-0.85741	0.460914	-1.86023	0.062852	0.249516	chr9	43844690	43845140	+	0	NA	IntergeniALR/Alphe	718749	NR_160666	1.03E+08	NR_160669	LOC102724-		methylenepseudo	
chr8-858	20.76864	-0.91387	0.491873	-1.85794	0.063178	0.250369	chr8	85807267	85808792	+	0	NA	IntergeniMLT1F1 L	-4468	NR_003594	1E+08	Hs.535055NR_003594	REXO112P	-	REXO1 likpseudo	
chr20-271	23.75157	-0.85517	0.460428	-1.85733	0.063265	0.250369	chr20	27137540	27139324	+	0	NA	IntergeniALR/Alphe	-929199	NR_04009E	284801	Hs.370695NR_04009E	ENSG00000MIR663AHC	-	MIR663A lncRNA	
chr21-915	18.31005	-0.97715	0.526149	-1.85717	0.063286	0.250369	chr21	9134860	9135862	+	0	NA	IntergeniLIMA3 LII	-5600	NR_038327	1E+08	Hs.487562NM_174948	ENSG00000TEKT4P2	MAFIPL Tf	tektin 4 pseudo	
chr14-174	24.22971	-0.84697	0.456237	-1.85644	0.063391	0.250495	chr14	17473467	17475180	+	0	NA	IntergeniALR/Alphe	-1126794	NM_001013	440153	Hs.53488CNM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding	
chr19-265	80.41826	-0.49587	0.267196	-1.85582	0.063479	0.250552	chr19	26504013	26504551	+	0	NA	IntergeniALR/Alphe	-1289149	NR_14673E	1.02E+08	Hs.567934NR_110687	ENSG00000LOC101927-		uncharactncRNA	
chr13-175	41.9063	-0.65732	0.354418	-1.85464	0.063647	0.250786	chr13	17389762	17389987	+	0	NA	IntergeniALR/Alphe	-805423	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA	
chr21-122	23.68089	-0.85843	0.462918	-1.85438	0.063685	0.250786	chr21	12215718	12217633	+	0	NA	IntergeniALR/Alphe	-821491	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr15-194	20.83654	-0.91406	0.493244	-1.85316	0.06386	0.251186	chr15	19471999	19472261	+	0	NA	IntergeniALR/Alphe	-810614	NR_03883E	646096	Hs.448785NR_03883E	ENSG00000CHEK2P2	-	checkpoirpseudo	
chr21-121	22.20306	-0.88287	0.476853	-1.85145	0.064104	0.25126	chr21	12106183	12108626	+	0	NA	IntergeniALR/Alphe	-930762	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr21-104	18.3178	-1.00228	0.541374	-1.85137	0.064116	0.25126	chr21	10459729	10460002	+	0	NA	intron (AluX) SIN	46333	NM_18248E	85319	Hs.545785NM_18248E	BAGE2	CT2.2	BAGE famiprotein-coding	
chrY-568	22.29545	-0.8007	0.475742	-1.8512	0.06414	0.25126	chrY	56855301	56856401	+	0	NA	IntergeniIntergeni	-98404	NM_00584C	10251	Hs.381912NM_00584C	ENSG00000SPRY3	spry-3	sprouty fprotein-coding	
chr20-266	25.78101	-0.82049	0.443272	-1.85099	0.064172	0.25126	chr20	26616967	26617987	+	0	NA	IntergeniALR/Alphe	-408244	NR_04009E	284801	Hs.370695NR_04009E	ENSG00000MIR663AHC	-	MIR663A lncRNA	
chr1-124	98.67546	-0.46682	0.252409	-1.84946	0.064392	0.251683	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2565372	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1P	-	embigin ipseudo	
chr3-908	27.37291	-0.80226	0.433837	-1.84922	0.064427	0.251683	chr3	90835915	90836119	+	0	NA	IntergeniALR/Alphe	1728396	NM_00523E	2042	Hs.123642NM_00523E	ENSG00000EPAH3	EK4 ETK E	EPHF receptor-coding	
chr17-251	77.7682	-0.50231	0.272016	-1.84663	0.064801	0.252857	chr17	25101213	25101447	+	0	NA	IntergeniALR/Alphe	1987911	NR_13567E	1.05E+08	Hs.649918NR_135673	LOC105371-		uncharactncRNA	
chr21-122	26.16676	-0.8154	0.442012	-1.84474	0.065076	0.25364	chr21	12058674	12059558	+	0	NA	IntergeniALR/Alphe	-979050	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr13-175	29.63062	-0.77038	0.41887	-1.83918	0.065888	0.256514	chr13	17383417	17383830	+	0	NA	IntergeniALR/Alphe	-811674	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA	
chr1-1235	37.75115	-0.69268	0.377399	-1.83539	0.066448	0.258017	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	1997057	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1P	-	embigin ipseudo	
chr21-122	30.13325	-0.76351	0.416073	-1.83504	0.066499	0.258017	chr21	12247978	12248388	+	0	NA	IntergeniALR/Alphe	-789893	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr7-5936	169.2198	-0.37825	0.206174	-1.8346	0.066565	0.258017	chr7	59364544	59364859	+	0	NA	IntergeniALR/Alphe	1914524	NM_00115E	441234	Hs.533121NM_00115E	ENSG00000ZNF716	-	zinc fingprotein-coding	
chr18-184	17.64993	-0.99316	0.541465	-1.8342	0.066624	0.258017	chr18	18437833	18438129	+	0	NA	IntergeniALR/Alphe	2673832	NM_00540E	6093	Hs.306307NM_00540E	ENSG00000ROCK1	P160ROCK	Rho assocprotein-coding	
chr1-124	38.92338	-0.67233	0.366628	-1.83382	0.06668	0.258017	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3100324	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1P	-	embigin ipseudo	
chr21-122	52.2572	-0.59115	0.322412	-1.83352	0.066726	0.258017	chr21	12803177	12803466	+	0	NA	IntergeniALR/Alphe	-238485	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo	
chr5-494	76.9327	-0.49791	0.271991	-1.8306	0.067161	0.259405	chr5	49437287	49437564	+	0	NA	IntergeniALR/Alphe	1003863	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding	
chr1-124	34.42977	-0.7067	0.386734	-1.82736	0.067645	0.260607	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3007698	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1P	-	embigin ipseudo	
chr22-145	15.47518	-1.03742	0.567899	-1.82677	0.067734	0.260607	chr22	14950830	14952358	+	0	NA	IntergeniALR/Alphe	-576565	NR_00100E	81061	Hs.55470E	NM_00100E	ENSG00000OR11H1	OR11H12 C	olfactoryprotein-coding
chr10-141	37.44276	-0.68118	0.37294	-1.82651	0.067773	0.260607	chr10	41283017	41283360	+	0	NA	IntergeniALR/Alphe	-1084857	NR_02438E	441666	Hs.255725NR_02438E	ENSG00000LOC44166E	-	zinc fingpseudo	
chr1-124	91.52733	-0.47431	0.25975	-1.82602	0.067847	0.260607	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3026720	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1P	-	embigin ipseudo	
chr8-442	14.99146	-1.06876	0.585308	-1.82599	0.067852	0.260607	chr8	44250250	44250528	+	0	NA	IntergeniALR/Alphe	957947	NM_00100E	34044	Hs.531575NM_00100E	ENSG00000PTEA	A26A1 CT1	POTE ankyprotein-coding	
chr9-437	15.49409	-1.04471	0.572491	-1.82484	0.068025	0.260977	chr9	43734271	43734921	+	0	NA	IntergeniALR/Alphe	68430	NR_160666	1.03E+08	NR_160669	LOC102724-		methylenepseudo	
chr5-485	81.98461	-0.48655	0.266869	-1.82318	0.068276	0.26113	chr5	48596168	48596446	+	0	NA	IntergeniALR/Alphe	1844981	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding	
chr1-1235	59.57788	-0.55539	0.30464	-1.82311	0.068287	0.26113	chr1	1.24E+08	1.24E+08	+	0										



chr10-40c 32.62186	-0.70158	0.397706	-1.76407	0.07772	0.275071	chr10	40601150	40601645	+	0	NA	IntergeniALR/Alphe	1766648	NR_02438C	441666	Hs.255725NR_02438C	ENSG0000CLOC441666-	-	zinc_fingpseudo	
chr7-6031 64.18166	-0.51746	0.293506	-1.76302	0.077897	0.275411	chr7	60310640	60312035	+	0	NA	IntergeniALR/Alphe	2861160	NM_00115E	441234	Hs.533121NM_00115E	ENSG0000CZNF716	-	zinc_fingprotein-coding	
chr20-27c 32.60016	-0.70064	0.397868	-1.76099	0.078241	0.276344	chr20	27091205	27092210	+	0	NA	IntergeniALR/Alphe	-882474	NR_04009E	284801	Hs.370695NR_04009E	ENSG0000CMIR663AHC-	-	MIR663A lncRNA	
chr5-487c 76.06226	-0.51471	0.292566	-1.7593	0.078526	0.277066	chr5	48759336	48759542	+	0	NA	IntergeniALR/Alphe	1681849	NM_19844E	133418	Hs.561411NM_19844E	ENSG0000CEMB	GP70	embigin protein-coding	
chr20-27c 52.70026	-0.56443	0.321347	-1.75646	0.079011	0.278365	chr20	27975181	27976055	+	0	NA	IntergeniALR/Alphe	627047	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo	
chr5-482c 132.062	-0.39178	0.223086	-1.75618	0.079057	0.278365	chr5	48272813	48273035	+	0	NA	IntergeniALR/Alphe	2168364	NM_19844E	133418	Hs.561411NM_19844E	ENSG0000CEMB	GP70	embigin protein-coding	
chr9-638c 22.15013	-0.85643	0.488391	-1.75358	0.079502	0.279444	chr9	63830352	63830595	+	0	NA	IntergeniIntergeni	-10819	NR_03968E	1.01E+08	NR_03968E	ENSG0000CMIR4477A	-	microRNA ncRNA	
chr20-27c 39.33915	-0.63858	0.364271	-1.75305	0.079594	0.279444	chr20	27514264	27515536	+	0	NA	IntergeniALR/Alphe	1087765	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo	
chr12-35c 16.46432	-0.98248	0.560468	-1.75297	0.079608	0.279444	chr12	35302829	35303213	+	0	NA	IntergeniALR/Alphe	1280525	NM_03283A	84920	Hs.102971NM_03283A	ENSG0000CALG10	ALG10A DI	ALG10 alprotein-coding	
chr10-40c 62.19173	-0.50263	0.300776	-1.7498	0.080152	0.281067	chr10	40973814	40974124	+	0	NA	IntergeniALR/Alphe	1394076	NR_02438C	441666	Hs.255725NR_02438C	ENSG0000CLOC441666-	-	zinc_fingpseudo	
chr1-124c 39.0119	-0.65084	0.372078	-1.74921	0.080255	0.281138	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2542846	NR_00395E	647121	Hs.697682NR_00395E	ENSG0000CEMBP1	-	embigin fpseudo	
chr20-28c 34.82947	-0.69221	0.39604	-1.74782	0.080495	0.281693	chr20	28091190	28091526	+	0	NA	IntergeniALR/Alphe	511307	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo	
chr20-27c 28.63646	-0.7358	0.421743	-1.74466	0.081044	0.283324	chr20	27539269	27542138	+	0	NA	IntergeniALR/Alphe	1061962	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo	
chr9-437c 32.02684	-0.70839	0.406373	-1.74321	0.081297	0.283795	chr9	43777409	43777956	+	0	NA	IntergeniALR/Alphe	651516	NR_160669	1.03E+08	NR_160669	LOC102724-	-	methylenepseudo	
chr5-476c 77.22389	-0.4901	0.281205	-1.74284	0.081361	0.283795	chr5	47671646	47671878	+	0	NA	IntergeniALR/Alphe	-1975382	NM_02107E	348980	Hs.35317eNM_02107E	ENSG0000HCN1	BCNG-1 B	hyperpoleprotein-coding	
chr22-14c 15.15067	-0.99942	0.573689	-1.74209	0.081492	0.283795	chr2	14003031	14030862	+	0	NA	IntergeniALR/Alphe	-1497713	NM_00100E	81061	Hs.55470eNM_00100E	ENSG0000COR11H1	OR11H12 C	olfactoryprotein-coding	
chr7-592c 74.75688	-0.48099	0.276118	-1.74199	0.08151	0.283795	chr7	59251595	59251979	+	0	NA	IntergeniALR/Alphe	1801610	NM_00115E	441234	Hs.533121NM_00115E	ENSG0000CZNF716	-	zinc_fingprotein-coding	
chr11-53c 119.0882	-0.40946	0.235251	-1.74052	0.081767	0.284102	chr11	53204993	53205270	+	0	NA	IntergeniALR/Alphe	1398867	NM_00100A	119749	Hs.553564NM_00100A	ENSG0000COR4C46	-	olfactoryprotein-coding	
chr20-26c 27.17755	-0.75273	0.432507	-1.74039	0.081791	0.284102	chr20	26865858	26867743	+	0	NA	IntergeniALR/Alphe	-657567	NR_04009E	284801	Hs.370695NR_04009E	ENSG0000CMIR663AHC-	-	MIR663A lncRNA	
chr22-14c 27.63399	-0.74642	0.42896	-1.74007	0.081847	0.284102	chr22	14404561	14407328	+	0	NA	IntergeniALR/Alphe	-122215	NM_00100E	81061	Hs.55470eNM_00100E	ENSG0000COR11H1	OR11H12 C	olfactoryprotein-coding	
chr19-26c 27.19925	-0.75386	0.433413	-1.73936	0.081972	0.28419	chr19	26084678	26084976	+	0	NA	IntergeniALR/Alphe	-7078604	NR_146733	1.02E+08	Hs.567934NR_146733	ENSG0000CLOC101927-	-	uncharactncRNA	
chr9-434c 28.59027	-0.7366	0.423624	-1.7388	0.08207	0.28419	chr9	43465699	43466367	+	0	NA	IntergeniALR/Alphe	339867	NR_160666	1.03E+08	NR_160669	LOC102724-	-	methylenepseudo	
chr22-12c 15.65051	-0.98359	0.56579	-1.73844	0.082133	0.28419	chr22	12559228	12559535	+	0	NA	IntergeniMLTID LTF	661975	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr21-12c 15.12618	-1.00307	0.577128	-1.73804	0.082204	0.28419	chr21	12972007	12971029	+	0	NA	IntergeniALR/Alphe	-767638	NR_02691E	149992	Hs.55864eNM_153773	ANKRD30BF C21orf99	ankyrin rpseudo		
chr5-487c 56.51088	-0.53828	0.309811	-1.73746	0.082306	0.284255	chr5	48791286	48792197	+	0	NA	IntergeniALR/Alphe	1649547	NM_19844E	133418	Hs.561411NM_19844E	ENSG0000CEMB	GP70	embigin protein-coding	
chr14-17c 15.15346	-0.99398	0.57258	-1.73597	0.082569	0.284877	chr14	17469800	17472362	+	0	NA	IntergeniALR/Alphe	-1130036	NM_00101E	440153	Hs.53488eNM_00101E	ENSG0000COR11H12	-	olfactoryprotein-coding	
chr22-11c 15.67779	-0.97487	0.562648	-1.73264	0.08316	0.285529	chr22	11935389	11935651	+	0	NA	intron (intron)	38559	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr21-11c 25.72143	-0.76845	0.443574	-1.73241	0.0832	0.285529	chr21	11943773	11945248	+	0	NA	IntergeniALR/Alphe	-1093656	NR_02691E	149992	Hs.55864eNM_153773	ANKRD30BF C21orf99	ankyrin rpseudo		
chr22-14c 27.11244	-0.7494	0.432709	-1.73187	0.083297	0.285529	chr22	14416192	14418179	+	0	NA	IntergeniALR/Alphe	-1110664	NM_00100E	81061	Hs.55470eNM_00100E	ENSG0000COR11H1	OR11H12 C	olfactoryprotein-coding	
chr19-26c 70.64792	-0.48859	0.282247	-1.73107	0.08344	0.285529	chr19	26410342	26411379	+	0	NA	IntergeniALR/Alphe	-1382602	NR_146733	1.02E+08	Hs.567934NR_146733	ENSG0000CLOC101927-	-	uncharactncRNA	
chr22-13c 19.85749	-0.88784	0.513085	-1.7304	0.083559	0.285529	chr22	13386009	13386244	+	0	NA	IntergeniALR/Alphe	1488720	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr5-484c 27.76698	-0.75011	0.433509	-1.73032	0.083573	0.285529	chr5	48432744	48433024	+	0	NA	IntergeniALR/Alphe	2008415	NM_19844E	133418	Hs.561411NM_19844E	ENSG0000CEMB	GP70	embigin protein-coding	
chr21-11c 15.17795	-0.99043	0.572461	-1.73012	0.083609	0.285529	chr21	11915885	11915912	+	0	NA	IntergeniALR/Alphe	-1111177	NR_02691E	149992	Hs.55864eNM_153773	ANKRD30BF C21orf99	ankyrin rpseudo		
chr22-14c 15.17795	-0.99043	0.572461	-1.73012	0.083609	0.285529	chr22	14237520	14238209	+	0	NA	IntergeniALR/Alphe	-1290295	NM_00100E	81061	Hs.55470eNM_00100E	ENSG0000COR11H1	OR11H12 C	olfactoryprotein-coding	
chr21-79c 17.67995	-0.91731	0.530622	-1.72875	0.083854	0.285529	chr21	7982709	79893245	+	0	NA	IntergeniALR/Alphe	-153345	NM_00136E	1.03E+08	NM_00133E	ENSG0000KCNE1B	-	potassium protein-coding	
chr18-15c 15.10727	-0.99568	0.57604	-1.7285	0.083899	0.285529	chr18	15689059	15690133	+	0	NA	IntergeniALR/Alphe	346677	NR_027417	644669	Hs.579474NR_027417	ENSG0000CLOC64466E-	-	ankyrin rpseudo	
chr22-13c 25.24329	-0.77453	0.44819	-1.72812	0.083967	0.285529	chr22	13496768	13497424	+	0	NA	IntergeniALR/Alphe	1599690	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr22-13c 24.12394	-0.79247	0.459018	-1.72644	0.084268	0.285529	chr22	13637866	13638442	+	0	NA	IntergeniALR/Alphe	1740748	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr3-19c 16.68026	-0.9418	0.545576	-1.72625	0.084303	0.285529	chr3	91987861	91988216	+	0	NA	IntergeniALR/Alphe	1986044	NM_00131A	5627	Hs.64016	NM_00031E	ENSG0000CPRO1	PRO1 PS21	protein fprotein-coding
chr20-27c 22.71401	-0.812	0.470669	-1.72521	0.08449	0.285529	chr20	27533374	27533614	+	0	NA	IntergeniALR/Alphe	1069171	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo	
chr22-15c 17.70444	-0.9143	0.530084	-1.72482	0.084559	0.285529	chr22	15021994	15022633	+	0	NA	IntergeniALR/Alphe	-505846	NM_00100E	81061	Hs.55470eNM_00100E	ENSG0000COR11H1	OR11H12 C	olfactoryprotein-coding	
chr5-488c 20.16024	-0.86182	0.499888	-1.72403	0.084703	0.285529	chr5	48861644	48861965	+	0	NA	IntergeniALR/Alphe	1579484	NM_19844E	133418	Hs.561411NM_19844E	ENSG0000CEMB	GP70	embigin protein-coding	
chr14-16c 16.60958	-0.94652	0.549302	-1.72314	0.084863	0.285529	chr14	16821092	16822416	+	0	NA	IntergeniALR/Alphe	-1779363	NM_00101E	440153	Hs.53488eNM_00101E	ENSG0000COR11H12	-	olfactoryprotein-coding	
chr10-40c 42.13335	-0.61133	0.354781	-1.72312	0.084866	0.285529	chr10	40594513	40596731	+	0	NA	IntergeniALR/Alphe	1772423	NR_02438C	441666	Hs.255725NR_02438C	ENSG0000CLOC441666-	-	zinc_fingpseudo	
chr13-17c 16.18042	-0.95525	0.55446	-1.72284	0.084917	0.285529	chr13	17408988	17409414	+	0	NA	IntergeniALR/Alphe	-782608	NR_02727E	26080	Hs.448582NR_02727E	ENSG0000FAM230C	LINC00281	family wincRNA	
chr21-88c 19.22845	-0.88013	0.510939	-1.72258	0.084965	0.285529	chr21	8833564	8834663	+	0	NA	IntergeniLIMC4a LJ	-152886	NR_037421	1.01E+08	NR_037421	ENSG0000CMIR3648-	IMR3648 E	microRNA ncRNA	
chr22-13c 17.20459	-0.92607	0.537716	-1.72223	0.085027	0.285529	chr22	13701894	13703219	+	0	NA	IntergeniALR/Alphe	1805150	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr6-596c 18.13638	-0.90296	0.524343	-1.72209	0.085053	0.285529	chr6	59683252	59683754	+	0	NA	IntergeniALR/Alphe	-1722057	NR_13299E	1.07E+08	Hs.56153eNR_13299E	ENSG0000CLOC10068C-	-	long intencRNA	
chr22-12c 18.70691	-0.88837	0.515983	-1.7217	0.085123	0.285529	chr22	12868316	12872660	+	0	NA	IntergeniIntergeni	973082	NR_110761	1.03E+08	Hs.65292eNR_110761	LOC102722-	-	uncharactncRNA	
chr17-26c 101.6333	-0.42273	0.245542	-1.72163	0.085137	0.285529	chr17	26468498	26468746	+	0	NA	IntergeniALR/Alphe	620619	NR_13567E	1.05E+08	Hs.64991eNR_135673	LOC105371-	-	uncharactncRNA	
chr21-10c 22.12178	-0.82069	0.476924	-1.72079	0.085289	0.285529	chr21	12845730	12846119	+	0	NA	IntergeniALR/Alphe	-192244	NR_02691E	149992	Hs.55864eNM_153773	ANKRD30BF C21orf99	ankyrin rpseudo		
chr10-40c 34.82942	-0.66227																			

chr13-171 25.88064	-0.73218	0.440951	-1.66045	0.096824	0.303734	chr13	17114028	17115564	+	0 NA	IntergeniALR/Alphe	-1080501 NR_027278	26080 Hs. 448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr10-405 64.08984	-0.49095	0.295839	-1.65952	0.097012	0.303734	chr10	40923972	40925120	+	0 NA	IntergeniALR/Alphe	1443499 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC441666	-	zinc fingpseudo
chr5-483 36.59834	-0.64066	0.38653	-1.65745	0.097428	0.303734	chr5	48321979	48322219	+	0 NA	IntergeniALR/Alphe	2119189 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr15-17 25.3563	-0.73832	0.445515	-1.65724	0.097471	0.303734	chr15	17093382	17093632	+	0 NA	IntergeniALR/Alphe	-3189237 NR_03883E	646096 Hs. 448785NR_03883E	ENSG00000CHEK2P2	-	checkpoirpseudo
chr1-1226 55.48944	-0.51937	0.313429	-1.65706	0.097507	0.303734	chr1	1639663	1639695E	+	0 NA	IntergeniALR/Alphe	1639663 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMB1	-	embigin fpseudo
chr1-124 33.59761	-0.64586	0.390147	-1.65544	0.097835	0.303734	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alphe	2993717 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMB1	-	embigin fpseudo
chr20-284 22.84594	-0.77621	0.468907	-1.65536	0.097851	0.303734	chr20	28417539	28417949	+	0 NA	IntergeniALR/Alphe	184921 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr20-276 22.87043	-0.77392	0.467599	-1.65509	0.097907	0.303734	chr20	27658635	27659718	+	0 NA	IntergeniALR/Alphe	943489 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr8-8564 15.89653	-0.92687	0.560354	-1.65408	0.098111	0.303734	chr8	85645401	85649011	+	0 NA	Intergeni Intergeni	8470 NR_003594	1E+08 Hs. 535055NR_003594	REXO1L2P	-	REXO1 likpseudo
chr20-275 24.83197	-0.74473	0.450581	-1.65282	0.098368	0.303734	chr20	27537881	27538227	+	0 NA	IntergeniALR/Alphe	1064561 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr3-9184 33.14117	-0.64951	0.392976	-1.65258	0.098371	0.303734	chr3	91846693	91847208	+	0 NA	IntergeniALR/Alphe	1212731 NM_001314	5627 Hs. 64016 NM_00031E	ENSG00000PROS1	PROS PS21	protein Sprotein-coding
chr13-17 22.82145	-0.77854	0.471047	-1.65278	0.098375	0.303734	chr13	17029104	17029907	+	0 NA	IntergeniALR/Alphe	-1165792 NR_027278	26080 Hs. 448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr17-251 101.4624	-0.40937	0.247743	-1.65241	0.098452	0.303734	chr17	25139805	25140052	+	0 NA	IntergeniALR/Alphe	1949313 NR_135673	1.05E+08 Hs. 649918NR_135673	LOC105371	-	uncharactncRNA
chr19-267 69.52076	-0.46927	0.284143	-1.65153	0.09863	0.303734	chr19	26754027	26754268	+	0 NA	IntergeniALR/Alphe	-1039284 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927	-	uncharactncRNA
chr19-254 27.96301	-0.73063	0.442516	-1.65109	0.098721	0.303734	chr19	25496035	25496273	+	0 NA	IntergeniALR/Alphe	-1332707 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG00000HAVCRIP1	-	hepatitispseudo
chr7-5917 15.39947	-0.9351	0.566566	-1.65047	0.098848	0.303734	chr7	59172526	59172973	+	0 NA	IntergeniALR/Alphe	1722572 NM_00115E	441234 Hs. 533121NM_00115E	ENSG00000ZNF716	-	zinc fingprotein-coding
chr3-758 16.37746	-0.90738	0.549861	-1.6502	0.098902	0.303734	chr3	75859662	75860574	+	0 NA	Intergeni Intergeni	-74569 NR_00129C	1E+08 Hs. 556877NM_00112E	ENSG00000ZNF717	OB1 X17	zinc fingprotein-coding
chr10-41 22.37059	-0.77955	0.472411	-1.65016	0.09891	0.303734	chr10	41537733	41538078	+	0 NA	IntergeniALR/Alphe	830140 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC441666	-	zinc fingpseudo
chr4-4957 19.88471	-0.82602	0.500623	-1.64998	0.098947	0.303734	chr4	49572377	49578989	+	0 NA	IntergeniMSTA-int1	589041 NM_00128E	80157 Hs. 479702NM_02508E	ENSG00000CWH43	CWH43-C	cell wallprotein-coding
chr20-296 20.36285	-0.81705	0.495215	-1.64988	0.098968	0.303734	chr20	29873133	29882324	+	0 NA	Intergeni Intergeni	-2656 NR_03968E	1.01E+08 NR_03968E	ENSG00000MIR4477B	-	microRNA ncRNA
chr19-265 71.91035	-0.47166	0.286066	-1.64878	0.099192	0.303734	chr19	26358831	26359037	+	0 NA	IntergeniALR/Alphe	-1434497 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927	-	uncharactncRNA
chr21-117 20.38735	-0.81447	0.49399	-1.64875	0.099198	0.303734	chr21	11703771	11703970	+	0 NA	IntergeniALR/Alphe	1182356 NM_19926C	7179 Hs. 122986NM_19925E	ENSG00000TPTE	CT44 PTEN	transmem protein-coding
chr5-493 92.925	-0.4234	0.256808	-1.6487	0.099208	0.303734	chr5	49351635	49351914	+	0 NA	IntergeniALR/Alphe	1089514 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr8-857 21.34363	-0.79793	0.484022	-1.64854	0.099242	0.303734	chr8	85772118	85778993	+	0 NA	non-codiri non-codiri	538 NR_003594	1E+08 Hs. 535055NR_003594	REXO1L2P	-	REXO1 likpseudo
chr21-12 15.87761	-0.91988	0.558016	-1.64848	0.099255	0.303734	chr21	12015277	12017193	+	0 NA	IntergeniALR/Alphe	-1021931 NR_02691E	149992 Hs. 558645NM_153773	ANKRD30BF C21orf99	ankyrin rpseudo	
chr22-128 17.92596	-0.86842	0.527128	-1.64746	0.099463	0.303734	chr22	12873492	12878924	+	0 NA	IntergeniLIP4 LID	978802 NR_110761	1.03E+08 Hs. 652929NR_110761	LOC10272E	-	uncharactncRNA
chr9-4351 19.90921	-0.82338	0.499825	-1.64734	0.099489	0.303734	chr9	43516621	43516925	+	0 NA	IntergeniALR/Alphe	390167 NR_16066E	1.03E+08 NR_16066E	LOC10272E	-	methylencpseudo
chr20-285 19.35759	-0.84098	0.510516	-1.64732	0.099492	0.303734	chr20	28330403	28331249	+	0 NA	IntergeniALR/Alphe	271839 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr21-884 18.3824	-0.85566	0.519482	-1.64713	0.099531	0.303734	chr21	8849453	8850376	+	0 NA	Intergeni Intergeni	-137085 NR_037421	1.01E+08 NR_037421	ENSG00000MIR3648	MIR3648	microRNA ncRNA
chr13-17 32.51888	-0.65941	0.400349	-1.6471	0.099538	0.303734	chr13	17359794	17360299	+	0 NA	IntergeniALR/Alphe	-835251 NR_027278	26080 Hs. 448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr22-14 20.83431	-0.83103	0.504634	-1.64679	0.099601	0.303734	chr22	14590484	14590768	+	0 NA	IntergeniALR/Alphe	-937533 NM_00100E	81061 Hs. 554706NM_00100E	ENSG00000OR11H1	OR11H12	Colfactoryprotein-coding
chr13-17 19.83852	-0.8272	0.502391	-1.64653	0.099654	0.303734	chr13	17654342	17657039	+	0 NA	IntergeniALR/Alphe	-539607 NR_027278	26080 Hs. 448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr21-927 15.92381	-0.91835	0.557905	-1.64606	0.099751	0.303734	chr21	9275740	9276951	+	0 NA	Intergeni Intergeni	-146584 NR_03832E	1E+08 Hs. 487562NM_17494E	ENSG00000TEKT4P2	MAFIPL T	tektin 4 pseudo
chr21-91 19.43107	-0.83277	0.506301	-1.6448	0.10001	0.303734	chr21	9186026	9190432	+	0 NA	IntergeniLIP4 LID	-58468 NR_03832E	1E+08 Hs. 487562NM_17494E	ENSG00000TEKT4P2	MAFIPL T	tektin 4 pseudo
chrY-568 19.43107	-0.83277	0.506301	-1.6448	0.10001	0.303734	chrY	56868600	56875371	+	0 NA	Intergeni Intergeni	-82270 NR_00584C	10251 Hs. 381912NM_00584C	ENSG00000SPRY3	spry-3	sprouty fprotein-coding
chr21-10 18.88503	-0.84235	0.512463	-1.64372	0.100234	0.303734	chr21	10368104	10368958	+	0 NA	Intergeni Intergeni	-44989 NM_001187	574 Hs. 545785NM_001187	BAGE	BAGE1 CTE2B	melaninprotein-coding
chr13-17 17.35823	-0.8783	0.534435	-1.64341	0.100297	0.303734	chr13	17392507	17393993	+	0 NA	IntergeniALR/Alphe	-802047 NR_027278	26080 Hs. 448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr20-27 18.83326	-0.8524	0.518692	-1.64336	0.100308	0.303734	chr20	27099228	27102270	+	0 NA	IntergeniALR/Alphe	-891516 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AH	MIR663A	lncRNA
chr20-27 19.36317	-0.83245	0.506554	-1.64336	0.100309	0.303734	chr20	27389969	27392240	+	0 NA	IntergeniALR/Alphe	-1721071 NM_00101E	440153 Hs. 534888NM_00101E	ENSG00000OR11H12	-	olfactoryprotein-coding
chr4-5904 18.3607	-0.85407	0.519884	-1.64282	0.100421	0.303734	chr4	59041222	59042642	+	0 NA	IntergeniALR/Alphe	-1080468 NR_13299E	1.07E+08 Hs. 561535NR_125727	ENSG00000LINC0068C	-	long intencRNA
chr5-484 46.92089	-0.55542	0.338091	-1.64281	0.100423	0.303734	chr5	48445423	48454422	+	0 NA	IntergeniALR/Alphe	-1089696 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr20-277 32.79223	-0.66325	0.403865	-1.64226	0.100536	0.303734	chr20	27779784	27780072	+	0 NA	IntergeniALR/Alphe	822737 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr14-16 21.29464	-0.80295	0.488988	-1.64206	0.100578	0.303734	chr14	16515439	16515800	+	0 NA	IntergeniALR/Alphe	-2085498 NM_00101E	440153 Hs. 534888NM_00101E	ENSG00000OR11H12	-	olfactoryprotein-coding
chr12-35 19.97431	-0.82788	0.504484	-1.64104	0.100789	0.303734	chr12	35315739	35316190	+	0 NA	IntergeniALR/Alphe	1293468 NM_032834	84920 Hs. 102971NM_032834	ENSG00000ALG10	ALG10A DIALG10	alprotein-coding
chr6-586 23.32966	-0.76247	0.464766	-1.64054	0.100893	0.303734	chr6	58690312	58691148	+	0 NA	IntergeniALR/Alphe	-729284 NR_13299E	1.07E+08 Hs. 561535NR_125727	ENSG00000LINC0068C	-	long intencRNA
chr1-123 20.91447	-0.80099	0.488302	-1.64036	0.10093	0.303734	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1769817 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMB1	-	embigin fpseudo
chr20-268 23.8078	-0.75618	0.461225	-1.63951	0.101107	0.303734	chr20	26848548	26848774	+	0 NA	IntergeniALR/Alphe	-639428 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AH	MIR663A	lncRNA
chr20-268 19.8658	-0.82043	0.500462	-1.63934	0.101142	0.303734	chr20	26892280	26893265	+	0 NA	IntergeniALR/Alphe	-683539 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AH	MIR663A	lncRNA
chr5-488 63.48529	-0.48389	0.295207	-1.63915	0.101182	0.303734	chr5	48850687	48851635	+	0 NA	IntergeniALR/Alphe	1590127 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr10-41 35.61092	-0.62757	0.383187	-1.63775	0.101473	0.303734	chr10	41295912	41296133	+	0 NA	IntergeniALR/Alphe	1072023 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC441666	-	zinc fingpseudo
chr7-5954 45.68736	-0.56101	0.342564	-													



chr10-414	29.99686	-0.67724	0.429912	-1.57529	0.115189	0.320691	chr10	41481944	41482143	+	0	NA	IntergeniALR/Alphe	886002	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud		
chr16-368	20.08175	-0.78951	0.501224	-1.57517	0.115216	0.320691	chr16	36858852	36859102	+	0	NA	IntergeniALR/Alphe	112425	NR_03398E	400533	Hs.499135	NR_03398E	ENSG0000C.LINC02167	-	long	intencRNA		
chr20-268	20.06005	-0.78801	0.500416	-1.57471	0.115324	0.320691	chr20	26849707	26851918	+	0	NA	IntergeniALR/Alphe	-641579	NR_04009E	284801	Hs.370695	NR_04009E	ENSG0000C.MIR663AHC	-	MIR663A	lncRNA		
chr10-121	19.6281	-0.79515	0.505609	-1.57434	0.11541	0.320691	chr10	1.26E+08	1.26E+08	+	0	NA	intron (N	8851	NM_00136E	92565	Hs.352591	NM_14523E	ENSG0000C.FANK1	HSD13		fibronect	protein-coding	
chr5-49084	20.54098	-0.77609	0.493355	-1.57308	0.1157	0.320691	chr5	49117822	49118084	+	0	NA	IntergeniALR/Alphe	1323335	NM_19844E	133418	Hs.561411	NM_19844E	ENSG0000C.EMB	GP70		embigin	protein-coding	
chr22-148	21.9971	-0.75624	0.480754	-1.57303	0.115713	0.320691	chr22	14850201	14850442	+	0	NA	IntergeniALR/Alphe	-677838	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG0000C.COR1IH1	OR11H12		Colfatory	protein-coding	
chr22-144	29.80925	-0.64834	0.412355	-1.57228	0.115885	0.320691	chr22	14362795	14363344	+	0	NA	IntergeniALR/Alphe	-116590	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG0000C.COR1IH1	OR11H12		Colfatory	protein-coding	
chr1-1228	37.05366	-0.58619	0.373017	-1.57148	0.116071	0.320691	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1282941	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1P1	-	embigin	pseudo		
chr5-4918	19.07928	-0.80788	0.514109	-1.57142	0.116084	0.320691	chr5	49186256	49186517	+	0	NA	IntergeniALR/Alphe	1254902	NM_19844E	133418	Hs.561411	NM_19844E	ENSG0000C.EMB	GP70		embigin	protein-coding	
chr13-179	60.919	-0.78946	0.502636	-1.57063	0.116267	0.320691	chr13	17231269	17233559	+	0	NA	IntergeniALR/Alphe	-962283	NR_02727E	26080	Hs.448582	NR_02727E	ENSG0000C.FAM230C	LINC00281	family	wincRNA		
chr21-122	20.58996	-0.77103	0.491027	-1.57024	0.116358	0.320691	chr21	12274782	12276093	+	0	NA	IntergeniALR/Alphe	-762729	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30BF.C21orf99	ankryn	rpseudo			
chr18-155	15.09667	-0.89768	0.571735	-1.5701	0.116392	0.320691	chr18	15512512	15517435	+	0	NA	IntergeniALR/Alphe	-189054	NR_02741E	644669	Hs.579474	NR_02741E	ENSG0000C.LOC64466E	-	ankryn	rpseudo		
chr9-440	15.09667	-0.89768	0.571735	-1.5701	0.116392	0.320691	chr9	44023347	44026039	+	0	NA	IntergeniALR/Alphe	898527	NR_16066E	1.03E+08	NR_160669	LOC102724	-	methylene	pseudo			
chr20-274	21.99989	-0.75247	0.47927	-1.57003	0.116407	0.320691	chr20	27484652	27487833	+	0	NA	IntergeniALR/Alphe	1116395	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGC1P	-	FSHD	regipseudo		
chr19-265	55.02139	-0.49831	0.31744	-1.56976	0.11647	0.320691	chr19	26390793	26391708	+	0	NA	IntergeniALR/Alphe	-1402181	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG0000C.LOC101927	-	uncharact	ncRNA		
chr5-4762	23.12203	-0.73129	0.465895	-1.56965	0.116496	0.320691	chr5	47690718	47690982	+	0	NA	IntergeniALR/Alphe	-1994470	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG0000C.HCN1	BCNG-1		BC	hyperpole	protein-coding
chr21-122	24.93104	-0.72531	0.462104	-1.56959	0.116511	0.320691	chr21	12273736	12273942	+	0	NA	IntergeniALR/Alphe	-764327	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30BF.C21orf99	ankryn	rpseudo			
chr1-2367	21.57073	-0.75434	0.480887	-1.56865	0.11673	0.320691	chr1	2.37E+08	2.37E+08	+	0	NA	intron (N	27429	NM_00127E	88	Hs.49817E	NM_00110E	ENSG0000C.ACTN2	CMD1AA		C	actinin	aprotein-coding
chr22-145	17.10161	-0.84333	0.537629	-1.56861	0.116739	0.320691	chr22	14535855	14536750	+	0	NA	IntergeniALR/Alphe	-991857	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG0000C.COR1IH1	OR11H12		Colfatory	protein-coding	
chr20-265	16.09914	-0.86874	0.553831	-1.56861	0.116739	0.320691	chr20	26904891	26906112	+	0	NA	IntergeniALR/Alphe	-696268	NR_04009E	284801	Hs.370695	NR_04009E	ENSG0000C.MIR663AHC	-	MIR663A	lncRNA		
chr17-245	20.04114	-0.78242	0.498811	-1.56857	0.116747	0.320691	chr17	24921274	24921533	+	0	NA	IntergeniALR/Alphe	2167838	NR_135673	1.05E+08	Hs.56491E	NR_135673	LOC105371	-	uncharact	ncRNA		
chr21-104	15.621	-0.88197	0.562322	-1.56844	0.116779	0.320691	chr21	10447517	10448766	+	0	NA	intron (N	34609	NM_18248E	85319	Hs.54578E	NM_18248E	BAGE2	CT2.2	2	BAGE	fami	protein-coding
chr3-9218	15.57481	-0.8835	0.563417	-1.5681	0.116857	0.320691	chr3	92184253	92194667	+	0	NA	IntergeniALR/Alphe	1789621	NM_001314	5627	Hs.64016	NM_00031E	ENSG0000C.PROS1	PROS PS21	protein	S	protein-coding	
chr20-275	19.13105	-0.79805	0.509029	-1.56779	0.11693	0.320691	chr20	27989115	27991056	+	0	NA	IntergeniALR/Alphe	612600	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGC1P	-	FSHD	regipseudo		
chr13-167	24.0566	-0.71892	0.45857	-1.56773	0.116943	0.320691	chr13	16779623	16779842	+	0	NA	IntergeniALR/Alphe	-1415565	NR_02727E	26080	Hs.448582	NR_02727E	ENSG0000C.FAM230C	LINC00281	family	wincRNA		
chr20-276	16.57728	-0.85635	0.546255	-1.56767	0.116958	0.320691	chr20	27591933	27593508	+	0	NA	IntergeniALR/Alphe	1009945	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGC1P	-	FSHD	regipseudo		
chr9-6062	17.12052	-0.84991	0.542185	-1.56757	0.116981	0.320691	chr9	60623190	60625999	+	0	NA	IntergeniALR/Alphe	-2896233	NM_00111E	727905	Hs.645497	NM_00111E	ENSG0000C.SPATA31A	FAM75A5	SPATA31	s	protein-coding	
chr9-4398	22.98066	-0.73769	0.470662	-1.56735	0.117033	0.320691	chr9	43981511	43981991	+	0	NA	IntergeniALR/Alphe	855585	NR_16066E	1.03E+08	NR_160669	LOC102724	-	methylene	pseudo			
chr20-288	20.54377	-0.77211	0.492733	-1.567	0.117116	0.320691	chr20	28876175	28877139	+	0	NA	IntergeniALR/Alphe	-203733	NR_13231E	1.03E+08	NR_132316	FRG1DP	-	FSHD	regipseudo			
chr21-114	20.54377	-0.77211	0.492733	-1.567	0.117116	0.320691	chr21	11472981	11473951	+	0	NA	IntergeniALR/Alphe	917232	NM_19926E	7179	Hs.12298E	NM_19925E	ENSG0000C.TPTE	CT44		PTEN	transmem	protein-coding
chr20-271	20.51928	-0.77465	0.494378	-1.56692	0.117133	0.320691	chr20	27104308	27107213	+	0	NA	IntergeniALR/Alphe	-896527	NR_04009E	284801	Hs.370695	NR_04009E	ENSG0000C.MIR663AHC	-	MIR663A	lncRNA		
chr10-412	30.31467	-0.64094	0.49095	-1.56689	0.11714	0.320691	chr10	41250085	41250665	+	0	NA	IntergeniALR/Alphe	1117670	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud		
chr19-265	56.33499	-0.48629	0.310457	-1.56636	0.117264	0.320691	chr19	26572432	26573801	+	0	NA	IntergeniALR/Alphe	-1220315	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG0000C.LOC101927	-	uncharact	ncRNA		
chr22-120	18.12858	-0.81795	0.52244	-1.56564	0.117432	0.320691	chr22	12048847	12049289	+	0	NA	IntergeniL3 LINE(C	151662	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272E	-	uncharact	ncRNA		
chr22-141	18.12858	-0.81795	0.52244	-1.56564	0.117432	0.320691	chr22	14169500	14170799	+	0	NA	IntergeniALR/Alphe	-1358010	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG0000C.COR1IH1	OR11H12		Colfatory	protein-coding	
chr21-127	16.60177	-0.85319	0.544968	-1.56557	0.117449	0.320691	chr21	12747617	12748120	+	0	NA	IntergeniALR/Alphe	-290271	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30BF.C21orf99	ankryn	rpseudo			
chr20-275	18.53603	-0.81239	0.518946	-1.56546	0.117474	0.320691	chr20	27932864	27934346	+	0	NA	IntergeniALR/Alphe	669060	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGC1P	-	FSHD	regipseudo		
chr9-4428	18.53603	-0.81239	0.518946	-1.56546	0.117474	0.320691	chr9	44292218	44292667	+	0	NA	IntergeniALR/Alphe	1166276	NR_16066E	1.03E+08	NR_160669	LOC102724	-	methylene	pseudo			
chr22-148	19.03866	-0.80043	0.511517	-1.56481	0.117628	0.320691	chr22	14863795	14865314	+	0	NA	IntergeniALR/Alphe	-663605	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG0000C.COR1IH1	OR11H12		Colfatory	protein-coding	
chr20-278	18.0334	-0.82506	0.527286	-1.56473	0.117646	0.320691	chr20	27840066	27843246	+	0	NA	IntergeniALR/Alphe	761009	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGC1P	-	FSHD	regipseudo		
chr22-148	16.12363	-0.86549	0.553141	-1.56468	0.117659	0.320691	chr22	14884859	14889386	+	0	NA	IntergeniALR/Alphe	-639237	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG0000C.COR1IH1	OR11H12		Colfatory	protein-coding	
chr14-177	29.26321	-0.6511	0.416231	-1.56428	0.117751	0.320691	chr14	17777773	17793281	+	0	NA	IntergeniALR/Alphe	-822590	NM_00101E	440153	Hs.53488E	NM_00101E	ENSG0000C.COR1IH12	-	olfactory	protein-coding		
chr10-412	19.55463	-0.80351	0.513888	-1.56359	0.117915	0.320691	chr10	41278530	41278819	+	0	NA	IntergeniALR/Alphe	1089371	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud		
chr21-114	15.55311	-0.88165	0.564049	-1.56307	0.118036	0.320691	chr21	11450003	11450297	+	0	NA	IntergeniALR/Alphe	928636	NM_19926E	7179	Hs.12298E	NM_19925E	ENSG0000C.TPTE	CT44		PTEN	transmem	protein-coding
chr14-18	15.09946	-0.89229	0.517101	-1.56265	0.118134	0.320691	chr14	18062304	18063213	+	0	NA	IntergeniALR/Alphe	-538359	NM_00101E	440153	Hs.53488E	NM_00101E	ENSG0000C.COR1IH12	-	olfactory	protein-coding		
chr5-4865	35.59196	-0.59499	0.380769	-1.56261	0.118144	0.320691	chr5	48696127	48696344	+	0	NA	IntergeniALR/Alphe	1745053	NM_19844E	133418	Hs.561411	NM_19844E	ENSG0000C.EMB	GP70		embigin	protein-coding	
chr6-586E	19.51123	-0.80036	0.512221	-1.56252	0.118165	0.320691	chr6	58662243	58665899	+	0	NA	IntergeniALR/Alphe	-702470	NR_13299E	1.07E+08	Hs.56153E	NR_12572E	ENSG0000C.LINC0068C	-	long	intencRNA		
chr22-128	17.65044	-0.82813	0.530124	-1.56215	0.118252	0.320691	chr22	12881981	12884494	+	0	NA	IntergeniALR/Alphe	985831	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272E	-	uncharact	ncRNA		

chr20-267 22.36278	-0.71174	0.472358	-1.50677	0.131869	0.337541	chr20	26718733	26719245	+	0 NA	IntergeniALR/Alphe	-509756 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr10-405 20.7842	-0.74055	0.491598	-1.50641	0.131961	0.337541	chr10	40966719	40967697	+	0 NA	IntergeniALR/Alphe	1400837 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC441666-	zinc fingpseudo	
chr21-917 21.33582	-0.72676	0.482462	-1.50635	0.131978	0.337541	chr21	9170867	9171997	+	0 NA	Intergeni Intergeni	-41671 NR_038327	1E+08 Hs. 487562NM_17494E	ENSG00000TEK74P2	MAFIPL TE	tektin 4 pseudo
chr10-402 48.84729	-0.5013	0.33283	-1.50618	0.132021	0.337541	chr10	40267010	40269017	+	0 NA	IntergeniALR/Alphe	1571420 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5 FKSG74	ACTR3B	pspseudo
chr21-121 33.38891	-0.5978	0.397301	-1.50568	0.132148	0.337614	chr21	12199547	12199866	+	0 NA	IntergeniALR/Alphe	838960 NR_02691E	149992 Hs. 558645NM_153773	ANKRD30BF C21orf99	ankyrin rpsudo	uncharactncRNA
chr19-265 30.58517	-0.61387	0.408129	-1.5041	0.132555	0.337827	chr19	26531815	26532040	+	0 NA	IntergeniALR/Alphe	-1261504 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr13-172 23.44547	-0.71967	0.478843	-1.50293	0.132857	0.337827	chr13	17296206	17296588	+	0 NA	IntergeniALR/Alphe	-898900 NR_02727E	26080 Hs. 448582NR_02727E	ENSG00000FAM230C	LINC00281	family wincRNA
chr19-265 70.5566	-0.4257	0.283337	-1.50245	0.132998	0.337827	chr19	26919480	26920402	+	0 NA	IntergeniALR/Alphe	-873490 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr20-268 21.81675	-0.71701	0.47732	-1.50216	0.133055	0.337827	chr20	26832769	26834323	+	0 NA	IntergeniALR/Alphe	-624313 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr3-2697 21.72157	-0.72274	0.481181	-1.50201	0.133096	0.337827	chr1	2697006	26978939	+	0 NA	intron (n intron (n	-64435 NR_033467	79258 Hs. 591452NM_033467	ENSG00000MMEL1	MMEL2 NEF	membrane protein-coding
chr21-122 21.72157	-0.72274	0.481181	-1.50201	0.133096	0.337827	chr21	12009315	12010639	+	0 NA	IntergeniALR/Alphe	-1028189 NR_02691E	149992 Hs. 558645NM_153773	ANKRD30BF C21orf99	ankyrin rpsudo	
chr17-237 28.48227	-0.63278	0.421625	-1.50082	0.133403	0.337827	chr17	23733642	23733865	+	0 NA	IntergeniALR/Alphe	1210642 NM_00119C	1E+08 Hs. 740182NM_00119C	ENSG00000MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr10-412 20.83598	-0.73164	0.487852	-1.49971	0.133689	0.337827	chr10	41046158	41046373	+	0 NA	IntergeniALR/Alphe	1321780 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC441666-	zinc fingpseudo	
chr21-121 19.80901	-0.74886	0.499732	-1.49851	0.134	0.337827	chr21	12725267	12726745	+	0 NA	IntergeniALR/Alphe	-312160 NR_02691E	149992 Hs. 558645NM_153773	ANKRD30BF C21orf99	ankyrin rpsudo	
chr22-142 18.80375	-0.76956	0.514239	-1.49651	0.134522	0.337827	chr22	14234351	14236688	+	0 NA	IntergeniALR/Alphe	-1292640 NM_00100E	81061 Hs. 554706NM_00100E	ENSG00000COR11H1	OR11H12 Col	factoryprotein-coding
chr7-5807 18.80375	-0.76956	0.514239	-1.49651	0.134522	0.337827	chr7	58071938	58072207	+	0 NA	Intergeni Intergeni	-821895 NM_00115E	441234 Hs. 533121NM_00115E	ENSG00000ZNF716	-	zinc fingprotein-coding
chr22-142 19.20648	-0.63919	0.427195	-1.49625	0.134588	0.337827	chr22	14662843	14663124	+	0 NA	IntergeniALR/Alphe	-865176 NM_00100E	81061 Hs. 554706NM_00100E	ENSG00000COR11H1	OR11H12 Col	factoryprotein-coding
chr14-172 19.73833	-0.75261	0.503576	-1.49453	0.135038	0.337827	chr14	17226564	17227753	+	0 NA	IntergeniALR/Alphe	-1373959 NM_00101E	440153 Hs. 534888NM_00101E	ENSG00000COR11H12	-	olfactoryprotein-coding
chr10-415 19.78731	-0.74736	0.500072	-1.49445	0.135044	0.337827	chr10	41529680	41532258	+	0 NA	IntergeniALR/Alphe	837076 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC441666-	zinc fingpseudo	
chr13-175 18.32561	-0.77794	0.52071	-1.49401	0.135174	0.337827	chr13	17532823	17533695	+	0 NA	IntergeniALR/Alphe	-662038 NR_02727E	26080 Hs. 448582NR_02727E	ENSG00000FAM230C	LINC00281	family wincRNA
chr20-267 27.5232	-0.64182	0.42965	-1.49382	0.135223	0.337827	chr20	26841191	26842064	+	0 NA	IntergeniALR/Alphe	-632394 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr1-125 18.80654	-0.76522	0.512394	-1.49343	0.135326	0.337827	chr1	1.25E+08	1.25E+08	+	0 NA	Intergeni Intergeni	3562341 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMB1P1	-	embigin rpsudo
chr10-402 18.80654	-0.76522	0.512394	-1.49343	0.135326	0.337827	chr10	40216834	40218898	+	0 NA	IntergeniALR/Alphe	1521270 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5 FKSG74	ACTR3B	pspseudo
chr3-757 18.80654	-0.76522	0.512394	-1.49343	0.135326	0.337827	chr3	75709189	75713774	+	0 NA	IntergeniMER101-ir	-26799 NR_03623E	1E+08 Hs. 530638NM_001511E	ENSG00000MIR4273	-	microRNA ncRNA
chr20-288 18.30391	-0.77632	0.519853	-1.49334	0.135348	0.337827	chr20	28366453	28367444	+	0 NA	IntergeniALR/Alphe	235717 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr4-932 18.30391	-0.77632	0.519853	-1.49334	0.135348	0.337827	chr4	9323055	9325890	+	0 NA	promoter-promoter-	-693 NM_00124E	728369 Hs. 55381CNM_00124E	ENSG00000USP17L24	USP17L25	ubiquitinprotein-coding
chr22-134 23.0625	-0.71953	0.481896	-1.49312	0.135407	0.337827	chr22	13473303	13473577	+	0 NA	IntergeniALR/Alphe	1576034 NM_110761	1.03E+08 Hs. 652929NR_110761	LOC102722-	uncharactncRNA	
chr13-166 18.84715	-0.77281	0.517601	-1.49306	0.135421	0.337827	chr13	16652247	16652833	+	0 NA	IntergeniALR/Alphe	-1542757 NR_02727E	26080 Hs. 448582NR_02727E	ENSG00000FAM230C	LINC00281	family wincRNA
chr20-266 29.1113	-0.6435	0.431143	-1.49254	0.135558	0.337827	chr20	26626943	26627201	+	0 NA	IntergeniALR/Alphe	-417839 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr21-122 19.30917	-0.74732	0.50574	-1.49232	0.135616	0.337827	chr21	12257025	12258186	+	0 NA	IntergeniALR/Alphe	-870561 NR_02691E	149992 Hs. 558645NM_153773	ANKRD30BF C21orf99	ankyrin rpsudo	
chr5-493 37.64761	-0.55941	0.375122	-1.49127	0.135891	0.337827	chr5	49358787	49359042	+	0 NA	IntergeniALR/Alphe	1082374 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr21-107 17.82577	-0.78514	0.526594	-1.49098	0.135967	0.337827	chr21	10767387	10773121	+	0 NA	IntergeniLIP3 LID	248740 NM_19926C	7179 Hs. 122988NM_19926E	ENSG00000TPTE	CT44 PTEN	transmemt protein-coding
chr14-177 18.28221	-0.7747	0.519853	-1.49024	0.136162	0.337827	chr14	17787628	17788239	+	0 NA	IntergeniALR/Alphe	-831384 NM_00101E	440153 Hs. 534888NM_00101E	ENSG00000COR11H12	-	olfactoryprotein-coding
chr20-275 19.71384	-0.75531	0.50689	-1.49009	0.1362	0.337827	chr20	27517493	27520725	+	0 NA	IntergeniALR/Alphe	1083556 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr20-267 17.32314	-0.7975	0.535218	-1.49004	0.136214	0.337827	chr20	26706877	26707607	+	0 NA	IntergeniALR/Alphe	-498009 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr6-5946 19.23849	-0.75855	0.509175	-1.48977	0.136286	0.337827	chr6	59461858	59462542	+	0 NA	IntergeniALR/Alphe	-1500754 NR_13299E	1.07E+08 Hs. 561535NR_125727	ENSG00000LINC0068C-	long intencRNA	
chr19-268 62.68431	-0.44243	0.296981	-1.48976	0.136287	0.337827	chr19	26889035	26889359	+	0 NA	IntergeniALR/Alphe	-904234 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr5-4926 62.18057	-0.44617	0.299601	-1.48921	0.136431	0.337827	chr5	49289538	49289853	+	0 NA	IntergeniALR/Alphe	1151593 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr4-5075 18.25493	-0.78211	0.525203	-1.48916	0.136446	0.337827	chr4	50792074	50790653	+	0 NA	IntergeniALR/Alphe	-1052537 NM_01511E	23142 Hs. 605388NM_01511E	ENSG00000DCUN1D4	-	defectiveprotein-coding
chr10-404 34.17817	-0.57646	0.387473	-1.48775	0.136817	0.337827	chr10	40097742	40099433	+	0 NA	IntergeniALR/Alphe	1401991 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5 FKSG74	ACTR3B	pspseudo
chr20-276 17.75509	-0.78938	0.530609	-1.48768	0.136835	0.337827	chr20	27630457	27633777	+	0 NA	IntergeniALR/Alphe	970598 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr5-4803 68.41308	-0.42585	0.286266	-1.48759	0.136859	0.337827	chr5	48031598	48031840	+	0 NA	IntergeniALR/Alphe	-2335339 NM_02107E	348980 Hs. 353176NM_02107E	ENSG00000HCN1	BCNG-1 B	hyperpoleprotein-coding
chr22-143 17.32035	-0.80232	0.539417	-1.48739	0.136911	0.337827	chr22	14357689	14358968	+	0 NA	IntergeniALR/Alphe	-1169831 NM_00100E	81061 Hs. 554706NM_00100E	ENSG00000COR11H1	OR11H12 Col	factoryprotein-coding
chr20-298 16.32067	-0.81953	0.551128	-1.487	0.137014	0.337827	chr20	29824024	29824473	+	0 NA	IntergeniLIM2 LID	-56136 NR_03968E	1.01E+08 Hs. NR_03968E	ENSG00000MIR4477B	-	microRNA ncRNA
chr21-127 17.85026	-0.78224	0.526151	-1.48672	0.137088	0.337827	chr21	12727955	12728275	+	0 NA	IntergeniALR/Alphe	-310051 NR_02691E	149992 Hs. 558645NM_153773	ANKRD30BF C21orf99	ankyrin rpsudo	
chr9-434 19.33366	-0.75206	0.505948	-1.48644	0.137162	0.337827	chr9	43431280	43431866	+	0 NA	IntergeniALR/Alphe	330407 NR_16066E	1.03E+08 Hs. NR_16066E	LOC102724-	methylenepseudo	
chr9-4356 16.29617	-0.82279	0.553818	-1.48568	0.137365	0.337827	chr9	43583488	43584384	+	0 NA	IntergeniALR/Alphe	457770 NR_16066E	1.03E+08 Hs. NR_16066E	LOC102724-	methylenepseudo	
chr7-5971 17.75788	-0.78475	0.528246	-1.48558	0.137391	0.337827	chr7	59711039	59713467	+	0 NA	IntergeniALR/Alphe	2262076 NM_00115E	441234 Hs. 533121NM_00115E	ENSG00000ZNF716	-	zinc fingprotein-coding
chr14-174 16.8016	-0.80399	0.541223	-1.48551	0.137408	0.337827	chr14	17476913	17478166	+	0 NA	IntergeniALR/Alphe	-1123578 NM_00101E	440153 Hs. 534888NM_00101E	ENSG00000COR11H12	-	olfactoryprotein-coding
chr22-135 15.79633	-0.83237	0.560327	-1.4855	0.137411	0.337827	chr22	13997607	13998096	+	0 NA	IntergeniALR/Alphe	-1530308 NM_00100E	81061 Hs. 554706NM_00100E	ENSG00000COR11H1	OR11H12 Col	factoryprotein-coding
chr20-292 18.35289	-0.77068	0.519067	-1.48474	0.137612	0.337827	chr20	92925729	92925964	+	0 NA	IntergeniALR/Alphe	984713 NR_02771A	440888 Hs. 730235NM_00103241E	ACTR3BP2 FKSG73	ACTR3B	pspseudo
chr20-267 18.26051	-0.7731	0.520713	-1.48469	0.137627	0.337827	chr20	26722837	26723594	+	0 NA	IntergeniALR/Alphe	-513982 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr5-4792 34.31675	-0.57475	0.387211	-1.48433	0.137722	0.337827	chr5	47921050	47921376	+	0 NA	IntergeniALR/Alphe	-2224833 NM_02107E	348980 Hs. 353176NM_02107E	ENSG00000HCN1	BCNG-1 B	hyperpoleprotein-coding
chr4-5068 15.29649	-0.84263	0.567716	-1.48425	0.137742	0.337827	chr4	50684948	50685472	+	0 NA	IntergeniALR/Alphe	-1157790 NM_01511E	23142 Hs. 605388NM_01511E	ENSG00000DCUN1D4		



chr7-5914	27.76921	-0.6139	0.428411	-1.43298	0.151864	0.356359	chr7	59148624	59149858	+	0	NA	IntergeniALR/Alphe	1699064	NM_001155	441234	Hs.533121NM_001155	ENSG000003ZNF716	-	zinc_fingprotein-coding	
chr20-268	22.97564	-0.66866	0.467101	-1.4315	0.152286	0.357055	chr20	26859852	26860072	+	0	NA	IntergeniALR/Alphe	-650729	NR_040095	284801	Hs.370695NR_040095	ENSG000003MIR663AHC	-	MIR663A lncRNA	
chr20-272	20.98961	-0.69532	0.485913	-1.43096	0.152441	0.357055	chr20	27254886	27256914	+	0	NA	IntergeniALR/Alphe	-1046667	NR_040095	284801	Hs.370695NR_040095	ENSG000003MIR663AHC	-	MIR663A lncRNA	
chr20-282	37.65034	-0.52978	0.370255	-1.43085	0.152473	0.357055	chr20	28270356	28271464	+	0	NA	IntergeniALR/Alphe	331755	NR_132315	1E+08	Hs.529357NR_132315	ENSG000003FRG1CP	-	FSHD regipseudo	
chr1-1241	35.47843	-0.54633	0.382429	-1.42857	0.153129	0.358347	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2654403	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMB1P	-	embigin fpseudo	
chr8-4552	20.51147	-0.70094	0.490896	-1.42788	0.153326	0.358564	chr8	45526878	45528428	+	0	NA	IntergeniALR/Alphe	1089990	NR_146077	389652	NR_146077	ENSG000003ASNSP1	ASNSL1	asparagirpseuso	
chr17-262	132.4283	-0.31765	0.222729	-1.42615	0.153824	0.359026	chr17	26299343	26299599	+	0	NA	IntergeniALR/Alphe	789770	NR_135677	1.05E+08	Hs.649915NR_135673	LOC105371-	uncharactcRNA		
chr8-4586	23.40759	-0.66519	0.466536	-1.42615	0.153925	0.359026	chr8	45866419	45866767	+	0	NA	IntergeniALR/Alphe	751050	NR_146077	389652	NR_146077	ENSG000003ASNSP1	ASNSL1	asparagirpseuso	
chr6-5944	20.05503	-0.70834	0.496865	-1.42561	0.153981	0.359026	chr6	59446091	59447443	+	0	NA	IntergeniALR/Alphe	-1485321	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG000003LINC0068C	-	long_intencRNA	
chr14-18C	42.21853	-0.50854	0.356733	-1.42555	0.153999	0.359026	chr14	18060858	18061280	+	0	NA	IntergeniALR/Alphe	-540048	NM_001013	440153	Hs.53488CNM_001013	ENSG000003COR11H12	-	olfactoryprotein-coding	
chr19-265	77.98196	-0.39385	0.276398	-1.42494	0.154174	0.359026	chr19	26986841	26987080	+	0	NA	IntergeniALR/Alphe	-806471	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-	uncharactcRNA		
chr5-4897	58.61769	-0.43592	0.305953	-1.42478	0.154219	0.359026	chr5	48972894	48974315	+	0	NA	IntergeniALR/Alphe	1467684	NM_198445	133418	Hs.561411NM_198445	ENSG000003EMB	GP70	embigin protein-coding	
chr10-414	29.1686	-0.59579	0.418244	-1.42445	0.154303	0.359026	chr10	41410236	41410349	+	0	NA	IntergeniALR/Alphe	993778	NR_02438C	441666	Hs.255725NR_02438C	ENSG000003LOC441666-	zinc_fingpseuso		
chr7-6008	21.47054	-0.6862	0.481781	-1.42429	0.154363	0.359026	chr7	60081468	60081755	+	0	NA	IntergeniALR/Alphe	2631400	NM_001155	441234	Hs.533121NM_001155	ENSG000003ZNF716	-	zinc_fingprotein-coding	
chr19-266	109.4176	-0.34704	0.243739	-1.42338	0.154503	0.359111	chr19	26643030	26643252	+	0	NA	IntergeniALR/Alphe	-1150290	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-	uncharactcRNA		
chr22-136	19.5307	-0.71566	0.502851	-1.42321	0.154676	0.359268	chr22	13655316	13655946	+	0	NA	IntergeniALR/Alphe	1758225	NR_110761	1.03E+08	Hs.652925NR_110761	LOC102722-	uncharactcRNA		
chr22-145	19.509	-0.71413	0.502818	-1.42026	0.155531	0.360931	chr22	14395521	14396628	+	0	NA	IntergeniALR/Alphe	-1132085	NM_001005	81061	Hs.554705NM_001005	ENSG000003COR11H1	OR11H12	Colfactoryprotein-coding	
chr19-256	64.42321	-0.42533	0.29832	-1.41971	0.155692	0.360931	chr19	25631101	25631362	+	0	NA	IntergeniALR/Alphe	-1467784	NR_003603	1E+08	Hs.149312NR_003603	ENSG000003HAVCR1P1	-	hepatitispsseudo	
chr21-117	27.18257	-0.6109	0.430318	-1.41965	0.155708	0.360931	chr21	11724600	11725232	+	0	NA	IntergeniALR/Alphe	1203402	NM_19926C	7179	Hs.122986NM_199255	ENSG000003TPTE	CT44 PTEN	transmemprotein-coding	
chr9-445	23.33412	-0.6719	0.473533	-1.41891	0.155924	0.361044	chr9	44593968	44594286	+	0	NA	IntergeniALR/Alphe	1467961	NR_160665	1.03E+08	NR_160669	LOC102724-	methylenepseuso		
chr21-936	19.55519	-0.71305	0.502586	-1.41876	0.155968	0.361044	chr21	9360015	9361765	+	0	NA	IntergeniCER SateI	-182140	NR_135512	1.05E+08	Hs.462322NR_135512	LOC105375-	nuclear rpseuso		
chr19-248	32.92187	-0.55819	0.393653	-1.41799	0.156195	0.361101	chr19	24848165	24848381	+	0	NA	IntergeniALR/Alphe	-684826	NR_003603	1E+08	Hs.149312NR_003603	ENSG000003HAVCR1P1	-	hepatitispsseudo	
chr9-435	19.59859	-0.71612	0.505038	-1.41796	0.156203	0.361101	chr9	43531239	43531541	+	0	NA	IntergeniALR/Alphe	405224	NR_160665	1.03E+08	NR_160669	LOC102724-	methylenepseuso		
chr21-905	18.52822	-0.73039	0.515743	-1.41619	0.156272	0.362052	chr21	9098429	9101252	+	0	NA	intron (CER SateI)	29921	NR_03832E	1E+08	Hs.487562NM_174948	ENSG000003TEKT4P2	MAFIPL TE	tektin 4 pseuso	
chr20-275	19.43831	-0.71789	0.507116	-1.41563	0.156885	0.362108	chr20	27919335	27919594	+	0	NA	IntergeniALR/Alphe	683201	NR_132315	1E+08	Hs.529357NR_132315	ENSG000003FRG1CP	-	FSHD regipseudo	
chr20-284	18.98466	-0.72182	0.509985	-1.41539	0.156956	0.362108	chr20	28458853	28459070	+	0	NA	IntergeniALR/Alphe	143704	NR_132315	1E+08	Hs.529357NR_132315	ENSG000003FRG1CP	-	FSHD regipseudo	
chr19-266	18.02559	-0.74063	0.523551	-1.41463	0.157176	0.362108	chr19	26666497	26667668	+	0	NA	IntergeniALR/Alphe	-1126349	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-	uncharactcRNA		
chr10-415	18.48203	-0.73156	0.517168	-1.41454	0.157203	0.362108	chr10	41581166	41584614	+	0	NA	IntergeniALR/Alphe	785155	NR_02438C	441666	Hs.255725NR_02438C	ENSG000003LOC441666-	zinc_fingpseuso		
chr13-166	18.50652	-0.72879	0.515741	-1.41309	0.15763	0.362421	chr13	16699070	16700145	+	0	NA	IntergeniALR/Alphe	-1495690	NR_02727E	26080	Hs.448582NR_02727E	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr22-136	18.93568	-0.7273	0.514801	-1.41277	0.157722	0.362421	chr22	13675960	13676290	+	0	NA	IntergeniALR/Alphe	1778719	NR_110761	1.03E+08	Hs.652925NR_110761	LOC102722-	uncharactcRNA		
chr10-414	31.77414	-0.57609	0.407776	-1.41276	0.157727	0.362421	chr10	41418100	41418388	+	0	NA	IntergeniALR/Alphe	949801	NR_02438C	441666	Hs.255725NR_02438C	ENSG000003LOC441666-	zinc_fingpseuso		
chr19-261	32.44373	-0.55961	0.396149	-1.41262	0.157768	0.362421	chr19	26180855	26181058	+	0	NA	IntergeniALR/Alphe	-1612475	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-	uncharactcRNA		
chr14-18C	20.52201	-0.71911	0.509138	-1.41224	0.157832	0.362421	chr14	18005414	18005786	+	0	NA	IntergeniALR/Alphe	-595517	NM_001013	440153	Hs.53488CNM_001013	ENSG000003COR11H12	-	olfactoryprotein-coding	
chr22-115	18.05008	-0.73779	0.522593	-1.41178	0.158014	0.362513	chr22	11914667	11922207	+	0	NA	intron (MSTA-int	21031	NR_110761	1.03E+08	Hs.652925NR_110761	LOC102722-	uncharactcRNA		
chr19-261	20.53875	-0.6945	0.492103	-1.41129	0.158159	0.362513	chr19	26162022	26162250	+	0	NA	IntergeniALR/Alphe	-1631295	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG000003LOC101927-	uncharactcRNA		
chr6-5956	17.54745	-0.74854	0.530665	-1.41107	0.158371	0.362513	chr6	59584744	59585038	+	0	NA	IntergeniALR/Alphe	-1623445	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG000003LINC0068C	-	long_intencRNA	
chr1-1241	35.82078	-0.54439	0.385941	-1.41055	0.158378	0.362513	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2607370	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMB1P	-	embigin fpseudo	
chr14-175	17.52575	-0.74684	0.529777	-1.40973	0.158619	0.362513	chr14	17947453	17945128	+	0	NA	IntergeniALR/Alphe	-626177	NM_001013	440153	Hs.53488CNM_001013	ENSG000003COR11H12	-	olfactoryprotein-coding	
chr13-175	18.46033	-0.72995	0.518026	-1.40911	0.158804	0.362513	chr13	17947921	17949276	+	0	NA	IntergeniALR/Alphe	-246669	NR_02727E	26080	Hs.448582NR_02727E	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr21-127	18.96296	-0.72026	0.511211	-1.40893	0.158857	0.362513	chr21	12720190	12720497	+	0	NA	IntergeniALR/Alphe	-317823	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BF C21orf99	ankyrin rpseuso		
chr3-920	32.04403	-0.5729	0.406862	-1.40811	0.159099	0.362513	chr3	92035956	92036287	+	0	NA	IntergeniALR/Alphe	1937690	NM_001314	5627	Hs.64016	NM_000313	ENSG000003PROS1	PROS PS21	protein Sprotein-coding
chr12-356	28.73944	-0.59446	0.422258	-1.40782	0.159185	0.362513	chr12	35998324	35999126	+	0	NA	IntergeniALR/Alphe	1976229	NM_03283A	84920	Hs.102971NM_03283A	ENSG000003ALG10	ALG10A DIALG10	al protein-coding	
chr5-475	36.05564	-0.53309	0.379097	-1.4062	0.159664	0.362513	chr5	47593939	47595076	+	0	NA	IntergeniALR/Alphe	-1898127	NM_021072	348980	Hs.353176NM_021072	ENSG000003HCN1	BCNG-1 BCHyperpole	protein-coding	
chr22-113	17.06652	-0.76177	0.542084	-1.40526	0.159945	0.362513	chr22	11357217	11357428	+	0	NA	IntergeniIntergeni	-395793	NR_13232C	1.03E+08	NR_132320	FRG1FP	-	FSHD regipseudo	
chr10-40C	29.24207	-0.59048	0.420301	-1.40489	0.160054	0.362513	chr10	40001878	40002158	+	0	NA	IntergeniALR/Alphe	1305422	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo	
chr18-47C	16.54498	-0.76714	0.546056	-1.40487	0.160059	0.362513	chr18	47025261	47026562	+	0	NA	intron (intron (	-1748	NM_145653	162699	Hs.515381NM_145653	ENSG000003ELOA3	ELOA3A Hselongin	l protein-coding	
chr21-52	16.54498	-0.76714	0.546056	-1.40487	0.160059	0.362513	chr21	5235605	5238454	+	0	NA	IntergeniTHE1C-int	-82371	NR_160695	1.03E+08	Hs.449076NM_001368	ENSG000003LOC102724-	periodic protein-coding		
chr13-174	20.51705	-0.69301	0.493541	-1.40415	0.160273	0.362513	chr13	17410264	17411521	+	0	NA	IntergeniALR/Alphe	-784405	NR_02727E	26080	Hs.448582NR_02727E	ENSG000003FAM230C	LINC00281	family_wincRNA	
chr1-1247	172.0962	-0.28529	0.203273	-1.40349	0.160472	0.362513	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3238599	NR_003955	647121	Hs.697682NR_003955	ENSG000003EMB1P	-	embigin fpseudo	
chr20-284	25.19932	-0.62515	0.445469	-1.40336	0.160509	0.362513	chr20	28461197	28461398	+	0	NA	IntergeniALR/Alphe	141368	NR_132315	1E+08	Hs.529357NR_132315	ENSG000003FRG1CP	-	FSHD regipseudo	
chr8-445	18.50931	-0.72443	0.516245	-1.40326	0.160539	0															

chr5-4836	19.9738	-0.69392	0.507494	-1.36734	0.17152	0.37121	chr5	48361010	48361343	+	0 NA	IntergeniALR/Alphe	2080112	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin protein-coding	
chr22-135	22.1702	-0.64797	0.47409	-1.36677	0.171698	0.371362	chr22	13566779	13567041	+	0 NA	IntergeniALR/Alphe	1669504	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC102722	-	uncharactericrNA	
chr11-526	41.44595	-0.48747	0.356787	-1.36627	0.171854	0.371466	chr11	52690104	52690478	+	0 NA	IntergeniALR/Alphe	1913707	NM_001004	119749	Hs.553564NM_001004	ENSG00000	OR4C46	-	olfactoryprotein-coding	
chr1-124	31.18302	-0.57072	0.418239	-1.36457	0.172389	0.372283	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2687997	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMB1P	-	embigin fpseudo	
chr18-19C	21.23562	-0.65797	0.482485	-1.36372	0.172656	0.372283	chr18	19025255	19025516	+	0 NA	IntergeniALR/Alphe	2086428	NM_00540E	6093	Hs.306307NM_00540E	ENSG00000	ROCK1	P16G0RCK	Rho assocprotein-coding	
chr21-11f	21.23562	-0.65797	0.482485	-1.36372	0.172656	0.372283	chr21	11602814	11603047	+	0 NA	IntergeniALR/Alphe	1081416	NM_19926C	7179	Hs.12298E	NR_19925E	ENSG00000	TPTE	CT44 PTEN	transmemtprotein-coding
chr20-27f	17.91988	-0.7277	0.533653	-1.36363	0.172684	0.372283	chr20	27610883	27611265	+	0 NA	IntergeniALR/Alphe	991591	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1CP	-	FSHD regipseudo	
chr12-35f	36.82878	-0.50935	0.373665	-1.36313	0.172842	0.372283	chr12	35597039	35598194	+	0 NA	IntergeniALR/Alphe	1575120	NM_032834	84920	Hs.102971NM_032834	ENSG00000	ALG10	ALG10A DIALG10	alIprotein-coding	
chr20-27f	20.7302	-0.66899	0.490825	-1.36299	0.172884	0.372283	chr20	27257976	27259977	+	0 NA	IntergeniALR/Alphe	1049743	NR_04009E	284801	Hs.37069E	NR_04009E	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr20-284	19.44947	-0.70085	0.515411	-1.3598	0.173894	0.374222	chr20	28471884	28472172	+	0 NA	IntergeniALR/Alphe	130637	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1CP	-	FSHD regipseudo	
chr11-537	46.35143	-0.46047	0.338963	-1.35847	0.174315	0.374892	chr11	53700305	53700620	+	0 NA	IntergeniALR/Alphe	903536	NM_001004	119749	Hs.553564NM_001004	ENSG00000	OR4C46	-	olfactoryprotein-coding	
chr7-589f	21.20277	-0.67232	0.495303	-1.35738	0.17466	0.375359	chr7	58939023	58939427	+	0 NA	IntergeniALR/Alphe	1489048	NM_00115E	441234	Hs.533121NM_00115E	ENSG00000	ZNF716	-	zinc fingprotein-coding	
chr5-4927	48.36196	-0.45636	0.336274	-1.35709	0.174751	0.375359	chr5	49275640	49275847	+	0 NA	IntergeniALR/Alphe	1165545	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin protein-coding	
chr10-40	20.25485	-0.66998	0.494138	-1.35585	0.175146	0.375971	chr10	40829612	40831838	+	0 NA	IntergeniALR/Alphe	957320	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E	-	zinc fingpseudo
chr5-4924	54.13523	-0.43156	0.318672	-1.35423	0.175661	0.376564	chr5	49243227	49244204	+	0 NA	IntergeniALR/Alphe	1197573	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin protein-coding	
chr19-26f	49.05605	-0.44643	0.329659	-1.35422	0.175668	0.376564	chr19	26807954	26808214	+	0 NA	IntergeniALR/Alphe	985347	NR_146732	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927	-	uncharactericrNA	
chr20-27f	21.69485	-0.64843	0.478991	-1.35375	0.175817	0.376564	chr20	27847634	27847967	+	0 NA	IntergeniALR/Alphe	754865	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1CP	-	FSHD regipseudo	
chr1-124	42.98391	-0.47807	0.35318	-1.35361	0.175862	0.376564	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2892521	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMB1P	-	embigin fpseudo	
chr15-19C	20.27934	-0.66748	0.493943	-1.35133	0.176588	0.377779	chr15	19640129	19641451	+	0 NA	IntergeniALR/Alphe	641954	NR_03883E	646096	Hs.44878E	NR_03883E	ENSG00000	CHEK2P2	-	checkpoirpseudo
chr1-124	54.25211	-0.42995	0.318277	-1.35087	0.176738	0.377779	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2580966	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMB1P	-	embigin fpseudo	
chr1-122f	43.7214	-0.46793	0.346407	-1.3508	0.17676	0.377779	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1360881	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMB1P	-	embigin fpseudo	
chr5-476f	31.51863	-0.54815	0.406259	-1.34926	0.177253	0.378169	chr5	47694563	47697120	+	0 NA	IntergeniALR/Alphe	1999461	NM_021072	348980	Hs.35317E	NM_021072	ENSG00000	HCN1	BCNG-1 BChyperpole	protein-coding
chr20-27f	19.70882	-0.67468	0.500204	-1.3488	0.177401	0.378169	chr20	27250959	27251191	+	0 NA	IntergeniALR/Alphe	1042197	NR_04009E	284801	Hs.37069E	NR_04009E	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr5-4901	25.8745	-0.59637	0.442204	-1.34863	0.177456	0.378169	chr5	49010782	49011102	+	0 NA	IntergeniALR/Alphe	1430341	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin protein-coding	
chr20-26f	19.75501	-0.67364	0.499532	-1.34853	0.177487	0.378169	chr20	26994114	26998377	+	0 NA	IntergeniALR/Alphe	787012	NR_04009E	284801	Hs.37069E	NR_04009E	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr17-26f	84.50941	-0.36036	0.267225	-1.34851	0.177494	0.378169	chr17	26098077	26098327	+	0 NA	IntergeniALR/Alphe	991039	NR_135673	1.05E+08	Hs.64991E	NR_135673	LOC105371	-	uncharactericrNA	
chr19-254	31.24417	-0.55607	0.408771	-1.34713	0.177938	0.378433	chr19	25400559	25400789	+	0 NA	IntergeniALR/Alphe	1237227	NR_00360E	1E+08	Hs.149312NR_00360E	ENSG00000	HAVCR1P1	-	hepatitispseudo	
chr21-12f	26.40441	-0.58699	0.435768	-1.34703	0.177971	0.378433	chr21	12571974	12572998	+	0 NA	IntergeniALR/Alphe	465680	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30B C21orf99	-	ankyrin rpseudo	
chr19-251	37.26631	-0.50483	0.374815	-1.34687	0.178022	0.378433	chr19	25182688	25184148	+	0 NA	IntergeniALR/Alphe	1019971	NR_00360E	1E+08	Hs.149312NR_00360E	ENSG00000	HAVCR1P1	-	hepatitispseudo	
chr20-26f	31.13845	-0.54288	0.4032	-1.34644	0.178162	0.378433	chr20	26589322	26589556	+	0 NA	IntergeniALR/Alphe	380206	NR_04009E	284801	Hs.37069E	NR_04009E	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr5-488f	19.20619	-0.68276	0.507095	-1.34641	0.17817	0.378433	chr5	48872041	48872256	+	0 NA	IntergeniALR/Alphe	1569140	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin protein-coding	
chr10-411	34.83996	-0.51852	0.385257	-1.34559	0.178335	0.378549	chr10	41187878	41188619	+	0 NA	IntergeniALR/Alphe	1179797	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000	LOC44166E	-	zinc fingpseudo
chr11-53f	35.31252	-0.52668	0.388454	-1.34549	0.178452	0.378549	chr11	53620742	53621085	+	0 NA	IntergeniALR/Alphe	983085	NM_001004	119749	Hs.553564NM_001004	ENSG00000	OR4C46	-	olfactoryprotein-coding	
chr20-28C	19.23068	-0.68012	0.505831	-1.34456	0.178769	0.37889	chr20	28049227	28050735	+	0 NA	IntergeniALR/Alphe	552684	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1CP	-	FSHD regipseudo	
chr22-141	19.66263	-0.67574	0.502642	-1.34437	0.178828	0.37889	chr22	14107384	14108579	+	0 NA	IntergeniALR/Alphe	1420178	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG00000	COR11H1	OR11H12 Col	factoryprotein-coding
chr8-450f	36.26105	-0.50868	0.378536	-1.34382	0.179006	0.379005	chr8	45039184	45039618	+	0 NA	IntergeniALR/Alphe	1578242	NR_146077	389652	NR_146077	ENSG00000	ASNSP1	ASNSL1	asparagirpseudo	
chr20-271	30.63582	-0.54576	0.406244	-1.34343	0.179133	0.379005	chr20	27116910	27118097	+	0 NA	IntergeniALR/Alphe	908270	NR_04009E	284801	Hs.37069E	NR_04009E	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr16-342	21.52789	-0.66921	0.498261	-1.34309	0.179244	0.379005	chr16	34276979	34277178	+	0 NA	IntergeniALR/Alphe	104402	NR_15815E	1.03E+08	Hs.69271C	NR_15815E	CCNYL3	-	cyclin Y pseudo	
chr20-30f	20.28213	-0.6635	0.49423	-1.34249	0.179439	0.379005	chr20	30384149	30384595	+	0 NA	IntergeniALR/Alphe	7208	NR_145491	284802	Hs.37069E	NR_04009E	ENSG00000	FRG1BP	C20orf80 F	SHD regipseudo
chr5-500C	19.18449	-0.6812	0.507488	-1.3423	0.1795	0.379005	chr5	50004449	50004742	+	0 NA	IntergeniALR/Alphe	436693	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin protein-coding	
chr19-26f	25.37076	-0.61073	0.455084	-1.34201	0.179592	0.379005	chr19	26999135	26999354	+	0 NA	IntergeniALR/Alphe	794817	NR_146732	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927	-	uncharactericrNA	
chr13-17f	18.51768	-0.7107	0.529659	-1.34181	0.179657	0.379005	chr13	17587372	17587704	+	0 NA	IntergeniALR/Alphe	667759	NR_02727E	26080	Hs.44858E	NR_02727E	ENSG00000	FAM230C	LINC00281	family wincRNA
chr20-26f	25.97246	-0.58857	0.438799	-1.34132	0.179816	0.379107	chr20	26873075	26875553	+	0 NA	IntergeniALR/Alphe	665081	NR_04009E	284801	Hs.37069E	NR_04009E	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr7-5971	17.71161	-0.67059	0.500257	-1.3405	0.180084	0.379382	chr7	59718394	59718606	+	0 NA	IntergeniALR/Alphe	2268233	NM_00115E	441234	Hs.533121NM_00115E	ENSG00000	ZNF716	-	zinc fingprotein-coding	
chr20-27f	18.72247	-0.69743	0.520374	-1.34024	0.180168	0.379382	chr20	27713326	27714682	+	0 NA	IntergeniALR/Alphe	886631	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1CP	-	FSHD regipseudo	
chr20-27f	18.70635	-0.68696	0.512917	-1.33932	0.180465	0.37944	chr20	27749039	27752947	+	0 NA	IntergeniALR/Alphe	851672	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1CP	-	FSHD regipseudo	
chr4-936f	18.75254	-0.68586	0.512094	-1.33932	0.180467	0.37944	chr4	9368140	9368966	+	0 NA	non-codir non-codir	679	NR_02727E	391622	Hs.72265E	NR_02727E	ENSG00000	USP17L6P	DUBA USP1	ubiquitirpseudo
chr7-604f	18.22542	-0.69749	0.520851	-1.33913	0.180528	0.37944	chr7	60437651	60439204	+	0 NA	IntergeniALR/Alphe	2865629	NR_00395E	643955	Hs.58330E	NR_00395E	ENSG00000	ZNF733P	ZNF733	zinc fingpseudo
chr3-925f	18.65737	-0.69247	0.517763	-1.33743	0.181081	0.380371	chr3	92589103	92590819	+	0 NA	IntergeniALR/Alphe	1384120	NM_001314	5627	Hs.64016	NM_00031E	ENSG00000	PROS1	PROS PS21	protein Sprotein-coding
chr17-25f	52.85941	-0.42812	0.320246	-1.33684	0.181274	0.380434	chr17	25769639	25769856	+	0 NA	IntergeniALR/Alphe	1319494	NR_135673	1.05E+08	Hs.64991E	NR_135673</				



chr15-184 15.74791	-0.72697	0.557177	-1.30474	0.191982	0.385318	chr15	18414891	18416291	+	0 NA	IntergeniALR/Alphe	-1867153 NR_03883E	646096 Hs. 448785NR_03883E	ENSG00000CHEK2P2	-	checkpoirpseudo
chr10-405 39.77104	-0.47658	0.365272	-1.30473	0.191984	0.385318	chr10	40598530	40599669	+	0 NA	IntergeniALR/Alphe	1768946 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC44166E	-	zinc fingpseudo
chr21-122 16.68249	-0.70944	0.543889	-1.30438	0.192103	0.385333	chr21	12263187	12264263	+	0 NA	IntergeniALR/Alphe	-774441 NR_02691E	149992 Hs. 558645NR_153773	ANKRD30BFC21orf99	ankyrin rpseudo	
chr19-265 36.15913	-0.4943	0.3791	-1.30389	0.192272	0.385438	chr19	26578832	26579081	+	0 NA	IntergeniALR/Alphe	-1214475 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr20-281 27.55214	-0.56497	0.433456	-1.30304	0.192437	0.385438	chr20	28127151	28127706	+	0 NA	IntergeniALR/Alphe	4752737 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr19-252 31.78914	-0.52311	0.401393	-1.30324	0.192494	0.385438	chr19	25294053	25296620	+	0 NA	IntergeniALR/Alphe	-1131889 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG00000HAVCR1P1	-	hepatitispseudo
chr5-4917 32.05022	-0.54492	0.418419	-1.30234	0.192801	0.385826	chr5	49177635	49177835	+	0 NA	IntergeniALR/Alphe	1263553 NR_19844E	133418 Hs. 561411NR_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr5-4775 27.21537	-0.56149	0.43147	-1.30135	0.19314	0.386121	chr5	47735165	47736048	+	0 NA	IntergeniALR/Alphe	-2039226 NR_02107E	348980 Hs. 353176NR_02107E	ENSG00000CHCN1	BCNG-1 BChyperpoleprotein-coding	
chr10-402 22.44071	-0.6111	0.469721	-1.30099	0.19326	0.386121	chr10	40284697	40285334	+	0 NA	IntergeniALR/Alphe	1588419 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5 FKS74	ACTR3B pspseudo	
chr17-258 48.61745	-0.43233	0.33234	-1.30086	0.193306	0.386121	chr17	25828576	25827997	+	0 NA	IntergeniALR/Alphe	1260554 NR_13567E	1.05E+08 Hs. 649918NR_13567E	LOC105371-	uncharactncRNA	
chr20-277 29.19309	-0.54378	0.418106	-1.30059	0.193399	0.386121	chr20	27056659	27056907	+	0 NA	IntergeniALR/Alphe	-847550 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr1-1242 36.50706	-0.48865	0.375986	-1.29964	0.193723	0.38622	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2731896 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMBP1	-	embigin fpseudo
chr9-4462 21.93808	-0.61669	0.474676	-1.29918	0.193883	0.38622	chr9	44625226	44653006	+	0 NA	IntergeniALR/Alphe	1526000 NR_16066E	1.03E+08 NR_160669	LOC102724-	methylenepseudo	
chr13-174 23.16213	-0.62328	0.479759	-1.29914	0.193895	0.38622	chr13	17474907	1745122	+	0 NA	IntergeniALR/Alphe	-702283 NR_02727E	26080 Hs. 448582NR_02727E	ENSG00000FAM230C	LINC00281family wincRNA	
chr5-4786 73.46047	-0.36003	0.277129	-1.29913	0.193899	0.38622	chr5	47863888	47865016	+	0 NA	IntergeniALR/Alphe	-2168072 NR_02107E	348980 Hs. 353176NR_02107E	ENSG00000CHCN1	BCNG-1 BChyperpoleprotein-coding	
chr20-265 15.65553	-0.72966	0.562017	-1.29829	0.194187	0.386331	chr20	26956340	26956605	+	0 NA	IntergeniALR/Alphe	-747239 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr20-268 16.75317	-0.70513	0.543245	-1.298	0.194286	0.386331	chr20	26815500	26816097	+	0 NA	IntergeniALR/Alphe	-606565 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr5-4904 32.79998	-0.51333	0.3955	-1.29792	0.194314	0.386331	chr5	49041539	49041747	+	0 NA	IntergeniALR/Alphe	1339645 NR_19844E	133418 Hs. 561411NR_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr10-41E 21.41096	-0.62489	0.48155	-1.29765	0.194406	0.386331	chr10	41574567	41577274	+	0 NA	IntergeniALR/Alphe	792125 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC44166E-	zinc fingpseudo	
chr21-103 16.6363	-0.71068	0.548185	-1.29643	0.194828	0.386524	chr21	10336840	10337084	+	0 NA	IntergeniALuY SINE	-76558 NR_001187	574 Hs. 545785NR_001187	BAGE	BAGE1 CT2B melanonprotein-coding	
chr3-909C 21.43545	-0.62253	0.480202	-1.2964	0.194839	0.386524	chr3	90909531	90909800	+	0 NA	IntergeniALR/Alphe	1802044 NR_00523E	2042 Hs. 123642NR_00523E	ENSG00000EPAH3	EK4 ETK EFPH	receptprotein-coding
chr10-414 27.56051	-0.55595	0.428846	-1.29639	0.194842	0.386524	chr10	41438905	41440486	+	0 NA	IntergeniALR/Alphe	928350 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC44166E-	zinc fingpseudo	
chr20-267 46.18831	-0.4407	0.340068	-1.29591	0.195008	0.386591	chr20	26784806	26785701	+	0 NA	IntergeniALR/Alphe	-575705 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr10-404 35.59419	-0.49107	0.379053	-1.29552	0.195139	0.386591	chr10	40465789	40467720	+	0 NA	IntergeniALR/Alphe	1770158 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5 FKS74	ACTR3B pspseudo	
chr1-1227 47.29433	-0.43302	0.334509	-1.29449	0.195497	0.386591	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1258780 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMBP1	-	embigin fpseudo
chr19-261 17.13893	-0.70052	0.514344	-1.29404	0.195651	0.386591	chr19	26139615	26139819	+	0 NA	IntergeniALR/Alphe	-1653714 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr10-41E 20.93003	-0.63258	0.489025	-1.29355	0.195821	0.386591	chr10	41840858	41841708	+	0 NA	IntergeniALR/Alphe	526762 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC44166E-	zinc fingpseudo	
chr4-498E 19.21735	-0.6657	0.514646	-1.29351	0.195836	0.386591	chr4	49860100	49860489	+	0 NA	IntergeniALR/Alphe	873652 NR_00128E	80157 Hs. 479703NR_025087	ENSG00000CWH43	CWH43-C Fcell wallprotein-coding	
chr17-257 24.56532	-0.59056	0.456886	-1.29343	0.195864	0.386591	chr17	25796406	25796639	+	0 NA	IntergeniALR/Alphe	1292719 NR_13567E	1.05E+08 Hs. 649918NR_13567E	LOC105371-	uncharactncRNA	
chr13-171 21.45994	-0.6202	0.479685	-1.29293	0.196037	0.386591	chr13	17144723	17146236	+	0 NA	IntergeniALR/Alphe	-1049923 NR_02727E	26080 Hs. 448582NR_02727E	ENSG00000FAM230C	LINC00281family wincRNA	
chr5-476C 38.74966	-0.47424	0.366827	-1.29282	0.196073	0.386591	chr5	47607622	47608338	+	0 NA	IntergeniALR/Alphe	-1911600 NR_02107E	348980 Hs. 353176NR_02107E	ENSG00000CHCN1	BCNG-1 BChyperpoleprotein-coding	
chr10-41E 26.67213	-0.55975	0.433007	-1.29227	0.196114	0.386591	chr10	41533473	41534497	+	0 NA	IntergeniALR/Alphe	834060 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000LOC44166E-	zinc fingpseudo	
chr19-217 17.40492	-0.71226	0.550992	-1.29227	0.196116	0.386591	chr19	25178729	25179170	+	0 NA	IntergeniALR/Alphe	-1015502 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG00000HAVCR1P1	-	hepatitispseudo
chr5-482C 27.22095	-0.5555	0.429831	-1.29237	0.196229	0.386591	chr5	48203296	48203870	+	0 NA	IntergeniALR/Alphe	2237705 NR_19844E	133418 Hs. 561411NR_19844E	ENSG00000EMB	GP70	embigin protein-coding
chr1-1236 27.15306	-0.55505	0.429617	-1.29198	0.196365	0.386637	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2364351 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMBP1	-	embigin fpseudo
chr19-262 45.09514	-0.44399	0.343924	-1.29096	0.196718	0.387108	chr19	26266562	26266806	+	0 NA	IntergeniALR/Alphe	-1526747 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr20-274 20.95731	-0.62626	0.485365	-1.29029	0.196949	0.38725	chr20	27478082	27479647	+	0 NA	IntergeniALR/Alphe	1123801 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr11-52E 21.00071	-0.62919	0.487708	-1.2901	0.197016	0.38725	chr11	52839833	52840936	+	0 NA	IntergeniALR/Alphe	1763614 NR_001004	119749 Hs. 553564NR_001004	ENSG00000OR4C46	-	olfactoryprotein-coding
chr1-122E 21.43824	-0.61878	0.479968	-1.28921	0.197324	0.387591	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1301836 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMBP1	-	embigin fpseudo
chr2-929E 22.94613	-0.6022	0.467205	-1.28895	0.197416	0.387591	chr2	92920834	92921111	+	0 NA	IntergeniALR/Alphe	979839 NR_027714	440888 Hs. 730235NR_001032412	ACTR3BP2 FKS73	ACTR3B pspseudo	
chr20-264 43.29336	-0.46107	0.358509	-1.28609	0.198411	0.388906	chr20	26484555	26484799	+	0 NA	IntergeniALR/Alphe	-275444 NR_04009E	284801 Hs. 370695NR_04009E	ENSG00000MIR663AHC-	MIR663A lncRNA	
chr3-918S 35.09434	-0.49052	0.381507	-1.28573	0.198536	0.388906	chr3	91835551	91835900	+	0 NA	IntergeniALR/Alphe	2138356 NR_001314	5627 Hs. 64016 NR_000315	ENSG00000PROS1	PROS1 PS21protein Sprotein-coding	
chr10-402 30.30574	-0.52923	0.411708	-1.28545	0.198636	0.388906	chr10	40213435	40213647	+	0 NA	IntergeniALR/Alphe	1516945 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5 FKS74	ACTR3B pspseudo	
chr19-267 68.60676	-0.36666	0.285328	-1.28504	0.198777	0.388906	chr19	26781782	26782860	+	0 NA	IntergeniALR/Alphe	-1011110 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927-	uncharactncRNA	
chr1-122S 30.37921	-0.52421	0.40798	-1.28489	0.198829	0.388906	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1394132 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMBP1	-	embigin fpseudo
chr20-28E 20.43298	-0.63115	0.491262	-1.28475	0.19888	0.388906	chr20	28829808	28834993	+	0 NA	IntergeniALR/Alphe	-229735 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo
chr22-13E 20.43298	-0.63115	0.491262	-1.28475	0.19888	0.388906	chr22	13396334	13396596	+	0 NA	IntergeniALR/Alphe	1499059 NR_110761	1.03E+08 Hs. 65292E NR_110761	LOC10272E-	uncharactncRNA	
chr10-401 34.95298	-0.49443	0.385297	-1.28325	0.199406	0.389407	chr10	40100244	40100614	+	0 NA	IntergeniALR/Alphe	1403833 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5 FKS74	ACTR3B pspseudo	
chr9-435A 20.50087	-0.63167	0.492228	-1.28315	0.199438	0.389407	chr9	43545964	43547355	+	0 NA	IntergeniALR/Alphe	420493 NR_16066E	1.03E+08 NR_160669	LOC102724-	methylenepseudo	
chr14-16E 15.27256	-0.73027	0.569172	-1.28304	0.199477	0.389407	chr14	16869339	16869551	+	0 NA	IntergeniALR/Alphe	-1731672 NR_00101E	440153 Hs. 53488C NR_00101E	ENSG00000OR11H12	-	olfactoryprotein-coding
chr14-17E 20.91391	-0.62337	0.485981	-1.2827	0.199597	0.389418	chr14	17267006	17268338	+	0 NA	IntergeniALR/Alphe	-1333445 NR_00101E	440153 Hs. 53488			

chr20-277 23.09697	-0.57445	0.464496	-1.23673	0.216189	0.404479	chr20	27712619	27714581	+	0 NA	IntergeniALR/Alphe	889065 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr19-256 116.4038	-0.29475	0.238364	-1.23655	0.216253	0.404479	chr19	25601050	25601304	+	0 NA	IntergeniALR/Alphe	-1437730 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG0000CHAVCR1P1	-	hepatitispseudo
chr6-589C 16.90402	-0.66533	0.538301	-1.23598	0.216467	0.404479	chr6	58906421	58908599	+	0 NA	IntergeniALR/Alphe	-946064 NR_13299E	1.07E+08 Hs. 561535NR_125727	ENSG0000CLINCO068C	-	long intencRNA
chr1-124 31.01098	-0.50076	0.405223	-1.23577	0.216545	0.404479	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2927380 NR_00395E	647121 Hs. 697682NR_00395E	ENSG0000EMB1P	-	embigin ppsseudo
chr22-142 16.37689	-0.67756	0.548669	-1.23492	0.216864	0.404479	chr22	14295354	14295504	+	0 NA	IntergeniALR/Alphe	-1229680 NR_00100E	81061 Hs. 554706NR_00100E	ENSG0000COR1IH1	OR11H12 Col	factoryprotein-coding
chr20-281 16.40139	-0.67447	0.546246	-1.23474	0.216928	0.404479	chr20	28170803	28172989	+	0 NA	IntergeniALR/Alphe	430769 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr19-266 46.85184	-0.42418	0.343551	-1.23468	0.216951	0.404479	chr19	26875132	26875365	+	0 NA	IntergeniALR/Alphe	-918183 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG0000CLOC101927-	-	uncharactncRNA
chr20-267 26.93705	-0.53613	0.434242	-1.23462	0.216977	0.404479	chr20	26724437	26725594	+	0 NA	IntergeniALR/Alphe	-515782 NR_04009E	284801 Hs. 370695NR_04009E	ENSG0000MIR663AH	-	MIR663A lncRNA
chr20-276 15.94495	-0.6829	0.553192	-1.23447	0.217026	0.404479	chr20	27600678	27602183	+	0 NA	IntergeniALR/Alphe	1001235 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr7-591C 26.11276	-0.55032	0.4458	-1.23446	0.21703	0.404479	chr7	59130196	59130407	+	0 NA	IntergeniALR/Alphe	1680214 NR_00115E	441234 Hs. 533121NR_00115E	ENSG0000CZNF716	-	zinc fingprotein-coding
chr19-257 22.59434	-0.57904	0.469153	-1.23424	0.217115	0.404479	chr19	25735783	25737545	+	0 NA	IntergeniALR/Alphe	-1573217 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG0000CHAVCR1P1	-	hepatitispseudo
chr20-275 18.52599	-0.64029	0.519047	-1.23359	0.217356	0.404518	chr20	27983835	27984144	+	0 NA	IntergeniALR/Alphe	618676 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr10-401 16.9964	-0.66294	0.537425	-1.23355	0.217372	0.404518	chr10	40141928	40142351	+	0 NA	IntergeniALR/Alphe	1445543 NR_04500C	399746 Hs. 742607NR_04500C	ACTR3BP5 FKSG74	ACTR3B ppsseudo	
chr20-265 23.23555	-0.57198	0.463902	-1.23298	0.217584	0.404693	chr20	26585738	26586006	+	0 NA	IntergeniALR/Alphe	-376639 NR_04009E	284801 Hs. 370695NR_04009E	ENSG0000MIR663AH	-	MIR663A lncRNA
chr19-255 34.79154	-0.47192	0.382913	-1.23244	0.217786	0.404848	chr19	25512451	25514293	+	0 NA	IntergeniALR/Alphe	-1349925 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG0000CHAVCR1P1	-	hepatitispseudo
chr21-107 21.65697	-0.58938	0.478589	-1.23149	0.21814	0.404859	chr21	10760977	10763429	+	0 NA	IntergeniALR/Alphe	240689 NR_19926C	7179 Hs. 122988NR_19926E	ENSG0000CTPT	CT44 PTEN	transmemprotein-coding
chr21-104 15.99114	-0.68163	0.553574	-1.23132	0.218205	0.404859	chr21	10463461	10466048	+	0 NA	IntergeniALR/Alphe	51222 NR_18248E	85319 Hs. 545785NR_18248E	BAGE2	CT2	BAGE famiprotein-coding
chr5-481 15.99114	-0.68163	0.553574	-1.23132	0.218205	0.404859	chr5	48185528	48186711	+	0 NA	IntergeniALR/Alphe	1255169 NR_19844E	133418 Hs. 561411NR_19844E	ENSG0000EMB	GP70	embigin protein-coding
chr12-366 15.87426	-0.68744	0.55849	-1.23088	0.218366	0.404859	chr12	36626864	36627206	+	0 NA	IntergeniALR/Alphe	-1689739 NR_00130E	144245 Hs. 259305NR_00101E	ENSG0000ALG10B	ALG10 KCF	ALG10 alpprotein-coding
chr18-154 15.92325	-0.68104	0.55331	-1.23084	0.218383	0.404859	chr18	15488524	15493689	+	0 NA	IntergeniALR/Alphe	-165187 NR_02741E	644669 Hs. 579474NR_02741E	ENSG0000CLOC64466E	-	ankyrin rpsseudo
chr22-156 16.9747	-0.66117	0.537494	-1.2301	0.218659	0.404946	chr22	15034168	15034716	+	0 NA	IntergeniALR/Alphe	493717 NR_00100E	81061 Hs. 554706NR_00100E	ENSG0000COR1IH1	OR11H12 Col	factoryprotein-coding
chr20-285 15.96944	-0.67976	0.552611	-1.23008	0.218666	0.404946	chr20	28868610	28873492	+	0 NA	IntergeniALR/Alphe	-209339 NR_13231E	1.03E+08 Hs. NR_132316	FRG1DP	-	FSHD regipseudo
chr9-446 21.63527	-0.58796	0.478158	-1.22963	0.218836	0.404958	chr9	44621005	44621252	+	0 NA	IntergeniALR/Alphe	1494962 NR_16066E	1.03E+08 Hs. NR_160669	LOC102724-	-	methylenepseudo
chr5-485 34.23714	-0.47882	0.389464	-1.22943	0.218909	0.404958	chr5	48504932	48506174	+	0 NA	IntergeniALR/Alphe	1935735 NR_19844E	133418 Hs. 561411NR_19844E	ENSG0000EMB	GP70	embigin protein-coding
chr20-276 15.42061	-0.69129	0.562584	-1.22878	0.219154	0.405069	chr20	27604681	27607727	+	0 NA	IntergeniALR/Alphe	996461 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr10-408 15.39612	-0.6946	0.565341	-1.22864	0.219205	0.405069	chr10	40870173	40871118	+	0 NA	IntergeniALR/Alphe	1497400 NR_02438C	441666 Hs. 255725NR_02438C	ENSG0000CLOC44166E	-	zinc fingpseudo
chr20-282 22.54815	-0.57991	0.472301	-1.22783	0.219511	0.405414	chr20	28034414	28035463	+	0 NA	IntergeniALR/Alphe	567727 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr11-534 22.64332	-0.57464	0.468337	-1.22699	0.219826	0.405725	chr11	53435098	53435303	+	0 NA	IntergeniALR/Alphe	1168798 NR_00100A	119749 Hs. 553564NR_00100A	ENSG0000ORAC46	-	olfactoryprotein-coding
chr18-158 16.00726	-0.69397	0.565696	-1.22675	0.219916	0.405725	chr18	15888389	15888792	+	0 NA	IntergeniALR/Alphe	-562671 NR_02741E	644669 Hs. 579474NR_02741E	ENSG0000CLOC64466E	-	ankyrin rpsseudo
chr20-280 21.61357	-0.58655	0.47844	-1.22595	0.220216	0.405869	chr20	28006703	28006966	+	0 NA	IntergeniALR/Alphe	595831 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr20-275 15.4451	-0.68804	0.561242	-1.22591	0.220231	0.405869	chr20	27965609	27968361	+	0 NA	IntergeniALR/Alphe	635680 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr6-592 21.15434	-0.59466	0.485228	-1.22553	0.220375	0.405917	chr6	59270485	59271059	+	0 NA	IntergeniALR/Alphe	-1309326 NR_13299E	1.07E+08 Hs. 561535NR_125727	ENSG0000CLINCO068C	-	long intencRNA
chr10-406 26.30143	-0.53527	0.436925	-1.22508	0.220545	0.406012	chr10	40643315	40645650	+	0 NA	IntergeniALR/Alphe	17236315 NR_02438C	441666 Hs. 255725NR_02438C	ENSG0000CLOC44166E	-	zinc fingpseudo
chr20-276 22.18689	-0.57848	0.472408	-1.22454	0.220748	0.406116	chr20	27644318	27645464	+	0 NA	IntergeniALR/Alphe	957774 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr4-923 15.39891	-0.68937	0.563299	-1.22381	0.221023	0.406116	chr4	9233648	9237494	+	0 NA	IntergeniALR/Alphe	1186 NR_00125E	1E+08 Hs. 528621NR_00125E	ENSG0000CUSP17L15	-	ubiquitinprotein-coding
chr6-585 92.31051	-0.32724	0.267405	-1.22377	0.221039	0.406116	chr6	58560738	58560981	+	0 NA	IntergeniALR/Alphe	-599413 NR_13299E	1.07E+08 Hs. 561535NR_125727	ENSG0000CLINCO068C	-	long intencRNA
chr19-276 15.37442	-0.69267	0.566062	-1.22367	0.221076	0.406116	chr19	27000422	27000627	+	0 NA	IntergeniALR/Alphe	-792907 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG0000CLOC101927-	-	uncharactncRNA
chr20-277 21.15713	-0.59082	0.483067	-1.22307	0.221303	0.40627	chr20	27583937	27585889	+	0 NA	IntergeniALR/Alphe	1017753 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG0000CFRG1CP	-	FSHD regipseudo
chr7-587 21.74936	-0.58763	0.480639	-1.22259	0.221483	0.40627	chr7	58730505	58730839	+	0 NA	IntergeniALR/Alphe	1280495 NR_00115E	441234 Hs. 533121NR_00115E	ENSG0000CZNF716	-	zinc fingprotein-coding
chr21-801 26.89923	-0.52775	0.431722	-1.22243	0.221545	0.40627	chr21	8019335	8020688	+	0 NA	IntergeniALR/Alphe	-177609 NR_03895E	1.01E+08 Hs. 426704NR_03895E	LOC100507-	-	uncharactncRNA
chr19-266 53.78122	-0.39084	0.319782	-1.22219	0.221634	0.40627	chr19	26842726	26843706	+	0 NA	IntergeniALR/Alphe	-950200 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG0000CLOC101927-	-	uncharactncRNA
chr20-265 21.11094	-0.59175	0.484361	-1.2217	0.22182	0.406393	chr20	26914824	26918005	+	0 NA	IntergeniALR/Alphe	-707181 NR_04009E	284801 Hs. 370695NR_04009E	ENSG0000MIR663AH	-	MIR663A lncRNA
chr13-175 15.92603	-0.67602	0.553933	-1.22204	0.222314	0.406862	chr13	17592511	17593034	+	0 NA	IntergeniALR/Alphe	-602525 NR_02727E	26080 Hs. 448582NR_02727E	ENSG0000FAM230C	LINC00281	family wincRNA
chr20-268 15.92603	-0.67602	0.553933	-1.22204	0.222314	0.406862	chr20	26804671	26807420	+	0 NA	IntergeniALR/Alphe	-596812 NR_04009E	284801 Hs. 370695NR_04009E	ENSG0000MIR663AH	-	MIR663A lncRNA
chr19-255 21.18162	-0.58848	0.482546	-1.21952	0.222645	0.406875	chr19	25274916	25276192	+	0 NA	IntergeniALR/Alphe	-1112107 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG0000CHAVCR1P1	-	hepatitispseudo
chr1-125 59.23942	-0.37243	0.30541	-1.21943	0.222682	0.406875	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1414770 NR_00395E	647121 Hs. 697682NR_00395E	ENSG0000EMB1P	-	embigin ppsseudo
chr12-372 22.52645	-0.57854	0.47461	-1.21897	0.222855	0.406875	chr12	37266624	37266892	+	0 NA	IntergeniALR/Alphe	-1050016 NR_00130E	144245 Hs. 259305NR_00101E	ENSG0000ALG10B	ALG10 KCF	ALG10 alpprotein-coding
chr10-403 33.6911	-0.47859	0.392636	-1.2189	0.222881	0.406875	chr10	40391847	40393491	+	0 NA	IntergeniALR/Alphe	1696073 NR_04500C	399746 Hs. 742607NR_04500C	ACTR3BP5 FKSG74	ACTR3B ppsseudo	
chr19-264 16.42867	-0.66553	0.546864	-1.21881	0.222914	0.406875	chr19	26483377	26483903	+	0 NA	IntergeniALR/Alphe	-1309326 NR_13299E	1.07E+08 Hs. 567934NR_110687	ENSG0000CLOC101927-	-	uncharactncRNA
chr20-265 21.61636	-0.58283	0.478557	-1.21789	0.223265	0.407132	chr20	26582324	26584207	+	0 NA	IntergeniALR/Alphe	-374032 NR_04009E	284801 Hs. 370695NR_04009E	ENSG0000MIR663AH	-	MIR663A lncRNA
chr14-175 15.85535	-0.68047	0.5														





chr22-13	16.26722	-0.61979	0.556653	-1.11343	0.265523	0.438293	chr22	13326379	13326853	+	0	NA	IntergeniALR/Alphe	1429210	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC102723-		uncharactncRNA		
chr19-26	38.4068	-0.40887	0.367266	-1.11329	0.265586	0.438293	chr19	26352889	26353692	+	0	NA	IntergeniALR/Alphe	1440141	NR_146732	1.02E+08	Hs.567934NR	110687	ENSG0000C	LOC101927-		uncharactncRNA	
chr22-10	15.675	-0.62541	0.562136	-1.11257	0.265895	0.438592	chr22	10696200	10696539	+	0	NA	IntergeniL2 LINE I	265160	NR_13232C	1.03E+08		NR_132320	FRG1FP	-		FSHD regipseudo	
chr13-167	17.85254	-0.62767	0.56432	-1.11226	0.266028	0.438601	chr13	16767717	16767927	+	0	NA	IntergeniALR/Alphe	1427475	NR_02727E	26808	Hs.44858	NR_02727E	ENSG0000C	FAM230C	LINC00281	family wincRNA	
chr5-486	19.42548	-0.55982	0.503503	-1.11185	0.266204	0.438679	chr5	48653815	48655259	+	0	NA	IntergeniALR/Alphe	1786751	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr5-4981	24.0904	0.521645	0.469524	1.111007	0.266565	0.439064	chr5	49811174	49811405	+	0	NA	IntergeniALR/Alphe	629999	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr1-1231	34.14531	-0.42963	0.386887	-1.11053	0.266771	0.439077	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1588807	NR_00395E	647121	Hs.697682NR	00395E	ENSG0000C	EMB1	-	embigin fpseudo	
chr3-9121	19.35759	-0.5592	0.50361	-1.11039	0.266883	0.439077	chr3	91213803	91214234	+	0	NA	IntergeniALR/Alphe	1206397	NR_00523E	2042	Hs.123642NR	00523E	ENSG0000C	EPHA3	EK4 ETK E EPH	recepprotein-coding	
chr5-492	50.89899	-0.36102	0.32532	-1.10974	0.267111	0.439328	chr5	49208430	49208716	+	0	NA	IntergeniALR/Alphe	1232715	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr7-6001	18.39573	-0.57295	0.516723	-1.10881	0.267513	0.439779	chr7	60013344	60013980	+	0	NA	IntergeniALR/Alphe	2563485	NR_00115E	441234	Hs.533121NR	00115E	ENSG0000C	ZNF716	-	zinc fingprotein-coding	
chr20-26	18.85496	-0.56428	0.509378	-1.10778	0.267956	0.440085	chr20	26538057	26540701	+	0	NA	IntergeniALR/Alphe	330146	NR_04009E	284801	Hs.370695NR	04009E	ENSG0000C	MIR663AHC	-	MIR663A lncRNA	
chr20-27	18.85496	-0.56428	0.509378	-1.10778	0.267956	0.440085	chr20	27865478	27865702	+	0	NA	IntergeniALR/Alphe	737075	NR_13231E	1E+08	Hs.529357NR	13231E	ENSG0000C	FRG1CP	-	FSHD regipseudo	
chr1-122	30.81562	-0.45836	0.413935	-1.10732	0.268155	0.440201	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1311253	NR_00395E	647121	Hs.697682NR	00395E	ENSG0000C	EMB1	-	embigin fpseudo	
chr5-494	49.70896	-0.36228	0.327256	-1.10702	0.268286	0.440205	chr5	49464927	49466069	+	0	NA	IntergeniALR/Alphe	975790	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr20-267	16.63407	-0.61075	0.552046	-1.10633	0.268582	0.440315	chr20	26779108	26779529	+	0	NA	IntergeniALR/Alphe	570085	NR_04009E	284801	Hs.370695NR	04009E	ENSG0000C	MIR663AHC	-	MIR663A lncRNA	
chr17-25	49.22803	-0.36293	0.32807	-1.10627	0.268661	0.440315	chr17	25082611	25082851	+	0	NA	IntergeniALR/Alphe	2006510	NR_135673	1.05E+08	Hs.649918NR	135673	LOC105371-		uncharactncRNA		
chr19-257	44.48172	-0.38151	0.345187	-1.10522	0.269066	0.440851	chr19	25733804	25734023	+	0	NA	IntergeniALR/Alphe	1570466	NR_00360E	1E+08	Hs.149312NR	00360E	ENSG0000C	HAVCR1P1	-	hepatitispsseudo	
chr1-1217	34.24048	-0.42626	0.385962	-1.10441	0.269415	0.441212	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	226991	NR_00395E	647121	Hs.697682NR	00395E	ENSG0000C	EMB1	-	embigin fpseudo	
chr21-83	57.70592	-0.34218	0.309998	-1.10382	0.269673	0.441272	chr21	8385781	8387075	+	0	NA	intron (intron (delta	-1934	NR_12871E	1.04E+08		NR_12871E	ENSG0000C	MIR6724-	hsa-mir-	microRNA ncRNA	
chr1-123	19.38208	-0.56665	0.504334	-1.10373	0.269709	0.441272	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1706296	NR_00395E	647121	Hs.697682NR	00395E	ENSG0000C	EMB1	-	embigin fpseudo	
chr7-608	26.77455	-0.4759	0.431821	-1.10208	0.270428	0.442076	chr7	60803527	60803803	+	0	NA	IntergeniALR/Alphe	2506391	NR_00395E	643955	Hs.583308NR	00395E	ENSG0000C	ZNF733P	ZNF733	zinc fingpseudo	
chr5-490	19.26521	-0.56111	0.509256	-1.10182	0.270538	0.442076	chr5	49032207	49032931	+	0	NA	IntergeniALR/Alphe	1408719	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr11-534	18.83326	-0.56265	0.51071	-1.10171	0.270588	0.442076	chr11	53454475	53455701	+	0	NA	IntergeniALR/Alphe	1148910	NR_001004	119749	Hs.553564NR	001004	ENSG0000C	OR4C46	-	olfactoryprotein-coding	
chr19-25	26.29362	-0.47194	0.435372	-1.10054	0.271097	0.442698	chr19	25802797	25803357	+	0	NA	IntergeniALR/Alphe	1639630	NR_00360E	1E+08	Hs.149312NR	00360E	ENSG0000C	HAVCR1P1	-	hepatitispsseudo	
chr6-5934	17.8497	-0.57527	0.523134	-1.09966	0.271482	0.443114	chr6	59342733	59345761	+	0	NA	IntergeniALR/Alphe	1382801	NR_13299E	1.07E+08	Hs.561535NR	125727	ENSG0000C	LINC0068C	-	long intencRNA	
chr5-478	33.21073	-0.42952	0.390872	-1.09886	0.271827	0.443467	chr5	47855246	47857101	+	0	NA	IntergeniALR/Alphe	2159794	NR_02107E	348980	Hs.35317E	NR_02107E	ENSG0000C	HCN1	BCNG-1 B	hyperpolprotein-coding	
chr5-480	26.27192	-0.47795	0.435505	-1.09746	0.272439	0.444228	chr5	48068271	48068578	+	0	NA	IntergeniALR/Alphe	2372044	NR_02107E	348980	Hs.35317E	NR_02107E	ENSG0000C	HCN1	BCNG-1 B	hyperpolprotein-coding	
chr17-22	79.76978	-0.30043	0.273811	-1.0972	0.272553	0.444228	chr17	22976497	22977768	+	0	NA	IntergeniALR/Alphe	454021	NR_00119C	1E+08	Hs.740185NR	00119C	ENSG0000C	MTRNR2L1	HN1	MT-RNR2	lprotein-coding
chr5-490	36.39627	-0.4112	0.375058	-1.09638	0.272914	0.444406	chr5	49055825	49058084	+	0	NA	IntergeniALR/Alphe	1384434	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr5-484	22.12731	-0.51961	0.473951	-1.09633	0.272934	0.444406	chr5	48483143	48483579	+	0	NA	IntergeniALR/Alphe	1957924	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr5-493	18.85775	-0.56004	0.510952	-1.09606	0.273052	0.444406	chr5	49381192	49381512	+	0	NA	IntergeniALR/Alphe	1059936	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr6-5907	17.36877	-0.58302	0.532215	-1.09546	0.273314	0.444621	chr6	59070324	59071091	+	0	NA	IntergeniALR/Alphe	1109261	NR_13299E	1.07E+08	Hs.561535NR	125727	ENSG0000C	LINC0068C	-	long intencRNA	
chr19-261	42.76735	-0.38285	0.349825	-1.0944	0.27378	0.445169	chr19	26120147	26120524	+	0	NA	IntergeniALR/Alphe	1673096	NR_146733	1.02E+08	Hs.567934NR	110687	ENSG0000C	LOC101927-		uncharactncRNA	
chr20-27	17.85249	-0.57082	0.522804	-1.09184	0.274904	0.446479	chr20	27354139	27356616	+	0	NA	IntergeniALR/Alphe	1146144	NR_04009E	284801	Hs.370695NR	04009E	ENSG0000C	MIR663AHC	-	MIR663A lncRNA	
chr20-28	17.85249	-0.57082	0.522804	-1.09184	0.274904	0.446479	chr20	28820977	28821467	+	0	NA	IntergeniALR/Alphe	218557	NR_13231E	1E+08	Hs.529357NR	13231E	ENSG0000C	FRG1CP	-	FSHD regipseudo	
chr19-25	33.16733	-0.42758	0.391675	-1.09167	0.274977	0.446479	chr19	25087989	25090286	+	0	NA	IntergeniALR/Alphe	925699	NR_00360E	1E+08	Hs.149312NR	00360E	ENSG0000C	HAVCR1P1	-	hepatitispsseudo	
chr10-41	19.24351	-0.55948	0.512771	-1.09109	0.275232	0.446515	chr10	41373034	41373346	+	0	NA	IntergeniALR/Alphe	994855	NR_02438C	441666	Hs.255725NR	02438C	ENSG0000C	LOC44166E	-	zinc fingpseudo	
chr5-491	64.57567	-0.31897	0.292373	-1.09095	0.275294	0.446515	chr5	49182237	49183369	+	0	NA	IntergeniALR/Alphe	1258485	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr20-27	17.32537	-0.5795	0.531354	-1.09061	0.275446	0.446515	chr20	27827668	27829743	+	0	NA	IntergeniALR/Alphe	773960	NR_13231E	1E+08	Hs.529357NR	13231E	ENSG0000C	FRG1CP	-	FSHD regipseudo	
chr1-1241	21.55678	-0.52251	0.479176	-1.09044	0.27552	0.446515	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2583125	NR_00395E	647121	Hs.697682NR	00395E	ENSG0000C	EMB1	-	embigin fpseudo	
chr21-11	15.22135	-0.62716	0.575889	-1.08902	0.276144	0.447314	chr21	11904755	11904848	+	0	NA	IntergeniALR/Alphe	1133455	NR_02691E	149992	Hs.55864E	NR_153773	ANKRD30BF	C21orf99	ankyrin fpseudo		
chr11-51	86.81098	-0.28222	0.259414	-1.08792	0.276632	0.447825	chr11	51097822	51098096	+	0	NA	IntergeniALR/Alphe	688812	NR_024504	646813	Hs.684175NR	024504	LOC646813-		DEXH-box pseudo		
chr5-492	35.87194	-0.41092	0.377884	-1.08742	0.276851	0.447825	chr5	49260323	49261153	+	0	NA	IntergeniALR/Alphe	1180550	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr2-9341	26.66046	-0.47601	0.437747	-1.08742	0.276851	0.447825	chr2	93414411	93414616	+	0	NA	IntergeniALR/Alphe	73906	NR_146105	728034	Hs.561411NR	146105	BMS1P14	-	BMS1 psetpseudo		
chr5-489	26.15393	-0.48952	0.450581	-1.08642	0.277293	0.448255	chr5	48962019	48962232	+	0	NA	IntergeniALR/Alphe	1479163	NR_19844E	133418	Hs.561411NR	19844E	ENSG0000C	EMB	GP70	embigin protein-coding	
chr10-404	21.55957	-0.51879	0.477876	-1.08562	0.277646	0.448255	chr10	40476464	40478829	+	0	NA	IntergeniALR/Alphe	1781050	NR_04500C	339746	Hs.742607NR	045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr20-27	22.0405	-0.51398	0.473647	-1.08516	0.27785	0.448255	chr20	27212045	27212885	+	0	NA	IntergeniALR/Alphe	1003232	NR_04009E	284801	Hs.370695NR	04009E	ENSG0000C	MIR663AHC	-	MIR663A lncRNA	
chr6-596	17.30366	-0.57775	0.532417	-1.08515	0.277855	0.448255	chr6	59686391	59686595	+	0	NA	IntergeniALR/Alphe	1725974	NR_13299E	1.07E+08	Hs.561535NR	125727	ENSG0000C	LINC0068C	-	long intencRNA	
chr1-124	35.94262	-0.40909	0.377705	-1.0849	0.277966	0.448255	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2979795	NR_00395E	647121	Hs.697682NR						



chr10-406	30.2061	-0.42496	0.408228	-1.04097	0.297887	0.464314	chr10	40673460	40673667	+	0	NA	IntergeniALR/Alphe	1694482	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud	
chr13-17	20.15243	-0.51629	0.496183	-1.04053	0.298094	0.464412	chr13	17315416	17315692	+	0	NA	IntergeniALR/Alphe	-879743	NR_027278	26080	Hs.44858	NR_027278	ENSG0000C.FAM230C	LINC00281	family	wincRNA	
chr10-408	22.82976	-0.48484	0.466073	-1.04025	0.298221	0.464412	chr10	40833171	40834292	+	0	NA	IntergeniALR/Alphe	1534314	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud	
chr1-123	34.76096	-0.40511	0.39046	-1.03751	0.299499	0.466189	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1578717	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr10-407	18.62005	-0.50857	0.513302	-1.03243	0.301027	0.468278	chr10	40763185	40764350	+	0	NA	IntergeniALR/Alphe	1604278	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud	
chr1-123	32.93521	-0.40551	0.392247	-1.03381	0.301225	0.468278	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1531111	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr1-124	27.2211	-0.47905	0.46343	-1.03371	0.30127	0.468278	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3232285	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr20-265	17.33652	-0.56069	0.542569	-1.03339	0.30142	0.468278	chr20	26935661	26935885	+	0	NA	IntergeniALR/Alphe	-726540	NR_04009E	284801	Hs.370695	NR_04009E	ENSG0000C.MIR663AHC	-	MIR663A	lncRNA	
chr1-124	18.55215	-0.53019	0.513171	-1.03317	0.301524	0.468278	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2511304	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr6-602	19.48283	-0.54118	0.524351	-1.03209	0.30203	0.468683	chr6	60234132	60234340	+	0	NA	IntergeniALR/Alphe	-1339894	NR_00119C	1E+08	Hs.	1190706	MTRNR2L9	HN9	MT-RNR2	lprotein-coding	
chr2-9401	22.76466	-0.48703	0.465809	-1.03203	0.302059	0.468683	chr2	94011196	94011422	+	0	NA	IntergeniALR/Alphe	197110	NR_146105	728034	NR.146105	BMS1P14	-	BMS1	pseudoprotein-coding		
chr4-4984	16.28507	-0.5739	0.556295	-1.03165	0.302236	0.468747	chr4	49841247	49841696	+	0	NA	IntergeniALR/Alphe	854829	NR_00128E	80157	Hs.479702	NR_025087	ENSG0000C.CWH43	CWH43-C	Cell	wallprotein-coding	
chr1-125	18.57664	-0.52757	0.512439	-1.02953	0.30323	0.469862	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1388345	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr20-266	18.57664	-0.52757	0.512439	-1.02953	0.30323	0.469862	chr20	26922289	26924253	+	0	NA	IntergeniALR/Alphe	-714328	NR_04009E	284801	Hs.370695	NR_04009E	ENSG0000C.MIR663AHC	-	MIR663A	lncRNA	
chr1-244	16.47256	0.571272	0.556181	1.027134	0.304358	0.47137	chr1	2440413	2440671	+	0	NA	IntergeniCpG	-26909	NR_00130E	9651	Hs.17015E	NR_014638	ENSG0000C.PLCH2	PLC-L4	PL	phospholiprotein-coding	
chr5-4795	55.61579	-0.31955	0.311186	-1.02688	0.304478	0.47137	chr5	47924481	47924712	+	0	NA	IntergeniALR/Alphe	-2228216	NR_02107E	348980	Hs.35317E	NR_02107E	ENSG0000C.HCN1	BCNG-1	BC	hyperpolprotein-coding	
chr1-127	31.88096	-0.40976	0.399559	-1.02554	0.305108	0.472132	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1370751	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr19-27	53.00078	-0.32621	0.31825	-1.025	0.305364	0.472166	chr19	27020554	27020787	+	0	NA	IntergeniALR/Alphe	-772761	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG0000C.LOC101927	-	uncharactncRNA		
chr5-4904	31.21694	-0.41777	0.407646	-1.02484	0.305436	0.472166	chr5	49042810	49043746	+	0	NA	IntergeniALR/Alphe	1398010	NR_19844E	133418	Hs.561411	NR_19844E	ENSG0000C.EMB	GP70	embigin	protein-coding	
chr18-205	25.42029	-0.45528	0.444667	-1.02388	0.305894	0.472166	chr18	20920232	20923103	+	0	NA	IntergeniALR/Alphe	190146	NR_00540E	6093	Hs.306307	NR_00540E	ENSG0000C.ROCK1	P160ROCK	Rho	assocprotein-coding	
chr19-27	53.00078	-0.40524	0.393162	-1.02385	0.305906	0.472166	chr19	27069326	27069544	+	0	NA	IntergeniALR/Alphe	-723996	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG0000C.LOC101927	-	uncharactncRNA		
chr12-372	21.7811	-0.4873	0.475985	-1.02377	0.305944	0.472166	chr12	37235338	37236302	+	0	NA	IntergeniALR/Alphe	-1080954	NR_00130E	144245	Hs.25930E	NR_00101E	ENSG0000C.ALG10B	ALG10	KCF	ALG10	alprotein-coding
chr8-4417	22.16685	-0.4885	0.477228	-1.02362	0.306013	0.472166	chr8	44174599	44175592	+	0	NA	IntergeniALR/Alphe	882653	NR_00100E	340441	Hs.53157E	NR_00100E	ENSG0000C.POTE	A26A1	CT1	POTE	ankyprotein-coding
chr8-456	18.00333	-0.53571	0.523435	-1.02345	0.306095	0.472166	chr8	45639961	45640835	+	0	NA	IntergeniALR/Alphe	977245	NR_146077	389652	NR.146077	ENSG0000C.ASNP1	ASNSL1	asparagipseudo			
chr10-402	21.7349	-0.48812	0.477482	-1.02228	0.306647	0.472592	chr10	40246748	40248460	+	0	NA	IntergeniALR/Alphe	1551008	NR_04500C	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr10-403	21.7349	-0.48812	0.477482	-1.02228	0.306647	0.472592	chr10	40396648	40397790	+	0	NA	IntergeniALR/Alphe	40396648	NR_04500C	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr10-411	36.55827	-0.38617	0.377966	-1.02169	0.306926	0.47281	chr10	41143920	41144303	+	0	NA	IntergeniALR/Alphe	1220634	NR_02438C	441666	Hs.255725	NR_02438C	ENSG0000C.LOC441666	-	zinc	fingerpseud	
chr3-918	32.56836	-0.40708	0.398821	-1.0207	0.307396	0.473321	chr3	91865256	91865540	+	0	NA	IntergeniALR/Alphe	2108683	NR_001314	5627	Hs.64016	NR_00031E	ENSG0000C.PROS1	PROS1	PS21	protein	protein-coding
chr5-4897	35.17669	-0.40063	0.392961	-1.01953	0.307953	0.473756	chr5	48979351	48979602	+	0	NA	IntergeniALR/Alphe	1461812	NR_19844E	133418	Hs.561411	NR_19844E	ENSG0000C.EMB	GP70	embigin	protein-coding	
chr9-4098	17.5224	-0.54227	0.53189	-1.01952	0.307955	0.473756	chr9	40982447	40983912	+	0	NA	IntergeniLIMAG LID	-9082	NR_15673C	1E+08	Hs.	15673C	FRG1H	-	FSHD	regipseudo	
chr1-122	60.00084	-0.30687	0.301194	-1.01886	0.308269	0.474026	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1052348	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr20-287	17.57138	-0.5366	0.526907	-1.0184	0.308486	0.474147	chr20	28780595	28787216	+	0	NA	IntergeniALR/Alphe	-181240	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGL1CP	-	FSHD	regipseudo	
chr5-495	22.26482	-0.47966	0.471197	-1.01796	0.308696	0.474257	chr5	49567719	49569712	+	0	NA	IntergeniALR/Alphe	872543	NR_19844E	133418	Hs.561411	NR_19844E	ENSG0000C.EMB	GP70	embigin	protein-coding	
chr1-124	18.00612	-0.53128	0.52256	-1.01668	0.309305	0.474852	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2938015	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr20-287	29.0694	0.426568	0.419683	1.016403	0.309437	0.474852	chr20	28534153	28534745	+	0	NA	IntergeniALR/Alphe	68216	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGL1CP	-	FSHD	regipseudo	
chr21-127	21.25119	-0.49636	0.488427	-1.01624	0.309516	0.474852	chr21	12711699	12711929	+	0	NA	IntergeniALR/Alphe	-326352	NR_02691E	149992	Hs.55864E	NR_153773	ANKRD30B	C21orf99	ankyrin	fpseudo	
chr11-51	17.63928	-0.53734	0.528888	-1.01598	0.309638	0.474852	chr11	51925566	51926266	+	0	NA	IntergeniALR/Alphe	1516769	NR_024504	646813	Hs.68417E	NR_024504	LOC64681E	-	DEXH-box	pseudo	
chr5-4791	34.59115	-0.38922	0.383954	-1.01372	0.310714	0.476289	chr5	47912908	47914813	+	0	NA	IntergeniALR/Alphe	-2217480	NR_02107E	348980	Hs.35317E	NR_02107E	ENSG0000C.HCN1	BCNG-1	BC	hyperpolprotein-coding	
chr1-122	30.39366	-0.41993	0.414474	-1.01317	0.310977	0.476363	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1476114	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr19-24	22.67506	-0.4787	0.472552	-1.013	0.311059	0.476363	chr19	24976648	24978063	+	0	NA	IntergeniALR/Alphe	-813908	NR_00360E	1E+08	Hs.149312	NR_00360E	ENSG0000C.HAVCR1P1	-	hepatitis	pseudo	
chr13-16	19.10656	-0.51659	0.510086	-1.01275	0.31118	0.476363	chr13	16366093	16366324	+	0	NA	IntergeniALR/Alphe	-1659899	NR_027278	26080	Hs.44858	NR_027278	ENSG0000C.FAM230C	LINC00281	family	wincRNA	
chr14-17	17.09045	-0.54336	0.536942	-1.01196	0.311558	0.476531	chr14	17362088	17362349	+	0	NA	IntergeniALR/Alphe	-1238899	NR_00101E	440153	Hs.53488C	NR_00101E	ENSG0000C.ORI1H1	ORI1H1	Col	factoryprotein-coding	
chr20-284	29.06506	-0.42588	0.420852	-1.01194	0.311567	0.476531	chr20	28473938	28474450	+	0	NA	IntergeniALR/Alphe	128471	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG0000C.FRGL1CP	-	FSHD	regipseudo	
chr9-605	40.4596	-0.36308	0.358923	-1.01159	0.311733	0.476572	chr9	60591243	60591488	+	0	NA	IntergeniALR/Alphe	-323042	NR_00111E	727905	Hs.645497	NR_00111E	ENSG0000C.SPATA31A	FAM75A5	SPATA31	sprotein-coding	
chr11-534	70.49088	-0.28529	0.282106	-1.01128	0.311883	0.476589	chr11	53456744	53456998	+	0	NA	IntergeniALR/Alphe	1147127	NR_001004	119749	Hs.553564	NR_001004	ENSG0000C.ORAC46	-	olfactory	protein-coding	
chr5-472	17.11494	-0.54047	0.535448	-1.00938	0.312793	0.477369	chr5	47292625	47297963	+	0	NA	IntergeniALR/Alphe	-1600749	NR_02107E	348980	Hs.35317E	NR_02107E	ENSG0000C.HCN1	BCNG-1	BC	hyperpolprotein-coding	
chr6-5964	17.6554	-0.54878	0.54377	-1.00921	0.312872	0.477369	chr6	59648794	59649186	+	0	NA	IntergeniALR/Alphe	-1687544	NR_13299E	1.07E+08	Hs.56153E	NR_125727	ENSG0000C.LINC0068C	-	long	intencRNA	
chr1-124	34.80604	-0.40949	0.405817	-1.00904	0.312955	0.477369	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2973183	NR_00395E	647121	Hs.697682	NR_00395E	ENSG0000C.EMB1	-	embigin	fpseudo	
chr19-251	21.78668	-0.47998	0.475751	-1.0089	0.313024	0.477369	chr19	25192098	25194107	+	0	NA											

chr5-4828	23.4916	-0.44621	0.495511	-0.97106	0.331516	0.489313	chr5	48280249	48280723	+	0	NA	IntergeniALR/Alphe	2160802	NM_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr1-1234	51.89537	-0.3172	0.326735	-0.97082	0.331636	0.489313	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1949633	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr19-265	20.143	-0.4869	0.501881	-0.97014	0.331976	0.489393	chr19	26980787	26980999	+	0	NA	IntergeniALR/Alphe	-812538	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-		uncharactncRNA
chr17-263	84.95413	-0.2619	0.269956	-0.97014	0.331976	0.489393	chr17	26328659	26328911	+	0	NA	IntergeniALR/Alphe	760456	NR_135673	1.05E+08	Hs.649918NR_135673	ENSG00000	LOC105371-		uncharactncRNA
chr6-5866	15.0666	-0.54866	0.566437	-0.96861	0.33274	0.490308	chr6	58685069	58685926	+	0	NA	IntergeniALR/Alphe	58685069	NR_132995	1.07E+08	Hs.561535NR_125727	ENSG00000	LINC00681-		long intencRNA
chr1-1245	16.14254	-0.53329	0.5514	-0.96716	0.333462	0.490973	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	2988616	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr11-516	26.11253	-0.42386	0.438384	-0.96686	0.333615	0.490973	chr11	51800188	51800415	+	0	NA	IntergeniALR/Alphe	1391154	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC646813-		DEXH-box pseudo
chr20-266	15.11279	-0.54745	0.566225	-0.96668	0.333644	0.490973	chr20	26696172	26698193	+	0	NA	IntergeniALR/Alphe	-487949	NR_040095	284801	Hs.370695NR_040095	ENSG00000	MIR663AHC-		MIR663A lncRNA
chr19-252	19.34699	-0.48685	0.503689	-0.96656	0.333764	0.490973	chr19	25299835	25300693	+	0	NA	IntergeniALR/Alphe	-1136817	NR_003603	1E+08	Hs.149312NR_003603	ENSG00000	HAVCR1P1		hepatitispseudo
chr19-271	37.49559	-0.35802	0.370916	-0.96524	0.334426	0.491735	chr19	27138456	27140712	+	0	NA	IntergeniALR/Alphe	-653847	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-		uncharactncRNA
chr10-395	18.75198	-0.49183	0.51077	-0.96293	0.335584	0.493226	chr10	39936594	39937584	+	0	NA	IntergeniALR/Alphe	29936594	NR_003955	399746	Hs.742607NR_045000	ENSG00000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr16-377	28.39262	-0.40757	0.423538	-0.96229	0.335904	0.493485	chr16	37749960	37750295	+	0	NA	IntergeniALR/Alphe	2003575	NR_033985	400533	Hs.499135NR_033985	ENSG00000	LINC02167-		long intencRNA
chr7-5953	38.24708	-0.36427	0.378997	-0.96114	0.33648	0.49412	chr7	59538057	59538324	+	0	NA	IntergeniALR/Alphe	2088013	NR_001155	441234	Hs.533121NM_001155	ENSG00000	ZNF716		zinc fingprotein-coding
chr5-1752	34.35624	-0.3702	0.385635	-0.95999	0.337062	0.494762	chr5	17525188	17527945	+	0	NA	IntergeniIntergeni	82556	NR_13427C	1.03E+08	NR_13427C	ENSG00000	LINC02218-		long intencRNA
chr17-236	47.81698	-0.32074	0.334309	-0.95942	0.337349	0.494971	chr17	23696720	23696930	+	0	NA	IntergeniALR/Alphe	1173714	NR_00119C	1E+08	Hs.740185NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr22-137	23.49439	-0.44276	0.461798	-0.95878	0.337669	0.495129	chr22	13741327	13741546	+	0	NA	IntergeniALR/Alphe	-1786723	NR_001005	81061	Hs.554706NM_001005	ENSG00000	OR11H1	OR11H12	Colfactoryprotein-coding
chr5-4913	37.56906	-0.35413	0.369412	-0.95863	0.337746	0.495129	chr5	49197568	49197861	+	0	NA	IntergeniALR/Alphe	1243574	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr1-1233	18.31724	-0.49594	0.518362	-0.95675	0.338696	0.49631	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1741699	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr17-255	18.80096	-0.48669	0.509402	-0.95542	0.339367	0.49708	chr17	25963986	25964529	+	0	NA	IntergeniALR/Alphe	1124984	NR_135673	1.05E+08	Hs.649918NR_135673	ENSG00000	LOC105371-		uncharactncRNA
chr10-406	34.42692	-0.36833	0.38589	-0.9545	0.339832	0.497165	chr10	40609163	40609464	+	0	NA	IntergeniALR/Alphe	1758732	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000	LOC441666-		zinc fingpseudo
chr1-1247	21.98371	-0.4515	0.473046	-0.95444	0.33986	0.497165	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3211559	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr8-4405	21.98371	-0.4515	0.473046	-0.95444	0.33986	0.497165	chr8	44056069	44057021	+	0	NA	IntergeniALR/Alphe	764103	NR_001002	340441	Hs.531575NM_001002	ENSG00000	POTEA	A26A1	CTIPOTE ankyprotein-coding
chr19-265	15.6644	-0.53541	0.561352	-0.9538	0.340187	0.497431	chr19	26538547	26539620	+	0	NA	IntergeniALR/Alphe	-1254348	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-		uncharactncRNA
chr15-186	18.19758	-0.50535	0.530279	-0.95298	0.340598	0.49782	chr15	18668862	18669455	+	0	NA	IntergeniALR/Alphe	-1613586	NR_03883C	646096	Hs.448785NR_03883C	ENSG00000	CHEK2P2		checkpoirpseudo
chr1-1237	19.2357	-0.4829	0.506966	-0.95253	0.34083	0.497947	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2213547	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr10-414	34.70138	-0.36828	0.387048	-0.9515	0.34135	0.498473	chr10	41466548	41466900	+	0	NA	IntergeniALR/Alphe	901321	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000	LOC441666-		zinc fingpseudo
chr10-408	22.48913	-0.44612	0.469015	-0.95118	0.341511	0.498473	chr10	40822031	40822542	+	0	NA	IntergeniALR/Alphe	1545759	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000	LOC441666-		zinc fingpseudo
chr19-245	28.88191	-0.39735	0.417845	-0.95096	0.341627	0.498473	chr19	24959239	24960235	+	0	NA	IntergeniALR/Alphe	-796290	NR_003603	1E+08	Hs.149312NR_003603	ENSG00000	HAVCR1P1		hepatitispseudo
chr2-9302	22.53532	-0.44537	0.468741	-0.95014	0.342042	0.498866	chr2	93025965	93026265	+	0	NA	IntergeniALR/Alphe	1084982	NR_027714	440888	Hs.730235NM_001032412	ENSG00000	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr12-357	18.73307	-0.48595	0.512402	-0.94839	0.342933	0.499543	chr12	33786055	35786498	+	0	NA	IntergeniALR/Alphe	1763780	NR_032834	84920	Hs.102971NM_032834	ENSG00000	ALG10	ALG10A	DIALG10 alprotein-coding
chr14-171	17.79291	-0.49776	0.525241	-0.94768	0.343292	0.500263	chr14	17128289	17128995	+	0	NA	IntergeniALR/Alphe	-1472475	NR_001013	440153	Hs.534888NM_001013	ENSG00000	OR11H12		olfactoryprotein-coding
chr10-395	21.52727	-0.45262	0.478266	-0.94638	0.343953	0.501013	chr10	39599775	39990787	+	0	NA	IntergeniALR/Alphe	1293685	NR_045000	399746	Hs.742607NR_045000	ENSG00000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr19-256	27.6173	-0.4135	0.437108	-0.946	0.344148	0.501024	chr19	26605006	26605224	+	0	NA	IntergeniALR/Alphe	-1441668	NR_003603	1E+08	Hs.149312NR_003603	ENSG00000	HAVCR1P1		hepatitispseudo
chr19-264	18.27663	-0.48821	0.516324	-0.94556	0.344375	0.501024	chr19	26489812	26491742	+	0	NA	IntergeniALR/Alphe	-1302654	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-		uncharactncRNA
chr5-4946	43.78265	-0.33327	0.35248	-0.94551	0.344399	0.501024	chr5	49467892	49468145	+	0	NA	IntergeniALR/Alphe	973270	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr10-407	45.69405	-0.32099	0.339681	-0.94497	0.344675	0.501213	chr10	40736163	40736461	+	0	NA	IntergeniALR/Alphe	1631732	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000	LOC441666-		zinc fingpseudo
chr5-4998	33.85919	-0.36546	0.387179	-0.94389	0.345224	0.501476	chr5	49989733	49990011	+	0	NA	IntergeniALR/Alphe	451416	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr1-1217	24.71821	-0.42262	0.44776	-0.94385	0.345247	0.501476	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	2045572	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr17-235	15.96056	-0.53265	0.564526	-0.94353	0.345407	0.501476	chr17	23523166	23523369	+	0	NA	IntergeniALR/Alphe	100156	NR_00119C	1E+08	Hs.740185NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr5-4901	27.94454	-0.39897	0.422879	-0.94347	0.345442	0.501476	chr5	49012955	49013196	+	0	NA	IntergeniALR/Alphe	1428213	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr1-1224	15.11837	-0.53692	0.569438	-0.94289	0.345736	0.501691	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	881023	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr21-822	57.95619	-0.29505	0.313352	-0.9416	0.346399	0.502439	chr21	8202682	82023996	+	0	NA	Intergeni intron (LIMC4 L1)	-1976	NR_10678	1.02E+08	NR_10678	ENSG00000	MIR6724-1	MIR6724	lmiRNA ncRNA
chr1-1241	18.84994	-0.48151	0.511794	-0.94082	0.346795	0.502597	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2612578	NR_003955	647121	Hs.697682NR_003955	ENSG00000	EMB	GP70	emigin protein-coding
chr5-4927	20.74638	-0.47032	0.499908	-0.94081	0.346801	0.502597	chr5	49277240	49277443	+	0	NA	IntergeniALR/Alphe	1163947	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr5-4932	36.52039	-0.35199	0.374443	-0.94003	0.347203	0.502611	chr5	49324904	49326221	+	0	NA	IntergeniALR/Alphe	1115726	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr5-4888	18.30112	-0.48557	0.516563	-0.94001	0.347213	0.502611	chr5	48805625	48806140	+	0	NA	IntergeniALR/Alphe	1635406	NR_198444	133418	Hs.561411NM_198444	ENSG00000	EMB	GP70	emigin protein-coding
chr11-516	18.71136	-0.48427	0.515212	-0.93994	0.347251	0.502611	chr11	51619036	51619259	+	0	NA	IntergeniALR/Alphe	1210000	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC646813-		DEXH-box pseudo
chr11-515	57.07079	-0.29238	0.311267	-0.93933	0.347563	0.502851	chr11	51387664	51387991	+	0	NA	IntergeniALR/Alphe	978680	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC646813-		DEXH-box pseudo
chr7-6147	19.29028	-0.50153	0.534475	-0.93836	0.34806	0.503358	chr7	61409848	61410802	+	0	NA	IntergeniALR/Alphe	1893731	NR_003955	643955	Hs.583308NR_003955	ENSG00000	ZNF733P	ZNF733	zinc fingpseudo
chr5-4774	27.90114	-0.39668																			



chr20-27	18.99799	-0.45359	0.507057	-0.89455	0.371028	0.519691	chr20	27010125	27012140	+	0	NA	IntergeniALR/Alphe	-801899	NR_040095	284801	Hs.370695	NR_040095	ENSG00000	MIR663AHC-	MIR663A	lncRNA						
chr17-244	15.72286	-0.49813	0.556863	-0.89454	0.371035	0.519691	chr17	24416819	24417018	+	0	NA	IntergeniALR/Alphe	1893807	NM_00119C	1E+08	Hs.74018E	NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2	lprotein-coding					
chr17-252	15.72286	-0.49813	0.556863	-0.89454	0.371035	0.519691	chr17	25211314	25211808	+	0	NA	IntergeniALR/Alphe	1877680	NR_135673	1.05E+08	Hs.64991E	NR_135673	LOC105371-				uncharactncRNA					
chr1-1247	36.76641	-0.33332	0.372958	-0.89372	0.371472	0.520091	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3222246	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr1-1247	15.79354	-0.49398	0.553313	-0.89276	0.371986	0.520598	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3184691	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr11-512	15.32874	-0.51279	0.574722	-0.89224	0.372262	0.520771	chr11	51234761	51235677	+	0	NA	IntergeniALR/Alphe	826072	NR_024504	646813	Hs.68417E	NR_024504	LOC646813-				DEXH-box	pseudo				
chr1-1245	53.88029	-0.28642	0.3213	-0.89144	0.372695	0.521164	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3167800	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr2-945	15.31261	-0.50003	0.562175	-0.88946	0.373755	0.522282	chr2	94501867	94502562	+	0	NA	IntergeniALR/Alphe	84969	NR_02444E	1E+08	Hs.645502	NR_02444E	ENSG00000	LOC101033-				methylene	pseudo			
chr20-265	18.90561	-0.45543	0.512075	-0.88938	0.373799	0.522282	chr20	26557541	26559101	+	0	NA	IntergeniALR/Alphe	-349088	NR_040095	284801	Hs.370695	NR_040095	ENSG00000	MIR663AHC-	MIR663A	lncRNA						
chr1-1215	51.37768	-0.28998	0.326312	-0.88866	0.374184	0.522607	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	256140	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr22-113	30.82728	-0.35896	0.404293	-0.88788	0.374608	0.522986	chr22	11365760	11371503	+	0	NA	IntergeniALR/Alphe	-408602	NR_13232E	1.03E+08	NR_132320	FRG1FP					FSHD	regipseudo				
chr1-1233	26.92874	-0.38687	0.436019	-0.88728	0.37493	0.523222	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1878537	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr21-107	15.29091	-0.49803	0.561755	-0.88657	0.375311	0.523541	chr21	10782326	10793392	+	0	NA	IntergeniALR/Alphe	266345	NM_19926E	7179	Hs.12298E	NM_19925E	ENSG00000	TPTE	CT44 PTEN	transmem	protein-coding					
chr8-458	18.49536	-0.45587	0.514563	-0.88593	0.375653	0.523804	chr8	45835192	45835535	+	0	NA	IntergeniALR/Alphe	782280	NR_146077	389652	NR_146077	ENSG00000	ASNSP1	ASNSL1	asparagir	pseudo						
chr21-911	15.24472	-0.49918	0.563754	-0.88546	0.37591	0.52395	chr21	9118416	9119046	+	0	NA	IntergeniALR/Alphe	11030	NR_03832E	1E+08	Hs.487562	NM_17494E	ENSG00000	TEKT4P2	MAFIPL TE	tektin	4	pseudo				
chr13-171	17.71447	-0.4769	0.539212	-0.88445	0.376456	0.524497	chr13	17147317	17147694	+	0	NA	IntergeniALR/Alphe	-1047792	NR_02727E	26080	Hs.44858E	NR_02727E	ENSG00000	FAM230C	LINC00281	family	wincRNA					
chr20-284	19.5741	-0.44403	0.502509	-0.88362	0.376899	0.524525	chr20	28402493	28402701	+	0	NA	IntergeniALR/Alphe	200068	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG00000	FRG1CP				FSHD	regipseudo			
chr22-114	21.6809	-0.42124	0.476871	-0.88334	0.37705	0.524525	chr22	11466744	11493678	+	0	NA	IntergeniTiger1 I	-417195	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272E-					uncharactncRNA				
chr22-152	21.6809	-0.42124	0.476871	-0.88334	0.37705	0.524525	chr22	15054057	15054297	+	0	NA	IntergeniALR/Alphe	-473982	NM_00100E	81061	Hs.55470E	NM_00100E	ENSG00000	OR11H1	OR11H12 C	olfactory	protein-coding					
chr11-527	16.25277	-0.48628	0.550665	-0.88308	0.377194	0.524525	chr11	52772891	52773111	+	0	NA	IntergeniALR/Alphe	1830997	NM_001004	119749	Hs.553564	NM_001004	ENSG00000	OR4C46					olfactory	protein-coding		
chr20-298	46.63694	-0.29627	0.335533	-0.88299	0.377242	0.524525	chr20	29884986	29886222	+	0	NA	IntergeniALR/Alphe	-5141	NR_03968E	1.01E+08	NR_03968E	ENSG00000	MTR4477A					microRNA	ncRNA			
chr19-255	95.48595	-0.22648	0.257169	-0.88066	0.378503	0.526066	chr19	25316739	25316983	+	0	NA	IntergeniALR/Alphe	-1153414	NR_00360E	1E+08	Hs.14931E	NR_00360E	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr20-276	18.49815	-0.45159	0.512965	-0.88034	0.378673	0.526088	chr20	27603384	27603668	+	0	NA	IntergeniALR/Alphe	999139	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG00000	FRG1CP					FSHD	regipseudo		
chr20-265	21.6592	-0.41979	0.477192	-0.87971	0.379015	0.526272	chr20	26551030	26551655	+	0	NA	IntergeniALR/Alphe	-342109	NR_04009E	284801	Hs.370695	NR_04009E	ENSG00000	MIR663AHC-	MIR663A	lncRNA						
chr19-265	31.74573	-0.35508	0.40379	-0.87937	0.379201	0.526272	chr19	26965786	26967996	+	0	NA	IntergeniALR/Alphe	-826540	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-					uncharactncRNA			
chr11-532	27.50205	-0.38393	0.436652	-0.87925	0.379266	0.526272	chr11	53099267	53099525	+	0	NA	IntergeniALR/Alphe	1504602	NM_001004	119749	Hs.553564	NM_001004	ENSG00000	OR4C46					olfactory	protein-coding		
chr1-1236	28.12546	-0.3707	0.422081	-0.87826	0.379801	0.526445	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2116354	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr2-934	18.54435	-0.45068	0.513181	-0.87821	0.37983	0.526445	chr2	93432421	93432801	+	0	NA	IntergeniALR/Alphe	775808	NR_14610E	728034	NR_146105	BMS1P14					BMS1	pset	pseudo			
chr19-271	56.945	-0.27117	0.308793	-0.87817	0.379851	0.526445	chr19	27187513	27187794	+	0	NA	IntergeniALR/Alphe	-605778	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-					uncharactncRNA			
chr8-857	15.84252	-0.48784	0.555993	-0.87742	0.380261	0.526798	chr8	85788548	85788747	+	0	NA	IntergeniLIPAS LID	2721	NR_003594	1E+08	Hs.53505E	NR_003594	REX0112P					REX01	lik	pseudo		
chr1-1245	23.83558	-0.40775	0.464917	-0.87703	0.380471	0.526876	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3074632	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr19-252	21.6375	-0.41834	0.478275	-0.87469	0.381741	0.528422	chr19	25694265	25694501	+	0	NA	IntergeniALR/Alphe	-1530936	NR_00360E	1E+08	Hs.14931E	NR_00360E	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr19-257	24.3883	-0.39417	0.450935	-0.87412	0.382052	0.528639	chr19	25766146	25766379	+	0	NA	IntergeniALR/Alphe	-602815	NR_00360E	1E+08	Hs.14931E	NR_00360E	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr7-604	18.91119	-0.44699	0.512661	-0.87191	0.383257	0.529942	chr7	60421222	60421497	+	0	NA	IntergeniALR/Alphe	2882697	NR_00395E	643955	Hs.58330E	NR_00395E	ENSG00000	ZNF733P	ZNF733					zinc	finger	pseudo
chr17-23	80.89192	-0.23554	0.270169	-0.87183	0.383303	0.529942	chr17	23255947	23256199	+	0	NA	IntergeniALR/Alphe	732962	NM_00119C	1E+08	Hs.74018E	NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2	lprotein-coding					
chr10-404	30.41982	-0.35514	0.407546	-0.87141	0.383532	0.530045	chr10	40408276	40409172	+	0	NA	IntergeniALR/Alphe	1712128	NR_04500C	399746	Hs.742607	NR_04500C	ACTR3BP5	FKSG74					ACTR3B	ps	pseudo	
chr11-512	21.24896	-0.41943	0.481626	-0.87087	0.383827	0.530238	chr11	51951183	51951777	+	0	NA	IntergeniALR/Alphe	1542333	NR_024504	646813	Hs.68417E	NR_024504	LOC646813-					DEXH-box	pseudo			
chr1-1226	96.51565	-0.21735	0.249853	-0.86992	0.384345	0.530734	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1392312	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr1-1235	15.272	-0.49086	0.564702	-0.86923	0.384721	0.530832	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2388316	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr12-357	15.272	-0.49086	0.564702	-0.86923	0.384721	0.530832	chr12	35721680	35722161	+	0	NA	IntergeniALR/Alphe	1699424	NM_032834	84920	Hs.102971	NM_032834	ENSG00000	ALG10	ALG10A DI	ALG10	al	protein-coding				
chr19-267	18.02001	-0.4512	0.519525	-0.86849	0.385125	0.531175	chr19	26778873	26779725	+	0	NA	IntergeniALR/Alphe	-1014312	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-					uncharactncRNA			
chr5-481	43.26663	-0.3012	0.349416	-0.86745	0.385694	0.531746	chr5	48138016	48138016	+	0	NA	IntergeniALR/Alphe	2303575	NM_19844E	133418	Hs.561411	NM_19844E	ENSG00000	EMB	GP70				embigin	protein-coding		
chr2-926	25.35295	-0.38744	0.447208	-0.86635	0.386299	0.532365	chr2	92677643	92678079	+	0	NA	IntergeniALR/Alphe	376728	NR_027714	440888	Hs.73023E	NM_01032412	ACTR3BP2	FKSG73					ACTR3B	ps	pseudo	
chr19-258	18.47924	-0.44563	0.514716	-0.86578	0.386611	0.532581	chr19	25849171	25850610	+	0	NA	IntergeniALR/Alphe	-1686443	NR_00360E	1E+08	Hs.14931E	NR_00360E	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr1-1225	17.99831	-0.44948	0.519583	-0.86509	0.386992	0.532698	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	994655	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000	EMBPI	-		embigin	fpseudo				
chr19-266	40.65441	-0.30864	0.356884	-0.86482	0.387135	0.532698	chr19	26008797	26009053	+	0	NA	IntergeniALR/Alphe	-1784506	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-					uncharactncRNA			
chr1-1243	18.06621	-0.45027	0.520683	-0.86478	0.387162	0.532698	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2854765	NR_00395E	647121	Hs.											

chr19-252	16.49879	-0.44238	0.54452	-0.81242	0.416552	0.555943	chr19	25272374	25273031	+	0	NA	IntergeniALR/Alphe	-1109255	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr1-1245	33.21575	-0.31806	0.39203	-0.81133	0.417177	0.556373	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3042347	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr12-345	19.2034	-0.40902	0.504542	-0.81068	0.417547	0.556373	chr12	34952200	34954363	+	0	NA	IntergeniALR/Alphe	930785	NM_032834	84920	Hs.102971NM_032834	ENSG00000CALG10	ALG10A DIALG10	al protein-coding
chr11-514	18.74417	-0.41342	0.5102	-0.81031	0.417763	0.556373	chr11	51424567	51425380	+	0	NA	IntergeniALR/Alphe	1015826	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEXH-box pseudo
chr1-1235	15.49074	-0.45216	0.558113	-0.81016	0.417848	0.556373	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1815473	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr10-415	15.49074	-0.45216	0.558113	-0.81016	0.417848	0.556373	chr10	41563244	41566698	+	0	NA	IntergeniALR/Alphe	803074	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000LOC441666	-	zinc fingpseudo
chr13-162	15.49074	-0.45216	0.558113	-0.81016	0.417848	0.556373	chr13	16250294	16253530	+	0	NA	IntergeniALR/Alphe	-1943385	NR_027278	26080	Hs.448582NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr1-1225	15.44454	-0.45325	0.560665	-0.80845	0.418834	0.55719	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1072922	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr8-443	15.44454	-0.45325	0.560665	-0.80845	0.418834	0.55719	chr8	44337474	44338946	+	0	NA	IntergeniALR/Alphe	1045768	NM_001002	340441	Hs.531575NM_001002	ENSG00000POTEA	A26A1 CT1POTE	ankypotein-coding
chr2-9305	16.61287	-0.44216	0.547295	-0.80779	0.419146	0.55719	chr2	93091154	93091381	+	0	NA	IntergeniALR/Alphe	117152	NR_146105	728034	NR_146105	BMS1P14	-	BMS1 psepseudo
chr5-4905	22.41343	-0.3801	0.470574	-0.80773	0.419244	0.55719	chr5	49030698	49031399	+	0	NA	IntergeniALR/Alphe	1410204	NM_198445	133418	Hs.561411NM_198445	ENSG00000EMB	GP70	embigin protein-coding
chr19-266	24.1723	-0.37195	0.460521	-0.80768	0.419275	0.55719	chr19	26682633	26682832	+	0	NA	IntergeniALR/Alphe	-1110699	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000LOC101927	-	uncharactncRNA
chr4-5046	15.99616	-0.44468	0.551029	-0.80701	0.419662	0.557489	chr4	50466450	50466823	+	0	NA	IntergeniALR/Alphe	-1376644	NM_015115	23142	Hs.605388NM_015115	ENSG00000DCUN1D4	-	defectiveprotein-coding
chr5-4933	35.42052	-0.3067	0.380615	-0.80581	0.420353	0.557925	chr5	49304347	49305347	+	0	NA	IntergeniALR/Alphe	1363641	NM_198444	133418	Hs.561411NM_198444	ENSG00000EMB	GP70	embigin protein-coding
chr21-725	15.46903	-0.45017	0.558914	-0.80544	0.420564	0.557925	chr21	7291506	7292108	+	0	NA	IntergeniALR/Alphe	-138830	NM_001322	1.03E+08	Hs.743984NM_001322	LOC102724	-	uncharactprotein-coding
chr17-228	15.51523	-0.4491	0.557619	-0.80539	0.420596	0.557925	chr17	22863386	22864343	+	0	NA	IntergeniALR/Alphe	340753	NM_00119C	1E+08	Hs.740185NM_00119C	ENSG00000MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr5-4921	39.32074	-0.29563	0.367286	-0.80489	0.420882	0.557925	chr5	49218769	49219303	+	0	NA	IntergeniALR/Alphe	1222403	NM_198444	133418	Hs.561411NM_198444	ENSG00000EMB	GP70	embigin protein-coding
chr1-1245	73.95802	-0.22878	0.284352	-0.80456	0.421071	0.557925	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3394913	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr1-1225	19.1817	-0.40737	0.506383	-0.80446	0.42113	0.557925	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1078346	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr19-250	19.1817	-0.40737	0.506383	-0.80446	0.42113	0.557925	chr19	25069251	25069463	+	0	NA	IntergeniALR/Alphe	-905910	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr5-4901	16.28563	-0.46669	0.580365	-0.80413	0.421324	0.557966	chr5	49014486	49014703	+	0	NA	IntergeniALR/Alphe	1426694	NM_198445	133418	Hs.561411NM_198445	ENSG00000EMB	GP70	embigin protein-coding
chr4-5065	15.03151	-0.45909	0.571198	-0.80373	0.421553	0.558053	chr4	50653424	50653690	+	0	NA	IntergeniALR/Alphe	-1189443	NM_015115	23142	Hs.605388NM_015115	ENSG00000DCUN1D4	-	defectiveprotein-coding
chr19-252	21.40538	-0.38433	0.478652	-0.80295	0.422005	0.558436	chr19	25225896	25226959	+	0	NA	IntergeniALR/Alphe	-1062980	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr5-4735	27.27662	-0.3437	0.429169	-0.80086	0.423215	0.559821	chr5	47359728	47360728	+	0	NA	IntergeniALR/Alphe	-1663848	NM_021072	348980	Hs.353176NM_021072	ENSG00000HCN1	BCNG-1 BChyperpolaprotein-coding	
chr17-253	34.43417	-0.30827	0.385085	-0.80051	0.423413	0.559866	chr17	25359989	25360417	+	0	NA	IntergeniALR/Alphe	1729038	NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371	-	uncharactncRNA
chr21-122	15.0343	-0.45378	0.567327	-0.79944	0.424036	0.560377	chr21	12226050	12226794	+	0	NA	IntergeniALR/Alphe	-811744	NR_02691E	149992	Hs.558645NM_153773	ANKRD30BFC21orf99	ankyrin ipseudo	
chr21-104	18.81485	-0.41001	0.513032	-0.79919	0.424181	0.560377	chr21	10457795	10458386	+	0	NA	IntergeniALR/Alphe	44558	NM_182482	85319	Hs.545785NM_182482	BAGE2	CT2.2	BAGE famiprotein-coding
chr9-6382	18.17365	-0.41379	0.517886	-0.799	0.42429	0.560377	chr9	63828119	63828793	+	0	NA	IntergeniIntergeni	-8802	NR_039688	1.01E+08	NR_039688	ENSG00000MIR4477A	-	microRNA ncRNA
chr11-523	33.42501	-0.31475	0.394532	-0.79777	0.425002	0.561101	chr11	52323112	52323363	+	0	NA	IntergeniALR/Alphe	1914090	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEXH-box pseudo
chr19-245	15.0126	-0.45172	0.566568	-0.7973	0.425279	0.56125	chr19	24922027	24925960	+	0	NA	IntergeniALR/Alphe	-760546	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr5-1755	31.65609	-0.32137	0.403269	-0.7969	0.425506	0.561322	chr5	17595475	17596280	+	0	NA	IntergeniCharlie2e	59761	NM_001355	391769	NM_001355	ENSG00000CH3.Y	-	histone cprotein-coding
chr19-246	26.31086	-0.35591	0.446763	-0.79664	0.425661	0.561322	chr19	24642615	24642885	+	0	NA	IntergeniALR/Alphe	-479303	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr7-6035	36.61445	-0.29923	0.375846	-0.79616	0.425938	0.561471	chr7	60350305	60350581	+	0	NA	IntergeniALR/Alphe	2900276	NM_001155	441234	Hs.533121NM_001155	ENSG00000ZNF716	-	zinc fingprotein-coding
chr11-518	18.19814	-0.41118	0.516712	-0.79577	0.426167	0.561556	chr11	51809660	51810920	+	0	NA	IntergeniALR/Alphe	1401143	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEXH-box pseudo
chr10-405	17.73612	-0.42049	0.530009	-0.79324	0.427638	0.563125	chr10	40377877	40379220	+	0	NA	IntergeniALR/Alphe	1681952	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr8-4532	20.94894	-0.38393	0.484056	-0.79316	0.427686	0.563125	chr8	45327990	45329357	+	0	NA	IntergeniALR/Alphe	2288290	NR_146077	389652	NR_146077	ENSG00000ASNSP1	ASNSL1	asparagipseudo
chr1-1238	30.97037	-0.32616	0.41157	-0.79249	0.428076	0.563386	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2371184	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr8-4574	17.69272	-0.41682	0.526122	-0.79225	0.428213	0.563386	chr8	45747859	45748224	+	0	NA	IntergeniALR/Alphe	869602	NR_146077	389652	NR_146077	ENSG00000ASNSP1	ASNSL1	asparagipseudo
chr2-9233	15.03709	-0.44856	0.566654	-0.7916	0.428594	0.563367	chr2	92339878	92330566	+	0	NA	IntergeniALR/Alphe	3980989	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr5-4896	29.59826	-0.32549	0.412335	-0.78937	0.429895	0.565165	chr5	48960928	48961191	+	0	NA	IntergeniALR/Alphe	1480229	NM_198444	133418	Hs.561411NM_198444	ENSG00000EMB	GP70	embigin protein-coding
chr20-275	29.02485	-0.32691	0.415556	-0.78669	0.431466	0.567012	chr20	27654057	27654612	+	0	NA	IntergeniALR/Alphe	948331	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000FRG1C	-	F5HD regipseudo
chr19-1255	50.44087	-0.25495	0.324943	-0.78461	0.432683	0.568378	chr19	25929996	25930244	+	0	NA	IntergeniALR/Alphe	-766673	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr1-1225	23.10473	-0.36429	0.464447	-0.78435	0.432837	0.568378	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1410581	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr19-246	29.04944	-0.32528	0.415308	-0.78322	0.433496	0.568958	chr19	24605343	24605546	+	0	NA	IntergeniALR/Alphe	-441997	NR_003602	1E+08	Hs.149312NR_003602	ENSG00000HACVCR1P1	-	hepatitispsseudo
chr10-411	21.45715	-0.37619	0.480428	-0.78303	0.43361	0.568958	chr10	41131045	41131285	+	0	NA	IntergeniALR/Alphe	1268980	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000LOC441666	-	zinc fingpseudo
chr5-4862	23.61294	-0.35764	0.457327	-0.78201	0.434207	0.569523	chr5	48603204	48605281	+	0	NA	IntergeniALR/Alphe	1837046	NM_198444	133418	Hs.561411NM_198444	ENSG00000EMB	GP70	embigin protein-coding
chr10-415	17.76619	-0.40877	0.523847	-0.78031	0.435206	0.570204	chr10	41586835	41587134	+	0	NA	IntergeniALR/Alphe	781061	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000LOC441666	-	zinc fingpseudo
chr19-265	54.1797	-0.25351	0.324879	-0.78031	0.435206	0.570204	chr19	26505417	26505643	+	0	NA	IntergeniALR/Alphe	-1287901	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000LOC101927	-	uncharactncRNA
chr1-1225	23.10752	-0.36802	0.462418	-0.78028	0.435225	0.570204	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1417205	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBMP1	-	embigin ipseudo
chr16-365	17.69829	-0.40791	0.523768	-0.77881	0.436093	0.571122	chr16	36907498	36908263	+	0	NA	IntergeniALR/Alphe	1161328	NR_03398E	400533	Hs.499135NR_03398E	ENSG00000LINC02167	-	long intncRNA
chr5-485	18.75254	-0.40065	0.515299	-0.77751	0.436855	0.571487	chr5	48500661	48501011	+	0	NA</								



chr2-9243	15.66607	-0.41076	0.557099	-0.73732	0.460928	0.586841	chr2	92432640	92433299	+	0	NA	IntergeniALR/Alphe	491836	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo
chr11-535	31.58044	-0.3066	0.415861	-0.73727	0.460955	0.586841	chr11	53951923	53952123	+	0	NA	IntergeniALR/Alphe	651975	NM_001004	119749	Hs.553564NM_001004	ENSG0000C	OR4C46	-	olfactoryprotein-coding
chr7-5895	16.26387	-0.40268	0.54637	-0.73701	0.461114	0.586841	chr7	58956269	58956796	+	0	NA	IntergeniALR/Alphe	1506355	NM_001155	441234	Hs.533121NM_001155	ENSG0000C	ZNF716	-	zinc fingprotein-coding
chr5-4735	18.90059	-0.37379	0.507581	-0.73641	0.461482	0.587092	chr5	47397705	47397904	+	0	NA	IntergeniALR/Alphe	-1701427	NM_021072	348980	Hs.353176NM_021072	ENSG0000C	HCHN1	BCNG-1 BCh	hyperpolprotein-coding
chr6-5946	16.02733	-0.41796	0.570191	-0.73301	0.463555	0.589503	chr6	59404658	59405254	+	0	NA	IntergeniALR/Alphe	-1443510	NR_132992	1.07E+08	Hs.561535NR_125727	ENSG0000C	LINC0068C	-	long intencRNA
chr7-6055	16.14979	-0.40271	0.550025	-0.73216	0.464071	0.589898	chr7	60559487	60560146	+	0	NA	IntergeniALR/Alphe	2744240	NR_003952	643955	Hs.583308NR_003952	ENSG0000C	ZNF733P	ZNF733	zinc fingpseudo
chr11-526	26.51737	-0.31701	0.4334	-0.73146	0.4645	0.589898	chr11	52071729	52072652	+	0	NA	IntergeniALR/Alphe	1663043	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEfH-box pseudo	
chr19-256	21.72208	-0.34932	0.477615	-0.73138	0.464545	0.589898	chr19	25613373	25613583	+	0	NA	IntergeniALR/Alphe	-1443510	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr1-1235	24.36158	-0.32961	0.450677	-0.73138	0.464549	0.589898	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2032161	NR_003952	647121	Hs.697682NR_003952	ENSG0000C	EMBP1	-	embigin fpseudo
chr20-271	15.71505	-0.40473	0.553828	-0.73079	0.464909	0.590136	chr20	27122885	27123784	+	0	NA	IntergeniALR/Alphe	-914101	NR_040095	284801	Hs.370695NR_040095	ENSG0000C	MIR663AHC	-	MIR663A lncRNA
chr17-233	20.68015	-0.37674	0.516082	-0.72999	0.465395	0.590331	chr17	23207571	23207826	+	0	NA	IntergeniALR/Alphe	684587	NM_00119C	1E+08	Hs.740185NM_00119C	ENSG0000C	MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr5-481	21.14876	-0.3518	0.481934	-0.72997	0.465407	0.590331	chr5	48132228	48132427	+	0	NA	IntergeniALR/Alphe	2308961	NM_198445	133418	Hs.561411NM_198445	ENSG0000C	EMB	GP70	embigin protein-coding
chr5-4768	15.80465	-0.40772	0.55893	-0.72946	0.465721	0.59043	chr5	47683032	47683379	+	0	NA	IntergeniALR/Alphe	-1986825	NR_021072	348980	Hs.353176NM_021072	ENSG0000C	HCHN1	BCNG-1 BCh	hyperpolprotein-coding
chr19-265	18.48756	-0.37649	0.516251	-0.72928	0.46583	0.59043	chr19	26861861	26863256	+	0	NA	IntergeniALR/Alphe	-930873	NM_146732	1.02E+08	Hs.567934NR_110687	ENSG0000C	LOC101927	-	uncharactncRNA
chr5-4925	27.04728	-0.31326	0.4304	-0.72784	0.466713	0.591331	chr5	49252151	49252758	+	0	NA	IntergeniALR/Alphe	1188834	NM_198445	133418	Hs.561411NM_198445	ENSG0000C	EMB	GP70	embigin protein-coding
chr5-4714	21.17325	-0.34957	0.481539	-0.72595	0.46787	0.592578	chr5	47140632	47140896	+	0	NA	IntergeniALR/Alphe	-1444384	NM_021072	348980	Hs.353176NM_021072	ENSG0000C	HCHN1	BCNG-1 BCh	hyperpolprotein-coding
chr19-252	66.66413	-0.21017	0.289719	-0.72542	0.468197	0.592773	chr19	25271153	25271389	+	0	NA	IntergeniALR/Alphe	-1075824	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr12-372	23.30455	-0.33543	0.463297	-0.724	0.469065	0.593652	chr12	37259970	37261633	+	0	NA	IntergeniALR/Alphe	-1107973	NM_001308	144245	Hs.259305NM_001011	ENSG0000C	ALG10B	ALG10 KCF	ALG10 alprotein-coding
chr5-485	31.81698	-0.29893	0.413267	-0.72333	0.469478	0.593955	chr5	48507078	48507309	+	0	NA	IntergeniALR/Alphe	1934095	NM_198445	133418	Hs.561411NM_198445	ENSG0000C	EMB	GP70	embigin protein-coding
chr19-96	15.14174	-0.41008	0.567896	-0.7221	0.470235	0.594693	chr19	9608205	9615695	+	0	NA	intron (AluSx SIN)	9282	NM_00133C	93134	Hs.720081NM_152285	ENSG0000C	ZNF561	-	zinc fingprotein-coding
chr20-265	24.36437	-0.32633	0.452264	-0.72156	0.470568	0.594895	chr20	26964000	26964240	+	0	NA	IntergeniALR/Alphe	-754887	NR_040095	284801	Hs.370695NR_040095	ENSG0000C	MIR663AHC	-	MIR663A lncRNA
chr19-265	18.46864	-0.3705	0.513701	-0.72124	0.470763	0.594923	chr19	26955410	26955635	+	0	NA	IntergeniALR/Alphe	-837544	NR_146732	1.02E+08	Hs.567934NR_110687	ENSG0000C	LOC101927	-	uncharactncRNA
chr19-255	15.16623	-0.40692	0.564859	-0.72039	0.471284	0.595142	chr19	25962793	25965809	+	0	NA	IntergeniALR/Alphe	-1800854	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr5-4711	15.16623	-0.40692	0.564859	-0.72039	0.471284	0.595142	chr5	47113907	47115974	+	0	NA	IntergeniALR/Alphe	-1418559	NM_021072	348980	Hs.353176NM_021072	ENSG0000C	HCHN1	BCNG-1 BCh	hyperpolprotein-coding
chr10-405	20.68954	-0.35458	0.492681	-0.7197	0.471709	0.595336	chr10	40934550	40936374	+	0	NA	IntergeniALR/Alphe	1432583	NR_02438C	441666	Hs.255725NR_02438C	ENSG0000C	LOC441666	-	zinc fingpseudo
chr5-489	18.88168	-0.36791	0.511284	-0.71958	0.471785	0.595336	chr5	48937500	48937725	+	0	NA	IntergeniALR/Alphe	1503676	NM_198445	133418	Hs.561411NM_198445	ENSG0000C	EMB	GP70	embigin protein-coding
chr5-4761	20.62443	-0.34983	0.487582	-0.71748	0.473079	0.596372	chr5	47611037	47612273	+	0	NA	IntergeniALR/Alphe	-1915275	NM_021072	348980	Hs.353176NM_021072	ENSG0000C	HCHN1	BCNG-1 BCh	hyperpolprotein-coding
chr15-195	17.89533	-0.374	0.52147	-0.71721	0.473244	0.596372	chr15	19336497	19336924	+	0	NA	IntergeniALR/Alphe	-946034	NR_03883E	646096	Hs.448785NR_03883E	ENSG0000C	CHEK2P2	-	checkpoirpseudo
chr1-124	15.19072	-0.40382	0.56311	-0.71712	0.473303	0.596372	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2706514	NR_003952	647121	Hs.697682NR_003952	ENSG0000C	EMBP1	-	embigin fpseudo
chr7-5864	15.19072	-0.40382	0.56311	-0.71712	0.473303	0.596372	chr7	58640826	58641867	+	0	NA	IntergeniALR/Alphe	1191169	NM_001155	441234	Hs.533121NM_001155	ENSG0000C	ZNF716	-	zinc fingprotein-coding
chr3-910	17.94152	-0.37313	0.520719	-0.71657	0.473637	0.59642	chr3	91022140	91022382	+	0	NA	IntergeniALR/Alphe	1914640	NM_005233	2042	Hs.123642NM_005233	ENSG0000C	EPHA3	EK4 ETK EPEH	receptprotein-coding
chr5-175	15.23691	-0.40277	0.56239	-0.71618	0.473883	0.59642	chr5	17528573	17530394	+	0	NA	Intergeni Intergeni	85473	NR_134272	1.03E+08	Hs.134272	ENSG0000C	LINC02215	-	long intencRNA
chr2-122	15.62546	-0.40175	0.561012	-0.71611	0.473925	0.59642	chr2	12024447	12024944	+	0	NA	IntergeniLIP4 LID	137789	NR_110761	1.03E+08	Hs.652925NR_110761	LOC102722	-	uncharactncRNA	
chr1-1241	28.21951	-0.30195	0.421763	-0.71593	0.474037	0.59642	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2636015	NR_003952	647121	Hs.697682NR_003952	ENSG0000C	EMBP1	-	embigin fpseudo
chr5-495	24.8236	-0.3244	0.453574	-0.71522	0.474475	0.596544	chr5	49560537	49560740	+	0	NA	IntergeniALR/Alphe	880650	NM_198445	133418	Hs.561411NM_198445	ENSG0000C	EMB	GP70	embigin protein-coding
chr17-24	15.14453	-0.40488	0.566371	-0.71486	0.474695	0.596544	chr17	24502813	24503194	+	0	NA	IntergeniALR/Alphe	1559452	NM_00119C	1E+08	Hs.740185NM_00119C	ENSG0000C	MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr19-256	20.60273	-0.34829	0.487564	-0.71434	0.475014	0.596544	chr19	25665974	25666574	+	0	NA	IntergeniALR/Alphe	-1502827	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr19-252	28.60806	-0.30302	0.424267	-0.71422	0.475089	0.596544	chr19	25235725	25235936	+	0	NA	IntergeniALR/Alphe	-1072383	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr11-533	23.35632	-0.32793	0.459225	-0.7141	0.475166	0.596544	chr11	53306319	53307889	+	0	NA	IntergeniALR/Alphe	1296894	NM_001004	119749	Hs.553564NM_001004	ENSG0000C	OR4C46	-	olfactoryprotein-coding
chr18-168	17.91982	-0.37138	0.520288	-0.71379	0.475355	0.596544	chr18	16858707	16859131	+	0	NA	IntergeniALR/Alphe	-1533000	NR_027417	644669	Hs.579474NR_027417	ENSG0000C	LOC644669	-	ankyrin ipseudo
chr5-500	17.91982	-0.37138	0.520288	-0.71379	0.475355	0.596544	chr5	50053482	50053723	+	0	NA	IntergeniALR/Alphe	367686	NM_198445	133418	Hs.561411NM_198445	ENSG0000C	EMB	GP70	embigin protein-coding
chr21-111	17.98771	-0.37228	0.521943	-0.71326	0.475687	0.596686	chr21	11117295	11118199	+	0	NA	IntergeniALR/Alphe	518263	NR_13231E	7179	Hs.122988NM_199255	ENSG0000C	TPT	CT44 PTEN	transmem protein-coding
chr20-28	17.87363	-0.37225	0.522055	-0.71305	0.475816	0.596686	chr20	28084296	28084508	+	0	NA	IntergeniALR/Alphe	518263	NR_13231E	7179	Hs.122988NM_199255	ENSG0000C	TPT	CT44 PTEN	transmem protein-coding
chr19-252	28.19781	-0.3008	0.422145	-0.71255	0.476125	0.596855	chr19	25085848	25086059	+	0	NA	IntergeniALR/Alphe	-922506	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr2-927	15.16902	-0.40177	0.564614	-0.71158	0.476723	0.597386	chr2	92730380	92731263	+	0	NA	IntergeniALR/Alphe	785688	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo
chr7-5892	23.33462	-0.32656	0.459492	-0.7107	0.477269	0.597852	chr7	58924761	59785203	+	0	NA	IntergeniALR/Alphe	1475107	NM_001155	441234	Hs.533121NM_001155	ENSG0000C	ZNF716	-	zinc fingprotein-coding
chr19-255	81.97009	-0.19253	0.271199	-0.70992	0.477751	0.598236	chr19	25933316	25933548	+	0	NA	IntergeniALR/Alphe	-1769985	NR_003602	1E+08	Hs.149312NR_003602	ENSG0000C	HAVCR1P1	-	hepatitispseudo
chr2-924	17.89812	-0.36963	0.520871	-0.70963	0.477932	0.598245	chr2	92473048	92474841	+	0	NA	IntergeniALR/Alphe	5224118	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo
chr1-1237	17.94431	-0.36877	0.520064	-0.70908	0.478277	0.598457	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2340426	NR_003952	647121	Hs.697682NR_003952	ENSG0000C	EMBP1	-	embigin fpseudo
chr21-127	17.4144	-0.37597	0.530645	-0.70851	0.478626	0.598675	chr21	12758727</													





chr1-1234	20.50533	-0.27499	0.489339	-0.56196	0.574146	0.669968	chr1	1.23E+08	1.23E+08	0	NA	IntergeniALR/Alphe	1924961	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo	
chr19-262	22.75629	-0.26089	0.464806	-0.56129	0.574602	0.670271	chr19	26202697	26204858	+	0	NA	IntergeniALR/Alphe	-1589654	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-	-	uncharactncRNA	
chr19-268	27.57886	-0.24101	0.429874	-0.56064	0.575041	0.670555	chr19	26856341	26856551	+	0	NA	IntergeniALR/Alphe	-936985	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-	-	uncharactncRNA	
chr11-542	15.63935	-0.31043	0.55494	-0.55939	0.575894	0.671321	chr11	54221939	54223088	+	0	NA	IntergeniALR/Alphe	381485	NM_001004	1.197949	Hs.553564NM_001004	ENSG00000	OR4C46	-	olfactoryprotein-coding	
chr15-192	20.13569	-0.27045	0.498476	-0.55866	0.576437	0.671725	chr15	19226162	19226420	+	0	NA	IntergeniALR/Alphe	-1056453	NR_03883E	646969	Hs.448785NR_03883E	ENSG00000	CHEK2P2	-	checkpoirpseudo	
chr17-234	16.50882	-0.31152	0.558097	-0.55817	0.576725	0.671833	chr17	23453743	23453942	+	0	NA	IntergeniALR/Alphe	930731	NM_00119C	1E+08	Hs.740185NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2	lprotein-coding
chr17-246	17.86582	-0.29057	0.520951	-0.55776	0.577006	0.671931	chr17	24660607	24660822	+	0	NA	IntergeniALR/Alphe	21376003	NM_00119C	1E+08	Hs.740185NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2	lprotein-coding
chr12-352	15.15563	-0.31571	0.566631	-0.55717	0.577413	0.672177	chr12	35204680	35204971	+	0	NA	IntergeniALR/Alphe	11823299	NM_032834	84920	Hs.102971NM_032834	ENSG00000	ALG10	ALG10A	DIALG10	alprotein-coding
chr2-923E	16.71808	-0.30525	0.549429	-0.55558	0.578496	0.672421	chr2	92395819	92396249	+	0	NA	IntergeniALR/Alphe	454901	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr2-923E	26.36044	-0.24984	0.449784	-0.55548	0.578569	0.672421	chr2	93003783	93004042	+	0	NA	IntergeniALR/Alphe	1062779	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr1-1228	20.0244	-0.27424	0.493956	-0.5552	0.578761	0.672421	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1375644	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr11-517	20.0244	-0.27424	0.493956	-0.5552	0.578761	0.672421	chr11	51793531	51793774	+	0	NA	IntergeniALR/Alphe	1384505	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box	pseudo	
chr10-411	15.13393	-0.31358	0.564873	-0.55514	0.5788	0.672421	chr10	41176766	41178267	+	0	NA	IntergeniALR/Alphe	1190529	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000	LOC441666-	-	zinc	finfpseudo
chr8-857E	15.13393	-0.31358	0.564873	-0.55514	0.5788	0.672421	chr8	85726990	85728015	+	0	NA	IntergeniALR/Alphe	-8796	NR_003594	1E+08	Hs.535055NR_003594	REXO1L2P	-	REXO1	likpseudo	
chr18-204	15.18012	-0.31264	0.56557	-0.55279	0.58041	0.674062	chr18	20492194	20492530	+	0	NA	IntergeniALR/Alphe	619451	NM_00540E	6093	Hs.306307NM_00540E	ENSG00000	ROCK1	P160ROCK	Rho	asokprotein-coding
chr14-164	15.11223	-0.31149	0.564454	-0.55184	0.581057	0.674492	chr14	16498939	16499154	+	0	NA	IntergeniALR/Alphe	-2102071	NM_001013	440153	Hs.53488CNR_001013	ENSG00000	OR11H12	-	olfactoryprotein-coding	
chr1-1244	48.2901	-0.18252	0.330856	-0.55167	0.581173	0.674492	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2883509	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr1-1247	20.66839	-0.27065	0.490939	-0.55129	0.581435	0.674557	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3264701	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr17-266	37.16271	-0.20553	0.373005	-0.55102	0.581623	0.674557	chr17	26624945	26626420	+	0	NA	IntergeniALR/Alphe	463559	NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371-	-	uncharactncRNA		
chr20-284	22.25366	-0.25846	0.469636	-0.55035	0.582079	0.674772	chr20	28433074	28433359	+	0	NA	IntergeniALR/Alphe	169449	NR_13231E	1E+08	Hs.529357NR_13231E	ENSG00000	FRG1C1P	-	FSHD	regipseudo
chr11-52E	25.56165	-0.24479	0.445183	-0.54987	0.582409	0.674772	chr11	52327339	52327935	+	0	NA	IntergeniALR/Alphe	1918490	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box	pseudo	
chr5-487E	22.20746	-0.25909	0.471301	-0.54973	0.582502	0.674772	chr5	48784845	48786749	+	0	NA	IntergeniALR/Alphe	1655491	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding
chr11-51E	17.82242	-0.287	0.522193	-0.5496	0.582597	0.674772	chr11	51948668	51950096	+	0	NA	IntergeniALR/Alphe	1540235	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box	pseudo	
chr20-264	24.36604	-0.24858	0.45401	-0.54753	0.584014	0.676186	chr20	26486370	26486743	+	0	NA	IntergeniALR/Alphe	26486370	NR_04009E	284801	Hs.370695NR_04009E	ENSG00000	MIR663AHC-	-	MIR663A	lncRNA
chr1-121E	17.2953	-0.28727	0.53003	-0.54199	0.587827	0.679895	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	281724	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr7-604E	15.16121	-0.30542	0.563535	-0.54197	0.587842	0.679895	chr7	60486328	60486977	+	0	NA	IntergeniALR/Alphe	2817404	NR_00395E	643955	Hs.583308NR_00395E	ENSG00000	ZNF733P	ZNF733	zinc	finfpseudo
chr19-268	19.47557	-0.27256	0.503152	-0.54171	0.588016	0.679895	chr19	26823520	26823730	+	0	NA	IntergeniALR/Alphe	-969806	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-	-	uncharactncRNA	
chr2-927E	19.47557	-0.27256	0.503152	-0.54171	0.588016	0.679895	chr2	92726049	92726388	+	0	NA	IntergeniALR/Alphe	785085	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr2-926E	21.72723	-0.25742	0.475443	-0.54143	0.58821	0.679895	chr2	92665533	92666448	+	0	NA	IntergeniALR/Alphe	724767	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr11-51E	26.20676	-0.23252	0.435949	-0.53963	0.589449	0.68106	chr11	51310637	51310951	+	0	NA	IntergeniALR/Alphe	9101647	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box	pseudo	
chr1-1224	19.95929	-0.26939	0.499436	-0.53939	0.589616	0.68106	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	918021	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr14-192	15.2074	-0.30445	0.56528	-0.53858	0.590176	0.681477	chr14	19264915	19265143	+	0	NA	IntergeniALR/Alphe	-36675	NR_13391E	1.06E+08	Hs.643607NR_13391E	ENSG00000	BMS1P22	-	BMS1	psetpseudo
chr8-459E	21.79722	-0.2553	0.474794	-0.5377	0.590783	0.681949	chr8	45927307	45929522	+	0	NA	IntergeniALR/Alphe	689014	NR_146077	389652	NR_146077	ENSG00000	ASNSP1	ASNSL1	asparagipseudo	
chr2-926E	19.45387	-0.27092	0.504595	-0.5369	0.591335	0.682355	chr2	92602076	92603750	+	0	NA	IntergeniALR/Alphe	661780	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr5-474E	19.52456	-0.26781	0.499747	-0.53589	0.592033	0.682931	chr5	47411073	47411306	+	0	NA	IntergeniALR/Alphe	-171484	NR_021072	348980	Hs.353176NM_021072	ENSG00000	HCN1	BCNG-1	BC	hyperpolprotein-coding
chr9-638E	19.01635	-0.2735	0.511459	-0.53475	0.592822	0.683604	chr9	63816703	68319606	+	0	NA	non-codir	-1420	NR_03968E	1.01E+08	NR_03968E	ENSG00000	MIR4477B	-	microRNA	ncRNA
chr5-488E	15.64493	-0.30029	0.561844	-0.53447	0.593015	0.683604	chr5	48873895	48874728	+	0	NA	IntergeniALR/Alphe	1566977	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding
chr2-927E	21.68313	-0.25509	0.477882	-0.53378	0.593491	0.683919	chr2	92727679	92728159	+	0	NA	IntergeniALR/Alphe	786786	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr20-30E	17.34428	-0.28196	0.528594	-0.53342	0.59374	0.683919	chr20	30818122	30820036	+	0	NA	IntergeniALR/Alphe	-415617	NR_04511E	140678	Hs.653095NR_04511E	MLL1T10P1	MLL1T10L	MLL1T10	pspseudo	
chr2-931E	21.82171	-0.25318	0.474826	-0.53321	0.593887	0.683919	chr2	93119510	93120232	+	0	NA	IntergeniALR/Alphe	1088548	NR_14610E	728034	NR_14610E	BMSIP14	-	BMS1	psetpseudo	
chr5-484E	20.05447	-0.26408	0.496516	-0.53187	0.594818	0.684761	chr5	48460664	48460663	+	0	NA	IntergeniALR/Alphe	2035025	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding
chr21-127	15.11781	-0.3012	0.566715	-0.53148	0.595088	0.684841	chr21	12778233	12778455	+	0	NA	IntergeniALR/Alphe	-259822	NR_02691E	149992	Hs.55864ENM_153773	ANKRD30BF	C21orf99	ankryrin	fpseudo	
chr1-1234	26.18784	-0.23098	0.435364	-0.53055	0.595729	0.685191	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1914031	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr19-251	19.59524	-0.26475	0.499098	-0.53046	0.595792	0.685191	chr19	25123792	25124733	+	0	NA	IntergeniALR/Alphe	-960815	NR_00360E	1E+08	Hs.149312NR_00360E	ENSG00000	HAVCR1P1	-	hepatitis	pseudo
chr5-474E	16.79266	-0.28483	0.538082	-0.52934	0.596573	0.685858	chr5	47480931	47481357	+	0	NA	IntergeniALR/Alphe	-1784764	NR_021072	348980	Hs.353176NM_021072	ENSG00000	HCN1	BCNG-1	BC	hyperpolprotein-coding
chr1-1237	23.93688	-0.24207	0.454761	-0.52834	0.597266	0.686425	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2279215	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBP1	-	embigin	fpseudo
chr2-926E	17.36877	-0.2793	0.529324	-0.52766	0.597734	0.686583	chr2	92689875	92690188	+	0	NA	IntergeniALR/Alphe	748898	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr20-294	20.84204	0.258728	0.490243	0.527561	0.597804	0.686583	chr20	29448473	29449975	+	0	NA	intron	707	NR_134504	1.05E+08	Hs.70227CNR_134504	LOC105377-	-	uncharactncRNA		
chr2-929E	19.04363	-0.26683	0.506088	-0.52724	0.598025	0.686606	chr2	92943419	92933539	+	0	NA	IntergeniALR/Alphe	994110	NR_02771A	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr1-124E	19.57354	-0.26311	0.49959	-0.526																		

chr5-4884	21.45101	-0.21954	0.478064	-0.45922	0.646074	0.723586	chr5	48847443	48847675	+	0	NA	IntergeniALR/Alphe	1593729	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chr2-9238	21.26173	0.220934	0.42889	0.457524	0.647294	0.724716	chr2	92387034	92387631	+	0	NA	IntergeniALR/Alphe	446199	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspsseudo	
chr19-266	51.82235	-0.14784	0.323781	-0.4566	0.647955	0.725169	chr19	26024094	26024311	+	0	NA	IntergeniALR/Alphe	-1769229	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr7-586	17.06317	-0.24297	0.532395	-0.45637	0.648123	0.725169	chr7	58632312	58635947	+	0	NA	IntergeniALR/Alphe	1183952	NM_00115E	441234	Hs.533121NM_00115E	ENSG00000	ZNF716	-		zinc	fingerprotein-coding
chr2-9367	29.81923	-0.18674	0.410062	-0.45538	0.648832	0.725601	chr2	93672523	93672946	+	0	NA	IntergeniALR/Alphe	5368835	NR_146105	728034	NR_146105	ENSG00000	BMS1P14	-		BMS1	pseupseudo
chr2-922	16.97079	-0.24459	0.537258	-0.45525	0.648932	0.725601	chr2	92231925	92233925	+	0	NA	IntergeniALR/Alphe	291792	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspsseudo	
chr11-52	25.38241	-0.20037	0.442137	-0.45319	0.650414	0.727021	chr11	52320619	52321209	+	0	NA	IntergeniALR/Alphe	1911767	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC64681E	-		DEXH-box	pseudo
chr19-27	17.08766	-0.24031	0.532158	-0.45157	0.651578	0.728084	chr19	27095943	27097148	+	0	NA	IntergeniALR/Alphe	-6968886	NR_146732	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr1-124	21.49999	-0.21529	0.477441	-0.45092	0.652045	0.728369	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2829172	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chr1-122	24.79514	0.201017	0.450075	0.446629	0.655143	0.73159	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1009361	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chr11-524	30.96975	-0.18038	0.405433	-0.4449	0.656393	0.732747	chr11	52492890	52493168	+	0	NA	IntergeniALR/Alphe	2083882	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC64681E	-		DEXH-box	pseudo
chr2-922	23.24832	-0.20392	0.461021	-0.44231	0.658264	0.73413	chr2	92253871	92254831	+	0	NA	IntergeniALR/Alphe	313218	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspsseudo	
chr2-34	17.09045	-0.23576	0.53303	-0.4423	0.658274	0.73413	chr2	34946695	34946988	+	0	NA	IntergeniALR/Alphe	924345	NM_032834	84920	Hs.102971NM_032834	ENSG00000	ALG10	ALG10A	DIALG10	alprprotein-coding	
chr5-487	17.09045	-0.23576	0.53303	-0.4423	0.658274	0.73413	chr5	48957535	48958003	+	0	NA	IntergeniALR/Alphe	1465611	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chr5-494	30.90354	-0.18254	0.413531	-0.44141	0.658914	0.734605	chr5	49469821	49470050	+	0	NA	IntergeniALR/Alphe	971353	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chr5-483	21.86962	-0.21306	0.48678	-0.43768	0.661617	0.737378	chr5	48325069	48325315	+	0	NA	IntergeniALR/Alphe	2116096	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chrX-623	30.55672	-0.17921	0.411523	-0.43549	0.663207	0.738909	chrX	62362395	62362960	+	0	NA	IntergeniALR/Alphe	98655	NM_00101E	139886	Hs.612782NM_00101E	ENSG00000	SPIN4	TDRD28	spindlin	protein-coding	
chr11-521	18.38119	-0.22577	0.520459	-0.43378	0.664445	0.739502	chr11	52183468	52183708	+	0	NA	IntergeniALR/Alphe	1774441	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC64681E	-		DEXH-box	pseudo
chr2-925	20.51364	-0.21326	0.491637	-0.43377	0.664458	0.739502	chr2	92533572	92534498	+	0	NA	IntergeniALR/Alphe	592902	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspsseudo	
chrX-594	38.23753	-0.1615	0.372455	-0.43362	0.664567	0.739502	chrX	59488012	59489036	+	0	NA	IntergeniALR/Alphe	-1577891	NM_00715E	7789	Hs.550094NM_00715E	ENSG00000	ZXDA	ZNF896	zinc	fingerprotein-coding	
chrX-6207	18.70021	-0.22189	0.511775	-0.43357	0.664602	0.739502	chrX	62074740	62075452	+	0	NA	IntergeniALR/Alphe	1276236	NM_00101E	139886	Hs.612782NM_00101E	ENSG00000	SPIN4	TDRD28	spindlin	protein-coding	
chr17-25	16.00893	-0.24098	0.556441	-0.43307	0.664961	0.739661	chr17	25375417	25375617	+	0	NA	IntergeniALR/Alphe	1713724	NR_135673	1.05E+08	Hs.649918NR_135673	ENSG00000	LOC105371-			uncharactncRNA	
chr5-467	22.94216	0.200851	0.4654	0.431566	0.666057	0.740464	chr5	46721258	46721593	+	0	NA	IntergeniALR/Alphe	-1025045	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG00000	HCN1	BCNG-1	BC	hyperpolaprotein-coding
chr10-40	29.2053	-0.18065	0.418662	-0.43149	0.666115	0.740464	chr10	40315195	40315534	+	0	NA	IntergeniALR/Alphe	1618768	NR_04500C	399746	Hs.742607NR_04500C	ENSG00000	ACTR3BP5	FKSG74	ACTR3B	pspsseudo	
chr5-4801	17.13943	-0.2303	0.537414	-0.42854	0.66826	0.742608	chr5	48013865	48014073	+	0	NA	IntergeniALR/Alphe	-2317589	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG00000	HCN1	BCNG-1	BC	hyperpolaprotein-coding
chr11-51	24.33095	-0.19408	0.453664	-0.4278	0.668797	0.742963	chr11	51284263	51285088	+	0	NA	IntergeniALR/Alphe	875528	NR_024504	646813	Hs.684175NR_024504	ENSG00000	LOC64681E	-		DEXH-box	pseudo
chr1-1218	26.60919	-0.1841	0.432278	-0.42589	0.670189	0.744268	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	340944	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chr5-478	20.56262	-0.20877	0.490881	-0.42531	0.670613	0.744498	chr5	47891967	47892176	+	0	NA	IntergeniALR/Alphe	-2195691	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG00000	HCN1	BCNG-1	BC	hyperpolaprotein-coding
chr1-122	16.03621	-0.23309	0.549312	-0.42433	0.671328	0.74505	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alphe	744801	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chr2-926	18.24377	-0.21714	0.515798	-0.42097	0.673774	0.747335	chr2	92622879	92625785	+	0	NA	IntergeniALR/Alphe	683199	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspsseudo	
chr1-124	19.96482	-0.21006	0.499077	-0.42091	0.673823	0.747335	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3343248	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chrX-624	54.54592	-0.13651	0.324699	-0.42008	0.674429	0.747765	chrX	62471948	62473142	+	0	NA	IntergeniALR/Alphe	878787	NM_00101E	139886	Hs.612782NM_00101E	ENSG00000	SPIN4	TDRD28	spindlin	protein-coding	
chr5-495	25.39356	-0.18678	0.447634	-0.41955	0.674817	0.747953	chr5	49553310	49553674	+	0	NA	IntergeniALR/Alphe	887796	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chr1-124	34.45308	-0.1607	0.383964	-0.41853	0.675562	0.748537	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3200768	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chr5-465	29.92277	-0.17493	0.418372	-0.41812	0.675859	0.748624	chr5	46524164	46524408	+	0	NA	IntergeniALR/Alphe	-827906	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG00000	HCN1	BCNG-1	BC	hyperpolaprotein-coding
chr2-927	18.33615	-0.21571	0.516384	-0.41774	0.67614	0.748693	chr2	92755302	92756056	+	0	NA	IntergeniALR/Alphe	814546	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspsseudo	
chr2-933	16.039	-0.22826	0.548137	-0.41643	0.677097	0.749511	chr2	93346297	93348275	+	0	NA	IntergeniALR/Alphe	861133	NR_146105	728034	NR_146105	ENSG00000	BMS1P14	-		BMS1	pseupseudo
chr17-24	15.1684	0.238033	0.573516	0.415041	0.678112	0.750391	chr17	24821226	24821427	+	0	NA	IntergeniALR/Alphe	2267913	NR_135673	1.05E+08	Hs.649918NR_135673	ENSG00000	LOC105371-			uncharactncRNA	
chr17-23	20.47582	-0.2024	0.489139	-0.41379	0.679031	0.750898	chr17	23632413	23632635	+	0	NA	IntergeniALR/Alphe	1109413	NM_00119C	1E+08	Hs.74018E	NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2	lprotein-coding
chr5-500	27.16577	0.178564	0.431742	0.413591	0.679174	0.750898	chr5	50031670	50031890	+	0	NA	IntergeniALR/Alphe	409508	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chr5-499	23.92071	-0.18938	0.457972	-0.41352	0.679227	0.750898	chr5	49975993	49976456	+	0	NA	IntergeniALR/Alphe	465064	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000	EMB	GP70	embigin	protein-coding	
chr2-932	27.71533	-0.17767	0.43033	-0.41286	0.679707	0.751186	chr2	93286111	93286606	+	0	NA	IntergeniALR/Alphe	93286111	93286606	728034	NR_146105	ENSG00000	BMS1P14	-		BMS1	pseupseudo
chr1-124	28.29242	-0.1732	0.420392	-0.41201	0.680335	0.751637	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3386895	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000	EMBMP1	-		embigin	fpseudo
chr19-26	18.29275	-0.21218	0.515521	-0.41158	0.680649	0.751695	chr19	26675488	26677143	+	0	NA	IntergeniALR/Alphe	-1117116	NM_04573E	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr18-19	23.9669	-0.18888	0.45918	-0.41134	0.680826	0.751695	chr18	19426410	19426749	+	0	NA	IntergeniALR/Alphe	1685234	NM_00540E	6093	Hs.306307NM_00540E	ENSG00000	ROCK1	P160ROCK	Rho	assocprotein-coding	
chr19-27	17.787	-0.17256	0.424678	-0.40634	0.684491	0.755304	chr19	27152820	27153185	+	0	NA	IntergeniALR/Alphe	-640429	NR_146732	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr17-24	42.01981	-0.14769	0.363515	-0.40628	0.684536	0.755304	chr17	24062456	24062699	+	0	NA	IntergeniALR/Alphe	1539466	NM_00119C	1E+08	Hs.74018E	NM_00119C	ENSG00000	MTRNR2L1	HN1	MT-RNR2	lprotein-coding
chr19-27	34.21258	0.157916	0.389093	0.405857	0.684847	0.755405	chr19	27125210	27125436	+	0	NA	IntergeniALR/Alphe	-668108	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr11-																							



chr2-9258	28.75438	-0.13592	0.420957	-0.32289	0.746775	0.803966	chr2	92588763	92589501	+	0	NA	IntergeniALR/Alphe	647999	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr11-51f	27.03054	-0.1388	0.430331	-0.32254	0.747041	0.803966	chr11	51547851	51548070	+	0	NA	IntergeniALR/Alphe	1138813	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEXH-box	pseudo	
chr20-28f	18.40571	0.16621	0.515637	0.322339	0.747196	0.803966	chr20	28552122	28554482	+	0	NA	IntergeniALR/Alphe	49363	NR_13231f	1E+08	Hs.529357NR_13231f	ENSG00000FRG1CP	-	FSHD	regipseudo	
chrX-599f	15.73898	-0.17827	0.553546	-0.32205	0.747411	0.803966	chrX	59928180	59929689	+	0	NA	IntergeniALR/Alphe	-2018301	NM_00715e	7789	Hs.550094NM_00715e	ENSG00000CXDA	ZNF896	-	zinc	fingerprotein-coding
chr21-79f	17.46282	-0.16939	0.52732	-0.32122	0.748042	0.804392	chr21	7956171	79969566	+	0	NA	IntergeniALR/Alphe	-133236	NM_00136e	1.03E+08	NM_00133C	ENSG00000KCNE1B	-	potassium	protein-coding	
chr1-124f	16.26889	-0.1765	0.55013	-0.32084	0.748334	0.804454	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3336534	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr1-124f	16.91646	-0.13848	0.437395	-0.31924	0.749548	0.805505	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3290571	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr8-448f	15.20907	-0.1801	0.567159	-0.31755	0.750824	0.806624	chr8	44887108	44887375	+	0	NA	IntergeniALR/Alphe	1594799	NM_001002	340441	Hs.531575NM_001002	ENSG00000POTEA	A26A1 CT1POTE	an	kyprotein-coding	
chr1-124f	16.80831	0.106729	0.33657	0.317108	0.751162	0.806734	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3367860	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr11-53f	19.71936	-0.1572	0.497665	-0.31588	0.752091	0.807478	chr11	53519613	53519917	+	0	NA	IntergeniALR/Alphe	1084233	NM_001004	119749	Hs.553564NM_001004	ENSG00000OR4C46	-	olfactory	protein-coding	
chr7-587f	17.53335	-0.16612	0.52706	-0.31519	0.752619	0.807793	chr7	58783892	58784334	+	0	NA	IntergeniALR/Alphe	1333936	NM_00115e	441234	Hs.533121NM_00115e	ENSG00000CZNF716	-	zinc	fingerprotein-coding	
chr2-923f	19.09707	-0.15941	0.508898	-0.31325	0.754092	0.809119	chr2	92367835	92369326	+	0	NA	IntergeniALR/Alphe	427447	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr7-597f	16.9574	-0.16823	0.540257	-0.31139	0.755504	0.810381	chr7	59726595	59727021	+	0	NA	IntergeniALR/Alphe	2276631	NM_00115e	441234	Hs.533121NM_00115e	ENSG00000CZNF716	-	zinc	fingerprotein-coding	
chr11-51f	26.60305	0.134611	0.434173	0.31004	0.756531	0.811228	chr11	51264609	51264866	+	0	NA	IntergeniALR/Alphe	855590	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEXH-box	pseudo	
chr11-94f	19.48834	0.156411	0.507032	0.308483	0.757715	0.812244	chr11	94233618	94237470	+	0	NA	IntergeniLIPA2 L1N	-70093	NM_00119e	390243	Hs.553758NM_00108C	ENSG00000IZUM01R	FOLR4 FolI	IZUM01	reprotein-coding	
chr1-123f	15.72007	-0.17122	0.559061	-0.30626	0.75941	0.813806	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2196956	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr19-26f	15.81245	-0.1697	0.555742	-0.30536	0.760094	0.814254	chr19	26912931	26913508	+	0	NA	IntergeniALR/Alphe	-880212	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000CLOC101927-	-	uncharact	ncRNA	
chr11-52f	16.96109	-0.16353	0.536011	-0.30508	0.760303	0.814254	chr11	52821308	52821780	+	0	NA	IntergeniALR/Alphe	1782454	NM_001004	119749	Hs.553564NM_001004	ENSG00000OR4C46	-	olfactory	protein-coding	
chr10-41f	20.89438	-0.14706	0.484295	-0.30366	0.761385	0.815157	chr10	41553296	41553751	+	0	NA	IntergeniALR/Alphe	814522	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000CLOC44166e-	-	zinc	fingerpsudo	
chr2-924f	16.93849	-0.16159	0.535583	-0.30171	0.76287	0.816492	chr2	92429171	92431455	+	0	NA	IntergeniALR/Alphe	489180	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr7-25f	16.44143	0.168259	0.558303	0.301376	0.763128	0.816513	chr7	25257831	25258060	+	0	NA	IntergeniALR/Alphe	1831296	NR_135673	1.05E+08	Hs.64991fNR_135673	LOC105371-	-	uncharact	ncRNA	
chr12-36f	15.74456	-0.16832	0.559802	-0.30067	0.763666	0.816834	chr12	36000128	36000740	+	0	NA	IntergeniALR/Alphe	1977938	NM_032834	84920	Hs.102971NM_032834	ENSG00000ALG10	ALG10A DI	ALG10	al protein-coding	
chr10-40f	15.37493	-0.1696	0.566051	-0.29962	0.764463	0.817432	chr10	40926465	40926722	+	0	NA	IntergeniALR/Alphe	1441452	NR_02438C	441666	Hs.255725NR_02438C	ENSG00000CLOC44166e-	-	zinc	fingerpsudo	
chr20-28f	16.96298	-0.15894	0.533953	-0.29767	0.765953	0.818769	chr20	28930371	28930482	+	0	NA	IntergeniALR/Alphe	298669	NR_13231f	1E+08	Hs.529357NR_13231f	ENSG00000FRG1CP	-	FSHD	regipseudo	
chr19-25f	15.28533	-0.16617	0.561415	-0.29598	0.767244	0.819734	chr19	25960505	25960837	+	0	NA	IntergeniALR/Alphe	-1797224	NR_00360f	1E+08	Hs.149312NR_00360f	ENSG00000HAVCR1P1	-	hepatitis	pspseudo	
chr7-60f	15.19295	-0.16773	0.566934	-0.29586	0.767334	0.819734	chr7	60400908	60401460	+	0	NA	IntergeniALR/Alphe	2902872	NR_00395f	643955	Hs.583308NR_00395f	ENSG00000CZNF733P	ZNF733	-	zinc	fingerpsudo
chr14-10f	20.45685	-0.14673	0.497746	-0.29479	0.768158	0.820358	chr14	1.07E+08	1.07E+08	+	0	NA	IntergeniIntergeni	98598	NR_049827	1.01E+08	NR_049827	ENSG00000M1R5195	-	microRNA	ncRNA	
chr19-25f	15.33152	-0.16535	0.562423	-0.294	0.768756	0.820741	chr19	25042546	25042923	+	0	NA	IntergeniALR/Alphe	-879287	NR_00360f	1E+08	Hs.149312NR_00360f	ENSG00000HAVCR1P1	-	hepatitis	pspseudo	
chrX-590f	21.81836	0.139968	0.476966	0.293455	0.769175	0.820932	chrX	59050923	59051317	+	0	NA	IntergeniALR/Alphe	-1140487	NM_00715e	7789	Hs.550094NM_00715e	ENSG00000CXDA	ZNF896	-	zinc	fingerprotein-coding
chr2-926f	16.89509	-0.15775	0.538324	-0.29304	0.769494	0.821018	chr2	92614929	92615386	+	0	NA	IntergeniALR/Alphe	674024	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr1-124f	22.04769	-0.13665	0.47579	-0.28721	0.773951	0.825516	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3407694	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr2-929f	20.37004	-0.14003	0.490408	-0.28553	0.77524	0.826213	chr2	92994226	92995894	+	0	NA	IntergeniALR/Alphe	1053927	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr1-124f	20.32385	-0.14063	0.492682	-0.28544	0.775305	0.826213	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3415162	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chrX-600f	65.06546	-0.08358	0.293043	-0.28521	0.775487	0.826213	chrX	60082937	60083380	+	0	NA	IntergeniALR/Alphe	-2172525	NM_00715e	7789	Hs.550094NM_00715e	ENSG00000CXDA	ZNF896	-	zinc	fingerprotein-coding
chr19-26f	17.58917	0.151033	0.529758	0.285908	0.775569	0.826213	chr19	26003948	26004172	+	0	NA	IntergeniALR/Alphe	-1789371	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000CLOC101927-	-	uncharact	ncRNA	
chr11-54f	29.5264	0.118284	0.415759	0.284501	0.776026	0.826297	chr11	54132879	54133109	+	0	NA	IntergeniALR/Alphe	471004	NM_001004	119749	Hs.553564NM_001004	ENSG00000OR4C46	-	olfactory	protein-coding	
chr1-123f	47.57258	-0.09657	0.339596	-0.28436	0.776131	0.826297	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2099651	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr7-613f	20.39454	-0.13782	0.489345	-0.28165	0.778214	0.828199	chr7	61378493	61379469	+	0	NA	IntergeniALR/Alphe	1925075	NR_00395f	643955	Hs.583308NR_00395f	ENSG00000CZNF733P	ZNF733	-	zinc	fingerpsudo
chr18-18f	18.73859	-0.14351	0.509987	-0.2814	0.778401	0.828199	chr18	18533091	18533449	+	0	NA	IntergeniALR/Alphe	2578593	NM_00540e	6093	Hs.306307NR_00540e	ENSG00000ROCK1	P16OROCK	-	Rho	assocprotein-coding
chr1-124f	61.36113	-0.08542	0.304982	-0.28007	0.779427	0.828883	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2948036	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chrX-612f	25.91678	-0.12359	0.441489	-0.27993	0.779528	0.828883	chrX	61282489	61282799	+	0	NA	IntergeniALR/Alphe	2068688	NM_001012	139886	Hs.612782NM_001012	ENSG00000SP1N4	TDR28	-	spindlin	protein-coding
chrX-585f	22.9416	0.126531	0.468406	0.270131	0.780706	0.836382	chrX	58545094	58555512	+	0	NA	IntergeniALR/Alphe	-637600	NM_00715e	7789	Hs.550094NM_00715e	ENSG00000CXDA	ZNF896	-	zinc	fingerprotein-coding
chr11-52f	22.07776	-0.12747	0.472013	-0.27006	0.78711	0.836382	chr11	52815040	52815527	+	0	NA	IntergeniALR/Alphe	1788715	NM_001004	119749	Hs.553564NM_001004	ENSG00000OR4C46	-	olfactory	protein-coding	
chr1-124f	16.55552	-0.14644	0.542752	-0.2698	0.787312	0.836382	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3197910	NR_00395f	647121	Hs.697682NR_00395f	ENSG00000EMB1P	-	embigin	fpseudo	
chr2-928f	25.38965	-0.12064	0.447825	-0.26939	0.787629	0.836459	chr2	92829616	92830994	+	0	NA	IntergeniALR/Alphe	889172	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr5-484f	18.8977	-0.13798	0.516337	-0.26722	0.789299	0.837973	chr5	48418744	48418979	+	0	NA	IntergeniALR/Alphe	2022427	NM_19844f	133418	Hs.561411NM_19844f	ENSG00000EMB	GP70	-	embigin	protein-coding
chr2-930f	21.45547	-0.12887	0.487395	-0.2644	0.791472	0.839856	chr2	93050067	93050876	+	0	NA	IntergeniALR/Alphe	1109338	NR_027714	440888	Hs.730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr19-26f	23.96467	-0.12133	0.459745	-0.2639	0.791858	0.839856	chr19	26443785	26444012	+	0	NA	IntergeniALR/Alphe	-1349533	NR_146733	1.02E+08	Hs.567934NR_110687	ENSG00000CLOC101927-	-	uncharact	ncRNA	
chr22-13f	16.41973	-0.14389	0.545601	-0.26373	0.791987	0.839856	chr22	13245088	13245442	+	0	NA	IntergeniALR/Alphe	1347859	NR_110761	1.03E+08	Hs.65292fNR_110761	LOC1021927-	-	uncharact	ncRNA	
chr20-28f	29.33773	0.109776	0.416376</																			

chr17-26c	16.2121	-0.09246	0.547225	-0.16896	0.865826	0.897381	chr17	26076962	26077872	+	0 NA	IntergeniALR/Alphe	1011824	NR_135673	1.05E+08	Hs. 649918NR_135673	LOC105371-	uncharactncRNA	
chrX-618c	15.57419	0.094345	0.558897	0.168807	0.865949	0.897381	chrX	61821708	61822772	+	0 NA	IntergeniALR/Alphe	1529092	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr2-937f	15.528	0.093825	0.558459	0.168007	0.866578	0.897761	chr2	93752978	93753370	+	0 NA	IntergeniALR/Alphe	455245	NR_146108	728034	NR_146105	BMS1P14	-	BMS1 psepseudo
chrX-5867	25.90339	-0.0736	0.440496	-0.16709	0.867297	0.897918	chrX	58674237	58674469	+	0 NA	IntergeniALR/Alphe	-763720	NM_007156	7789	Hs. 550094NM_007156	ENSG00000CXDA	ZNF896	zinc fingprotein-coding
chr6-595f	17.43052	-0.08853	0.529911	-0.16707	0.867314	0.897918	chr6	59505624	59505862	+	0 NA	IntergeniALR/Alphe	-1544297	NR_132995	1.07E+08	Hs. 561535NR_132995	ENSG00000LINC0068C	-	long intencRNA
chrX-602f	21.2779	-0.07994	0.481904	-0.16589	0.86824	0.897918	chrX	60282652	60283683	+	0 NA	IntergeniALR/Alphe	-2372534	NM_007156	7789	Hs. 550094NM_007156	ENSG00000CXDA	ZNF896	zinc fingprotein-coding
chr1-123c	18.48141	0.085047	0.514334	0.165354	0.868665	0.897918	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1832223	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr20-28f	18.48141	0.085047	0.514334	0.165354	0.868665	0.897918	chr20	28521783	28521774	+	0 NA	IntergeniALR/Alphe	78187	NR_13231f	1E+08	Hs. 529357NR_13231f	ENSG00000FRG1CP	-	FSHD regipseudo
chr3-9117	19.55127	-0.08317	0.503057	-0.16532	0.86869	0.897918	chr3	91177444	91177958	+	0 NA	IntergeniALR/Alphe	2070080	NM_00523c	2042	Hs. 123642NM_00523c	ENSG00000EPAH3	EK4 ETK E	EPH receptorprotein-coding
chr1-123c	18.48141	0.085047	0.514334	0.165354	0.868665	0.897918	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2146108	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chrX-624c	30.46098	-0.06895	0.418069	-0.16492	0.869004	0.897918	chrX	62462860	62463979	+	0 NA	IntergeniALR/Alphe	887913	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr2-9234	17.36263	-0.08725	0.529351	-0.16482	0.869089	0.897918	chr2	92349336	92350186	+	0 NA	IntergeniALR/Alphe	408628	NR_027714	440888	Hs. 730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr19-26f	40.07769	0.059065	0.360264	0.163949	0.869771	0.898353	chr19	26818302	26818513	+	0 NA	IntergeniALR/Alphe	-975024	NR_14673c	1.02E+08	Hs. 567934NR_14673c	ENSG00000LOC101927-	-	uncharactncRNA
chr5-466f	15.77457	-0.08999	0.557723	-0.16135	0.87182	0.900198	chr5	46671863	46672182	+	0 NA	IntergeniALR/Alphe	-975642	NM_021072	348980	Hs. 353176NM_021072	ENSG00000HCN1	BCNG-1 B	hyperpolaprotein-coding
chr5-4744	17.34093	-0.08535	0.530104	-0.161	0.872095	0.90021	chr5	47443011	47443295	+	0 NA	IntergeniALR/Alphe	-1746773	NM_021072	348980	Hs. 353176NM_021072	ENSG00000HCN1	BCNG-1 B	hyperpolaprotein-coding
chr19-261f	37.44376	-0.05828	0.373368	-0.15661	0.875952	0.903528	chr19	26118342	26118546	+	0 NA	IntergeniALR/Alphe	-1674987	NR_14673c	1.02E+08	Hs. 567934NR_14673c	ENSG00000LOC101927-	-	uncharactncRNA
chr11-52c	15.68498	-0.08647	0.554181	-0.15604	0.876003	0.903528	chr11	52362936	52363178	+	0 NA	IntergeniALR/Alphe	1953910	NR_024504	646813	Hs. 684175NR_024504	LOC646813-	-	DEH-box pseudo
chr1-124c	19.13824	-0.07866	0.50451	-0.15591	0.8761	0.903528	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alphe	2987258	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr17-22f	18.58384	-0.07995	0.5179	-0.15437	0.877316	0.90451	chr17	22869445	22869741	+	0 NA	IntergeniALR/Alphe	346482	NM_00119C	1E+08	Hs. 740185NM_00119C	ENSG00000MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr19-25c	17.34372	-0.0809	0.530572	-0.15247	0.878817	0.905784	chr19	25391904	25392256	+	0 NA	IntergeniALR/Alphe	-1228633	NR_00360c	1E+08	Hs. 149312NR_00360c	ENSG00000HAVCR1P1	-	hepatitispseudo
chr9-606f	16.8817	-0.08093	0.531915	-0.15013	0.880665	0.907417	chr9	60602817	60603293	+	0 NA	IntergeniALR/Alphe	-311352	NM_00111c	727905	Hs. 645497NM_00111c	ENSG00000SPATA31A	FAM75A5	SPATA31 sprotein-coding
chrX-615c	27.63839	-0.06316	0.425538	-0.14843	0.882004	0.908522	chrX	61538233	61539410	+	0 NA	IntergeniALR/Alphe	1812511	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr5-484c	16.60952	0.078397	0.549475	0.142676	0.886546	0.912927	chr5	48404425	48404641	+	0 NA	IntergeniALR/Alphe	2036755	NM_19844f	133418	Hs. 561411NM_19844f	ENSG00000EMB	GP70	embigin protein-coding
chr1-124c	15.1167	-0.08081	0.56782	-0.14232	0.88683	0.912944	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alphe	3374869	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr22-124	15.15786	-0.08006	0.564267	-0.14188	0.887175	0.913025	chr22	12489037	12490680	+	0 NA	IntergeniALR/Alphe	592452	NR_110761	1.03E+08	Hs. 652929NR_110761	LOC10272c-	-	uncharactncRNA
chrX-592c	25.40634	-0.06163	0.44257	-0.13925	0.889255	0.914891	chrX	59239676	59241388	+	0 NA	IntergeniALR/Alphe	-1329599	NM_007156	7789	Hs. 550094NM_007156	ENSG00000CXDA	ZNF896	zinc fingprotein-coding
chrX-6144	18.91336	0.070366	0.5089	0.138271	0.890026	0.91541	chrX	61444891	61446426	+	0 NA	IntergeniALR/Alphe	1905674	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr1-168f	15.13616	-0.07789	0.565298	-0.13779	0.890407	0.915526	chr1	16865910	16866658	+	0 NA	IntergeniLIPAS L1I	-5942	NR_160657	1.12E+08	NR_160657	LOC112267-	-	uncharactncRNA
chr1-124c	15.18235	-0.07717	0.562854	-0.13711	0.890947	0.915672	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alphe	3383866	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chrX-624c	27.20365	-0.05843	0.428273	-0.13643	0.891482	0.915672	chrX	62469769	62470908	+	0 NA	IntergeniALR/Alphe	880996	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr1-123c	71.64028	-0.03855	0.282827	-0.13631	0.891578	0.915672	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	2030595	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr7-602f	18.52152	-0.07027	0.515842	-0.13622	0.891649	0.915672	chr7	60273892	60274200	+	0 NA	IntergeniALR/Alphe	2823869	NM_00115f	441234	Hs. 533121NM_00115f	ENSG00000ZNF716	-	zinc fingprotein-coding
chr2-939c	17.71385	0.071367	0.525066	0.135919	0.891885	0.915672	chr2	93935328	93935523	+	0 NA	IntergeniALR/Alphe	2729699	NR_146105	728034	NR_146105	BMS1P14	-	BMS1 psepseudo
chr19-25d	22.3288	0.063017	0.474418	0.13283	0.894328	0.917905	chr19	25436960	25437336	+	0 NA	IntergeniALR/Alphe	-1273701	NR_00360c	1E+08	Hs. 149312NR_00360c	ENSG00000HAVCR1P1	-	hepatitispseudo
chr5-494f	17.44168	-0.07064	0.533492	-0.1324	0.894666	0.917977	chr5	49405855	49406138	+	0 NA	IntergeniALR/Alphe	1035292	NM_19844f	133418	Hs. 561411NM_19844f	ENSG00000EMB	GP70	embigin protein-coding
chrX-611c	21.8178	0.062144	0.477368	0.130181	0.896424	0.919485	chrX	61120291	61121922	+	0 NA	IntergeniALR/Alphe	2230226	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr19-25c	26.43274	0.056634	0.436092	0.129866	0.896672	0.919485	chr19	25304519	25304791	+	0 NA	IntergeniALR/Alphe	-1141208	NR_00360c	1E+08	Hs. 149312NR_00360c	ENSG00000HAVCR1P1	-	hepatitispseudo
chrX-606c	20.29713	-0.06362	0.49128	-0.12949	0.89697	0.919515	chrX	60691088	60692269	+	0 NA	IntergeniALR/Alphe	2659564	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr20-28f	17.75726	0.067532	0.523494	0.129003	0.897356	0.919635	chr20	28530792	28533213	+	0 NA	IntergeniALR/Alphe	70663	NR_13231f	1E+08	Hs. 529357NR_13231f	ENSG00000FRG1CP	-	FSHD regipseudo
chr1-1247	38.65665	0.045296	0.365816	0.123823	0.901455	0.923561	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alphe	3279729	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr5-477c	23.22327	-0.05594	0.461139	-0.12131	0.903445	0.925322	chr5	47713357	47718109	+	0 NA	IntergeniALR/Alphe	-2035203	NM_021072	348980	Hs. 353176NM_021072	ENSG00000HCN1	BCNG-1 B	hyperpolaprotein-coding
chr5-491f	19.8379	-0.0593	0.496687	-0.1194	0.904959	0.926522	chr5	49192139	49192355	+	0 NA	IntergeniALR/Alphe	1249041	NM_19844f	133418	Hs. 561411NM_19844f	ENSG00000EMB	GP70	embigin protein-coding
chrX-624c	16.40635	-0.06471	0.54353	-0.11906	0.905228	0.926522	chrX	62497812	62500437	+	0 NA	IntergeniALR/Alphe	852208	NM_001012	139886	Hs. 612782NM_001012	ENSG00000CPIN4	TDRD28	spindlin protein-coding
chr5-467f	19.46219	0.059526	0.501031	0.118807	0.905428	0.926522	chr5	46730498	46732360	+	0 NA	IntergeniALR/Alphe	-1035049	NM_021072	348980	Hs. 353176NM_021072	ENSG00000HCN1	BCNG-1 B	hyperpolaprotein-coding
chr1-122c	15.23412	-0.06631	0.566071	-0.11715	0.906743	0.927591	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alphe	1336743	NR_00395f	647121	Hs. 697682NR_00395f	ENSG00000EMB1P	-	embigin fpseudo
chr19-24f	17.15555	0.061288	0.54147	0.113188	0.909881	0.930406	chr19	24625227	24625497	+	0 NA	IntergeniALR/Alphe	-461915	NR_00360c	1E+08	Hs. 149312NR_00360c	ENSG00000HAVCR1P1	-	hepatitispseudo
chr19-247	27.90053	-0.04807	0.4254	-0.11299	0.910038	0.930406	chr19	24765071	24765344	+	0 NA	IntergeniALR/Alphe	-601760	NR_00360c	1E+08	Hs. 149312NR_00360c	ENSG00000HAVCR1P1	-	hepatitispseudo
chr20-28f	18.23																		



Supplementary Information

Supplementary Table 7. Genome-wide profiling of differential peaks between proliferating and bleomycin-induced senescent cells (ChIP-seq for H3K36me3).

geneID	baseMea	log2Fold	lfcSE	stat	pvalue	padj	Chr	Start	End	Stran	Peak	Focus	Annotati	Detailed	Distance	Nearest	F	Entrez	ID	Nearest	L	Nearest	F	Nearest	E	Gene	Nar	Gene	Ali	Gene	De	Gene	Type			
chr5-464	56.27501	1.540953	0.386873	3.983093	6.80E-05	0.981636	chr5	46434582	46434946	+	0	NA	IntergeniALR/Alp	-738384	NM_021072	348980	Hs.	353176	NR_021072	ENS00000	HCN1	BCNG-1	[BC	hyperpol	protein-coding											
chr3-441	5.836925	-5.97783	1.66186	-3.59707	0.000322	0.981636	chr3	44815289	44815596	+	0	NA	intron (NM)T1K L	-46444	NR_03029C	693149	NR_03029C	ENS00000	MIR564	MIRN564	[mi	croRNA	ncRNA													
chr1-214	6.888664	-5.39213	1.756285	-3.07019	0.002139	0.981636	chr1	2.15E+08	2.15E+08	+	0	NA	intron (C)Pg	5361	NM_016343	1063	Hs.	497741	NR_016343	ENS00000	CENPF	CENF	[C	IL1	centromer	protein-coding										
chr5-467	19.5447	1.78688	0.592184	3.017442	0.002549	0.981636	chr5	46731825	46732204	+	0	NA	IntergeniALR/Alp	-1035634	NM_021072	348980	Hs.	353176	NR_021072	ENS00000	HCN1	BCNG-1	[BC	hyperpol	protein-coding											
chr4-739	8.432759	-2.80103	0.946173	-2.99067	0.002567	0.981636	chr4	73906089	73906784	+	0	NA	IntergeniLIPA3 L	37043	NM_001511	2919	Hs.	789	NR_001511	ENS00000	CXCL1	FSP GR01	[C-X-C	mot	protein-coding											
chr12-286	3.641203	-5.29767	1.776977	-2.98128	0.00287	0.981636	chr12	2861178	2861741	+	0	NA	intron (N)IME3G L	-4420	NM_00136E	1.02E+08	Hs.	63462E	NR_00136E	ENS00000	TEX52															
chr17-266	773.7942	0.720193	0.242394	2.971167	0.002967	0.981636	chr17	26603798	26604053	+	0	NA	IntergeniALR/Alp	485316	NR_135673	1.05E+08	Hs.	64991E	NR_135673	LOC105371																
chr20-28	18.53599	1.793789	0.607525	2.952618	0.003151	0.981636	chr20	28517445	28519255	+	0	NA	IntergeniALR/Alp	84315	NR_13231E	1E+08	Hs.	529357	NR_13231E	ENS00000	FRG1CP															
chr20-28	16.98956	1.865205	0.634361	2.94029	0.003279	0.981636	chr20	28523377	28524675	+	0	NA	IntergeniALR/Alp	78639	NR_13231E	1E+08	Hs.	529357	NR_13231E	ENS00000	FRG1CP															
chr4-745	8.315302	-2.47978	0.939137	-2.61084	0.003717	0.981636	chr4	74597145	74598143	+	0	NA	IntergeniTHE1B-int	152508	NM_001657	374	Hs.	27083E	NR_001657	ENS00000	CAREG	AR AREGB	[am	phireg	protein-coding											
chr10-12	3.393741	-5.19658	1.801836	-2.88404	0.003926	0.981636	chr10	1.28E+08	1.28E+08	+	0	NA	exon (NM)exon (NM)	14612	NM_002417	4288	Hs.	80976	NR_002417	ENS00000	MKI67	KIA MI6	[mar	ker	of	protein-coding										
chr19-36	12.93097	2.107527	0.736323	2.86223	0.004207	0.981636	chr19	36288833	36289139	+	0	NA	IntergeniSST1 S	-22357	NR_02938E	1E+08	Hs.	46655C	NR_02938E	LOC100134																
chr5-492	37.7132	1.284362	0.454933	2.823188	0.004755	0.981636	chr5	49203138	49203392	+	0	NA	IntergeniALR/Alp	1238023	NM_19844E	133418	Hs.	561411	NR_19844E	ENS00000	EMB	GP70														
chr20-28	35.18259	1.282136	0.454411	2.821533	0.004779	0.981636	chr20	28643737	28644855	+	0	NA	IntergeniALR/Alp	-41631	NR_13231E	1E+08	Hs.	529357	NR_13231E	ENS00000	FRG1CP															
chr4-746	6.013237	-2.7512	1.148472	-2.42768	0.005196	0.981636	chr4	74616713	74616924	+	0	NA	IntergeniAluYg6 S	176182	NM_001657	374	Hs.	27083E	NR_001657	ENS00000	CAREG	AR AREGB	[am	phireg	protein-coding											
chr19-36	13.55283	2.012879	0.723684	2.781433	0.005412	0.981636	chr19	36273945	36274230	+	0	NA	IntergeniSST1 S	-28159	NR_00136E	147929	Hs.	59633E	NR_00136E	ENS00000	ZNF565															
chr1-462	3.146279	-5.08785	1.832379	-2.77663	0.005492	0.981636	chr1	46250430	46250881	+	0	NA	intron (N)intron (N)	2892	NM_00357E	8438	Hs.	642042	NR_00357E	ENS00000	RAD54L	HR54 RAD	[RAD	54	lik	protein-coding										
chr17-82	3.146279	-5.08785	1.832379	-2.77663	0.005492	0.981636	chr17	8203263	8203952	+	0	NA	IntergeniAluSx S	618	NR_132731	9212	Hs.	44265E	NR_004217	ENS00000	AURKB	ATK2 ATM	[aur	ora	k	protein-coding										
chr3-908	18.79917	1.708134	0.617911	2.76468	0.005703	0.981636	chr3	9086855	90869676	+	0	NA	IntergeniALR/Alp	1761504	NM_182644	2042	Hs.	123642	NR_00523E	ENS00000	EPHA3	EK4 ETK	[E	PH	recep	protein-coding										
chr19-36	13.22928	1.974391	0.718478	2.748018	0.005996	0.981636	chr19	36305538	36306094	+	0	NA	IntergeniIntergeni	-5527	NR_02938E	1E+08	Hs.	46655C	NR_02938E	LOC100134																
chr20-38	2.914534	-4.97635	1.846932	-2.69439	0.007052	0.981636	chr20	38943012	38943485	+	0	NA	intron (N)AluSx S	16831	NR_03091E	81610	Hs.	726442	NR_03091E	ENS00000	FAM83D	C20orf12	[fam	ily	w	protein-coding										
chr19-18	7.529523	2.749781	1.021015	2.693185	0.007077	0.981636	chr19	18386706	18386963	+	0	NA	TTS (NR_C)TTS (NR_C)	272	NR_03615E	1E+08	Hs.	03615E	NR_03615E	ENS00000	MIR3189	mir-3189	[mi	croRNA	ncRNA											
chr19-36	10.69956	2.163039	0.81901	2.641042	0.008265	0.981636	chr19	36294349	36294924	+	0	NA	IntergeniSST1 S	-16707	NR_02938E	1E+08	Hs.	46655C	NR_02938E	LOC100134																
chr9-36	8.324024	-2.48178	0.946173	-2.62297	0.008717	0.981636	chr9	36653166	36653493	+	0	NA	intron (N)AluJo S	80434	NM_014791	9833	Hs.	18433E	NR_014791	ENS00000	MELK	HPK38														
chr4-746	5.234628	-2.08902	0.856385	-2.62073	0.008743	0.981636	chr4	74498802	74499010	+	0	NA	IntergeniLIME2 L	53770	NM_001657	374	Hs.	27083E	NR_001657	ENS00000	CAREG	AR AREGB	[am	phireg	protein-coding											
chr21-25	7.589682	-2.69283	1.027551	-2.62063	0.008777	0.981636	chr21	25972664	25973000	+	0	NA	intron (N)IMEc L	167558	NM_00113E	351	Hs.	43498C	NR_00048E	ENS00000	APP	AAA ABET	[am	yl	oid	protein-coding										
chr7-955	7.264681	2.691055	1.029079	2.615014	0.008922	0.981636	chr7	95592568	95595189	+	0	NA	intron (N)intron (N)	2638	NM_00261E	5166	Hs.	8364	NR_00261E	ENS00000	PDK4															
chr19-36	5.802375	3.439154	1.316238	2.612866	0.008979	0.981636	chr19	36626461	36626843	+	0	NA	exon (NM)exon (NM)	21339	NM_03282E	84911	Hs.	631591	NR_03282E	ENS00000	ZNF382	KS1														
chr4-103	5.846263	-3.40899	1.304734	-2.61278	0.008981	0.981636	chr4	1.03E+08	1.03E+08	+	0	NA	exon (NM)exon (NM)	-33991	NM_02013E	56898	Hs.	12469E	NR_02013E	ENS00000	BDH2	DHRS6 EF	[3-h	ydrox	y	protein-coding										
chr7-588	21.73201	4.38733	0.552591	2.603612	0.009225	0.981636	chr7	58893059	58893259	+	0	NA	IntergeniALR/Alp	1442982	NM_00115E	441234	Hs.	533121	NR_00115E	ENS00000	ZNF716															
chr17-78	5.094355	-4.27535	1.6729	-2.55565	0.010599	0.981636	chr17	78217917	78218199	+	0	NA	intron (N)AluJo S	3795	NM_00101E	332	Hs.	74487E	NR_00116E	ENS00000	BTRC5	API4 EPR	[bac	ulo	vir	protein-coding										
chr1-197	7.350078	-2.63875	1.033828	-2.55241	0.010698	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	exon (NM)exon (NM)	14927	NM_00662E	26227	Hs.	48729E	NR_00662E	ENS00000	PHGDH															
chr19-36	4.690022	2.183611	0.861275	2.535322	0.011234	0.981636	chr19	36270412	36272955	+	0	NA	IntergeniSST1 S	-25755	NR_00136E	147929	Hs.	59633E	NR_00136E	ENS00000	ZNF565															
chr10-40	173.637	0.709559	0.285612	2.484347	0.012979	0.981636	chr10	40593352	40593438	+	0	NA	IntergeniALR/Alp	1774566	NR_02438C	441666	Hs.	25572E	NR_02438C	ENS00000	LOC44166E															
chr19-36	9.973448	2.040305	0.821388	2.483973	0.012993	0.981636	chr19	36299211	36301092	+	0	NA	IntergeniCpG	-11192	NR_02938E	1E+08	Hs.	46655C	NR_02938E	LOC100134																
chr5-138	4.701862	4.204168	1.705862																																	

chr15-805.4.410491	-2.9281	1.394136	-2.10029	0.035703	0.981636	chr15	80933495	80934129	+ 0 NA	intron (NMIR SINE	56007	NR_12632E	23184	Hs.57845C	NR_015154	ENSG000000MESD	BOCA MESL	mesoderm protein-coding	
chr5-4961.179.2379	0.614564	0.292931	2.097981	0.035907	0.981636	chr5	49616438	49617194	+ 0 NA	IntergeniALR/Alph	824472	NR_19844E	133418	Hs.561411	NR_19844E	ENSG000000EMB	GP70	embigin protein-coding	
chr10-408.20.6046	1.171331	0.558458	2.09744	0.035955	0.981636	chr10	40806076	40806313	+ 0 NA	IntergeniALR/Alph	1561851	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000000CLOC44166C-		zinc fingpseudo	
chr10-402.38.19696	0.92218	0.440596	2.093209	0.036347	0.981636	chr10	40267076	40268087	+ 0 NA	IntergeniALR/Alph	1570985	NR_04500C	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo	
chr16-846.7.591162	-1.99474	0.95306	-2.09299	0.03635	0.981636	chr16	84615586	84615924	+ 0 NA	intron (Nintron (N	2323	NR_02114E	23406	Hs.28909E	NR_02114E	ENSG000000COTL1	CLP	coactosin protein-coding	
chr19-436.4.238745	2.938944	1.406556	2.089461	0.036666	0.981636	chr19	43875108	43875569	+ 0 NA	intron (Nintron (N	4798	NR_00103E	342908	Hs.76561	NR_00103E	ENSG000000ZNF404		zinc fingprotein-coding	
chr6-4796.4.238745	2.938944	1.406556	2.089461	0.036666	0.981636	chr6	47989216	47990117	+ 0 NA	intron (NTH1A-int	79023	NR_00101E	442213	Hs.65940E	NR_20749E	ENSG000000PTCHD4	G6orf138	patched protein-coding	
chr1-1245.14.27016	1.40362	0.673417	2.084325	0.037131	0.981636	chr1	12588001	1.25E+08	+ 0 NA	IntergeniALR/Alph	3406518	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG000000EMBP1		embigin psseudo	
chr2-739.7.357566	-1.95207	0.937843	-2.08145	0.037393	0.981636	chr2	73907971	73912171	+ 0 NA	intron (NAluSx1 SI	-16755	NR_13489E	1716	Hs.46902E	NR_00192E	ENSG000000CDGUOK	MTDPS3 NC	deoxyguar protein-coding	
chr8-1332.6.63894	-2.08572	1.003234	-2.079	0.037617	0.981636	chr8	1.33E+08	1.33E+08	+ 0 NA	intron (Nintron (N	25933	NR_00113E	10397	Hs.372914	NR_00609E	ENSG000000NDRG1	CAP43 CM1-	nuclyc dowprotein-coding	
chr4-2684.7.349708	-1.95067	0.938723	-2.078	0.037709	0.981636	chr4	2684380	2684579	+ 0 NA	intron (NLMEd LIN	59047	NR_04633E	8603	Hs.652364	NR_003704	ENSG000000FAM193A	C4orf8 RE	familyp wiprotein-coding	
chr12-108.8.820242	-1.75691	0.847451	-2.07317	0.038157	0.981636	chr12	1.09E+08	1.09E+08	+ 0 NA	intron (Nintron (N	26146	NR_039717	1.01E+08	NR_039717	ENSG000000CIR4496			microRNA ncRNA	
chr8-143.6.615366	-2.07106	1.006381	-2.06787	0.038653	0.981636	chr8	1.44E+08	1.44E+08	+ 0 NA	IntergeniIntergeni	27535	NR_20138E	5339	Hs.43424E	NR_00044E	ENSG000000PLEC	EBS1 EBSv	plectin protein-coding	
chr7-5925.62.4047	0.787932	0.377467	2.065693	0.038857	0.981636	chr7	59292394	59292611	+ 0 NA	IntergeniALR/Alph	1842325	NR_00115E	441234	Hs.533121	NR_00115E	ENSG000000ZNF716		zinc fingprotein-coding	
chr19-264.75.15622	0.725538	0.351299	2.065302	0.038894	0.981636	chr19	26460000	26460272	+ 0 NA	IntergeniALR/Alph	-133295	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG000000LOC101927-		uncharactncRNA	
chr14-886.6.582085	-2.09053	1.012931	-2.06384	0.039033	0.981636	chr14	88538470	88538669	+ 0 NA	intron (Nintron (N	16438	NR_00703E	11099	Hs.43704C	NR_00703E	ENSG000000PTNP21	PTPD1 PTF	protein tprotein-coding	
chr6-5956.50.04129	0.822985	0.399562	2.059716	0.039426	0.981636	chr6	59586841	59587042	+ 0 NA	IntergeniALR/Alph	-1625495	NR_132994	1.07E+08	Hs.56153E	NR_125727	ENSG000000CLNCO068C-		long intencRNA	
chr1-2013.4.442553	-3.64925	1.772274	-2.05908	0.039487	0.981636	chr1	2.02E+08	2.02E+08	+ 0 NA	intron (Nintron (N	1498	NR_00119E	1465	Hs.10808E	NR_00407E	ENSG000000CSRP1	CRP CRP1	cysteine protein-coding	
chr7-3641.3.393556	-3.65484	1.77675	-2.05704	0.039683	0.981636	chr7	36419496	36420375	+ 0 NA	intron (Nintron (N	-29578	NR_00110C	23366	Hs.6224	NR_015314	ENSG000000KIAA0895		KIAA0895 protein-coding	
chr18-241.6.419492	2.103774	1.023135	2.056203	0.039763	0.981636	chr18	24146467	24146749	+ 0 NA	intron (NLMEd LIN	7124	NR_138644	26256	Hs.51198E	NR_01218E	ENSG000000CABYR	CABYR Ca	calcium tprotein-coding	
chr17-236.330.4404	0.542952	0.264229	2.054852	0.039893	0.981636	chr17	23016338	23016540	+ 0 NA	IntergeniALR/Alph	493328	NR_00119C	1E+08	Hs.74018E	NR_00119C	ENSG000000MTRNR2L1	HNI	MT-RNR2 lprotein-coding	
chr17-618.4.161179	-2.86055	1.392121	-2.05482	0.039897	0.981636	chr17	61845152	61846160	+ 0 NA	intron (NCharlieL	17903	NR_03204E	83990	Hs.12890E	NR_03204E	ENSG000000BRIP1	BACH1 FAN	BRCA1 intrprotein-coding	
chr2-3056.6.607508	-2.0794	1.012061	-2.05462	0.039916	0.981636	chr2	30569159	30569358	+ 0 NA	intron (Nintron (N	122012	NR_00130A	253558	Hs.46804E	NR_182551	ENSG000000LCLAT1	IAGPAT8 A	lysocardiprotein-coding	
chr6-152.6.607508	-2.0794	1.012061	-2.05462	0.039916	0.981636	chr6	152E+08	1.52E+08	+ 0 NA	intron (Nintron (N	10909	NR_012177	26271	Hs.52050E	NR_012177	ENSG000000FBX05	EM11 FBX	F-box prcprotein-coding	
chr12-454.3.41898	-3.64118	1.772982	-2.05371	0.040004	0.981636	chr12	4544342	45442740	+ 0 NA	intron (NLM7 LIN	5901	NR_00113C	10635	Hs.73069E	NR_00647E	ENSG000000RAD51AP1	PIR51	RAD51 assprotein-coding	
chr15-413.3.41898	-3.64118	1.772982	-2.05371	0.040004	0.981636	chr15	41347185	41347845	+ 0 NA	intron (Nintron (N	14604	NR_01635E	51203	Hs.61509E	NR_01635E	ENSG000000NUSAP1	ANKT BMO	cellular protein-coding	
chr18-795.4.145464	-2.85599	1.396053	-2.04576	0.04078	0.981636	chr18	79900796	79901362	+ 0 NA	IntergeniIntergeni	37411	NR_01228E	26251	Hs.24790E	NR_01228E	ENSG000000KCNG2	KCNF2 KVC	potassium protein-coding	
chr22-463.3.385698	-3.65224	1.785918	-2.04502	0.040853	0.981636	chr22	46316880	46317311	+ 0 NA	intron (NAluSx1 SI	-18306	NR_104241	55687	Hs.439524	NR_01800E	ENSG000000TRMU	L3CAL3 MT	tRNA 5-mcprotein-coding	
chr1-2116.3.411122	-3.63821	1.782005	-2.04164	0.041188	0.981636	chr1	2.12E+08	2.12E+08	+ 0 NA	intron (Nintron (N	4538	NR_002497	4751	Hs.15370E	NR_002497	ENSG000000CNEK2	HSK21 NF	NEM1a relprotein-coding	
chr2-1756.7.326134	-1.94633	0.953714	-2.04079	0.041272	0.981636	chr2	1.76E+08	1.76E+08	+ 0 NA	intron (NLP1A3 LIN	38639	NR_03065E	80856	Hs.209561	NR_03065E	ENSG000000LNPK	KIAA1715 lunapark,	protein-coding	
chr7-364E.4.137606	-2.85364	1.403819	-2.03277	0.042076	0.981636	chr7	36452347	36454460	+ 0 NA	3' UTR (N3' UTR (N	-63046	NR_00110C	23366	Hs.6224	NR_015314	ENSG000000KIAA0895		KIAA0895 protein-coding	
chr7-158.4.137606	-2.85364	1.403819	-2.03277	0.042076	0.981636	chr7	1.59E+08	1.59E+08	+ 0 NA	intron (NAluY SINE	44938	NR_01776E	54892	Hs.18616	NR_01776E	ENSG000000NCAPG2	3KS CAP-	non-SMC cprotein-coding	
chr14-556.6.548803	-2.10072	1.035961	-2.0278	0.042581	0.981636	chr14	55631694	55631897	+ 0 NA	intron (Nintron (N	51588	NR_00107E	3895	Hs.509414	NR_00498E	ENSG000000KTN1	CG1 KNT	kinectin protein-coding	
chr10-408.168.482	0.618197	0.305386	2.024314	0.042938	0.981636	chr10	40892151	40892527	+ 0 NA	IntergeniALR/Alph	1475706	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000000CLOC44166C-		zinc fingpseudo	
chr1-6847.4.871947	-2.45966	1.217932	-2.01954	0.043431	0.981636	chr1	68479629	68479901	+ 0 NA	intron (NAluJr SIN	-16911	NR_110671	1.02E+08	Hs.38285E	NR_110671	ENSG000000DEPDC1-AS-		DEPDC1 arncRNA	
chr15-805.4.410491	-2.9281	1.394136	-2.10029	0.035703	0.981636	chr15	80805796	80806551	+ 0 NA	intron (NCharlie2E	26803	NR_00129E	57214	Hs.45908E	NR_01868E	ENSG000000CEMIP	CCSP1 HYE	cell migrprotein-coding	
chr15-406.4.178745	-2.83775	1.405379	-2.01921	0.043465	0.981636	chr15	40621023	40621625	+ 0 NA	exon (NM exon (NM	27075	NR_14450E	57082	Hs.18185E	NR_14450E	ENSG000000CNKL1	AF15Q14 C	kinetoch protein-coding	
chr3-1006.4.178745	-2.83775	1.405379	-2.01921	0.043465	0.981636	chr3	10068230	10068803	+ 0 NA	intron (NLM3A3 LIN	39739	NR_17347E	115795	Hs.19041E	NR_17347E	ENSG000000FANCD20S	C3orf24	FANCD2 pprotein-coding	
chr15-402.4.905229	-2.44603	1.211975	-2.01822	0.043568	0.981636	chr15	40108699	40109574	+ 0 NA	intron (Nintron (N	-8292	NR_00112E	1.07E+08	Hs.73237E	NR_00112E	ENSG000000BUB1B-PAK	PAK-5 PAK	BUB1B-PAK protein-coding	
chr11-748.4.129748	-2.85122	1.41607	-2.01348	0.044065	0.981636	chr11	74838783	74839035	+ 0 NA	3' UTR (N3' UTR (N	90060	NR_00109E	254225	Hs.37014E	NR_00109E	ENSG000000CRNF169		ring fingprotein-coding	
chr10-114.7.744073	1.831101	0.90977	2.012708	0.044145	0.981636	chr10	1.14E+08	1.14E+08	+ 0 NA	intron (NAluSg SIN	31750	NR_031747	1E+08	NR_031747	ENSG000000MIR2110			hsa-mir-2	microRNA ncRNA
chr20-317.4.170087	-2.83521	1.409446	-2.01158	0.044264	0.981636	chr20	31772407	31772929	+ 0 NA	intron (NLM1E4C LI	33378	NR_01211E	22974	Hs.24458C	NR_01211E	ENSG000000TPX2	C20orf1 C	TPX2 micrprotein-coding	
chr12-506.5.639571	-2.20102	1.094948	-2.01016	0.044414	0.981636	chr12	50631387	50631669	+ 0 NA	intron (NAluS6 SI	126543	NR_17360E	57609	Hs.50551E	NR_02084E	ENSG000000DIP2B		disco intrprotein-coding	
chr1-1481.7.18693	1.96479	0.97808	2.008825	0.044556	0.981636	chr1	1.48E+08	1.48E+08	+ 0 NA	intron (NAluSx1 SI	9549	NR_001101	200030	Hs.72158E	NR_18337E	ENSG000000NBPF11	NBPF24	NBPF memprotein-coding	
chr9-1347.4.864009	-2.45774	1.224606	-2.00696	0.044754	0.981636	chr9	1.35E+08	1.35E+08	+ 0 NA	intron (Nintron (N	-53848	NR_13804E	414316	Hs.571561	NR_13804E	ENSG000000COL5A1-AS-	C9orf104 G	COL5A1 arncRNA	
chrX-4912.4.743191	2.4552	1.22456	2.004965	0.044967	0.981636	chrX	49120465	49120966	+ 0 NA	intron (NAluSx SIN	3020	NR_01569E	27238	Hs.50366E	NR_01569E	ENSG000000GPKW0	GPAT5 G	6-patch protein-coding	
chr9-128.5.487056	2.213379	1.104267	2.004387	0.045029	0.981636	chr9	1.28E+08	1.28E+08	+ 0 NA	3' UTR (N3' UTR (N	4367	NR_19795E	203245	Hs.37360E	NR_19795E	ENSG000000NAIF1	C9orf90 t	nuclear pprotein-coding	
chr10-74.5.606289	-2.21233	1.105061	-2.002	0															



chr5-4908 14. 71608	1.2342	0.642964	1.919547	0.054915	0.981636	chr5	49088837	49089492 +	0 NA	IntergeniALR/Alpha	1352124 NM_198444	133418 Hs. 561411NM_198444	ENSG000000CEMB	GP70	emigin protein-coding
chr2-2675 4. 657768	-2.35714	1.229029	-1.91789	0.055125	0.981636	chr2	26790705	26792687 +	0 NA	intron (Nintron (N	5640 NM_001805	1058 Hs. 1594 NM_001805	ENSG000000CENPA	CENP-A C	centromere protein-coding
chr8-9504 4. 657768	-2.35714	1.229029	-1.91789	0.055125	0.981636	chr8	95045645	95045900 +	0 NA	intron (Nintron (N	20783 NR_148913	137682 Hs. 435500NM_152414	ENSG000000NDUFAP6	C8orf38 N	NADH:ubiquinone protein-coding
chr8-417 6. 717801	1.849174	0.965073	1.916098	0.055353	0.981636	chr8	41707497	41707701 +	0 NA	intron (Nintron (N	42325 NM_02048C	286 Hs. 654438NM_000037	ENSG000000ANK1	ANK1 SPH1	ankyrin 1 protein-coding
chr12-105 5. 399967	-2.12396	1.109148	-1.91495	0.055499	0.981636	chr12	1.057078	1.057081 +	0 NA	IntergeniALR/Alpha	42466 NM_00114F	387882 Hs. 368983NM_207377	ENSG000000C12orf75	AGK3 OCC	chromosome protein-coding
chr19-564 7. 502805	1.758828	0.918838	1.914186	0.055596	0.981636	chr19	56460915	56461342 +	0 NA	intron (NMIR SINE	16217 NM_001321	63934 Hs. 67660NM_022103	ENSG000000ZNF667	MIPU1	zinc finger protein-coding
chr2-3202 7. 502805	1.758828	0.918838	1.914186	0.055596	0.981636	chr2	32024460	32024737 +	0 NA	intron (NLM3C3A LI	-13599 NR_126034	51072 Hs. 444966NM_015955	ENSG000000MEMO1	C2orf4 C	mediator protein-coding
chr11-665 5. 991502	1.974324	1.03206	1.912993	0.055749	0.981636	chr11	66535964	66536516 +	0 NA	3' UTR (N3' UTR (N	9808 NM_20734C	254359 Hs. 209587NM_20734C	ENSG000000ZDHH24	-	zinc finger protein-coding
chr10-404 50. 79542	0.7396	0.38665	1.912842	0.055768	0.981636	chr10	40412688	40414995 +	0 NA	IntergeniALR/Alpha	1717245 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B ps_pseudo
chr3-2146 4. 384251	-2.12024	1.109116	-1.91164	0.055922	0.981636	chr3	2.15E+08	2.15E+08 +	0 NA	exon (NM exon (NM	54016 NM_016343	1063 Hs. 497741NM_016343	ENSG000000CENPF	CENF CILL	centromere protein-coding
chr10-408 13. 94476	1.354961	0.709003	1.911078	0.055995	0.981636	chr10	40898298	40898519 +	0 NA	IntergeniALR/Alpha	1469637 NR_02438C	441666 Hs. 255725NR_02438C	ENSG000000LOC441666	-	zinc finger pseudo
chr19-105 5. 99936	1.970665	1.031772	1.909982	0.056136	0.981636	chr19	1056868	1060029 +	0 NA	intron (N3b LINE	-7511 NM_00125E	23526 Hs. 465521NM_012292	ENSG000000ARHGAP45	HA-1 HLA-Rho	GTPase protein-coding
chr19-40C 5. 99936	1.970665	1.031772	1.909982	0.056136	0.981636	chr19	40034687	40035214 +	0 NA	exon (NM exon (NM	21281 NM_00100E	163131 Hs. 101135NM_00100E	ENSG000000ZNF780B	ZNF779	zinc finger protein-coding
chr2-1555 5. 99936	1.970665	1.031772	1.909982	0.056136	0.981636	chr2	15552908	15553233 +	0 NA	intron (NAluSc SIN	8264 NM_01590E	51594 Hs. 407155NM_01590E	ENSG000000CNBAS	ILF52 NAC	neuroblastin protein-coding
chr3-1836 5. 99936	1.970665	1.031772	1.909982	0.056136	0.981636	chr3	1.84E+08	1.84E+08 +	0 NA	intron (NAluSp SIN	-24991 NM_001351	55689 Hs. 632575NM_018023	ENSG000000YEATS2	-	YEATS domain protein-coding
chr8-2332 5. 366686	-2.13551	1.118168	-1.90983	0.056155	0.981636	chr8	23324274	23325985 +	0 NA	intron (NAluJb SIN	-10844 NR_038322	1.01E+08 Hs. 661133NR_038322	ENSG000000LOC100507	-	uncharacterized ncRNA
chr5-6718 8. 170399	1.675699	0.877712	1.909247	0.05623	0.981636	chr5	67142994	67143302 +	0 NA	intron (NFMAM_C SI	53651 NM_00558E	4064 Hs. 87205 NM_00558E	ENSG000000CD180	LY64 Ly7c	CD180 mol protein-coding
chr10-404 41. 71549	0.78331	0.410351	1.908877	0.056278	0.981636	chr10	40587921	40588148 +	0 NA	IntergeniALR/Alpha	178011 NR_02438C	441666 Hs. 255725NR_02438C	ENSG000000LOC441666	-	zinc finger pseudo
chr5-1215 6. 862643	-1.82497	0.957442	-1.90609	0.056639	0.981636	chr5	1.22E+08	1.22E+08 +	0 NA	intron (NLIAP7 LIN	2913 NM_15254E	153443 Hs. 107622NM_15254E	ENSG000000SRFBP1	BUD22 P4	serum response protein-coding
chr5-4945 85. 83963	0.69468	0.364496	1.905864	0.056668	0.981636	chr5	49492298	49492628 +	0 NA	IntergeniALR/Alpha	948825 NM_19844F	133418 Hs. 561411NM_19844F	ENSG000000CEMB	GP70	emigin protein-coding
chr5-3347 6. 837219	-1.83492	0.963356	-1.90471	0.056817	0.981636	chr5	33470230	33470502 +	0 NA	IntergeniIntergeni	29590 NR_04767E	6897 Hs. 481866NM_15229F	ENSG000000TARS	ThrRS	threonyl-tRNA protein-coding
chr20-505 5. 966078	1.968861	1.03477	1.902704	0.057079	0.981636	chr20	5096548	5097333 +	0 NA	intron (Nintron (N	16136 NM_00100E	29058 Hs. 472024NM_01414F	ENSG000000TMEM230	C2orf30 C	transmembrane protein-coding
chr19-564 6. 725659	1.845095	0.970441	1.90213	0.057154	0.981636	chr19	56441478	56444947 +	0 NA	intron (NLMIB7 LIN	34133 NM_001321	63934 Hs. 67660NM_022103	ENSG000000ZNF667	MIPU1	zinc finger protein-coding
chr3-1704 5. 376393	-2.11834	1.113709	-1.90206	0.057163	0.981636	chr3	1.7E+08	1.7E+08 +	0 NA	intron (Nintron (N	3313 NR_10688E	1.02E+08 Hs. 10688E	ENSG000000MIR6828	hsa-mir-6828	microRNA ncRNA
chr6-334 4. 616628	-2.36919	1.246821	-1.90018	0.057409	0.981636	chr6	33406024	33406324 +	0 NA	intron (Nintron (N	-4840 NM_02416E	5252 Hs. 166204NM_00263E	ENSG000000PHF1	MTF2L2 PC	HD finger protein-coding
chr16-145 5. 222213	2.127513	1.206882	1.898408	0.057642	0.981636	chr16	1457033	1457396 +	0 NA	intron (Nintron (N	-12740 NM_00114E	645811 Hs. 355232NM_00114E	ENSG000000CCDC154	C16orf29	coiled-coil protein-coding
chr16-302 6. 102877	-1.95442	1.029643	-1.89816	0.057676	0.981636	chr16	3021770	3022334 +	0 NA	TTS (NM_C TTS (NM_C	1684 NM_01663E	51330 Hs. 355899NM_01663E	ENSG000000TNFRSF12	CD266 FN1	TNFR protein-coding
chr8-1332 6. 136159	-1.94473	1.024803	-1.89766	0.057741	0.981636	chr8	1.33E+08	1.33E+08 +	0 NA	intron (NMER5A DNA	24136 NM_08083E	8840 Hs. 492974NM_00388E	ENSG000000CCN4	WISP1 WIS	cellular protein-coding
chr6-1392 6. 829361	-1.83345	0.966763	-1.89648	0.057896	0.981636	chr6	1.39E+08	1.39E+08 +	0 NA	exon (NM exon (NM	14020 NM_02124E	58527 Hs. 600861NM_02124E	ENSG000000ABRACL	C6orf115 ABRA	C-terminus protein-coding
chr1-1928 13. 98978	2.12472	0.657959	1.89635	0.057914	0.981636	chr1	1.93E+08	1.93E+08 +	0 NA	intron (Nintron (N	1827 NM_00292E	5997 Hs. 78944 NM_00292E	ENSG000000RGS2	GOSR	regulator protein-coding
chr5-7925 6. 684519	1.847389	0.975542	1.893705	0.058264	0.981636	chr5	79290640	79290900 +	0 NA	intron (NAluSg7 SI	54639 NM_15240E	133746 Hs. 482606NM_15240E	ENSG000000JMY	WHAMM2 WJ	junction protein-coding
chr19-444 6. 101228	-1.97126	1.041129	-1.89338	0.058307	0.981636	chr19	44676444	44676643 +	0 NA	intron (Nintron (N	5091 NM_02021E	56971 Hs. 416922NM_02021E	ENSG000000CEACAM19	CEACAM19	carcinoembryonic protein-coding
chr17-404 4. 642052	-2.3525	1.244004	-1.89107	0.058615	0.981636	chr17	40404772	40407422 +	0 NA	intron (NAluSg2 SI	11799 NM_001067	7153 Hs. 15634NM_001067	ENSG000000TOP2A	TOP2 TP2A	DNA topoisomerase protein-coding
chr6-1445 5. 425391	-2.1104	1.116557	-1.89009	0.058745	0.981636	chr6	1.45E+08	1.45E+08 +	0 NA	intron (Nintron (N	126067 NR_13277E	1.07E+08 Hs. 13277E	SNORA98	-	small nucleolar RNA
chr9-5465 11. 425391	-2.1104	1.116557	-1.89009	0.058745	0.981636	chr9	5462599	5463108 +	0 NA	exon (NM exon (NM	12311 NM_001314	29126 Hs. 521989NM_01414F	ENSG000000CD274	B7-H B7H1	CD274 mol protein-coding
chr7-1375 5. 107578	-1.40387	0.743834	-1.88734	0.059114	0.981636	chr7	1.38E+08	1.38E+08 +	0 NA	intron (NLIAP8 LIN	6471 NM_00131E	64764 Hs. 490275NM_194071	ENSG000000CREB3L2	BBF2H7	cAMP response protein-coding
chr11-28C 5. 368536	-2.1164	1.121588	-1.88697	0.059164	0.981636	chr11	28087724	28089555 +	0 NA	exon (NM exon (NM	19517 NM_03121E	81930 Hs. 301052NM_03121E	ENSG000000KIF18A	MS-KIF18A	kinesin I protein-coding
chr2-1527 5. 368536	-2.1164	1.121588	-1.88697	0.059164	0.981636	chr2	1.53E+08	1.53E+08 +	0 NA	intron (NHERV1P OI	11316 NM_00136E	55660 Hs. 64358NM_01789E	ENSG000000PRP40A	FBP-11 F	pre-mRNA processing protein-coding
chr5-1294 8. 317461	-1.64711	0.873047	-1.88662	0.059211	0.981636	chr5	1.29E+08	1.29E+08 +	0 NA	intron (NAluSx1 SI	-8283 NR_12574F	1.04E+08 Hs. 628635NR_12574F	ENSG000000ADAMTS19	-	ADAMTS19 ncRNA
chr20-317 5. 343112	-2.13019	1.13249	-1.88098	0.059974	0.981636	chr20	31779835	31780153 +	0 NA	intron (N2b LINE	-39381 NM_03311E	85366 Hs. 86092 NM_03311E	ENSG000000MYLK2	KMLC MLC	myosin I protein-coding
chr9-3805 5. 343112	-2.13019	1.13249	-1.88098	0.059974	0.981636	chr9	38055980	38055980 +	0 NA	intron (Nintron (N	9533 NM_00302E	6461 Hs. 521482NM_00302E	ENSG000000SHB	BA3J10.2	SH2 domain protein-coding
chr16-884 6. 007218	1.96681	1.046087	1.880159	0.060086	0.981636	chr16	884159	885094 +	0 NA	intron (NLMIEc LIN	-36407 NR_11094E	1.02E+08 Hs. 737087NR_11094E	ENSG000000LMF1-AS1	LA136-36E	LMF1 antinuclear RNA
chr19-574 5. 230071	2.12304	1.12942	1.879761	0.060141	0.981636	chr19	57452347	57452546 +	0 NA	IntergeniMST LTR	4293 NM_02063E	57191 Hs. 677422NM_02063E	ENSG000000VNIR1	VNIR1 VN	von Willebrand factor protein-coding
chr17-281 7. 12952	-1.86211	0.991981	-1.87716	0.060496	0.981636	chr17	28101275	28101474 +	0 NA	intron (NLMIE1 LIN	58697 NM_016231	51701 Hs. 208755NM_016231	ENSG000000NLK	-	nemo like protein-coding
chr1-1745 8. 758974	1.57614	0.83999	1.876379	0.060603	0.981636	chr1	50710 NM_00136E	50710 NM_00136E +	0 NA	intron (NLMIA6 LIN	50710 NM_00136E	9910 Hs. 585375NM_014857	ENSG000000RABGAP1L	HHL TB	IC1 RAB GTPase protein-coding
chr6-5936 55. 08224	0.725062	0.386781	1.874605	0.060847	0.981636	chr6	59383276	59383494 +	0 NA	IntergeniALR/Alpha	-1421939 NR_132994	1.07E+08 Hs. 561535NR_125727	ENSG000000LINC0068C	-	long intergenic RNA
chr1-1228 11. 956447	1.326251	0.707629	1.874217	0.060901	0.981636	chr1	1.23E+08	1.23E+08 +	0 NA	IntergeniALR/Alpha	133121 NR_00395E	647121 Hs. 697682NR_00395E	ENSG000000EMBPI	-	emigin ps_pseudo
chr11-117 9. 554399	-1.494	0.797534	-1.87328	0.06103	0.981636	chr11	1.17E+08	1.17E+08 +	0 NA	3' UTR (N3' UTR (N	-5104 NR_04521E	1.01E+08 Hs. 732365NR_04521E	ENSG000000LOC100652	-	uncharacterized ncRNA
chr10-40C 8. 99379	0.834661	0.446167	1.870737	0.061381	0.981636	chr10	40019658	40020581 +	0 NA	IntergeniALR/Alpha	1323523 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B ps_pseudo
chr1-1628 7. 991535	1.636747	0.875458	1.869589	0.061541	0.981636	chr1	1.63E+08	1.63E+08 +	0 NA	intron (Nintron (N	10578 NM_016371	51478 Hs. 492922NM_016371	ENSG000000HSD17B7	PRAP SDR	hydroxysteroid protein-coding
chr18-764 7. 991535	1.6367														

chr1-1967	9.271277	1.479612	0.81799	1.80884	0.070476	0.981636	chr1	1.97E+08	1.97E+08	0	NA	intron (THE1C-int	-35692	NM_021023	10878	Hs.709217NM_021023	ENSG00000CFHR3	CFHL3 DOW	complemer protein-coding				
chr1-2418	4.377024	-2.277	1.260254	-1.80677	0.070797	0.981636	chr1	2.42E+08	2.42E+08	0	NA	intron (NLTR12C LI	6053	NM_006027	9156	Hs.498244NM_003688	ENSG00000EX01	HEX1 hEx	exonucleo protein-coding				
chr2-112	4.377024	-2.277	1.260254	-1.80677	0.070797	0.981636	chr2	1.12E+08	1.12E+08	0	NA	intron (NAluSp SIN	21797	NM_024953	80018	Hs.530941NM_024953	ENSG00000NAA25	C12orf30 N(alpha)	protein-coding				
chr2-7385	5.896555	-1.87138	1.035836	-1.80664	0.070819	0.981636	chr2	73899178	73904633	0	NA	intron (Nintron (N	8897	NM_001199	72	Hs.516105NM_001616	ENSG00000ACTG2	ACT ACT3	actin gα protein-coding				
chr15-412	5.111366	-2.05049	1.136616	-1.80403	0.071226	0.981636	chr15	14345606	14346736	0	NA	intron (NL2 LINE I	12960	NM_001635	51203	Hs.615092NM_016355	ENSG00000NUSAP1	ANKT BMO2	nucleolar protein-coding				
chr15-694	5.111366	-2.05049	1.136616	-1.80403	0.071226	0.981636	chr15	69438121	69438854	0	NA	intron (Nintron (N	-14331	NM_001003	6176	Hs.356502NM_001003	ENSG00000CRPLP1	LP1 P1 RF	ribosomal protein-coding				
chr1-771C	4.264354	2.268934	1.258642	1.802684	0.071438	0.981636	chr1	7710111	771579	0	NA	intron (Nintron (N	7939	NR_033908	1E+08	Hs.527521NR_033908	LOC100288		uncharactercna				
chr10-681	6.519222	-1.75534	0.97418	-1.80187	0.071566	0.981636	chr10	68002688	68003162	0	NA	intron (NLIMA3 LIN	7958	NR_131184	1E+08	Hs. NR_131184	POU5F1P5	Oct4-pg5	POU class pseudo				
chr15-892	6.607323	-1.75534	0.97418	-1.80187	0.071566	0.981636	chr15	89248846	89250381	0	NA	intron (NAluJb SIN	5634	NM_018193	55215	Hs.513122NM_018193	ENSG00000FANCI	KIAA1794	FA comple	protein-coding			
chr10-377	4.982795	2.042757	1.134187	1.801076	0.071691	0.981636	chr10	37747025	37971146	0	NA	intron (NL2a LINE	5045	NR_138066	219749	Hs.499422NM_145011	ENSG00000ZNF25	KOX19 Zfz	zinc fing	protein-coding			
chr19-374	4.982795	2.042757	1.134187	1.801076	0.071691	0.981636	chr19	37474646	37749901	0	NA	intron (NAluY SINE	-28012	NM_032685	84775	Hs.116622NM_032685	ENSG00000ZNF607			zinc fing	protein-coding		
chr5-3782	4.982795	2.042757	1.134187	1.801076	0.071691	0.981636	chr5	37822987	37824795	0	NA	intron (Nintron (N	10931	NM_001278	2668	Hs.248114NM_000514	ENSG00000GDNF	ATF ATF1 glial	cell	protein-coding			
chr6-2614	4.982795	2.042757	1.134187	1.801076	0.071691	0.981636	chr6	26137347	26139842	0	NA	Intergeni LIME4b LI	14449	NM_003512	8334	Hs.484952NM_003512	ENSG00000HIST1H2AC	H2A H1 H2	histone c	protein-coding			
chr9-379	6.5819	-1.76561	0.980348	-1.801	0.071702	0.981636	chr9	37991654	37991853	0	NA	intron (Nintron (N	77474	NM_030302	6461	Hs.521482NM_030302	ENSG00000SHB	ba3J10.2	SH2	domai	protein-coding		
chr11-345	6.648463	-1.74834	0.971952	-1.79879	0.072051	0.981636	chr11	34944680	34944933	0	NA	intron (NLIMEi LIN	2969	NR_039833	1.01E+08	NR_039833	ENSG00000MIR1343			microRNA	ncRNA		
chr10-176	5.855416	-1.87949	1.045408	-1.79786	0.0722	0.981636	chr10	17612604	17612831	0	NA	intron (NAluY SINE	4657	NM_014241	9200	Hs.114062NM_014241	ENSG00000HACD1	CAP PTPLA	3-hydroxy	protein-coding			
chr1-214C	4.402448	-2.25994	1.25735	-1.79738	0.072275	0.981636	chr1	2.15E+08	2.15E+08	0	NA	3' UTR (N3' UTR (N	61002	NM_016343	1063	Hs.497741NM_016343	ENSG00000CCENPF	CENF CILL	centromer	protein-coding			
chr17-404	4.402448	-2.25994	1.25735	-1.79738	0.072275	0.981636	chr17	40397611	40401221	0	NA	intron (NAluJb SIN	18480	NM_001067	7153	Hs.156342NM_001067	ENSG00000TOP2A	TOP2 TP2	DNA topoi	protein-coding			
chr17-404	4.402448	-2.25994	1.25735	-1.79738	0.072275	0.981636	chr17	40402179	40403015	0	NA	intron (NL2a LINE	15299	NM_001067	7153	Hs.156342NM_001067	ENSG00000TOP2A	TOP2 TP2	DNA topoi	protein-coding			
chr1-1965	5.701236	1.887575	1.050773	1.796368	0.072436	0.981636	chr1	19625455	19625748	0	NA	3' UTR (N3' UTR (N	-17628	NM_182744	4681	Hs.654502NM_005383	ENSG00000CNBL1	D1S1733E NBL1	DA	protein-coding			
chr1-2355	5.701236	1.887575	1.050773	1.796368	0.072436	0.981636	chr1	2.36E+08	2.36E+08	0	NA	intron (NChap1_Man	-45269	NM_001098	2786	Hs.159711NM_004488	ENSG00000GNG4			G	protein-coding		
chr8-8654	9.161725	1.466446	0.817351	1.794145	0.07279	0.981636	chr8	86544904	86545385	0	NA	intron (NMER70C LI	30709	NM_003905	8895	Hs.191215NM_003905	ENSG00000CPNE3	CPN3 PRO1	copine 3	protein-coding			
chr4-9427	9.306937	-1.44283	0.804567	-1.7933	0.072925	0.981636	chr4	94275780	94276037	0	NA	intron (NAluY SINE	22599	NM_001254	56916	Hs.410402NM_020155	ENSG00000SMARCAD1	ADERM BAS	SWI/SNF-1	protein-coding			
chr14-705	4.23893	2.261471	1.261248	1.793043	0.072966	0.981636	chr14	70520346	70521207	0	NA	Intergeni Tigger1 I	14228	NM_003814	8748	Hs.177984NM_003814	ENSG00000ADAM20			ADAM	meta	protein-coding	
chr19-524	4.23893	2.261471	1.261248	1.793043	0.072966	0.981636	chr19	52468433	52469429	0	NA	intron (NMLT2B3 LI	15378	NM_001095	147660	Hs.157287NM_152472	ENSG00000ZNF578			zinc	fing	protein-coding	
chr10-40	23.62776	0.950094	0.529967	1.792743	0.073014	0.981636	chr10	40367454	40368623	0	NA	Intergeni ALR Alpha	1671442	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo		
chr19-105	5.016076	2.044747	1.141308	1.791582	0.0732	0.981636	chr19	10545456	10560038	0	NA	exon (NM exon (NM	-10667	NM_001258	23256	Hs.465521NM_012292	ENSG00000ARHGAP45	HA-1 HLA	Rho	GT	Pas	protein-coding	
chr4-1031	3.675964	-2.62305	1.464154	-1.79151	0.073211	0.981636	chr4	1.03E+08	1.03E+08	0	NA	intron (NL2c LINE	-9898	NM_020135	56898	Hs.124692NM_020135	ENSG00000BDH2	DHR56 EF	3-hydroxy	protein-coding			
chr5-8107	7.300526	-1.67692	0.936219	-1.79117	0.073266	0.981636	chr5	81070686	81070913	0	NA	intron (Nintron (N	-109892	NR_105015	1.03E+08	Hs.737155NR_105015	ENSG00000RASGRF2-1			RASGRF2	ε	ncRNA	
chr7-5927	8.494131	1.517431	0.847798	1.78985	0.073478	0.981636	chr7	59274995	59275528	0	NA	Intergeni ALR Alpha	1825084	NM_001155	441234	Hs.533121NM_001155	ENSG00000ZNF716			zinc	fing	protein-coding	
chr3-1235	5.880839	-1.8677	1.04446	-1.7882	0.073744	0.981636	chr3	1.24E+08	1.24E+08	0	NA	intron (NHAL1b LI	21676	NM_001366	64770	Hs.645022NM_022757	ENSG00000CCDC14			coiled-c	protein-coding		
chr2-1217	6.564334	-1.77801	0.994443	-1.78795	0.073784	0.981636	chr2	1.22E+08	1.22E+08	0	NA	intron (Nintron (N	2859	NM_004622	7247	Hs.75066	NM_004622	ENSG00000TSN	BCLF-1 C	transl	in	protein-coding	
chr17-682	6.957371	2.036221	1.139893	1.786326	0.074046	0.981636	chr17	68227184	68227732	0	NA	intron (NMLT1D LTF	-20116	NM_001346	51321	Hs.293566	NM_016627	ENSG00000AMZ2			archaeal	ys	protein-coding
chr2-365	6.599465	-1.75368	0.981816	-1.78616	0.074073	0.981636	chr2	36507731	36507930	0	NA	intron (Nintron (N	90338	NM_001042	9637	Hs.258563NM_005102	ENSG00000FEZ2	HUM3CL	fascicul	ε	protein-coding		
chr15-326	6.574042	-1.76411	0.988074	-1.78541	0.074195	0.981636	chr15	32625149	32626377	0	NA	intron (Nintron (N	10259	NM_001286	9824	Hs.591133NM_014783	ENSG00000ARHGAP11	11	GAP (1-12	Rho	GT	Pas	protein-coding
chr6-616	6.519522	1.779739	0.997801	1.783301	0.074537	0.981636	chr6	26132458	26132815	0	NA	Intergeni AluSx4 SI	8491	NM_003512	8334	Hs.484952NM_003512	ENSG00000HIST1H2AC	H2A H1 H2	histone c	protein-coding			
chr15-477	4.990653	2.038206	1.143282	1.782767	0.074624	0.981636	chr15	47764022	47765974	0	NA	exon (NM exon (NM	46509	NM_153615	80031	Hs.511265NM_020855	ENSG00000SEMA6D			semaphori	protein-coding		
chr6-1497	5.847558	-1.87776	1.054409	-1.78086	0.074935	0.981636	chr6	1.5E+08	1.5E+08	0	NA	intron (NAluSg SIN	33628	NM_001366	5110	Hs.279257NM_005383	ENSG00000PCMT1	P1MT		protein-l	protein-coding		
chr12-585	5.121074	-2.03254	1.143105	-1.77808	0.07539	0.981636	chr12	58868014	58868405	0	NA	Intergeni Intergeni	51337	NM_001136	121227	Hs.253737NM_153377	ENSG00000LRIG3	LIG3		leucine	in	protein-coding	
chr2-1355	5.121074	-2.03254	1.143105	-1.77808	0.07539	0.981636	chr2	1.36E+08	1.36E+08	0	NA	intron (NLIMA2 LIN	-13673	NR_110200	1.02E+08	Hs.602175NR_110195	ENSG00000DARS-AS1			DARS	ant	ncRNA	
chr15-58	9.365642	-1.4304	0.804486	-1.77803	0.075399	0.981636	chr15	58654692	58654974	0	NA	intron (NLIMA2 LIN	38774	NR_073415	664618	Hs.670224NM_002927	HSP90ABF HSP90b			heat	shoc	pseudo	
chr7-4507	7.245821	1.688798	0.950904	1.775992	0.075734	0.981636	chr7	45072720	45072979	0	NA	intron (Nintron (N	16095	NM_001146	23148	Hs.96633	NM_001146	ENSG00000NACAD			NAC	alphan	protein-coding
chr8-4317	7.709127	1.566054	0.882196	1.775176	0.075869	0.981636	chr8	43177116	43177530	0	NA	intron (NAluY SINE	36859	NM_152415	138050	Hs.600384NM_152415	ENSG00000HGSNAT	HGNAT MPS	heparan-ε	protein-coding			
chr5-478	139.0327	0.506707	0.285495	1.774835	0.075925	0.981636	chr5	47864769	47864981	0	NA	Intergeni ALR Alpha	-2168495	NM_021072	348980	Hs.353176NM_021072	ENSG00000HCN1	BCNG-1 BC	hyperpol	ε	protein-coding		
chr17-565	7.742409	1.567868	0.884348	1.772908	0.076244	0.981636	chr17	56941715	56941955	0	NA	intron (Nintron (N	19215	NM_004645	8161	Hs.532795NM_004645	ENSG00000COIL	CLN80 p8C	coilin	protein-coding			
chr2-1732	8.062141	-1.58812	0.896322	-1.77182	0.076424	0.981636	chr2	1.73E+08	1.73E+08	0	NA	intron (NAluSx SIN	74591	NR_033882	339751	Hs.570085NR_033882	ENSG00000MAP3K20-1	MLK7-AS1	MAP3K20	ε	ncRNA		
chr8-4255	5.872982	-1.86573	1.053458	-1.77106	0.076551	0.981636	chr8	42532310	42532652	0	NA	intron (Nintron (N	-8667	NM_001135	114926	Hs.655322NM_138433	ENSG00000SMIM19	C8orf40		small	in	protein-coding	
chr6-839	5.921979	-1.85912	1.049836	-1.77087	0.076583	0.981636	chr6	83934671	83935202	0	NA	intron (Nintron (N	75247	NM_016233	51167	Hs.5741	NM_016233	ENSG00000CCYB5R4	NCB50R ct	cytochro	protein-coding		
chr4-267	8.613735	-1.47865	0.836267	-1.76815	0.077037	0.981636	chr4	26735694	26735981	0	NA	intron (NLIPA2 LIN	124407	NR_134675	1.05E+08	Hs.548855NR_134673	STIM2-AS1			STIM2	ant	ncRNA	
chr4-1135	6.624889	-1.7431	0.987095	-1.76589	0.077415	0.9816																	



chr17-417 5.495099	1.80979	1.058738	1.709385	0.08738	0.981636	chr17	41769422	41771610	+	0 NA	intron (Nintron (N	15579 NM_001352	3728 Hs. 514174NM_00223C	ENSG00000CJUP	CTNNG DP2 junction protein-coding
chr5-487 22.43233	0.905459	0.529751	1.709217	0.087411	0.981636	chr5	48785857	48786704	+	0 NA	IntergeniALR/Alph	1655008 NM_198445	133418 Hs. 561411NM_198445	ENSG00000EMB	GP70 embigin protein-coding
chr3-532 6.188116	1.698572	0.994013	1.708802	0.087488	0.981636	chr3	53251108	53251491	+	0 NA	intron (Nintron (N	4723 NM_001064	7086 Hs. 89643 NM_001064	ENSG00000CKT	HEL-S-48 transketcprotein-coding
chr17-417 4.973087	2.025941	1.185604	1.708783	0.087491	0.981636	chr17	41755718	41756125	+	0 NA	intron (Nintron (N	-21275 NM_001079	9001 Hs. 158303NM_00394C	ENSG00000HAP1	HAP2 HPE huntingtin protein-coding
chr2-1106 4.137421	-2.17849	1.275642	-1.70776	0.087681	0.981636	chr2	1.11E+08	1.11E+08	+	0 NA	intron (Nintron (N	4662 NR_132975	1.07E+08 NR_132975	SNORD132	small nucsnoRNA
chr11-124 5.615812	-1.80227	1.055605	-1.70734	0.087759	0.981636	chr11	1.25E+08	1.25E+08	+	0 NA	intron (NAluS6 SI	4551 NM_001312	79684 Hs. 146079NM_02463I	ENSG00000MSANTD2	C11orf61 Myb/SANT protein-coding
chr2-364 5.615812	-1.80227	1.055605	-1.70734	0.087759	0.981636	chr2	36454282	36454546	+	0 NA	intron (Nintron (N	98636 NM_016441	51232 Hs. 699247NM_01644I	ENSG00000CRIMI	CRIM-1 5E cysteine protein-coding
chr2-2018 5.615812	-1.80227	1.055605	-1.70734	0.087759	0.981636	chr2	2.02E+08	2.02E+08	+	0 NA	intron (Nintron (N	20476 NM_001261	65061 Hs. 348711NM_13915E	ENSG00000CDK15	ALS2CR7 Fyclin deprotein-coding
chr5-176 5.615812	-1.80227	1.055605	-1.70734	0.087759	0.981636	chr5	1.76E+08	1.76E+08	+	0 NA	TTS (NM_TTS (NM_I	-1582 NM_00125E	51491 Hs. 696282NM_01639I	ENSG00000CNO16	HSPC111 FNOP16 nucprotein-coding
chr8-6161 5.615812	-1.80227	1.055605	-1.70734	0.087759	0.981636	chr8	61612440	61613003	+	0 NA	intron (NLM4a LI	77659 NM_001164	444 Hs. 332422NM_00431E	ENSG00000ASPH	AAH BAH Caspartat protein-coding
chr5-134 5.649094	-1.79223	1.049905	-1.70704	0.087815	0.981636	chr5	1.35E+08	1.35E+08	+	0 NA	intron (NLMBA LI	23654 NM_17801I	347732 Hs. 631804NM_17801E	ENSG00000CATSPER3	CACR carotid cprotein-coding
chr10-10 8.196007	1.454459	0.852246	1.706618	0.087893	0.981636	chr10	1.02E+08	1.02E+08	+	0 NA	intron (Nintron (N	2887 NM_001322	4791 Hs. 73090 NM_00250E	ENSG00000CNFKB2	CVID10 H2 nuclear fprotein-coding
chr1-1231 36.12926	0.756761	0.443899	1.704806	0.088231	0.981636	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alph	1588203 NR_00395E	647121 Hs. 697682NR_00395E	ENSG00000EMB1	embigin fpseudo
chr7-3061 9.62623	-1.33891	0.785531	-1.70446	0.088295	0.981636	chr7	30614287	30615066	+	0 NA	intron (NAluYh3 SI	19798 NM_002047	2617 Hs. 404321NM_002047	ENSG00000GARS	CMT2D DSM glycy1-tfprotein-coding
chr19-19 6.401001	-1.67684	0.983996	-1.70411	0.088361	0.981636	chr19	19907795	19908024	+	0 NA	intron (Nintron (N	6963 NM_03121E	81931 Hs. 301059NM_03121E	ENSG00000ZNF93	HPF34 HTF zinc fingprotein-coding
chr7-593 10.83821	1.285295	0.754306	1.703943	0.088392	0.981636	chr7	59321009	59321546	+	0 NA	IntergeniALR/Alph	1871000 NM_00115E	441234 Hs. 533121NM_00115E	ENSG00000ZNF716	zinc fingprotein-coding
chr7-116 9.051618	-1.38859	0.815781	-1.70216	0.088725	0.981636	chr7	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	510 NM_00117E	857 Hs. 74034 NM_00175E	ENSG00000CAV1	BSC13 GLI caveolin protein-coding
chr7-448 6.898698	-1.94791	1.144485	-1.702	0.088756	0.981636	chr7	44882763	44883448	+	0 NA	3' UTR (N3' UTR (N	-1305 NR_039801	1.01E+08 NR_039801	ENSG00000MIR4657	mir-4657 microRNA ncRNA
chr16-88 5.598246	-1.81641	1.067311	-1.70186	0.088782	0.981636	chr16	8887427	8887626	+	0 NA	Intergeni (GT)n LIN	-18514 NM_00127E	23589 Hs. 632184NM_01431E	ENSG00000CARHSP1	CRHSP-24 calcium rprotein-coding
chrX-774 5.598246	-1.81641	1.067311	-1.70186	0.088782	0.981636	chrX	77645607	77646029	+	0 NA	intron (NLM4c LI	140398 NM_13827E	546 Hs. 533521NM_00048E	ENSG00000CATR	JMS MRX52 ATR chrprotein-coding
chr17-64 6.359862	-1.68387	0.993536	-1.70168	0.088815	0.981636	chr17	64652637	64652836	+	0 NA	intron (NAluSx1 SI	9571 NM_002273E	64750 Hs. 515011NM_002273E	ENSG00000SMURF2	SMAD specprotein-coding
chr8-664 5.461817	1.807573	1.062437	1.701346	0.088878	0.981636	chr8	66448695	66449303	+	0 NA	intron (Nintron (N	16495 NM_14465E	137872 Hs. 720022NM_14465E	ENSG00000ADHFE1	ADH8 HMF1 alcohol cprotein-coding
chr20-62 9.477599	1.341688	0.78871	1.701116	0.088921	0.981636	chr20	62339742	62340049	+	0 NA	intron (Nintron (N	-7338 NR_03991E	1.01E+08 NR_03991E	ENSG00000MIR4758	microRNA ncRNA
chr19-48 6.898698	1.621269	0.953865	1.699683	0.089191	0.981636	chr19	48626257	48626501	+	0 NA	intron (Nintron (N	1350 NM_001204	56848 Hs. 528006NM_02012E	ENSG00000SPHK2	SK 2 SK-2 sphingosiprotein-coding
chr8-9494 4.743376	1.952667	1.149667	1.698464	0.08942	0.981636	chr8	94945630	94946551	+	0 NA	intron (NLM4e LI	3288 NM_00113E	94241 Hs. 492261NM_03328E	ENSG00000TP53INP1	SIP TP53E tumor prprotein-coding
chr19-93 5.469675	1.803713	1.062125	1.698211	0.089468	0.981636	chr19	9357696	9357941	+	0 NA	intron (Nintron (N	-5195 NM_00345E	7730 Hs. 728944NM_00345I	ENSG00000ZNF177	PIGX zinc fngprotein-coding
chr12-11 7.520556	1.513211	0.891139	1.698063	0.089496	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	intron (NAluSx1 SI	49770 NM_17066E	488 Hs. 506755NM_00168I	ENSG00000ATP2A2	ATP2B DAF ATPase sprotein-coding
chr10-89 5.641236	-1.7903	1.054622	-1.69757	0.089589	0.981636	chr10	89760956	89763466	+	0 NA	intron (NMLT1H1 LI	60621 NM_001284	9585 Hs. 240 NM_01619E	ENSG00000KIF20B	CT90 KRMF kinesin fprotein-coding
chr1-117 4.86309	-1.96223	1.156323	-1.69696	0.089705	0.981636	chr1	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	-6977 NR_03064E	1E+08 NR_03064E	ENSG00000MIR942	MIRN942 microRNA ncRNA
chr1-205 5.504807	1.82376	1.075099	1.696364	0.089817	0.981636	chr1	2.05E+08	2.05E+08	+	0 NA	intron (Nintron (N	12700 NM_001331	9911 Hs. 6360 NM_01485E	ENSG00000TMCC2	HUCEP11 transment protein-coding
chr12-95 6.393143	-1.67506	0.988017	-1.69537	0.090005	0.981636	chr12	95775500	95775857	+	0 NA	intron (NLM4a LI	14517 NM_00132E	59277 Hs. 201034NM_02122E	ENSG00000CNTN4	PRO3091 netrin 4 protein-coding
chr19-24 38.77165	0.72194	0.426006	1.694669	0.090138	0.981636	chr19	24893005	24893298	+	0 NA	IntergeniALR/Alph	-729704 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG00000HAVCRIP1	hepatitis fpseudo
chr7-70 7.053064	-1.61212	0.951632	-1.69406	0.090254	0.981636	chr7	1.04E+08	1.04E+08	+	0 NA	intron (NAluJo SIN	12427 NM_00255E	5001 Hs. 432948NM_00255E	ENSG00000COC5	ORC5L ORC origin rprotein-coding
chr14-10 7.512698	1.515929	0.895159	1.693475	0.090365	0.981636	chr14	1E+08	1E+08	+	0 NA	exon (NM_exon (NM	13606 NM_00135E	123096 Hs. 578109NM_15233E	ENSG00000SLC25A29	C14orf69 solute cprotein-coding
chr19-26 10.73377	1.254869	0.741154	1.692887	0.090477	0.981636	chr19	26938609	26939623	+	0 NA	IntergeniALR/Alph	-854315 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927	uncharactncRNA
chr3-123 4.930468	-1.93785	1.145201	-1.69215	0.090618	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (NFLAM_A SI	28517 NM_00132E	201562 Hs. 705488NM_19840E	ENSG00000HACD2	PTPLB 3-hydroxyprotein-coding
chr5-15 7.024935	2.165878	1.280023	1.692061	0.090634	0.981636	chr5	1.57E+08	1.57E+08	+	0 NA	intron (Nintron (N	21577 NM_00100I	408263 Hs. 437066NM_00100I	ENSG00000FNDC9	C5orf40 fibronectprotein-coding
chr11-62 8.170584	1.450115	0.857082	1.691921	0.090661	0.981636	chr11	62677167	62677666	+	0 NA	intron (Nintron (N	1657 NM_00128E	51035 Hs. 35129E NM_01585E	ENSG00000UBXN1	2B28 SARX UBX domaiprotein-coding
chr19-36 8.170584	1.450115	0.857082	1.691921	0.090661	0.981636	chr19	36359663	36360256	+	0 NA	intron (NLM5 LINE	19242 NM_020917	57677 Hs. 35524 NM_020917	ENSG00000ZFP14	ZNF531 ZFP14 xzprotein-coding
chr1-151 5.479383	1.817628	1.075059	1.690724	0.090889	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	13217 NR_13013E	58497 Hs. 78524 NM_02122E	ENSG00000PRUNE1	DRES-17 lprune excprotein-coding
chr19-36 6.922273	1.612024	0.953699	1.690286	0.090973	0.981636	chr19	36615931	36616363	+	0 NA	intron (NAluJr SIN	10834 NM_03282E	84911 Hs. 631591NM_03282E	ENSG00000ZNF382	KS1 zinc fingprotein-coding
chr2-423 9.04376	-1.3874	0.820954	-1.68998	0.091031	0.981636	chr2	42320134	42320392	+	0 NA	intron (NFLAM_C SI	39775 NR_13494E	9167 Hs. 33963E NM_00471E	ENSG00000COX7A2L	COX7AR CC cytochroprotein-coding
chr19-19 7.006402	1.623867	0.961043	1.689693	0.091087	0.981636	chr19	1987070	1987293	+	0 NA	exon (NM_exon (NM	28533 NM_017797	55643 Hs. 46554E NM_017797	ENSG00000BTBD2	BTB domaiprotein-coding
chr1-230 6.162692	1.692962	1.002995	1.687906	0.091429	0.981636	chr1	2.3E+08	2.3E+08	+	0 NA	intron (Nintron (N	179044 NM_00448I	2590 Hs. 743964NM_00448I	ENSG00000GALNT2	GalNAc-T2 polypept protein-coding
chr19-32 7.528414	1.510556	0.895171	1.68745	0.091517	0.981636	chr19	32639005	32639464	+	0 NA	intron (Nintron (N	-30765 NR_14571E	1.1E+08 NR_14571E	ENSG00000SNORA68B	small nucsnoRNA
chr19-36 7.528414	1.510556	0.895171	1.68745	0.091517	0.981636	chr19	36862773	36864054	+	0 NA	intron (NERVL-E ir	11762 NM_00124E	25850 Hs. 362324NM_00341E	ENSG00000ZNF345	HZF10 zinc fngprotein-coding
chr10-10 4.92261	-1.93569	1.147114	-1.68744	0.091518	0.981636	chr10	1.02E+08	1.02E+08	+	0 NA	IntergeniAluSx1 SI	17096 NM_00389E	8861 Hs. 45441E NM_00389E	ENSG00000LDB1	CLIM-2 CLIM domaiprotein-coding
chr19-78 4.717952	1.945781	1.153801	1.686409	0.091717	0.981636	chr19	7858623	7859453	+	0 NA	intron (NAluSx SIN	15352 NM_00119C	80164 Hs. 28854CNM_00108E	ENSG00000PRR36	proline rprotein-coding
chr11-27 3.999511	2.17916	1.280524	1.685181	0.091954	0.981636	chr11	27541270	27542402	+	0 NA	intron (NLM9A LI	-17005 NR_107054	1.02E+08 NR_107054	ENSG00000MIR8087	hsa-mir-5microRNA ncRNA
chr17-50 6.254679	1.702463	1.010535	1.684714	0.092044	0.981636	chr17	50115680	50115942	+	0 NA	intron (Nintron (N	14349 NM_17492C	201191 Hs. 567766NM_17492C	ENSG00000SAMD14	sterile eprotein-coding
chr1-73 7.46185	1.506628	0.844394	1.684524	0.092081	0.981636	chr1	2.31E+08	2.31E+08	+	0 NA	intron (NLM4e LI	45221 NR_110681	1.02E+08 Hs. 63892E NR_110681	ENSG00000LOC101927	uncharactncRNA
chr13-29 8.366273	-1.42133														

chr2-189f.6.733702	1.55403	0.950794	1.634456	0.102163	0.981636	chr2	1.9E+08	1.9E+08	0	NA	intron (Nintron (N	6539	NM_01458E	30061	Hs.64300E	NM_01458E	ENSG00000	SLC40A1	FPN1 HFE4	solute cation protein-coding		
chr1-149c.6.01711	1.643254	1.005864	1.633674	0.102327	0.981636	chr1	1.49E+08	1.49E+08	0	NA	3' UTR (N3' UTR (N	49952	NM_001277	400818	Hs.44508C	NM_001037	ENSG00000	NBP9	AE01	NBP9 mem protein-coding		
chr2-134f.6.143832	-1.61575	0.989568	-1.63279	0.102514	0.981636	chr2	1.35E+08	1.35E+08	0	NA	intron (NAluJb SIN	24453	NM_001241	905	Hs.74411E	NM_001241	ENSG00000	CCNT2	CYCT2	cyclin T2 protein-coding		
chr1-108f.6.118408	-1.62629	0.996023	-1.63278	0.102515	0.981636	chr1	1.09E+08	1.09E+08	0	NA	3' UTR (N3' UTR (N	9432	NM_00134E	55119	Hs.342307	NM_018061	ENSG00000	PRPF38B	NET1	pre-mRNA protein-coding		
chr19-52f.7.982012	1.399349	0.857618	1.631668	0.102749	0.981636	chr19	52150911	52512607	0	NA	exon (NM exon (NM	-15897	NM_001321	388558	Hs.729294	NM_00103E	ENSG00000	ZNF808		zinc finger protein-coding		
chr2-203f.7.982012	1.399349	0.857618	1.631668	0.102749	0.981636	chr2	2.03E+08	2.03E+08	0	NA	intron (Nintron (N	-108131	NM_17753E	57404	Hs.44606E	NM_020674	ENSG00000	CYP20A1	CYP-M	cytochrome protein-coding		
chr5-494f.5.18549	0.632789	0.387885	1.631384	0.102809	0.981636	chr5	49465510	49466309	0	NA	IntergeniALR/Alpha	975514	NM_19844E	133418	Hs.561411	NM_19844E	ENSG00000	EMB	GP70	emigin protein-coding		
chr8-852f.6.135974	-1.617403	0.989496	-1.631164	0.102857	0.981636	chr8	85213831	85213831	0	NA	TTS (NM_C TTS (NM_C	6665	NR_120681	401466	Hs.44307E	NM_00109E	ENSG00000	CRB1S	C8orf59	ribosomal protein-coding		
chr1-702f.6.11055	-1.62455	0.995953	-1.63115	0.102859	0.981636	chr1	70225689	70225943	0	NA	intron (Nintron (N	4436	NM_00135E	9295	Hs.47969E	NM_00476E	ENSG00000	SRSP11	NET2 SFRS	serine ar protein-coding		
chr1-227f.7.816629	1.603181	0.83409	1.6309	0.102911	0.981636	chr1	1.28E+08	1.28E+08	0	NA	3' UTR (N3' UTR (N	-2762	NM_00132E	116841	Hs.325081	NM_05305E	ENSG00000	SNAP47	Clorf142	synaptos protein-coding		
chr1-124f.54.80824	0.631841	0.387515	1.630495	0.102997	0.981636	chr1	1.25E+08	1.25E+08	0	NA	IntergeniALR/Alpha	3215871	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000	EMB1P		emigin pseudo		
chr1-155f.4.784516	1.949815	1.196512	1.629583	0.10319	0.981636	chr1	1.55E+08	1.55E+08	0	NA	exon (NM exon (NM	2867	NR_030281	693235	NR_030281	ENSG00000	MIR92B	MIRN92B	microRNA ncRNA			
chr19-36f.5.974121	1.628467	0.999345	1.629535	0.1032	0.981636	chr19	21765	NM_00136E	0	NA	IntergeniAluSj SIN	164312	HS.412517	15260E	ENSG00000	ZNF567				zinc finger protein-coding		
chr20-60f.6.821318	-1.54712	0.950595	-1.62752	0.103626	0.981636	chr20	6034450	6034728	0	NA	intron (Nintron (N	19471	NM_152611	164312	HS.412517	15261E	ENSG00000	LRRN4	C20orf75	leucine r protein-coding		
chr2-112f.7.179191	-2.41025	1.481887	-1.62647	0.103849	0.981636	chr2	1.13E+08	1.13E+08	0	NA	intron (Nintron (N	20576	NM_001304	150468	HS.43425E	NM_15251E	ENSG00000	CKAP2L			cytoskel protein-coding	
chr6-437f.6.102692	-1.62286	0.998837	-1.62475	0.104217	0.981636	chr6	43772255	43772666	0	NA	intron (Nintron (N	492	NM_001287	7422	HS.73793	NM_00337E	ENSG00000	VEGFA	MVCD1 VEF	vascular protein-coding		
chr14-10f.6.007403	1.630718	1.003764	1.624603	0.104247	0.981636	chr14	1.03E+08	1.03E+08	0	NA	intron (NMIRb SINE	7728	NM_006291	7127	HS.525607	NM_006291	ENSG00000	TNFAIP2	B94 ELOC3	TNF alpha protein-coding		
chr1-252f.7.434577	1.488718	0.91645	1.624439	0.104282	0.981636	chr1	25262846	25263045	0	NA	intron (NMLT2B3 LI	4980	NR_135777	57035	HS.25941E	NM_02031E	ENSG00000	SRSP1	Clorf60C	arginine protein-coding		
chr1-550f.5.966263	1.631867	1.005529	1.622894	0.104612	0.981636	chr1	55087814	55088152	0	NA	intron (NLT2b LINE	47761	NR_110451	255738	HS.18844	NM_17493E	ENSG00000	PCSK9	FH3 HCHO1	proprate protein-coding		
chr3-184f.5.966263	1.631867	1.005529	1.622894	0.104612	0.981636	chr3	1.84E+08	1.84E+08	0	NA	intron (Nintron (N	5617	NM_003907	8893	HS.283551	NM_003907	ENSG00000	EIF2B5	CACH CLE	eukaryoti protein-coding		
chr11-86f.6.708278	1.5488	0.954692	1.622304	0.104738	0.981636	chr11	8623947	8624909	0	NA	exon (NM exon (NM	-30200	NM_00128E	65975	HS.50183E	NM_03090E	ENSG00000	STK33			serine/t protein-coding	
chr10-404f.32.87888	0.799561	0.492973	1.621916	0.104821	0.981636	chr10	40462784	40463063	0	NA	IntergeniALR/Alpha	1766327	NR_04500C	399746	HS.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps pseudo		
chr14-30f.6.838884	-1.53598	0.948125	-1.62002	0.105228	0.981636	chr14	30680776	30681209	0	NA	intron (NAluSv6 SI	58673	NM_01610E	23256	HS.36916E	NM_01610E	ENSG00000	SCFD1	C14orf16C	secl fami protein-coding		
chr7-102f.6.838884	-1.53598	0.948125	-1.62002	0.105228	0.981636	chr7	1.03E+08	1.03E+08	0	NA	intron (NAluSx SIN	2642	NM_03295E	246721	HS.61025E	NM_03295E	ENSG00000	POLR2J2	HRPB11B FRNA	polyn protein-coding		
chr13-11f.9.238181	1.289096	0.795786	1.619904	0.105253	0.981636	chr13	1.13E+08	1.13E+08	0	NA	intron (Nintron (N	-4013	NR_10704E	1.02E+08	NR_10704E	ENSG00000	MIR8075				hsa-mir-ε microRNA ncRNA	
chr16-19f.5.384066	-1.72259	1.063731	-1.61930	0.105364	0.981636	chr16	69002932	69003441	0	NA	intron (NHERV35 I	-102467	NM_00119E	3038	HS.59206E	NM_00532E	ENSG00000	HAS3				hyaluron protein-coding
chr18-17f.10.48649	1.209311	0.747367	1.618095	0.105642	0.981636	chr18	10755628	10756081	0	NA	IntergeniALR/Alpha	-1729935	NR_027417	644669	HS.579474	NR_027417	ENSG00000	LOC64466E				ankyrin r pseudo
chr12-98f.7.530237	-1.4999	0.927085	-1.61787	0.105691	0.981636	chr12	9856952	9857167	0	NA	intron (NLT2c LINE	12800	NM_005127	9976	HS.85201	NM_005127	ENSG00000	CLEC2B	A1CL CLEC	C-type I protein-coding		
chr1-214f.3.171333	-2.40717	1.488649	-1.61701	0.105875	0.981636	chr1	2.15E+08	2.15E+08	0	NA	intron (Nintron (N	19442	NM_01634E	1063	HS.497741	NM_01634E	ENSG00000	CENPF	CENF CILI	centromer protein-coding		
chr15-89f.3.171333	-2.40717	1.488649	-1.61701	0.105875	0.981636	chr15	89594806	89597651	0	NA	intron (NLM5 LINE	20641	NM_00130E	90381	HS.44170E	NM_15225E	ENSG00000	TICRR	C15orf42 TOPBP1	r protein-coding		
chr1-856f.8.878577	-1.32328	0.818435	-1.61684	0.105912	0.981636	chr1	85653059	85653491	0	NA	3' UTR (N3' UTR (N	55158	NM_00117C	54680	HS.5111	NM_01795E	ENSG00000	ZNHIT6	BCD1 Clor	zinc finger protein-coding		
chr13-32f.5.981979	1.625018	1.005193	1.616623	0.10596	0.981636	chr13	32671213	32674133	0	NA	intron (NMLT1C LIT	135539	NM_023037	10129	HS.50766E	NM_023037	ENSG00000	FRY	13CDNA73 FRY	micro protein-coding		
chr19-13f.5.981979	1.625018	1.005193	1.616623	0.10596	0.981636	chr19	13969844	13970056	0	NA	intron (Nintron (N	-16558	NM_00114E	79883	HS.44849E	NM_02482E	ENSG00000	PODNL1	SLRR5B	podocan r protein-coding		
chr19-36f.5.981979	1.625018	1.005193	1.616623	0.10596	0.981636	chr19	36809977	36811092	0	NA	intron (Nintron (N	12971	NR_04002E	284408	HS.57001E	NR_04002E	ENSG00000	ZNF790-AS				ZNF790 ar ncRNA
chr9-987f.5.981979	1.625018	1.005193	1.616623	0.10596	0.981636	chr9	98772749	98773144	0	NA	intron (NLT2c LINE	23609	NM_173551	203286	HS.40689E	NM_173551	ENSG00000	ANKS6	ANKRD14	ankyrin r protein-coding		
chr19-12f.9.212757	1.285202	0.796187	1.614196	0.106485	0.981636	chr19	12763201	12763738	0	NA	intron (Nintron (N	11678	NM_01768E	54381	HS.43561E	NM_01768E	ENSG00000	BEST2	VMD2L1	bestrophin protein-coding		
chr3-132f.6.094834	-1.6212	1.004778	-1.61349	0.106639	0.981636	chr3	1.33E+08	1.33E+08	0	NA	TTS (NM_C TTS (NM_C	19023	NM_001321	79876	HS.170737	NM_02481E	ENSG00000	CUBA5	EIEE44 SC	ubiquitin r protein-coding		
chr11-28f.6.120258	-1.6105	0.998214	-1.61339	0.106661	0.981636	chr11	28062023	28061887	0	NA	intron (NME68 LIT	4260	NR_030341	693195	NR_030341	ENSG00000	MIR610	MIRN610	microRNA ncRNA			
chr10-14f.6.929021	-1.52491	0.945194	-1.61333	0.106673	0.981636	chr10	14533985	14534695	0	NA	intron (Nintron (N	-1626	NM_00132C	83641	HS.44631E	NM_03145E	ENSG00000	FAM107B	C10orf45	family w protein-coding		
chr12-50f.6.169256	-1.60515	0.994952	-1.6133	0.10668	0.981636	chr12	50461612	50461866	0	NA	TTS (NM_C TTS (NM_C	5168	NR_13275E	1.07E+08	NR_13275E	SNORD133					ZL142 ZL4	small nucsnoRNA
chr11-64f.5.376208	-1.72068	1.067166	-1.61238	0.10688	0.981636	chr11	64762505	64763414	0	NA	Intergeni Intergeni	-824	NM_001164	5837	HS.154084	NM_00560E	ENSG00000	PYGM				glycogen protein-coding
chr17-77f.5.376208	-1.72068	1.067166	-1.61238	0.10688	0.981636	chr17	77405653	77406105	0	NA	intron (Nintron (N	2024	NM_00129E	10801	HS.44093E	NM_00664E	ENSG00000	SEPTIN9	AF17q25 SEPTIN9	protein-coding		
chr2-365f.5.376208	-1.72068	1.067166	-1.61238	0.10688	0.981636	chr2	36553431	36553842	0	NA	intron (Nintron (N	44532	NM_00104E	9637	HS.25856E	NM_00510E	ENSG00000	FEZ2	HUM3CL	fascicul protein-coding		
chr3-187f.5.376208	-1.72068	1.067166	-1.61238	0.10688	0.981636	chr3	1.87E+08	1.87E+08	0	NA	intron (NLT2a LINE	-15091	NR_135551	1.02E+08	NR_135551	ENSG00000	LOC10192E				uncharact ncRNA	
chr8-254f.5.376208	-1.72068	1.067166	-1.61238	0.10688	0.981636	chr8	25483899	25485067	0	NA	intron (NLM5 LINE	25250	NM_15256E	157313	HS.33366	NM_15256E	ENSG00000	CDC42	PPP1R81 Fcell	divi protein-coding		
chr12-98f.6.161398	-1.60342	0.994881	-1.61167	0.107034	0.981636	chr12	9855176	9855633	0	NA	intron (Nintron (N	14455	NM_005127									



chr2-4756 5.393774	-1.7064	1.073191	-1.59002	0.11183	0.981636	chr2	45388192	45388391	+	0 NA	TTS (NM_C/TTS (NM_C	-133520 NR_033831	400952 Hs. 468368 NR_033831	ENSG000001LINC01121UNQ6975	long intencRNA
chr3-1604 5.393774	-1.7064	1.073191	-1.59002	0.11183	0.981636	chr3	1.6E+08	1.6E+08	+	0 NA	intron (Nintron (N	8184 NR_029525	406951 NR_029525	ENSG000001MIR16-2	MIRN16-2 microRNA ncRNA
chr7-1301 5.393774	-1.7064	1.073191	-1.59002	0.11183	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	TTS (NM_C/TTS (NM_C	22994 NR_149034	1E+08 Hs. 105944 NR_149034	ENSG000001CLOC100128-	uncharactncRNA
chr1-152 7.238148	1.436319	0.903668	1.589433	0.119663	0.981636	chr1	152219	1523222	+	0 NA	intron (NCPg-113	10490 NM_001177	55210 Hs. 23413 NM_018188	ENSG000001ATAD3	HAYOS ATPase fε protein-coding
chr9-1108 8.110954	-1.36024	0.855831	-1.58938	0.11974	0.981636	chr9	1.11E+08	1.11E+08	+	0 NA	intron (NAluY SINE	147624 NM_001351	1902 Hs. 126667 NM_001401	ENSG000001LPAR1	EDG2 GPR2 lysophosf protein-coding
chr15-307 3.204615	-2.38579	1.50179	-1.58863	0.112144	0.981636	chr15	30755863	30756600	+	0 NA	intron (Nintron (N	-61805 NR_072991	390561 Hs. 72129 NR_072991	HERC2P10	hect domε pseudo
chr13-95 8.911859	-1.31719	0.829229	-1.58845	0.112184	0.981636	chr13	95061382	95061581	+	0 NA	intron (Nintron (N	101440 NR_047487	1.01E+08 Hs. 48706 NR_047487	ENSG000001LINC00557-	long intencRNA
chr6-5875 116.4778	0.518456	0.326422	1.588299	0.112219	0.981636	chr6	58793454	58793676	+	0 NA	IntergeniALR/Alphe	-832119 NR_132994	1.07E+08 Hs. 561535 NR_125727	ENSG000001LINC00687-	long intencRNA
chr10-88 4.641867	-1.85335	1.167053	-1.58806	0.112273	0.981636	chr10	88928240	88929609	+	0 NA	IntergeniIntergeni	-3760 NR_125373	1E+08 NR_125373	ENSG000001ACTA2-AS1UC001kfo ACTA2	antncRNA
chr5-388 4.641867	-1.85335	1.167053	-1.58806	0.112273	0.981636	chr5	38838907	38839289	+	0 NA	intron (NLMER1 LIN	6731 NR_109951	1.02E+08 Hs. 546623 NR_109951	OSMR-AS1	CTD-2127 OSMR antncRNA
chr9-553 4.641867	-1.85335	1.167053	-1.58806	0.112273	0.981636	chr9	5535098	5535799	+	0 NA	intron (NLMER112 DN	24913 NM_025235	80380 Hs. 532275 NM_025235	ENSG000001PDCD1L G2	B7DC Btdc program protein-coding
chr2-233 3.889959	-2.07027	1.304317	-1.58724	0.112458	0.981636	chr2	2.34E+08	2.34E+08	+	0 NA	intron (Nintron (N	6894 NM_01841C	55355 Hs. 532968 NM_01841C	ENSG000001HJURP	FAKTS URI Holliday protein-coding
chr4-8405 5.196975	1.716393	1.081496	1.587054	0.1125	0.981636	chr4	8409273	8409472	+	0 NA	intron (Nintron (N	31351 NM_003501	8310 Hs. 479122 NM_003501	ENSG000001ACOX3	acyl-CoA protein-coding
chr5-45 6.41867	-1.85335	1.167053	-1.58806	0.112273	0.981636	chr5	47450769	47451138	+	0 NA	IntergeniALR/Alphe	-1754573 NM_021072	348980 Hs. 353172 NM_021072	ENSG000001HCN1	BCNG-1 BC hyperpolε protein-coding
chr13-75 4.683006	-1.84317	1.162939	-1.58493	0.112983	0.981636	chr13	75691825	75693003	+	0 NA	intron (NAluJr SIN	56084 NM_00130E	4008 Hs. 207631 NM_00535E	ENSG000001LM07	FBX20 FBX LIM domai protein-coding
chr6-972 4.683006	-1.84317	1.162939	-1.58493	0.112983	0.981636	chr6	97268070	97268765	+	0 NA	intron (NAluYf1 SI	14799 NM_00135C	253714 Hs. 444292 NM_19846E	ENSG000001MMS22L	G6orf167 MMS22 lik protein-coding
chr8-12 4.683006	-1.84317	1.162939	-1.58493	0.112983	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (Nintron (N	-8094 NR_03038E	693130 NR_03038E	ENSG000001MIR548D1	MIRN548D1 microRNA ncRNA
chr19-36 8.486458	1.312155	0.82792	1.584881	0.112993	0.981636	chr19	36995858	36998082	+	0 NA	exon (NM exon (NM	80638 NM_001204	734900 Hs. 404222 NM_19853E	ENSG000001ZNF568	ZFP568 zinc fing protein-coding
chr12-117 5.931132	1.613317	1.018076	1.584672	0.113041	0.981636	chr12	1.17E+08	1.17E+08	+	0 NA	intron (NAluSz SIN	33297 NM_015002	23014 Hs. 74037E NM_015002	ENSG000001FBX021	FBX21 F-box prc protein-coding
chr2-157 5.204833	1.712409	1.081169	1.583849	0.113228	0.981636	chr2	1.57E+08	1.57E+08	+	0 NA	intron (Nintron (N	3598 NM_00132E	11227 Hs. 269027 NM_01456E	ENSG000001GALNT5	GALNAC-Tε polypepti protein-coding
chr1-171 10.42594	1.195103	0.755044	1.582826	0.113461	0.981636	chr1	1.72E+08	1.72E+08	+	0 NA	3' UTR (N3' UTR (N	37871 NR_003704	8674 Hs. 6651 NM_00376E	ENSG000001VAMP4	VAMP-4 Vvesicle ε protein-coding
chr21-63 10.06051	-1.2207	0.771365	-1.58251	0.113533	0.981636	chr21	6331889	6333916	+	0 NA	IntergeniAluSc SIN	-65566 NM_001322	1.03E+08 Hs. 743984 NM_001322044	LOC102724-	uncharact protein-coding
chr19-397 7.357196	-1.42117	0.898125	-1.58237	0.113565	0.981636	chr19	3973073	3973708	+	0 NA	IntergeniAluSx1 SI	-2291 NM_00134E	1613 Hs. 631844 NM_00134E	ENSG000001DAPK3	DLK ZIP Zdeath ass protein-coding
chr11-94 10.51007	1.20382	0.76114	1.581601	0.113741	0.981636	chr11	94235881	94237578	+	0 NA	IntergeniL1P2 LIN	-68908 NM_00119E	390243 Hs. 55375E NM_00108C	ENSG000001IZUMO1R	FOLR4 FolIZUMO1 re protein-coding
chr19-47 5.989837	1.621239	1.02514	1.581481	0.113768	0.981636	chr19	47488426	47488834	+	0 NA	intron (Nintron (N	4348 NR_03845E	1.01E+08 Hs. 65732E NR_03845E	ENSG000001NAPA-AS1	NAPA antncRNA
chr12-504 7.374762	-1.41125	0.892731	-1.58082	0.113919	0.981636	chr12	50416496	50416844	+	0 NA	intron (NAluJb SIN	15260 NM_00135E	113251 Hs. 26613 NM_05287E	ENSG000001CLARP4	PP1296 La ribon protein-coding
chr11-8507 4.478534	1.849233	1.169944	1.580616	0.113966	0.981636	chr11	85074850	85075112	+	0 NA	intron (NLa2 LINE	12657 NM_14517E	126820 Hs. 97933 NM_14517E	ENSG000001WDR63	DIC3 NYD-WD repeat protein-coding
chr17-57 4.478534	1.849233	1.169944	1.580616	0.113966	0.981636	chr17	57310649	57311380	+	0 NA	intron (NMLRb SINE	53995 NM_170721	124540 Hs. 658922 NM_13896E	ENSG000001MSI2	MSI2H musashi f protein-coding
chr17-27 6.716136	1.545183	0.977624	1.580549	0.113981	0.981636	chr17	27594905	27595126	+	0 NA	intron (Nintron (N	-36173 NM_00230E	3965 Hs. 81337 NM_00230E	ENSG000001GLALS9	HUAT Lgal galactin protein-coding
chr2-885 9.253897	1.284799	0.812889	1.580534	0.113985	0.981636	chr2	88585240	88586032	+	0 NA	intron (NLa2-3_Crp	32993 NM_00131E	9451 Hs. 59158E NM_00483E	ENSG000001EIF2AK3	PEK PERK eukaryoti protein-coding
chr3-142 7.212724	1.431451	0.905859	1.580213	0.114058	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (Nintron (N	18014 NM_00128E	54464 Hs. 43510E NM_019001	ENSG000001CXRN1	1-Sep 5'-3' exc protein-coding
chr8-143 7.212724	1.431451	0.905859	1.580213	0.114058	0.981636	chr8	1.43E+08	1.43E+08	+	0 NA	intron (NMSTA-int	-18487 NM_20158E	389692 NM_20158E	ENSG000001MAFA	INSDM RTF maf Z1P protein-coding
chr8-94 7.38262	-1.41273	0.894032	-1.58017	0.114067	0.981636	chr8	94769786	94770110	+	0 NA	intron (NAluSz SIN	50048 NM_181787	286148 Hs. 56782E NM_181787	ENSG000001DPY19L4	PAP-1 PGI pyrogluta protein-coding
chr19-197 5.263538	1.721195	1.089482	1.579829	0.114146	0.981636	chr19	19703805	19704852	+	0 NA	IntergeniAluSz SIN	28784 NM_02103C	7561 Hs. 65993E NM_02103C	ENSG000001ZNF14	GIOT-4 KC zinc fing protein-coding
chr8-123 8.107254	-1.38428	0.876394	-1.57952	0.114217	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (NAluS6 SI	-12992 NR_03038E	693130 NR_03038E	ENSG000001MIR548D1	MIRN548D1 microRNA ncRNA
chr19-18 4.4961	1.861309	1.178634	1.579209	0.114288	0.981636	chr19	18353281	18353709	+	0 NA	intron (NAluJb SIN	12897 NM_00132E	54858 Hs. 13177E NM_01771E	ENSG000001PGPEP1	PAP-1 PGI pyrogluta protein-coding
chr20-28 10.9988	1.152018	0.729793	1.578555	0.114438	0.981636	chr20	28525634	28526317	+	0 NA	IntergeniALR/Alphe	76690 NR_13231E	1E+08 Hs. 529357 NR_13231E	ENSG000001FRG1CP	FSHD regipseudo
chr11-439 7.365054	-1.42272	0.901826	-1.57776	0.114656	0.981636	chr11	43929915	43930341	+	0 NA	intron (Nintron (N	-3192 NM_05709E	9048 Hs. 632404 NM_00397E	ENSG000001ARTN	ART ENOV artemin protein-coding
chr10-141 65.69286	0.596608	0.377846	1.57754	0.11467	0.981636	chr10	1124957	1125502	+	0 NA	IntergeniALR/Alphe	1242816 NR_02438C	441666 Hs. 25572E NR_02438C	ENSG000001LOC44166E-	zinc fing pseudo
chr11-12 7.366904	-1.40976	0.893781	-1.5773	0.114727	0.981636	chr11	1.22E+08	1.22E+08	+	0 NA	intron (Nintron (N	-9693 NR_13718E	399959 Hs. 44098 NR_02443C	ENSG000001MIR100HG	AGD1 lincmir-100-lncRNA
chr16-28 7.366904	-1.40976	0.893781	-1.5773	0.114727	0.981636	chr16	28721979	28722178	+	0 NA	intron (Nintron (N	-2174 NR_10705E	1.02E+08 Hs. 51403E NM_00447E	ENSG000001MIR6862-2	hsa-mir-ε microRNA ncRNA
chr14-61 6.137824	-1.59764	1.012922	-1.57726	0.114736	0.981636	chr14	61749638	61750155	+	0 NA	promoter-promoter-	-807 NR_04540E	1.01E+08 Hs. 59721E NR_04540E	HIF1A-AS2-3	aHIF-1 HIF1A antncRNA
chr3-123 6.137824	-1.59764	1.012922	-1.57726	0.114736	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	10250 NM_00136E	64770 Hs. 64502E NM_02275E	ENSG000001CCDC14	- coiled-cp protein-coding
chr6-57 6.137824	-1.59764	1.012922	-1.57726	0.114736	0.981636	chr6	57187074	57181208	+	0 NA	intron (NLMIE5 LIN	8665 NM_00428E	9532 Hs. 74504E NM_00428E	ENSG000001BAG2	BAG-2 d4BCL2 assc protein-coding
chr2-297 8.494316	1.309894	0.831059	1.576175	0.114986	0.981636	chr2	29792564	29793287	+	0 NA	intron (NAluJb SIN	25606 NM_01338E	29796 Hs. 28429E NM_01338E	ENSG000001UCRQ10	HSPC0501 Fubiquinol protein-coding
chr6-896 7.390478	-1.41241	0.89771	-1.57535	0.115175	0.981636	chr6	89684808	89685007	+	0 NA	exon (NM exon (NM	-46160 NM_02046E	57226 Hs. 17727E NM_02046E	ENSG000001LYRM2	DJ12208.εLYR motif protein-coding
chr1-123 123.0855	0.478808	0.304177	1.574112	0.115462	0.981636	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alphe	1991822 NR_00395E	647121 Hs. 69768E NR_00395E	ENSG000001EMBP1	- embigin f pseudo
chr1-157 3.752235	2.052116	1.304131	1.57355	0.115592	0.981636	chr1	1.57E+08	1.57E+08	+	0 NA	intron (NLMIB7 LIN	22387 NM_014784	9826 Hs. 516954 NM_014784	ENSG000001CARHGF11	GTRAP48 FRho guaniprotein-coding
chr17-28 5.89785	1.610917	1.02397	1.573207	0.115671	0.981636	chr17	28884584	28884809	+	0 NA	intron (Nintron (N	13037 NM_00447E	2319 Hs. 51403E NM_00447E	ENSG000001FLOT2	ECS-1 ECS Flotillir protein-coding
chr10-14 12.17869	1.088909	0.692383	1.572698	0.115789	0.981636	chr10	41380177	41380376	+	0 NA	IntergeniALR/Alphe	987769 NR_02438C	441666 Hs. 25572E NR_02438C	ENSG000001LOC44166E-	zinc fing pseudo
chr19-41 4.511815	1.851799	1.177498	1.572655	0.115799	0.981636	chr19	1460788	1461577	+	0 NA	intron (Nintron (N	8194 NM_00135E	1029		

chr10-40f.24.53054	0.833078	0.540727	1.540662	0.123399	0.981636	chr10	40595496	40596559	+	0	NA	IntergeniALR/Alph	1772018	NR_02438C	441666	Hs.25572ENR_02438C	ENSG000004C0441666	-	zinc fingpseudo					
chr17-73f.6.581715	-1.47754	0.959124	-1.54051	0.123436	0.981636	chr17	73238148	73238362	+	0	NA	intron (intron)	5594	NR_11010F	55028	Hs.12929	NM_017941	ENSG00000C170rF80	HLC-8 MITC	chromosomprotein-coding				
chr16-25f.7.709312	1.335282	0.867362	1.539476	0.123688	0.981636	chr16	2566414	2566670	+	0	NA	intron (intron)	28521	NM_001261	5170	Hs.459691	NM_00261E	ENSG00000C	PDPK1	PDPK3-phospho	protein-coding			
chrX-103f.9.27532	-1.25164	0.813493	-1.5386	0.123902	0.981636	chrX	1.04E+08	1.04E+08	+	0	NA	exon (NM exon)	10491	NM_01228E	9643	Hs.326387	NM_01228E	ENSG00000C	MORFL2	MORFL2 MF	mortalityprotein-coding			
chr1-145f.10.46708	1.19458	0.776407	1.538601	0.123902	0.981636	chr1	1.45E+08	1.45E+08	+	0	NA	intron (intron)	4389	NM_00127E	1E+08	Hs.44508C	NM_00127E	ENSG00000C	NBP20	NBP2	mentprotein-coding			
chr1-147f.6.632562	-1.45837	0.948434	-1.53766	0.124132	0.981636	chr1	1.47E+08	1.47E+08	+	0	NA	intron (AluJr SIN	47742	NM_00134E	9557	Hs.191164	NM_00428A	ENSG00000C	CHD1L	ALC1 CHD1	chromodon	protein-coding		
chr2-47f.6.632562	-1.45837	0.948434	-1.53766	0.124132	0.981636	chr2	1.4715781	47416989	+	0	NA	exon (NM exon)	13318	NM_00125E	4436	Hs.59765E	NM_000251	ENSG00000C	MSH2	COCA1 FCC	mutS	homc	protein-coding	
chr9-110f.6.632562	-1.45837	0.948434	-1.53766	0.124132	0.981636	chr9	111E+08	1.11E+08	+	0	NA	intron (AluSz SIN	121467	NM_001351	1902	Hs.126667	NM_001401	ENSG00000C	LPAR1	EDG2 GPR2	Lysophosf	protein-coding		
chr1-148f.7.71717	1.332801	0.867411	1.536528	0.124409	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (AluSx SIN	5598	NR_03718E	653513	Hs.632434	NR_03718E	LOC65351E	-	phosphodipe	pseudo			
chr1-236f.7.71717	1.332801	0.867411	1.536528	0.124409	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (intron)	16500	NR_01807E	55127	Hs.708114	NM_01807E	ENSG00000C	HEATR1	BAP28 UTF	HEAT	repe	protein-coding	
chr3-197f.7.71717	1.332801	0.867411	1.536528	0.124409	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (intron)	22076	NM_03322E	89782	Hs.51854C	NM_03302E	ENSG00000C	LMLN	GP63 INV	leishman	protein-coding		
chr10-11f.6.435578	1.47473	0.959975	1.536218	0.124485	0.981636	chr10	1131133	1131676	+	0	NA	3' UTR (3' UTR)	-28364	NR_01537E	399706	Hs.721191	NM_00101C	ENSG00000C	LINC0020C	C10orf13E	long	intencRNA		
chr6-301f.6.435578	1.47473	0.959975	1.536218	0.124485	0.981636	chr6	30185523	30185722	+	0	NA	3' UTR (3' UTR)	22076	NM_03322E	89870	Hs.59178E	NM_03322E	ENSG00000C	TRIM15	RNF93 ZNF	tripartit	protein-coding		
chr11-88f.4.600727	-1.86428	1.213578	-1.53619	0.124492	0.981636	chr11	88288155	88288354	+	0	NA	IntergeniLIMA4 LI	49482	NM_14817I	1075	Hs.12806E	NM_001814	ENSG00000C	CTSC	CPPI DPP-	cathepsin	protein-coding		
chr10-49f.5.760126	1.554611	1.012033	1.536127	0.124507	0.981636	chr10	49475788	49476646	+	0	NA	exon (NM exon)	48064	NM_17075E	267004	Hs.49063	NM_17075E	ENSG00000C	PGBD3	-	piggyBac	protein-coding		
chr20-27f.18.10871	0.893563	0.581838	1.535759	0.124597	0.981636	chr20	27966984	27967183	+	0	NA	IntergeniALR/Alph	635582	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG00000C	FRG1CP	-	FSHD	regipseudo		
chr20-27f.32.22904	0.753299	0.490697	1.535161	0.124744	0.981636	chr20	17811246	27811523	+	0	NA	IntergeniALR/Alph	791281	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG00000C	FRG1CP	-	FSHD	regipseudo		
chr4-105f.6.59928	-1.46622	0.95559	-1.53436	0.12494	0.981636	chr4	2.06E+08	1.06E+08	+	0	NA	intron (NLIP4S LIN	20736	NM_001031	79807	Hs.16142E	NM_024751	ENSG00000C	GSTCD	-	glutathio	protein-coding		
chr8-307f.6.59928	-1.46622	0.95559	-1.53436	0.12494	0.981636	chr8	30798567	30799040	+	0	NA	intron (intron)	14015	NM_00100E	5516	Hs.49144C	NM_00415E	ENSG00000C	PPP2CB	PP2beta	protein	protein-coding		
chr5-151f.6.589976	-1.27037	0.828403	-1.53351	0.125149	0.981636	chr5	1.52E+08	1.52E+08	+	0	NA	intron (MIR3 SINE	2590	NM_00130E	6678	Hs.11177E	NM_00311E	ENSG00000C	SPARC	BM-40 O1	secreted	protein-coding		
chr15-80f.5.904228	-1.53866	0.103368	-1.5335	0.125153	0.981636	chr15	80817583	80819594	+	0	NA	intron (intron)	23485	NR_03039E	693132	NR_03039E	ENSG00000C	MIR549A	MIR549 MI	microRNA	ncRNA			
chr1-156f.5.734702	1.548667	1.011905	1.530447	0.125906	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (intron)	-35133	NR_030527	768220	NR_030527	ENSG00000C	MIR765	MIRN765	mi	microRNA	ncRNA		
chr1-232f.5.734702	1.548667	1.011905	1.530447	0.125906	0.981636	chr1	2.33E+08	2.33E+08	+	0	NA	intron (intron)	26181	NR_138027	84284	Hs.64271E	NM_03232A	ENSG00000C	NTPCR	C1orf57	leucosic	protein-coding		
chr11-66f.5.734702	1.548667	1.011905	1.530447	0.125906	0.981636	chr11	66241403	66242245	+	0	NA	intron (intron)	-15470	NM_001134	64837	Hs.28079E	NM_02282E	ENSG00000C	KLC2	-	kinesin	I	protein-coding	
chr18-54f.5.734702	1.548667	1.011905	1.530447	0.125906	0.981636	chr18	54909856	54910155	+	0	NA	intron (MERS2D LI	48043	NM_00114E	80323	Hs.12079C	NM_02521A	ENSG00000C	CCDC68	SE57-1	coiled-cc	protein-coding		
chr2-259f.5.734702	1.548667	1.011905	1.530447	0.125906	0.981636	chr2	25946555	25947153	+	0	NA	intron (AluSz SIN	35643	NM_00225A	3797	Hs.21611	NM_00225A	ENSG00000C	KIF3C	-	kinesin	I	protein-coding	
chr12-66f.5.888512	-1.53504	1.00325	-1.53006	0.126001	0.981636	chr12	66165962	66166161	+	0	NA	intron (NLIM3 LINE	4011	NM_00128E	51643	Hs.505934	NM_01605E	ENSG00000C	TMBIM4	CG1-119	transmem	protein-coding		
chr14-55f.5.888512	-1.53504	1.00325	-1.53006	0.126001	0.981636	chr14	55313567	55313817	+	0	NA	intron (THEID LTF	41538	NM_152231	55030	Hs.52534E	NM_01794E	ENSG00000C	FBX034	CG1-301	FF-box	prc	protein-coding	
chr19-39f.5.888512	-1.53504	1.00325	-1.53006	0.126001	0.981636	chr19	39366551	39366895	+	0	NA	intron (intron)	24314	NM_00130E	55095	Hs.61233E	NM_01802E	ENSG00000C	SAMD4B	SMGB Sma	sterile	protein-coding		
chr1-124f.13.96288	1.005914	0.657693	1.529457	0.126151	0.981636	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alph	3084509	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000C	EMBP1	-	embin	pseudo		
chr1-150f.11.49353	1.095612	0.716753	1.528577	0.126369	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	exon (NM exon)	-15673	NM_001271	80222	Hs.288974	NM_02515C	ENSG00000C	TARS2	COXP21	threonyl-	protein-coding		
chr1-122f.7.801299	1.344144	0.879572	1.528179	0.126468	0.981636	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alph	968809	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000C	EMBP1	-	embin	pseudo		
chr5-488f.68.72361	0.535947	0.350835	1.527633	0.126604	0.981636	chr5	48860545	48860791	+	0	NA	IntergeniALR/Alph	1580620	NM_19844E	133418	Hs.561411	NM_19844E	ENSG00000C	EMB	GP70	embin	protein-coding		
chr11-10f.9.834772	-1.18249	0.774118	-1.52753	0.126629	0.981636	chr11	10589641	10590078	+	0	NA	intron (intron)	-21194	NM_006691	10894	Hs.65533E	NM_006691	ENSG00000C	LYVE1	CRSBP-1	lymphatic	protein-coding		
chr2-112f.7.750452	1.334872	0.873934	1.527428	0.126655	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	intron (intron)	54874	NM_005054	84220	Hs.46963C	NM_005054	ENSG00000C	RGPD5	BS-63	B5E	RANBP2	1	protein-coding
chr20-33f.8.623258	-1.26459	0.82793	-1.52741	0.12666	0.981636	chr20	33767468	33767719	+	0	NA	intron (Tigger1 I	24926	NM_01640E	51654	Hs.45837E	NM_01608E	ENSG00000C	CDK5RAP1	C20orf34	CDK5	regu	protein-coding	
chr1-462f.2.179822	-2.9561	1.936578	-1.52646	0.126896	0.981636	chr1	46265471	46266303	+	0	NA	intron (MIRb SINE	18124	NM_00357E	8438	Hs.64204E	NM_00357E	ENSG00000C	RAD54L	HR54	RAD54	lik	protein-coding	
chr1-124f.125.4758	0.448112	0.293705	1.525722	0.127079	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alph	2790635	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000C	EMBP1	-	embin	pseudo		
chr5-479f.22.11682	0.807174	0.52906	1.525676	0.127091	0.981636	chr5	47912961	47914327	+	0	NA	IntergeniALR/Alph	-221764	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG00000C	HCN1	BCNG-1	BC	hyperpol	protein-coding	
chr11-34f.7.368754	-1.39629	0.915874	-1.52454	0.127374	0.981636	chr11	34057825	34058024	+	0	NA	intron (AluSq2 SI	6193	NM_00589E	4076	Hs.47181E	NM_00589E	ENSG00000C	CAPRIN1	GPIAP1	GF	cell	cycl	protein-coding
chr12-93f.10.56496	-1.15076	0.754916	-1.52436	0.127419	0.981636	chr12	93490996	93491195	+	0	NA	intron (AluSz SIN	23581	NR_03816E	28977	Hs.19957E	NM_01405E	ENSG00000C	RPL27	HSPC204	mitochon	protein-coding		
chr2-231f.5.726844	1.55215	1.018272	1.524298	0.127434	0.981636	chr2	2.32E+08	2.32E+08	+	0	NA	intron (LIME3D LI	13009	NM_00128E	64708	Hs.335061	NM_02273C	ENSG00000C	COP57B	CG1-301	SMG	COP9	sig	protein-coding
chr3-184f.5.767984	1.551154	1.01804	1.523667	0.127592	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (intron)	3470	NM_001171	1181	Hs.436847	NM_00436E	ENSG00000C	CLCN2	C1C-2	CL	chloride	protein-coding	
chr17-57f.9.80334	-1.17781	0.773406	-1.52289	0.127787	0.981636	chr17	57997584	57998158	+	0	NA	IntergeniIntergeni	9375	NM_00107E	6426	Hs.68714								



chrX-41f 7.863492	-1.2979	0.867112	-1.49681	0.134442	0.981636	chrX	41350482	41350707	+	0	NA	TTS (NM_C	16428	NM_001363	1654	Hs.72856	NM_00135	ENS	G0000	DDX3X	CAP-Rf	DEAD-box	protein-coding			
chr22-41f 6.418012	1.465715	0.979571	1.496282	0.13458	0.981636	chr22	41882548	41882860	+	0	NA	intron (AluSj SIN	-18240	NR_029507	4077039	NR_029507	ENS	G0000	MIR33A	MIR33	MI	microRNA	ncRNA			
chr9-114f 6.418012	1.465715	0.979571	1.496282	0.13458	0.981636	chr9	1.15E+08	1.15E+08	+	0	NA	exon (NM_exon	14557	NM_001354	1.05E+08	Hs.14736	NM_001354	ENS	G0000	TEX53		testis	expression			
chr19-17f 3.666071	-1.9613	1.310797	-1.49627	0.134584	0.981636	chr19	17066684	17067411	+	0	NA	intron (AluSj SIN	8405	NM_033417	93323	Hs.40408	NM_033417	ENS	G0000	HAUS8	DGT4	HICE	HAUS	augm	protein-coding	
chr1-426f 4.410121	-1.75702	1.174586	-1.49586	0.134689	0.981636	chr1	42675312	42675684	+	0	NA	intron (AluSj SIN	-6920	NM_004555	4904	Hs.47358	NM_004555	ENS	G0000	YBX1	BP-8	CBCF-	Y-box	bir	protein-coding	
chr1-214f 4.410121	-1.75702	1.174586	-1.49586	0.134689	0.981636	chr1	2.15E+08	2.15E+08	+	0	NA	intron (AluSj SIN	16441	NM_016343	1063	Hs.49774	NM_016343	ENS	G0000	CENPF	CENF	CILL	centromer	protein-coding		
chr12-64f 4.410121	-1.75702	1.174586	-1.49586	0.134689	0.981636	chr12	64615259	64616199	+	0	NA	intron (AluSj SIN	5234	NM_178166	283349	Hs.64360	NM_178166	ENS	G0000	RASSF3	RASSF5	FAN	assoc	protein-coding		
chr17-61f 4.410121	-1.75702	1.174586	-1.49586	0.134689	0.981636	chr17	61768931	61770098	+	0	NA	intron (AluSj SIN	94045	NM_032042	83990	Hs.12890	NM_032042	ENS	G0000	BRIP1	BACH1	FAN	BRCA1	in	protein-coding	
chr1-235f 6.957589	1.368769	0.915155	1.495669	0.13474	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	intron (AluSp SIN	-57750	NR_039908	1.01E+08	NR_039908	ENS	G0000	MIR4753	mir-4753			microRNA	ncRNA		
chr10-40f 3.13119	0.701881	0.469553	1.494787	0.13497	0.981636	chr10	40598964	40599627	+	0	NA	Intergeni	1768750	NR_02438C	441666	Hs.25572	NR_02438C	ENS	G0000	LOC441666			zinc	finger	pseudo	
chr19-52f 7.67418	1.320775	0.88367	1.494647	0.135007	0.981636	chr19	5207543	5207849	+	0	NA	intron (AluSj SIN	133116	NM_130854	5802	Hs.74492	NM_02285C	ENS	G0000	PTPRS	PTPSIGMA		protein	protein-coding		
chr1-382f 4.990838	1.62872	1.090568	1.49346	0.135317	0.981636	chr1	3828979	3829334	+	0	NA	intron (AluSj SIN	28055	NM_014704	9731	Hs.13308	NM_014704	ENS	G0000	CPEP104	CFAP256		centrosom	protein-coding		
chr16-15f 4.990838	1.62872	1.090568	1.49346	0.135317	0.981636	chr16	1557202	1558082	+	0	NA	intron (AluSj SIN	-22885	NR_13517E	1.05E+08	Hs.66332	NR_13517E	ENS	G0000	LOC105371			uncharact	ncRNA		
chr8-949f 4.990838	1.62872	1.090568	1.49346	0.135317	0.981636	chr8	94942211	94944383	+	0	NA	intron (AluJo SIN	6081	NM_001135	94241	Hs.49226	NM_001135	ENS	G0000	TP53INP1	SIP	TP53I	umcor	protein-coding		
chrX-129f 4.990838	1.62872	1.090568	1.49346	0.135317	0.981636	chrX	1.3E+08	1.3E+08	+	0	NA	intron (AluSj SIN	18826	NM_001587	4952	Hs.12635	NM_00027E	ENS	G0000	OCRL	INPP5F		LC	OCRL	inos	protein-coding
chr7-116f 4.433695	-1.76407	1.181385	-1.49322	0.13538	0.981636	chr7	1.17E+08	1.17E+08	+	0	NA	TTS (NM_C	9229	NM_00120E	858	Hs.21233	NR_00123E	ENS	G0000	CAV2	CAV		caveolin	protein-coding		
chr18-48f 2.221616	1.248557	0.836356	1.492854	0.135475	0.981636	chr18	48718711	48719456	+	0	NA	intron (ML3 LINE C	48483	NR_039897	1.01E+08	NR_039897	ENS	G0000	MIR4743			microRNA	ncRNA			
chr11-201f 5.154171	-1.61957	1.085066	-1.4926	0.135541	0.981636	chr11	20100414	20101419	+	0	NA	intron (AluSj SIN	-51613	NR_046672	1.01E+08	Hs.55791	NR_046672	ENS	G0000	NAV2-AS2			NAV2	antinc	RNA	
chr7-143f 5.154171	-1.61957	1.085066	-1.4926	0.135541	0.981636	chr7	1.43E+08	1.43E+08	+	0	NA	intron (AluSj SIN	2364	NR_106952	1.02E+08	NR_106952	ENS	G0000	MIR6892	hsa-mir-6892			microRNA	ncRNA		
chr13-11f 7.394178	-1.38688	0.929309	-1.49238	0.135599	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (AluY SINE	71708	NM_00184E	1282	Hs.17441	NM_00184E	ENS	G0000	COL4A1	BSVD		BSVI	collagen	protein-coding	
chr4-802f 7.394178	-1.38688	0.929309	-1.49238	0.135599	0.981636	chr4	80275627	80275866	+	0	NA	intron (AluSj SIN	7301	NM_001291	2250	Hs.37055	NM_004464	ENS	G0000	PGF5	HBGF-5		Sn	fibroblas	protein-coding	
chr1-172f 4.384697	-1.77203	1.18741	-1.49235	0.135607	0.981636	chr1	1.72E+08	1.72E+08	+	0	NA	non-codir	-2643	NR_029627	406996	NR_029627	ENS	G0000	MIR214	MIRN214			microRNA	ncRNA		
chr8-132f 7.109735	-1.35343	0.907083	-1.49207	0.135681	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (AluSj SIN	15599	NM_01601E	51105	Hs.30436	NR_01601E	ENS	G0000	PHF20L1	CGI-72		TL	PHD	finger	protein-coding
chr17-59f 7.732886	1.327472	0.890474	1.490748	0.136028	0.981636	chr17	59292023	59292024	+	0	NA	intron (AluSx1 SI	27014	NR_16146E	6198	Hs.46364	NR_003161	ENS	G0000	RPS6KB1	PS6K		SR6	ribosomal	protein-coding	
chr3-101f 7.732886	1.327472	0.890474	1.490748	0.136028	0.981636	chr3	1.02E+08	1.02E+08	+	0	NA	exon (NM_exon	-6368	NM_00100E	64332	Hs.31971	NM_03141E	ENS	G0000	NFKB1Z	IKBZ		INAF	NFKB	inh	protein-coding
chr16-46f 3.658213	-1.95859	1.313926	-1.49064	0.136057	0.981636	chr16	46589953	46591522	+	0	NA	intron (MLIPA5 LIN	-21640	NR_02655E	124149	Hs.97414	NM_001004299	ANKRD26P1			ankryn	r	pseudo			
chr3-448f 3.658213	-1.95859	1.313926	-1.49064	0.136057	0.981636	chr3	44853426	44854978	+	0	NA	TTS (NM_C	7686	NR_03029C	693149	NR_03029C	ENS	G0000	MIR564	MIRN564			microRNA	ncRNA		
chr9-107f 3.658213	-1.95859	1.313926	-1.49064	0.136057	0.981636	chr9	1.07E+08	1.07E+08	+	0	NA	Intergeni	51624	NM_001244	5887	Hs.52164	NR_002874	ENS	G0000	RAD23B	HHR23B		HHR	RAD23	hon	protein-coding
chr10-13f 7.101877	-1.35188	0.906964	-1.49055	0.13608	0.981636	chr10	1.3E+08	1.3E+08	+	0	NA	intron (AluJb SIN	35496	NM_001321	10539	Hs.42644	NM_006541	ENS	G0000	GLRX3	GLRX4		GRX	glutared	protein-coding	
chr6-130f 7.101877	-1.35188	0.906964	-1.49055	0.13608	0.981636	chr6	1.31E+08	1.31E+08	+	0	NA	intron (AluSx SIN	30302	NM_00119E	1.01E+08	Hs.38871	NM_00119E	ENS	G0000	SMLR1			small	le	protein-coding	
chr2-201f 5.775842	1.547492	1.038552	1.490048	0.136212	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	intron (AluSj SIN	13422	NR_11062C	130540	Hs.10794	NR_13916E	ENS	G0000	FLACC1	ALS2CR12			flagellum	protein-coding	
chr14-73f 7.804787	-1.31226	0.880871	-1.48973	0.136294	0.981636	chr14	73316447	73316652	+	0	NA	intron (AluSj SIN	-70548	NR_13524E	1.02E+08	Hs.66059	NR_13524E	LOC10192E					uncharact	ncRNA		
chr9-922f 6.973305	1.363225	0.915148	1.489623	0.136323	0.981636	chr9	92290796	92290393	+	0	NA	intron (MLMB7 LIN	2313	NR_037424	1.01E+08	NR_037424	ENS	G0000	MIR3651	mir-3651			microRNA	ncRNA		
chr1-235f 6.973305	1.363225	0.915148	1.489623	0.136323	0.981636	chr1	2.36E+08	2.36E+08	+	0	NA	intron (AluSj SIN	-66741	NR_00109E	2786	Hs.15971	NM_00448E	ENS	G0000	CNG4			G	protein	protein-coding	
chr19-124f 6.973305	1.363225	0.915148	1.489623	0.136323	0.981636	chr19	12458423	12458962	+	0	NA	Intergeni	-17671	NM_00581E	10224	Hs.63689	NR_00581E	ENS	G0000	ZNF443	ZK1			zinc	finger	protein-coding
chr8-919f 6.973305	1.363225	0.915148	1.489623	0.136323	0.981636	chr8	91970184	91970618	+	0	NA	intron (AluSj SIN	47279	NM_17563E	862	Hs.36843	NR_00434E	ENS	G0000	RUNX1T1	AML1-MTG8		RUNX1	par	protein-coding	
chr9-116f 6.973305	1.363225	0.915148	1.489623	0.136323	0.981636	chr9	1.16E+08	1.16E+08	+	0	NA	intron (ML2b LINE	45893	NR_103711	493913	Hs.72883	NR_103711	ENS	G0000	PAPPA-AS1	DIPAS		NCF	PAPPA	ant	ncRNA
chr9-115f 7.135158	-1.34488	0.902893	-1.48952	0.136351	0.981636	chr9	1.15E+08	1.15E+08	+	0	NA	intron (AluSj SIN	4210	NM_00216E	3371	Hs.14325	NM_00216E	ENS	G0000	TNC	150-225			Tenascin	protein-coding	
chr11-55f 10.68111	1.094253	0.735138	1.488868	0.136522	0.981636	chr11	53416348	53416621	+	0	NA	Intergeni	1187514	NM_001004	119749	Hs.55356	NM_001004	ENS	G0000	COR4C4			o	factory	protein-coding	
chr1-185f 8.254898	1.250639	0.840011	1.488837	0.13653	0.981636	chr1	1.85E+08	1.85E+08	+	0	NA	intron (MLIMA6 LIN	65886	NM_01767E	54823	Hs.13418	NR_01767E	ENS	G0000	SWT1	Clorf26			SWT1	RNA	protein-coding
chr1-155f 9.452361	1.607116	0.780036	1.488028	0.136744	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	exon (NM_exon	-32019	NR_132767	1.07E+08	NR_132767	SCARNA26E					small	Ca	ncRNA		
chr2-21f 7.1273	1.34333	0.902773	-1.48801	0.13675	0.981636	chr22	19601272	21961538	+	0	NA	intron (AluSj SIN	-8557	NM_014634	9647	Hs.11272	NR_014634	ENS	G0000	PPM1F	CAMKP		Ca	protein	protein-coding	
chr17-63f 6.940024	1.360938	0.914741	1.487786	0.136807	0.981636	chr17	63738492	63738766	+	0	NA	intron (AluSx3 SI	3170	NM_00100E	92335	Hs.51440	NR_15333E	ENS	G0000	STRADA	LYK5		NY	-ESTE20	rel	protein-coding
chr3-567f 6.940024	1.360938	0.914741	1.487786	0.136807	0.981636	chr3	56736988	56737247	+	0	NA	intron (AluSj SIN	38600	NM_00112E	50650	Hs.47640	NR_01955E	ENS	G0000	ARHGFE3	GEF3		STA3	Rho	guanin	protein-coding
chr6-432f 6.940024	1.360938	0.914741	1.487786	0.136807	0.981636	chr6	43216546	43217457	+	0	NA	intron (AluSj SIN	12480	NM_199184	10591	Hs.10975	NR_00644E	ENS	G0000	CNDP1H	C6orf108			2'	-deoxy	protein-coding
chr10-145f 5.821949	-1.55403	1.044645	-1.48762	0.136852	0.981636	chr10	14576375	14576695	+	0	NA	intron (AluSg SIN	-4160	NM_00128E	83641	Hs.44631	NR_003145E	ENS	G0000	FAM107B	C10orf45			family	wi	protein-coding
chr3-314f 5.821949	-1.55403	1.044645	-1.48762	0.136852	0.981636	chr3	3146781	3146980	+																	

chr2-594 8. 237332	1.243863	0.849378	1.464439	0.143074	0.981636	chr2	1.9E+08	1.9E+08	0	NA	intron (Nintron (N	16321 NM_01458E	30061 Hs. 643000ENM_01458E	ENSG00000SLC40A1	FPN1 HFE4	solute cation protein-coding	
chr1-2675 6. 683409	-1.43748	0.98169	-1.4643	0.143113	0.981636	chr1	26756055	26756502	0	NA	intron (NAluSx SIN	-31685 NM_017837	55650 Hs. 259600ENM_017837	ENSG00000PIGV	GPI-MT-II	phosphatidylinositol protein-coding	
chr9-1364 8. 178626	1.237393	0.845386	1.463701	0.143276	0.981636	chr9	1.36E+08	1.36E+08	0	NA	intron (Nintron (N	9231 NM_00131E	56623 Hs. 120999ENM_01989E	ENSG00000INPP5E	CORS1 CPI	inositol protein-coding	
chr18-58 6. 383251	-1.39802	0.955266	-1.46348	0.143335	0.981636	chr18	58557093	58558106	0	NA	intron (NLM1C1 LIN	-43021 NR_13296E	1.07E+08	SNORA108		small nucleolar RNA	
chr7-105 6. 383251	-1.39802	0.955266	-1.46348	0.143335	0.981636	chr7	58557093	58558106	0	NA	intron (Nintron (N	6102 NM_00131E	54517 Hs. 520619ENM_01904E	ENSG00000PUS1	IDDABS	pseudouridine protein-coding	
chr17-74 6. 247006	1.410145	0.963639	1.463355	0.14337	0.981636	chr17	74868404	74870193	0	NA	promoter-promoter-	-545 NM_00125E	2232 Hs. 69745 NM_00411E	ENSG00000CFDXR	ADR ADXR	ferredoxin protein-coding	
chr13-45 11. 87086	1.034782	0.707238	1.463132	0.143431	0.981636	chr13	45530396	45530395	0	NA	intron (Nintron (N	65556 NM_031431	83548 Hs. 50794ENM_031431	ENSG00000COG3	SEC34	component protein-coding	
chr18-87 8. 373946	-1.21609	0.831728	-1.46213	0.143706	0.981636	chr18	8796366	8797230	0	NA	intron (Nintron (N	79417 NM_01521E	23255 Hs. 70792ENM_01521E	ENSG00000MCTCL1	CCDC165	microtubule protein-coding	
chr20-264 24. 84149	0.747364	0.511241	1.461863	0.143779	0.981636	chr20	26468721	26469385	0	NA	IntergeniALR/Alph	-259820 NR_04009E	284801 Hs. 370699ENM_04009E	ENSG00000MIR663AHC	MIR663A	lincRNA	
chr14-39 6. 375393	-1.39631	0.955178	-1.46183	0.143788	0.981636	chr14	39124559	39124758	0	NA	intron (NAluSx SIN	10374 NM_00361E	8487 Hs. 652307NM_00361E	ENSG00000GEM12	SIP1 SIP1em	nucleic acid protein-coding	
chr15-494 6. 375393	-1.39631	0.955178	-1.46183	0.143788	0.981636	chr15	49487944	49488396	0	NA	3' UTR (N3' UTR (N	64928 NM_00200E	2252 Hs. 56726ENM_00200E	ENSG00000FG7	B CYP-S1	peptidyl protein-coding	
chr3-490 6. 375393	-1.39631	0.955178	-1.46183	0.143788	0.981636	chr3	49086231	49086627	0	NA	intron (NAluY SINE	7203 NM_00132E	54870 Hs. 29738ENM_01773E	ENSG00000QRICH1	AB-DIP VF	glutamine protein-coding	
chr11-51 20. 20092	0.812947	0.562632	1.461524	0.143872	0.981636	chr11	51912546	51912766	0	NA	IntergeniALR/Alph	1503509 NR_024504	646813 Hs. 684179NR_024504	LOC64681E		DEH-hom pseudo	
chr7-189 6. 922458	1.352871	0.957552	1.461375	0.143912	0.981636	chr7	5914051	5914362	0	NA	intron (NAluJr SIN	15473 NM_01562E	51622 Hs. 53000ENM_01562E	ENSG00000CCZ1	C7orf28A CCZ1	home protein-coding	
chr15-80 6. 391109	-1.39976	0.958311	-1.46065	0.144112	0.981636	chr15	80871550	80874331	0	NA	intron (NMLT1J LTF	-30867 NR_03039E	693132	ENSG00000MIR549A	MIR549	microRNA	
chr20-35 12. 45944	1.002293	0.686301	1.460429	0.144172	0.981636	chr20	35502322	35502521	0	NA	exon (NM exon (NM	27231 NR_02693E	140873 Hs. 15868ENM_08082E	ENSG00000C20orf17E	dJ47704.4	chromosome protein-coding	
chr11-19 4. 427687	-1.73923	1.191009	-1.4603	0.144209	0.981636	chr11	19887682	19887946	0	NA	intron (Nintron (N	-127731 NR_03984E	1.01E+08	NR_03984E	ENSG00000MIR4694		microRNA
chr15-30 4. 427687	-1.73923	1.191009	-1.4603	0.144209	0.981636	chr15	30646245	30646874	0	NA	intron (NAluYe5 SI	444 NR_03825E	1E+08	Hs. 66895ENM_03825E	ENSG00000LOC100208E		OTU deubiquitination pseudo
chr7-158 2. 916014	-2.26385	1.550486	-1.46009	0.144266	0.981636	chr7	1.59E+08	1.59E+08	0	NA	intron (Nintron (N	55046 NR_04989E	1.01E+08	NR_04989E	ENSG00000MIR5707		microRNA
chr19-25 17. 19384	0.863099	0.591191	1.459933	0.144309	0.981636	chr19	25021130	25021580	0	NA	IntergeniALR/Alph	-857908 NR_00360E	1E+08	Hs. 149312NR_00360E	ENSG00000HACVCRIP1		hepatitis pseudo
chr10-92 6. 358223	-1.21339	0.831418	-1.45943	0.144447	0.981636	chr10	92691184	92693071	0	NA	intron (Nintron (N	2172 NM_00272E	3087 Hs. 118651NM_00272E	ENSG00000HHX	HEX HMHP1	hematopoietic protein-coding	
chr12-12 5. 179594	-1.60623	1.100906	-1.45901	0.144563	0.981636	chr12	1.21E+08	1.21E+08	0	NA	intron (NAluSx1 SI	9591 NM_032314	84274 Hs. 17250 NM_032314	ENSG00000COQ5		coenzyme protein-coding	
chr3-119 6. 179594	-1.60623	1.100906	-1.45901	0.144563	0.981636	chr3	1.19E+08	1.19E+08	0	NA	intron (NLTR12D LI	-14981 NR_04674E	1.01E+08	Hs. 607097NR_04674E	ENSG00000ARHGAP31-		ARHGAP31 ncRNA
chr15-64 6. 213725	1.407644	0.965094	1.458556	0.144687	0.981636	chr15	64195685	64196092	0	NA	intron (Nintron (N	-32733 NM_00094E	5479 Hs. 434937NM_00094E	ENSG00000PP1B	B CYP-S1	peptidyl protein-coding	
chr9-116 6. 213725	1.407644	0.965094	1.458556	0.144687	0.981636	chr9	1.16E+08	1.16E+08	0	NA	intron (Nintron (N	97033 NR_103711	493913 Hs. 728832NR_103711	ENSG00000PAPPA-AS1	DIPAS NCF	PAPPA lincRNA	
chrX-48 6. 213725	1.407644	0.965094	1.458556	0.144687	0.981636	chrX	48933820	48934992	0	NA	intron (Nintron (N	-15382 NM_00687E	11040 Hs. 72714ENM_00687E	ENSG00000PIM2		Pim-2 precursor protein-coding	
chr13-24 7. 103726	-1.33855	0.91803	-1.45807	0.144822	0.981636	chr13	24499251	24499774	0	NA	intron (Nintron (N	13266 NM_006437	143 Hs. 744855NM_006437	ENSG00000PARP4	ADPRTL1 Apol	ADP-protein-coding	
chr13-33 6. 642497	-1.95326	1.339774	-1.4579	0.144868	0.981636	chr13	33834887	33836410	0	NA	intron (Nintron (N	17499 NM_00291E	5983 Hs. 115474NM_00291E	ENSG00000RFC3	RFC38	replicator protein-coding	
chr20-31 7. 642497	-1.95326	1.339774	-1.4579	0.144868	0.981636	chr20	31743951	31745072	0	NA	intron (Nintron (N	5221 NM_01211E	22974 Hs. 24458ENM_01211E	ENSG00000TPX2	C20orf1 CTPX2	micro protein-coding	
chr3-12 6. 642497	-1.95326	1.339774	-1.4579	0.144868	0.981636	chr3	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	36631 NM_00728E	11343 Hs. 27703ENM_00728E	ENSG00000MGLL	HU-K5 HU	monoclonal protein-coding	
chr1-18 6. 10946	0.992363	0.680753	1.457743	0.144911	0.981636	chr1	1.86E+08	1.86E+08	0	NA	intron (Nintron (N	28107 NM_00329E	7175 Hs. 27964ENM_00329E	ENSG00000TPR		translocase protein-coding	
chr20-50 8. 324949	-1.21919	0.837243	-1.4562	0.145338	0.981636	chr20	50150549	50150978	0	NA	intron (NAluSx1 SI	2960 NM_19912E	387521 Hs. 74483ENM_19912E	ENSG00000TMEM189	KUA	transmembrane protein-coding	
chr6-31 6. 211908	1.239398	0.851186	1.456084	0.145369	0.981636	chr6	31505897	31506131	0	NA	intron (Nintron (N	7869 NM_00128E	4277 Hs. 73144ENM_005931	ENSG00000M1CB	PERB1.2	MHC class protein-coding	
chr13-27 6. 367535	-1.39461	0.958051	-1.45567	0.145483	0.981636	chr13	27114803	27115041	0	NA	intron (NAluJr SIN	-10611 NR_046547	1.01E+08	Hs. 524922NR_046547	USP12-AS1-		USP12 lincRNA
chr2-39 6. 367535	-1.39461	0.958051	-1.45567	0.145483	0.981636	chr2	39321207	39321933	0	NA	intron (NLTR5_Hs L	-77587 NR_144521	344387 Hs. 403201NM_00100E	ENSG00000CDKL4		cyclin dependent protein-coding	
chr3-47 6. 367535	-1.39461	0.958051	-1.45567	0.145483	0.981636	chr3	47621236	47621435	0	NA	intron (NLM1P17 LI	40359 NR_145791	1.1E+08	NR_145791	SNORD146		small nucleolar RNA
chr3-14 6. 367535	-1.39461	0.958051	-1.45567	0.145483	0.981636	chr3	1.46E+08	1.46E+08	0	NA	intron (NTHE1B LTF	13941 NM_00112E	57088 Hs. 47786ENM_02035E	ENSG00000PLSCR4	TRA1	phospholipase protein-coding	
chr5-38 6. 367535	-1.39461	0.958051	-1.45567	0.145483	0.981636	chr5	38927438	38925673	0	NA	exon (NM exon (NM	79193 NM_00132E	9180 Hs. 12066ENM_00399E	ENSG00000OSMR	IL-31R	beccanostatin protein-coding	
chr6-18 6. 367535	-1.39461	0.958051	-1.45567	0.145483	0.981636	chr6	18223556	18226034	0	NA	TTS (NM_TTS (NM_I	39735 NM_001134	7913 Hs. 48481ENM_00347E	ENSG00000DEK	D6S231E	DEK prototypic protein-coding	
chr1-15 6. 221583	1.404546	0.965012	1.45547	0.145539	0.981636	chr1	1.58E+08	1.58E+08	0	NA	intron (N2a LINE	29355 NR_145471	1.01E+08	Hs. 66465ENM_145471	KIRREL1-KIRREL-1	KIRREL1 lincRNA	
chr17-17 6. 221583	1.404546	0.965012	1.45547	0.145539	0.981636	chr17	17132817	17132266	0	NA	intron (Nintron (N	73292 NR_17883E	201164 Hs. 72907ENM_17883E	ENSG00000PLD6	SIC	phospholipase protein-coding	
chr8-94 6. 221583	1.404546	0.965012	1.45547	0.145539	0.981636	chr8	94925442	94926423	0	NA	TTS (NM_TTS (NM_C	23446 NM_00113E	91424 Hs. 492261NM_03328E	ENSG00000TP53INP1	ZUP TP53	tumor protein-coding	
chr9-20 6. 221583	1.404546	0.965012	1.45547	0.145539	0.981636	chr9	2086822	2087021	0	NA	exon (NM exon (NM	64976 NM_00128E	6595 Hs. 29899ENM_00307E	ENSG00000SMARCA2	BAF190 BFSWI SNF	r protein-coding	
chr9-54 0 6. 213691	1.73784	1.194264	1.455156	0.145626	0.981636	chr9	5408338	5408797	0	NA	intron (NTHE1D-int	29358 NM_01846E	55848 Hs. 584424NM_01846E	ENSG00000PLGRKT	AD025	C9c plasminogen protein-coding	
chr12-6 6. 365685	-1.40964	0.96899	-1.45475	0.145738	0.981636	chr12	65456764	65457508	0	NA	intron (Nintron (N	100175 NR_13503E	1.05E+08	Hs. 738044NR_13503E	ENSG00000LOC10536E		uncharacterized RNA
chr12-28 6. 365685	-1.40964	0.96899	-1.45475	0.145738	0.981636	chr12	28401523	28401779	0	NA	intron (NTHE1C LTF	-210913 NR_14501E	729291 Hs. 12927ENM_14893E	LOC729291-		uncharacterized RNA	
chr10-31 6. 408674	-1.38845	0.955	-1.45388	0.14598	0.981636	chr10	3120805	3121445	0	NA	intron (Nintron (N	12979 NR_13275E	1.07E+08	NR_13275E	SNORD142	SNORA85	small nucleolar RNA
chr3-7 6. 408674	-1.38845	0.955	-1.45388	0.14598	0.981636	chr3	72922448	72923056	0	NA	intron (Nintron (N	34706 NM_00108E	727936 Hs. 71027ENM_00108E	ENSG00000GXLYT2	GLT8D4	glucosylase protein-coding	
chr5-7 6. 408674	-1.38845	0.955	-1.45388	0.14598	0.981636	chr5	78089125	78089450	0	NA	intron (Nintron (N	131040 NR_10501E	1.02E+08	Hs. 25289ENM_10501E	LOC10192E-		uncharacterized RNA
chr19-20 6. 4359274	-1.78913	1.230604	-1.45386	0.145985	0.981636	chr19	20935071	20935908	0	NA	intron (NLM3a LIN	12236 NR_04583E	7639 Hs. 37138 NM_00342E	ENSG00000ZNF85	HPF4 HTF1	zinc finger protein-coding	



chr5-3594	8.24519	1.241268	0.867439	1.430957	0.152443	0.981636	chr5	359456	359888	+	0	NA	intron (Nintron (N	55496 NM_020731	57491 Hs. 50823 NM_020731	ENSG000004AHRH	AHH AHRH aryl-hydriprotein-coding
chrX-6245	11.72528	1.004899	0.702441	1.430581	0.15255	0.981636	chrX	62499326	62499605	+	0	NA	IntergeniALR/Alpha	851867 NM_001012	139886 Hs. 612782 NM_001012	ENSG000004SPIN4	TDRD28 spindlin protein-coding
chr10-395	35.34092	0.660611	0.461889	1.430238	0.152649	0.981636	chr10	39983438	39983710	+	0	NA	IntergeniALR/Alpha	1286978 NR_045000	399746 Hs. 742607 NR_045000	ACTR3BP5	FKSG74 ACTR3B pspseudo
chr15-822	7.588757	-1.25306	0.876538	-1.42955	0.152845	0.981636	chr15	82226710	82227188	+	0	NA	intron (NL2-3_Crp)	35579 NM_001322	79631 Hs. 459114 NM_024588	ENSG000004EFL1	EFTUD1 F elongaticprotein-coding
chr7-1587	7.606323	-1.24367	0.870402	-1.42881	0.153058	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	intron (NLIMB3 LIN	38361 NM_020728	57488 Hs. 490796 NM_020728	ENSG000004ESY2	CHR2SYT E xtended protein-coding
chr9-2716	6.434098	-1.37854	0.965158	-1.4283	0.153206	0.981636	chr9	27187159	27187500	+	0	NA	intron (Nintron (N	78188 NM_000455	7010 Hs. 89640 NM_000455	ENSG000004CTEY	CD202B G TEK recep protein-coding
chr6-1305	5.915786	-1.50545	1.054982	-1.42699	0.153584	0.981636	chr6	1.31E+08	1.31E+08	+	0	NA	intron (NALuX LI	27725 NM_001195	1.01E+08 Hs. 388715 NM_001195	ENSG000004SMLR1	- small let protein-coding
chr17-395	5.495284	1.464155	1.02612	1.426885	0.153613	0.981636	chr17	39339443	39339765	+	0	NA	intron (NLIMC4a LI	42204 NR_162098	1.14E+08 NR_162098	MIR548BC	- microRNA ncRNA
chr19-524	5.495284	1.464155	1.02612	1.426885	0.153613	0.981636	chr19	52462494	52463902	+	0	NA	intron (NHERVK4-i	9645 NM_001095	147660 Hs. 157287 NM_152472	ENSG000004ZNF578	- zinc fing protein-coding
chr8-1864	5.495284	1.464155	1.02612	1.426885	0.153613	0.981636	chr8	18648856	18649717	+	0	NA	intron (NMSTA-int)	159581 NM_206905	23362 Hs. 434255 NM_015311	ENSG000004PSD3	EFA6D E F pleckstrin protein-coding
chr19-174	8.127779	1.228139	0.860923	1.426538	0.153713	0.981636	chr19	17423738	17424084	+	0	NA	intron (Nintron (N	3864 NM_138401	93343 Hs. 515243 NM_138401	ENSG000004MVB12A	CFBP FAM multivesiprotein-coding
chr11-134	5.130597	-1.61229	1.13063	-1.42601	0.153865	0.981636	chr11	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	-15326 NR_145790	1.1E+08 NR_145790	SNORD153	- small nucsnRNA
chr3-9782	6.615627	-1.4625	1.026056	-1.42536	0.154054	0.981636	chr3	9782147	9782352	+	0	NA	TTS (NM_TTS (NM_1	-10246 NM_001024	10093 Hs. 323342 NM_005715	ENSG000004ARPC4	ARC20 P2 actin rel protein-coding
chr5-3238	9.814898	-1.15873	0.813328	-1.42468	0.15425	0.981636	chr5	32386056	32386342	+	0	NA	intron (NMIR SINE)	8276 NR_030305	693164 NR_030305	ENSG000004MIR579	MIRN579 microRNA ncRNA
chr1-1495	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr1	14957085	14957526	+	0	NA	intron (Nintron (N	11386 NM_001017	23254 Hs. 368822 NM_015205	ENSG000004KAZN	KAZ kazrin, f protein-coding
chr1-7864	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr1	78641676	78642609	+	0	NA	3' UTR (N3' UTR (N	-7647 NR_135640	10561 Hs. 82316 NM_006417	ENSG000004IF144	MTAP44 TI interferc protein-coding
chr1-154	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (Nintron (N	2986 NR_036212	1E+08 NR_036212	ENSG000004MIR4258	- microRNA ncRNA
chr11-205	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr11	20097797	20098294	+	0	NA	intron (Nintron (N	-48742 NR_046672	1.01E+08 Hs. 557915 NM_046672	ENSG000004NAV2-AS2	- NAV2 anticnRNA
chr15-515	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr15	51930672	51930871	+	0	NA	IntergeniIntergeni	-6651 NR_109775	1E+08 Hs. 664788 NR_109775	LOC100422	- LEO1 homc pseudo
chr2-3317	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr2	33177753	33178200	+	0	NA	intron (Nintron (N	43379 NM_001166	4052 Hs. 619315 NM_000627	ENSG000004LTBP1	- latent tr protein-coding
chr4-9905	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr4	99057556	99057906	+	0	NA	intron (Nintron (N	31057 NM_000671	128 Hs. 78989 NM_000671	ENSG000004ADH5	ADH-3 AD alcohol protein-coding
chr6-2046	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr6	20463983	20464603	+	0	NA	intron (NMER2-int	60614 NM_001243	1871 Hs. 269405 NM_001945	ENSG000004E2F3	E2F-3 E2F trans protein-coding
chr6-151	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chr6	1.51E+08	1.51E+08	+	0	NA	intron (NMSTB LTR	25297 NM_001355	25902 Hs. 591343 NM_015440	ENSG000004MTHFD1L	FTHFSDC1 methyleneprotein-coding
chrX-2196	5.641051	-1.45147	1.018976	-1.42444	0.154318	0.981636	chrX	12967290	12967574	+	0	NA	intron (Nintron (N	26723 NM_004595	6611 Hs. 724874 NM_004595	ENSG000004SMS	MRSR SPM spermine protein-coding
chr1-2438	7.426904	1.25819	0.883368	1.42431	0.154357	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (NLIPA10 LI	20435 NM_181690	10000 Hs. 498292 NM_005465	ENSG000004AKT3	MPPH MPP AKT serir protein-coding
chr20-284	88.26594	0.453982	0.31875	1.424257	0.154372	0.981636	chr20	28494794	28498050	+	0	NA	IntergeniALR/Alpha	106243 NR_132315	1E+08 Hs. 529357 NR_132315	ENSG000004FRG1CP	- FSHD rep pseudo
chr2-7391	7.639604	-1.23733	0.8695	-1.42304	0.154725	0.981636	chr2	73912994	73920395	+	0	NA	exon (NM_exon (NM_	-10132 NR_134895	1716 Hs. 469022 NM_001925	ENSG000004DGUOK	MTDPS3 NC deoxyguar protein-coding
chr5-4962	128.5629	0.415534	0.292075	1.422695	0.154825	0.981636	chr5	49625564	49627067	+	0	NA	IntergeniALR/Alpha	814973 NM_198445	133418 Hs. 561141 NM_198445	ENSG000004EMB	GP70 embigin protein-coding
chr11-133	7.460186	1.260424	0.886037	1.422541	0.154869	0.981636	chr11	13369641	13369935	+	0	NA	intron (Nintron (N	70491 NM_001297	84280 Hs. 332382 NM_032320	ENSG000004BTBD10	GMRP-1 GN BTB domai protein-coding
chr16-195	7.460186	1.260424	0.886037	1.422541	0.154869	0.981636	chr16	19577048	19577247	+	0	NA	intron (NMSTB1 LTR	21444 NM_001365	57020 Hs. 654964 NM_020314	ENSG000004VPS35L	C16orf62 VPS35 enc protein-coding
chr17-637	7.460186	1.260424	0.886037	1.422541	0.154869	0.981636	chr17	63713164	63713568	+	0	NA	intron (Nintron (N	13028 NR_046273	729683 Hs. 534931 NR_046273	LOC729683	- uncharactncRNA
chr7-5996	15.98526	0.904777	0.635898	1.422362	0.154921	0.981636	chr7	59908457	59908731	+	0	NA	IntergeniALR/Alpha	2458417 NM_001155	441234 Hs. 533121 NM_001155	ENSG000004ZNF716	- zinc fing protein-coding
chr1-1246	33.84719	0.647218	0.455181	1.421892	0.155058	0.981636	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alpha	3167475 NR_003955	641234 Hs. 697682 NR_003955	ENSG000004EMB1P	- embigin f pseudo
chr3-1231	10.76538	1.094239	0.769983	1.421121	0.155282	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	IntergeniIntergeni	3023 NR_106960	1.02E+08 NR_106960	ENSG000004MIR7110	hsa-mir-7 microRNA ncRNA
chr19-187	5.487426	1.467733	1.032838	1.421609	0.155297	0.981636	chr19	18342870	18344069	+	0	NA	intron (NMIR SINE	2871 NM_001322	54858 Hs. 131775 NM_017712	ENSG000004PGPEP1	PAP-1 PG pyroglyt protein-coding
chr10-506	6.418382	-1.37498	0.968	-1.42043	0.155481	0.981636	chr10	50746266	50746465	+	0	NA	intron (NLIMA8 LIN	6429 NM_001321	653308 Hs. 659820 NM_001075	ENSG000004ASAH2B	ASAH2 ASN-acylsp protein-coding
chr5-9887	6.418382	-1.37498	0.968	-1.42043	0.155481	0.981636	chr5	98871874	98872313	+	0	NA	exon (NM_exon (NM_	54441 NM_001270	1105 Hs. 643465 NM_001270	ENSG000004CHD1	CHD-1 PII chromodon protein-coding
chr7-6657	6.418382	-1.37498	0.968	-1.42043	0.155481	0.981636	chr7	66571346	66571545	+	0	NA	intron (NMIR3 SINE	20962 NR_111974	493754 Hs. 732405 NR_002933	ENSG000004GS1-124E1	- RAB guanipseudo
chr16-485	6.377243	-1.38127	0.972954	-1.41967	0.155705	0.981636	chr16	48594413	48594636	+	0	NA	intron (NLIMC4a LI	15656 NM_153025	9683 Hs. 511835 NM_153025	ENSG000004NBP1	- NEDD4 bi protein-coding
chr5-144	6.377243	-1.38127	0.972954	-1.41967	0.155705	0.981636	chr5	14434373	14434796	+	0	NA	intron (NLIMC4a LI	-29399 NR_145815	1.1E+08 NR_145815	SNORD170	- small nucsnRNA
chr6-8722	7.631746	-1.23585	0.87055	-1.41962	0.155719	0.981636	chr6	87220695	87220989	+	0	NA	intron (Nintron (N	65277 NM_015021	23036 Hs. 444800 NM_015021	ENSG000004ZNF292	Nbla00365 zinc fing protein-coding
chr9-107	7.631746	-1.23585	0.87055	-1.41962	0.155719	0.981636	chr9	1.07E+08	1.07E+08	+	0	NA	IntergeniL3 LINE C	53994 NM_001244	5887 Hs. 521640 NM_02874	ENSG000004RAD23B	HHR23B HF RAD23 hon protein-coding
chr10-74	7.573041	-1.25017	0.881096	-1.41888	0.155933	0.981636	chr10	74015241	74015842	+	0	NA	intron (NALuS SIN	17425 NM_003373	7414 Hs. 643895 NM_003373	ENSG000004CVL	CMD1W CMF vinculin protein-coding
chr2-1277	7.573041	-1.25017	0.881096	-1.41888	0.155933	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	TTS (NM_TTS (NM_C	40751 NM_018383	55339 Hs. 554831 NM_018383	ENSG000004WDR33	NET14 WDC WD repeat protein-coding
chr1-8508	5.46986	1.457874	1.027958	1.418222	0.156126	0.981636	chr1	85081436	85083456	+	0	NA	intron (Nintron (N	20119 NM_145172	126820 Hs. 97933 NM_145172	ENSG000004WDR63	DIC3 NYD- WD repeat protein-coding
chr19-122	5.46986	1.457874	1.027958	1.418222	0.156126	0.981636	chr19	12207998	12209709	+	0	NA	IntergeniIntergeni	13838 NR_104175	1E+08 Hs. 662620 NR_104175	LOC100285	- uncharactncRNA
chr7-1497	5.46986	1.457874	1.027958	1.418222	0.156126	0.981636	chr7	1.5E+08	1.5E+08	+	0	NA	intron (NMIR SINE	8361 NM_001290	84626 Hs. 299560 NM_032534	ENSG000004KRBA1	- KRAB-A d protein-coding
chr22-431	8.852968	-1.14004	0.805679	-1.415	0.157067	0.981636	chr22	43161236	43161476	+	0	NA	intron (Nintron (N	9421 NM_001255	706 Hs. 202 NM_000714	ENSG000004TSPO	BPBS BZRF transloc protein-coding
chr2-929	17.66316	0.834004	0.589453	1.414878	0.157104	0.981636	chr2	92934828	92935157	+	0	NA	IntergeniALR/Alpha	993859 NR_027714	440888 Hs. 730235 NM_001032412	ACTR3BP2	FKSG73 ACTR3B pspseudo
chr1-2282	5.503142	1.460606	1.03246	1.414685	0.157161	0.981636	chr1	2.28E+08	2.28E+08	+	0	NA	intron (Nintron (N	-70335 NR_073154	574407 Hs. 650035 NM_001025	ENSG000004OBSCN-AS1	C1orf145 OBSCN anticnRNA
chr4-281	5.503142	1.460606	1.03246	1.414685	0.157161	0.981636	chr4	2821434	2821938	+	0	NA	intron (NALuJb SIN	2872 NM_003023	6452 Hs. 167675 NM_003023	ENSG000004SH3BP2	3BP-2 3BP SH3 domai protein-coding
chr17-315	5.607769	-1.46066	1.033249	-1.41366	0.157462	0.981636	chr17	31591189	31591511	+	0	NA	IntergeniHALLME LI	15939 NR_029855	1E+08 NR_029855	ENSG000004MIR365B	MIR365-2 microRNA ncRNA
chr18-51	5.607769	-1.46066	1.033249	-1.41366	0.157462	0.981636	chr18	51086476	51086757	+	0	NA	IntergeniLIMD1 LIN	56403 NM_005355	4089 Hs. 75862 NM_005355	ENSG000004SMAD4	DPC4 JIP SMAD fami protein-coding

chr20-60: 4.922425	-1.52942	1.094359	-1.39755	0.162249	0.981636	chr20	6032876	6033549	+	0	NA	intron (AluS2) SI	20848	NM_152611	164312	Hs.14913:NM_152611:ENS00000CLRRN4	C20orf75 leucine rprotein-coding	
chr20-58: 4.922425	-1.52942	1.094359	-1.39755	0.162249	0.981636	chr20	5852898	5853166	+	0	NA	intron (L1MB1) LIN	-14903	NM_15336C	164284	Hs.11928:NM_15336C:ENS00000APCDL1L	- APC down-protein-coding	
chr3-180: 4.922425	-1.52942	1.094359	-1.39755	0.162249	0.981636	chr3	1.81E+08	1.81E+08	+	0	NA	TTS (NM_C TTS (NM_C	16145	NM_001042	151613	Hs.43213:NM_001042:ENS00000TTC14	DRDL5813 tetratric protein-coding	
chr8-233: 4.922425	-1.52942	1.094359	-1.39755	0.162249	0.981636	chr8	23334285	23334615	+	0	NA	intron (N intron (N	-1758	NR_038322	1.01E+08	Hs.66113:NR_038322:ENS00000LOC100507-	uncharactncRNA	
chr9-115: 4.922425	-1.52942	1.094359	-1.39755	0.162249	0.981636	chr9	1.53E+08	1.15E+08	+	0	NA	intron (N intron (N	57228	NM_00216C	3371	Hs.14325:NM_00216C:ENS00000TNC	150-225 tenascin protein-coding	
chr1-150: 7.956774	1.182053	0.845938	1.397327	0.162315	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (N intron (N	-3035	NM_022664	1893	Hs.81071:NM_00442:ENS00000CECM1	URBWD extracell protein-coding	
chr15-23: 7.956774	1.182053	0.845938	1.397327	0.162315	0.981636	chr15	23311286	23311783	+	0	NA	intron (N intron (N	189	NR_145475	1.01E+08	NR_145479	HERC2P11	hect dom pseudo
chr18-17: 7.956774	1.182053	0.845938	1.397327	0.162315	0.981636	chr18	17240247	17240454	+	0	NA	IntergeniALR Alpha	-1914431	NR_027417	644669	Hs.579474:NR_027417:ENS00000LOC644669-	ankyrin rpseudo	
chr7-106: 7.956774	1.182053	0.845938	1.397327	0.162315	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	intron (N intron (N	15932	NM_00574E	10135	Hs.48961:NM_00574E:ENS00000CNAMPT	11100350 nicotinan protein-coding	
chr9-104: 7.956774	1.182053	0.845938	1.397327	0.162315	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (AluSc) SIN	27539	NR_13076C	55335	Hs.4929294:NM_01837:ENS00000NIPSNAP3EFP944	NIPSNAP3 protein-coding	
chr1-113: 5.599911	-1.45884	1.044484	-1.39671	0.162501	0.981636	chr1	1.14E+08	1.14E+08	+	0	NA	exon (NM exon (NM	85808	NM_00660E	10745	Hs.655824:NM_00660E:ENS00000PHTF1	PHTF putative protein-coding	
chr20-32: 5.599911	-1.45884	1.044484	-1.39671	0.162501	0.981636	chr20	32701946	32702264	+	0	NA	TTS (NM_C TTS (NM_C	-28164	NM_182584	284805	Hs.353262:NM_182584:ENS00000C20orf20-	mitochondrion protein-coding	
chr8-12: 5.599911	-1.45884	1.044484	-1.39671	0.162501	0.981636	chr8	1.25E+08	1.23E+08	+	0	NA	exon (NM exon (NM	-11115	NR_030382	693130	NR_030382:ENS00000MIR5482D-	MIR5482D microRNA ncRNA	
chr19-25: 12.21216	0.960881	0.688102	1.396422	0.162587	0.981636	chr19	25693106	25693327	+	0	NA	IntergeniALR Alpha	-1529769	NR_003603	1E+08	Hs.14931:NR_003603:ENS00000HACVCR1P1	hepatitis rpseudo	
chr11-13: 5.582346	-1.47256	1.055282	-1.39542	0.162891	0.981636	chr11	1.31E+08	1.31E+08	+	0	NA	IntergeniAlu Jo SIN	-3993	NR_125382	1.04E+08	Hs.43030:NR_125382:ENS00000LOC103611-	uncharactncRNA	
chr14-50: 5.625335	-1.44746	1.037347	-1.39535	0.162911	0.981636	chr14	50356190	50356529	+	0	NA	intron (N intron (N	40522	NM_00419E	8814	Hs.280881:NM_00419E:ENS00000CDKL1	KKIALRE F cyclin d protein-coding	
chr1-31: 6.733887	1.291579	0.925637	1.395341	0.162913	0.981636	chr1	31364806	31365427	+	0	NA	TTS (NM_C TTS (NM_C	7960	NM_00410E	2170	Hs.576372:NM_00410E:ENS00000FABP3	FABP11 H-fatty aciprotein-coding	
chr1-20: 6.733887	1.291579	0.925637	1.395341	0.162913	0.981636	chr1	2.08E+08	2.08E+08	+	0	NA	intron (N intron (N	-5228	NR_026817	148696	Hs.125511:NM_01039568	LOC14869E-	uncharactncRNA
chr8-43: 6.733887	1.291579	0.925637	1.395341	0.162913	0.981636	chr8	43170476	43171175	+	0	NA	intron (N intron (N	30361	NM_15241E	138050	Hs.600384:NM_15241E:ENS00000HGSNAT	HGNAT MPS heparan-ε protein-coding	
chr12-16: 6.887697	-1.27369	0.912944	-1.39514	0.162973	0.981636	chr12	1632139	1632476	+	0	NA	intron (ML2c LINE	3076	NM_03264E	81029	Hs.306051:NM_03077:ENS00000WNT5B	- Wnt fami protein-coding	
chr7-16: 6.887697	-1.27369	0.912944	-1.39514	0.162973	0.981636	chr7	16316773	16164038	+	0	NA	intron (N LMB7 LIN	-10709	NR_145787	1.1E+08	NR_145787	SNORD163	small nucsnRNA
chr19-10: 6.887697	-1.27369	0.912944	-1.39514	0.162973	0.981636	chr19	10390379	10390665	+	0	NA	TTS (NM_C TTS (NM_C	-9950	NM_003331	7297	Hs.75516:NM_003331:ENS00000TYK2	TYK2 JTK tyrosine protein-coding	
chr7-100: 6.887697	-1.27369	0.912944	-1.39514	0.162973	0.981636	chr7	1.01E+08	1.01E+08	+	0	NA	3' UTR (N3' UTR (N	-23673	NM_00136E	56996	Hs.521087:NM_02024:ENS00000SLC12A9	SLC12A9 CIP1 solute c protein-coding	
chr8-13: 6.887697	-1.27369	0.912944	-1.39514	0.162973	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	non-codirnon-codir	37071	NM_08083E	8840	Hs.4929294:NM_003882:ENS00000CCN4	CCN4 WISP1 WISC cellular protein-coding	
chr13-36: 6.700605	1.289113	0.924008	1.395132	0.162976	0.981636	chr13	36247146	36247618	+	0	NA	intron (N Tiger1 E	-32767	NM_00128E	54937	Hs.12451:NM_01782:ENS00000SOHLH2	SOHLH2 SP1 spermatog protein-coding	
chr17-64: 6.700605	1.289113	0.924008	1.395132	0.162976	0.981636	chr17	64046008	64046291	+	0	NA	intron (N intron (N	-25515	NM_00109E	3384	Hs.43146:NM_00087:ENS00000ICAM2	ICAM2 CD102 intercell protein-coding	
chr2-27: 6.948916	1.184375	0.849012	1.395003	0.163015	0.981636	chr2	27695842	27696148	+	0	NA	IntergeniIntergeni	19737	NR_13520C	1E+08	Hs.51587:NR_13520C:ENS00000LINC0146C-	long intencRNA	
chr8-105: 7.582749	-1.23921	0.888431	-1.39483	0.163067	0.981636	chr8	1.05E+08	1.05E+08	+	0	NA	intron (N intron (N	174168	NM_00136E	23414	Hs.43100:NM_01208:ENS00000ZFPM2	ZFPM2 DIH3 FOG2 zinc fing protein-coding	
chr6-5: 6.895555	-1.2753	0.914423	-1.39465	0.163123	0.981636	chr6	52529350	52530927	+	0	NA	intron (N MER53 DNA	46922	NM_01228E	9697	Hs.520182:NM_01228E:ENS00000TRAM2	TRAM2 - transloc protein-coding	
chr20-28: 6.895555	-1.4382	1.032043	-1.39355	0.163454	0.981636	chr20	28118593	28118792	+	0	NA	IntergeniALR Alpha	483973	NR_13231E	1E+08	Hs.529357:NR_13231E:ENS00000FRGLCP	- FSHD regpseudo	
chr8-13: 6.586817	-1.4382	1.032043	-1.39355	0.163454	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (N intron (N	30676	NM_00113E	10397	Hs.372914:NM_00609:ENS00000CNRG1	CNRG1 CAP43 CMN-myc down protein-coding	
chr9-11: 5.658617	-1.4382	1.032043	-1.39355	0.163454	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (N intron (N	26374	NM_001351	1902	Hs.126667:NM_001401:ENS00000LPAR1	LPAR1 EDG2 GPR2 lysophosph protein-coding	
chr5-490: 10.01366	1.0987	0.789227	1.392122	0.163886	0.981636	chr5	49096248	49096467	+	0	NA	IntergeniALR Alpha	1344931	NM_19844E	133418	Hs.561411:NM_19844E:ENS00000EMB	EMB GP70 embigin protein-coding	
chr6-27: 4.522294	1.447825	1.040173	1.391908	0.16395	0.981636	chr6	27845387	27845772	+	0	NA	IntergeniIntergeni	6917	NM_00352C	8341	Hs.53436:NM_00352C:ENS00000HIST1H2B H2B/d H2E histone c protein-coding		
chr6-4: 4.522294	1.447825	1.040173	1.391908	0.16395	0.981636	chr6	41566731	41567015	+	0	NA	intron (N intron (N	-18252	NR_12641E	1.01E+08	Hs.57109:NR_12641E:ENS00000POXP4-AS1-	POXP4 antncRNA	
chr4-76: 6.879839	-1.27207	0.914199	-1.39145	0.164088	0.981636	chr4	762179	762657	+	0	NA	intron (N intron (N	19475	NR_036511	1E+08	Hs.73175:NR_036511:ENS00000LOC10012E-	uncharactncRNA	
chr5-43: 6.879839	-1.27207	0.914199	-1.39145	0.164088	0.981636	chr5	43135517	43135718	+	0	NA	intron (AluS2) SIN	14052	NM_00133C	7690	Hs.535804:NM_00343:ENS00000ZNF131	ZNF131 ZBTB35 p/zinc fing protein-coding	
chr6-7: 6.879839	-1.27207	0.914199	-1.39145	0.164088	0.981636	chr6	75147248	75156865	+	0	NA	intron (N intron (N	-23274	NR_14578E	1.1E+08	NR_145788	SNORD156	small nucsnRNA
chr7-23: 6.879839	-1.27207	0.914199	-1.39145	0.164088	0.981636	chr7	23330673	23331642	+	0	NA	intron (N intron (N	31818	NM_13844E	115416	Hs.87385:NM_13844E:ENS00000MALSU1	C7orf30 mi to micro protein-coding	
chr19-23: 9.195376	1.099966	0.79092	1.390742	0.164304	0.981636	chr19	23344503	23345218	+	0	NA	IntergeniMER48 LTF	50611	NM_00343C	7644	Hs.58834:NM_00343C:ENS00000ZNF91	ZNF91 HPF7 HTF1 zinc fing protein-coding	
chr12-54: 4.914567	-1.52717	1.098625	-1.39008	0.164506	0.981636	chr12	54414594	54415017	+	0	NA	intron (AluU) SINE	4461	NM_00220E	3678	Hs.505654:NM_00220E:ENS00000ITGA5	ITGA5 CD49E FN1 integrin protein-coding	
chr1-54: 7.964632	1.179709	0.849184	1.389225	0.164764	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	exon (NM exon (NM	-22870	NR_14785E	1.02E+08	Hs.61708:NR_14785E:ENS00000IL6R-AS1-	IL6R antncRNA	
chr1-16: 7.964632	1.179709	0.849184	1.389225	0.164764	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (N intron (N	14526	NM_016371	51478	Hs.49292:NM_016371:ENS00000HSD17B7	HSD17B7 PRAP SDR2 hydroxyst protein-coding	
chr1-18: 7.964632	1.179709	0.849184	1.389225	0.164764	0.981636	chr1	1.85E+08	1.85E+08	+	0	NA	intron (N intron (N	17643	NM_00131E	80267	Hs.523811:NM_025191:ENS00000EDEM3	EDEM3 Clorf22 ER degrad protein-coding	
chr1-19: 7.964632	-1.13485	0.817018	-1.38901	0.164829	0.981636	chr1	19730217	19730571	+	0	NA	intron (N MLT1 LTF	65519	NM_000871	3362	Hs.22180:NM_000871:ENS00000CHTR6	CHTR6 5-HT6 5-β hydroxy protein-coding	
chr10-49: 8.821537	-1.13485	0.817018	-1.38901	0.164829	0.981636	chr10	49947371	49947755	+	0	NA	intron (AluSx1) SI	5510	NR_15865E	1.13E+08	NR_158654	TMM23B-β	TMM23B-β ncRNA
chr1-16: 8.81285	-1.53783	1.108346	-1.3875	0.165289	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (N LIMEc LIN	9729	NM_145697	83540	Hs.65195:NM_03142:ENS00000NUF2	NUF2 CDCA1 CT1NUP2 com protein-coding	
chr11-8: 8.81285	-1.53783	1.108346	-1.3875	0.165289	0.981636	chr11	86253034	86253286	+	0	NA	intron (N intron (N	8407	NM_003797	8726	Hs.50351:NM_003797:ENS00000CEED	CEED COG15 HEF embryonic protein-coding	
chr12-9: 8.81285	-1.53783	1.108346	-1.3875	0.165289	0.981636	chr12	95665125	95665538	+	0	NA	intron (N intron (N	16076	NR_07722E	1E+08	Hs.676211:NR_07722E:ENS00000PGAM1P5	PGAM1P5 - phosphog pseudo	
chr20-56: 4.881285	-1.53783	1.108346	-1.3875	0.165289	0.981636	chr20	56372061	56373505	+	0	NA	intron (N intron (N	13809	NM_080821	116151	Hs.14373:NM_080821:ENS00000FAM210B	FAM210B 5A3 C20orf family wiprotein-coding	
chr15-90: 9.279505	1.110032	0.800275	1.387062	0.165423	0.981636	chr15	90911401	90911602	+	0	NA	non-codirnon-codir	7311	NR_135504	4122	Hs.11645:NM_00612:ENS00000MAN2A2	MAN2A2 MANA2X mannosi d protein-coding	
chr2-32: 9.279505	1.110032	0.800275	1.387062	0.165423	0.981636	chr2	32282411	32282615	+	0	NA	intron (AluUx4) SI	4609	NM_03231E	84272	Hs.468099:NM_03231E:ENS00000YIPF4	YIPF4 FinGER4 Yip1 dom protein-coding	
chr16-70: 7.93135	1.17748	0.849088	1.386758	0.165515	0.981636	chr16	70463586	70464263	+	0</								



chr17-821.6.741745	1.288605	0.939427	1.371693	0.170159	0.981636	chr17	82170931	82171733	+	0 NA	intron (Nintron (N	41510 NM_001316	284001 Hs. 631724NM_152677	ENSG00000CCDC57	-	coiled-coil protein-coding	
chr15-896.6.864123	-1.26874	0.925178	-1.37135	0.170267	0.981636	chr15	89637136	89637579	+	0 NA	intron (NLIAPA3 LIN	18110 NM_198525	374654 Hs. 513134NM_198525	ENSG00000KIF7	-	ACLS AGBB kinesin protein-coding	
chr3-114.6.864123	-1.26874	0.925178	-1.37135	0.170267	0.981636	chr3	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	12009 NM_024638	79691 Hs. 477162NM_024638	ENSG00000QTRT2	-	QTRTD1 queuine t protein-coding	
chr5-1135.6.864123	-1.26874	0.925178	-1.37135	0.170267	0.981636	chr5	1.14E+08	1.14E+08	+	0 NA	exon (NM exon (NM	65967 NM_001346	64848 Hs. 231942NM_022828	ENSG00000YTHDC2	-	CAHL HYTH YTH domain protein-coding	
chr6-8765.6.864123	-1.26874	0.925178	-1.37135	0.170267	0.981636	chr6	87696527	87696919	+	0 NA	intron (Nintron (N	5510 NM_018064	55122 Hs. 485915NM_018064	ENSG00000AKIRIN2	-	G6orf166 akirin 2 protein-coding	
chr16-277.6.683039	1.280833	0.934116	1.371172	0.170321	0.981636	chr16	27727583	27727878	+	0 NA	intron (NLMC5a LI	-8701 NR_147898	1E+08 Hs. 610277NR_147898	LOC100128	-	uncharactericnRNA	
chr19-161.6.683039	1.280833	0.934116	1.371172	0.170321	0.981636	chr19	1612443	1613146	+	0 NA	intron (Nintron (N	-7332 NM_00683C	10975 Hs. 8372	ENSG00000UQCR11	0710008DC ubiquinol protein-coding		
chrX-7135.6.683039	1.280833	0.934116	1.371172	0.170321	0.981636	chrX	71389943	71391024	+	0 NA	intron (Nintron (N	24126 NR_104387	6872 Hs. 158566NM_004600	ENSG00000TAF1	BA2R CCG1TATA-box protein-coding		
chr8-1177.6.067779	-1.16728	0.851484	-1.37087	0.170414	0.981636	chr8	1.18E+08	1.18E+08	+	0 NA	Intergeni LIPREC2 I	144007 NR_145799	1.1E+08	NR_145799	SNORD168	-	small nucleosnoRNA
chr9-9595.0.963850	0.995961	0.727405	1.369198	0.170937	0.981636	chr9	95958301	95959278	+	0 NA	intron (NLIAPA3 LIN	63022 NR_024125	1.0E+08 Hs. 43431CNR_024125	ENSG00000LINC00092	NCRNA0009	long intencnRNA	
chr14-754.8.110769	-1.15121	0.841142	-1.36863	0.171116	0.981636	chr14	75443137	75443336	+	0 NA	intron (Nintron (N	11102 NM_001135	122953 Hs. 196482NM_130466	ENSG00000JDP2	JUNDM2	Jun dimer protein-coding	
chr6-7512.8.110769	-1.15121	0.841142	-1.36863	0.171116	0.981636	chr6	75121737	75130595	+	0 NA	intron (Nintron (N	2616 NR_145788	1.1E+08	NR_145788	SNORD156	-	small nucleosnoRNA
chrX-3057.8.110769	-1.15121	0.841142	-1.36863	0.171116	0.981636	chrX	305759	307264	+	0 NA	intron (Nintron (N	12308 NM_012227	8225 Hs. 437145NM_012227	ENSG00000GTPBP6	PGPL	GTP bindi protein-coding	
chr1-1494.12.61918	0.92203	0.674145	1.367703	0.171405	0.981636	chr1	1.49E+08	1.49E+08	+	0 NA	intron (Nintron (N	3711 NM_001351	1.01E+08 Hs. 44508CNR_001351	ENSG00000NBPF19	-	NBPF memt protein-coding	
chr17-618.6.897404	-1.26157	0.92249	-1.36757	0.171445	0.981636	chr17	61820732	61820936	+	0 NA	intron (NAluSz SIN	42725 NM_032043	83990 Hs. 128903NM_032043	ENSG00000BRIP1	BACHI FANBRCA1 intr protein-coding		
chr2-2245.6.897404	-1.26157	0.92249	-1.36757	0.171445	0.981636	chr2	2.25E+08	2.25E+08	+	0 NA	intron (N Tiger2a	56835 NM_001257	8452 Hs. 372288NM_00359C	ENSG00000CUL3	CUL-3 PH1 cullin 3 protein-coding		
chr17-422.9.725246	1.048146	0.766459	1.367518	0.171463	0.981636	chr17	42614592	42616045	+	0 NA	TTS (NM_TTS (NM_C	5635 NM_00107C	7283 Hs. 279665NM_00107C	ENSG00000TUBG1	CDCMB4 Gc tubulin 3 protein-coding		
chr4-185.9.793659	1.061704	0.776395	1.367479	0.171475	0.981636	chr4	1.85E+08	1.85E+08	+	0 NA	exon (NM exon (NM	19595 NM_001151	291 Hs. 246505NM_001151	ENSG00000SLC25A4	AAC1 ANT solute c protein-coding		
chr10-404.19.15893	0.771612	0.564909	1.365905	0.171969	0.981636	chr10	40466158	40467631	+	0 NA	Intergeni ALR Alpha	1770298 NR_04500C	399746 Hs. 742607NR_04500C	ACTR3BP5	FKSG74	ACTR3B ps pseudo	
chr10-705.5.99973	1.333724	0.97756	1.36434	0.172461	0.981636	chr10	70884825	70885309	+	0 NA	intron (Nintron (N	2814 NM_001285	5092 Hs. 3192	NM_000281	ENSG00000PCBD1	DCOH PCBE pterin-4 protein-coding	
chr2-727.5.99973	1.333724	0.97756	1.36434	0.172461	0.981636	chr2	72760822	72762009	+	0 NA	intron (Nintron (N	64618 NM_001321	23233 Hs. 303454NM_01518C	ENSG00000EXOC6B	SEC15B SE exocyst protein-coding		
chr19-125.7.913784	1.170409	0.858045	1.364042	0.172554	0.981636	chr19	12517669	12518106	+	0 NA	Intergeni Intergeni	-33071 NM_152601	163051 Hs. 631622NM_152601	ENSG00000ZNF709	-	zinc fing protein-coding	
chr1-2804.6.135789	-1.31921	0.967146	-1.36403	0.172559	0.981636	chr1	28000413	28001568	+	0 NA	intron (NAluJb SIN	41528 NM_018055	55113 Hs. 55024	NM_018055	ENSG00000XKR8	XRG8 hXkr XK relate protein-coding	
chr8-222.6.135789	-1.31921	0.967146	-1.36403	0.172559	0.981636	chr8	22246584	22246908	+	0 NA	intron (Nintron (N	1634 NM_001722	661 Hs. 148352NM_001722	ENSG00000POLR3D	BN51T RPC RNA polyn protein-coding		
chr12-567.8.077487	-1.15707	0.848413	-1.3638	0.172629	0.981636	chr12	56719171	56719407	+	0 NA	exon (NM exon (NM	6010 NM_005594	4666 Hs. 505735NM_005594	ENSG00000NACA	HSD48 NAC nascent f protein-coding		
chr19-101.6.143647	-1.32102	0.968828	-1.36352	0.172718	0.981636	chr19	10167863	10168979	+	0 NA	intron (Nintron (N	26532 NM_001318	1786 Hs. 202672NM_001318	ENSG00000DNMT1	ADCAN AIDNA methyl protein-coding		
chr4-8395.7.417196	1.247338	0.915149	1.362989	0.172886	0.981636	chr4	83961128	8399474	+	0 NA	intron (Nintron (N	41424 NM_003501	8310 Hs. 479122NM_003501	ENSG00000ACOX3	-	acyl-CoA protein-coding	
chr11-117.4.203799	-1.63813	1.202667	-1.36208	0.173173	0.981636	chr11	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	1228 NM_003188	6876 Hs. 410977NM_003188	ENSG00000TAGLN	SM22 SM22 transgelin protein-coding		
chr1-1501.9.349556	-1.046308	0.782609	-1.36194	0.173215	0.981636	chr1	1.5E+08	1.5E+08	+	0 NA	promoter-promoter-	-618 NR_135098	1.05E+08 Hs. 599366NR_135098	LOC105371	-	uncharactericnRNA	
chr1-2356.9.699822	-1.065307	0.766827	-1.361857	0.173243	0.981636	chr1	2.36E+08	2.36E+08	+	0 NA	intron (NHERVPI0F	-20154 NM_001098	2786 Hs. 159711NM_004488	ENSG00000GNG4	-	G protein binding	
chr10-395.46.18847	0.544894	0.400116	1.361842	0.173248	0.981636	chr10	39986368	39987336	+	0 NA	Intergeni ALR Alpha	1290256 NR_04500C	399746 Hs. 742607NR_04500C	ACTR3BP5	FKSG74	ACTR3B ps pseudo	
chr5-9554.8.872384	-1.12112	0.823389	-1.36159	0.173329	0.981636	chr5	95548626	95549008	+	0 NA	intron (Nintron (N	6188 NM_014638	9652 Hs. 482868NM_014638	ENSG00000TTC37	KIAA0372 tetraatric protein-coding		
chr1-8888.3.410752	-1.83169	1.345441	-1.3614	0.173387	0.981636	chr1	88802725	88803057	+	0 NA	intron (Nintron (N	88676 NM_001514	2959 Hs. 481852NM_001514	ENSG00000GTF2B	TF2B TFII general protein-coding		
chr11-102.4.692714	1.522148	1.118205	1.361242	0.173437	0.981636	chr11	1.02E+08	1.02E+08	+	0 NA	intron (NAluSg SIN	25645 NM_001195	10413 Hs. 503692NM_006100	ENSG00000YAP1	COB1 YAP Yes assoc protein-coding		
chr5-113.4.692714	1.522148	1.118205	1.361242	0.173437	0.981636	chr5	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	67774 NM_152624	167227 Hs. 443875NM_152624	ENSG00000DCP2	NUD20 decapping protein-coding		
chr1-3172.6.007588	1.330572	0.977471	1.36124	0.173438	0.981636	chr1	31727062	31728236	+	0 NA	intron (NMR SINE	-23632 NM_001856	1307 Hs. 368921NM_001856	ENSG00000COL16A1	447AA FPII collagen protein-coding		
chr10-308.4.154801	-1.64601	1.209725	-1.36065	0.173625	0.981636	chr10	3086532	3087509	+	0 NA	intron (NAluSz SIN	-17589 NM_001323	5214 Hs. 26010	NM_002627	ENSG00000PFKP	ATP-PFK f phosphofr protein-coding	
chr9-129.8.151925	1.118656	0.822664	1.360128	0.173789	0.981636	chr9	1.29E+08	1.29E+08	+	0 NA	intron (NAluSx SIN	19984 NM_003280	84895 Hs. 632692NM_03280C	ENSG00000MIGA2	C9orf54 Fmi toguar protein-coding		
chr12-96.6.127931	-1.31743	0.968676	-1.36003	0.17382	0.981636	chr12	96312255	96312516	+	0 NA	intron (Nintron (N	56887 NM_001303	2004 Hs. 46523	NM_00523C	ENSG00000ELK3	ERP NET SET trans protein-coding	
chr4-763.6.127931	-1.31743	0.968676	-1.36003	0.17382	0.981636	chr4	76309845	76310640	+	0 NA	3' UTR (3' UTR (N	4216 NM_003943	8987 Hs. 109599NM_003943	ENSG00000STBD1	GENEX34 starch bi protein-coding		
chr6-7511.6.127931	-1.31743	0.968676	-1.36003	0.17382	0.981636	chr6	75111596	75114071	+	0 NA	intron (Nintron (N	15949 NR_145788	1.1E+08	NR_145788	SNORD156	-	small nucleosnoRNA
chr8-1335.6.127931	-1.31743	0.968676	-1.36003	0.17382	0.981636	chr8	17900 NM_080838	8840 Hs. 492974NM_080838	ENSG00000CCN4	WISPI WIS cellular protein-coding							
chr2-5532.8.102911	-1.14977	0.845502	-1.35987	0.173872	0.981636	chr2	55322215	55322488	+	0 NA	intron (N2a LINE	40032 NR_027258	344405 Hs. 445292NM_00108C	ENSG00000PRORSD1P	NCRNA0011	prolyl-tf pseudo	
chr15-735.8.14405	-1.14536	0.84246	-1.35954	0.173976	0.981636	chr15	73917896	73918359	+	0 NA	non-codir-non-codir	-8335 NM_005576	4016 Hs. 65436	NM_005576	ENSG00000LOXL1	LOL LOXL llysl oxiprotein-coding	
chr2-2745.8.494501	1.114301	0.819744	1.359328	0.174043	0.981636	chr2	27439615	27440117	+	0 NA	exon (NM exon (NM	-2500 NM_001168	200634 Hs. 59509	NM_17385C	ENSG00000KRTCAP3	KCP3 keratinoc protein-coding	
chr11-645.7.255898	1.207364	0.888286	1.359207	0.174081	0.981636	chr11	649380	649983	+	0 NA	intron (NAluSz SIN	12412 NM_000797	1815 Hs. 599922	NM_000797	ENSG00000DRD4	D4DR dopamine protein-coding	
chr14-496.2.684268	-2.11658	1.557647	-1.35883	0.174201	0.981636	chr14	49612203	49613537	+	0 NA	intron (Nintron (N	7756 NM_001001	6166 Hs. 444745NM_001001	ENSG00000RPL36AL	RPL36A ribosomal protein-coding		
chr19-365.5.974306	1.327844	0.977375	1.358582	0.174279	0.981636	chr19	36978787	36979637	+	0 NA	intron (NAluSp SIN	62908 NM_001204	374900 Hs. 404222NM_198535	ENSG00000ZNF568	ZFP568 zinc fing protein-coding		
chr3-754.5.974306	1.327844	0.977375	1.358582	0.174279	0.981636	chr3	75748969	75750477	+	0 NA	intron (N CER Sate1	11443 NR_036238	1E+08	NR_036238	ENSG00000MIR4273	microRNA ncRNA	
chr9-1365.4.129378	-1.66184	1.223575	-1.35819	0.174404	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	-5932 NM_001145	26086 Hs. 23937CNR_015597	ENSG00000GPSM1	AGS3	G protein binding	
chr5-1067.6.281322	1.212429	0.89281	1.357992	0.174466	0.981636	chr5	10686966	10687423	+	0 NA	intron (N Tiger1 I	74040 NM_004394	1611 Hs. 7				



chr20-321.9.367122	-1.05834	0.788118	-1.34287	0.179314	0.981636	chr20	32138883	32139123	+	0	NA	intron (Nintron (N	29275	NM_001363	9777	Hs.654666	NM_014742	ENSG000002TM9SF4	dJ836N17	transmembrane protein-coding	
chr7-8735.4.865569	-1.53342	1.142299	-1.3424	0.179466	0.981636	chr7	87336151	87336427	+	0	NA	intron (Nintron (N	9203	NR_015381	11257	Hs.274325	NM_007233	ENSG000002TP53TG1	LINC00099	TP53 target RNA	
chrX-135.4.865569	-1.53342	1.142299	-1.3424	0.179466	0.981636	chrX	1.35E+08	1.35E+08	+	0	NA	IntergeniLTR16A2 I	6632	NM_001078	8933	Hs.522788	NM_003928	ENSG000002RTL8C	CXX1 FAM1retrotransposon	protein-coding	
chr2-1275.9.682257	1.038512	0.773712	1.342246	0.179516	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	37748	NM_001141	75959	Hs.32995	NM_024545	ENSG000002SAP130	-	Sin3A associated protein-coding	
chr1-377.2.658844	-2.14374	1.597187	-1.3422	0.179532	0.981636	chr1	37709410	37710252	+	0	NA	TTS (NM_C TTS (NM_C	17315	NM_081110	55143	Hs.524571	NM_018101	ENSG000002CDC48	BOR BOR cell	dividing protein-coding	
chr10-145.6.145497	-1.30579	0.973191	-1.34176	0.179673	0.981636	chr10	14541170	14543234	+	0	NA	intron (NAluS SIN	-3660	NM_00132C	83641	Hs.446315	NM_031455	ENSG000002FAM107B	C10orf45 family	wiprotein-coding	
chr12-795.6.145497	-1.30579	0.973191	-1.34176	0.179673	0.981636	chr12	79562649	79562949	+	0	NA	IntergeniLTR12C LI	127781	NM_001354	5074	Hs.64313C	NM_002585	ENSG000002PAWR	PAR4 Par-pro-apopt	protein-coding	
chr15-225.6.145497	-1.30579	0.973191	-1.34176	0.179673	0.981636	chr15	22555243	22555442	+	0	NA	intron (Nintron (N	60464	NM_001367	8924	Hs.43489C	NM_004667	ENSG000002HERC2	D15F37S1 HECT	and protein-coding	
chr3-8751.6.145497	-1.30579	0.973191	-1.34176	0.179673	0.981636	chr3	8751669	8753082	+	0	NA	3' UTR (N3' UTR (N	16356	NM_001354	5021	Hs.2820	NM_000915	ENSG000002COXR	OT-R	oxytocin protein-coding	
chr6-8546.6.145497	-1.30579	0.973191	-1.34176	0.179673	0.981636	chr6	85468890	85470268	+	0	NA	intron (N2a LINE	19496	NM_00252E	4907	Hs.153952	NM_00252E	ENSG000002NT5E	CALJA CD75	protein-coding	
chr7-1054.6.145497	-1.30579	0.973191	-1.34176	0.179673	0.981636	chr7	10546889	10546889	+	0	NA	intron (Nintron (N	22153	NM_00131E	54517	Hs.520615	NM_019042	ENSG000002PUS7	IDDAB3	pseudouridine protein-coding	
chr2-1902.7.197193	1.199967	0.895023	1.34071	0.180015	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (Nintron (N	68443	NM_014362	26275	Hs.65668E	NM_014362	ENSG000002HIBCH	HIBYLCOAF-3	hydroxy protein-coding	
chr3-1701.7.374577	-1.17882	0.879345	-1.34056	0.180063	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (NAluSx1 SI	15959	NM_024947	80012	Hs.529592	NM_024947	ENSG000002PHC3	EDR3 HPH2	polyhomeoprotein-coding	
chr7-4465.6.677031	1.297941	0.968937	1.339551	0.180391	0.981636	chr7	44650188	44650408	+	0	NA	intron (Nintron (N	43671	NM_001003	4967	Hs.488181	NM_002541	ENSG000002CGDH	AKG8H Elk	oxoglutarate protein-coding	
chr12-245.11.841	-0.96167	0.717987	-1.3394	0.18044	0.981636	chr12	24828914	24829135	+	0	NA	intron (N(AAAT)n S	73198	NM_00117E	586	Hs.43899E	NM_005504	ENSG000002BCAT1	BCATC BC1	branched protein-coding	
chr6-5916.270.4006	0.356235	0.265994	1.339258	0.180487	0.981636	chr6	59163123	59163348	+	0	NA	IntergeniALR Alpha	-1201789	NR_132994	1.07E+08	Hs.56153E	NR_125727	ENSG000002LINC0068C	-	long intencRNA	
chr19-233.3.974273	1.625694	1.214002	1.33912	0.180532	0.981636	chr19	23341176	23342005	+	0	NA	IntergeniLIM3 LINE	53881	NM_00343C	7644	Hs.58834	NM_00343C	ENSG000002ZNF9F	HPF7 HTF1	zinc finger protein-coding	
chr1-9324.7.366719	-1.17729	0.879214	-1.33902	0.180564	0.981636	chr1	93241758	93243663	+	0	NA	intron (NTHEIB-int	61994	NM_001130C	343099	Hs.48287E	NM_20688E	ENSG000002CCDC18	NY-SAR-4	coiled-coil protein-coding	
chr10-111.7.366719	-1.17729	0.879214	-1.33902	0.180564	0.981636	chr10	1.14E+08	1.14E+08	+	0	NA	intron (NLM4c LIN	6464	NM_198514	374354	Hs.369924	NM_198514	ENSG000002NHLRC2	FINCA	NHL repeat protein-coding	
chr15-807.7.366719	-1.17729	0.879214	-1.33902	0.180564	0.981636	chr15	80790022	80796271	+	0	NA	intron (Nintron (N	13776	NM_00129E	57214	Hs.45908E	NM_01868E	ENSG000002CEMIP	CCSP1 HYE	cell migr protein-coding	
chr3-1944.7.366719	-1.17729	0.879214	-1.33902	0.180564	0.981636	chr3	1.94E+08	1.94E+08	+	0	NA	intron (Nintron (N	8986	NM_001367	79752	Hs.52960E	NM_024524	ENSG000002ATP13A3	AFURS1	ATPase 1	protein-coding
chr1-2256.7.246191	1.197221	0.894147	1.338954	0.180586	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (N2a LINE	27755	NM_01469E	9725	Hs.119387	NM_01469E	ENSG000002TMEM63A	KIAA0792	transmembrane protein-coding	
chr10-125.7.246191	1.197221	0.894147	1.338954	0.180586	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (NMIRb SINE	-18336	NM_147191	118856	Hs.314141	NM_147191	ENSG000002MMP21	HTX7 MMP-	matrix metalloproteinase	
chr16-156.7.246191	1.197221	0.894147	1.338954	0.180586	0.981636	chr16	15599400	15599865	+	0	NA	intron (Nintron (N	11463	NR_106761	1.02E+08	NR_106761	ENSG000002MIR6506	hsa-mir-61	microRNA ncRNA		
chr20-317.4.146943	-1.64328	1.22779	-1.3384	0.180765	0.981636	chr20	31793377	31794532	+	0	NA	exon (NM exon (NM	-25421	NM_03311E	85366	Hs.86092	NM_03311E	ENSG000002MYLK2	KMLC MLC	myosin liprotein-coding	
chr10-877.6.112215	-1.31384	0.981765	-1.33824	0.180817	0.981636	chr10	87747869	87748317	+	0	NA	TTS (NM_C TTS (NM_C	70138	NM_001321	84896	Hs.43594E	NM_03281C	ENSG000002ATAD1	AFDC1 FNF	ATPase f	protein-coding
chr11-781.6.112215	-1.31384	0.981765	-1.33824	0.180817	0.981636	chr11	78103382	78103748	+	0	NA	intron (NAluSp SIN	-23703	NM_001203	1.01E+08	Hs.40786C	NM_001203	ENSG000002NDUFC2-KC-	-	NDUFC2-kc	protein-coding
chr3-1967.7.382435	-1.18037	0.882034	-1.33823	0.18082	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	3' UTR (N3' UTR (N	-36252	NM_00130E	205564	Hs.24077C	NM_15269E	ENSG000002SEN5P	-	SUMO spec protein-coding	
chr6-2644.7.382435	-1.18037	0.882034	-1.33823	0.18082	0.981636	chr6	26443655	26444015	+	0	NA	intron (Nintron (N	3331	NM_006994	10384	Hs.167741	NM_006994	ENSG000002BTN3A3	BTf3 BTN2	butyrophilin protein-coding	
chr1-2354.7.179627	1.192361	0.891328	1.337735	0.180983	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	3' UTR (N3' UTR (N	40043	NM_15249C	148789	Hs.49814E	NM_15249C	ENSG000002B3GALNT2	B3GALNac-beta-1,3-	protein-coding	
chr8-1278.7.179627	1.192361	0.891328	1.337735	0.180983	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (NAluJo SIN	8057	NR_03160E	1E+08	NR_03160E	ENSG000002MIR1204	hsa-mir-1	microRNA ncRNA		
chr16-296.4.032978	1.637518	1.22419	1.337633	0.181016	0.981636	chr16	29682401	29683195	+	0	NA	intron (NLM5C LIN	3618	NR_13453E	23475	Hs.513484	NM_01429E	ENSG000002QPRT	HEL-5-90r	quinoline protein-coding	
chr11-691.8.103399	1.103399	0.824926	1.337574	0.181035	0.981636	chr11	69068089	69068164	+	0	NA	intron (Nintron (N	-14811	NR_036122	1E+08	NR_036122	ENSG000002MIR3164	-	microRNA ncRNA		
chr17-765.9.185669	1.091394	0.815988	1.337512	0.181055	0.981636	chr17	76347693	76347989	+	0	NA	intron (N2 LINE I	6075	NM_00276E	5635	Hs.77498	NM_00276E	ENSG000002PRPSAP1	PAP39	phosphoriprotein-coding	
chr1-2251.5.990022	1.321434	0.988009	1.337472	0.181069	0.981636	chr1	2.25E+08	2.25E+08	+	0	NA	intron (NLM1A4 LIN	239218	NM_00114E	127602	Hs.133977	NM_00137E	ENSG000002DNAH14	Clorf67 dynein	alpha protein-coding	
chr19-125.5.990022	1.321434	0.988009	1.337472	0.181069	0.981636	chr19	12224566	12225093	+	0	NA	IntergeniLTR19A LI	29814	NR_10417E	1E+08	Hs.66260E	NR_104179	LOC10028E-	-	uncharacterized RNA	
chr7-1492.5.990022	1.321434	0.988009	1.337472	0.181069	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	-6903	NR_03657E	155060	Hs.490512	NR_015357	ENSG000002LOC15506C-	-	AT894139 pseudo	
chr17-374.6.922282	-1.25217	0.936266	-1.33741	0.18109	0.981636	chr17	31794538	31794720	+	0	NA	intron (NAluS6 SI	12364	NM_00148E	6871	Hs.50066E	NM_00148E	ENSG000002TADA2A	ADA2 ADA2	transcriptase protein-coding	
chr2-4357.6.922282	-1.25217	0.936266	-1.33741	0.18109	0.981636	chr2	43570345	43570544	+	0	NA	exon (NM exon (NM	25530	NM_00108E	63892	Hs.369592	NM_00206E	ENSG000002THADA	ARMC13 G1THADA	arm protein-coding	
chr8-1184.7.341295	-1.18532	0.886539	-1.33702	0.181216	0.981636	chr8	11840352	11841040	+	0	NA	IntergeniIntergeni	27391	NM_00190E	1508	Hs.52089E	NM_00190E	ENSG000002CTSB	APPS CPSE	cathepsin protein-coding	
chr12-702.4.180225	-1.62994	1.219622	-1.33643	0.181409	0.981636	chr12	70285023	70285203	+	0	NA	intron (Nintron (N	41457	NM_00119E	4848	Hs.13335C	NM_01451E	ENSG000002CNOT2	CDC36 HSF	CCKR4-NOT	protein-coding
chr7-809.4.180225	-1.62994	1.219622	-1.33643	0.181409	0.981636	chr7	80911285	80912761	+	0	NA	intron (Nintron (N	7028	NM_00637E	10512	Hs.26910E	NM_00637E	ENSG000002SEMA3C	SEMAE Semaphorin	protein-coding	
chr1-1494.5.941024	1.325128	0.991682	1.336242	0.18147	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	22818	NM_001364	1.01E+08	NM_001364	ENSG000002NOTCH2NL2C-	N2N NOTCH	notch 2 protein-coding		
chr16-524.5.941024	1.325128	0.991682	1.336242	0.18147	0.981636	chr16	57458496	57458717	+	0	NA	intron (Nintron (N	-4073	NM_03294C	5432	Hs.79402	NM_002694	ENSG000002POLR2C	RPB3 RPB3	RNA polymerase protein-coding	
chr2-9237.16.10101	0.811921	0.608081	1.335218	0.181805	0.981636	chr2	92374494	92374819	+	0	NA	IntergeniALR Alpha	433523	NR_027714	440888	Hs.73023E	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	ps pseudo
chr7-1396.8.061771	-1.15429	0.864537	-1.33516	0.181825	0.981636	chr7															

chr19-517.8.564367	-1.08463	0.822258	-1.31909	0.187138	0.981636	chr19	51701858	51702599	+	0 NA	intron (Nintron (N	-8772 NR_10810C	1.02E+08	Hs. 64018E	NR_10810C	ENSG000003PACA6P	-	LINC01125	SPACA6P	ncRNA
chr19-287.7.162062	1.18464	0.898102	1.319049	0.187153	0.981636	chr19	2808862	2809297	+	0 NA	intron (Nintron (N	-10789 NM_001102	115196	Hs. 30704E	NR_15230E	ENSG000003ZNF554	-			zinc finger protein-coding
chr1-251.5.255865	1.374347	1.042665	1.31811	0.187467	0.981636	chr1	2513376	2514276	+	0 NA	intron (Nintron (N	12770 NM_01821E	55229	Hs. 26156	NM_01821E	ENSG000003PANK4	-			panthothenic acid synthase protein-coding
chr1-2124.5.255865	1.374347	1.042665	1.31811	0.187467	0.981636	chr1	12770	12770	+	0 NA	intron (N2 LINE N	11787 NM_01334E	29937	Hs. 461787	NM_01334E	ENSG000003NENF	VAMP-2 SCF1	neudesin	protein-coding	
chr1-1717.11.94732	0.913451	0.693046	1.318023	0.187496	0.981636	chr1	1.72E+08	1.72E+08	+	0 NA	intron (NAluSz SIN	5883 NR_033704	8674	Hs. 6651	NM_00376E	ENSG000003VAMP4	VAMP-4 VAV	vesicle protein-coding		
chr6-5956.109.3849	0.427096	0.324061	1.317951	0.18752	0.981636	chr6	59566217	59566459	+	0 NA	IntergeniALR/Alpha	-1604892 NR_132994	1.07E+08	Hs. 56153E	NR_12572E	ENSG000003LINC0068C			long intencRNA	
chr17-401.0.27083	0.998654	0.758023	1.317446	0.187689	0.981636	chr17	4014871	40149092	+	0 NA	intron (NAluSz6 S1	8399 NM_00735E	22794	Hs. 743287	NM_00735E	ENSG000003CAS3	BTZ MLN51	CASC3	exc protein-coding	
chr11-1119.9.869718	-1.00374	0.762193	-1.31691	0.187869	0.981636	chr11	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	15066 NM_00125E	143903	Hs. 503831	NM_17883E	ENSG000003LAYN			laylin protein-coding	
chr19-1316.0.078934	-1.32238	1.005278	-1.31544	0.188362	0.981636	chr19	13107771	13108017	+	0 NA	intron (Nintron (N	-5036 NM_00558E	4066	Hs. 46446	NM_00558E	ENSG000003LYL1	bHLHa18	LYL1	basiprotein-coding	
chr1-2075.7.376427	-1.16618	0.886828	-1.315	0.188508	0.981636	chr1	12025842	12025508	+	0 NA	intron (NAluSc8 S1	-20508 NM_001103	400745	Hs. 591522	NM_001103	ENSG000003SH2D5			SH2 domain protein-coding	
chr12-1272.7.376427	-1.16618	0.886828	-1.315	0.188508	0.981636	chr12	1.22E+08	1.22E+08	+	0 NA	intron (Nintron (N	-31962 NR_04538E	1.01E+08	Hs. 62425E	NR_04538E	ENSG000003CLIP1-AS1			CLIP1 antncRNA	
chr14-954.7.376427	-1.16618	0.886828	-1.315	0.188508	0.981636	chr14	95438694	95439146	+	0 NA	intron (Nintron (N	36915 NM_00136E	161176	Hs. 41502	NM_02463E	ENSG000003SYNE3	C14orf13E	spectrin	protein-coding	
chr4-1456.7.29472	1.199583	0.912329	1.314859	0.188557	0.981636	chr4	1.46E+08	1.46E+08	+	0 NA	exon (NM exon (NM	36517 NM_17883E	152485	Hs. 13391E	NM_17883E	ENSG000003ZNF827			zinc finger protein-coding	
chr11-466.8.97481	1.044929	0.795073	1.314257	0.18876	0.981636	chr11	46665302	46665799	+	0 NA	intron (Nintron (N	35069 NM_00430E	392	Hs. 13886C	NM_00430E	ENSG000003ARHGAP1	CDC42GAP Rho	GTPase	protein-coding	
chr19-636.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr19	630536	630735	+	0 NA	intron (Nintron (N	2902 NM_00503E	5442	Hs. 25411E	NM_00503E	ENSG000003POLRMT	APOLMT MRNA	polynprotein-coding		
chr19-125.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr19	12286883	12287408	+	0 NA	intron (Nintron (N	7467 NM_00135E	51710	Hs. 296731	NM_01626E	ENSG000003ZNF44	GIOT-2 KC	zinc finger protein-coding		
chr3-1604.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr3	1.6E+08	1.6E+08	+	0 NA	intron (Nintron (N	12886 NR_02952E	406951	NR_02952E	ENSG000003MIR16-2	MIRN16-2 microRNA	ncRNA			
chr3-1604.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr3	1.6E+08	1.6E+08	+	0 NA	intron (Nintron (N	16589 NR_02952E	406951	NR_02952E	ENSG000003MIR16-2	MIRN16-2 microRNA	ncRNA			
chr4-1031.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr4	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	28236 NM_00128E	1062	Hs. 75573	NM_00181E	ENSG000003CENPE	CENP-E KI	centromere protein-coding		
chr7-551E.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr7	55185174	55185698	+	0 NA	intron (Nintron (N	3513 NR_047551	1.01E+08	Hs. 72048E	NR_047551	ENSG000003CEGRF-AS1			EGFR antncRNA	
chr7-400.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	TTS (NM_C TTS (NM_C	39940 NM_02275E	64761	Hs. 12646	NM_02275E	ENSG000003PARP12	ARTD12 MS	poly(ADP-ribosyl) transferase protein-coding		
chr8-641E.5.393589	-1.36278	1.037459	-1.31357	0.18899	0.981636	chr8	6416339	6416538	+	0 NA	intron (Nintron (N	9285 NM_00132E	79648	Hs. 593807	NM_02459E	ENSG000003MCPH1	BRIT1 MC1	microcephalin protein-coding		
chr8-144E.5.248007	1.378034	0.949619	1.31289	0.18922	0.981636	chr8	1.45E+08	1.45E+08	+	0 NA	intron (NAluJb SIN	668 NM_00130E	80728	Hs. 14898E	NM_02525E	ENSG000003ARHGAP39	CrGAP Vil	Rho GTPase	protein-coding	
chr16-577.2.54048	1.194469	0.910564	1.311791	0.189591	0.981636	chr16	5779556	5779788	+	0 NA	intron (Nintron (N	7345 NM_00113C	3801	Hs. 23131	NM_00555E	ENSG000003KIFC3			kinesin f protein-coding	
chr10-608.5.230441	1.367702	1.042666	1.311743	0.189607	0.981636	chr10	60883060	60883629	+	0 NA	intron (Nintron (N	60841 NM_00135C	9886	Hs. 737374	NM_01483E	ENSG000003RHOBTB1			Rho related protein-coding	
chr16-196.5.230441	1.367702	1.042666	1.311743	0.189607	0.981636	chr16	19871240	19872158	+	0 NA	intron (Nintron (N	13149 NM_01623E	51704	Hs. 14868E	NM_01623E	ENSG000003GPRC5B	RAIG-2 RfG	protein protein-coding		
chr19-366.5.230441	1.367702	1.042666	1.311743	0.189607	0.981636	chr19	36345974	36347227	+	0 NA	intron (Nintron (N	-14882 NR_03827E	1.01E+08	Hs. 59515E	NR_03827E	ENSG000003LINC0066E			long intencRNA	
chr22-418.5.230441	1.367702	1.042666	1.311743	0.189607	0.981636	chr22	41873835	41875875	+	0 NA	intron (Nintron (N	-26089 NR_029507	407039	NR_029507	ENSG000003MIR33A	MIR33 MI	microRNA	ncRNA		
chr3-141E.5.230441	1.367702	1.042666	1.311743	0.189607	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (Nintron (N	6967 NR_13619E	646730	Hs. 570677	NR_13619E	ENSG000003LINC0261E			long intencRNA	
chr10-68.9.384688	-1.0504	0.80079	-1.31171	0.189619	0.981636	chr10	68067149	68067364	+	0 NA	TTS (NM_C TTS (NM_C	8027 NM_00127E	26091	Hs. 51891	NM_015601	ENSG000003HERC4			HECT and protein-coding	
chr5-466E.3.255832	1.782972	1.359443	1.311546	0.189673	0.981636	chr5	46665392	46666191	+	0 NA	IntergeniALR/Alpha	-969411 NM_02107E	348980	Hs. 35317E	NM_02107E	ENSG000003HCN1	BCNG-1 Bc	hyperpolarized protein-coding		
chr2-390E.5.898035	1.309796	0.998889	1.311253	0.189772	0.981636	chr2	39054512	39054719	+	0 NA	exon (NM exon (NM	65848 NM_00563E	6654	Hs. 70989E	NM_00563E	ENSG000003SOS1	GF1 G6F1	SOS Ras/Fra	protein-coding	
chr16-156.5.939175	1.309278	0.998615	1.311094	0.189826	0.981636	chr16	1561709	1561319	+	0 NA	intron (Nintron (N	-18103 NR_13517E	1.05E+08	Hs. 66332E	NR_13517E	ENSG000003LOC105371			uncharacterized protein-coding	
chr5-115E.7.343145	-1.17266	0.894559	-1.31088	0.189897	0.981636	chr5	1.16E+08	1.16E+08	+	0 NA	exon (NM exon (NM	-21331 NR_10987E	1.02E+08	Hs. 74534E	NR_10987E	ENSG000003LOC101927			uncharacterized ncRNA	
chr5-493E.56.21002	0.50863	0.388023	1.310822	0.189918	0.981636	chr5	49368045	49368499	+	0 NA	IntergeniALR/Alpha	1073016 NM_19844E	133418	Hs. 561411	NM_19844E	ENSG000003EMB	GP70	emigin	protein-coding	
chr1-212E.7.260344	1.128995	0.861294	1.310812	0.189921	0.981636	chr1	2.12E+08	2.12E+08	+	0 NA	intron (NMER5A DNA	30023 NM_01825E	55248	Hs. 44538E	NM_01825E	ENSG000003PACC1	Clorf75 Fro	topon acron protein-coding		
chr17-161E.8.615215	-1.0711	0.817319	-1.3105	0.190025	0.981636	chr17	16146274	16146589	+	0 NA	exon (NM exon (NM	6765 NR_14578E	1.1E+08	NR_14578E	ENSG000003SNORD163			small nucleolar RNA		
chr8-899E.8.615215	-1.0711	0.817319	-1.3105	0.190025	0.981636	chr8	89977405	89977701	+	0 NA	intron (Nintron (N	7118 NM_00248E	4683	Hs. 49220E	NM_00248E	ENSG000003NBN	AT-V1 AT	nibrin	protein-coding	
chr12-77E.6.129781	-1.30177	0.993597	-1.31016	0.190141	0.981636	chr12	77945851	77946199	+	0 NA	intron (Nintron (N	115131 NM_01490E	89795	Hs. 655301	NM_01490E	ENSG000003NAV3	POMF1 L1	neuron	protein-coding	
chr5-129E.6.129781	-1.30177	0.993597	-1.31016	0.190141	0.981636	chr5	1.3E+08	1.3E+08	+	0 NA	intron (Nintron (N	-102597 NR_12574E	1.04E+08	Hs. 62863E	NR_12574E	ENSG000003ADAMTS19			ADAMTS19 ncRNA	
chr1-206E.11.45859	0.474769	0.723593	1.309921	0.19026	0.981636	chr1	2.06E+08	2.06E+08	+	0 NA	intron (N2c LINE N	-49130 NM_01400E	9641	Hs. 32104E	NM_01400E	ENSG000003IKBKE	IKK-E IKK	inhibitor protein-coding		
chr5-112E.13.64923	0.853434	0.651613	1.309785	0.190289	0.981636	chr5	71204016	71204433	+	0 NA	intron (Nintron (N	3907 NR_02702E	728411	Hs. 88181	NM_207331	ENSG000003GUSP1			GUSB pseudo	
chr10-40E.15.45884	0.810488	0.618828	1.309714	0.190293	0.981636	chr10	40835250	40835639	+	0 NA	IntergeniALR/Alpha	1532601 NR_02438E	441666	Hs. 25572E	NR_02438E	ENSG000003LOC44166E			zinc finger pseudo	
chr3-1551.4.641866	1.506869	1.15058	1.309661	0.19031	0.981636	chr3	1.55E+08	1.55E+08	+	0 NA	intron (N2 LINE L	-71203 NR_12539E	1.02E+08	Hs. 12141E	NR_12539E	ENSG000003LINC01487			long intencRNA	
chr15-484.8.581933	-1.07649	0.822148	-1.30936	0.190413	0.981636	chr15	48494896	48495130	+	0 NA	intron (Nintron (N	150775 NM_00013E	2200	Hs. 59113E	NM_00013E	ENSG000003FBN1	ACM1C D	EC fibriillin	protein-coding	
chr20-59E.7.417566	-1.1621	0.886938	-1.30924	0.190454	0.981636	chr20	59034163	59034630	+	0 NA	3' UTR (N3' UTR (N	-2061 NM_00688E	514	Hs. 17753E	NM_00688E	ENSG000003ATP5F1E	ATP5E ATF	ATP synth	protein-coding	
chr17-31E.7.317721	-1.1809	0.902058	-1.30912	0.190493	0.981636	chr17	31939780	31939979	+	0 NA	intron (Nintron (N	2872 NM_01535E	23512	Hs. 46273E	NM_01535E	ENSG000003SUZ12	CHEY9 JJA	SUZ12		



chr9-6751	6.461186	1.213481	0.934493	1.298545	0.1941	0.981636	chr9	37524074	37525032	+	0	NA	intron (NL2b LINE	38605	NM_02249C	64425	Hs.591087NM_02249C	ENSG00000POLR1E	PAF53 PRF	RNA polyn	protein-coding		
chr9-1287	6.461186	1.213481	0.934493	1.298545	0.1941	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (intron (N	20121	NM_00633F	10444	Hs.14795C	00633F	ENSG00000ZER1	C9orf60 Zygy-11	reprotein-coding		
chr9-1354	6.461186	1.213481	0.934493	1.298545	0.1941	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	TTS (NM_C TTS (NM_C	9060	NM_01481I	9858	Hs.53326C	01481I	ENSG00000PPP1R26	KIAA0649 protein	protein-coding		
chr15-808	6.461893	-1.2005	0.924504	-1.29853	0.194105	0.981636	chr15	80882296	80883096	+	0	NA	intron (intron (N	-40623	NR_03039F	693132	NR_03039F	ENSG00000MIR549A	MIR549 Mimicr	ncRNA			
chr12-295	7.691931	1.112358	0.856869	1.298165	0.194231	0.981636	chr12	29342929	29343229	+	0	NA	intron (intron (N	-25231	NR_10386E	1.01E+08	Hs.298851NR_10386E	ENSG00000LOC10050E		uncharacterncRNA			
chr2-2025	7.691931	1.112358	0.856869	1.298165	0.194231	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (NLIPB LINE	11101	NM_00135E	79800	Hs.444982NM_024744	ENSG00000CCARF	ALS2CR8 AL	calcium	protein-coding		
chr6-3731	7.691931	1.112358	0.856869	1.298165	0.194231	0.981636	chr6	37312743	37314679	+	0	NA	intron (intron (N	-40272	NM_18307F	9025	Hs.485278NM_00395E	ENSG00000RN8F	hRN8	ring	protein-coding		
chr12-125	8.930534	1.038714	0.800348	1.297828	0.194347	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NL2a LINE	-18263	NR_135044	1.01E+08	Hs.53633E	NR_135044	ENSG00000LOC10050E		uncharacterncRNA		
chr1-6694	4.657397	-1.44379	1.112831	-1.2974	0.194494	0.981636	chr1	66942710	66943288	+	0	NA	intron (intron (N	12743	NM_001077	57708	Hs.605432NM_02094E	ENSG00000MIER1	ER1 MI-EFMIER1	tra	protein-coding		
chr11-311	4.657397	-1.44379	1.112831	-1.2974	0.194494	0.981636	chr1	3112735	3113690	+	0	NA	intron (MER4-int	52098	NM_001144	114879	Hs.436166NM_02089E	ENSG00000OSBPL5	OBPH1 ORF	sterol	protein-coding		
chr15-805	4.657397	-1.44379	1.112831	-1.2974	0.194494	0.981636	chr15	80914933	80916276	+	0	NA	intron (LTR85b LI	-73531	NR_03039F	693132	NR_03039F	ENSG00000MIR549A	MIR549 Mimicr	ncRNA			
chr17-597	4.657397	-1.44379	1.112831	-1.2974	0.194494	0.981636	chr17	59704123	59705108	+	0	NA	intron (NL2b LINE	2983	NM_016077	51651	Hs.12677	NM_016077	ENSG00000PTRH2	BIT1 CFAF	peptidyl-	protein-coding	
chr4-7705	4.657397	-1.44379	1.112831	-1.2974	0.194494	0.981636	chr4	77050100	77050925	+	0	NA	intron (intron (N	24398	NM_00134E	10983	Hs.518827NM_00683E	ENSG00000CCNI	CCNI1 CYC	cyclin I	protein-coding		
chr7-6749	4.657397	-1.44379	1.112831	-1.2974	0.194494	0.981636	chr7	64917106	64917881	+	0	NA	intron (intron (N	14251	NM_02114E	10793	Hs.520889NM_02114E	ENSG00000ZNF273	HZF9	zinc	protein-coding		
chr3-9081	6.494468	1.216154	0.937541	1.297174	0.194571	0.981636	chr3	90811765	90812886	+	0	NA	IntergeniALR/Alpha	1704704	NM_182644	2042	Hs.123642NM_00523E	ENSG00000EPHA3	EK4 ETK E	EPH	recep	protein-coding	
chr4-6601	6.494468	1.216154	0.937541	1.297174	0.194571	0.981636	chr4	6601980	6603256	+	0	NA	intron (intron (N	27429	NM_015274	23324	Hs.188464NM_015274	ENSG00000MAN2B2		mannoside	protein-coding		
chr9-1165	6.494468	1.216154	0.937541	1.297174	0.194571	0.981636	chr9	1.16E+08	1.16E+08	+	0	NA	intron (intron (N	36499	NR_103711	493913	Hs.728832NR_103711	ENSG00000PAPPA-AS1	DIPAS NCF	PAPPA	antncRNA		
chr1-124	3.15539	0.582805	0.49321	1.297081	0.194603	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alpha	2486311	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB1		emigin	pseudo		
chr1-8906	6.640235	-1.19881	0.924401	-1.29685	0.194682	0.981636	chr1	89061175	89063060	+	0	NA	intron (NLIMB3 LI	3091	NM_02020E	2633	Hs.62661	NM_02020E	ENSG00000GBP1		guanylate	protein-coding	
chr17-955	6.640235	-1.19881	0.924401	-1.29685	0.194682	0.981636	chr17	955924	956394	+	0	NA	intron (intron (N	23617	NM_02246E	64359	Hs.527989NM_02246E	ENSG00000CNXN	NRX TRG-4	nucleoc	protein-coding		
chr19-235	6.640235	-1.19881	0.924401	-1.29685	0.194682	0.981636	chr19	23392042	23393448	+	0	NA	intron (ALuSg SI	2726	NM_00343C	7644	Hs.58834	NM_00343C	ENSG00000ZNF91	HPF7 HTF1	zinc	protein-coding	
chr6-1105	6.640235	-1.19881	0.924401	-1.29685	0.194682	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (ALuSx SI	16873	NM_032194	84154	Hs.37226E	NM_032194	ENSG00000RPF2	BXDC1 ba	ribosome	protein-coding	
chr9-1105	6.640235	-1.19881	0.924401	-1.29685	0.194682	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	17521	NM_00113E	445815	Hs.591098NM_00720E	ENSG00000PALM2-AK	AKAP-2 AK	PALM2-AK	protein-coding		
chr9-1101	4.662555	-1.44612	1.115133	-1.29681	0.194696	0.981636	chr9	1.15E+08	1.15E+08	+	0	NA	intron (intron (N	53910	NM_00216C	3371	Hs.14325E	NM_00216C	ENSG00000TNC	150-225 T	enascin	protein-coding	
chr3-1797	4.883135	-1.5167	1.169756	-1.2966	0.194769	0.981636	chr3	1.8E+08	1.8E+08	+	0	NA	intron (intron (N	102007	NM_00394C	8975	Hs.175322NM_00394C	ENSG00000CUSP13	ISOT3 I	scubiquitin	protein-coding		
chr12-194	7.684073	1.114709	0.860011	1.296157	0.194921	0.981636	chr12	19465785	19465984	+	0	NA	intron (ALuSx SI	25285	NM_001267	121536	Hs.126497NM_15320E	ENSG00000AEBP2		AE	bindir	protein-coding	
chr15-654	6.453328	1.216331	0.938918	1.29546	0.195162	0.981636	chr15	65556818	65557239	+	0	NA	intron (NLIMC3 LI	26565	NM_01639E	51945	Hs.51297E	NM_01639E	ENSG00000HCB3	B-IND1 BI	3-hydroxy	protein-coding	
chr20-385	6.453328	1.216331	0.938918	1.29546	0.195162	0.981636	chr20	38566372	38566933	+	0	NA	intron (intron (N	-14545	NR_130907	149685	Hs.36802E	NM_17490E	ENSG00000ADIG	SMAF1	adipogeni	protein-coding	
chr1-1562	10.25327	0.993074	0.76663	1.295376	0.195191	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	exon (NM exon (NM	-2637	NM_00119E	11243	Hs.53047E	NM_00722I	ENSG00000PMF1		polymine	protein-coding	
chr4-1275	7.292298	-1.1896	0.918552	-1.29508	0.195291	0.981636	chr4	1.28E+08	1.28E+08	+	0	NA	3' UTR (3' UTR (N	39357	NM_00119C	10733	Hs.17205E	NM_014264	ENSG00000PLK4	MCCR2 SA	poly	like	protein-coding
chr1-1975	5.419013	-1.35132	1.04355	-1.29493	0.195346	0.981636	chr1	19795092	19795954	+	0	NA	intron (intron (N	3826	NM_00134E	255104	Hs.46672E	NM_18171E	ENSG00000TMC04		transmem	protein-coding	
chr1-150	5.419013	-1.35132	1.04355	-1.29493	0.195346	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (ALuSx5 SI	2174	NM_00127E	11311	Hs.44375E	NM_00725E	ENSG00000VPS45	HI H1VPS4	vacuolar	protein-coding	
chr19-125	5.419013	-1.35132	1.04355	-1.29493	0.195346	0.981636	chr19	12632513	12632887	+	0	NA	3' UTR (3' UTR (N	2780	NM_15335E	163049	Hs.72077E	NM_15335E	ENSG00000ZNF791		zinc	protein-coding	
chr3-1387	5.419013	-1.35132	1.04355	-1.29493	0.195346	0.981636	chr3	1.39E+08	1.39E+08	+	0	NA	intron (intron (N	-3559	NM_00125E	5291	Hs.23981E	NM_00621E	ENSG00000CIK3CB	P110BETA	phosphati	protein-coding	
chr8-478	5.419013	-1.35132	1.04355	-1.29493	0.195346	0.981636	chr8	47837742	47838572	+	0	NA	intron (intron (N	-99993	NM_00519E	1052	Hs.44082E	NM_00519E	ENSG00000CEBPD	C/EBP-delta	CCAAT	en	protein-coding
chr6-1324	5.19716	1.364632	1.053948	1.294781	0.195396	0.981636	chr6	1.32E+08	1.32E+08	+	0	NA	intron (THE1B LTF	19520	NM_00132E	8417	Hs.59314E	NM_00356E	ENSG00000STX7		syntxin	protein-coding	
chr18-752	6.606953	-1.20597	0.931709	-1.29437	0.195539	0.981636	chr18	75201839	75202038	+	0	NA	exon (NM exon (NM	3575	NM_00130E	284273	Hs.46543E	NM_17590E	ENSG00000ZADH2	PRG-3	zinc	bin	protein-coding
chr2-112	6.606953	-1.20597	0.931709	-1.29437	0.195539	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	intron (intron (N	-22931	NM_001137	84172	Hs.745127NM_019014	ENSG00000POLR1B	HPA135 RF	RNA polyn	protein-coding		
chr15-494	9.838287	-0.99882	0.772168	-1.29533	0.195828	0.981636	chr15	49485488	49485966	+	0	NA	3' UTR (3' UTR (N	62485	NM_00200E	2252	Hs.56726E	NM_00200E	ENSG00000FGF7	HBFG-7 K	fibroblast	protein-coding	
chr20-622	7.203201	1.184109	0.915545	1.293338	0.195894	0.981636	chr20	62272190	62273445	+	0	NA	intron (ALuJr SI	-30079	NM_17557E	11047	Hs.90107	NM_00700E	ENSG00000ADRM1	ARM-1 AR	adhesion	protein-coding	
chr5-559E	12.7519	-0.876	0.677668	-1.29267	0.196124	0.981636	chr5	55962763	55963594	+	0	NA	intron (intron (N	31830	NM_175767	3572	Hs.53208E	NM_002184	ENSG00000IL6ST	CD130 CD	130	interleuk	protein-coding
chr1-112E	4.64954	-1.4415	1.115234	-1.29255	0.196166	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (LJM4 LINE	41172	NM_024494	7482	Hs.25857E	NM_00418E	ENSG00000WNT2B	WNT13	Wnt	family	protein-coding
chr10-684	4.64954	-1.4415	1.115234	-1.29255	0.196166	0.981636	chr10	68464357	68465154	+	0	NA	intron (ALuSp SI	7218	NM_00108C	1763	Hs.53244E	NM_00108C	ENSG00000DNA2	DNA2L hd	hDNA	repl	protein-coding
chr16-374	4.64954	-1.4415	1.115234	-1.29255	0.196166	0.981636	chr16	3749818	3750399	+	0	NA	intron (ALuJb SI	-32584	NM_01629E	10131	Hs.30345	NM_01629E	ENSG00000TRAP1	HSP 75 HS	TNF	recep	protein-coding
chr18-471	4.64954	-1.4415	1.115234	-1.29255	0.196166	0.981636	chr18	47136460	47137106	+	0	NA	intron (intron (N	13717	NM_00131E	84064	Hs.465041NM_032124	ENSG00000HDHD2	HSP 70 HSP	70	recep	protein-coding	
chr8-170E	4.64954	-1.4415	1.115234	-1.29255	0.196166	0.981636	chr8	17086790	17087450	+	0	NA	intron (intron (N	59882	NR_14623C	286097	Hs.460359NM_18172E	ENSG00000MICU3	EFHA2	mitochond	protein-coding		
chr9-135E	6.071076	-1.32076	1.021977	-1.29236	0.196233	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (intron (N	91910	NM_015447	157922	Hs.52249E	NM_015447	ENSG00000CAMSAP1		calmodul	protein-coding	
chr6-124E	8.963816	1.040801	0.805547	1.292042	0.196343	0.981636	chr6	1.25E+08	1.25E+08	+	0	NA	intron (intron (N	-33257	NR_136734	154214	Hs.12876	NM_15255E	ENSG00000CRNF27	G6orf172	ring	protein-coding	
chr9-104E	8.963816	1.040801	0.805547	1.292042	0.196343	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (MTRb SINE										

chr3-138C.7.837883	-1.09359	0.855143	-1.27883	0.200955	0.981636	chr3	1.38E+08	1.38E+08	+	0	NA	intron (N)LP1B LIN	37165	NM_00117C	199221	Hs.35140C	NM_17354C	ENSG00000CDZIP1L	DZIP2 PKI DAZ	interprotein-coding
chr5-496C.215.915	0.339047	0.265125	1.278818	0.200961	0.981636	chr5	49630809	49632109	+	0	NA	IntergeniALR Alpha	809829	NM_198445	133418	Hs.561411	NM_198445	ENSG00000EMB	GP70	emigin protein-coding
chr1-551F.5.377873	-1.35844	1.062601	-1.27841	0.201105	0.981636	chr1	55160000	55160244	+	0	NA	intron (N)intron (N)	55242	NM_01530C	23358	Hs.47700E	NM_01530C	ENSG00000CASP24	-	ubiquitin protein-coding
chr12-104F.5.377873	-1.35844	1.062601	-1.27841	0.201105	0.981636	chr12	1.04E+08	1.04E+08	+	0	NA	intron (N)HAL LINE	26106	NM_01332C	29915	Hs.50655E	NM_01332C	ENSG00000HCFC2	HCF-2 HCF	cell protein-coding
chr15-74F.5.377873	-1.35844	1.062601	-1.27841	0.201105	0.981636	chr15	74638594	74638870	+	0	NA	intron (N)L2c LINE	23738	NM_001113C	1198	Hs.51179C	NM_001129C	ENSG00000CLK3	PHCLK3 PE CDC	like protein-coding
chr3-131C.5.377873	-1.35844	1.062601	-1.27841	0.201105	0.981636	chr3	1.31E+08	1.31E+08	+	0	NA	intron (N)intron (N)	16246	NM_01406E	28990	Hs.10087E	NM_01406E	ENSG00000ASTE1	HT001	asteroid protein-coding
chr7-152F.5.377873	-1.35844	1.062601	-1.27841	0.201105	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (N)AluS6 SI	141929	NM_17060E	58508	Hs.64712C	NM_02123C	ENSG00000KMT2C	HALR KLEF	lysine m protein-coding
chr1-1504I.10.67358	0.939861	0.735669	1.277559	0.201405	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	exon (NM)exon (NM)	29872	NM_001271	80222	Hs.288974	NM_02515C	ENSG00000TARS2	CXPD21 T	threonyl- protein-coding
chr9-999F.10.67358	0.939861	0.735669	1.277559	0.201405	0.981636	chr9	99952192	99952546	+	0	NA	intron (N)LP1A3 LIN	45715	NM_01791E	55014	Hs.704031	NM_01791E	ENSG00000CSTX17	-	syntaxin protein-coding
chr21-41F.5.171736	1.357816	1.062875	1.277493	0.201428	0.981636	chr21	41809882	41810448	+	0	NA	non-codiron-codir	-43113	NM_02063E	54101	Hs.51731C	NM_02063E	ENSG00000RIPK4	ANKK2 ANK	receptor protein-coding
chr16-167I.9.444688	0.993344	0.777749	1.277203	0.201531	0.981636	chr16	1670773	16710220	+	0	NA	intron (N)intron (N)	-7383	NM_14457C	90861	Hs.513261	NM_14457C	ENSG00000JPT2	C16orf34 Jupit	r protein-coding
chr12-105F.6.443621	1.204961	0.943546	1.277056	0.201583	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (N)MIRb SINE	22319	NM_01643C	51228	Hs.38125E	NM_01643C	ENSG00000GLTP	-	glycolipin protein-coding
chr17-60F.6.443621	1.204961	0.943546	1.277056	0.201583	0.981636	chr17	60690000	60691272	+	0	NA	intron (N)LM1B2 LIN	12785	NM_00132C	54828	Hs.65502E	NM_01767E	ENSG00000BCAS3	GAOB1 MA	BCAS3 mic protein-coding
chr19-162F.6.443621	1.204961	0.943546	1.277056	0.201583	0.981636	chr19	1622032	1622231	+	0	NA	exon (NM)exon (NM)	-16669	NM_00683C	10975	Hs.8372	NM_00683C	ENSG00000UCR11	071008DC	ubiquinol protein-coding
chr7-152I.4.52841	-0.80815	0.633091	-1.27651	0.201774	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	exon (NM)exon (NM)	59141	NM_00135C	55193	Hs.18992C	NM_01816E	ENSG00000PBRM1	BAF180 PF	polybrom protein-coding
chr3-526E.9.051247	-1.02125	0.800287	-1.27611	0.201918	0.981636	chr3	52626259	52626657	+	0	NA	intron (N)intron (N)	-12	NR_029501	40718	Hs.029501	ENSG00000MIR27A	hsa-mir-27A	microRNA ncRNA	
chr19-13F.13.58978	-0.85888	0.673267	-1.27569	0.202066	0.981636	chr19	13836372	13836687	+	0	NA	promoter-promoter	9067	NR_10678E	1072E+08	NR_10678E	ENSG00000MIR6728	hsa-mir-6728	microRNA ncRNA	
chr1-885F.6.657801	-1.18815	0.93159	-1.2754	0.202166	0.981636	chr1	8857258	8857789	+	0	NA	IntergeniMERS5 DNA	1443476	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG00000LOC44166E	-	zinc fing pseudo
chr10-40E.27.92521	0.622803	0.488365	1.275283	0.202209	0.981636	chr10	40924037	40925101	+	0	NA	IntergeniALR Alpha	3757	NM_03243C	84446	Hs.182081	NM_03243C	ENSG00000CBRSK1	hSAD1	BR serine protein-coding
chr19-55F.5.947033	1.205323	1.02376	1.275029	0.202299	0.981636	chr19	55287631	55287878	+	0	NA	intron (N)intron (N)	11205	NM_00104C	222962	Hs.4302	NM_15324E	ENSG00000SLC29A4	ENT4 PMA1	solute c protein-coding
chr7-529F.6.502326	1.213175	0.95163	1.274838	0.202367	0.981636	chr7	5293633	5294663	+	0	NA	intron (N)AluJr SIN	11259	NM_00117C	192111	Hs.10255E	NM_13857E	ENSG00000PGAM5	BXLBV68	PGAM fam protein-coding
chr12-13F.7.863307	-1.08622	0.852179	-1.27464	0.202436	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	3' UTR (N)3' UTR (N)	-25472	NM_00226E	3837	Hs.53279E	NM_00226E	ENSG00000KPMB1	IMB1 IPO1	karyopher protein-coding
chr17-47F.7.863307	-1.08622	0.852179	-1.27464	0.202436	0.981636	chr17	47623882	47625012	+	0	NA	IntergeniAluSx SIN	13189	NM_00111E	10801	Hs.44093C	NM_00664C	ENSG00000SEPTIN9	AF17q25 S	septin 9 protein-coding
chr17-77F.6.689636	-1.06106	0.832983	-1.27381	0.202731	0.981636	chr17	77488255	77488609	+	0	NA	intron (N)intron (N)	15258	NM_17385A	254428	Hs.20274	NM_17385A	ENSG00000SLC41A1	MgtE	solute c protein-coding
chr1-2057I.9.493685	0.991636	0.778784	1.273314	0.202907	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	exon (NM)exon (NM)	27583	NM_02477E	79830	Hs.47124E	NM_02477E	ENSG00000ZMYM1	MYM	zinc fing protein-coding
chr1-351F.7.81246	-1.10117	0.864925	-1.27314	0.20297	0.981636	chr1	35106854	35107082	+	0	NA	intron (N)AluY SINE	-19689	NM_00598E	6615	Hs.48029	NM_00598E	ENSG00000SNA11	SLUGH2 S	snail fam protein-coding
chr20-49F.9.902597	-1.09355	0.859001	-1.27305	0.203001	0.981636	chr20	49963143	49963439	+	0	NA	IntergeniAluY SINE	14507	NM_00104C	51752	Hs.666524	NM_01644E	ENSG00000CERAP1	A-LAP AL	endoplasm protein-coding
chr5-967F.4.667105	-1.42598	1.121325	-1.27169	0.203484	0.981636	chr5	96792940	96793937	+	0	NA	exon (NM)exon (NM)	-42749	NR_02989E	442893	NR_02989E	ENSG00000MIR151A	MIR151 MI	microRNA ncRNA	
chr8-140F.6.667105	-1.42598	1.121325	-1.27169	0.203484	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (N)AluS6 SI	8347	NM_032637	6502	Hs.23348	NM_00598E	ENSG00000SKP2	FBL1 FBX1	S-phase k protein-coding
chr5-361F.7.327429	-1.12694	0.919674	-1.27156	0.203531	0.981636	chr5	36160321	36160595	+	0	NA	intron (N)L2c LINE	16866	NR_13296E	192217	Hs.472491	NR_13296E	ENSG00000CXCT2P1	CXCT2P	3-oxoacid pseudo
chr1-395F.7.650792	1.112275	0.874905	1.27131	0.203618	0.981636	chr1	39531557	39531907	+	0	NA	intron (N)intron (N)	35907	NR_104387	6872	Hs.15856C	NM_00460C	ENSG00000TAF1	BA2R CCG1	TATA-box protein-coding
chrX-714F.5.189302	1.368411	1.076498	1.271169	0.203668	0.981636	chrX	71401994	71402534	+	0	NA	intron (N)AluS6 SI	15420	NM_00135E	10587	Hs.44343C	NM_00644C	ENSG00000TXNRD2	GCCD5 SEL	thioredox protein-coding
chr22-19F.5.187452	1.350351	1.062462	1.203741	0.981636	chr22	19116875	19117392	+	0	NA	intron (N)LM14 LINE	1994	NM_001001	861	Hs.149261	NM_00175A	ENSG00000CRUX1	AML1 AML1	RUNX fam protein-coding	
chr21-34F.7.912304	-1.08325	0.85246	-1.27074	0.203822	0.981636	chr21	34886445	34886966	+	0	NA	intron (N)CpG	33023	NR_03370A	8674	Hs.6651	NM_00376E	ENSG00000VAMP4	VAMP-4 V	vesicle e protein-coding
chr1-1717I.11.19559	0.905328	0.712828	1.270051	0.204067	0.981636	chr1	1.72E+08	1.72E+08	+	0	NA	intron (N)intron (N)	-19466	NR_03961E	1.01E+08	NR_03961E	ENSG00000MIR4423	MIR-4423	microRNA ncRNA	
chr1-851I.4.504142	1.433575	1.128766	1.270037	0.204071	0.981636	chr1	85113587	85115070	+	0	NA	intron (N)LM1E1 LIN	31495827	31496618	117583	Hs.65738E	NM_05717E	ENSG00000PARD3B	ALS2 PBR19	par-3 fan protein-coding
chr10-314F.6.591238	-1.20268	0.947035	-1.26994	0.204107	0.981636	chr10	2.05E+08	2.05E+08	+	0	NA	intron (N)intron (N)	21782	NM_00130E	26896	Hs.387804	NM_00256E	ENSG00000PABPC1	PAB1 PABF	poly(A) t protein-coding
chr2-2047F.6.591238	-1.20268	0.947035	-1.26994	0.204107	0.981636	chr2	1.01E+08	1.01E+08	+	0	NA	intron (N)MERE1E LI	8033	NM_01763E	54795	Hs.467101	NM_01763E	ENSG00000TRPM4	LTrpC4 PF	transient protein-coding
chr8-949F.9.468262	0.987644	0.77823	1.269901	0.204409	0.981636	chr8	94932124	94941324	+	0	NA	intron (N)intron (N)	12654	NM_00113E	94241	Hs.492261	NM_03328E	ENSG00000TP53INP1	SIP1 TP53	tumor p protein-coding
chr11-66F.7.641084	1.102644	0.869228	1.268533	0.204608	0.981636	chr11	66238920	66239126	+	0	NA	intron (N)intron (N)	-18271	NM_001134	64837	Hs.28079E	NM_02282E	ENSG00000KLC2	-	kinesin l protein-coding
chr17-57F.7.641084	1.102644	0.869228	1.268533	0.204608	0.981636	chr17	57300557	57300801	+	0	NA	intron (N)THE1B LTF	43660	NM_170721	124540	Hs.65892E	NM_13896E	ENSG00000CMS12	MSI2H	musashi f protein-coding
chr22-29F.7.641084	1.102644	0.869228	1.268533	0.204608	0.981636	chr22	29678271	29678490	+	0	NA	intron (N)intron (N)	-41623	NM_182527	164633	Hs.64360E	NM_182527	ENSG00000CABP7	CALN2	calcium t protein-coding
chr15-68F.8.280506	1.057039	0.833682	1.267917	0.204828	0.981636	chr15	68092311	68092810	+	0	NA	intron (N)MLT1A0 LI	37984	NM_00132C	8554	Hs.16245E	NM_01616E	ENSG00000PIAS1	DDXB1 GE	protein-coding
chr5-179F.8.280506	1.057039	0.833682	1.267917	0.204828	0.981636	chr5	1.79E+08	1.79E+08	+	0	NA	3' UTR (N)3' UTR (N)	22548	NM_014594	30832	Hs.27232E	NM_014594	ENSG00000ZNF354C	KID3	zinc fing protein-coding
chr3-157F.9.094237	-1.00726	0.794822	-1.26728	0.205056	0.981636	chr3	15733172	15733385	+	0	NA	intron (N)intron (N)	23269	NM_00119E	23243	Hs.33523E	NM_01519E	ENSG00000ANKRD28	PITK PPP1	ankyrin l protein-coding
chr1-538F.6.476902	1.207519	0.953019	1.267046	0.205139	0.981636	chr1	53854263	53855136												



chr3-4841 5.768169	1.246327	0.993386	1.254626	0.209615	0.981636	chr3	48411578	48412477	+	0 NA	intron (Nintron (N	17436 NM_002673	5364 Hs. 476209NM_002673	ENSG00000PLXNB1	PLEXIN-B1plexin B1protein-coding
chr14-31:8.237517	1.045772	0.833789	1.25424	0.209755	0.981636	chr14	31307462	31307904	+	0 NA	intron (Nintron (N	-99890 NM_015382	25831 Hs. 708017NM_015382	ENSG00000HECTD1	EULR HECT domain protein-coding
chr1-227:5.734887	1.243329	0.991421	1.254088	0.20981	0.981636	chr1	2.28E+08	2.28E+08	+	0 NA	3' UTR (N3' UTR (N	36432 NR_036753	401983 Hs. 681816NR_036753	ZNF847P	gml27 zinc finger pseudo
chr2-426:6.965632	1.12576	0.897714	1.25403	0.209831	0.981636	chr2	42682719	42683597	+	0 NA	intron (Nintron (N	81103 NM_148962	165140 Hs. 168439NM_148962	ENSG00000CXER1	GPCR GPR10xoeicos protein-coding
chr4-324:6.965632	1.12576	0.897714	1.25403	0.209831	0.981636	chr4	3240088	3240451	+	0 NA	3' UTR (N3' UTR (N	-4100 NM_00133C	345222 Hs. 442291NM_001012	ENSG00000MSANTD1	Corf444 Myb/SANT protein-coding
chr5-149:6.965632	1.12576	0.897714	1.25403	0.209831	0.981636	chr5	1.5E+08	1.5E+08	+	0 NA	intron (NLINE2z/LI	9608 NM_001271	1452 Hs. 529862NM_001892	ENSG00000CCSNK1A1	CK1 CK1a casein k protein-coding
chr8-518:6.965632	1.12576	0.897714	1.25403	0.209831	0.981636	chr8	51831102	51831319	+	0 NA	intron (NAluSz SIN	-21765 NM_144651	137902 Hs. 444882NM_144651	ENSG00000PDXNL	PMR1 PM1peroxidase protein-coding
chr20-266:64.62055	0.448571	0.357773	1.253786	0.20992	0.981636	chr20	26605426	26607869	+	0 NA	IntergeniALR/Alph	-397414 NR_04009E	ENSG00000MIR663AHC	MIR663A lncRNA	
chr1-112:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr1	1.13E+08	1.13E+08	+	0 NA	TTS (NM_TTS (NM_I	32529 NM_024494	7482 Hs. 258577NM_00418E	ENSG00000WNT2B	WNT13 Wnt family protein-coding
chr10-14:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr10	14551100	14552394	+	0 NA	intron (Nintron (N	-3110 NM_00132C	83641 Hs. 446311NM_03145E	ENSG00000FAM107B	C10orf45 family wiprotein-coding
chr17-45:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr17	45281501	45282497	+	0 NA	intron (Nintron (N	-19905 NM_00132C	124783 Hs. 412711NM_15234E	ENSG00000SPATA32	AEP2 C17c spermatog protein-coding
chr19-914:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr19	9142010	9142541	+	0 NA	intron (Nintron (N	1878 NR_10243E	57693 Hs. 465822NM_02093E	ENSG00000ZNF317	zinc finger protein-coding
chr2-875:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr2	87526558	87527310	+	0 NA	Intergeni Intergeni	56984 NR_14646C	112597 Hs. 652166NR_02420A	ENSG00000CYTOR	C2orf59 lyctoskelcRNA
chr2-1731:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr2	1.73E+08	1.73E+08	+	0 NA	intron (Nintron (N	87219 NM_00136E	51776 Hs. 444511NM_01665E	ENSG00000MAP3K20	AZK CNM6 mitogen- protein-coding
chr2-199:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr2	2E+08	2E+08	+	0 NA	intron (Nintron (N	-12129 NM_00136E	79568 Hs. 154494NM_02452C	ENSG00000MAIP1	C2orf47 matrix A protein-coding
chr20-49:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr20	49267003	49268038	+	0 NA	intron (Nintron (N	10537 NM_02103E	51769 Hs. 371794NM_02103E	ENSG00000ZNF1	zinc finger protein-coding
chr4-119:5.880469	-1.23399	0.984257	-1.25373	0.20994	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (NHAL1 LINE	9340 NM_001371396			
chr5-491:11.21131	0.902138	0.720013	1.252947	0.210225	0.981636	chr5	49134512	49136221	+	0 NA	IntergeniALR/Alph	1305922 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70 embigin protein-coding
chr11-124:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr11	12484936	12486262	+	0 NA	intron (NLMC3 LIN	108028 NM_01822E	55742 Hs. 432914NM_01822E	ENSG00000PARVA	CH-ILKBP parvin al protein-coding
chr15-80:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr15	80802077	80804203	+	0 NA	intron (Nintron (N	23770 NM_00129E	57214 Hs. 459085NM_01868E	ENSG00000CEMIP	CCSP1 HYE cell migr protein-coding
chr19-12:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr19	12699211	12699744	+	0 NA	3' UTR (N3' UTR (N	-2846 NM_032301	84261 Hs. 515154NM_032301	ENSG00000FBXW9	Fbw9 MEC-F-box anc protein-coding
chr2-745:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr2	74546958	74547986	+	0 NA	intron (NLS LINE C	-1548 NM_001197	1796 Hs. 103854NM_001381	ENSG00000DOK1	P62DOK p docking p protein-coding
chr3-102:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr3	10252671	10252870	+	0 NA	intron (NAluJo SIN	4311 NM_01476C	9797 Hs. 475401NM_01476C	ENSG00000TATDN2	TatD DNase protein-coding
chr4-267:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr4	26777407	26778034	+	0 NA	IntergeniALuSz6 SI	82524 NR_13467E	1.05E+08 Hs. 548856NR_134673	STIM2-AS1	STIM2 antncRNA
chr8-122:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr8	12209487	12210892	+	0 NA	Intergeni Intergeni	-16056 NR_14887E	65333 Hs. 458413NM_001137	ENSG00000FAM86B2	family wiprotein-coding
chr9-33:5.921609	-1.22783	0.980526	-1.25222	0.210491	0.981636	chr9	33127081	33127522	+	0 NA	intron (Nintron (N	18609 NR_162131	1.13E+08 NR_162131	MIR12117	microRNA ncRNA
chr1-149:8.170954	1.04112	0.831681	1.251826	0.210633	0.981636	chr1	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	-2466 NM_00585C	10262 Hs. 516166NM_00585C	ENSG00000SF3B4	AFD1 Hsh4splicing protein-coding
chr2-13:8.170954	1.04112	0.831681	1.251826	0.210633	0.981636	chr2	1.32E+08	1.32E+08	+	0 NA	intron (Nintron (N	16029 NR_00329C	347918 Hs. 122115NM_18261E	ENSG00000EP400P1	EP400NL EP400 psc pseudo
chr3-988:8.170954	1.04112	0.831681	1.251826	0.210633	0.981636	chr3	98800689	98801240	+	0 NA	intron (Nintron (N	37657 NM_00132E	10402 Hs. 148711NM_00610C	ENSG00000ST3GAL6	SIAT10 ST13 beta- protein-coding
chr19-57:7.740929	1.109612	0.88688	1.25114	0.210883	0.981636	chr19	57879690	57879889	+	0 NA	intron (NLS LINE L	9248 NM_001144	730051 Hs. 634148NM_001144	ENSG00000ZNF814	zinc finger protein-coding
chr1-155:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr1	1.55E+08	1.55E+08	+	0 NA	intron (Nintron (N	8648 NM_00125E	51043 Hs. 729275NM_00125E	ENSG00000ZBTB7B	CKROX THF zinc finger protein-coding
chr1-168:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr1	1.68E+08	1.68E+08	+	0 NA	intron (Nintron (N	14623 NR_03170Z	1E+08 NR_03170Z	ENSG00000MIR1255B	MIR1255B-microRNA ncRNA
chr13-98:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr13	98385392	98385771	+	0 NA	intron (Nintron (N	136544 NM_00357E	8428 Hs. 508514NM_00357E	ENSG00000STK24	HEL-S-95 serine/t protein-coding
chr16-47:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr16	47688973	47689473	+	0 NA	intron (Nintron (N	-169358 NR_11065C	1.02E+08 Hs. 589404NR_11065C	ENSG00000CLINC0213C	long intncRNA
chr18-20:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr18	20972945	20973521	+	0 NA	intron (NLSa LINE	138530 NM_00540E	6193 Hs. 306307NM_00540E	ENSG00000ROCK1	P160ROCK Rho assoc protein-coding
chr19-20:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr19	20027064	20021640	+	0 NA	intron (NMER30 DNA	18103 NM_001077	9120 Hs. 306296NR_03319E	ENSG00000ZNF682	BC39498 zinc finger protein-coding
chr19-564:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr19	56445847	56446388	+	0 NA	intron (NMER33 DNA	31228 NM_001321	63934 Hs. 676605NM_02210E	ENSG00000ZNF667	MIPU1 zinc finger protein-coding
chr9-116:6.97349	1.123167	0.89775	1.25109	0.210902	0.981636	chr9	1.16E+08	1.16E+08	+	0 NA	intron (N(GAAA)n S	58946 NM_002581	5069 Hs. 643596NM_002581	ENSG00000PAPPA	ASBAB27 pappalysiprotein-coding
chr1-1851:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr1	1.85E+08	1.85E+08	+	0 NA	intron (NLP1A7 LIN	40672 NM_01767E	54823 Hs. 134188NM_01767E	ENSG00000SWT1	Corf26 ESWT1 RNA protein-coding
chr16-164:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr16	1643760	1645278	+	0 NA	intron (Nintron (N	29879 NM_02082E	57585 Hs. 603676NM_02082E	ENSG00000CRAMP1	CRAMP1L cramped c protein-coding
chr16-29:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr16	29684589	29685060	+	0 NA	intron (Nintron (N	5644 NR_13453E	23475 Hs. 513484NM_01429E	ENSG00000QPRT	HEL-S-90 quinoline protein-coding
chr16-47:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr16	47599067	47591966	+	0 NA	intron (NLS2c LINE	130135 NM_001031	5257 Hs. 78060 NM_00029E	ENSG00000PHK6	phosphory protein-coding
chr22-49:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr22	49866839	49867653	+	0 NA	intron (NLM4 LINE	13402 NM_01483E	9889 Hs. 475205NM_01483E	ENSG00000ZBED4	zinc finger protein-coding
chr4-866:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr4	86650231	86651194	+	0 NA	intron (NLM4A LIN	56397 NM_00626A	5783 Hs. 436142NM_00626A	ENSG00000PTPN13	FAP-1 PNF protein t protein-coding
chr7-643:5.742745	1.240117	0.991321	1.250974	0.210944	0.981636	chr7	64330804	64332128	+	0 NA	intron (NLM1 LINE	17505 NM_00117C	728927 Hs. 386162NM_00117C	ENSG00000ZNF736	zinc finger protein-coding
chr3-114:6.642085	-1.18434	0.946919	-1.25073	0.211032	0.981636	chr3	1.14E+08	1.14E+08	+	0 NA	intron (NLM1E3G LI	19167 NM_02463E	79691 Hs. 477162NM_02463E	ENSG00000QTRT2	QTRTD1 queuine t protein-coding
chr9-108:6.642085	-1.18434	0.946919	-1.25073	0.211032	0.981636	chr9	1.09E+08	1.09E+08	+	0 NA	intron (NKangalla L	12207 NM_006687	10881 Hs. 12353C	ENSG00000ACTL7A	actin lik protein-coding
chr1-173:5.913751	-1.22595	0.980461	-1.25038	0.211162	0.981636	chr1	1.74E+08	1.74E+08	+	0 NA	intron (NLP1A6 LIN	6574 NM_001171	91687 Hs. 531856NM_03331E	ENSG00000CCENPL	C1orf155 centromer protein-coding
chr11-12:5.913751	-1.22595	0.980461	-1.25038	0.211162	0.981636	chr11	1.28E+08	1.28E+08	+	0 NA	3' UTR (N3' UTR (N	62318 NM_00523E	2113 Hs. 369438NM_00523E	ENSG00000ETS1	ETS-1 EWS ETS protc protein-coding
chr12-46:5.913751	-1.22595	0.980461	-1.25038	0.211162	0.981636	chr12	46211975	46212489	+	0 NA	intron (Nintron (N	54284 NM_00127E	81539 Hs. 53377C	ENSG00000SLC38A1	ATA1 NAT2 solute c protein-coding
chr12-96:5.913751	-1.22595	0.980461	-1.25038	0.211162	0.981636	chr12	96273138	96273387	+	0 NA	IntergeniALuSx SIN	17764 NM_00130E	2004 Hs. 46523 NM_00523C	ENSG00000CELK3	ERP NET ETS trans protein-coding
chr12-13:5.913751	-1.22595	0.980461	-1.25038	0.211162	0.981636	chr12	1.33E+08	1.33E+08	+						

chr3-1411 6.948067	1.117926	0.90039	1.241602	0.214384	0.981636	chr3	14112352	14113341	+	0 NA	3' UTR (N3' UTR (N	12024 NM_001098	131474 Hs. 51781ENM_14463ENS	ENSG000004CHCHD4	MIA40 TIM	coiled-coiled protein-coding	
chr6-264 6.948067	1.117926	0.90039	1.241602	0.214384	0.981636	chr6	26430379	26430790	+	0 NA	TTS (NR_C TTS (NR_C	9193 NR_027795	54718 Hs. 729655ENM_02401ENS	ENSG000004BTN2A3P	BTN2.3 BTB	butyrophilic pseudo	
chr5-1284 8.365903	-1.01983	0.821621	-1.24124	0.214518	0.981636	chr5	1.28E+08	1.28E+08	+	0 NA	intron (NMIRB SINE	130942 NM_001995	2201 Hs. 519294NM_001995ENS	ENSG000004FBN2	CCA DA9 E	fibriin protein-coding	
chr12-10 9.563551	-0.95918	0.727871	-1.24106	0.214583	0.981636	chr12	1.04E+08	1.04E+08	+	0 NA	TTS (NM_C TTS (NM_C	211330 NM_003211	6996 Hs. 584809NM_003211ENS	ENSG000004TDG	hTDG	thymine I protein-coding	
chr5-4892 59.41868	0.45026	0.362862	1.240856	0.214659	0.981636	chr5	48929424	48930402	+	0 NA	IntergeniALR/Alpha	1511375 NM_198445	133418 Hs. 561411NM_198445ENS	ENSG000004EMB	GP70	thymine I protein-coding	
chr6-751 7.117407	-1.11921	0.902499	-1.24012	0.21493	0.981636	chr6	75105487	75107064	+	0 NA	intron (Nintron (N	22507 NR_145788	1.1E+08	SNORD156	-	small nucsnoRNA	
chr6-158 8.332622	-1.02528	0.826811	-1.24004	0.214961	0.981636	chr6	1.59E+08	1.59E+08	+	0 NA	intron (Nintron (N	4556 NM_001291	6993 Hs. 445999NM_00651ENS	ENSG000004DYNLT1	CW-1 TCT	dynein I protein-coding	
chr6-354 9.588975	-0.95328	0.768866	-1.23985	0.215032	0.981636	chr6	35468561	35473568	+	0 NA	TTS (NM_C TTS (NM_C	556 NR_106961	1.02E+08	NR_106961ENS	ENSG000004MIR7111	hsa-mir-7	microRNA ncRNA
chr6-419 8.358045	-1.01844	0.821461	-1.23979	0.215053	0.981636	chr6	41924526	41924937	+	0 NA	intron (N2b LINE	3232 NM_004055	705 Hs. 106888NM_004055ENS	ENSG000004BYSL	BYSTIN E	rbystin I protein-coding	
chr19-27 24.81644	0.626768	0.505571	1.239724	0.215078	0.981636	chr19	27008326	27009103	+	0 NA	IntergeniALR/Alpha	-784717 NR_146735	1.02E+08	Hs. 567934NR_110687ENS	ENSG000004LOC101927	-	uncharactercna
chr15-805 8.373761	-1.02123	0.824019	-1.23933	0.215224	0.981636	chr15	80024123	80926037	+	0 NA	intron (Nintron (N	64739 NR_126325	23184 Hs. 578455NM_015154ENS	ENSG000004MESD	BOCA MES	mesoderm protein-coding	
chr5-132 8.373761	-1.02123	0.824019	-1.23933	0.215224	0.981636	chr5	1.32E+08	1.32E+08	+	0 NA	intron (Nintron (N	13689 NR_106888	1.02E+08	NR_106888ENS	ENSG000004MIR6830	hsa-mir-6	microRNA ncRNA
chr17-29 9.947284	0.936547	0.755863	1.239043	0.21533	0.981636	chr17	29632044	29632644	+	0 NA	exon (NM exon (NM	-10921 NM_032854	84940 Hs. 143045NM_032854ENS	ENSG000004COR06	-	coronin f protein-coding	
chr4-754 5.847188	-1.24241	1.002867	-1.23886	0.215397	0.981636	chr4	81745839	81746338	+	0 NA	intron (Nintron (N	162811 NM_001263	1040 Hs. 654895NM_001263ENS	ENSG000004CDS1	CDS 1	CDP-diacyl protein-coding	
chr1-1247 19.12583	0.692645	0.55947	1.238038	0.215702	0.981636	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alpha	3187382 NR_003955	647121 Hs. 697682NR_003955ENS	ENSG000004EMBP1	-	emigin f pseudo	
chr12-10 5.776027	1.243107	1.004408	1.237651	0.215846	0.981636	chr12	1.06E+08	1.06E+08	+	0 NA	intron (Nintron (N	16824 NM_001288	255394 Hs. 696047NM_152777ENS	ENSG000004TCP11L2	-	t-complex protein-coding	
chr2-48 5.776027	1.243107	1.004408	1.237651	0.215846	0.981636	chr2	48478073	48478490	+	0 NA	intron (NMLTIC LTF	37512 NM_001193	129285 Hs. 654615NM_152994ENS	ENSG000004PPP1R21	CCDC128 K	protein I protein-coding	
chr16-28 8.186669	1.036636	0.837685	1.237502	0.215901	0.981636	chr16	28391588	28391862	+	0 NA	promoter-promoter-	-674 NR_106922	1.02E+08	NR_106922ENS	ENSG000004MIR6862	hsa-mir-6	microRNA ncRNA
chr7-752 8.186669	1.036636	0.837685	1.237502	0.215901	0.981636	chr7	752242	752458	+	0 NA	intron (NCPG	-24674 NM_001164	5575 Hs. 520851NM_002733ENS	ENSG000004PRKAR1B	PRKAR1	protein I protein-coding	
chr19-181 6.981348	1.12051	0.905469	1.237492	0.215904	0.981636	chr19	18127899	18129444	+	0 NA	intron (Nintron (N	-24919 NR_162071	5296 Hs. 371344NM_005027ENS	ENSG000004PIK3R2	MPPH MPPI	phosphoin protein-coding	
chr19-18 6.981348	1.12051	0.905469	1.237492	0.215904	0.981636	chr19	18877024	18877255	+	0 NA	TTS (NM_C TTS (NM_C	19492 NM_001492	2657 Hs. 412355NM_001492ENS	ENSG000004GDF1	CERS1 CHI	growth di protein-coding	
chr22-31 6.981348	1.12051	0.905469	1.237492	0.215904	0.981636	chr22	31267809	31269463	+	0 NA	intron (Nintron (N	20252 NM_016733	3985 Hs. 474599NM_005566ENS	ENSG000004LIMK2	-	LIM domain protein-coding	
chr1-205 6.932351	1.123142	0.908025	1.236907	0.216122	0.981636	chr1	2.36E+08	2.36E+08	+	0 NA	intron (Nintron (N	-92454 NM_001098	2786 Hs. 159711NM_004488ENS	ENSG000004CNG4	-	G protein-coding	
chr3-102 6.932351	1.123142	0.908025	1.236907	0.216122	0.981636	chr3	10239150	10239430	+	0 NA	intron (N2 LINE L	-9169 NM_014766	9797 Hs. 475401NM_014766ENS	ENSG000004TADN2	-	TadD NAs protein-coding	
chr9-1104 7.914154	-1.07101	0.865995	-1.23673	0.216186	0.981636	chr9	1.1E+08	1.1E+08	+	0 NA	intron (NLMES3Cz L	-86625 NM_001286	255220 Hs. 147064NM_001000ENS	ENSG000004TXNDC8	SPTRX-3 S	thioedox protein-coding	
chr19-211 7.152539	-1.09966	0.889271	-1.23658	0.216241	0.981636	chr19	21185479	21186240	+	0 NA	3' UTR (N3' UTR (N	43819 NM_133475	170959 Hs. 156255NM_133475ENS	ENSG000004ZNF431	-	zinc fing protein-coding	
chr7-17 8.270798	1.048069	0.847759	1.236282	0.216354	0.981636	chr7	74119684	74120517	+	0 NA	intron (NMLTID LTF	26883 NM_001204	3984 Hs. 647035NM_002314ENS	ENSG000004LIMK1	LIMK LIML	domain protein-coding	
chr8-254 3.171148	-1.6957	1.371769	-1.23614	0.216407	0.981636	chr8	25463936	25465963	+	0 NA	intron (Nintron (N	5716 NM_152562	157313 Hs. 33366 NM_152562ENS	ENSG000004CDA2	PPP1R81 F	cell divi protein-coding	
chr17-61 6.510184	1.209883	0.979003	1.235832	0.216521	0.981636	chr17	61920131	61920347	+	0 NA	intron (NAluSq10 S	7743 NM_020748	57508 Hs. 279644NM_020748ENS	ENSG000004INTS2	INT2 KIAI	integratc protein-coding	
chr17-37 12.1174	-0.85702	0.693616	-1.23558	0.216613	0.981636	chr17	37557619	37557942	+	0 NA	intron (NAluJr SIN	5163 NM_080555	11276 Hs. 594647NM_007247ENS	ENSG000004SYNRG	APIGBP1 S	ynnergim protein-coding	
chr22-41 5.701606	1.240391	1.004445	1.234902	0.216867	0.981636	chr22	41877473	41878504	+	0 NA	exon (NM exon (NM	-22956 NR_029507	407039	NR_029507ENS	ENSG000004MIR33A	MIR33 MI	microRNA ncRNA
chr3-515 5.701606	1.240391	1.004445	1.234902	0.216867	0.981636	chr3	51565559	51567008	+	0 NA	intron (NAluSp SIN	15194 NM_001322	23132 Hs. 105399NM_015100ENS	ENSG000004RAD54L2	ARIP4 HSF	RAD54 l1 protein-coding	
chr1-851 7.111399	-1.1045	0.894471	-1.23481	0.216902	0.981636	chr1	85186330	85186641	+	0 NA	intron (NLIAP3 LIN	14531 NM_032184	84144 Hs. 533855NM_032184ENS	ENSG000004SYDE2	-	synase c protein-coding	
chr11-281 7.111399	-1.1045	0.894471	-1.23481	0.216902	0.981636	chr11	28112308	28112591	+	0 NA	intron (Nintron (N	4061 NM_152636	196074 Hs. 243322NM_152636ENS	ENSG000004METTL15	METT5D1	methyltrc protein-coding	
chr5-3884 7.111399	-1.1045	0.894471	-1.23481	0.216902	0.981636	chr5	38848197	38849772	+	0 NA	intron (NLMES3G LI	3072 NM_001322	9180 Hs. 120655NM_003999ENS	ENSG000004OSMR	IL-31R	beoncostat1 protein-coding	
chr2-75 8.356195	-1.02962	0.8341	-1.23441	0.21705	0.981636	chr2	75492977	75493259	+	0 NA	3' UTR (N3' UTR (N	-30950 NR_110281	1.02E+08	Hs. 671111NR_110281ENS	ENSG000004LOC101927	-	uncharactercna
chr19-134 5.750603	1.236833	1.002318	1.233972	0.217213	0.981636	chr19	13451545	13451944	+	0 NA	intron (NMLT1J2 LI	54716 NM_001127	773 Hs. 501632NM_000068ENS	ENSG000004CACNA1A	APCA BI C	alcium v protein-coding	
chr19-16 5.750603	1.236833	1.002318	1.233972	0.217213	0.981636	chr19	16680519	16681135	+	0 NA	intron (Nintron (N	19688 NM_024074	79041 Hs. 436068NM_024074ENS	ENSG000004TMEM38A	TRIC-A T	transcript protein-coding	
chr20-62 5.750603	1.236833	1.002318	1.233972	0.217213	0.981636	chr20	62327165	62328905	+	0 NA	intron (Nintron (N	4522 NR_039915	1.01E+08	NR_039915ENS	ENSG000004MIR4758	-	microRNA ncRNA
chr5-694 10.43102	-0.94474	0.765851	-1.23359	0.217357	0.981636	chr5	69415090	69415355	+	0 NA	TTS (NM_C TTS (NM_C	106 NM_001038	153562 Hs. 657687NM_144724ENS	ENSG000004MARVELD2	DFNB49 MA	MARVEL dc protein-coding	
chr1-130 7.085976	-1.11271	0.902017	-1.23359	0.217358	0.981636	chr1	1309913	1310112	+	0 NA	intron (Nintron (N	1415 NM_153339	126789 Hs. 400655NM_153339ENS	ENSG000004PUSL1	-	pseudour1 protein-coding	
chr12-10 7.085976	-1.11271	0.902017	-1.23359	0.217358	0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	13146 NM_001276	23603 Hs. 330384NM_014327ENS	ENSG000004COR10C	HCRN4	coronin I protein-coding	
chr12-111 8.245375	1.04347	0.846065	1.233322	0.217456	0.981636	chr12	1.12E+08	1.12E+08	+	0 NA	exon (NM exon (NM	-22059 NM_000699	217 Hs. 604551NM_000699ENS	ENSG000004ALDH2	ALDH-E2 A	aldehyde protein-coding	
chr1-703 7.144681	-1.09804	0.890523	-1.23303	0.217564	0.981636	chr1	70322616	70322942	+	0 NA	intron (NAluSp SIN	31943 NM_030816	81573 Hs. 744989NM_030816ENS	ENSG000004ANKRD13C	dJ67H15.	ankyrin I protein-coding	
chr12-121 7.144681	-1.09804	0.890523	-1.23303	0.217564	0.981636	chr12	1.21E+08	1.21E+08	+	0 NA	3' UTR (N3' UTR (N	30772 NM_00127C	10645 Hs. 297343NM_006544ENS	ENSG000004CAMK2	CAMKK CAM	calcium/c protein-coding	
chr19-19 7.144681	-1.09804	0.890523	-1.23303	0.217564	0.981636	chr19	19022036	19022631	+	0 NA	intron (Nintron (N	11184 NR_147913	10147 Hs. 77876 NM_014884ENS	ENSG000004SUGP2	SFRS14 S	SRP and protein-coding	
chr20-39 7.144681	-1.09804	0.890523	-1.23303	0.217564	0.981636	chr20	3921619	3921831	+	0 NA	intron (NAluSz SIN	-4162 NR_031722	1E+08	NR_031722ENS	ENSG000004MIR103B2	MIR103-2	microRNA ncRNA
chr10-40 17.71234	0.747912	0.606598	1.232962	0.21759	0.981636	chr10	40476615	40477209	+	0 NA	IntergeniALR/Alpha	1780316 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B ps pseudo	
chr10-87 5.898035	-1.22199	0.991107	-1.23295	0.217594	0.981636	chr10	87520816	87521279	+	0 NA	exon (NM exon (NM	13214 NM_001178	9562 Hs. 121269NM_004897ENS	ENSG000004M1NPP1	HIPER1 M	multiple protein-coding	
chr18-70 5.898035	-1.22199	0.991107	-1.23295	0.217594	0.981636	chr18	70104566	70104779	+	0 NA	intron (NLIAP8A LI	101015 NM_001318	25914 Hs. 654809NM_173633ENS	ENSG000004RTTN	MSSP	rotatin protein-coding	
chr2-189 5.898035	-1.22199	0.991107	-1.23295	0.217594	0.981636	chr2	1.9E+08	1.9E+08	+	0 NA	TTS (NM_C TTS (NM_C	-5082 NM_144708	150709 Hs. 60772 NM_144708ENS	ENSG000004ANKAR	-	ankyrin f protein-coding	
chr22-45 5.898035	-1.22199	0.991107	-1.23295	0.217594	0.981636	chr22	45699029	45699438	+	0 NA	intron (Nintron (N	19347 NM_013236	25814 Hs. 475122NM_013236ENS	ENSG000004ATXN10	E46L HUM	ataxin I protein-coding	
chr3-283 5.898035	-1.22199	0.991107	-1.23295	0.217594	0.981636	chr3	28353066	28353354	+	0 NA	intron (NCharlie2E	4061 NM_001324	152098 Hs. 510633NM_001040ENS	ENSG000004ZCWFW2	ZCW2	zinc fing protein-coding	
chr4-47 5.898035	-1.22199	0.991107	-1.23295	0.217594	0.981636												



chr17-197 11.72361	0.864689	0.70837	1.220675	0.222209	0.981636	chr17	19796132	19797296	+	0 NA	intron (NLTR22C0 I	-48416 NM_000691	218 Hs. 531682NM_000691	ENSG000004ALDH3A1	ALDH3 ALI	aldehyde protein-coding
chr12-105 5.144278	-1.28624	1.053743	-1.220664	0.222224	0.981636	chr12	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	387882 Hs. 368936NM_207377	ENSG000004C12orf75	AGD3 OCC	-chromosom protein-coding	
chr8-4241 5.144278	-1.28624	1.053743	-1.220664	0.222224	0.981636	chr8	42418391	42418740	+	0 NA	intron (NAluSz SIN	26685 NM_005662	7419 Hs. 699301NM_005662	ENSG000004VDAC3	HD-VDAC3 voltage c	protein-coding
chr8-1234 5.144278	-1.28624	1.053743	-1.220664	0.222224	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (Nintron (N	20622 NM_018024	55093 Hs. 18029 NM_018024	ENSG000004WDYHV1	C8orf32	WDYHV motprotein-coding
chr21-29 5.931317	-1.21362	0.994648	-1.220115	0.222408	0.981636	chr21	429043974	29044726	+	0 NA	intron (NLMC5 LIN	19682 NM_006447	10600 Hs. 99819 NM_006447	ENSG000004USP16	UBP-MUB	ubiquitin protein-coding
chr6-289 5.931317	-1.21362	0.994648	-1.220115	0.222408	0.981636	chr6	28908334	28908785	+	0 NA	intron (Nintron (N	12029 NR_104117	414760 Hs. 211006NR_104117	ENSG000004HCG14	dJ111M5.4HLA	complncRNA
chr8-589 5.931317	-1.21362	0.994648	-1.220115	0.222408	0.981636	chr8	58938007	58938948	+	0 NA	intron (NLM3 LINE C	180670 NM_014722	9760 Hs. 491806NM_014722	ENSG000004TOX	TOX1	thymocyte protein-coding
chr13-421 8.120106	1.031803	0.845694	1.220666	0.22244	0.981636	chr13	42159969	42160168	+	0 NA	exon (NM exon (NM	22010 NM_001204	160851 Hs. 630383NM_152911	ENSG000004DGKH	DGKeta	diacylglycerol protein-coding
chr12-121 8.683257	0.981202	0.804367	1.219844	0.222524	0.981636	chr12	1.22E+08	1.22E+08	+	0 NA	intron (NAluY SINE	12003 NM_00108C	144404 Hs. 644504NM_00108C	ENSG000004TMEM120B	-	transmemt protein-coding
chr19-366 8.683257	0.981202	0.804367	1.219844	0.222524	0.981636	chr19	368761307	36878331	+	0 NA	exon (NM exon (NM	25598 NM_001242	25850 Hs. 362324NM_003411	ENSG000004ZNF345	HZF10	zinc fing protein-coding
chr2-1311 8.683257	0.981202	0.804367	1.219844	0.222524	0.981636	chr2	1.31E+08	1.31E+08	+	0 NA	intron (NHALb LIN	23428 NM_00130C	55041 Hs. 469944NM_017951	ENSG000004PLEKH2	EV22	pleckstrin protein-coding
chr3-433 8.683257	0.981202	0.804367	1.219844	0.222524	0.981636	chr3	43303771	43304609	+	0 NA	intron (Nintron (N	17650 NM_017711	54861 Hs. 476052NM_017711	ENSG000004SNRR	HSNFRK	SNF relat protein-coding
chr1-1541 5.13642	-1.28409	1.05374	-1.2186	0.222995	0.981636	chr1	1.54E+08	1.54E+08	+	0 NA	promoter-promoter-	-734 NM_001278	7170 Hs. 535581NM_152263	ENSG000004TPM3	CAPM1 CFI	tropomyosin protein-coding
chr4-705 5.13642	-1.28409	1.05374	-1.2186	0.222995	0.981636	chr4	7059111	7059516	+	0 NA	3' UTR (N3' UTR (N	8751 NM_02519E	80273 Hs. 443723NM_02519E	ENSG000004GRPEL1	GrpE HMGCGrpE	like protein-coding
chr18-318 5.169701	-1.27477	1.046208	-1.21847	0.223045	0.981636	chr18	31898006	31898500	+	0 NA	intron (NMER2 DNA	44875 NM_014931	22878 Hs. 202001NM_014931	ENSG000004TRAPPC8	GSGL HsT2	traffickiprotein-coding
chr7-8402 5.169701	-1.27477	1.046208	-1.21847	0.223045	0.981636	chr7	84024203	84024524	+	0 NA	intron (NAluSz6 SI	170516 NM_00608C	10371 Hs. 252451NM_00608C	ENSG000004SEMA3A	COLL1 HHI	semaphoriprotein-coding
chr5-129 5.962749	-1.22109	1.002229	-1.21838	0.22308	0.981636	chr5	1.3E+08	1.3E+08	+	0 NA	intron (NAluSc SIN	-137202 NR_125744	1.04E+08 Hs. 628631NR_125744	ENSG000004ADAMTS19-	ADAMTS19	ncRNA
chr1-264 5.962749	-1.22109	1.002229	-1.21838	0.22308	0.981636	chr1	26453392	26454014	+	0 NA	intron (NAluJb SIN	13834 NR_125952	1.02E+08 Hs. 663251NR_125952	LOC101928-	-	uncharactncRNA
chr12-22 8.367753	-1.0088	0.828255	-1.21798	0.223233	0.981636	chr12	22531035	22532033	+	0 NA	intron (Nintron (N	12663 NM_00128C	9847 Hs. 271014NM_014802	ENSG000004C2CD5	CDP138 KIC2	calcit protein-coding
chr12-76 8.367753	-1.0088	0.828255	-1.21798	0.223233	0.981636	chr12	76073112	76073813	+	0 NA	intron (Nintron (N	11223 NM_00130C	4673 Hs. 524599NM_004537	ENSG000004NAP1L1	NAP1 NAP1	nucleoson protein-coding
chr11-65 6.924493	1.125873	0.924726	1.21752	0.223406	0.981636	chr11	65282887	65283150	+	0 NA	intron (NAluJr4 SI	21056 NM_002688	23649 Hs. 201897NM_002688	ENSG000004POLA2	-	DNA polyn protein-coding
chr16-22 6.924493	1.125873	0.924726	1.21752	0.223406	0.981636	chr16	22371134	22371550	+	0 NA	intron (Nintron (N	3277 NM_001802	1039 Hs. 513433NM_001802	ENSG000004CDR2	CDR62 Yo	cerebell protein-coding
chr18-54 5.890177	-1.21986	1.002323	-1.21704	0.22359	0.981636	chr18	54283204	54283751	+	0 NA	intron (NMIR SINE	13903 NM_001351	11201 Hs. 438533NM_007191	ENSG000004POLI	RAD30B RADNA	polyn protein-coding
chr19-101 5.161843	-1.27264	1.046202	-1.21644	0.223817	0.981636	chr19	10127739	10128541	+	0 NA	IntergeniAluSz SIN	-8244 NM_00375E	8666 Hs. 529051NM_00375E	ENSG000004EIF3G	EIF3-P42 eukaryotiprotein-coding	
chr3-105 5.161843	-1.27264	1.046202	-1.21644	0.223817	0.981636	chr3	1.06E+08	1.06E+08	+	0 NA	intron (N(AT)n Sin	192314 NM_001627	214 Hs. 591293NM_001627	ENSG000004ALCAM	CD166 MEM	activatc protein-coding
chr4-127 5.161843	-1.27264	1.046202	-1.21644	0.223817	0.981636	chr4	1272905	1272910	+	0 NA	exon (NM exon (NM	7026 NM_006342	10460 Hs. 104011NM_006342	ENSG000004TACC3	ERIC-1 EF	transforn protein-coding
chr7-121 5.161843	-1.27264	1.046202	-1.21644	0.223817	0.981636	chr7	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	-157955 NM_016087	51384 Hs. 272371NM_016087	ENSG000004WNT16	-	Wnt fami protein-coding
chr9-167 5.161843	-1.27264	1.046202	-1.21644	0.223817	0.981636	chr9	16775541	16776125	+	0 NA	intron (Nintron (N	49019 NR_151723	1.11E+08 Hs. 609211NR_151723	ENSG000004BNC2-AS1	BNC2	antncRNA
chr19-507 7.50336	1.053994	0.866459	1.216438	0.223818	0.981636	chr19	5078508	5079548	+	0 NA	intron (Nintron (N	109915 NM_00137C	23030 Hs. 654811NM_015011	ENSG000004KDM4B	JMJD2B TI	lysine d protein-coding
chr3-5674 7.528784	1.058997	0.87103	1.215798	0.224062	0.981636	chr3	56749086	56750490	+	0 NA	intron (Nintron (N	25929 NM_00112E	50650 Hs. 474002NM_019551	ENSG000004ARHGEF3	GEF3 STA3	Rho guaniprotein-coding
chr1-168 3.734854	1.504004	1.237169	1.215682	0.224106	0.981636	chr1	1682612	1683551	+	0 NA	intron (NAluXs1 SI	9714 NM_00111C	728661 Hs. 655251NM_00111C	ENSG000004SLC35E2B	SLC35E2	solute c protein-coding
chr7-6071 3.734854	1.504004	1.237169	1.215682	0.224106	0.981636	chr7	60712859	60713751	+	0 NA	IntergeniALR/Alph	2590751 NR_00395E	643955 Hs. 583301NR_00395E	ENSG000004ZNF73P	ZNF733	zinc fing pseudo
chr2-9721 8.309048	-1.02122	0.840138	-1.21554	0.224159	0.981636	chr2	97219642	97219814	+	0 NA	intron (NAluSp SIN	-58976 NR_103732	1.01E+08 Hs. 732611NR_103732	LOC100505C-	-	uncharactncRNA
chr17-404 10.45173	0.894378	0.735813	1.215496	0.224177	0.981636	chr17	40443944	40457865	+	0 NA	intron (Nintron (N	7454 NM_001552	3487 Hs. 462999NM_001552	ENSG000004IGFBP4	BP-4 HT21	insulin l protein-coding
chr5-2747 10.45173	0.894378	0.735813	1.215496	0.224177	0.981636	chr5	27473395	27479165	+	0 NA	intron (NMER61-int	3988 NR_03884F	643401 Hs. 533211NR_03884F	ENSG000004PURPL	LINC01021 p53	upregncRNA
chr6-751 9.663396	-0.94507	0.777714	-1.21519	0.224293	0.981636	chr6	75163156	75164257	+	0 NA	intron (Nintron (N	-34924 NR_145788	1.1E+08 NR_145788	SNORD156	-	small ncsoRNA
chr6-108 8.334471	-1.01424	0.834686	-1.21511	0.224324	0.981636	chr6	1.08E+08	1.08E+08	+	0 NA	intron (NLIPA8 LIN	15806 NM_00130C	8724 Hs. 12102 NM_003791	ENSG000004CSNX3	Grd19 MCC	sorting r protein-coding
chr6-144 8.334471	-1.01424	0.834686	-1.21511	0.224324	0.981636	chr6	1.44E+08	1.44E+08	+	0 NA	intron (NLIPA11 LI	56455 NM_132778	1.07E+08 NR_132778	SNORA98	-	small ncsoRNA
chr17-824 6.930501	1.109805	0.913965	1.214275	0.224643	0.981636	chr17	82485425	82486630	+	0 NA	intron (Nintron (N	27286 NM_01233C	26502 Hs. 256521NM_01233C	ENSG000004NARF	TOP2	nuclear r protein-coding
chr17-61 8.408893	-1.00474	0.827862	-1.21365	0.224881	0.981636	chr17	61993882	61994099	+	0 NA	intron (Nintron (N	-66008 NM_00133C	57508 Hs. 279641NM_020741	ENSG000004INTS2	INT2 KIA1	integratc protein-coding
chr19-41 8.408893	-1.00474	0.827862	-1.21365	0.224881	0.981636	chr19	41224327	41225297	+	0 NA	intron (Nintron (N	-1943 NM_00127E	558 Hs. 590977NM_001691	ENSG000004AXL	ARK JTK11 AXL	recep protein-coding
chr6-157 42.86859	0.495293	0.4082	1.213359	0.224993	0.981636	chr6	1.57E+08	1.57E+08	+	0 NA	intron (Nintron (N	13170 NM_018452	729515 Hs. 157211NM_018452	ENSG000004TMEM242	BM033 C6c	transmemt protein-coding
chr11-66 8.691115	0.979139	0.80703	1.213263	0.225029	0.981636	chr11	66537335	66537565	+	0 NA	3' UTR (N3' UTR (N	8598 NM_20734C	254359 Hs. 209587NM_20734C	ENSG000004ZDHHC24	-	zinc fing protein-coding
chr17-48 8.691115	0.979139	0.80703	1.213263	0.225029	0.981636	chr17	48056509	48058156	+	0 NA	3' UTR (N3' UTR (N	8973 NM_003204	4779 Hs. 514284NM_003204	ENSG000004NFEZL1	LCR-F1 NFC	nuclear l protein-coding
chr6-159 8.691115	0.979139	0.80703	1.213263	0.225029	0.981636	chr6	1.6E+08	1.6E+08	+	0 NA	3' UTR (N3' UTR (N	1251 NM_001024	6648 Hs. 457041NM_000631	ENSG000004SOD2	IPO-B IPC	superoxid protein-coding
chr7-139 8.691115	0.979139	0.80703	1.213263	0.225029	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (Nintron (N	43440 NM_00136E	6916 Hs. 520757NM_001061	ENSG000004TBXAS1	BDPLT14 C	thromboxe protein-coding
chr16-307 7.477936	1.049052	0.864673	1.213236	0.22504	0.981636	chr16	30751699	30757289	+	0 NA	TTS (NM_C TTS (NM_C	-4868 NM_001207	9810 Hs. 65238 NM_014771	ENSG000004RNF40	BRE1B RBF	ring fing protein-coding
chr18-797 7.477936	1.049052	0.864673	1.213236	0.22504	0.981636	chr18	79717515	79717908	+	0 NA	intron (Nintron (N	36281 NM_001202	9150 Hs. 465491NM_004711	ENSG000004CTDP1	CCFDN FCF	CTD phosph protein-coding
chr4-8884 7.477936	1.049052	0.864673	1.213236	0.22504	0.981636	chr4	88850	89231	+	0 NA	TTS (NM_C TTS (NM_C	-35436 NR_11052E	255403 Hs. 636631NM_001031	ENSG000004ZNF718	-	zinc fing protein-coding
chr7-2774 7.477936	1.049052	0.864673	1.213236	0.22504	0.981636	chr7	27749343	27749813	+	0 NA	intron (NTiger15e	9483 NM				

chr4-5542	10.10914	-0.89967	0.748796	-1.20149	0.229559	0.981636	chr4	55420365	55421735	+	0	NA	intron (AluSx SIN	25093	NM_018475	55858	Hs.479766	NM_018475	ENSG000002TMEM165	CDG2K FT2	transmem protein-coding	
chr12-163	8.253233	1.040979	0.866455	1.201423	0.229587	0.981636	chr12	1632712	1633219	+	0	NA	intron (intron (N	3734	NM_032642	81029	Hs.306051	NM_030777	ENSG000002WNT5B	-	Wnt fam1 protein-coding	
chr2-6919	9.624107	-0.93875	0.781572	-1.20111	0.229711	0.981636	chr2	69194621	69194863	+	0	NA	intron (AluSz SIN	91060	NR_036073	1E+08	NR_036073	ENSG000002MIR3126	mir-3126	microRNA ncRNA		
chr11-301	3.70943	1.494846	1.244816	1.200857	0.229807	0.981636	chr11	1.02E+08	1.02E+08	+	0	NA	intron (intron (N	-34547	NM_178127	253935	Hs.318373	NM_178127	ENSG000002ANGPTL5	-	angiopoietin protein-coding	
chr9-341C	7.46222	1.053966	0.878007	1.200457	0.229981	0.981636	chr9	34109158	34109793	+	0	NA	intron (intron (N	17223	NM_015397	25853	Hs.49375C	NM_015397	ENSG000002DCAF12	CT102 K1A DDB1	and protein-coding	
chr10-414	13.94569	0.781436	0.651146	1.200093	0.230103	0.981636	chr10	41438956	41440503	+	0	NA	IntergeniALR/Alph	928316	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000002LOC441666	-	zinc fing pseudo	
chr1-779C	4.676813	-1.40578	1.171477	-1.20001	0.230136	0.981636	chr1	77903520	77904158	+	0	NA	intron (AluJb SIN	-14300	NR_103535	374987	Hs.632414	NM_19934E	ENSG000002NEXN-AS1	C1orf118	NEXN anticnRNA	
chr22-38E	3.742712	1.498738	1.248988	1.199962	0.230154	0.981636	chr22	38635703	38636592	+	0	NA	intron (intron (N	20245	NM_00101E	646851	Hs.542707	NM_00101E	ENSG000002FAM227A	-	family wiprotein-coding	
chr3-6907	10.11699	-0.90085	0.750746	-1.19994	0.230162	0.981636	chr3	69070773	69070972	+	0	NA	intron (AluJo SIN	9493	NM_19819E	9039	Hs.15432C	NM_00396E	ENSG000002CUBA3	NAE2 UBE1	ubiquitin protein-coding	
chr1-178E	10.43416	0.888988	0.740888	1.198995	0.23018	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (L1PA2 LIN	-26125	NM_00467E	9068	Hs.591474	NM_00467E	ENSG000002ANGPTL1	ANG3 ANGF	angiopoietin protein-coding	
chr14-67E	5.120704	-1.27995	1.066983	-1.1996	0.230296	0.981636	chr14	67279329	67280477	+	0	NA	intron (intron (N	38468	NM_00125E	64398	Hs.65231E	NM_02247E	ENSG000002MPP5	PALS1	membrane protein-coding	
chr2-174E	5.120704	-1.27995	1.066983	-1.1996	0.230296	0.981636	chr2	1.74E+08	1.74E+08	+	0	NA	intron (MER30 DNA	7710	NM_00488E	9541	Hs.632531	NM_00488E	ENSG000002CIR1	CIR	corepress protein-coding	
chr2-177E	10.04257	-0.90847	0.757319	-1.19958	0.230301	0.981636	chr2	1.77E+08	1.77E+08	+	0	NA	non-codiron-codir	9675	NR_13847C	220988	Hs.51653E	NM_19424E	ENSG000002HNRNP3	2610510D1	heterolog protein-coding	
chr17-35E	8.844925	-0.95791	0.798709	-1.19932	0.230404	0.981636	chr17	35138852	35139201	+	0	NA	intron (AluJo SIN	3225	NM_00101A	54475	Hs.85570	NM_01809E	ENSG000002SNLE1	NLE	notogless protein-coding	
chr18-58E	8.844925	-0.95791	0.798709	-1.19932	0.230404	0.981636	chr18	58573947	58575813	+	0	NA	intron (intron (N	-25740	NR_13296E	1.07E+08	NR_13296E	SNORA108	-	small nucsnRNA		
chr2-1114	8.844925	-0.95791	0.798709	-1.19932	0.230404	0.981636	chr2	1.11E+08	1.11E+08	+	0	NA	intron (intron (N	2426	NR_13616E	541471	Hs.56080E	NM_01539E	ENSG000002MIR4435	-	AGD2 LINMIR4435	zncRNA
chr15-711	8.852783	-0.95295	0.79993	-1.19917	0.230464	0.981636	chr15	71154967	71155746	+	0	NA	intron (MSTA LTR	13907	NM_02481E	79875	Hs.387057	NM_02481E	ENSG000002THSD4	ADAMTSL- $\epsilon$	thrombospondin protein-coding	
chr10-49E	7.460371	1.041707	0.868989	1.198758	0.230622	0.981636	chr10	4966920	4973715	+	0	NA	intron (L1MC4 LIN	6902	NM_00135E	1645	Hs.46026C	NM_00135E	ENSG000002AKR1C1	2-ALPHA-H	aldo-ketoprotein-coding	
chr11-64E	7.460371	1.041707	0.868989	1.198758	0.230622	0.981636	chr11	6456486	6458557	+	0	NA	intron (intron (N	16420	NM_03327E	10612	Hs.59199E	NM_00645E	ENSG000002TRIM3	BERP HAC1	tripartite protein-coding	
chr16-897	7.460371	1.041707	0.868989	1.198758	0.230622	0.981636	chr16	89726752	89727062	+	0	NA	intron (AluSg SIN	5370	NM_00111E	92822	Hs.290154	NM_15228E	ENSG000002ZNF276	CENP-7	Cfzinc fing protein-coding	
chr2-743C	7.460371	1.041707	0.868989	1.198758	0.230622	0.981636	chr2	74331067	74331366	+	0	NA	intron (intron (N	12229	NM_13347E	57835	Hs.59409E	NM_02119E	ENSG000002SLCA45	NBC4 NBCe	solute c protein-coding	
chr3-115E	7.460371	1.041707	0.868989	1.198758	0.230622	0.981636	chr3	11562645	11563527	+	0	NA	intron (intron (N	5712	NM_00112E	9686	Hs.74038E	NM_01466E	ENSG000002VGLL4	VGL-4	vestigial protein-coding	
chr9-129E	7.460371	1.041707	0.868989	1.198758	0.230622	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (AluSc8 SI	-7076	NR_106914	1.02E+08	NR_106914	ENSG000002MIR6855	hsa-mir- $\epsilon$	microRNA ncRNA		
chr1-156E	8.698973	0.976983	0.814997	1.198757	0.230622	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	exon (NM exon (NM	5450	NM_00109E	92312	Hs.59149E	NM_00109E	ENSG000002MEX3A	MEX-3A FR	mex-3 RN <sup>4</sup> protein-coding	
chr12-34E	8.698973	0.976983	0.814997	1.198757	0.230622	0.981636	chr12	34928803	34929002	+	0	NA	IntergeniALR/Alph	906406	NM_03283A	84920	Hs.102971	NM_03283A	ENSG000002ALG10	ALG10A DIALG10	al protein-coding	
chr16-47E	8.698973	0.976983	0.814997	1.198757	0.230622	0.981636	chr16	47550434	47550871	+	0	NA	intron (L1PRE2 I	89351	NM_00103I	5257	Hs.78060	NM_00029E	ENSG000002PHKB	-	phosphoryl protein-coding	
chr5-53E	8.698973	0.976983	0.814997	1.198757	0.230622	0.981636	chr5	47353625	47354378	+	0	NA	IntergeniALR/Alph	-1657621	NM_02107E	348980	Hs.35317E	NM_02107E	ENSG000002HCN1	BCNG-1 B	hyperpol protein-coding	
chr11-10C	6.42118	0.980919	0.818515	1.198412	0.230757	0.981636	chr11	10079794	10080116	+	0	NA	intron (L1M2 LINE	214252	NM_03096E	81846	Hs.57725E	NM_03096E	ENSG000002SFB2	CMT4B2 DFSET	bindi protein-coding	
chr19-53E	5.187267	-1.26111	1.052363	-1.19836	0.230777	0.981636	chr19	53559080	53559558	+	0	NA	intron (AC)n Sin	4012	NM_00107E	55422	Hs.185674	NM_01855E	ENSG000002ZNF331	RITA ZNF $\epsilon$	zinc fing protein-coding	
chr5-969E	5.187267	-1.26111	1.052363	-1.19836	0.230777	0.981636	chr5	96902315	96902758	+	0	NA	intron (intron (N	26597	NR_13763E	64167	Hs.48291C	NM_02235E	ENSG000002ERAP2	64167	ERAP2	endoplasm protein-coding
chr9-278E	5.187267	-1.26111	1.052363	-1.19836	0.230777	0.981636	chr9	2789174	2790028	+	0	NA	IntergeniIntergeni	54494	NM_01487E	9933	Hs.49330E	NM_01487E	ENSG000002PUM3	HA-8 HLA	pumilio f protein-coding	
chr12-72E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr12	78042689	78043559	+	0	NA	intron (L1PA7 LIN	212230	NM_01490E	89795	Hs.655301	NM_01490E	ENSG000002NAV3	POMF1L1 S	neurone protein-coding	
chr15-28E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr15	22668038	22669313	+	0	NA	intron (AluSx SIN	3936	NR_00352I	339005	Hs.51267C	NR_00352I	WHAMMP3	WHAMML1 W	was prote pseudo	
chr3-127E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr3	1.28E+08	1.28E+08	+	0	NA	intron (L2a LINE	20676	NM_17202E	80325	Hs.10781E	NM_03254E	ENSG000002ABTB1	BPOZ BTB $\epsilon$	ankyrin f protein-coding	
chr4-779E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr4	77924792	77926172	+	0	NA	intron (AluYh3 SI	62652	NM_00202E	65008	Hs.53201E	NM_02023E	ENSG000002MRPL1	SMEC2 L1M	mitochon protein-coding	
chr5-131E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr5	1.31E+08	1.31E+08	+	0	NA	intron (L1PA5 LIN	80423	NM_00103E	56990	Hs.50882E	NM_02024E	ENSG000002CDC425E2	SPEC2	CDC42 sm $\epsilon$ protein-coding	
chr7-755E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr7	75590864	75591063	+	0	NA	intron (intron (N	-62840	NR_02805E	5387	Hs.659871	NM_00539E	ENSG000002PMS2P3	PMS2L3 P	PMS1 homc pseudo	
chr9-122E	6.400631	-1.12162	0.936016	-1.19829	0.230803	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (intron (N	-43727	NM_00529A	2844	Hs.72203E	NM_00529A	ENSG000002GPR21	-	G protein protein-coding	
chr16-29E	6.36735	-1.12884	0.942078	-1.19824	0.230823	0.981636	chr16	29557832	29558327	+	0	NA	intron (intron (N	37013	NR_13530E	440354	Hs.55270C	NR_00247E	SMGIP2	-	SMG1 pset pseudo	
chr7-124E	6.36735	-1.12884	0.942078	-1.19824	0.230823	0.981636	chr7	1.25E+08	1.25E+08	+	0	NA	intron (intron (N	-34432	NM_00102A	154872	Hs.44416E	NM_00102A	ENSG000002C7orf77	-	chromoson protein-coding	
chr1-786E	6.408489	-1.12339	0.937722	-1.198	0.230919	0.981636	chr1	78658834	78659261	+	0	NA	intron (L2a LINE	9216	NM_00641E	10561	Hs.8231E	NM_00641E	ENSG000002IF14E	MTAP44 T	interfer protein-coding	
chr13-41E	6.408489	-1.12339	0.937722	-1.198	0.230919	0.981636	chr13	41364271	41364731	+	0	NA	intron (intron (N	-52463	NM_00135A	9617	Hs.38217E	NM_00429A	ENSG000002MTRF1	MRF1 MTF	mitochon protein-coding	
chr15-80E	6.408489	-1.12339	0.937722	-1.198	0.230919	0.981636	chr15	80812865	80816462	+	0	NA	intron (L2c LINE	27410	NR_03039E	693132	NR_03039E	ENSG000002MIR549A	MIR549 M	microRNA ncRNA		
chr9-115E	6.408489	-1.12339	0.937722	-1.198	0.230919	0.981636	chr9	1.15E+08	1.15E+08	+	0	NA	exon (NM exon (NM	75911	NM_00216E	3371	Hs.14325C	NM_00216E	ENSG000002TNC	150-225 E	tenascin protein-coding	
chr11-791	6.221768	1.133621	0.946419	1.197801	0.230995	0.981636	chr11	791938	792143	+	0	NA	exon (NM exon (NM	-1950	NM_01656A	51286	Hs.73211E	NM_01656A	ENSG000002CEND1	BM88	cell cycl protein-coding	
chr13-324	6.221768	1.133621	0.946419	1.197801	0.230995	0.981636	chr13	32456919	32457971	+	0	NA	intron (L1MA4A LI	-29315	NM_00128E	90634	Hs.73211E	NM_05281E	ENSG000002N4BP2L1	CG108	NEDD4	bir protein-coding
chr17-657	6.221768	1.133621	0.946419	1.197801	0.230995	0.981636	chr17	657341	657765	+	0	NA	intron (intron (N	57286	NM_00112E	55275	Hs.46181E	NM_01828E	ENSG000002VPS53	HCCS1 PCF	VPS53 sub protein-coding	
chr19-23E	6.221768	1.133621	0.946419	1.197801	0.230995	0.981636	chr19	2348010	2349870	+	0	NA	intron (CpG	20256	NM_15298E	56928	Hs.74402E	NM_15298E	ENSG000002SPPL2B	IMP-4 IMF	signal p protein-coding	
chr19-104	6.221768	1.133621	0.946419	1.197801	0.230995	0.981636	chr19	10641856	10643705	+	0	NA	intron (intron (N	11092	NR_02433E	14727						



chr14-92c	4.965599	1.26439	1.062075	1.19049	0.233854	0.981636	chr14	92066989	92068732	+	0	NA	intron (N)LMIDa LIN	-27801 NM_001321	9321 Hs. 63233cENM_00423cENSG00000TRIP11	ACG1A CEV	thyroid f protein-coding
chr2-999f	4.965599	1.26439	1.062075	1.19049	0.233854	0.981636	chr2	9995679	9996496	+	0	NA	intron (N)intron (N)	44394 NM_198182	29841 Hs. 41849cENM_19818cENSG00000GRHL1	LBP32 MGF	grainyhead protein-coding
chr14-10f	6.359492	-1.1271	0.946924	-1.19028	0.233938	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	IntergeniAluS6 SI	13159 NM_00182c	1152 Hs. 173724NM_00182cENSG00000CKBK	B-CK BCK	creatine protein-coding
chr5-406f	6.359492	-1.1271	0.946924	-1.19028	0.233938	0.981636	chr5	40692524	40693290	+	0	NA	3' UTR (N)3' UTR (N)	12992 NM_00095f	5734 Hs. 19924fENM_00095fENSG00000PTGER4	EP4 EP4R	prostaglandin protein-coding
chr5-753f	6.359492	-1.1271	0.946924	-1.19028	0.233938	0.981636	chr5	75374759	75375497	+	0	NA	intron (N)intron (N)	37908 NM_00085f	3156 Hs. 62809cENM_00085fENSG00000MGCCR	LDLcCQ3	3-hydroxy protein-coding
chr9-132f	6.359492	-1.1271	0.946924	-1.19028	0.233938	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (N)L2a LINE	63896 NM_00135f	23064 Hs. 460317NM_01504cENSG00000CSETX	ALS4 AOA2	senataxir protein-coding
chr19-20f	6.341926	-1.13823	0.956407	-1.19011	0.234005	0.981636	chr19	20655936	20651135	+	0	NA	intron (N)AluSg4 SI	10536 NM_00107f	19777 Hs. 657001NM_145297ENSG00000ZNF626	-	zinc finger protein-coding
chr3-198f	8.783102	0.987974	0.83061	1.189457	0.23426	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (N)intron (N)	35376 NR_04666e	1.01E+08 Hs. 63716cNR_04666cENSG00000LMLN-AS1	-	LMLN antincRNA
chr3-134d	10.08556	-0.89609	0.753547	-1.18917	0.234373	0.981636	chr3	1.34E+08	1.34E+08	+	0	NA	intron (N)LIMA4A LI	9582 NM_00135c	80254 Hs. 443301NM_02518cENSG00000CCEP63	SCKL6	centrosome protein-coding
chr5-358f	10.08556	-0.89609	0.753547	-1.18917	0.234373	0.981636	chr5	35864208	35865690	+	0	NA	intron (N)LIME2 LIN	8058 NM_00218f	3575 Hs. 591742NM_00218fENSG00000IL7R	CD127 CDW	interleukin protein-coding
chr1-206f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr1	20638142	20638693	+	0	NA	intron (N)AluJb SIN	4738 NR_10673z	ENSG00000MIR6084	hsa-mir-6084	microRNA ncRNA
chr1-206a	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (N)intron (N)	-54199 NM_01400z	9641 Hs. 32104cENM_01400zENSG00000IKBKE	IKK-E IKK	inhibitor protein-coding
chr1-246f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr1	2.47E+08	2.47E+08	+	0	NA	intron (N)intron (N)	16633 NM_01544f	25909 Hs. 300887NM_01544fENSG00000AHCTF1	ELYS MS1AT	hook protein-coding
chr17-41f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr17	41760601	41767979	+	0	NA	intron (N)AluSx1 SI	21805 NM_00135z	3728 Hs. 514174NM_00223cENSG00000JUP	CTNNG DP2	junction protein-coding
chr17-47f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr17	47807180	47808305	+	0	NA	3' UTR (N)3' UTR (N)	14052 NM_14579f	114881 Hs. 46332cNM_017731ENSG00000OSBPL7	ORP7	oxysterol protein-coding
chr22-35f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr22	35317440	35320613	+	0	NA	intron (N)intron (N)	-16614 NR_037471	1.01E+08 NR_037471ENSG00000MIR3909	mir-3909	microRNA ncRNA
chr22-46f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr22	46666622	46668656	+	0	NA	intron (N)intron (N)	47253 NM_015124	23151 Hs. 47515cNM_015124ENSG00000GRAMD4	DAD	GRAM domain protein-coding
chr5-134f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr5	1.65E+08	1.35E+08	+	0	NA	exon (NM)exon (NM)	11966 NM_01528f	23338 Hs. 73215cNM_01528fENSG00000JADE2	JADE2 PF	jade family protein-coding
chr8-143f	6.229626	1.130703	0.950897	1.189091	0.234404	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	intron (N)intron (N)	17070 NR_03063z	ENSG00000MIR937	MIRN937	lmiRNA ncRNA
chr15-72f	7.493652	1.044203	0.878346	1.18883	0.234507	0.981636	chr15	72356034	72356538	+	0	NA	intron (N)intron (N)	19728 NM_00131f	3073 Hs. 60447cENM_00052cENSG00000CHEXA	TSD	hexosaminidase protein-coding
chr20-50f	4.93652	1.044203	0.878346	1.18883	0.234507	0.981636	chr20	50831342	50831675	+	0	NA	intron (N)MER102c I	36614 NM_19879f	55653 Hs. 38117cNM_01784cENSG00000BCASA	CNOL	breast cancer protein-coding
chr11-60f	6.938359	1.106722	0.930936	1.188826	0.234508	0.981636	chr11	60941556	60941755	+	0	NA	intron (N)intron (N)	10521 NM_01658z	51296 Hs. 23785cNM_01658zENSG00000SLC15A3	OCTP PHT2	solute carrier protein-coding
chr11-88c	4.998881	1.26775	1.066395	1.188818	0.234511	0.981636	chr11	886615	887497	+	0	NA	intron (N)AluJb SIN	23754 NM_00114z	66005 Hs. 14446cENM_023947ENSG00000CHHID1	GL008 SI	chitinase protein-coding
chr14-73f	4.998881	1.26775	1.066395	1.188818	0.234511	0.981636	chr14	73967145	73968081	+	0	NA	intron (N)AluS6 SI	17311 NM_18247f	51004 Hs. 13155cNM_18247cENSG00000COQ6	CG1-10 CC	coenzyme protein-coding
chr9-343f	4.998881	1.26775	1.066395	1.188818	0.234511	0.981636	chr9	34397601	34398339	+	0	NA	promoter-promoter-	-160 NM_03259f	84688 Hs. 50334 NM_03259cENSG00000C9orf24	CBE1 NYD	chromosome protein-coding
chr9-137f	4.998881	1.26775	1.066395	1.188818	0.234511	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (N)intron (N)	-12862 NM_20751f	401563 Hs. 52250cENM_20751f	C9orf139	chromosome protein-coding
chr2-324f	10.1267	-0.89294	0.751156	-1.18875	0.234537	0.981636	chr2	32494188	32494427	+	0	NA	intron (N)AluS5 SI	-3784 NR_03028f	693143 NR_03028fENSG00000MIR558	MIRN558	lmiRNA ncRNA
chr17-63f	8.757679	0.98355	0.827778	1.188179	0.234763	0.981636	chr17	63010574	63010773	+	0	NA	intron (N)MER21C LI	44438 NM_02518f	26115 Hs. 41088cNM_01562cENSG00000TANC2	ROLSA rol	tetratric protein-coding
chr1-229f	9.195561	0.928505	0.7816	1.187955	0.234851	0.981636	chr1	2.3E+08	2.3E+08	+	0	NA	intron (N)AluSx3 SI	5332 NM_01823z	55746 Hs. 12457cNM_01823cENSG00000NUP133	GAMOS8 NF	nucleoporin protein-coding
chr14-90f	9.195561	0.928505	0.7816	1.187955	0.234851	0.981636	chr14	90769435	90769736	+	0	NA	intron (N)AluJo SIN	46832 NM_00132z	145567 Hs. 655697NM_00101cENSG00000TTC7B	TTCTL1 CT	tetratric protein-coding
chr6-319f	9.195561	0.928505	0.7816	1.187955	0.234851	0.981636	chr6	31969067	31969266	+	0	NA	TTS (NM)TTS (NM)C	-2009 NR_02671f	8859 Hs. 654371NM_004197ENSG00000CSTK19	D6S60 D6S	serine/t protein-coding
chr1-150f	7.434947	1.036693	0.872777	1.187809	0.234908	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (N)intron (N)	8786 NM_00116z	55793 Hs. 74395cNM_01837fENSG00000MINDY1	PAM63A MI	MINDY lysine protein-coding
chr16-161f	7.434947	1.036693	0.872777	1.187809	0.234908	0.981636	chr16	16164682	16165735	+	0	NA	intron (N)AluJr SIN	58263 NM_00107f	368 Hs. 44218cNM_001171ENSG00000ABC6	ABC34 ARA	ATP binding protein-coding
chr4-321f	7.434947	1.036693	0.872777	1.187809	0.234908	0.981636	chr4	3217908	3218595	+	0	NA	intron (N)intron (N)	-26118 NM_00133z	345222 Hs. 442291NM_00101zENSG00000MSANTD1	C4orf44	Myb/SANT protein-coding
chr11-62f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr11	62782434	62782743	+	0	NA	intron (N)Charlie1f	-4814 NM_00136z	373495 Hs. 381134NM_199337ENSG00000TMEM1795	-	transmembrane protein-coding
chr11-10f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (N)MLT1f LTF	116105 NM_00133z	160140 Hs. 65318cNM_152587ENSG00000C11orf6B	-	chromosome protein-coding
chr14-10f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	intron (N)intron (N)	-4705 NR_02986z	442915 NR_02986zENSG00000MIR370	MIRN370	lmiRNA ncRNA
chr2-218f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (N)AluSp SIN	-10854 NM_01464z	9654 Hs. 47140cENM_01464zENSG00000TTL4	-	tubulin protein-coding
chr22-27f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr22	27982465	27983427	+	0	NA	exon (NM)exon (NM)	-62424 NR_03616z	ENSG00000MIR3199	mir-3199	microRNA ncRNA
chr3-113f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr3	1.14E+08	1.14E+08	+	0	NA	intron (N)intron (N)	19412 NM_00100z	205717 Hs. 63257cNM_00100zENSG00000USF3	KIAA2018	upstream protein-coding
chr3-123f	6.196344	1.127792	0.949579	1.187675	0.234961	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	intron (N)intron (N)	-43477 NR_10696z	1.02E+08 NR_10696zENSG00000MIR7110	hsa-mir-7110	microRNA ncRNA
chr19-94f	5.144463	1.330753	1.120913	1.187205	0.235147	0.981636	chr19	9468869	9469113	+	0	NA	intron (N)AluSx4 SI	147741 Hs. 63161cENM_15247cENSG00000ZNF560	-	zinc finger protein-coding	
chr11-94f	6.384915	-1.11804	0.942202	-1.18662	0.235377	0.981636	chr11	94813839	94814745	+	0	NA	intron (N)intron (N)	45936 NM_00130f	154810 Hs. 503594NM_130847ENSG00000AMOTL1	JEAP	angiomin protein-coding
chr2-101f	6.384915	-1.11804	0.942202	-1.18662	0.235377	0.981636	chr2	1.01E+08	1.01E+08	+	0	NA	intron (N)L1P3 LIN	14001 NM_00099z	6160 Hs. 46947cNM_00099zENSG00000RPL31	L31	ribosomal protein-coding
chr2-173f	6.384915	-1.11804	0.942202	-1.18662	0.235377	0.981636	chr2	1.73E+08	1.73E+08	+	0	NA	exon (NM)exon (NM)	15322 NR_03388z	339751 Hs. 57008cNR_03388zENSG00000MAP3K20	MLK7-AS1	RAP3K20 εncRNA
chr3-111f	6.384915	-1.11804	0.942202	-1.18662	0.235377	0.981636	chr3	11161946	11162547	+	0	NA	intron (N)LTR79 LTF	7753 NM_00109f	3269 Hs. 1570 NM_000861ENSG00000HRH1	HR1-R HR1	histamine protein-coding
chr4-139f	6.384915	-1.11804	0.942202	-1.18662	0.235377	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	IntergeniIntergeni	31741 NM_01211f	25819 Hs. 63984cNM_01211fENSG00000NOCT	CCR4L CCF	nocturnin protein-coding
chr17-60f	7.179846	0.932328	0.785856	1.186386	0.23547	0.981636	chr17	60624608	60624910	+	0	NA	intron (N)AluSp SIN	24576 NM_00362z	8493 Hs. 28607cNM_00362cENSG00000PPM1D	IDDDG PF	protein f protein-coding
chr14-73f	6.23703	-1.01974	0.859706	-1.18615	0.235565	0.981636	chr14	73450688	73450946	+	0	NA	intron (N)intron (N)	7763 NM_00100z	8650 Hs. 52544cNM_00374cENSG00000NUMB	C14orf41 NUMB	end protein-coding
chr16-29f	7.623703	-1.01974	0.859706	-1.18615	0.235565	0.981636	chr16	29286675	29288148	+	0	NA	IntergeniIntergeni	-14876 NR_00293z	440352 Hs. 65814cNR_00293z	SNX29P2	sorting rpsudo
chr2-247f	7.623703	-1.01974	0.859706	-1.18615	0.235565	0.981636	chr2	24798751	24802720	+	0	NA	intron (N)L1PA4 LIN	7310 NM_00119f	79172 Hs. 73156cENM_02432cENSG00000CCENP0	CENP-0 IC	centromere protein-coding
chr2-365f	7.623703	-1.01974	0.859706	-1.18615	0.235565	0.981636	chr2	36588922	36589525	+	0	NA	intron (N)L2c LINE	8945 NM_00104z	9637 Hs. 22585cENM_00510zENSG00000FE22	HMB3CL	fasciculin protein-coding
chr3-123f	7.623703	-1.01974	0.859706	-1.18615	0.235565	0.981636	chr3	12382629	12383395	+	0	NA	intron (N)MIR3 SINE	31510 NM_0158			

chr3-9088.6.007806	0.990106	0.840651	1.177784	0.238883	0.981636	chr3	90888721	908889568	+	0	NA	IntergeniALR/Alpha	1781523	NM_182644	2042	Hs.123642NM_005233	ENSG00000EPAH3	EK4 ETK E EPH	recep	protein-coding	
chr7-645f.4.425652	-1.34077	1.138571	-1.17759	0.238961	0.981636	chr7	64557362	64558099	+	0	NA	intron (NAluSz SIN	5341	NM_17855f	340252	Hs.52088fNM_17855f	ENSG00000ZNF680	-	zinc fing	protein-coding	
chr19-44f.11.02274	0.860348	0.730645	1.177519	0.238988	0.981636	chr19	44273424	44274715	+	0	NA	exon (NM_exon (NM	14155	NM_18175f	353355	Hs.466891NM_18175f	ENSG00000ZNF233	-	zinc fing	protein-coding	
chr1-117f.7.615845	-1.01818	0.864775	-1.17739	0.239041	0.981636	chr1	1.17fE+08	1.17fE+08	+	0	NA	intron (Nintron (N	16507	NM_003594	8458	Hs.32333	ENSG00000TTF2	HuF2 ZGRF	transcrip	protein-coding	
chr14-147f.7.615845	-1.01818	0.864775	-1.17739	0.239041	0.981636	chr14	73083914	73084238	+	0	NA	intron (NAluSx SIN	25542	NM_02123f	58517	Hs.53110fNM_02123f	ENSG00000RBM25	NET52 REI	RNA bindi	protein-coding	
chr3-150f.7.615845	-1.01818	0.864775	-1.17739	0.239041	0.981636	chr3	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	17025	NM_03202f	83939	Hs.65578fNM_03202f	ENSG00000EIF2A	CDAO2 EIF	eukaryoti	protein-coding	
chr4-802f.7.615845	-1.01818	0.864775	-1.17739	0.239041	0.981636	chr4	80286497	80292204	+	0	NA	3' UTR (N3' UTR (N	21085	NM_001291	2250	Hs.37055	ENSG00000PGF5	HBGf-5 Sn	fibroblas	protein-coding	
chr6-875f.7.615845	-1.01818	0.864775	-1.17739	0.239041	0.981636	chr6	87506137	87506520	+	0	NA	intron (Nintron (N	33354	NM_00641f	10550	Hs.42771fNM_00641f	ENSG00000SLC35A1	CGD2f CMF	solute ce	protein-coding	
chr8-9107.7.672701	-1.01681	0.863622	-1.17738	0.239045	0.981636	chr8	91073785	91074560	+	0	NA	intron (NMIRb SINE	3828	NM_00128f	51633	Hs.30532	ENSG00000OTUD6B	CGI-77 DU	OTU doma	protein-coding	
chr2-223f.7.982382	0.985379	0.837625	1.176396	0.239436	0.981636	chr2	2.24fE+08	2.24fE+08	+	0	NA	intron (Nintron (N	26509	NM_002291f	65080	Hs.20355fNM_002291f	ENSG00000MRPL44	COXP16 L	mitochon	protein-coding	
chr1-207f.8.846775	-0.94753	0.805677	-1.17607	0.239567	0.981636	chr1	20754531	20755470	+	0	NA	intron (NLIMB7 LIN	-22297	NM_00110f	400745	Hs.59152fNM_00110f	ENSG00000SH2D5	-	SH2 doma	protein-coding	
chr11-781.4.940175	1.257208	1.069415	1.175604	0.239753	0.981636	chr11	78193290	78194083	+	0	NA	intron (Nintron (N	4767	NM_02079f	57558	Hs.53124fNM_02079f	ENSG00000CUSP35	-	ubiquiti	protein-coding	
chr14-102.4.940175	1.257208	1.069415	1.175604	0.239753	0.981636	chr14	1.02fE+08	1.02fE+08	+	0	NA	intron (NL2a LINE	54529	NM_01484f	9895	Hs.19566fNM_01484f	ENSG00000TECPR2	KIAA0329	tectonin	protein-coding	
chr1-1237.182.2106	0.343188	0.2921	1.174902	0.240034	0.981636	chr1	1.24fE+08	1.24fE+08	+	0	NA	IntergeniALR/Alpha	2264529	NR_00395f	647121	Hs.69768fNR_00395f	ENSG00000EMBP1	-	embigin	psudo	
chr19-26f.15.64575	0.738361	0.628532	1.174738	0.240099	0.981636	chr19	26519309	26519508	+	0	NA	IntergeniALR/Alpha	-1274023	NR_14673f	1.02E+08	Hs.567934NR_110687	ENSG00000LOC101927	-	uncharact	ncRNA	
chr11-12f.6.377058	-1.11618	0.950651	-1.17412	0.240347	0.981636	chr11	12879195	12879476	+	0	NA	intron (Nintron (N	110213	NR_038904	1.01E+08	Hs.15340fNR_038904	ENSG00000LINC0095f	BLACAT2	long	intcncRNA	
chr13-110f.6.377058	-1.11618	0.950651	-1.17412	0.240347	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	15339	NM_00184f	1282	Hs.17441	ENSG00000COL4A1	BSVD BSV	collagen	protein-coding	
chr14-104f.6.377058	-1.11618	0.950651	-1.17412	0.240347	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	3' UTR (N3' UTR (N	-4577	NM_15232f	122622	Hs.59232fNM_15232f	ENSG00000ADSSL1	Adss1 MP	adenylos	protein-coding	
chr22-42f.6.377058	-1.11618	0.950651	-1.17412	0.240347	0.981636	chr22	42088919	42089623	+	0	NA	intron (Nintron (N	1501	NM_00249f	4700	Hs.27441fNM_00249f	ENSG00000NDUFA6	B14 CI-B	INDAH:u	bic	protein-coding
chr5-435f.6.377058	-1.11618	0.950651	-1.17412	0.240347	0.981636	chr5	43554898	43555155	+	0	NA	intron (NLIME3A LI	2051	NM_00645f	10605	Hs.48203fNM_00645f	ENSG00000PAIP1	-	poly(A)	t	protein-coding
chr10-132.6.262907	1.13355	0.965548	1.173996	0.240397	0.981636	chr10	1.32fE+08	1.32fE+08	+	0	NA	exon (NM_exon (NM	8257	NM_00109f	170394	Hs.52775fNM_13849f	ENSG00000PWWP2B	PWWP2 bA	A4PWWP	lome	protein-coding
chr9-130f.6.262907	1.13355	0.965548	1.173996	0.240397	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	TTS (NM_TTS (NM_C	12424	NR_10691f	1.02E+08	NR_10691f	ENSG00000MIR6856	hsa-mir- $\epsilon$	microRNA	ncRNA	
chr12-98f.7.99024	0.98317	0.837734	1.173607	0.240552	0.981636	chr12	98661001	98661244	+	0	NA	intron (NAluY SINE	15822	NM_18186f	317	Hs.55256fNM_00116f	ENSG00000CAPAF1	APAF-1 C	apoptotic	protein-coding	
chr17-82f.7.99024	0.98317	0.837734	1.173607	0.240552	0.981636	chr17	82083461	82089842	+	0	NA	intron (Nintron (N	3489	NR_13275f	1.07E+08	NR_13275f	SNORD134	ZL12	small	nucsnRNA	
chr2-219f.7.99024	0.98317	0.837734	1.173607	0.240552	0.981636	chr2	2.19fE+08	2.19fE+08	+	0	NA	exon (NM_exon (NM	5053	NM_01808f	55139	Hs.43764fNM_01808f	ENSG00000ANKZF1	Vms1 ZNF	7ankyrin	protein-coding	
chr16-74f.6.17092	1.121859	0.956589	1.17277	0.240888	0.981636	chr16	74928794	74929091	+	0	NA	intron (NLIMA3 LIN	56181	NM_03058f	79726	Hs.28095fNM_03058f	ENSG00000WDR59	CDW12 FP	RD	repeat	protein-coding
chr20-62f.6.17092	1.121859	0.956589	1.17277	0.240888	0.981636	chr20	62306458	62307049	+	0	NA	intron (Nintron (N	3756	NM_00700f	11047	Hs.90107	ENSG00000ADRM1	ARM-1 AR	adhesion	protein-coding	
chr6-335f.6.17092	1.121859	0.956589	1.17277	0.240888	0.981636	chr6	33572702	33573155	+	0	NA	3' UTR (N3' UTR (N	7348	NM_00118f	578	Hs.48513fNM_00118f	ENSG00000BAK1	BAK BAK-1	ECL2	ant	protein-coding
chr7-149f.6.17092	1.121859	0.956589	1.17277	0.240888	0.981636	chr7	1.5E+08	1.5E+08	+	0	NA	non-codiron-codir	-51511	NM_15255f	155061	Hs.24643	ENSG00000ZNF746	PARIS	zinc	fing	protein-coding
chr1-148f.18.89427	0.661711	0.564335	1.172551	0.240976	0.981636	chr1	1.49fE+08	1.49fE+08	+	0	NA	intron (Nintron (N	37900	NM_01538f	25832	Hs.53467fNM_01538f	ENSG00000NBPF14	DJ328E19	NBPF	mem	protein-coding
chr17-384.9.575109	-0.94063	0.802759	-1.17175	0.241299	0.981636	chr17	38471609	38471852	+	0	NA	intron (Nintron (N	43266	NM_00119f	57636	Hs.37444fNM_02087f	ENSG00000ARHGAP23	-	Rho	GTPas	protein-coding
chr10-10f.7.956959	0.980691	0.837164	1.171444	0.24142	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (NAluSx SI	34037	NM_03272f	9118	Hs.50091fNM_03272f	ENSG00000INA	NEF5 NF- $\epsilon$	interne	protein-coding	
chr9-122f.7.956959	0.980691	0.837164	1.171444	0.24142	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	IntergeniLIM4c LIN	-4247	NM_01219f	23637	Hs.27134fNM_01219f	ENSG00000RABGAP1	CAGPCNA	TRAB	GTPas	protein-coding
chr9-1274.7.956959	0.980691	0.837164	1.171444	0.24142	0.981636	chr9	1.27E+08	1.27E+08	+	0	NA	intron (NAluY SINE	33210	NM_00100f	90678	Hs.49518fNM_13836f	ENSG00000LRSAM1	CMT2P RIF	leucine	protein-coding	
chr3-566f.6.410339	-1.10888	0.946758	-1.17124	0.241502	0.981636	chr3	56627966	56628165	+	0	NA	intron (Nintron (N	35981	NM_015224	23272	Hs.11687fNM_015224	ENSG00000TASOR	C3orf63 F	transcrip	protein-coding	
chr6-272f.6.410339	-1.10888	0.946758	-1.17124	0.241502	0.981636	chr6	22723161	22723360	+	0	NA	IntergeniMLT1H2-ir	-5336	NR_13461f	1.05E+08	Hs.48488fNR_13461f	LOC105374	-	uncharact	ncRNA	
chr9-100f.6.410339	-1.10888	0.946758	-1.17124	0.241502	0.981636	chr9	1E+08	1E+08	+	0	NA	intron (Nintron (N	39772	NM_00116f	54881	Hs.49464fNM_01774f	ENSG00000CTEX10	Ipi1 ba2C	testis	es	protein-coding
chrX-742f.6.410339	-1.10888	0.946758	-1.17124	0.241502	0.981636	chrX	74269300	74269565	+	0	NA	intron (Nintron (N	17777	NR_03025f	664614	NR_03025f	ENSG00000MIR545	MIRN545  $\mu$	microRNA	ncRNA	
chr12-12f.6.997064	1.114477	0.951679	1.171064	0.241573	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	exon (NM_exon (NM	6433	NM_00124f	23457	Hs.51195fNM_01962f	ENSG00000ABCB9	EST12254ATP	bindi	protein-coding	
chr17-471.6.912935	1.101027	0.940236	1.171012	0.241594	0.981636	chr17	47163903	47164102	+	0	NA	intron (NAluSq2 SI	25293	NM_00125f	996	Hs.46329fNM_00125f	ENSG00000CDC27	ANAPC3 A	F cell	divi	protein-coding
chr11-68f.7.442805	1.034083	0.883191	1.170849	0.24166	0.981636	chr11	68907383	68907582	+	0	NA	intron (Nintron (N	3631	NM_00218f	3508	Hs.50304fNM_00218f	ENSG00000IGHMBP2	CATF1 CM	immunogl	protein-coding	
chr21-46f.7.442805	1.034083	0.883191	1.170849	0.24166	0.981636	chr21	46560699	46561194	+	0	NA	intron (Nintron (N	44136	NM_00627f	6285	Hs.42218fNM_00627f	ENSG00000CS100B	NEF S100	S100	calc	protein-coding
chr7-1521.7.442805	1.034083	0.883191	1.170849	0.24166	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	26106	NM_001371474	80084	NR_03408f	1E+08	Hs.73266fNR_03408f	CCDC18-AS-	CCDC18	arncRNA
chr1-932f.4.402078	-1.33334	1.138824	-1.1708	0.241679	0.981636	chr1	93265173	93266282	+	0	NA	intron (NLIPA5 LIN	24469	NM_00662f	26227	Hs.48729fNM_00662f	ENSG00000PHGDH	3-PGDH 3F	phosphog	protein-coding	
chr12-26f.4.402078	-1.33334	1.138824	-1.1708	0.241679	0.981636	chr12	26916371	26917230	+	0	NA	intron (Nintron (N	2181	NM_01816f	55726	Hs.50530fNM_01816f	ENSG00000INTS13	ASUN C1c2	integrac	protein-coding	
chr17-301.4.402078	-1.33334	1.138824	-1.1708	0.241679																	



chr4-7612.6.402481	-1.10688	0.955117	-1.15889	0.2465	0.981636	chr4	76123945	76124548	+	0	NA	intron (NLIMEj LIN	24151	NR_017426	53371	Hs.43043ENM_017426	ENSG000005	UNC5P4	-	nucleoporin protein-coding		
chr4-8807.6.751637	-1.055844	0.911216	-1.15872	0.24657	0.981636	chr4	88074880	88075672	+	0	NA	intron (Nintron (N	67641	NR_156488	5311	Hs.181272ENM_000297	ENSG000005	PKD2	-	APK2 PC2 polycystin protein-coding		
chr1-1544.13.21939	0.770392	0.665015	-1.158459	0.246677	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	intron (NMLT1H1 LI	-29633	NR_147855	1.02E+08	Hs.61708ENR_147855	ENSG000005	IL6R-AS1	-	IL6R anticRNA		
chr17-756.6.21206	0.121632	0.968737	-1.15783	0.246933	0.981636	chr17	75820387	75821921	+	0	NA	intron (Nintron (N	23928	NM_199242	201294	Hs.41045	ENM_199242	ENSG000005	UNC13D	-	FHL3 HLH3 unc-13 hc protein-coding	
chr19-574.6.21206	0.121632	0.968737	-1.15783	0.246933	0.981636	chr19	57469837	57472042	+	0	NA	3' UTR (N3' UTR (N	7527	NM_001144	4001270	Hs.38881CNM_001024	ENSG000005	ZNF772	-	zinc finger protein-coding		
chr22-204.6.21206	0.121632	0.968737	-1.15783	0.246933	0.981636	chr22	20464434	20465430	+	0	NA	exon (NM_exon (NM_	-27107	NM_182895	91179	Hs.474251NM_153334	ENSG000005	SCARF2	-	NSR1 SREC scavenger protein-coding		
chr1-1602.7.972674	0.976235	0.843211	-1.157759	0.246962	0.981636	chr1	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	-18308	NR_123722	729867	Hs.674191NR_123722	ENSG000005	LOC729867	-	uncharacterized protein-coding		
chr1-2235.7.972674	0.976235	0.843211	-1.157759	0.246962	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (NMLRb SINE	19267	NR_132119	441124	Hs.52058ENR_132119	ENSG000005	GTF2IP20	-	general tpsudo		
chr17-291.7.972674	0.976235	0.843211	-1.157759	0.246962	0.981636	chr17	29113094	29113323	+	0	NA	intron (Nintron (N	27181	NM_001346	399687	Hs.46259CNM_078471	ENSG000005	MYO18A	-	MAJN MYSF myosin XI protein-coding		
chr19-436.7.972674	0.976235	0.843211	-1.157759	0.246962	0.981636	chr19	43872412	43874032	+	0	NA	exon (NM_exon (NM_	6914	NM_001033	342908	Hs.674191NR_123722	ENSG000005	ZNF404	-	zinc finger protein-coding		
chr1-2235.7.972674	0.976235	0.843211	-1.157759	0.246962	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (NMLRb SINE	19267	NR_132119	441124	Hs.52058ENR_132119	ENSG000005	GTF2IP20	-	general tpsudo		
chr22-395.9.349371	-0.8973	0.775338	-1.1573	0.247152	0.981636	chr22	39529655	39530437	+	0	NA	intron (Nintron (N	2702	NR_130151	91582	Hs.52693ENM_194326	ENSG000005	RPS19BP1	-	AROS S19E ribosomal protein-coding		
chr14-775.6.3692	-1.11245	0.962813	-1.15728	0.247157	0.981636	chr14	77552082	77552361	+	0	NA	exon (NM_exon (NM_	-53405	NM_199296	145501	Hs.29742	ENM_182505	ENSG000005	ISM2	-	TAIL1 HIS1 thimazin 2 protein-coding	
chr12-106.4.39422	-1.33089	1.150085	-1.15721	0.247188	0.981636	chr12	1.07E+08	1.07E+08	+	0	NA	intron (Nintron (N	-9443	NR_040246	14029	NR_037433	1.01E+08	NR_037433	ENSG000005	MIR3657	-	microRNA ncRNA
chr12-112.4.39422	-1.33089	1.150085	-1.15721	0.247188	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	-52050	NM_001024	2643	Hs.86724	NM_000161	ENSG000005	GCHI1	-	DYT14 DYT1 GTP cyclc protein-coding	
chr14-545.4.39422	-1.33089	1.150085	-1.15721	0.247188	0.981636	chr14	54954637	54955116	+	0	NA	exon (NAluSp SIN	6726	NM_024032	78995	Hs.43705ENM_024032	ENSG000005	CC1orf53	-	chromosom protein-coding		
chr17-441.4.39422	-1.33089	1.150085	-1.15721	0.247188	0.981636	chr17	44148533	44148779	+	0	NA	exon (NM_exon (NM_	29262	NM_001292	54946	Hs.64022ENM_019022	ENSG000005	PRMT7	-	SBIDDS protein protein-coding		
chr16-685.11.40977	0.815207	0.704644	-1.156906	0.247311	0.981636	chr16	68338970	68341783	+	0	NA	intron (NLIME4b LI	9561	NM_014955	51603	Hs.49470ENM_014955	ENSG000005	EEF1AKNM1	-	5630401D2eEFL1 lys protein-coding		
chr1-1717.9.707865	0.881775	0.762487	-1.156445	0.247499	0.981636	chr1	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	455	NR_137195	399959	Hs.44098	NR_024432	ENSG000005	MIR100HG	-	AGD1 lincmir-100-1ncRNA	
chr11-125.5.648724	-1.14941	0.994519	-1.15574	0.247787	0.981636	chr11	1.22E+08	1.22E+08	+	0	NA	non-codinn-codir	11936	NM_002097	2971	Hs.445977NM_002097	ENSG000005	GTF3A	-	AP2 TFIIIf general tprotein-coding		
chr13-274.5.648724	-1.14941	0.994519	-1.15574	0.247787	0.981636	chr13	27436079	27437032	+	0	NA	TTS (NM_CTS (NM_C	16599	NM_001164	444	Hs.332422NM_004318	ENSG000005	ASPH	-	AAH BAH Caspartate protein-coding		
chr8-6152.5.648724	-1.14941	0.994519	-1.15574	0.247787	0.981636	chr8	61523389	61524315	+	0	NA	intron (NAluJr SIN	-59798	NM_004176	6720	Hs.59212ENM_004176	ENSG000005	SREBF1	-	SREBP1 bf sterol r protein-coding		
chr17-178.6.726214	0.150363	0.909279	-1.15516	0.248025	0.981636	chr17	17896203	17897415	+	0	NA	intron (NTigger15a	-24002	NM_001142	84514	Hs.38039	NM_032484	ENSG000005	GHDC	-	D11LGP1 LGH3 domai protein-coding	
chr17-425.6.726214	0.150363	0.909279	-1.15516	0.248025	0.981636	chr17	42818075	42818917	+	0	NA	intron (Nintron (N	40016	NM_031407	10075	Hs.13690ENM_031407	ENSG000005	HUWE1	-	ARF-BP1 FHECT, UB1 protein-coding		
chrX-5364.6.726214	0.150363	0.909279	-1.15516	0.248025	0.981636	chrX	53646375	53647032	+	0	NA	intron (Nintron (N	-1227	NM_001288	255403	Hs.63663ENM_001035	ENSG000005	ZNF718	-	zinc finger protein-coding		
chr4-1266.9.306382	-0.91073	0.788539	-1.15495	0.24811	0.981636	chr4	126668	127120	+	0	NA	intron (NAluSc5 SI	1222498	NR_003955	647121	Hs.69768ENR_003955	ENSG000005	EMBP1	-	emigin ppsudo		
chr1-1227.89.12074	0.375943	0.325592	-1.154643	0.248237	0.981636	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniAlR/Alph	13189	NM_001127	51324	Hs.24245ENM_016633	ENSG000005	SPG21	-	ABHD21 ACSPG21 abt protein-coding		
chr15-645.11.41763	0.813692	0.704847	-1.154424	0.248327	0.981636	chr15	64976169	64976393	+	0	NA	intron (NAluS2 SIN	9610	NM_033278	10612	Hs.59199ENM_006455	ENSG000005	TRIM3	-	BERP HAC1 tripartit protein-coding		
chr11-647.9.666276	0.881418	0.763556	-1.153436	0.248353	0.981636	chr11	66613703	66649599	+	0	NA	intron (NL2c LINE	32465	NM_001522	2975	Hs.37171ENM_001522	ENSG000005	GTF3C1	-	TFIIIC TFIIIf general tprotein-coding		
chr16-276.7.476086	0.103642	0.898375	-1.153466	0.248359	0.981636	chr16	27657307	27517594	+	0	NA	intron (Nintron (N	-1589467	NR_146735	1.02E+08	Hs.567934NR_106875	ENSG000005	LOC101927	-	uncharacterized protein-coding		
chr19-262.65.82624	0.407636	0.353437	-1.153348	0.248768	0.981636	chr19	26203861	26204067	+	0	NA	IntergeniAlR/Alph	10744	NM_152498	148789	Hs.49814ENM_152498	ENSG000005	B3GALNT2	-	B3GAlNAc-beta-1,3- protein-coding		
chr1-2354.11.45091	0.815777	0.702225	-1.153208	0.248825	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	intron (NAluSx1 SI	13773	NM_175767	3572	Hs.53208ENM_002184	ENSG000005	IL6ST	-	CD130 CDW interl leuk protein-coding		
chr5-5598.9.341514	-0.89602	0.777137	-1.15298	0.248918	0.981636	chr5	55980018	55982363	+	0	NA	intron (Nintron (N	78857	NM_001145	222234	Hs.20254ENM_147194	ENSG000005	FAM185A	-	family wiprotein-coding		
chr7-1028.9.341514	-0.89602	0.777137	-1.15298	0.248918	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (NAluP4 LIN	3534	NR_026903	201283	Hs.396447NM_153035	ENSG000005	AMZP21	-	archaelys pseudo		
chr17-645.9.11432	0.917809	0.796035	-1.152976	0.24892	0.981636	chr17	64971890	64972212	+	0	NA	intron (NAluJb SIN	2385	NM_001344	1603	Hs.82890	NM_001344	ENSG000005	DAD1	-	OST2 defender protein-coding	
chr14-225.6.145497	0.115742	0.967839	-1.152818	0.248985	0.981636	chr14	22587639	22587040	+	0	NA	intron (Nintron (N	6190	NM_001317	51657	Hs.11615	NM_016085	ENSG000005	STYXL1	-	DUSP24 MS serine/t protein-coding	
chr7-7602.6.145497	0.115742	0.967839	-1.152818	0.248985	0.981636	chr7	76024183	76024485	+	0	NA	intron (NTigger19f	23858	NM_001318	23268	Hs.500771NM_015221	ENSG000005	DNMBP	-	ARHGFB3 dynamn l protein-coding		
chr10-996.5.6233	-1.15976	1.006228	-1.15258	0.249081	0.981636	chr10	99889986	99890483	+	0	NA	intron (Nintron (N	63045	NM_001277	400818	Hs.450078NM_001037	ENSG000005	BNP9F	-	AEO1 NBPF memt protein-coding		
chr1-149.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	-77517	NM_014002	9641	Hs.32104ENM_014002	ENSG000005	IKBKE	-	IKK-E IKK inhibitor protein-coding		
chr1-2062.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (Nintron (N	84791	HS.52393ENM_032705	220002	ENM_22546	1.1ENSG000005	CYB561A3	-	Cyorf93 l cytochron protein-coding		
chr1-211.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr1	2.11E+08	2.11E+08	+	0	NA	intron (NMLTIN2 LI	9806	NR_026761	145226	Hs.415322ENM_152444	ENSG000005	RDH12	-	LCAI3 RP retinol c protein-coding		
chr11-615.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr11	61552126	61554288	+	0	NA	3' UTR (N3' UTR (N	4107	NM_001161	8482	Hs.24640	NM_003612	ENSG000005	SEMA7A	-	CD108 CDW semaphorin protein-coding	
chr14-677.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr14	67750964	67753240	+	0	NA	intron (Nintron (N	50216	NM_152444	57448	Hs.150107NM_016252	ENSG000005	BLRC6	-	ADOLLON Ebaculovir protein-coding		
chr15-744.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr15	74445335	74449279	+	0	NA	intron (Nintron (N	1578	NM_016252	9448	Hs.70101ENM_004834	ENSG000005	MAP4K4	-	FLH21957 mitogen-ε protein-coding		
chr2-3235.6.734072	0.104729	0.909309	-1.152225	0.249229	0.981636	chr2	32358443	32358270	+	0	NA	intron (NTHEID LTF	25458	NM_145687	169834	Hs.192877NM_001101	ENSG000005	ZNF883	-			



chr18-88c	7.898253	0.973442	0.849819	1.145471	0.252014	0.981636	chr18	8807001	8807219	+	0	NA	intron (Nintron (N	89729	NM_01521C	23255	Hs. 70792C	01521C	ENSG000000MTC1	CCDC165	[K]microtubul protein-coding
chr5-1111	10.59001	-0.84587	0.738539	-1.14532	0.252075	0.981636	chr5	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	8673	NM_139281	134430	Hs. 533237	NM_139281	ENSG000000WDR36	GLC1G	TA-WD repeat protein-coding
chr1-363f	5.495469	1.153512	1.007457	1.144975	0.25222	0.981636	chr1	3635633	3636737	+	0	NA	intron (Nintron (N	11170	NM_182752	127262	Hs. 20529	NM_182752	ENSG000000TPRG1L	FAM79A	h-tumor prc protein-coding
chr11-10f	5.495469	1.153512	1.007457	1.144975	0.25222	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	exon (NM exon (NM	17396	NM_00001E	38	Hs. 23237E	NM_00001E	ENSG000000ACAT1	ACAT	[MAT] acetyl-Cc protein-coding
chr1-465f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr1	4658259	46583489	+	0	NA	intron (Nintron (N	21394	NM_19897f	8569	Hs. 371594	NM_003684	ENSG000000MKNK1	MNK1	MAPK intc protein-coding
chr1-156f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	exon (NM exon (NM	11598	NM_020131	56893	Hs. 28373E	NM_020131	ENSG000000CUBQLN4	A1U	[Alu] ubi quilir protein-coding
chr10-29f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr10	29674993	29677333	+	0	NA	intron (Nintron (N	41192	NM_021738	6840	Hs. 49290E	NM_003174	ENSG000000SVIL	-	supervill protein-coding
chr12-35f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr12	35845251	35845608	+	0	NA	Intergeni ALR/Alph	1822933	NM_032834	84920	Hs. 109971	NM_032834	ENSG000000ALG10	ALG10	[DIALG10] alr protein-coding
chr16-507f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr16	5075525	5076479	+	0	NA	intron (NMLTIK LTF	3754	NM_00133C	56052	Hs. 59208E	NM_01910E	ENSG000000ALG1	CDG1K	[HM] ALG1 chit protein-coding
chr16-16f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr16	16258283	16258758	+	0	NA	intron (NML2 LINE L	25925	NM_173614	283820	Hs. 460141	NM_173614	ENSG000000NOMO2	NOMO2	PM5 NODAL mcr protein-coding
chr19-181f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr19	18123390	18125267	+	0	NA	exon (NM exon (NM	25512	NM_00129C	3594	Hs. 567294	NM_00553E	ENSG000000IL12RB1	CD212	[IL- inter] leuk protein-coding
chr19-181f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr19	18135676	18137970	+	0	NA	intron (NAluSx1 SI	16340	NR_162071	5296	Hs. 371344	NM_005027	ENSG000000PIK3R2	MPPH	[MPP] phosphoir protein-coding
chr2-995f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr2	99550474	99552472	+	0	NA	3' UTR (N3' UTR (N	61456	NR_135652	51455	Hs. 443077	NM_01631E	ENSG000000REV1	AIBP80	[RE] REV1 DNA protein-coding
chr2-20f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr2	20054996	20056006	+	0	NA	intron (Nintron (N	22462	NR_02970E	406961	NR_02970E	ENSG000000MIR185	MIRN185	[m] microRNA ncRNA	
chr4-840f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr4	840530	8406465	+	0	NA	intron (Nintron (N	34976	NM_003501	8310	Hs. 479122	NM_003501	ENSG000000ACO3	-	acyl-CoA protein-coding
chr5-142f	6.708648	1.042258	0.910606	1.144576	0.252385	0.981636	chr5	1.42E+08	1.42E+08	+	0	NA	exon (NM exon (NM	6790	NM_005471	10007	Hs. 63385E	NM_005471	ENSG000000GNPDA1	GNP1	[GNP] glucosam protein-coding
chr6-158f	6.435763	-1.09917	0.961113	-1.14364	0.252772	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	intron (NLI PA7 LN	12090	NM_20711E	404672	Hs. 356224	NM_20711E	ENSG000000GTF2H5	C6orf175	[general] t protein-coding
chr1-244f	6.767353	1.050572	0.919123	1.143016	0.253032	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (Nintron (N	1210	NM_02516C	80232	Hs. 49787E	NM_02516C	ENSG000000WDR26	CDW2	[G1D7W] repeat protein-coding
chr2-197f	6.186636	1.115502	0.97597	1.142967	0.253052	0.981636	chr2	19719920	19720591	+	0	NA	intron (NCPg-1875E	1786	NR_03761E	1.01E+08	Hs. 28374E	NR_03761E	ENSG000000SEPT5-GP1	GP1B1B	[GP1SEPT5-GP1] ncRNA
chr10-86f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr10	86930622	86931264	+	0	NA	Intergeni Intergeni	24844	NM_00133C	6623	Hs. 34947C	NM_003087	ENSG000000CSNCG	BCSG1	[SR] synrho protein-coding
chr11-46f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr11	46677261	46677400	+	0	NA	3' UTR (N3' UTR (N	23259	NM_00430E	392	Hs. 13886C	NM_00430E	ENSG000000ARHGAP1	CDC42GAP	[Rho] GTPas protein-coding
chr11-12f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	intron (NAluJb SIN	24750	NM_006597	3312	Hs. 180414	NM_006597	ENSG000000HSPA8	HEL-33	[HE] heat shoc protein-coding
chr12-10f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (NMSTB1 LTF	7991	NM_00114E	387882	Hs. 36893E	NM_20737E	ENSG000000C12orf75	AGD3	[OCC-] chromoson protein-coding
chr15-39f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr15	39998768	40000119	+	0	NA	intron (Nintron (N	39738	NM_003134	6727	Hs. 53373E	NM_003134	ENSG000000SRP14	ALURBP	signal r protein-coding
chr17-21f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr17	21544950	21545340	+	0	NA	intron (NMSTB1 LTF	6533	NR_160801	339263	Hs. 51401E	NM_00111E	ENSG000000LINC0269E	C17orf51	[long] intc ncRNA
chr2-132f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (NHAL1 LINE	77536	NR_13557E	1.02E+08	Hs. 680114	NR_13557E	ENSG000000NCKAP5-AS-	NCKAP5	arncRNA
chr3-160f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr3	1.6E+08	1.6E+08	+	0	NA	TTS (NM_CTS (NM_C	13886	NM_173084	286827	Hs. 212957	NM_173084	ENSG000000TRIM59	IFT80L	[MF] tripartit protein-coding
chr6-429f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr6	42976648	42977065	+	0	NA	intron (N2c LINE	2325	NR_13300E	5190	Hs. 65642E	NM_000287	ENSG000000PEX6	HMLR2	[PAF] peroxisom protein-coding
chr7-148f	5.633008	-1.14544	1.002252	-1.14287	0.253093	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	78838	NM_00137C	8454	Hs. 14680E	NM_00359E	ENSG000000CUL1	-	cullin 1 protein-coding
chr1-156f	4.450663	1.031204	0.902299	1.142862	0.253096	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (NMIR3 SINE	25078	NR_030527	768220	NR_030527	ENSG000000MIR765	MIRN765	[t] microRNA ncRNA	
chr9-104f	4.2393	1.314289	1.150341	1.142522	0.253237	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	30073	NM_00550E	19	Hs. 659274	NM_00550E	ENSG000000ABCA1	ABC-1	[ABCATP] bindi protein-coding
chr1-214f	8.143865	-0.94817	0.830233	-1.14205	0.253433	0.981636	chr1	2.14E+08	2.14E+08	+	0	NA	intron (Nintron (N	38317	NM_020197	56950	Hs. 66170	NM_020197	ENSG000000SMYD2	HSKM-B	[K] SET and I protein-coding
chr14-60f	6.394623	-1.10475	0.967351	-1.14203	0.253441	0.981636	chr14	60983328	60984069	+	0	NA	intron (Nintron (N	2008	NM_00135C	57570	Hs. 38015E	NM_02081C	ENSG000000TRMT5	COXP226	[tRNA] met protein-coding
chr1-320f	8.077302	-0.9591	0.839885	-1.14194	0.253479	0.981636	chr1	32030855	32031439	+	0	NA	intron (NAluJo SIN	17279	NM_001271	10657	Hs. 44589E	NM_00655E	ENSG000000KHDRBS1	Sam68	[p62K] RNA bi protein-coding
chr14-50f	0.77302	-0.9591	0.839885	-1.14194	0.253479	0.981636	chr14	50442395	50442662	+	0	NA	intron (NLMJC4 LIN	45230	NM_001367	8814	Hs. 280881	NM_00419E	ENSG000000CDKL1	KKTLAR	[F] cyclin d protein-coding
chr11-93f	8.151723	-0.9496	0.831585	-1.14192	0.253489	0.981636	chr11	93702931	93703524	+	0	NA	intron (NAluSx1 SI	18287	NR_00256E	619383	Hs. 66066E	NR_00256E	ENSG000000SCARN9A	Z32	[mgU2-SUMO] small Cc ncRNA
chr17-54f	8.151723	-0.9496	0.831585	-1.14192	0.253489	0.981636	chr17	5448042	5448287	+	0	NA	intron (NAluSx SIN	9009	NM_00121E	708	Hs. 55586E	NM_00121E	ENSG000000C1QB	COXP33	[C] complemer protein-coding
chr2-222f	8.151723	-0.9496	0.831585	-1.14192	0.253489	0.981636	chr2	2.23E+08	2.23E+08	+	0	NA	intron (Nintron (N	9343	NR_130154	10056	Hs. 47145E	NM_005687	ENSG000000FARSB	FARSLB	[FF] phenylal pseudo
chr10-40f	5.503327	1.150232	1.007347	1.141843	0.253519	0.981636	chr10	40171908	40172571	+	0	NA	Intergeni ALR/Alph	165580	NR_02438C	441666	NR_02438C	ENSG000000LOC441666-	-	zinc fing pseudo	
chr16-207f	5.503327	1.150232	1.007347	1.141843	0.253519	0.981636	chr16	2074842	2075530	+	0	NA	intron (NAluSx1 SI	15098	NR_03064E	1E+08	NR_03064E	ENSG000000MIR1225	MIRN1225	microRNA ncRNA	
chr4-139f	5.503327	1.150232	1.007347	1.141843	0.253519	0.981636	chr4	1391481	1393125	+	0	NA	Intergeni L1M4 LINE	14139	NM_00129C	54729	Hs. 52639E	NM_00129C	ENSG000000NKX1-1	HSP-153	[NKK1] homec protein-coding
chr1-449f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr1	44971506	44971999	+	0	NA	intron (NAluSg SIN	14843	NM_02036E	8891	Hs. 53354E	NM_02036E	ENSG000000EIF2B3	EIF2B3	[E] Eukaryot protein-coding
chr1-842f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr1	84239468	84240268	+	0	NA	Intergeni Intergeni	58236	NM_00124E	5567	Hs. 48732E	NM_002731	ENSG000000PRKACB	PKA	C-beta protein-coding
chr1-844f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr1	84485117	84485920	+	0	NA	intron (NTiger4b	6252	NM_02506E	80135	Hs. 48120E	NM_02506E	ENSG000000RPF1	BXDC5	ribosome protein-coding
chr15-80f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr15	80781494	80782761	+	0	NA	intron (Nintron (N	2757	NM_00129E	57214	Hs. 45908E	NM_01868E	ENSG000000CEMP1	CCSP1	[HYE] cell migr protein-coding
chr16-88f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr16	88399883	88400082	+	0	NA	Intergeni MIR SINE	27489	NM_001367	84627	Hs. 54925	NM_001127	ENSG000000ZNF469	BCS1	[BCS1] zinc fing protein-coding
chr17-75f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr17	75220833	75221850	+	0	NA	intron (NAluS6 SI	15662	NM_024844	79902	Hs. 362817	NM_024844	ENSG000000NUP85	FRONT1	[NF] nucleopor protein-coding
chr2-106f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr2	10605802	10606714	+	0	NA	intron (NMIR SINE	83707	NM_024894	79954	Hs. 222494	NM_024894	ENSG000000NOL10	PQB5	nucleolar protein-coding
chr5-536f	6.871796	-1.03122	0.903252	-1.14168	0.253589	0.981636	chr5	53683													

chr20-635	11.05932	-0.81279	0.717084	-1.13347	0.257019	0.981636	chr20	63522180	63523939	+	0	NA	TTS (NM_C TTS (NM_C	2294	NM_024299	79144	Hs.79625	NM_024299	ENSG000000PPDPF	C20orf145	pancreatic protein-coding
chr19-245	28.04944	0.538294	0.475113	1.13298	0.257222	0.981636	chr19	24976712	24977057	+	0	NA	IntergeniALR Alpha	-813437	NR_003603	1E+08	Hs.149312	NR_003603	ENSG000000HAVCR1P1	-	hepatitis pseudo
chr13-505	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr13	50013618	50014093	+	0	NA	3' UTR (A3' UTR (A	-1589	NM_173605	283518	Hs.660161	NM_173605	ENSG000000KCNRG	DLTET	potassium protein-coding
chr2-3315	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr2	31976556	31982777	+	0	NA	intron (Nintron (N	63369	NM_001166	4052	Hs.619319	NM_000627	ENSG000000LTBP1	-	latent t protein-coding
chr2-1795	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr2	1.8E+08	1.8E+08	+	0	NA	intron (NAlu Jo SIN	30258	NM_020944	57703	Hs.311363	NM_020944	ENSG000000CWC22	EIF4GL NC	C22 s plprotein-coding
chr3-1235	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (N(A)n Simp	420	NM_053031	4638	Hs.477375	NM_005965	ENSG000000MYLK	AAT7 KRP	myosin I protein-coding
chr3-1574	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	3577	NM_002852	5806	Hs.591288	NM_002852	ENSG000000PTX3	TNFAIP5 T	tenaxin protein-coding
chr7-8175	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr7	81732363	81733575	+	0	NA	intron (Nintron (N	37058	NM_001010	3082	Hs.396533	NM_000601	ENSG000000HGF	DFNB39 F	hepatocyt protein-coding
chr8-6155	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr8	61586765	61587878	+	0	NA	intron (Nintron (N	102490	NM_001164	444	Hs.332422	NM_004315	ENSG000000ASPH	AAH BAH C	aspartate protein-coding
chr8-9096	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr8	90969935	90970828	+	0	NA	intron (Nintron (N	14696	NM_001362	1E+08	Hs.733266	NM_001199	ENSG000000C8orf88	-	chromosom protein-coding
chr8-1304	5.658432	-1.13519	1.002056	-1.13286	0.257271	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	21059	NM_001362	50807	Hs.655552	NM_018482	ENSG000000ASAP1	AMAP1 CEN	ArfGAP wiprotein-coding
chr1-5197	6.683224	1.036722	0.915211	1.132768	0.257312	0.981636	chr1	51976762	51977090	+	0	NA	exon (NM_exon (NM	13774	NM_002867	5865	Hs.123072	NM_002867	ENSG000000CRAB3B	-	RAB3B, me protein-coding
chr15-25	6.683224	1.036722	0.915211	1.132768	0.257312	0.981636	chr15	25086629	25087532	+	0	NA	promoter-promoter-	554	NR_001293	727708	NR_001293	ENSG000000SNORD116	HBII-85	-1 small nucsnoRNA	
chr19-135	6.683224	1.036722	0.915211	1.132768	0.257312	0.981636	chr19	35023453	35024152	+	0	NA	intron (NMLTIK LTF	-6668	NM_001037	6324	Hs.436645	NM_001037	ENSG000000SCN1B	ATFB13 BF	sodium vcprotein-coding
chr3-4741	6.683224	1.036722	0.915211	1.132768	0.257312	0.981636	chr3	47416228	47416548	+	0	NA	intron (Nintron (N	35367	NM_001304	25930	Hs.25524	NM_015466	ENSG000000PTPN23	HD-PTP HE	protein tyrosine-coding
chr5-4897	35.31809	0.497793	0.43955	1.132507	0.257422	0.981636	chr5	48973351	48974271	+	0	NA	IntergeniALR Alpha	1467477	NM_198445	133418	Hs.561411	NM_198445	ENSG000000EMB	GP70	emigin protein-coding
chr11-708	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr11	70807055	70807265	+	0	NA	exon (NM_exon (NM	-55630	NR_073535	220070	Hs.326766	NM_145305	ENSG000000SHANK2-AS	C11orf76	SHANK2 arncRNA
chr11-857	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr11	85706325	85708154	+	0	NA	intron (NMRB SINE	11855	NM_001362	54843	Hs.369523	NM_003237	ENSG000000SYTL2	CHR115YT	synaptot protein-coding
chr12-112	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	exon (NM_exon (NM	-22594	NR_037433	1.01E+08	NR_037433	ENSG000000MIR3657	-	microRNA ncRNA	
chr2-364	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr2	36463007	36463428	+	0	NA	intron (Nintron (N	107439	NM_016441	51232	Hs.699247	NM_016441	ENSG000000CRIM1	CRIM-1 SE	cysteine protein-coding
chr2-1896	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (NMLTIAO LI	33969	NM_001321	5378	Hs.111745	NM_000534	ENSG000000PMS1	HNPC3 MI	PMS1 homc protein-coding
chr2-2296	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (NAlu Jr4 SI	44868	NM_001345	9320	Hs.572642	NM_004235	ENSG000000TRIP12	MRD49 TRI	thyroid t protein-coding
chr20-137	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr20	13798590	13799079	+	0	NA	intron (N L2c LINE	13806	NR_147982	79133	Hs.472165	NM_024120	ENSG000000NDUFAF5	C20orf7 V	NADH:ubiq protein-coding
chr4-7103	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr4	71039074	71039350	+	0	NA	IntergeniAlu Jr SIN	45563	NM_000788	1633	Hs.709	NM_000788	ENSG000000DCK	-	deoxycytiprotein-coding
chr5-1686	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr5	16866983	16867499	+	0	NA	intron (Nintron (N	69047	NM_012334	4651	Hs.481720	NM_012334	ENSG000000MYO10	-	myosin X protein-coding
chr5-7818	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr5	78180905	78181375	+	0	NA	intron (Nintron (N	113558	NM_001271	8546	Hs.532091	NM_003664	ENSG000000AP3B1	ADTB3 AD1	adaptor t protein-coding
chr8-6656	6.897219	-1.02302	0.903337	-1.13249	0.25743	0.981636	chr8	66568904	66569584	+	0	NA	intron (N LIPA13 LI	43974	NM_001080	4603	Hs.445898	NM_001080	ENSG000000MYBL1	A-MYB AMY	MYB protc protein-coding
chr3-1111	8.361745	-0.9947	0.878425	-1.13237	0.25748	0.981636	chr3	1.11E+08	1.11E+08	+	0	NA	exon (NM_exon (NM	50387	NM_001243	25945	Hs.293917	NM_015480	ENSG000000NECTIN3	CD113 CD	wnectin cp protein-coding
chr12-163	8.128149	-0.94522	0.834735	-1.13236	0.257483	0.981636	chr12	1636734	16372921	+	0	NA	intron (NAlu Jr SIN	7782	NM_032642	81029	Hs.306051	NM_030775	ENSG000000WNT57	-	Wnt familprotein-coding
chr12-861	8.128149	-0.94522	0.834735	-1.13236	0.257483	0.981636	chr12	88195313	88195751	+	0	NA	exon (NM_exon (NM	53225	NM_001366	160418	Hs.331268	NM_181785	ENSG000000TMT3	LIS8 SMI	transment protein-coding
chr19-494	8.128149	-0.94522	0.834735	-1.13236	0.257483	0.981636	chr19	4948075	4948565	+	0	NA	intron (Nintron (N	15633	NR_039902	1.01E+08	NR_039902	ENSG000000MIR4747	mir-4747	microRNA ncRNA	
chr5-3888	8.128149	-0.94522	0.834735	-1.13236	0.257483	0.981636	chr5	38851238	38852209	+	0	NA	intron (N THE1B LTF	5711	NM_001322	9180	Hs.120655	NM_003990	ENSG000000OSMR	IL-31R	-beconostat iprotein-coding
chr6-7508	8.128149	-0.94522	0.834735	-1.13236	0.257483	0.981636	chr6	75083791	75086007	+	0	NA	3' UTR (N3' UTR (N	43883	NR_145788	1.1E+08	NR_145788	ENSG000000SNORD156	-	small nucsnoRNA	
chr1-2628	6.863938	-1.02954	0.909233	-1.13232	0.257501	0.981636	chr1	26281025	26281541	+	0	NA	TTS (NM_C TTS (NM_C	1197	NM_031285	83442	Hs.109051	NM_031285	ENSG000000SH3BGRL3	HEL-S-297	SH3 domaiprotein-coding
chr18-125	6.863938	-1.02954	0.909233	-1.13232	0.257501	0.981636	chr18	12598229	12599156	+	0	NA	intron (N LIMB4 LIN	10681	NM_001013	81929	Hs.301045	NM_031210	ENSG000000SEHL1	SEC13L SE	SEHL1 like protein-coding
chr8-6155	6.863938	-1.02954	0.909233	-1.13232	0.257501	0.981636	chr8	61650592	61651736	+	0	NA	intron (Nintron (N	38647	NM_001164	444	Hs.332422	NM_004315	ENSG000000ASPH	AAH BAH C	aspartate protein-coding
chr8-9372	6.863938	-1.02954	0.909233	-1.13232	0.257501	0.981636	chr8	93729945	93731092	+	0	NA	non-codiron-codir	-9593	NR_027255	55472	Hs.192788	NM_018605	ENSG000000RBM12B-AS	C8orf39 F	FRBM12B arncRNA
chr1-1742	8.47712	0.921446	0.813838	1.132223	0.257541	0.981636	chr1	1.74E+08	1.74E+08	+	0	NA	intron (N LTR12 LTF	6277	NM_001366	9910	Hs.585375	NM_014857	ENSG000000RABGAP1L	HHL TBC1I	RAB GTPas protein-coding
chr1-2064	8.47712	0.921446	0.813838	1.132223	0.257541	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	3' UTR (N3' UTR (N	-14947	NM_014002	9641	Hs.321045	NM_014002	ENSG000000IKKBE	IKK-E IKK	inhibitor protein-coding
chr3-3355	8.47712	0.921446	0.813838	1.132223	0.257541	0.981636	chr3	33531288	33532129	+	0	NA	intron (NAlu Sp SIN	-91303	NM_014517	7342	Hs.729120	NM_014517	ENSG000000CUBP1	LBP-1B L	upstream protein-coding
chr7-1567	8.47712	0.921446	0.813838	1.132223	0.257541	0.981636	chr7	1567011	1567523	+	0	NA	TTS (NM_C TTS (NM_C	2765	NM_032302	84262	Hs.446311	NM_032302	ENSG000000PSMG3	C7orf48 F	proteasom protein-coding
chr9-1311	8.47712	0.921446	0.813838	1.132223	0.257541	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	exon (NM_exon (NM	-26244	NM_001315	8021	Hs.654533	NM_005058	ENSG000000NUP214	CAIN CAN	nucleopor protein-coding
chr1-9988	8.443839	0.919041	0.811845	1.132041	0.257617	0.981636	chr1	99885341	99885743	+	0	NA	intron (N MERIA DNA	34567	NM_000645	178	Hs.904	NM_000025	ENSG000000CAGL	GDE	amyo-alf protein-coding
chr13-111	8.443839	0.919041	0.811845	1.132041	0.257617	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (N CpG	13936	NM_001354	8874	Hs.508735	NM_003895	ENSG000000ARHGFE7	BETA-PIX	Rho guaniprotein-coding
chr17-182	8.443839	0.919041	0.811845	1.132041	0.257617	0.981636	chr17	1804145	1804588	+	0	NA	intron (NAlu Sx SIN	25536	NM_052925	114826	Hs.514602	NM_052925	ENSG000000SMYD4	ZMYND21	SET and W protein-coding
chr19-424	8.443839	0.919041	0.811845	1.132041	0.257617	0.981636	chr19	42224254	42224463	+	0	NA	intron (Nintron (N	4042	NM_133444	116115	Hs.137282	NM_133444	ENSG000000ZNF526	-	zinc fingprotein-coding
chr4-5587	8.443839	0.919041	0.811845	1.132041	0.257617	0.981636	chr4	55877962	55878901	+	0	NA	intron (Nintron (N	24781	NM_018261	55763	Hs.269665	NM_018261	ENSG000000EXOC1	BM-102 S	exocyst c protein-coding
chr15-484	4.213876	1.306036	1.153753	1.131989	0.257639	0.981636	chr15	48843099	48841642	+	0	NA	intron (Nintron (N	-29951	NM_001194	22995	Hs.443005	NM_014985	ENSG000000CEP152	MCPH4 MC	centrosom protein-coding
chr21-418	4.213876	1.306036	1.153753	1.131989	0.257639	0.981636	chr21	41813601	41814993	+	0	NA	intron (Nintron (N	-47245	NM_020635	54101	Hs.517310				



chr7-7662 6.685074	1.050371	0.935387	1.22927	0.261469	0.981636	chr7	76622320	76622597	+	0 NA	intron (AluSg4 SI	4845 NM_152992	22932 Hs. 488877NM_01223C	ENS00000POMZP3	POM-ZP3 FPM121	ar protein-coding	
chr20-41C 9.810828	-0.85587	0.762291	-1.12275	0.261542	0.981636	chr20	41084832	41086569	+	0 NA	intron (L1ME3G LI	-51843 NM_182811	5335 Hs. 268177NM_00266C	ENS00000PLCG1	NCKAP3 PI	phospholipase protein-coding	
chr2-7454 8.120291	-0.94368	0.840715	-1.12247	0.261663	0.981636	chr2	74543513	74544395	+	0 NA	intron (intron (	-5066 NM_001197	1796 Hs. 103854NM_00138I	ENS00000COK1	P62DOK pf	docking protein-coding	
chr7-1301 8.120291	-0.94368	0.840715	-1.12247	0.261663	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (AluJb SIN	25538 NM_003284	84928 Hs. 26724E	ENS00000TMEM209	NET31	transmembrane protein-coding	
chr1-1142 8.161431	-0.93968	0.837415	-1.12212	0.261812	0.981636	chr1	1.14E+08	1.14E+08	+	0 NA	3' UTR (3' UTR (	114929 NM_03302C	51592 Hs. 26837	NM_01590C	ENS00000TRIM33	ECTO PTC7	tripartite protein-coding
chr7-1344 8.510402	0.923863	0.823592	1.121747	0.26197	0.981636	chr7	1.34E+08	1.34E+08	+	0 NA	intron (intron (	2509 NM_00162E	231 Hs. 52121E	NM_00162E	ENS00000AKR1B1	ADR ALDR1	aldo-ketose reductase protein-coding
chr2-1271 11.00062	-0.82197	0.823592	-1.12145	0.262096	0.981636	chr2	1.28E+08	1.28E+08	+	0 NA	intron (intron (	21879 NM_01796E	55677 Hs. 46987E	NM_01796E	ENS00000TWS1		interacts protein-coding
chr4-3927 7.896403	0.961699	0.857796	1.121127	0.262234	0.981636	chr4	39273399	39273860	+	0 NA	intron (MER68 LTF	91100 NM_025132	57728 Hs. 43848E	NM_025132	ENS00000WDR19	ATD5 CED4WD	repeat protein-coding
chr9-1282 7.896403	0.961699	0.857796	1.121127	0.262234	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	intron (LTR13A LI	3653 NM_00104C	375757 Hs. 259594NM_00104C	ENS00000SWI5	C9orf119 SWI5	homeobox protein-coding	
chr11-352 9.828394	-0.84897	0.757327	-1.12101	0.262284	0.981636	chr11	35203368	35211480	+	0 NA	intron (intron (	145794 NR_145794	1.1E+08	NR_145794	SNORD164		small nucleolar RNA
chr10-406 17.67924	0.662811	0.591413	1.120725	0.262405	0.981636	chr10	40643502	40644673	+	0 NA	IntergeniALR Alphe	1723958 NR_02438C	441666 Hs. 25572E	NR_02438C	ENS00000LOC441666		zinc finger pseudo
chr8-1312 6.938359	-1.01802	0.908434	-1.12063	0.262445	0.981636	chr8	13128428	13128856	+	0 NA	intron (AluY SINE	4647 NM_006094	10395 Hs. 13429E	NM_006094	ENS00000DLC1	ARHGAP7 F	DLC1 Rho protein-coding
chr4-1031 6.86765	-1.10245	0.984179	-1.12018	0.262639	0.981636	chr4	1.03E+08	1.03E+08	+	0 NA	intron (L2a LINE	-48895 NM_02013E	56898 Hs. 12469E	NM_02013E	ENS00000BDH2	DHRS6 EFA3	hydroxyprotein-coding
chr1-2562 6.691082	1.033917	0.923152	1.119986	0.26272	0.981636	chr1	22506262	22507232	+	0 NA	intron (intron (	54896 NM_00133C	9923 Hs. 41896E	NM_01487C	ENS00000ZBT40	ZNF923	zinc finger protein-coding
chr22-466 6.691082	1.033917	0.923152	1.119986	0.26272	0.981636	chr22	46673387	46674946	+	0 NA	intron (intron (	53780 NM_015124	23151 Hs. 47515E	NM_015124	ENS00000GRAMD4	DIP	GRAM domain protein-coding
chr7-9036 6.691082	1.033917	0.923152	1.119986	0.26272	0.981636	chr7	90361349	90361874	+	0 NA	intron (L1P46 LIN	14895 NM_033107	85865 Hs. 593547NM_033107	ENS00000GTPBP10	ObgH2 UGCGTP	bindin protein-coding	
chr1-1564 10.19475	0.836231	0.74672	1.119873	0.262768	0.981636	chr1	1.56E+08	1.56E+08	+	0 NA	exon (NM_exon (NM_	10939 NM_001271	4209 Hs. 314327NM_00592C	ENS00000MEF2D		myocyte protein-coding	
chr1-2202 10.19475	0.836231	0.74672	1.119873	0.262768	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (THE1C-int	17487 NR_001587	6791 Hs. 65484E	NR_001587	AURKAP1	AURKAPS1	aurora kinase pseudo
chr1-2325 10.19475	0.836231	0.74672	1.119873	0.262768	0.981636	chr1	2.33E+08	2.33E+08	+	0 NA	intron (L2a LINE	6897 NR_138027	84284 Hs. 64271E	NM_032324	ENS00000NTPCR	Clorf57	nucleoside protein-coding
chr3-4334 10.19475	0.836231	0.74672	1.119873	0.262768	0.981636	chr3	43343550	43343749	+	0 NA	intron (intron (	8131 NR_046757	1.01E+08	Hs. 600984NR_046757	SNRK-AS1		SNRK anticRNA
chr19-104 6.649943	1.033756	0.923303	1.119628	0.262872	0.981636	chr19	10464100	10464546	+	0 NA	intron (AluSg SIN	11831 NM_006202	5141 Hs. 89901	NR_006202	ENS00000PE4A	DPPE2 PDF	phosphodiesterase protein-coding
chr19-151 6.649943	1.033756	0.923303	1.119628	0.262872	0.981636	chr19	15186229	15186847	+	0 NA	intron (AluSx1 SI	-7188 NR_10685E	1.02E+08	NR_10685E	ENS00000MIR6795	hsa-mir-ε	microRNA ncRNA
chr21-366 6.649943	1.033756	0.923303	1.119628	0.262872	0.981636	chr21	36050308	36050560	+	0 NA	intron (intron (	9930 NM_001007	54093 Hs. 60620C	NM_01743E	ENS00000CSETD4	C21orf18 SET	domain protein-coding
chr4-8386 6.649943	1.033756	0.923303	1.119628	0.262872	0.981636	chr4	8386958	8387346	+	0 NA	intron (intron (	53571 NM_003501	8310 Hs. 47912E	NM_003501	ENS00000ACOX3		acyl-CoA protein-coding
chr5-1394 6.649943	1.033756	0.923303	1.119628	0.262872	0.981636	chr5	1.39E+08	1.39E+08	+	0 NA	intron (AluJr SIN	5019 NM_15268E	202052 Hs. 483537NM_15268E	ENS00000DNAJ18		DnaJ heat protein-coding	
chr1-2916 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr1	29164283	29165238	+	0 NA	intron (intron (	17140 NM_00562E	6429 Hs. 46997C	NM_00562E	ENS00000SRSP4	SFRS4 SRF	serine arginine protein-coding
chr1-180C 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (intron (	-67409 NM_001004	5768 Hs. 71917E	NM_00282E	ENS00000QSOX1	Q6 QSCN6	quiescin protein-coding
chr13-445 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr13	44960018	44960236	+	0 NA	intron (AluSg SIN	29344 NM_01234E	26747 Hs. 52500E	NM_01234E	ENS00000NUFIP1	NUFIP baE	nuclear protein-coding
chr13-11 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr13	1.1E+08	1.1E+08	+	0 NA	intron (THE1B LTF	-5449 NR_10704C	1.02E+08	NR_10704C	ENS00000MIR8073	hsa-mir-ε	microRNA ncRNA
chr19-192 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr19	1922607	1922806	+	0 NA	intron (intron (	17307 NM_00132E	113178 Hs. 14498E	NM_079834	ENS00000SCAMP	SCAMP-4	secretory protein-coding
chr3-129 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr3	1.29E+08	1.29E+08	+	0 NA	intron (intron (	9955 NR_00299E	677797 Hs. 71139E	NR_00299E	ENS00000SNORA7B	ACA7B	small nucleolar RNA
chr5-1507 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr5	1.51E+08	1.51E+08	+	0 NA	intron (AluSx SIN	7913 NM_032947	85027 Hs. 29444	NM_032947	ENS00000SMIM3	C5orf62	small intron protein-coding
chr9-122 5.650574	-1.133	1.012198	-1.11935	0.262991	0.981636	chr9	1.23E+08	1.23E+08	+	0 NA	intron (L2c LINE	36718 NM_012197	23637 Hs. 271341NM_012197	ENS00000RABGAP1	CAPGCNA TRAB	GTPase protein-coding	
chr1-439 5.485761	1.140275	1.01873	1.11931	0.263008	0.981636	chr1	43962536	43963553	+	0 NA	intron (intron (	-6966 NM_00131E	1802 Hs. 63239E	NM_001384	ENS00000DPH2	DPH2L2	diphthamide protein-coding
chr1-2302 5.485761	1.140275	1.01873	1.11931	0.263008	0.981636	chr1	2.3E+08	2.3E+08	+	0 NA	intron (AluSx1 SI	170155 NM_00125E	79605 Hs. 52046E	NM_024554	ENS00000PGDB5		piggyBac protein-coding
chr14-10C 5.485761	1.140275	1.01873	1.11931	0.263008	0.981636	chr14	1E+08	1E+08	+	0 NA	3' UTR (3' UTR (	14035 NR_10682E	1.02E+08	NR_10682E	ENS00000MIR6764	hsa-mir-ε	microRNA ncRNA
chr20-28 5.485761	1.140275	1.01873	1.11931	0.263008	0.981636	chr20	28315580	28316224	+	0 NA	IntergeniALR Alphe	286763 NR_13231E	1E+08	Hs. 529357NR_13231E	ENS00000FRG1CP		FSHD repeat pseudo
chr22-302 5.485761	1.140275	1.01873	1.11931	0.263008	0.981636	chr22	30283187	30286572	+	0 NA	TTS (NM_C	4748 NM_001037	652968 Hs. 44495E	NM_001037	ENS00000CASTOR1	GATSL3	cytosolic protein-coding
chr22-43 5.485761	1.140275	1.01873	1.11931	0.263008	0.981636	chr22	43932842	43934858	+	0 NA	intron (intron (	10045 NM_02522E	80339 Hs. 65480C	NM_02522E	ENS00000PNPLA3	ADPN C22c	patatin protein-coding
chr14-601 6.85608	-1.02783	0.918541	-1.11898	0.263149	0.981636	chr14	60130403	60130844	+	0 NA	intron (MLT1A LTF	34775 NM_01602E	51635 Hs. 59719	NM_01602E	ENS00000DHR57	CGI-86 SE	dehydrogenase protein-coding
chr5-623 6.85608	-1.02783	0.918541	-1.11898	0.263149	0.981636	chr5	62392330	62394271	+	0 NA	intron (FLAM_A SI	10605 NM_00134E	27292 Hs. 73166E	NM_01447E	ENS00000DITM1	DIM1 DITM1	rRNA protein-coding
chr10-87 5.691173	-1.12675	1.007125	-1.11878	0.263234	0.981636	chr10	87804794	87805522	+	0 NA	intron (intron (	13048 NM_001321	84896 Hs. 43594E	NM_03281C	ENS00000ATAD1	AFCDC1 FNF	ATPase protein-coding
chr15-654 6.830656	-1.03634	0.926393	-1.11868	0.263275	0.981636	chr15	65478419	65478659	+	0 NA	intron (AluSx SIN	38735 NM_19796C	54878 Hs. 45860E	NM_01774E	ENS00000DPPP8	DP8 DPRP	dipeptidyl protein-coding
chr2-179 6.830656	-1.03634	0.926393	-1.11868	0.263275	0.981636	chr2	1.8E+08	1.8E+08	+	0 NA	intron (MER44A DN	21542 NM_02094E	57703 Hs. 31136E	NM_02094E	ENS00000CWC22	E1F4GL NCWC22	spl protein-coding
chr6-117 6.830656	-1.03634	0.926393	-1.11868	0.263275	0.981636	chr6	1.18E+08	1.18E+08	+	0 NA	intron (LTR28B LI	19336 NM_001017	57120 Hs. 19153E	NM_02039E	ENS00000GOPC	CAL FIG1	golgi associated protein-coding
chr1-151 8.484978	0.919341	0.821882	1.118581	0.263319	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	exon (NM_exon (NM_	6883 NM_00125E	8991 Hs. 63246E	NM_003944	ENS00000SELENBP1	EHHM70 HEL	selenium protein-coding
chr10-324 8.484978	0.919341	0.821882	1.118581	0.263319	0.981636	chr10	32487655	32488363	+	0 NA	intron (L1P44 LIN	41869 NR_109827	79741 Hs. 585464NM_02468E	ENS00000CCDC7	BIOT2 Bic	coiled-coil protein-coding	
chr12-10 8.484978	0.919341	0.821882	1.118581	0.263319	0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	intron (AluSc SIN	5138 NM_001161	54434 Hs. 19976E	NM_018984	ENS00000CSSH1	SSH1L	slingshot protein-coding
chr9-669 8.484978	0.919341	0.821882	1.118581	0.263319	0.981636	chr9	66911917	66917414	+	0 NA	intron (L1MB7 LIN	11304 NR_13425E	26149 Hs. 52214E	NM_03316C	ENS00000ZNF658		zinc finger protein-coding
chr15-491 11.04361	-0.8106	0.724744	-1.11846	0.26337	0.981636	chr15											



chr5-135c	4.896816	-1.18584	1.070859	-1.10737	0.268133	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	Intergeni	Intergeni	-7125 NR_161235	1.01E+08	NR_161235	C5orf66	-	chromosomncRNA					
chr5-1494	4.896816	-1.18584	1.070859	-1.10737	0.268133	0.981636	chr5	1.49E+08	1.49E+08	+	0	NA	intron	(intron)	(N	3955 NR_105056	728264	Hs. 519666	NR_027180	CARMN	CARMEN MI cardiac nncRNA				
chr7-140c	4.896816	-1.18584	1.070859	-1.10737	0.268133	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron	(intron)	(N	21817 NM_02275c	64761	Hs. 12646	NM_02275c	ENSG000003PARP12	ARTD12 MS poly (ADP- protein-coding				
chr7-140c	4.896816	-1.18584	1.070859	-1.10737	0.268133	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron	(intron)	(N	17982 NM_02275c	64761	Hs. 12646	NM_02275c	ENSG000003PARP12	ARTD12 MS poly (ADP- protein-coding				
chr8-130c	4.896816	-1.18584	1.070859	-1.10737	0.268133	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron	(intron)	(N	-23590 NR_00276c	29065	Hs. 63931	NR_00276c	ASAP1-IT1 ASAP1 intrncRNA					
chr16-22c	9.894957	-0.84022	0.75876	-1.10736	0.268138	0.981636	chr16	22341282	22341668	+	0	NA	Intergeni	AluSx SIN	33144 NM_00180c	1039	Hs. 51343	CNM_00180c	ENSG000003CCR2	CCR2 Yo cerebellar protein-coding					
chr21-26c	4.904674	-1.18817	1.073236	-1.10709	0.268255	0.981636	chr21	26928679	26929224	+	0	NA	intron	(intron)	(N	-25010 NR_03991c	1.01E+08	NR_03991c	ENSG000003MIR4759	-	microRNA ncRNA				
chr17-43c	10.75004	0.807802	0.729743	1.106967	0.268308	0.981636	chr17	43399941	43400986	+	0	NA	3' UTR	(3' UTR)	(N	1470 NM_001661	379	Hs. 18315	NR_001661	ENSG000003ARL4D	ARF4 ARI ADP ribosom protein-coding				
chr14-761c	8.630745	-0.89085	0.804973	-1.10669	0.26843	0.981636	chr14	76180777	76182070	+	0	NA	intron	(intron)	(N	27069 NR_110314	55668	Hs. 41023	1NM_01792c	ENSG000003PATCH2L	C14orf118 G-patch c protein-coding				
chr19-124	10.69133	0.802097	0.724857	1.106559	0.268484	0.981636	chr19	12463898	12468080	+	0	NA	intron	(intron)	(N	18822 NM_152601	16305	Hs. 63162	2NM_152601	ENSG000003ZNF709	-	zinc fing protein-coding			
chr1-149c	12.44224	0.751638	0.679306	1.106478	0.26852	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron	(intron)	(N	19524 NM_001277	400818	Hs. 44508	CNM_001037	ENSG000003NBPF9	AEO1	NBPF memt protein-coding			
chr20-324	8.981566	0.87332	0.789562	1.106082	0.268691	0.981636	chr20	32451768	32453319	+	0	NA	intron	(intron)	(N	30947 NM_001351	140688	Hs. 51697	ENM_08061c	ENSG000003NOL4L	C20orf112 nucleolar protein-coding				
chr19-25c	21.18106	0.626697	0.566897	1.105964	0.268742	0.981636	chr19	25520214	25520844	+	0	NA	Intergeni	ALR/Alpha	-1357282 NR_00360c	399746	Hs. 14931	2NR_00360c	ENSG000003HAVCR1P1	-	hepatitis pseudo				
chr10-40c	10.2026	0.83444	0.754669	1.105705	0.268854	0.981636	chr10	40081263	40082143	+	0	NA	Intergeni	ALR/Alpha	1385102 NR_045000	441234	Hs. 53312	1NM_00115c	ENSG000003ZNF716	-	zinc fing protein-coding				
chr7-602c	10.2026	0.83444	0.754669	1.105705	0.268854	0.981636	chr7	60234792	60235021	+	0	NA	Intergeni	ALR/Alpha	2784729 NM_00115c	7750	Hs. 50743	3NR_00345c	ENSG000003ZMY2	FIM MYM Zinc fing protein-coding					
chr13-20c	8.589606	-0.8945	0.809016	-1.10567	0.268871	0.981636	chr13	20012393	20012592	+	0	NA	intron	(intron)	(N	52678 NR_14836c	26010	Hs. 12032	2NM_01553c	ENSG000003SPM2SL	DNAETP6 Spermatog protein-coding				
chr2-20c	8.589606	-0.8945	0.809016	-1.10567	0.268871	0.981636	chr2	2E+08	2E+08	+	0	NA	intron	(intron)	(N	22387 NM_00128c	28996	Hs. 73141	7NM_02274c	ENSG000003HIPK2	PROO593	homodome protein-coding			
chr7-1397	8.589606	-0.8945	0.809016	-1.10567	0.268871	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron	(intron)	(N	69711 NM_00111c	147837	Hs. 66351	CNM_14527c	ENSG000003ZNF563	-	zinc fing protein-coding			
chr19-12c	10.72462	0.804137	0.727367	1.105545	0.268924	0.981636	chr19	12318576	12321684	+	0	NA	intron	(intron)	(N	13503 NM_14527c	64934	Hs. 12560	ENM_00101c	ENSG000003C9orf152	ba470J20	chromosom protein-coding			
chr9-110c	8.622888	-0.88948	0.804805	-1.10521	0.269069	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	3' UTR	(3' UTR)	(N	36493 NM_00101c	401516	Hs. 12560	ENM_00101c	ENSG000003MIR610	MIRN610 miRNA ncRNA				
chr11-28c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr11	28033618	28037048	+	0	NA	intron	(intron)	(N	-21482 NR_030341	6814	Hs. 64839	4NM_00141c	ENSG000003EIF4B	EIF-4B PF eukaryot protein-coding				
chr12-53c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr12	53012833	53013707	+	0	NA	intron	(intron)	(N	6814 NM_00133c	221143	Hs. 26674	NM_17492c	ENSG000003EEF1AKMT1	ESP13 N6 EEF1A lys protein-coding				
chr13-207	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr13	20794752	20795762	+	0	NA	intron	(intron)	(N	-21296 NM_00131c	10128	Hs. 36808	4NM_13325c	ENSG000003LRP3C	CLONE-23c	leucine i protein-coding			
chr2-439c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr2	43969015	43969967	+	0	NA	intron	(intron)	(N	88042 NM_01461c	23200	Hs. 47842	2NM_01461c	ENSG000003ATP11B	ATP1F ATF ATPase p protein-coding				
chr3-182c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr3	1.83E+08	1.83E+08	+	0	NA	intron	(intron)	(N	27981 NM_00134c	10983	Hs. 51882	7NM_00683c	ENSG000003CCNI	CCNI1 CYC cyclin I protein-coding				
chr4-770c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr4	77046710	77047148	+	0	NA	TTS	(NM_C TTS)	(NM_C	27981 NM_00134c	3480	Hs. 48734	1NM_00735c	ENSG000003GNA12	NNX3 RMP G protein protein-coding				
chr7-283c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr7	2893737	2841920	+	0	NA	intron	(intron)	(N	3480 NM_00735c	6482	Hs. 37425	2NM_00303c	ENSG000003ST3GAL1	Gal-1 Nac6S ST3 beta protein-coding				
chr8-133c	4.92224	-1.17413	1.063048	-1.1045	0.269378	0.981636	chr8	1.34E+08	1.34E+08	+	0	NA	intron	(intron)	(N	56856 NM_00303c	9479	Hs. 46307	4NM_00517c	ENSG000003ATP6VOA1	ATP6N1 AT ATPase H+ protein-coding				
chr17-424	8.948285	0.870982	0.788873	1.104084	0.269557	0.981636	chr17	42468194	42468521	+	0	NA	intron	(intron)	(N	10949 NM_00312c	6713	Hs. 71465	NR_00312c	ENSG000003SQLE	-	qualene protein-coding			
chr8-125c	8.948285	0.870982	0.788873	1.104084	0.269557	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	intron	(intron)	(N	10949 NM_00312c	253827	Hs. 33902	4NM_19808c	ENSG000003MSRB3	DFNB74	methionin protein-coding			
chr12-65c	9.914785	-1.01269	0.91728	-1.10401	0.269588	0.981636	chr12	65309017	65309891	+	0	NA	intron	(intron)	(N	30467 NM_00119c	2821	Hs. 46647	1NM_00017c	ENSG000003GPI	AGN GPI glucose-C protein-coding				
chr19-34c	6.914785	-1.01269	0.91728	-1.10401	0.269588	0.981636	chr19	34320576	34321150	+	0	NA	intron	(intron)	(N	-43877 NM_001184	407040	NR_02961c	ENSG000003MIR34A	-	microRNA ncRNA				
chr1-915c	6.665658	1.02816	0.931369	1.103924	0.269626	0.981636	chr1	9157023	91571490	+	0	NA	intron	(intron)	(N	-5479 NR_02961c	5817	Hs. 17184	4NM_00650c	ENSG000003PVR	CD155 HVE PVR cell protein-coding				
chr19-44c	6.665658	1.02816	0.931369	1.103924	0.269626	0.981636	chr19	44632046	44632245	+	0	NA	intron	(intron)	(N	-11653 NM_00113c	10056	Hs. 47145	2NM_00568c	ENSG000003FARSB	FARSLB PF phenylal protein-coding				
chr2-222c	3.70118	-1.39009	1.259308	-1.10385	0.269656	0.981636	chr2	2.23E+08	2.23E+08	+	0	NA	intron	(intron)	(N	65162 NR_130154	1056	Hs. 47145	2NR_03993c	ENSG000003MIR4777	-	microRNA ncRNA			
chr2-231c	7.220952	0.970023	0.878957	1.103606	0.269764	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron	(intron)	(N	-69629 NR_03993c	10141	Hs. 17797	2NM_00575c	ENSG000003LINC01587	C4orf6 a c long intncRNA				
chr4-557c	7.220952	0.970023	0.878957	1.103606	0.269764	0.981636	chr4	5573642	5574272	+	0	NA	intron	(intron)	(N	48801 NR_126517	11163	NR_13621c	1.05E+08	08	Hs. 64380	1NR_13621c	ENSG000003VCAN-AS1	-	VCAN antincRNA
chr5-8357	7.220952	0.970023	0.878957	1.103606	0.269764	0.981636	chr5	83572794	83574161	+	0	NA	intron	(intron)	(N	-11163 NR_13621c	2878	Hs. 38679	2NM_00208c	ENSG000003GPX3	GPX-P GSE glutathic protein-coding				
chr5-151c	7.220952	0.970023	0.878957	1.103606	0.269764	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron	(intron)	(N	15230 NM_00132c	51622	Hs. 53000	CNM_01562c	ENSG000003CCZ1	C7orf28A CCZ1 homc protein-coding				
chr7-590c	7.220952	0.970023	0.878957	1.103606	0.269764	0.981636	chr7	5906036	5907324	+	0	NA	intron	(intron)	(N	7947 NM_01562c	9819	Hs. 72247	7NM_01477c	ENSG000003TSC22D2	TILZ4a T TSC22 don protein-coding				
chr3-1504	11.57163	-0.7222	0.700087	-1.10301	0.270024	0.981636	chr3	1.5E+08	1.5E+08	+	0	NA	intron	(intron)	(N	4245 NM_00130c	23627	NR_10672c	1.02E+08	08	NR_10672c	ENSG000003MIR6079	-	microRNA ncRNA	
chr1-4381	4.888958	-1.18359	1.07328	-1.10278	0.270122	0.981636	chr1	43814896	43815095	+	0	NA	intron	(intron)	(N	-23627 NR_10672c	24295	NR_13872c	54879	Hs. 20192	1NM_01774c	ENSG000003ST7L	-	uncharacterncRNA	
chr1-112c	4.888958	-1.18359	1.07328	-1.10278	0.270122	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron	(intron)	(N	24295 NM_13872c	41831	NR_11077c	1.02E+08	08	Hs. 43690	2NR_11077c	ENSG000003LOC101927	-	uncharacterncRNA
chr18-107	4.888958	-1.18359	1.07328	-1.10278	0.270122	0.981636	chr18	10703494	10704035	+	0	NA	intron	(intron)	(N	41831 NR_11077c	31376	NR_00137c	5723	Hs. 51265	5NM_00457c	ENSG000003PSPH	PSP PSPH phospho protein-coding		
chr7-561c	4.888958	-1.18359	1.07328	-1.10278	0.270122	0.981636	chr7	56109338	56202099	+	0	NA	intron	(intron)	(N	31376 NM_00137c	374768	Hs. 71059	9NM_19933c	ENSG000003SPEM1	C17orf83	spermatoc protein-coding			
chr17-741	8.400849	0.907834	0.823324	1.102645	0.270181	0.981636	chr17	7414862	7415798	+	0	NA	intron	(intron)	(N	-4994 NM_19933c	1300	Hs. 52033	3NM_00049c	ENSG000003COL10A1	-	collagen protein-coding			
chr6-1161	8.400849	0.907834	0.823324	1.102645	0.270181	0.981636	chr6	1.16E+08	1.16E+08	+	0	NA	intron	(intron)	(N	11277 NM_00049c	29563	NR_00113c	5610	Hs. 13143	1NM_00275c	ENSG000003EIF2AK2	EIF2AK1 F eukaryot protein-coding		
chr2-3711	7.366534	-0.95912	0.870051	-1.10237	0.270302	0.981636	chr2	37118060	37118459	+	0	NA	intron	(intron)	(N	29563 NM_00113c	39253	NR_00128c	79745	Hs. 12292	7NM_02469c	ENSG000003CLIP4	RNSL2	CAP-Gly c protein-coding	
chr2-291c	8.434131	0.910229	0.825758	1.102295	0.270334	0.981636	chr2	291																	

chr19-407.6.007773	1.055163	0.96204	1.096798	0.27273	0.981636	chr19	40711169	40711686	+	0 NA	intron (AluJo SIN	3692 NM_001142	79934 Hs. 130712NM_024876	ENSG00000CQ8B	ADCK4 NPF coenzyme protein-coding
chr4-8454.6.007773	1.055163	0.96204	1.096798	0.27273	0.981636	chr4	8454952	8455292	+	0 NA	intron (intron (N	14325 NM_00135C	152992 Hs. 566191NM_02495C	ENSG00000TRMT44	C4orf23 lncRNA methylprotein-coding
chr19-1015.6.675997	-1.12215	1.023392	-1.0965	0.272862	0.981636	chr19	10130170	10130369	+	0 NA	IntergeniAluSx SIN	-10370 NM_00375E	8666 Hs. 529055NM_00375E	ENSG00000EIF3G	EIF3-P42 eukaryotiprotein-coding
chr8-6711.6.69894	1.030843	0.940354	1.096229	0.272978	0.981636	chr8	67112919	67113250	+	0 NA	intron (AluSc8 SI	29236 NM_001291	79848 Hs. 370147NM_02479C	ENSG00000CSPPI	CSPPI JBTSCentrosomeprotein-coding
chr1-2431.12.93097	0.728425	0.664775	1.095747	0.273189	0.981636	chr1	2431008	2.43E+08	+	0 NA	exon (NM exon (NM	63908 NM_01481E	9859 Hs. 533636NM_01481E	ENSG00000CEP170	FAM68A KATcentrosomeprotein-coding
chr17-486.6.161028	-1.04005	0.949322	-1.09558	0.273265	0.981636	chr17	48911341	48912218	+	0 NA	intron (intron (N	-2796 NR_135674	1.05E+08 Hs. 655254NR_135674	ENSG00000CLOC105371	uncharacteractncRNA
chr17-591.6.161028	-1.04005	0.949322	-1.09558	0.273265	0.981636	chr17	59069887	59070226	+	0 NA	intron (MER5B DN	36824 NR_148347	4591 Hs. 579079NM_015294	ENSG00000TRIM37	MUL POB1 tripartitiprotein-coding
chr17-241.10.67377	0.796386	0.727911	1.094687	0.273654	0.981636	chr17	24188150	24188722	+	0 NA	IntergeniALR/Alph	1665325 NM_00119C	1E+08 Hs. 740188NM_00119C	ENSG00000MTRNR2L1	HNI  MT-NR2L1 protein-coding
chr17-378.8.957993	0.879303	0.803344	1.094554	0.273712	0.981636	chr17	37553404	37553857	+	0 NA	exon (NM exon (NM	55788 NM_08055C	11276 Hs. 594647NM_007247	ENSG00000CSYNRG	AP1GBP1 Synergina protein-coding
chr15-285.6.999915	1.058183	0.966838	1.094478	0.273746	0.981636	chr15	28289789	28290549	+	0 NA	intron (NLTR80A LI	36824 NR_148347	8924 Hs. 434899NM_004667	ENSG00000HERC2	D15F37S1 HECT and protein-coding
chr17-541.10.67377	0.796386	0.727911	1.094687	0.273772	0.981636	chr17	24188150	24188722	+	0 NA	IntergeniALR/Alph	1665325 NM_00119C	1E+08 Hs. 740188NM_00119C	ENSG00000MTRNR2L1	HNI  MT-NR2L1 protein-coding
chr17-378.8.957993	0.879303	0.803344	1.094554	0.273712	0.981636	chr17	37553404	37553857	+	0 NA	exon (NM exon (NM	55788 NM_08055C	11276 Hs. 594647NM_007247	ENSG00000CSYNRG	AP1GBP1 Synergina protein-coding
chr15-285.6.999915	1.058183	0.966838	1.094478	0.273746	0.981636	chr15	28289789	28290549	+	0 NA	intron (NLTR80A LI	36824 NR_148347	8924 Hs. 434899NM_004667	ENSG00000HERC2	D15F37S1 HECT and protein-coding
chr11-464.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr11	46407829	46409668	+	0 NA	intron (intron (N	-17080 NM_00136E	1132 Hs. 248100NM_000741	ENSG00000CHRM4	HM4 MAR cholinergeprotein-coding
chr16-1617.1.95528	0.964815	0.881579	1.094417	0.273772	0.981636	chr16	16170463	16174408	+	0 NA	intron (G-rich Lc	51036 NM_00107E	368 Hs. 442182NM_001171	ENSG00000ABC6C	ABC34 ARFATP bindiprotein-coding
chr16-227.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr16	22308875	22310428	+	0 NA	intron (intron (N	50364 NM_00125E	55718 Hs. 460298NM_01811E	ENSG00000POLR3E	RPC5 SIN RNA polyprotein-coding
chr17-183.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr17	1879746	1880993	+	0 NA	intron (intron (N	12668 NM_001007	6117 Hs. 461922NM_00294E	ENSG00000CPRA1	HSSB MSTCreplicatiprotein-coding
chr19-347.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr19	34759536	34761559	+	0 NA	exon (NM exon (NM	12668 NM_001007	148103 Hs. 590961NM_001007	ENSG00000ZNF599	zinc fingprotein-coding
chr19-365.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr19	36980532	36980765	+	0 NA	intron (MCR77B LI	64316 NM_001204	374900 Hs. 404222NM_19853E	ENSG00000ZNF568	ZFP568 zinc fingprotein-coding
chr19-527.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr19	52390114	52390800	+	0 NA	intron (intron (N	7300 NR_12534E	1.03E+08 Hs. 188688NR_12534E	ENSG00000ZNF528-AS-	ZNF528 arncRNA
chr4-1476.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr4	1.48E+08	1.48E+08	+	0 NA	intron (AluJb SIN	4826 NM_138364	90826 Hs. 591692NM_138364	ENSG00000PRMT9	PRMT10 protein eprotein-coding
chr9-1337.7.195528	0.964815	0.881579	1.094417	0.273772	0.981636	chr9	1.33E+08	1.33E+08	+	0 NA	intron (intron (N	-7696 NR_106937	1.02E+08 NR_106937	ENSG00000MIR6877	hsa-mir-6microRNA ncRNA
chr1-7795.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr1	77934995	77940286	+	0 NA	intron (AluSx1 SI	41432 NR_13015E	8880 Hs. 567388NM_00390C	ENSG00000FUBP1	FBP FUBP far upstrprotein-coding
chr14-582.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr14	58247843	58249899	+	0 NA	intron (AluSx SIN	4028 NM_00278E	5684 Hs. 558799NM_00278E	ENSG00000PSMA3	H8 P5C3 proteasoneprotein-coding
chr17-496.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr17	4969821	4970252	+	0 NA	promoter-promoter-	114 NR_10692E	1.02E+08 NR_10692E	ENSG00000MIR6865	hsa-mir-6microRNA ncRNA
chr2-1891.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr2	1.89E+08	1.89E+08	+	0 NA	intron (intron (N	-15534 NR_03607E	1E+08 NR_03607E	ENSG00000MIR3129	mir-3129 microRNA ncRNA
chr3-1505.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr3	1.51E+08	1.51E+08	+	0 NA	intron (intron (N	25890 NM_03202E	83939 Hs. 655782NM_03202E	ENSG00000EIF2A	CDAO2 EIFeukaryotiprotein-coding
chr4-9445.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr4	94456071	94456980	+	0 NA	exon (NM exon (NM	4583 NM_00125E	10611 Hs. 480311NM_006457	ENSG00000PDLIM5	ENH ENH1 PDZ and Iprotein-coding
chr8-1244.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chr8	1.24E+08	1.24E+08	+	0 NA	exon (NM exon (NM	12496 NM_00721E	11236 Hs. 744151NM_00721E	ENSG00000RNF139	HRCAL RCFring fingprotein-coding
chrX-1558.7.3841	-0.95002	0.868218	-1.09422	0.273858	0.981636	chrX	1.56E+08	1.56E+08	+	0 NA	intron (NL2b LINE	8745 NM_00118E	6845 Hs. 241161NM_00563E	ENSG00000VAMP7	SYB1 TI-vesicle eprotein-coding
chr3-474C.8.57019	-0.91383	0.835303	-1.09401	0.273949	0.981636	chr3	47408468	47409172	+	0 NA	exon (NM exon (NM	27799 NM_001304	25930 Hs. 25524 NM_01546E	ENSG00000PTPN23	HD-PTP HE protein tprotein-coding
chrX-1436.10.11062	0.826338	0.755339	1.093996	0.273957	0.981636	chrX	1436589	1437217	+	0 NA	intron (MLT1B LTF	16006 NM_00117E	8623 Hs. 533514NM_00419E	ENSG00000ASMTL1	ASMTLX AS acetylser protein-coding
chr1-270C.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr1	27000060	27001170	+	0 NA	3' UTR (3' UTR (N	6923 NM_00101E	388610 Hs. 355744NM_00101E	ENSG00000TRNP1	Clorf225 TMF1 regprotein-coding
chr10-156.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr10	15659712	15660170	+	0 NA	intron (MLT1C LTF	59981 NM_00363E	8516 Hs. 171311NM_00363E	ENSG00000ITGAS	integrin protein-coding
chr12-274.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr12	27401647	27405387	+	0 NA	exon (NM exon (NM	43117 NR_10997E	1.02E+08 Hs. 434262NR_10997E	ENSG00000ARNTL2-AS-	ARNTL2 arncRNA
chr12-462.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr12	46222764	46224720	+	0 NA	intron (intron (N	42774 NR_00127E	81539 Hs. 53377C	ENSG00000SLC38A1	ATA1 NAT2solute eprotein-coding
chr13-727.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr13	72743614	72744538	+	0 NA	intron (intron (N	16153 NM_00128E	79866 Hs. 643464NM_02480E	ENSG00000CBORA	C13orf34 BORA aurcprotein-coding
chr15-627.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr15	62766673	62766949	+	0 NA	intron (intron (N	-57146 NR_02979E	406965 NR_02979E	ENSG00000MIR190A	MIR190 MimicroRNA ncRNA
chr17-318.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr17	31855753	31856656	+	0 NA	intron (AluSx SIN	2758 NM_00133C	55352 Hs. 46272E	ENSG00000COPRS	C17orf79 coordinatprotein-coding
chr18-471.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr18	47112188	47112876	+	0 NA	intron (intron (N	37968 NM_00131E	84064 Hs. 465041NM_032124	ENSG00000CHDHD2	3110052NChaloacid protein-coding
chr19-492.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr19	4929487	4933361	+	0 NA	intron (AluSx1 SI	-1263 NR_03990E	1.01E+08 NR_03990E	ENSG00000MIR4747	mir-4747 microRNA ncRNA
chr2-4897.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr2	84977224	84978004	+	0 NA	intron (AluJb SIN	6452 NM_02012E	56888 Hs. 65496E	ENSG00000KCMF1	DEBT91 Fipotassiumprotein-coding
chr2-201C.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr2	2.01E+08	2.01E+08	+	0 NA	intron (intron (N	41474 NM_00132I	285172 Hs. 24701 NM_17382E	ENSG00000FAM126B	HYCC2 family wiprotein-coding
chr21-461.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr21	46106404	46109652	+	0 NA	intron (intron (N	9909 NM_05817E	1292 Hs. 40206E	ENSG00000CCL6A2	BTHLM1 PFcollagen protein-coding
chr5-7766.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr5	77689798	77690685	+	0 NA	TTS (NM_TTS (NM_C	-51544 NR_02310E	23440 Hs. 202247NM_03210E	ENSG00000COTP	orthopediprotein-coding
chr8-2336.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr8	23362046	23365198	+	0 NA	non-codiron-codir	27414 NR_03832E	1.01E+08 Hs. 661133NR_03832E	ENSG00000CLOC100507-	uncharacteractncRNA
chr8-1233.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (AluSx SIN	-2647 NR_03751E	1.01E+08 NR_03751E	ENSG00000MIR548A1	microRNA ncRNA
chr9-3107.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr9	36078734	36079821	+	0 NA	intron (intron (N	42364 NM_00131E	8434 Hs. 38891E	ENSG00000CRECK	ST15 reversiorprotein-coding
chr9-1168.6.15317	-1.03819	0.94924	-1.09371	0.274082	0.981636	chr9	1.11E+08	1.11E+08	+	0 NA	IntergeniIntergeni	141956 NM_00136E	4593 Hs. 52165E	ENSG00000MUSK	CMS9 FADSmuscle asprotein-coding
chr1-1602.8.930719	0.864782	0.790735	1.093644	0.274111	0.981636	chr1	1.6E+08	1.6E+08	+	0 NA	intron (AluSc SIN	-7187 NR_14761E	1E+08 Hs. 65764E	ENSG00000CLOC100287-	uncharacteractncRNA
chr1-2078.8.930719	0.864782	0.790735	1.093644	0.274111	0.981636	chr1	2.08E+08	2.08E+08	+	0 NA	intron (intron (N	-1927 NR_02951E	407025 NR_02951E	ENSG00000MIR29B2	MIRN29B2 microRNA ncRNA
chr13-405.8.930719	0.864782	0.790735	1.093644	0.274111											



chr10-145	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr10	14525373	14528790	+	0	NA	intron (AluY SINE	5633	NM_00132C	83641	Hs.44631ENM_031455	ENSG00000CFAM107B	C10orf45	family wiprotein-coding			
chr10-146	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr10	14596716	14599100	+	0	NA	intron (AluSz SIN	6493	NM_001282	83641	Hs.44631ENM_031455	ENSG00000CFAM107B	C10orf45	family wiprotein-coding			
chr12-502	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr12	50210335	50213242	+	0	NA	intron (AC)n Sin	-10255	NM_001243	51474	Hs.52541ENM_016357	ENSG00000CLIM1A1	EPLIN LDLIM	domain protein-coding			
chr13-476	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr13	47956907	47962339	+	0	NA	intron (LOR1-int)	-27392	NR_047492	1.01E+08	Hs.66097ENR_047492	ENSG00000LINC00562	long intncRNA				
chr13-111	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	43768	NM_001267	1.01E+08	Hs.64003ENM_001267044	COL4A2-AS-	COL4A2	ar protein-coding			
chr14-527	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr14	52779866	52782586	+	0	NA	intron (intron (N	10381	NM_198066	64841	Hs.47802ENM_198066	ENSG00000GNPNAT1	GNAI1 GNP	glucosamin protein-coding			
chr14-106	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	promoter-promoter-	-635	NR_003233	767565	NR_003233	ENSG00000SNORD113-	14q(1-5)	small ncnRNA			
chr17-625	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr17	62568586	62569081	+	0	NA	intron (AluSx SI	-58837	NR_006035	9902	Hs.7835	NM_006035	ENSG00000MRC2	CD280	CLF	mannose protein-coding	
chr2-331	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr2	33155131	33156388	+	0	NA	intron (intron (N	21162	NM_001166	4052	Hs.61931ENM_000627	ENSG00000CLTBP1		latent tr protein-coding			
chr2-132	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (intron (N	11614	NM_001321	116372	Hs.43239ENM_144586	ENSG00000LYPD1	LYPDC1 PF	LY6 PLAUF	protein-coding		
chr2-1527	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr2	1.53E+08	1.53E+08	+	0	NA	intron (HERV1 IOF	15600	NM_001365	55660	Hs.64358CNM_017892	ENSG00000PRPF40A		FBP-11 FF	pre-mRNA	protein-coding	
chr3-1116	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr3	11166757	11167770	+	0	NA	intron (intron (N	12770	NM_001098	3269	Hs.1570	NM_000861	ENSG00000CHRH1	H1-R H1R	histamine	protein-coding	
chr3-502	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr3	50239950	50240469	+	0	NA	intron (intron (N	3905	NM_001282	2771	Hs.77269	NM_002070	ENSG00000GNAI2	GIP GNAI2	G	protein-coding	
chr3-1586	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr3	1.59E+08	1.59E+08	+	0	NA	intron (intron (N	14042	NM_020165	56925	Hs.478067	NM_020165	ENSG00000CLXN	ECI TCI	unchar protein-coding		
chr4-1196	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr4	1196736	1197590	+	0	NA	non-codiron-codir	11799	NR_024565	1E+08	Hs.302962	NR_024569	LOC100130		uncharactncRNA		
chr7-1346	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr7	1.35E+08	1.35E+08	+	0	NA	intron (intron (N	39191	NM_033144	800	Hs.490203	NM_004342	ENSG00000CALD1	CDM H-CAI	caldesmon	protein-coding	
chr9-981	6.145312	-1.03631	0.952558	-1.08793	0.276628	0.981636	chr9	98116097	98116381	+	0	NA	intron (AluSz SIN	2983	NM_014788	9830	Hs.575631	NM_014788	ENSG00000TRIM14		tripartit	protein-coding	
chr1-1212	6.22881	0.967492	0.889466	1.087722	0.276718	0.981636	chr1	11203865	11204695	+	0	NA	intron (intron (N	14925	NM_021146	10218	Hs.14653ENM_021146	ENSG00000ANGPTL7	AngX CDT	angiopoie	protein-coding		
chr1-1565	6.22881	0.967492	0.889466	1.087722	0.276718	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (intron (N	-33194	NR_030527	768220	NR_030527	ENSG00000MIR765	MIRN765	l	microRNA	ncRNA	
chr15-655	6.22881	0.967492	0.889466	1.087722	0.276718	0.981636	chr15	65911387	65911809	+	0	NA	intron (AluSc SIN	42107	NM_001206	8766	Hs.321541	NM_004665	ENSG00000CRAB1A	YL8	RAB11A	n	protein-coding
chr19-425	6.22881	0.967492	0.889466	1.087722	0.276718	0.981636	chr19	42336611	42337141	+	0	NA	exon (NM exon (NM	11241	NM_001271	1954	Hs.13248ENM_001411	ENSG00000MEGF8	C19orf49	l	multiple	protein-coding	
chr22-502	6.22881	0.967492	0.889466	1.087722	0.276718	0.981636	chr22	50247665	50248016	+	0	NA	intron (intron (N	-2817	NM_020461	85378	Hs.336431	NM_020461	ENSG00000TUBGCP6	GCP-6 GCF	tubulin	protein-coding	
chr1-666	7.142807	-0.69594	0.640046	-1.08733	0.276892	0.981636	chr1	66630170	66630425	+	0	NA	intron (intron (N	1857	NR_030606	1E+08	NR_030606	ENSG00000MIR3117	mir-3117	microRNA	ncRNA		
chr1-466	7.142807	-0.69594	0.640046	-1.08733	0.276892	0.981636	chr1	46608473	46608684	+	0	NA	3' UTR (3' UTR (N	-4310	NR_024176	8569	Hs.371594	NM_003684	ENSG00000MKNK1	MNK1	MAPK	inte	protein-coding
chr1-7797	7.376242	-0.94841	0.872264	-1.08733	0.276906	0.981636	chr1	77973972	77975269	+	0	NA	intron (intron (N	4452	NR_130152	8880	Hs.56738CNM_003902	ENSG00000FUBP1	FBP FUBP	far	upstr	protein-coding	
chr12-647	7.376242	-0.94841	0.872264	-1.08733	0.276906	0.981636	chr12	64075157	64075812	+	0	NA	intron (MER9a2 LI	146812	NM_00130C	144577	Hs.444671	NM_15244C	ENSG00000C12orf66		chromoson	protein-coding	
chr12-797	7.376242	-0.94841	0.872264	-1.08733	0.276906	0.981636	chr12	79789813	79791470	+	0	NA	intron (intron (N	-99544	NM_001354	5074	Hs.64313CNM_002582	ENSG00000PAWR	PAR4 Par	pro-apopt	protein-coding		
chr12-112	7.376242	-0.94841	0.872264	-1.08733	0.276906	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (AluSg SIN	23725	NM_024953	80018	Hs.530941	NM_024953	ENSG00000NAA25	C12orf30	N(alpha)	protein-coding	
chr16-868	7.376242	-0.94841	0.872264	-1.08733	0.276906	0.981636	chr16	88390284	88390518	+	0	NA	IntergeniIntergeni	-37070	NM_001367	84627	Hs.54925	NM_001127	ENSG00000ZNF469	BKAS BCSI	zinc	finger	protein-coding
chr9-1367	7.376242	-0.94841	0.872264	-1.08733	0.276906	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (MER4E LTF	-2308	NR_024588	1E+08	Hs.734812	NR_024588	ENSG00000CCDC183	KIAA1984	CCDC183	ancRNA	
chr10-10C	8.57389	-0.89176	0.820198	-1.08726	0.276924	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (intron (N	7626	NM_001278	1147	Hs.19899ENM_001278	ENSG00000CHUK	IKKBA IKK	component	protein-coding		
chr14-10	10.35641	-0.8039	0.739423	-1.0872	0.276949	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	TTS (NR_C TTS (NR_C	159	NR_029863	442915	NR_029863	ENSG00000MIR370	MIRN370	l	microRNA	ncRNA	
chr18-957	10.35641	-0.8039	0.739423	-1.0872	0.276949	0.981636	chr18	9577334	9577533	+	0	NA	intron (AluJb SIN	37126	NR_052003	9989	Hs.74323ENM_005134	ENSG00000PPP4R1	MEG1 PP4	protein	protein-coding		
chr17-497	10.3407	-0.80155	0.737271	-1.08718	0.276957	0.981636	chr17	49705433	49705762	+	0	NA	intron (intron (N	2367	NM_001278	10237	Hs.15407ENM_005827	ENSG00000SLC35B1	UGTREL1	solute	protein-coding		
chr9-1307	10.3407	-0.80155	0.737271	-1.08718	0.276957	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	non-codiron-codir	-9749	NM_007313	25	Hs.43104ENM_005157	ENSG00000ABL1	ABL CHDS	ABL	protc	protein-coding	
chr8-4802	6.176744	-1.0438	0.960108	-1.08717	0.276963	0.981636	chr8	48021473	48022160	+	0	NA	intron (AluSx SIN	13385	NM_00335C	7336	Hs.49169ENM_00335C	ENSG00000UBE2V2	BDVIT1 DE	ubiquitir	protein-coding		
chr1-2242	7.154389	0.964451	0.887177	1.087101	0.276992	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (intron (N	16467	NR_110668	1.02E+08	Hs.71012ENR_110668	ENSG00000LOC101927		uncharactncRNA			
chr12-102	4.947664	-1.16236	1.069371	-1.08696	0.277056	0.981636	chr12	1.02E+08	1.02E+08	+	0	NA	intron (intron (N	10622	NM_016052	51019	Hs.405692	NM_016052	ENSG00000WASHC3	CCDC53	C	WASH	protein-coding
chr2-112	4.947664	-1.16236	1.069371	-1.08696	0.277056	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	3' UTR (3' UTR (N	-7906	NM_001304	84269	Hs.375707	NM_03230C	ENSG00000CHCHD5	CDorf9	C	coiled-co	protein-coding
chr2-2332	4.947664	-1.16236	1.069371	-1.08696	0.277056	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	promoter-promoter-	-257	NR_00300C	677772	Hs.689637	NR_00300C	ENSG00000SCARNA6	U88	small	Ca	ncRNA
chr5-1691	10.30557	-0.81471	0.749735	-1.08666	0.277185	0.981636	chr5	16915355	16915877	+	0	NA	intron (intron (N	20672	NM_012334	4651	Hs.48172CNM_012334	ENSG00000MYO10		myosin X	protein-coding		
chr1-1247	28.95601	0.54905	0.505494	1.086165	0.277406	0.981636	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	321421	NR_00395E	647121	Hs.697682	NR_00395E	ENSG00000EMB1P1		embigin	psudo	
chr8-3346	5.401632	1.123252	1.034475	1.085818	0.277559	0.981636	chr8	33460034	33460233	+	0	NA	intron (AluSx1 SI	13013	NM_032664	84750	Hs.45871ENM_032664	ENSG00000FUT10	FUCTX	fucosyltr	protein-coding		
chr1-1465	10.62477	0.797986	0.735517	1.084932	0.277952	0.981636	chr1	1.47E+08	1.47E+08	+	0	NA	exon (NM exon (NM	37208	NM_001278	149013	Hs.666981	NM_001278	ENSG00000NBPF12	COAS1 K1	NBPF	memt	protein-coding
chr1-1695	8.938577	0.862796	0.795529	1.084557	0.278118	0.981636	chr1	1.69E+08	1.69E+08	+	0	NA	intron (PABL_A-ir	22961	NM_00132C	8548	Hs.13074ENM_003666	ENSG00000BLZF1	COLG1N	4E	basic	let	protein-coding
chr15-748	8.938577	0.862796	0.795529	1.084557	0.278118	0.981636	chr15	74892770	74893215	+	0	NA	intron (intron (N	2950	NM_002433	4351	Hs.75694	NM_002433	ENSG00000MPL1	GDLB PMI	mannose	protein-coding	
chr17-288	8.938577	0.862796	0.795529	1.084557	0.278118	0.981636	chr17	28833097	28833757	+	0	NA	intron (intron (N	11731	NM_001321	9703	Hs.151761	NM_01468C	ENSG00000KIAA0100	BCOX BCOX	KIAA0100	protein-coding	
chr19-21F	8.938577	0.862796	0.795529	1.084557	0.278118	0.981636	chr19	21528543	21537791	+	0	NA	intron (L1M3 LINE	27565	NM_00134E	353088	Hs.572567	NM_001001	ENSG00000ZNF429		zinc	finger	protein-coding
chr1-1656	5.956925	1.042914	0.96166	1.084493	0.278146	0.981636	chr1	1.66E+08	1.66E+08	+	0	NA	intron (MTR SINE	17623	NM_004528	4259	Hs.191734						



chr22-28 7.203386	0.962205	0.892133	1.078544	0.280791	0.981636	chr22	28061478	28061740	+	0 NA	intron (NLIPI1 LINE	-140997 NR_036166	1E+08	NR_036166	ENSG000002MIR3199-1	mir-3199	microRNA	ncRNA
chr9-127 7.203386	0.962205	0.892133	1.078544	0.280791	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	promoter-promoter-	-83 NR_037473	1.01E+08	NR_037473	ENSG000002MIR3911	mir-3911	microRNA	ncRNA
chr22-20 4.743746	1.172159	1.086905	1.078437	0.280839	0.981636	chr22	20040490	20041353	+	0 NA	intron (Nintron (N	7782 NR_029706	406961	NR_029706	ENSG000002MIR185	MIRN185	microRNA	ncRNA
chr14-451 4.873242	-1.17922	1.093537	-1.07835	0.280877	0.981636	chr14	45112263	45112915	+	0 NA	intron (Nintron (N	1714 NR_003691	1E+08	NR_003691	ENSG000002SNORD127	small nucleosRNA		
chr17-161 4.873242	-1.17922	1.093537	-1.07835	0.280877	0.981636	chr17	16346686	16347560	+	0 NA	intron (NAluJb SIN	6346 NR_181716	201161	NR_181716	ENSG000002CENPV	3110013HC	transmembrane protein-coding	
chr20-944 7.776245	0.920254	0.853448	1.078277	0.28091	0.981636	chr20	9447118	9447476	+	0 NA	intron (NMLT1H LTF	-67061 NM_001199	24141	NR_012261	ENSG000002CLAMP5	BAD-LAMP	lysosomal protein-coding	
chr2-545 7.317536	-0.96229	0.892641	-1.07802	0.281203	0.981636	chr2	54535911	54536110	+	0 NA	intron (NAluSq2 SI	6788 NR_002225	56969	NR_002225	ENSG000002RPL23A3	RPL23A_9	ribosomal pseudo	
chr14-305 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr14	30562612	30563045	+	0 NA	intron (NLTR13 LSI	3670 NM_017766	55632	NR_017766	ENSG000002G2E3	KIAA1333 G2/M	phospho protein-coding	
chr15-671 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr15	67124031	67124623	+	0 NA	intron (Nintron (N	-1389 NM_001145	4088	NR_001145	ENSG000002SMAD3	HSPC193 SMAD	famiprotein-coding	
chr17-171 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr17	17102328	17102539	+	0 NA	intron (Nintron (N	59673 NM_201274	23164	NR_201274	ENSG000002MPRIP	M-RIP MRImyosin p	protein-coding	
chr2-939 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr2	9390947	9392312	+	0 NA	intron (NAluSx1 SI	30962 NM_001315	9270	NR_001315	ENSG000002ITGB1BP1	ICAP-1A Integrin	protein-coding	
chr22-357 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr22	35761065	35761814	+	0 NA	exon (NM exon (NM	43567 NM_030642	80831	NR_030642	ENSG000002APOL5	APOL-V AF apolipop	protein-coding	
chr6-158 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr6	1.58E+08	1.58E+08	+	0 NA	intron (Nintron (N	1732 NM_001178	8871	NR_001178	ENSG000002SYNJ2	INPP5H	synapto protein-coding	
chr7-101 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr7	1.01E+08	1.01E+08	+	0 NA	IntergeniAluJb SIN	-4203 NM_016066	51024	NR_016066	ENSG000002F1S1	CGI-135 Fission,	protein-coding	
chr8-106 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr8	1.07E+08	1.07E+08	+	0 NA	3' UTR (N3' UTR (N	18645 NM_139166	137735	NR_139166	ENSG000002ABRA	STARS	actin b protein-coding	
chr9-111 6.137454	-1.03438	0.959725	-1.07779	0.281126	0.981636	chr9	1.11E+08	1.11E+08	+	0 NA	intron (Nintron (N	3298 NM_001351	1902	NR_001351	ENSG000002LPAR1	EDG2 GPR2	lysophospho protein-coding	
chr4-867 12.05851	-0.73971	0.68635	-1.07774	0.28115	0.981636	chr4	86786860	86787106	+	0 NA	intron (NAluSz SIN	62401 NM_197966	345274	NR_197966	ENSG000002SLC10A6	SOAT	solute c protein-coding	
chr1-183 7.71754	0.912639	0.846907	1.077614	0.281206	0.981636	chr1	1.84E+08	1.84E+08	+	0 NA	intron (NAluJr4 SI	-62093 NM_001297	23179	NR_001297	ENSG000002RGL1	RGL	ran guaprotein-coding	
chr17-70 7.71754	0.912639	0.846907	1.077614	0.281206	0.981636	chr17	7002040	7002662	+	0 NA	intron (Nintron (N	6302 NM_000697	239	NR_000697	ENSG000002ALOX12	12-LOX 12	arachidon protein-coding	
chr20-33 7.71754	0.912639	0.846907	1.077614	0.281206	0.981636	chr20	33644523	33645908	+	0 NA	3' UTR (N3' UTR (N	-17112 NM_080825	128864	NR_080825	ENSG000002C2orf144	dJ63M2.6	chromoson protein-coding	
chr19-211 9.460589	0.826628	0.767674	1.076795	0.281572	0.981636	chr19	21116945	21117831	+	0 NA	exon (NM exon (NM	-24652 NM_001319	170959	NR_001319	ENSG000002ZNF431	-	zinc fing protein-coding	
chr2-262 9.460589	0.826628	0.767674	1.076795	0.281572	0.981636	chr2	26281056	26281307	+	0 NA	intron (NLS LINE C	36242 NM_001281	3032	NR_001281	ENSG000002HADHB	ECHB MSTF	hydroxyac protein-coding	
chr10-73 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr10	73034489	73034841	+	0 NA	intron (NAluJb SIN	62309 NM_000917	5033	NR_000917	ENSG000002P4HA1	P4HA	prolyl 4- protein-coding	
chr14-34 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr14	34712282	34713415	+	0 NA	non-codiron-codir	966 NM_021914	1073	NR_021914	ENSG000002CFL2	NEM7	cofilin 2 protein-coding	
chr14-50 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr14	50448128	50448533	+	0 NA	intron (Nintron (N	-51034 NM_001367	8814	NR_001367	ENSG000002CDKL1	KKIALRE F cyclin d	protein-coding	
chr14-95 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr14	95090587	95091013	+	0 NA	intron (Nintron (N	42703 NM_001199	23405	NR_001199	ENSG000002DICER1	DCR1 Dicer	1, protein-coding	
chr2-113 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr2	11318983	11319315	+	0 NA	intron (NLIPI5 LIN	25487 NM_00485C	9475	NR_00485C	ENSG000002ROCK2	ROCK-1 II	Rho assoc protein-coding	
chr21-74 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr21	74350117	74352566	+	0 NA	intron (Nintron (N	4499 NM_001322	1.03E+08	NR_001322	ENSG000002LOC102724	-	uncharact protein-coding	
chr22-23 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr22	23813091	23813527	+	0 NA	intron (NLMID2 LIN	25697 NM_001135	91319	NR_001135	ENSG000002CDERL3	C2orf14 derlin 3	protein-coding	
chr2-24 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr2	24057389	24057614	+	0 NA	intron (NHAL LINE	46131 NM_001199	23523	NR_001199	ENSG000002CABIN1	CABIN1 KB-ε	calcineur protein-coding	
chr8-133 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr8	1.34E+08	1.34E+08	+	0 NA	intron (Nintron (N	45684 NM_003033	6482	NR_003033	ENSG000002ST3GAL1	Gal-NAc6S ST3	beta- protein-coding	
chr9-839 7.368384	-0.94676	0.879249	-1.07678	0.281579	0.981636	chr9	83969689	83968133	+	0 NA	TTS (NM_C TTS (NM_C	2306 NR_029606	407043	NR_029606	ENSG000002MIR7-1	MIRN7-1	microRNA	ncRNA
chr22-501 5.403482	1.140294	1.059166	1.076596	0.281661	0.981636	chr22	50198135	50198507	+	0 NA	intron (NCpG-1933C	-2690 NM_031454	83642	NR_031454	ENSG000002SELENO	SELO	selenopr protein-coding	
chr1-243 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr1	24357926	24358617	+	0 NA	3' UTR (N3' UTR (N	35231 NM_02118C	57822	NR_02118C	ENSG000002GRHL3	SOM TFCP2	grainyhe protein-coding	
chr1-987 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr1	98727554	98728051	+	0 NA	intron (NLIPIA10 LI	66081 NM_001364	51375	NR_001364	ENSG000002SNX7	-	sorting r protein-coding	
chr1-123 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniAluJb SIN	1786487 NR_003955	647121	NR_003955	ENSG000002EMBP1	-	embigin pseudo	
chr1-248 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr1	2.49E+08	2.49E+08	+	0 NA	intron (Nintron (N	9847 NM_001017	267002	NR_001017	ENSG000002CPGBD2	-	piggyBac protein-coding	
chr10-10 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr10	1.04E+08	1.04E+08	+	0 NA	3' UTR (N3' UTR (N	-26700 NM_014631	9644	NR_014631	ENSG000002SH3PXD2A	FISH SH3	SH3 and F protein-coding	
chr10-12 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr10	1.26E+08	1.26E+08	+	0 NA	intron (Nintron (N	8432 NR_120633	1.02E+08	NR_120633	ENSG000002EDRF1-AS1	EDRF1	antncRNA	
chr16-69 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr16	69872306	69872525	+	0 NA	intron (NAluY SINE	33678 NM_00127C	11060	NR_00127C	ENSG000002WWP2	AIP2 Wwp2	WW domain protein-coding	
chr17-82 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr17	82429144	82480036	+	0 NA	intron (Nintron (N	20849 NM_01233C	26502	NR_01233C	ENSG000002NARF	IOP2	nuclear r protein-coding	
chr19-36 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr19	36991943	36992166	+	0 NA	exon (NM exon (NM	75422 NM_001204	374900	NR_001204	ENSG000002ZNF568	FZF568	zinc fing protein-coding	
chr19-41 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr19	41418889	41420786	+	0 NA	intron (NAluSq2 SI	8893 NM_19854C	374907	NR_19854C	ENSG000002B3GNT8	B3GALT7 EUDP-GlcN	protein-coding	
chr20-62 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr20	62009932	62003833	+	0 NA	intron (Nintron (N	-48720 NR_031658	1E+08	NR_031658	ENSG000002MIR1257	MIRN1257	microRNA	ncRNA
chr3-44 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr3	44716449	44718784	+	0 NA	intron (NAluSp SIN	4956 NM_001134	91392	NR_001134	ENSG000002ZNF502	-	zinc fing protein-coding	
chr5-374 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr5	37444808	37445325	+	0 NA	intron (NMER1B DNA	65748 NM_00134E	55100	NR_00134E	ENSG000002WDR70	-	WD repeat protein-coding	
chr9-35 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr9	35390188	35390851	+	0 NA	intron (Nintron (N	-16236 NR_11032C	158381	NR_11032C	ENSG000002ATP8B5P	FetA	ATPase p pseudo	
chr9-10 5.964783	1.039917	0.966394	1.076079	0.281892	0.981636	chr9	1.05E+08	1.05E+08	+	0 NA	intron (NLS LINE	75979 NR_13076C	55335	NR_13076C	ENSG000002NIPSNAP3E	FP944 NIP	nipsnap r protein-coding	
chr9-124 8.681593	-0.87777	0.816226	-1.0754	0.282198	0.981636	chr9	12002690	12003671	+	0 NA	intron (NAluSx4 SI	15563 NR_134927	1.02E+08	NR_134927	ENSG000002ZNF433-AC	ZNF433	arcnRNA	
chr1-889 4.898666																		

chr2-1178	7.699974	0.90551	0.847949	1.067883	0.285573	0.981636	chr2	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	-6851 NR_158150	1.08E+08	NR_158150	LOC10798E-		uncharactncRNA
chr2-24	7.699974	0.90551	0.847949	1.067883	0.285573	0.981636	chr22	24354567	24354865	+	0	NA	intron (NAluSc SIN	12608 NM_001254	23384 Hs. 474384NM_015330	ENSG00000SPECCIL	CYTA5 GBE	sperm antprotein-coding	
chr8-327	7.699974	0.90551	0.847949	1.067883	0.285573	0.981636	chr8	32759252	32761593	+	0	NA	3' UTR (N3' UTR (N	38587 NM_001322	3084 Hs. 453951NM_00449E	ENSG00000CNRG1	ARIA GGF	neureguliprotein-coding	
chr9-9594	7.699974	0.90551	0.847949	1.067883	0.285573	0.981636	chr9	95945090	95945302	+	0	NA	intron (NMER1 C LI	69188 NM_00101C	375748 Hs. 432364NM_020207	ENSG00000ERC6L2	BMP25 C9c	ERCC exciprotein-coding	
chr3-1574	6.104172	-1.04185	0.975923	-1.06755	0.285724	0.981636	chr3	15740000	1.57E+08	+	0	NA	intron (NLIPA16 LI	13811 NM_001167	79674 Hs. 658046NM_024621	ENSG00000VEPH1	MELT VEPF	ventricularprotein-coding	
chr5-1461	6.104172	-1.04185	0.975923	-1.06755	0.285724	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (Nintron (N	-32107 NM_00102E	153770 Hs. 162366NM_00102E	ENSG00000PLAC8L1		PLAC8 ltkprotein-coding	
chr19-117	7.335102	-0.95284	0.892587	-1.06751	0.285744	0.981636	chr19	11731070	11731310	+	0	NA	intron (NAluSp SIN	7756 NM_00108C	55552 Hs. 142169NM_017507	ENSG00000ZNF82F	HSZFP36	zinc fingprotein-coding	
chrX-1236	8.163281	-0.92705	0.868602	-1.06729	0.285843	0.981636	chrX	1.24E+08	1.24E+08	+	0	NA	intron (NLIPA5 LIN	69123 NM_001081	57187 Hs. 149991NM_02044E	ENSG00000THOC2	CXorf3 MF	THO compprotein-coding	
chr3-1111	11.65576	-0.75882	0.711	-1.06726	0.285854	0.981636	chr3	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	47305 NM_00124E	25945 Hs. 293917NM_01548C	ENSG00000NECTIN3	CD113 CD	wnectin cplprotein-coding	
chr10-72	9.074636	-0.85412	0.800457	-1.06704	0.285953	0.981636	chr10	72337920	72338229	+	0	NA	intron (Nintron (N	16795 NM_001002	54788 Hs. 50001E:NM_01762E	ENSG00000DNAJB12	DJ10	DnaJ heatprotein-coding	
chr16-31C	7.684258	0.910006	0.85366	1.066005	0.286422	0.981636	chr16	15057913	13058188	+	0	NA	IntergeniAluSx SIN	7037 NM_00117E	79759 Hs. 10292E:NM_02470E	ENSG00000ZNF668		zinc fingprotein-coding	
chr2-971E	7.684258	0.910006	0.85366	1.066005	0.286422	0.981636	chr2	97191142	97191413	+	0	NA	intron (NMER5A1 DN	78124 NM_001354	375248 Hs. 541894NM_19855E	ENSG00000ANKRD36	UNQ2430	ankyrin rprotein-coding	
chr2-21E	7.684258	0.910006	0.85366	1.066005	0.286422	0.981636	chr2	21693194	21693677	+	0	NA	intron (Nintron (N	27423 NM_14817E	23759 Hs. 438587NM_014337	ENSG00000PPIL2	CYC4 CYP	peptidyl protein-coding	
chr10-27C	7.177962	0.956814	0.897966	1.065535	0.286634	0.981636	chr10	27046014	27046269	+	0	NA	intron (NLI LINE I	54537 NM_00125E	22852 Hs. 361041NM_01491E	ENSG00000ANKRD26	THC2 hA1A	ankyrin i protein-coding	
chr9-3524	7.177962	0.956814	0.897966	1.065535	0.286634	0.981636	chr9	35245789	35246170	+	0	NA	intron (NLIPA5 LIN	83970 NM_00133C	10497 Hs. 493791NM_006377	ENSG00000UNC13B	MUNC13 U	unc-13 hcprotein-coding	
chr9-129E	7.177962	0.956814	0.897966	1.065535	0.286634	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (NAluJb SIN	2341 NM_01652C	51759 Hs. 27842E:NM_01652C	ENSG00000C9orf78	CSU2 HCA	metastasinprotein-coding	
chr2-425E	9.443023	0.820729	0.770398	1.065331	0.286726	0.981636	chr2	42581868	42582367	+	0	NA	intron (NAluY SINE	13485 NM_00133C	57504 Hs. 43451E:NM_02074E	ENSG00000CMTA3		metastasinprotein-coding	
chr12-10E	5.998065	1.043	0.979374	1.064966	0.286891	0.981636	chr12	10214570	10215123	+	0	NA	intron (Nintron (N	1969 NM_001341E	23710 Hs. 52425E:NM_03141E	ENSG00000GABARAPL1	APG8-LIKE	GABA typeprotein-coding	
chr2-8537	5.998065	1.043	0.979374	1.064966	0.286891	0.981636	chr2	85377198	85377530	+	0	NA	non-codirnon-codir	22595 NM_00113E	84173 Hs. 26999C:NM_03221E	ENSG00000ELMOD3	DFNB88 LS	ELMO domeprotein-coding	
chr4-5654	5.998065	1.043	0.979374	1.064966	0.286891	0.981636	chr4	5654576	5654964	+	0	NA	intron (Nintron (N	53378 NM_147127	132884 Hs. 87306 NM_147127	ENSG00000CEVC2	LBN WAD	EvC cilie protein-coding	
chr11-711	4.734038	1.156917	1.086599	1.064714	0.287005	0.981636	chr11	71107498	71108397	+	0	NA	intron (Nintron (N	116849 NM_01230E	22941 Hs. 26872E:NM_01230E	ENSG00000SHANK2	AUTS17 CS	SH3 and nprotein-coding	
chr21-514	4.734038	1.156917	1.086599	1.064714	0.287005	0.981636	chr21	5140369	5141020	+	0	NA	intron (Nintron (N	-12254 NR_13522C	8209 Hs. 41348E:NM_00464E	ENSG00000GATD3A	C21orf33	glutamine protein-coding	
chr19-12E	7.733256	0.908145	0.853033	1.064606	0.287054	0.981636	chr19	12655285	12655895	+	0	NA	intron (NMIRc SINE	11152 NM_00052E	4125 Hs. 35676E:NM_00052E	ENSG00000MAN2B1	LAMAN MAN	mannosid e protein-coding	
chr22-29E	7.733256	0.908145	0.853033	1.064606	0.287054	0.981636	chr22	29350818	29352636	+	0	NA	exon (NM exon (NM	-18469 NR_00368E	1E+08 NR_00368E	ENSG00000SNORD125		small nucsnoRNA	
chr4-152E	6.626369	1.041864	0.979135	1.064066	0.287299	0.981636	chr4	152269	152468	+	0	NA	intron (NLTR5E Hs I	24247 NM_00128E	255403 Hs. 63663E:NM_00103E	ENSG00000ZNF718		zinc fingprotein-coding	
chr2-218E	9.143049	-0.83437	0.784312	-1.06383	0.287407	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (NAluJr SIN	11256 NM_02093E	57695 Hs. 16606E:NM_02093E	ENSG00000CASP37		ubiquitin protein-coding	
chr20-19E	9.143049	-0.83437	0.784312	-1.06383	0.287407	0.981636	chr20	19990146	19990467	+	0	NA	exon (NM exon (NM	-26984 NR_18152E	51126 Hs. 36878E:NM_01610C	ENSG00000NAA20	NAT3 NAT	(alpha)-protein-coding	
chr3-1494	9.143049	-0.83437	0.784312	-1.06383	0.287407	0.981636	chr3	14944508	14945443	+	0	NA	non-codirnon-codir	2530 NR_046254	1.01E+08 Hs. 517821NR_046251	ENSG00000FGD5-AS1		FGD5 antncRNA	
chr4-6861	9.143049	-0.83437	0.784312	-1.06383	0.287407	0.981636	chr4	6861571	6862519	+	0	NA	exon (NM exon (NM	-47399 NM_00111E	57533 Hs. 518611NM_02077E	ENSG00000TBC1D14		TBC1 domeprotein-coding	
chr2-216E	7.393807	-0.93901	0.882827	-1.06364	0.287491	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (Nintron (N	7105 NM_021141	7520 Hs. 38873E:NM_021141	ENSG00000XRCC5	KARP-1 K	X-ray reprotein-coding	
chr2-1731	9.094052	-0.83641	0.786482	-1.06348	0.287564	0.981636	chr2	1.73E+08	1.73E+08	+	0	NA	intron (NAluSp SIN	64618 NM_01665E	51776 Hs. 444451NM_01665E	ENSG00000MAP3K20	AZK CNM6	mitogen- e protein-coding	
chr1-227E	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr1	2.28E+08	2.28E+08	+	0	NA	IntergeniLIPB1 LIN	-30943 NR_10230C	339500 Hs. 30323 NM_03275E	ENSG00000ZNF678		zinc fingprotein-coding	
chr1-243E	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (Nintron (N	198043 NM_18169C	10000 Hs. 49829E:NM_00546E	ENSG00000AKT3	MPPH MPPE	AKT serir protein-coding	
chr11-12E	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr11	1.3E+08	1.3E+08	+	0	NA	intron (NLI LINE I	27646 NM_00616E	4798 Hs. 53053E:NM_00616E	ENSG00000CFRKB	IN080G	nuclear fprotein-coding	
chr17-501	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr17	50109167	50109736	+	0	NA	TTS (NM_C	13756 NM_00119E	5164 Hs. 25666E:NM_00261E	ENSG00000PDK2	PDHK2 PDK	pyruvate protein-coding	
chr22-50E	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr22	50305080	50305376	+	0	NA	intron (Nintron (N	2418 NM_012401	23654 Hs. 3989 NM_012401	ENSG00000PLXNB2	NM1 Nblac	plexin B e protein-coding	
chr4-396C	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr4	39602170	39602696	+	0	NA	intron (NAluSx1 SI	24688 NM_001317	201895 Hs. 20595E:NM_17492E	ENSG00000CSMIM4	C4orf34	small intprotein-coding	
chr4-1194	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	IntergeniIntergeni	6278 NR_13511E	1.02E+08 Hs. 655864NR_13511E	ENSG00000GTF2P12		general tpsudo	
chr6-133E	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr6	13321344	13322445	+	0	NA	intron (Nintron (N	6643 NM_00131E	51256 Hs. 48467E:NM_01649E	ENSG00000TBC1D7	MGCPH PIC	TBC1 domeprotein-coding	
chr6-1121	5.93936	1.033655	0.972158	1.063258	0.287665	0.981636	chr6	1.12E+08	1.12E+08	+	0	NA	intron (NLI2c LINE I	-55252 NR_12119E	1.02E+08 Hs. 510007NR_12119E	LOC101927-		uncharactncRNA	
chr12-687	6.129596	-1.03238	0.971117	-1.06309	0.287741	0.981636	chr12	68703950	68704264	+	0	NA	intron (Nintron (N	17129 NM_020401	57122 Hs. 524574NM_020401	ENSG00000NUP107	NPHS1 N	ucleoporprotein-coding	
chr12-95E	6.129596	-1.03238	0.971117	-1.06309	0.287741	0.981636	chr12	95509964	95509934	+	0	NA	intron (Nintron (N	35662 NM_001317	10988 Hs. 44498E:NM_00683E	ENSG00000MPTAP2	MAP2 MNPF	methionyl protein-coding	
chr3-142E	6.129596	-1.03238	0.971117	-1.06309	0.287741	0.981636	chr3	1.43E+08	1.43E+08	+	0	NA	intron (NAluYh3 SI	64242 NM_001184	545 Hs. 271791NM_001184	ENSG00000ATR	FCTCS FRF	ATR serir protein-coding	
chr5-728E	6.129596	-1.03238	0.971117	-1.06309	0.287741	0.981636	chr5	72851916	72852418	+	0	NA	intron (Nintron (N	4028 NM_001364	3842 Hs. 48249E:NM_00227E	ENSG00000TNPO1	IPO2 KPNE	transportprotein-coding	
chr15-22E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr15	22970365	22970667	+	0	NA	intron (NLMIEc LIN	9852 NM_001324	23191 Hs. 26704 NM_01460E	ENSG00000CYFIP1	P140SRA-1	cytoplasm protein-coding	
chr12-135E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr12	2.36E+08	2.36E+08	+	0	NA	intron (Nintron (N	-2181 NR_11020C	1.02E+08 Hs. 60217E:NR_11019E	ENSG00000DARS-AS1		DARS antncRNA	
chr3-133E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr3	1.34E+08	1.34E+08	+	0	NA	intron (NAluJr4 SI	26500 NM_00136E	11073 Hs. 59337E:NM_00702E	ENSG00000TOPBP1	Dpb11 TOF	DNA topoi protein-coding	
chr4-802E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr4	80269741	80270829	+	0	NA	intron (Nintron (N	2020 NM_001291	2250 Hs. 37055 NM_00446E	ENSG00000CGF5	HBBF-5 S	n fibroblasprotein-coding	
chr8-133E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	3446 NM_00113E	10397 Hs. 372914NM_00609E	ENSG00000NDRG1	CAP43 Cn	myc dowprotein-coding	
chr9-545E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr9	5457046	5457365	+	0	NA	exon (NM exon (NM	6663 NM_001314	29126 Hs. 52198E:NM_01414E	ENSG00000CD274	B7-H B7H	CD274 molprotein-coding	
chr9-116E	6.162878	-1.02499	0.964396	-1.06284	0.287856	0.981636	chr9	1.12E+08	1.12E+08	+	0	NA	intron (NHERVK11-i	18055 NM_03230E	84263 Hs. 59486 NM_03230E	ENSG00000CHSD12	C9orf99 S	hydroxyst protein-coding	
chr16-26E	4.700757	1.153154	1.085154	1.062663	0.287935	0.981636	chr16	262											



chr4-5066 4.162474	-1.21903	1.157793	-1.05289	0.292389	0.981636	chr4	5066587	5067206	+	0	NA	intron (NL2b LINE)	15416 NM_001306	55351 Hs.133062NM_018401ENSG000003TK32B	HSA25083 serine/threonine protein-coding
chr4-8901 4.162474	-1.21903	1.157793	-1.05289	0.292389	0.981636	chr4	89015360	89016825	+	0	NA	intron (NTiger3b)	41093 NM_014888	10144 Hs.97270 NM_014888 ENSG000003FAM13A	ARHGAP48 family wiprotein-coding
chr7-9785 4.162474	-1.21903	1.157793	-1.05289	0.292389	0.981636	chr7	97851834	97852803	+	0	NA	exon (NM_exon NM)	19847 NM_133436	440 Hs.489207NM_001677 ENSG000003ASNS	ASNSD TS1asparagin protein-coding
chr12-72f 6.204017	-1.01927	0.968194	-1.05275	0.292454	0.981636	chr12	72636537	72636841	+	0	NA	intron (NL1PA3 LIN)	-363180 NR_026836	283392 Hs.363603NM_001022 ENSG000003TRHDE-AS1	TRHDE antncRNA
chr20-37c 6.204017	-1.01927	0.968194	-1.05275	0.292454	0.981636	chr20	20317073	20321819	+	0	NA	intron (NALuJb SIN)	64051 NM_001322	5933 Hs.207745NM_002899 ENSG000003RBL1	CP107 PRE RB transcrpotein-coding
chr1-231c 7.211244	0.959344	0.911532	1.052452	0.292592	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	IntergeniIntergeni	4442 NR_031599	1E+08 NR_031599 ENSG000003MIR1182	MIRN1182 microRNA ncRNA
chr11-40f 7.211244	0.959344	0.911532	1.052452	0.292592	0.981636	chr11	40826114	40837875	+	0	NA	intron (Nintron (N))	-11486 NM_001318	6240 Hs.445705NM_001033 ENSG000003RRM1	R1 R1R1 Fribonucle protein-coding
chr14-23z 7.211244	0.959344	0.911532	1.052452	0.292592	0.981636	chr14	23276381	23277189	+	0	NA	exon (NM_exon NM)	9347 NM_020834	57594 Hs.632323NM_020834 ENSG000003HOMEZ	KIAA1443 homeobox protein-coding
chr15-28c 6.486795	0.970773	0.922496	1.052333	0.292647	0.981636	chr15	28654288	28655693	+	0	NA	intron (NALuSx3 SI)	548 NR_036443	440248 Hs.531505NM_199044 ENSG000003HERC2P9	HERC2P9 hect domain pseudo
chr15-32f 6.486795	0.970773	0.922496	1.052333	0.292647	0.981636	chr15	32725516	32726040	+	0	NA	intron (NL1PA7 LIN)	-6913 NR_109767	1E+08 Hs.610545NR_109767 ENSG000003LOC100131	LOC100131 uncharacterized ncRNA
chr2-470c 6.486795	0.970773	0.922496	1.052333	0.292647	0.981636	chr2	47021901	47022275	+	0	NA	intron (Nintron (N))	-80483 NM_001171	90411 Hs.662152NM_139275 ENSG000003MCFD2	F5F8D F5F multiple protein-coding
chr18-541f 7.427089	-0.93277	0.886476	-1.05223	0.292696	0.981636	chr18	54162898	54163184	+	0	NA	intron (NALuSx4 SI)	59371 NR_002970	677819 Hs.655869NR_002970 ENSG000003SNORA37	ACA37 small nucleolar RNA
chr10-95z 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr10	95233154	95235818	+	0	NA	IntergeniAluJr SIN	40286 NM_207321	142827 Hs.134225NM_207321 ENSG000003ACSM6	C10orf12 acyl-CoA protein-coding
chr12-11f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N))	-5572 NM_001346	51347 Hs.644422NM_016281 ENSG000003TAKO3	DPK JIK WTAO kinase protein-coding
chr13-11f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N))	12134 NM_000820	2621 Hs.646344NM_000820 ENSG000003GAS6	AXLLG AXS growth ar protein-coding
chr17-281f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr17	28174668	28175279	+	0	NA	intron (Nintron (N))	-51590 NR_003064	23615 Hs.157195NM_021093 ENSG000003PYY2	PYY2 peptide lpsudo
chr2-746f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr2	74890293	74891517	+	0	NA	exon (NM_exon NM)	-18226 NR_125792	1.03E+08 Hs.708645NR_125792 ENSG000003LINC01291	LINC01291 long intencRNA
chr2-218f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr2	2.17E+08	2.17E+08	+	0	NA	intron (Nintron (N))	2937 NM_000599	3488 Hs.607212NM_000599 ENSG000003IGFBP5	IGFBP5 insulin lprotein-coding
chr4-249f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr4	2493975	2494777	+	0	NA	intron (NALuY SINE)	24923 NM_001188	6047 Hs.66394 NM_002938 ENSG000003RNF4	RNF4 RING fing protein-coding
chr8-304f 7.863122	-0.88567	0.841731	-1.05222	0.292707	0.981636	chr8	30486487	30487244	+	0	NA	intron (Nintron (N))	-10146 NR_046205	1E+08 Hs.126815NR_046205 ENSG000003RBPMS-AS1	RBPMS antncRNA
chr15-434 9.965035	0.788793	0.749676	1.052179	0.292718	0.981636	chr15	43430597	43432738	+	0	NA	intron (Nintron (N))	60566 NM_001288	27229 Hs.584887NM_014444 ENSG000003TUBGCP4	TUBGCP4 GCP-4 tubulin g protein-coding
chr19-43z 7.820133	-0.90151	0.856916	-1.05204	0.292782	0.981636	chr19	43989575	43990431	+	0	NA	intron (Nintron (N))	5815 NM_198088	7711 Hs.279567NM_003444 ENSG000003ZNF155	ZNF155 pH2-96 zinc fing protein-coding
chr4-410z 5.89822	1.033317	0.982322	1.051912	0.29284	0.981636	chr4	41024379	41024917	+	0	NA	intron (NLTR76 LTF)	-167456 NM_001166	323 Hs.479602NM_004307 ENSG000003APBB2	APBB2 FE65L FE65 amyloid t protein-coding
chr1-148z 13.93801	0.675843	0.642595	1.051741	0.292918	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N))	27011 NM_001350	9659 Hs.584841NM_014644 ENSG000003PDEAD1P	PDEAD1P CMY2 MMCP phosphodiprotein-coding
chr19-34f 6.520077	0.973872	0.926352	1.051298	0.293122	0.981636	chr19	34938794	34939555	+	0	NA	intron (NCTCC N)	12271 NR_024018	90075 Hs.657402NM_194322 ENSG000003ZNF30	ZNF30 KOX28 zinc fing protein-coding
chr5-482 16.15408	0.63851	0.607592	1.050886	0.293311	0.981636	chr5	48241487	48242221	+	0	NA	IntergeniAlu/Alph	2199434 NM_198444	133418 Hs.561411NM_198444 ENSG000003CEMB	CEMB GP70 embigin protein-coding
chr12-24f 7.904262	-0.88173	0.839776	-1.04996	0.293736	0.981636	chr12	41843300	418424158	+	0	NA	intron (NALuSx1 SI)	60478 NM_001178	586 Hs.438992NM_005504 ENSG000003BCAT1	BCAT1 BC1 branched protein-coding
chr5-9554 7.904262	-0.88173	0.839776	-1.04996	0.293736	0.981636	chr5	95545546	95546009	+	0	NA	intron (NL2a LINE)	9228 NM_014635	9652 Hs.482866NM_014635 ENSG000003TTC37	TTC37 KIAA0372 tetraatric protein-coding
chr5-129f 7.904262	-0.88173	0.839776	-1.04996	0.293736	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (NMLT1A LTF)	-76122 NM_001257	1E+08 Hs.582534NM_001257 ENSG000003MINAR2	MINAR2 KIAA1024 membrane protein-coding
chr13-197 9.37464	0.861102	0.777491	1.04966	0.293875	0.981636	chr13	19732569	19732839	+	0	NA	intron (NALuSx SIN)	50241 NM_001354	55269 Hs.213198NM_001042 ENSG000003PSPC1	PSPC1 paraspel protein-coding
chr1-255f 6.494653	0.968094	0.922519	1.049402	0.293993	0.981636	chr1	25558665	25560084	+	0	NA	intron (Nintron (N))	15789 NM_015627	26119 Hs.590911NM_015627 ENSG000003DLRAP1	DLRAP1 ARH ARH1 low densiprotein-coding
chr1-211f 6.494653	0.968094	0.922519	1.049402	0.293993	0.981636	chr1	2.11E+08	2.11E+08	+	0	NA	intron (NHAL1 LINE)	12114 NR_026761	84791 Hs.523932NM_032705	LINC00467 p29-197 long intencRNA
chr16-884 6.494653	0.968094	0.922519	1.049402	0.293993	0.981636	chr16	88655100	88656205	+	0	NA	intron (NCPg-10162)	-4599 NM_000101	1535 Hs.513803NM_000101 ENSG000003CYBA	CYBA C12-Phoenix cytochron protein-coding
chrX-143z 6.494653	0.968094	0.922519	1.049402	0.293993	0.981636	chrX	1432050	1432681	+	0	NA	exon (NM_exon NM)	20544 NM_001172	8623 Hs.533514NM_004192 ENSG000003ASMTL	ASMTL AS acetylser protein-coding
chr18-23z 7.103541	0.953155	0.909128	1.048824	0.294259	0.981636	chr18	23297621	23297967	+	0	NA	non-codirnon-codir	140167 NM_032933	85019 Hs.137562NM_032933 ENSG000003TMEM241	TMEM241 C18orf45 transmem protein-coding
chr15-42z 6.614262	-0.96417	0.919534	-1.04854	0.294391	0.981636	chr15	42963914	42964915	+	0	NA	intron (NALuSp SIN)	-43636 NM_173500	146057 Hs.646511NM_173500 ENSG000003TTBK2	TTBK2 KIAA11 TTE tubul protein-coding
chr17-47z 7.896404	-0.88023	0.839624	-1.04836	0.294471	0.981636	chr17	47588479	47589335	+	0	NA	intron (Nintron (N))	57799 NM_006310	9520 Hs.443837NM_006310 ENSG000003NPEPPS	NPEPPS AAP-S MAP1aminopept protein-coding
chr3-157f 7.896404	-0.88023	0.839624	-1.04836	0.294471	0.981636	chr3	15700591	15701071	+	0	NA	intron (Nintron (N))	-3460 NR_036088	1E+08 NR_036088 ENSG000003MIR3134	MIR3134 microRNA ncRNA
chr8-9987 7.912119	-0.88222	0.842503	-1.04832	0.29449	0.981636	chr8	99875069	99875455	+	0	NA	intron (Nintron (N))	18445 NM_004374	1345 Hs.351875NM_004374 ENSG000003COX6C	COX6C cytochron protein-coding
chr16-15z 6.64005	-0.95575	0.911713	-1.0483	0.294499	0.981636	chr16	15664652	15664947	+	0	NA	exon (NM_exon NM)	14554 NM_017668	54820 Hs.655377NM_017668 ENSG000003NDE1	NDE1 HOM-TES-ε nudE neur protein-coding
chr17-45z 6.64005	-0.95575	0.911713	-1.0483	0.294499	0.981636	chr17	45278916	45280043	+	0	NA	intron (NALuSx8 SI)	-17385 NM_152343	124783 Hs.412711NM_152343 ENSG000003SPATA32	SPATA32 AEP2 C17C spermatog protein-coding
chr18-19z 6.64005	-0.95575	0.911713	-1.0483	0.294499	0.981636	chr18	198043	200242	+	0	NA	intron (Nintron (N))	40585 NM_005151	9097 Hs.464411NM_005151 ENSG000003USP14	USP14 TGT ubiquitn protein-coding
chr22-41z 6.64005	-0.95575	0.911713	-1.0483	0.294499	0.981636	chr22	41676238	41676841	+	0	NA	intron (Nintron (N))	12328 NM_001005	4809 Hs.182255NM_005005 ENSG000003SNU13	SNU13 15.5K FA-small nuc protein-coding
chrX-464z 6.64005	-0.95575	0.911713	-1.0483	0.294499	0.981636	chrX	46467114	46469753	+	0	NA	intron (NALuSx6 SI)	21136 NM_001123	55634 Hs.632800NM_017777 ENSG000003KRBOX4	KRBOX4 ZNF673 KRAB box protein-coding
chr2-460z 6.15502	-1.02281	0.975697	-1.04829	0.294507	0.981636	chr2	46007605	46007804	+	0	NA	intron (Nintron (N))	-289703 NM_001432	2034 Hs.468411NM_001432 ENSG000003EPAS1	EPAS1 BAGY4 HIF endothel protein-coding
chr6-571z 6.15502	-1.02281	0.975697	-1.04829	0.294507	0.981636	chr6	57193232	57193464	+	0	NA	intron (NL4_B Mam)	21022 NM_004282	9532 Hs.745044NM_004282 ENSG000003BAG2	BAG2-2 dJ4BCL2 asc protein-coding
chr2-190z 4.965229	-1.14718	1.094373	-1.04826	0.29452	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (Nintron (N))	11763 NM_001321	4664 Hs.107474NM_005966 ENSG000003NAB1	NAB1 NGF1-A biprotein-coding
chr13-11z 6.647908	-0.95751	0.913441	-1.04825	0.294524	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (NLIMEf LIN)	-18523 NM_001278	8451 Hs.339735NM_003585 ENSG000003CUL4A	CUL4A cullin 4 protein-coding
chr6-144z 6.647908	-0.95751	0.913441	-1.04825	0.294524	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N))	16497 NR_132778	1.07E+08 NR_132778	SNORA98 small nucsnRNA
chr19-26z 21.92511	0.574227	0.548394	1.048019	0.29463	0.981636	chr19	26903950	26904752	+	0	NA	IntergeniALR/Alph	-889080 NR_146733	1.02E+08 Hs.567934NR_110687 ENSG000003LOC101927	LOC101927 uncharacterized ncRNA
chr1-31C 8.255268	0.863368														



chr12-112 7.855264	-0.88416	0.846807	-1.04411	0.296436	0.981636	chr12	1.12E+08	1.12E+08	0	NA	TTS (NM_C TTS (NM_C	10911 NM_006817	10961 Hs. 75841 NM_006817	ENSG000002CERP29	C12orf8	Fendoplasn protein-coding	
chr13-111 7.855264	-0.88416	0.846807	-1.04411	0.296436	0.981636	chr13	1.1E+08	1.1E+08	0	NA	intron (NL2c LINE	3334 NM_00184E	1282 Hs. 17441 NM_00184E	ENSG00000COL4A1	BSDV BSVI	collagen protein-coding	
chr4-119 7.855264	-0.88416	0.846807	-1.04411	0.296436	0.981636	chr4	1.2E+08	1.2E+08	0	NA	intron (NTigger12c	82862 NM_03343C	8654 Hs. 647971 NM_00108E	ENSG00000PDE5A	CGB-PDE C	phosphodi protein-coding	
chr8-103 7.855264	-0.88416	0.846807	-1.04411	0.296436	0.981636	chr8	1.03E+08	1.03E+08	0	NA	intron (NL2b LINE	4653 NM_001164	8323 Hs. 59186E NM_00350E	ENSG00000FZD6	Fz-6 FZ6	frizzled protein-coding	
chr2-653 7.855264	-1.05956	0.814887	-1.04402	0.296476	0.981636	chr2	65330967	65331856	0	NA	intron (Nintron (N	35367 NM_00112E	200734 Hs. 59332 NM_181784	ENSG00000SPRED2	SP-2	sprouty protein-coding	
chr4-475 5.416978	-1.05956	0.814887	-1.04402	0.296476	0.981636	chr4	47580228	47581114	0	NA	intron (NL3 LINE C	-71998 NR_10702C	1.02E+08	NR_10702C	ENSG00000MIR8053	hsa-mir-ε	microRNA ncRNA
chr4-767 5.416978	-1.05956	0.814887	-1.04402	0.296476	0.981636	chr4	76766053	76766695	0	NA	intron (NMIRc SINE	131770 NM_00102E	345079 Hs. 25729E NM_00102E	ENSG00000SOWAIB	ANKRD56	sonodow protein-coding	
chr11-65 5.947218	1.030332	0.98708	1.043818	0.29657	0.981636	chr11	65584811	65585273	0	NA	exon (NM exon (NM	8989 NM_00109E	254102 Hs. 502867 NM_00109E	ENSG00000EHP1L1	-	EH domain protein-coding	
chr9-121 5.947218	1.030332	0.98708	1.043818	0.29657	0.981636	chr9	1.22E+08	1.22E+08	0	NA	intron (Nintron (N	21579 NM_13870E	153090 Hs. 52237E NM_03255E	ENSG00000DAB2IP	AF9Q34 A	IDAB2 intε protein-coding	
chr9-131 5.947218	1.030332	0.98708	1.043818	0.29657	0.981636	chr9	1.32E+08	1.32E+08	0	NA	intron (N (ATTATAT)	36919 NM_00136E	642515 Hs. NM_00136E	ENSG00000PRRT1B	DSPD2 IF	Iproline protein-coding	
chr17-80 8.895588	0.851713	0.815994	1.043774	0.29659	0.981636	chr17	80009927	80010388	0	NA	intron (Nintron (N	25715 NM_01902C	125058 Hs. 36981E NM_01902C	ENSG00000TBC1D16	-	TBC1 dome protein-coding	
chr10-11 7.888546	-0.8787	0.84205	-1.04352	0.296706	0.981636	chr10	1.2E+08	1.2E+08	0	NA	TTS (NM_C TTS (NM_C	24363 NR_13666E	7073 Hs. 50120E NM_00325E	ENSG00000TIAL1	TCBP TIA	TIAI cytc protein-coding	
chr2-200 7.888546	-0.8787	0.84205	-1.04352	0.296706	0.981636	chr2	2E+08	2E+08	0	NA	intron (NL2c LINE	59213 NM_00132E	130535 Hs. 60577E NM_15238E	ENSG00000KCTD18	6530404F	Ipotassium protein-coding	
chr22-31 7.888546	-0.8787	0.84205	-1.04352	0.296706	0.981636	chr22	31740131	31740405	0	NA	intron (NAluSg SIN	9838 NM_17356E	253143 Hs. 43890E NM_17356E	ENSG00000PRL14L	C22orf30	proline i protein-coding	
chr3-12 7.888546	-0.8787	0.84205	-1.04352	0.296706	0.981636	chr3	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	49407 NM_17202E	80325 Hs. 10781E NM_03254E	ENSG00000ABTB1	BPOZ BTBε	ankyrin i protein-coding	
chr3-194 7.888546	-0.8787	0.84205	-1.04352	0.296706	0.981636	chr3	1.94E+08	1.94E+08	0	NA	intron (NLIME3Cz L	25561 NM_02452A	79572 Hs. 52960E NM_02452A	ENSG00000ATP13A3	AFURS1	ATPase Iε protein-coding	
chr2-390 10.00617	0.789328	0.756407	1.043523	0.296706	0.981636	chr2	39032667	39032931	0	NA	intron (NAluSx SIN	-72455 NR_02838E	37519E Hs. 65903E NR_02838E	ENSG00000LOC37519E	-	uncharactcRNA	
chr1-212 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr1	2.13E+08	2.13E+08	0	NA	intron (NAluSx SIN	13625 NM_00104E	128387 Hs. 53053E NM_00104E	ENSG00000CTADN3	-	TatD DNase protein-coding	
chr10-68 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr10	68199577	68200262	0	NA	intron (NL2b LINE	32194 NM_14517E	220202 Hs. 17539E NM_14517E	ENSG00000ATOH7	Math5 NCF	atonal bε protein-coding	
chr11-86 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr11	86321282	86321574	0	NA	intron (NLIME1 LIN	19188 NM_00132E	51501 Hs. 28332E NM_01640E	ENSG00000CHIKESHI	C11orf73	heat shoc protein-coding	
chr12-12 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr12	1.23E+08	1.23E+08	0	NA	Intergeni Intergeni	-26915 NM_00130C	57605 Hs. 27275E NM_02084E	ENSG00000PITPM2	NIR-7 NIF	phosphat i protein-coding	
chr15-67 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr15	67586812	67588402	0	NA	intron (NL3 LINE C	38513 NM_00120E	5607 Hs. 11419E NM_00275E	ENSG00000MAP2K5	HsT17454	mitogen-ε protein-coding	
chr16-14 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr16	14581379	14582881	0	NA	intron (Nintron (N	48130 NM_00258E	5073 Hs. 25319E NM_00258E	ENSG00000PARN	DAN DKCBε	poly (A)-s protein-coding	
chr9-104 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr9	1.05E+08	1.05E+08	0	NA	intron (Nintron (N	68158 NR_13076E	55335 Hs. 42929E NM_01837E	ENSG00000NIPSNAP3E	FP944 NIF	nipnasε protein-coding	
chr9-11 6.469229	0.962353	0.922232	1.043504	0.296715	0.981636	chr9	1.16E+08	1.16E+08	0	NA	intron (Nintron (N	118422 NM_00258I	5069 Hs. 64359E NM_00258I	ENSG00000PAPPA	ASBAP2 E	pappalys i protein-coding	
chr3-450 7.919977	-0.8847	0.847873	-1.04343	0.29675	0.981636	chr3	45070652	45071133	0	NA	Intergeni L2a LINE	40799 NM_00130E	7123 Hs. 47609E NM_00327E	ENSG00000CLEC3B	TN TNA	C-type iε protein-coding	
chr2-223 7.649127	0.895255	0.858396	1.043253	0.296831	0.981636	chr2	2.40E+08	2.40E+08	0	NA	intron (Nintron (N	29902 NM_02291E	65080 Hs. 20355E NM_02291E	ENSG00000MRPL44	CXXPD16 L	mitochon protein-coding	
chr3-113 6.681374	1.021231	0.979502	1.042602	0.297133	0.981636	chr3	1.13E+08	1.13E+08	0	NA	intron (NSVA_C Ret	-17204 NM_01833E	55779 Hs. 58493E NM_01833E	ENSG00000CFAP44	SPGF20 W	cilia anc protein-coding	
chr1-12 5.375838	-1.06587	1.022603	-1.04231	0.297268	0.981636	chr1	42937051	42937967	0	NA	intron (Nintron (N	21359 NM_00651E	6513 Hs. 473721 NM_00651E	ENSG00000SLC2A1	CSE DYT17	solute εε protein-coding	
chr10-12 5.375838	-1.06587	1.022603	-1.04231	0.297268	0.981636	chr10	17437	17437	0	NA	intron (NMIRb SINE	17437 NM_018117	55717 Hs. 14444E NM_018117	ENSG00000WDR11	BRWD2 DR	WD repeat protein-coding	
chr12-12 5.375838	-1.06587	1.022603	-1.04231	0.297268	0.981636	chr12	1.23E+08	1.23E+08	0	NA	TTS (NM_C TTS (NM_C	2771 NM_00127E	51329 Hs. 103561 NM_01663E	ENSG00000CARL6IP4	SFRS20 S	FADP ribos protein-coding	
chr2-232 5.375838	-1.06587	1.022603	-1.04231	0.297268	0.981636	chr2	2.32E+08	2.32E+08	0	NA	intron (N MamRep137	64141 NR_046477	129563 Hs. 73223E NM_15238E	ENSG00000DIS3L2	FAM6A PIR	DIS3 like protein-coding	
chr22-17 5.375838	-1.06587	1.022603	-1.04231	0.297268	0.981636	chr22	17821170	17821628	0	NA	intron (Nintron (N	44109 NR_10371E	200298 Hs. 51739E NR_10371E	ENSG00000LINC0052E	C22orf37	long intncRNA	
chr10-13 9.484163	0.821056	0.787741	1.042293	0.297276	0.981636	chr10	13631036	13631557	0	NA	TTS (NM_C TTS (NM_C	44331 NM_00367E	8559 Hs. 66064E NM_00367E	ENSG00000PRPF18	PRP18 h	Prpre-mRNA protein-coding	
chr13-39 9.484163	0.821056	0.787741	1.042293	0.297276	0.981636	chr13	39014124	39014433	0	NA	exon (NM exon (NM	-23419 NM_001144	161003 Hs. 32779E NM_14528E	ENSG00000STOML3	Epb7.21 S	stomatoin protein-coding	
chr11-17 4.187898	-1.20524	1.156444	-1.04219	0.297323	0.981636	chr11	17309211	17309967	0	NA	exon (NM exon (NM	32619 NM_00135E	4925 Hs. 65459E NM_00501E	ENSG00000NUCB2	HEL-S-10ε	nucleobir protein-coding	
chr12-31 4.187898	-1.20524	1.156444	-1.04219	0.297323	0.981636	chr12	31097041	31097808	0	NA	intron (NAluSc8 SI	23564 NM_00125E	1663 Hs. 44396E NM_00439E	ENSG00000CDDX11	CHL1 CHL	FDEAD/H-εc protein-coding	
chr2-18 4.187898	-1.20524	1.156444	-1.04219	0.297323	0.981636	chr2	1.9E+08	1.9E+08	0	NA	intron (NMERS DNA	90882 NM_00132E	5378 Hs. 11174E NM_00053A	ENSG00000PMS1	HNPPC3 M	PMS1 homc protein-coding	
chr21-46 4.187898	-1.20524	1.156444	-1.04219	0.297323	0.981636	chr21	46310314	46311324	0	NA	intron (Nintron (N	7401 NM_00128E	54058 Hs. 23657E NM_05818E	ENSG00000C21orf58	-	chromoson protein-coding	
chr22-40 4.187898	-1.20524	1.156444	-1.04219	0.297323	0.981636	chr22	40919641	40920135	0	NA	intron (NLIME2 LIN	-31490 NM_01424E	9978 Hs. 47494E NM_01424E	ENSG00000CRBX1	BA554C12.	ring-box protein-coding	
chr7-97 4.187898	-1.20524	1.156444	-1.04219	0.297323	0.981636	chr7	97856224	97857361	0	NA	exon (NM exon (NM	15373 NM_13343E	440 Hs. 48920E NM_00167E	ENSG00000ASNS	ASNSD TS	asparag i protein-coding	
chr11-28 4.154616	-1.21641	1.167273	-1.0421	0.297367	0.981636	chr11	28067643	28069841	0	NA	intron (Nintron (N	11927 NR_030341	693195 NR_030341	ENSG00000MIR610	MIRN610	microRNA ncRNA	
chr2-22 4.154616	-1.21641	1.167273	-1.0421	0.297367	0.981636	chr2	2.25E+08	2.25E+08	0	NA	intron (Nintron (N	132880 NM_00129C	55619 Hs. 46578 NM_01468E	ENSG00000DOCK10	DRIP2 N	bl dedicator protein-coding	
chr5-98 4.154616	-1.21641	1.167273	-1.0421	0.297367	0.981636	chr5	98882705	98884535	0	NA	intron (NLIPB1 LIN	42914 NM_00127E	1105 Hs. 64346E NM_00127E	ENSG00000CHD1	CHD-1 PII	chromodon protein-coding	
chr10-30 9.980751	0.785379	0.753833	1.041847	0.297482	0.981636	chr10	30022347	30022873	0	NA	intron (Nintron (N	36976 NM_00135C	57608 Hs. 53395E NM_02084E	ENSG00000JCAD	KIAA1462	junctionε protein-coding	
chr1-58 7.14.30619	-0.66101	0.634472	-1.04183	0.297489	0.981636	chr1	58781095	58783117	0	NA	exon (NM exon (NM	1941 NM_00222E	3725 Hs. 69668E NM_00222E	ENSG00000JUN	AP-1 AP1	Jun protc protein-coding	
chr21-31 7.419231	-0.9309	0.893584	-1.04176	0.297521	0.981636	chr21	31702921	31703313	0	NA	intron (Nintron (N	29001 NM_00114E	57466 Hs. 17255 NM_02070E	ENSG00000SCAF4	SFRS15 S	FRS-relate protein-coding	
chr22-41 8.20442	0.85405	0.820272	1.041179	0.297792	0.981636	chr22	41884897	41888130	0	NA	intron (NLIME3 LIN	-14431 NR_029507	407039 NR_029507	ENSG00000MIR33A	MIR33 MI	microRNA ncRNA	
chr5-37 8.20442	0.85405	0.820272	1.041179	0.297792	0.981636	chr5	37446188	37447009	0	NA	intron (NLIPA5 LIN	67280 NM_00134E	551100 Hs. 21369E NM_01803A	ENSG00000WDR70	WD	repeat protein-coding	
chr8-10 8.20442	0.85405	0.820272	1.041179	0.297792	0.981636	chr8	1.06E+08	1.06E+08	0	NA	intron (NMSTB-int	72397 NR_125797	1.03E+08 H				

chr3-1701 5.434544	-1.0471	1.010165	-1.03656	0.29994	0.981636	chr3	1.7E+08	1.7E+08	0 NA	intron (Nintron (N	57461 NM_024947	80012 Hs. 529592NM_024947	ENSG000003CASS3	EDR3 HPH2 polyhomec protein-coding	
chr9-7032 5.434544	-1.0471	1.010165	-1.03656	0.29994	0.981636	chr9	70325714	70327613	0 NA	intron (NLM5 LIN	67685 NM_01511C	23137 Hs. 534189NM_01511C	ENSG000003SMC5	SMC5L1 structure protein-coding	
chr13-274 6.435948	0.959271	0.925482	1.036509	0.299965	0.981636	chr13	27441335	27441608	0 NA	intron (Nintron (N	8718 NM_001166	219402 Hs. 534582NM_152912	ENSG000003MTIF3	IF3mt mitochondon protein-coding	
chr16-286 6.435948	0.959271	0.925482	1.036509	0.299965	0.981636	chr16	28662364	28662897	0 NA	intron (NHERV LI	4047 NR_039742	1.01E+08	NR_039742	ENSG000003MIR4517	mir-4517 microRNA ncRNA
chr19-96 6.435948	0.959271	0.925482	1.036509	0.299965	0.981636	chr19	9636019	9636787	0 NA	IntergeniHERV1B-int	15071 NR_122038	284385 Hs. 651747NM_001242	ENSG000003ZNF561-AS1	C19orf82 ZNF561 arncRNA	
chr19-121 6.435948	0.959271	0.925482	1.036509	0.299965	0.981636	chr19	12175420	12175677	0 NA	intron (NLM1C LIN	12452 NM_003437	7695 Hs. 479874NM_003437	ENSG000003ZNF136	pH2-20 zinc fing protein-coding	
chr9-129 6.435948	0.959271	0.925482	1.036509	0.299965	0.981636	chr9	1.29E+08	1.29E+08	0 NA	intron (Nintron (N	14137 NR_163192	56904 Hs. 460238NM_020144	ENSG000003SH3GLB2	PP6569 PF SH3 domain protein-coding	
chr7-8395 5.367981	-1.06383	1.026971	-1.03589	0.300255	0.981636	chr7	83959733	83959932	0 NA	3' UTR (N3' UTR (N	234957 NM_00608C	10371 Hs. 252451NM_00608C	ENSG000003SEMA3A	COLL11 HHI semaphorin protein-coding	
chr10-396 66.78385	0.393906	0.380396	1.035514	0.300429	0.981636	chr10	39967518	39968398	0 NA	IntergeniALR/Alpha	1271362 NR_04500C	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74 ACTR3B ps pseudo	
chr11-96 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr11	96383076	96384206	0 NA	intron (Nintron (N	6175 NM_001363	79780 Hs. 525088NM_014144	ENSG000003CCDC82	HSPC048 coiled-co protein-coding	
chr16-503 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr16	50325031	50325855	0 NA	intron (Nintron (N	32827 NR_106822	1.02E+08	NR_106822	ENSG000003MIR6771	hsa-mir-6771 microRNA ncRNA
chr17-664 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr17	6642832	6644630	0 NA	3' UTR (N3' UTR (N	2671 NM_032731	84817 Hs. 408233NM_032731	ENSG000003TXNDC17	TRP14 TXN thioredox protein-coding	
chr2-8747 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr2	87478599	87481682	0 NA	intron (Nintron (N	10190 NR_146466	112597 Hs. 652166NR_024204	ENSG000003CYTOR	C2orf59 L cytoskelncRNA	
chr20-564 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr20	56415570	56415973	0 NA	intron (Nintron (N	3577 NM_001164	57091 Hs. 473144NM_020354	ENSG000003CASC4	C2orf32 Cas scaff protein-coding	
chr22-41 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr22	41512436	41512888	0 NA	intron (Nintron (N	31808 NM_001018	171568 Hs. 712617NM_138333	ENSG000003POLR3H	RPC22.9 F RNA polyn protein-coding	
chr4-1691 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr4	1.69E+08	1.69E+08	0 NA	intron (Nintron (N	-110536 NM_032783	848669 Hs. 659311NM_032783	ENSG000003CBRA4	SDR45C1 carbonyl protein-coding	
chr8-382 6.657616	-0.9457	0.91329	-1.03549	0.300441	0.981636	chr8	38306933	38307356	0 NA	intron (N(AAAT)n S	-37912 NM_001354	84513 Hs. 567619NM_032483	ENSG000003PLPP5	DPPL1 HTF phospholiprotein-coding	
chr1-112 7.880688	-0.87712	0.847127	-1.0354	0.300482	0.981636	chr1	1.13E+08	1.13E+08	0 NA	intron (NAluSc8 SI	44123 NM_138727	54879 Hs. 201921NM_017744	ENSG000003STL7	FAM4B ST7 suppressin protein-coding	
chr12-121 7.880688	-0.87712	0.847127	-1.0354	0.300482	0.981636	chr12	1.21E+08	1.21E+08	0 NA	TTS (NM_C TTS (NM_C	19665 NR_106957	1.02E+08	NR_106957	ENSG000003MIR7107	hsa-mir-7107 microRNA ncRNA
chr13-44 6.68119	-0.95093	0.918535	-1.03527	0.300545	0.981636	chr13	44545344	44545776	0 NA	intron (Nintron (N	-30336 NR_038381	641467 Hs. 624196NR_038381	ENSG000003TSC22D1-1	TSC22D1 ncRNA	
chr16-65 6.68119	-0.95093	0.918535	-1.03527	0.300545	0.981636	chr16	65113862	65114886	0 NA	intron (NMTB SINE	7689 NM_001797	1009 Hs. 116471NM_001797	ENSG000003CDH11	CAD11 CDF cadherin protein-coding	
chr16-16 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr16	1639775	1640766	0 NA	intron (NLM1E LIN	25630 NM_02082E	57585 Hs. 603676NM_02082E	ENSG000003CRAMP1	CRAMP1L C cramped c protein-coding	
chr16-19 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr16	23629658	23630022	0 NA	exon (NM exon (NM	11517 NM_02467E	79728 Hs. 444664NM_02467E	ENSG000003PALB2	FANCN PNC partner e protein-coding	
chr19-237 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr19	19729174	19730979	0 NA	intron (NAluSx SIN	3036 NM_02103C	7561 Hs. 659932NM_02103C	ENSG000003ZNF14	GIOT-4 KC zinc fing protein-coding	
chr2-3881 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr2	38810683	38811603	0 NA	intron (Nintron (N	32933 NM_02477E	79833 Hs. 143818NM_02477E	ENSG000003GEM16	- gem nucle protein-coding	
chr2-238 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr2	2.38E+08	2.38E+08	0 NA	intron (NAluJb SIN	35884 NM_001133	26136 Hs. 631899NM_01565C	ENSG000003TRAF3IP1	IFT54 MIF TRAF3 int protein-coding	
chr22-378 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr22	37837970	37838471	0 NA	intron (NAluV SINE	5868 NM_001363	129138 Hs. 135255NM_138797	ENSG000003ANKRD54	LIATF ankyrin i protein-coding	
chr3-185 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr3	1.86E+08	1.86E+08	0 NA	intron (Nintron (N	-20917 NR_12632E	646600 Hs. 647945NR_027317	ENSG000003IGFBP2-1	C3orf65 IGF2BP2 ncRNA	
chr6-443 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr6	44305177	44305909	0 NA	intron (Nintron (N	7804 NM_02074E	57505 Hs. 158381NM_02074E	ENSG000003AARS2	AARSL COA alanyl-tE protein-coding	
chr6-1211 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr6	21.21E+08	1.21E+08	0 NA	intron (Nintron (N	208994 NM_15273C	221322 Hs. 121396NM_15273C	ENSG000003TBC1D32	BROMI C6c TBC1 dome protein-coding	
chr7-745 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr7	74539005	74540271	0 NA	intron (NAluSx SIN	-56330 NR_162111	1.13E+08	NR_162111	MIR10525	- microRNA ncRNA
chr8-100 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr8	1.01E+08	1.01E+08	0 NA	3' UTR (N3' UTR (N	37299 NR_00127C	157567 Hs. 530199NM_198401	ENSG000003ANKRD46	ANK-S GEM ankyrin i protein-coding	
chr9-127 8.212278	0.85196	0.822991	1.0352	0.300576	0.981636	chr9	1.27E+08	1.27E+08	0 NA	intron (NAluSx SIN	7594 NM_00100E	90678 Hs. 495188NM_138361	ENSG000003LRSAM1	CM2P2 RIF leucine i protein-coding	
chr10-414 15.20019	0.666307	0.64395	1.034718	0.3008	0.981636	chr10	41494385	41495161	0 NA	IntergeniALR/Alpha	873272 NR_02438C	441666 Hs. 255722NR_02438C	ENSG000003LOC441666	- zinc fing pseudo	
chr1-565 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr1	56564585	56567578	0 NA	intron (Nintron (N	13432 NM_00371E	8613 Hs. 405156NM_00371E	ENSG000003PLPP3	Dri42 LPF phospholiprotein-coding	
chr1-100 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr1	1E+08	1E+08	0 NA	intron (NAluSx3 SI	-25972 NM_03305E	64645 Hs. 124156NM_03305E	ENSG000003MFS14A	HIAT1 major fac protein-coding	
chr11-167 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr11	16757283	16758289	0 NA	3' UTR (N3' UTR (N	19139 NM_014267	10944 Hs. 368222NM_014267	ENSG000003C11orf58	IMAGE145C chromoson protein-coding	
chr13-32 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr13	32682962	32685007	0 NA	exon (NM exon (NM	97535 NM_015032	23047 Hs. 744901NM_015032	ENSG000003PDS5B	APRN ASE PDS5 cohe protein-coding	
chr2-2024 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr2	20249905	20250747	0 NA	3' UTR (N3' UTR (N	-24893 NM_00100E	6382 Hs. 224607NM_002997	ENSG000003SDC1	C13orf35 syndecan protein-coding	
chr2-5821 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr2	58211016	58211922	0 NA	intron (NTHE1B-int	29911 NR_156742	55120 Hs. 631899NM_01806E	ENSG000003FANCL	FAAP43 PFA comple protein-coding	
chr2-144 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr2	1.44E+08	1.44E+08	0 NA	intron (Nintron (N	-57274 NM_001354	79712 Hs. 44780 NM_02465E	ENSG000003GTDCl	Hmat-Xa nglycosyl protein-coding	
chr2-2016 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr2	2.02E+08	2.02E+08	0 NA	intron (Nintron (N	-10040 NM_00116E	151254 Hs. 335788NM_15252E	ENSG000003C2DC6	ALS2CR11 C2 calci protein-coding	
chr3-481 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr3	48180186	48182473	0 NA	intron (NLM1E3 LIN	7088 NM_00178E	993 Hs. 437705NM_00178E	ENSG000003CDC25A	CDC25A2 cell divi protein-coding	
chr4-159 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr4	1.59E+08	1.59E+08	0 NA	intron (Nintron (N	12904 NM_001351	9693 Hs. 744884NM_014247	ENSG000003RAPGEF2	CNrasGEF WPC guanin protein-coding	
chr4-183 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr4	1.83E+08	1.83E+08	0 NA	intron (Nintron (N	30940 NR_12647E	1.02E+08	Hs. 57071NR_12647E	ENSG000003WWC2-AS1	RWC2 antincRNA
chr5-810 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr5	81063364	81064400	0 NA	intron (NHALIME LI	-102975 NR_10501E	1.03E+08	Hs. 737156NR_10501E	ENSG000003RASGRF2-1	RASGRF2 ncRNA
chr5-969 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr5	96903757	96904733	0 NA	intron (Nintron (N	28306 NR_137637	64167 Hs. 482911NM_02235C	ENSG000003ERAP2	L-RAP LR1 endoplasm protein-coding	
chr9-8601 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr9	86019419	86020171	0 NA	intron (NLM1E4b LI	78276 NM_001321	60560 Hs. 436099NM_02192E	ENSG000003NAA35	EGAP MAK1N(alpha)- protein-coding	
chr9-9807 5.426686	-1.04499	1.010135	-1.03451	0.300898	0.981636	chr9	98079050	98079708	0 NA	intron (Nintron (N	22647 NM_01894E	54187 Hs. 522311NM_01894E	ENSG000003NANS	HEL-S-10CN-acetyl protein-coding	
chr19-144 7.821982	-0.88979	0.860348	-1.03422	0.301031	0.981636	chr19	14403035	14403234	0 NA	intron (NAluSx SIN	16207 NM_005804	10212 Hs. 311606NM_005804	ENSG000003DDX39A	BAT1 BAT1DEXD-box protein-coding	
chr20-36 7.821982	-0.88979	0.860348	-1.03422	0.301031	0.981636	chr20	36912119	36912318	0 NA	intron (Nintron (N	36080 NM_08062E	140711 Hs. 472633NM_08062E	ENSG000003TLDC2	C2orf11E TBC/LysM- protein-coding	
chr10-49 6.683191	1.141302	1.103749	1.034023	0.301125	0.981636	chr10	49516143	49516731	0 NA	exon (NM exon (NM	7844 NM_17075E	267004 Hs. 49063 NM_17075E	ENSG		



chr17-416 7.913969	-0.87155	0.84828	-1.02744	0.304215	0.981636	chr17	41806783	41807020	+	0 NA	intron (Nintron (N	5048 NM_006455	10609 Hs. 446459	ENSG000003P3H4	LEPREL4 N	prolyl 3-protein-coding	
chr8-1178 7.913969	-0.87155	0.84828	-1.02744	0.304215	0.981636	chr8	1.18E+08	1.18E+08	+	0 NA	intron (Nintron (N	96127 NR_145799	1.1E+08	NR_145799	SNORD168	small nucsnRNA	
chr15-443 3.677444	-1.37819	1.342062	-1.02692	0.304457	0.981636	chr15	44380785	44381064	+	0 NA	exon (NM_exon (NM_	-46705 NM_01639E	51496 Hs. 497967	ENSG000003CTD5PL2	HSPC058 E	CTD small protein-coding	
chr1-2401 8.186854	0.847279	0.825086	1.026898	0.304468	0.981636	chr1	2.4E+08	2.4E+08	+	0 NA	intron (Nintron (N	67840 NM_02006E	56715 Hs. 24889	ENSG000003FM2E	-	formin 2 protein-coding	
chr15-416 8.186854	0.847279	0.825086	1.026898	0.304468	0.981636	chr15	41536496	41537009	+	0 NA	intron (NMIR SINE	7505 NM_01554C	26015 Hs. 37104E	ENSG000003RPA1P	-	RNA polynprotein-coding	
chr17-119 8.186854	0.847279	0.825086	1.026898	0.304468	0.981636	chr17	11977213	11979457	+	0 NA	exon (NM_exon (NM_	19037 NM_14468C	7566 Hs. 37047E	ENSG000003ZNF18	HDSG1 K0	zinc fing protein-coding	
chr6-3088 8.186854	0.847279	0.825086	1.026898	0.304468	0.981636	chr6	30894668	30898594	+	0 NA	exon (NM_exon (NM_	5748 NR_03978E	1.01E+08	NR_03978E	ENSG000003MIR4640	-	microRNA ncRNA
chr11-201 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr11	20119888	20119649	+	0 NA	3' UTR (N3' UTR (N	41157 NM_00102E	120237	NR_00102E	ENSG000003DBX1	-	developiprotein-coding
chr11-128 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr11	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	58211 NM_00523E	2113 Hs. 36943E	ENSG000003ETS1	ETS-1 EWS	ETS protc protein-coding	
chr13-106 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr13	1.07E+08	1.07E+08	+	0 NA	TTS (NM_C TTS (NM_C	-6378 NM_00409E	1948 Hs. 14923E	ENSG000003EFN2E	EPLG5 HT	ephrin B2 protein-coding	
chr17-774 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr17	77411378	77411617	+	0 NA	intron (NAluS4 SI	6420 NM_00129E	10801 Hs. 44093E	ENSG000003SEPTIN9	AF17q25 A	septin 9 protein-coding	
chr2-173 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr2	1.73E+08	1.73E+08	+	0 NA	intron (Nintron (N	7097 NM_01665E	51776 Hs. 444451	ENSG000003MAP3K20	AZK CNM6	mitogen-ε protein-coding	
chr2-2274 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr2	20998 NM_00113E	2.27E+08	+	0 NA	intron (NLM1B LI	3267 Hs. 35296E	ENSG000003AGFG1	HRB IAB	FarfGAP wiprotein-coding		
chr20-205 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr20	36907584	36907810	+	0 NA	intron (NAluSg4 LI	31559 NM_00129E	140711 Hs. 47263E	ENSG000003TLD2C	C20orf11E	TBC/LysM protein-coding	
chr22-181 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr22	18158065	18158414	+	0 NA	intron (NAluSg4 SI	8069 NM_017414	11274 Hs. 38260	ENSG000003USP18	ISG43 PTC	ubiquitin protein-coding	
chr4-1223 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (Nintron (N	-68917 NM_13924E	132612 Hs. 518957	ENSG000003ADAD1	Tenr	adenosine protein-coding	
chr5-3587 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr5	35874616	35877737	+	0 NA	exon (NM_exon (NM_	19285 NM_00218E	3575 Hs. 59174E	ENSG000003IL7R	CD127 CDW	interleuk protein-coding	
chr6-2475 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr6	24785934	24787288	+	0 NA	TTS (NM_C TTS (NM_C	11198 NM_001251	51053 Hs. 23489E	ENSG000003GMNN	Gem MGOR	geminin I protein-coding	
chr7-1347 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr7	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	1587 NM_03313E	800 Hs. 49020E	ENSG000003CALD1	CDM H-CA	caldesmor protein-coding	
chr8-1331 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chr8	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	2356 NM_08083E	8840 Hs. 492974	ENSG000003CCN4	WISPI WIS	cellular protein-coding	
chrX-1415 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chrX	1415059	1415524	+	0 NA	non-codiron-codir	14760 NR_02671C	80161 Hs. 52185E	ENSG000003ASMTL-AS1	ASMTL-AS1	cellular antncRNA	
chrX-1015 5.385546	-1.0511	1.023657	-1.02681	0.304508	0.981636	chrX	1.01E+08	1.01E+08	+	0 NA	intron (NLM1A LI	2149 NM_00119E	1.01E+08	Hs. 43248E	ENSG000003RPL36A-HN	RPL36A-HN	protein-coding
chr19-498 11.34774	-0.72599	0.707094	-1.02673	0.30455	0.981636	chr19	49805909	49806109	+	0 NA	TTS (NM_C TTS (NM_C	7283 NR_03326E	80199 Hs. 28880E	ENSG000003CFUZ	CPLANE3 F	fuzzy plε protein-coding	
chr5-5594 11.34774	-0.72599	0.707094	-1.02673	0.30455	0.981636	chr5	55940822	55942726	+	0 NA	non-codiron-codir	53189 NM_175767	3572 Hs. 53208E	ENSG000003IL6ST	CDL30 CDW	interleuk protein-coding	
chr18-123 11.33202	-0.72381	0.705099	-1.02653	0.304641	0.981636	chr18	12309583	12320977	+	0 NA	intron (NLM1E4a LI	7039 NM_00130E	84617 Hs. 193491	ENSG000003TUBB6	FPVPEP H	tubulin t protein-coding	
chr2-691 11.33202	-0.72381	0.705099	-1.02653	0.304641	0.981636	chr2	69152670	69153351	+	0 NA	intron (Nintron (N	49328 NR_03607E	1E+08	NR_03607E	ENSG000003MIR3126	mir-3126	microRNA ncRNA
chr14-105 9.921794	1.023739	0.997389	1.026419	0.304694	0.981636	chr14	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	28256 NM_14568E	2972 Hs. 424484	ENSG000003BRF1	BRF1 BRF-1	BRF1 RNA protein-coding	
chr12-502 6.616476	-0.95047	0.926376	-1.02601	0.304886	0.981636	chr12	50208095	50208318	+	0 NA	intron (NAluSx3 SI	-6673 NM_00124E	51474 Hs. 52541E	ENSG000003LMA1A	EPLIN LDI	LIM domain protein-coding	
chr2-8647 6.616476	-0.95047	0.926376	-1.02601	0.304886	0.981636	chr2	86478268	86479068	+	0 NA	exon (NM_exon (NM_	37207 NM_00114E	55818 Hs. 55742E	ENSG000003KDM3A	JHDM2A JF	lysine deprotein-coding	
chr3-186 6.616476	-0.95047	0.926376	-1.02601	0.304886	0.981636	chr3	1.88E+08	1.88E+08	+	0 NA	intron (Nintron (N	-5133 NM_001167	4026 Hs. 52722E	ENSG000003LPP	-	LIM domain protein-coding	
chr4-1187 6.616476	-0.95047	0.926376	-1.02601	0.304886	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (Nintron (N	64263 NM_01482E	9871 Hs. 189641	ENSG000003SEC24D	CLCRP2	SEC24 hom protein-coding	
chr8-1802 6.616476	-0.95047	0.926376	-1.02601	0.304886	0.981636	chr8	18021502	18021298	+	0 NA	intron (NMER57A-ir	61481 NM_00136E	427 Hs. 52741E	ENSG000003ASAHI	ATC ADCase	N-acetyl sp protein-coding	
chr12-111 10.109599	-0.74751	0.729074	-1.02529	0.305227	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	37091 NM_17066E	488 Hs. 55765E	ENSG000003ATP2A2	ATP2B2 DAF	ATPase sp protein-coding	
chr8-6156 5.360123	-1.06184	1.035987	-1.02496	0.305383	0.981636	chr8	61564231	61565168	+	0 NA	intron (Nintron (N	125112 NM_001164	444 Hs. 33242E	ENSG000003ASPH	AAH BAH	Caspartate protein-coding	
chr19-206 29.65707	0.509013	0.496841	1.024499	0.3056	0.981636	chr19	26079823	26080137	+	0 NA	IntergeniALR Alpha	-1713451 NR_14673E	1.02E+08	Hs. 567934	ENSG000003LOC101927-	uncharactncRNA	
chr10-405 29.17805	0.517456	0.505104	1.024455	0.30562	0.981636	chr10	40975909	40976161	+	0 NA	IntergeniALR Alpha	1392010 NR_02438C	441666 Hs. 25572E	ENSG000003LOC44166E-	zinc fingpseudo		
chr11-126 6.445655	0.970656	0.947493	1.024446	0.305625	0.981636	chr11	1.26E+08	1.26E+08	+	0 NA	TTS (NM_C TTS (NM_C	-10093 NM_00135E	28960 Hs. 50424E	ENSG000003DCPS	ARS DCS1	decapping protein-coding	
chr1-123 40.46533	0.421614	0.411731	1.024002	0.305834	0.981636	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR Alpha	1539401 NR_00395E	647121 Hs. 69768E	ENSG000003EMBP1	-	embin g ppsudo	
chr10-136 6.088456	-1.03808	1.013757	-1.024	0.305837	0.981636	chr10	13342259	13342513	+	0 NA	intron (NAluSx SIN	5907 NM_012247	22929 Hs. 124027	ENSG000003SEPHS1	SELD SPS	selenophc protein-coding	
chr1-1114 5.238484	1.047355	1.023788	1.02302	0.306299	0.981636	chr1	1.11E+08	1.11E+08	+	0 NA	IntergeniL2c LINE	-3864 NM_00130C	128346 Hs. 28801E	ENSG000003C1orf162	-	chromoson protein-coding	
chr1-122 5.238484	1.047355	1.023788	1.02302	0.306299	0.981636	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR Alpha	1235972 NR_00395E	647121 Hs. 69768E	ENSG000003EMBP1	-	embin g ppsudo	
chr12-127 5.238484	1.047355	1.023788	1.02302	0.306299	0.981636	chr12	1.21E+08	1.21E+08	+	0 NA	3' UTR (N3' UTR (N	39121 NM_000017	35 Hs. 50707E	ENSG000003ACADS	ACAD3 SC	acyl-CoA protein-coding	
chr20-515 5.238484	1.047355	1.023788	1.02302	0.306299	0.981636	chr20	51598744	51600517	+	0 NA	3' UTR (N3' UTR (N	-36791 NM_00113E	4773 Hs. 74414E	ENSG000003NFATC2	NFAT1 NF	nuclear f protein-coding	
chr9-104 5.238484	1.047355	1.023788	1.02302	0.306299	0.981636	chr9	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	73153 NM_00550E	19 Hs. 659274	ENSG000003ABCA1	ABC-1 ABC	ATP bindiprotein-coding	
chr12-106 5.980499	1.033138	1.009982	1.022928	0.306342	0.981636	chr12	1.06E+08	1.06E+08	+	0 NA	exon (NM_exon (NM_	18842 NM_00128E	255394 Hs. 696047	ENSG000003TCP11L2	-	t-complex protein-coding	
chr9-133 5.980499	1.033138	1.009982	1.022928	0.306342	0.981636	chr9	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	-4776 NM_001807	1056 Hs. 53325E	ENSG000003CEL	BAL BSDL	carboxyl protein-coding	
chr11-464 8.220136	0.849805	0.831142	1.022454	0.306566	0.981636	chr11	46434547	46434926	+	0 NA	intron (Nintron (N	-17071 NR_03611E	1E+08	NR_03611E	ENSG000003MIR3160-	mir-3160	microRNA ncRNA
chr9-976 8.220136	0.849805	0.831142	1.022454	0.306566	0.981636	chr9	97600852	97601517	+	0 NA	3' UTR (N3' UTR (N	32184 NM_13924E	158427 Hs. 72323E	ENSG000003TSTD2	C9orf97	thiosulfε protein-coding	
chr4-2636 6.180443	-1.01267	0.990526	-1.02235	0.306614	0.981636	chr4	2636386	2636993	+	0 NA	intron (NCharliel	11257 NR_04633E	8603 Hs. 652364	ENSG000003FAM193A	C4orf8 RE	famil y wiprotein-coding	
chr14-61 9.655353	-0.78422	0.767087	-1.02234	0.306622	0.981636	chr14	61060879	61061251	+	0 NA	intron (NLIHS LINE	-79375 NM_00135E	57570 Hs. 38015E	ENSG000003TRMT5	COXP26 K	tRNA metl protein-coding	
chr22-192 7.774395	0.908351	0.888557	1.022277	0.30665	0.981636	chr22	19222653	19222948	+	0 NA	exon (NM_exon (NM_	-43937 NR_04629E	6576 Hs. 111024	ENSG000003SLC25A1	CMS23 CTF	solute cε protein-coding	
chr1																	



chr19-472.8.742148	0.811464	0.799103	0.015468	0.309883	0.981636	chr19	47260529	47261640	+	0	NA	intron (Nintron (N	4559	NM_015603	26093	Hs.227782	NM_015603	ENSG000000CCDC9	-		coiled-coiled protein-coding	
chr3-3164.8.742148	0.811464	0.799103	0.015468	0.309883	0.981636	chr3	3164210	3165443	+	0	NA	intron (Nintron (N	14891	NM_016302	51185	Hs.18925	NM_016302	ENSG000000CRBN	MRT2	MRT2	cerebrin protein-coding	
chr18-765.7.024523	0.907908	0.894079	0.015468	0.309883	0.981636	chr18	76900966	76901530	+	0	NA	intron (Nintron (N	77088	NM_007345	7776	Hs.719137	NM_007345	ENSG000000ZNF236	ZNF236A	ZNF236	zinc finger protein-coding	
chr7-8026.6.510369	0.962584	0.947933	0.015468	0.309888	0.981636	chr7	8026350	8027942	+	0	NA	intron (Nintron (N	58350	NM_138422	113263	Hs.13167	NM_138422	ENSG000000GLCC11	FAM117C	GLUCO	glucocorticoid protein-coding	
chr1-1784.6.999099	0.90242	0.888815	0.015307	0.30996	0.981636	chr1	1784085	1784177	+	0	NA	3' UTR (N3' UTR (N	-39354	NM_001117	84066	Hs.534501	NM_001117	ENSG000000TEX35	Clorf49	TESTIS	testis e protein-coding	
chr1-2131.6.999099	0.90242	0.888815	0.015307	0.30996	0.981636	chr1	2131085	2131177	+	0	NA	intron (Nintron (N	62053	NM_012424	26750	Hs.59141	NM_012424	ENSG000000RPS6K1	RPK118	RPS6K1	ribosomal protein-coding	
chr15-634.8.161431	0.842527	0.829844	0.015283	0.309971	0.981636	chr15	63676511	63676750	+	0	NA	intron (Nintron (N	-75803	NR_034088	1E+08	Hs.63116	NR_034088	ENSG000000USP3-AS1	-	USP3	antincRNA	
chr22-506.8.161431	0.842527	0.829844	0.015283	0.309971	0.981636	chr22	50465479	50467867	+	0	NA	exon (NM exon (NM	8362	NM_002972	6305	Hs.589924	NM_002972	ENSG000000SBF1	CMT4B3	DESET	bindiprotein-coding	
chr18-492.8.726432	0.815431	0.803483	0.01487	0.310168	0.981636	chr18	49257907	49258374	+	0	NA	intron (Nintron (N	202505	NM_001353	54808	Hs.16299	NM_001353	ENSG000000CDYM	DMC1	SMC	dymeclin protein-coding	
chr18-162.146.6285	0.286875	0.282685	0.01487	0.310119	0.981636	chr18	16265918	16266195	+	0	NA	IntergeniALR/Alpha	-940137	NR_027417	644669	Hs.579474	NR_027417	ENSG000000LOC644669	-		ankyrin r pseudo	
chr1-149.8.708866	0.808974	0.797233	0.014726	0.310236	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	exon (NM exon (NM	52902	NM_001353	9659	Hs.584841	NM_001353	ENSG000000PDE4DIP	CMYA2	MM	phosphodi protein-coding	
chr12-111.8.708866	0.808974	0.797233	0.014726	0.310236	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	39613	NM_025247	80724	Hs.331141	NM_025247	ENSG000000ACAD10	-	acyl-CoA	protein-coding	
chr8-473.8.708866	0.808974	0.797233	0.014726	0.310236	0.981636	chr8	47313540	47313742	+	0	NA	intron (Nintron (N	52703	NM_001088	23514	Hs.38105	NM_001088	ENSG000000SPIDR	KIAA0146	scalloid	protein-coding	
chr15-417.6.991241	0.904924	0.892134	0.014336	0.310422	0.981636	chr15	41766340	41766926	+	0	NA	exon (NM exon (NM	-7851	NM_001265	23005	Hs.513661	NM_001265	ENSG000000MAPKB1	JNKBP1	Jmi	protein-coding	
chr15-714.6.991241	0.904924	0.892134	0.014336	0.310422	0.981636	chr15	71400590	71401899	+	0	NA	intron (Nintron (N	-145992	NM_001288	79875	Hs.387057	NM_001288	ENSG000000THSD4	ADAMTSL-1	thrombos	protein-coding	
chr19-266.10.43435	0.744069	0.733615	0.014251	0.310463	0.981636	chr19	26033642	26033865	+	0	NA	IntergeniALR/Alpha	-1759678	NR_146733	1.02E+08	Hs.567934	NR_146733	ENSG000000LOC101927	-		uncharactericnRNA	
chr17-408.8.194712	0.845067	0.833265	0.014163	0.310505	0.981636	chr17	40029333	40029835	+	0	NA	intron (Nintron (N	-1969	NR_102365	1.01E+08	NR_102365	ENSG000000SNORD124	-		small nucsnoRNA		
chr19-101.8.194712	0.845067	0.833265	0.014163	0.310505	0.981636	chr19	10158509	10158794	+	0	NA	intron (Nintron (N	36332	NM_001318	1786	Hs.20267	NM_001318	ENSG000000DNMT1	ADCADN	AIDNA	methylprotein-coding	
chr7-149.8.194712	0.845067	0.833265	0.014163	0.310505	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	4697	NR_163909								
chr10-100.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (Nintron (N	26422	NM_003393	7479	Hs.421281	NM_003393	ENSG000000WNT8B	-		Wnt	family protein-coding
chr11-862.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr11	8622154	8622843	+	0	NA	intron (Nintron (N	-28270	NM_001288	65975	Hs.50183	NM_001288	ENSG000000STK33	-		serine/t protein-coding	
chr12-115.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr12	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	7826	NM_001143	53373	Hs.52476	NM_001143	ENSG000000TPCN1	TPC1	two pore	protein-coding	
chr16-216.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr16	2167271	2168444	+	0	NA	intron (Nintron (N	12075	NM_032271	84231	Hs.71363	NM_032271	ENSG000000TRAF7	CAFDADD	FTN	recept protein-coding	
chr17-147.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr17	47817028	47818869	+	0	NA	intron (Nintron (N	3846	NM_145798	114881	Hs.64332	NM_145798	ENSG000000OSBP17	ORP7	oxysterol	protein-coding	
chr4-2335.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr4	2335325	2335930	+	0	NA	intron (Nintron (N	29187	NM_001172	57732	Hs.292025	NM_001172	ENSG000000ZFVYE28	LST2	LYST	zinc finger protein-coding	
chr5-1574.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr5	1.57E+08	1.57E+08	+	0	NA	3' UTR (N3' UTR (N	-20778	NR_136205	1.03E+08	Hs.57088	NR_136205	ENSG000000LOC102724	-		uncharactericnRNA	
chr7-5865.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr7	58698599	58700039	+	0	NA	IntergeniALR/Alpha	1249142	NM_001155	441234	Hs.533121	NM_001155	ENSG000000ZNF716	-		zinc finger protein-coding	
chr9-8906.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr9	89063911	89065374	+	0	NA	intron (Nintron (N	73174	NM_005226	1903	Hs.58511	NM_005226	ENSG000000LIPR3	EDG-3	EDC	sphingosin protein-coding	
chr9-1365.5.213061	0.104038	0.102613	0.013843	0.310658	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (Nintron (N	20896	NR_039697	255130	NR_039697	ENSG000000MIR4479	-		microRNA ncRNA		
chr4-571C.7.788701	-0.8959	0.883703	-0.0138	0.310677	0.981636	chr4	57100892	57101289	+	0	NA	intron (Nintron (N	-8672	NR_034081	401941	Hs.691061	NR_034081	ENSG000000IGFBP7-AS	-		IGFBP7	arnRNA
chr14-347.4.213322	-1.19067	1.17482	-0.01349	0.310826	0.981636	chr14	34754092	34754714	+	0	NA	intron (Nintron (N	-39580	NR_028130	1073	Hs.180141	NR_028130	ENSG000000CFL2	NEM7	cofilin 2	protein-coding	
chr7-1286.10.49305	0.749991	0.740289	0.013101	0.31101	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	non-codiron-codir	11297	NR_024368	402483	Hs.72235	NR_024368	ENSG000000LINC0100C	-		long intncRNA	
chr2-1448.8.375426	-0.82458	0.814083	-0.01289	0.311112	0.981636	chr2	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	-72688	NR_040248	1E+08	Hs.56078	NR_040248	ENSG000000ZEB2-AS1	ZEB2-AS1	ZEB2	antincRNA	
chr3-7097.8.375426	-0.82458	0.814083	-0.01289	0.311112	0.981636	chr3	70974539	70975097	+	0	NA	intron (Nintron (N	90106	NM_001345	27086	Hs.59368	NM_001345	ENSG000000FOX1P	12CC4	HSF	forkhead protein-coding	
chr4-1688.8.375426	-0.82458	0.814083	-0.01289	0.311112	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N	37260	NM_001367	23022	Hs.15122	NM_001367	ENSG000000PALLD	CG1-151	CALLADIN	protein-coding	
chr7-1435.8.375426	-0.82458	0.814083	-0.01289	0.311112	0.981636	chr7	1.43E+08	1.43E+08	+	0	NA	intron (Nintron (N	12778	NM_001224	835	Hs.36898	NM_001224	ENSG000000CASP2	CASP-2	C	caspase 2 protein-coding	
chr12-911.9.59064	-0.78349	0.773672	-0.01269	0.311209	0.981636	chr12	91176600	91177914	+	0	NA	intron (Nintron (N	1389	NM_133505	1634	Hs.15631	NM_133505	ENSG000000CDN	CSCD	DSPC	decorin protein-coding	
chr19-941.12.68184	0.678375	0.669936	0.012596	0.311253	0.981636	chr19	9412168	9420477	+	0	NA	intron (Nintron (N	19251	NM_001370	10781	Hs.65618	NM_001370	ENSG000000ZNF266	HZF1	zinc finger	protein-coding	
chr9-265.8.381434	-0.83694	0.826682	-0.0124	0.311345	0.981636	chr9	2652451	2653203	+	0	NA	exon (NM exon (NM	30454	NR_015375	401491	Hs.41604	NR_015375	ENSG000000VLDLR-AS1	linc-VLDLR	VLDLR	antincRNA	
chr1-1921.8.716724	0.807028	0.797384	0.012095	0.311493	0.981636	chr1	19218421	19219423	+	0	NA	3' UTR (N3' UTR (N	8536	NR_135115	1.02E+08	Hs.660534	NR_135115	ENSG000000EMC1-AS1	-		EMC1	antincRNA
chr1-2191.8.716724	0.807028	0.797384	0.012095	0.311493	0.981636	chr1	2.19E+08	2.19E+08	+	0	NA	intron (Nintron (N	5411	NM_001320	127018	Hs.65761	NM_001320	ENSG000000LYPLAL1	Q96AV0	lysofos	protein-coding	
chr11-11.8.716724	0.807028	0.797384	0.012095	0.311493	0.981636	chr11	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	18101	NM_004724	9183	Hs.50388	NM_004724	ENSG000000ZWI10	HZW10	KNI	zinc protein-coding	
chr19-365.8.716724	0.807028	0.797384	0.012095	0.311493	0.981636	chr19	36943280	36951074	+	0	NA	intron (Nintron (N	30845	NM_001204	374900	Hs.40422	NM_001204	ENSG000000ZNF568	ZFP568	zinc finger	protein-coding	
chr20-558.8.716724	0.807028	0.797384	0.012095	0.311493	0.981636	chr20	5591449	5594859	+	0	NA	intron (Nintron (N	17852	NM_019593	56261	Hs.63635	NM_019593	ENSG000000GPCPD1	E103	GDEF	glycerol protein-coding	
chr10-146.8.342144	-0.82963	0.819726	-0.01209	0.311497	0.981636	chr10	14600394	14601159	+	0	NA	intron (Nintron (N	3629	NM_001282	83641	H						

chr2-1615	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr2	1.62E+08	1.62E+08	0 NA	intron (Nintron (N	74002 NM_001935	1803 Hs. 368912NM_001935	ENSG000004DPP4	ADABP ADC dipeptidylprotein-coding	
chr3-1842	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr3	1.84E+08	1.84E+08	0 NA	non-codiron-codir	2565 NR_03041C	1E+08	NR_03041C	ENSG000004MIR1224	MIRN1224 microRNA ncRNA
chr7-1295	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.3E+08	1.3E+08	0 NA	intron (NAluSp SIN	22774 NM_003344	7328 Hs. 643545NM_003344	ENSG000004UBE2H	E2-20K Gubiquitin protein-coding	
chr9-116	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr9	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	54260 NR_103711	493913 Hs. 728832NR_103711	ENSG000004PAPA-AS1	DIPAS NCF PAPA antncRNA	
chr13-786	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr13	1.16E+08	1.16E+08	0 NA	intron (NAluXs1 SI	18571 NM_024544	79596 Hs. 567575NM_024544	ENSG000004OBI1	C13orf7 FORC ubiq protein-coding	
chr2-1935	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr2	1.16E+08	1.16E+08	0 NA	intron (NCpG	1779 NM_14526C	130497 Hs. 123933NM_14526C	ENSG000004OSR1	ODD odd-skip protein-coding	
chr6-2814	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr6	1.16E+08	1.16E+08	0 NA	5' UTR (N5' UTR (N	2193 NM_001278	7745 Hs. 57679NM_006298	ENSG000004ZKSCAN8	L105-1 ZNF zinc finger protein-coding	
chr10-111	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr10	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-48862 NR_015376	399706 Hs. 721191NM_00101C	ENSG000004LINC00200C	CDorf135 long intncRNA	
chr12-296	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr12	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-101112 NM_001355	341350 Hs. 674585NM_183378	ENSG000004OVCH1	OVCH ovochymas protein-coding	
chr12-577	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr12	1.16E+08	1.16E+08	0 NA	intron (NLINE LINE	3171 NM_015433	25895 Hs. 63272C	ENSG000004EEFLAKMT7	FAM119B EEFLA lys protein-coding	
chr14-594	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr14	1.16E+08	1.16E+08	0 NA	IntergeniLIMb LIN	6980 NM_022571	64582 Hs. 647575NM_022571	ENSG000004GPR135	HUMNP11Y2G protein-coding	
chr17-784	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr17	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	34310 NR_110601	9489 Hs. 654671NM_024415	ENSG000004PGS1	phosphatidylprotein-coding	
chr19-975	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	TTS (NM_C TTS (NM_C	12037 NM_001077	162993 Hs. 665717NM_001077	ENSG000004ZNF846	zinc finger protein-coding	
chr2-202	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr2	1.16E+08	1.16E+08	0 NA	TTS (NR_C TTS (NR_C	118 NR_003058	692110	NR_003058	ENSG000004SNORD70	HBI1-234 small nucsnoRNA
chr21-414	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr21	1.16E+08	1.16E+08	0 NA	intron (NMER21C LI	17678 NM_001282	4599 Hs. 517307NM_002462	ENSG000004CMX1	IFI-78K IMX dynam protein-coding	
chr5-1714	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr5	1.16E+08	1.16E+08	0 NA	IntergeniIntergeni	-6331 NM_003862	8817 Hs. 87191 NM_003862	ENSG000004PGF18	PGF-18 Zf fibroblast protein-coding	
chr6-4108	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr6	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	11752 NM_001325	221443 Hs. 227457NM_145065	ENSG000004OARD1	C6orf130 O-acyl-AI protein-coding	
chr7-1508	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.16E+08	1.16E+08	0 NA	non-codiron-codir	18178 NR_022447	1E+08 Hs. 586358NR_022447	ENSG000004PAX11-AS	PAX1105 PAX11 arncRNA	
chr12-425	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr12	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	28314 NM_00113C	84318 Hs. 631656NM_032355	ENSG000004CCDC77	coiled-co protein-coding	
chr19-324	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	intron (NMER52C LI	2329 NM_03281E	84902 Hs. 599703NM_03281E	ENSG000004CEP89	CCDC123 Centron protein-coding	
chr1-125	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr1	1.16E+08	1.16E+08	0 NA	intron (NMIRb SINE	6687 NM_018252	55248 Hs. 445388NM_018252	ENSG000004PACC1	CRorf75 Proton ac protein-coding	
chr14-226	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr14	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	11723 NM_02206C	63874 Hs. 445665NM_02206C	ENSG000004ABHD4	ABH4 abhydrolase protein-coding	
chr7-526	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.16E+08	1.16E+08	0 NA	intron (NCpG	14019 NM_001035	26100 Hs. 122363NM_01561C	ENSG000004WIP12	ATG18B AtWD repeat protein-coding	
chr19-100	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	intron (NAluXs1 SI	19471 NM_00451E	3609 Hs. 465888NM_00451E	ENSG000004ILF3	CBTF DRBF interleaf protein-coding	
chr10-124	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr10	1.16E+08	1.16E+08	0 NA	intron (NAluJb SIN	16181 NM_001363	1488 Hs. 501345NM_001325	ENSG000004CTBP2	C-terminal protein-coding	
chr16-186	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr16	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-61693 NM_015161	23204 Hs. 634882NM_015161	ENSG000004ARL61P1	AIP1 ARL6 ADP ribos protein-coding	
chr6-1768	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr6	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-40998 NR_13461E	1.05E+08 Hs. 718703NR_13461E	ENSG000004LOC105374	uncharactncRNA	
chr17-362	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr17	1.16E+08	1.16E+08	0 NA	intron (NAluY SINE	-11088 NM_080704	7442 Hs. 579217NM_018727	ENSG000004TRPV1	VR1 transient protein-coding	
chr19-365	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	9510 NM_00130C	23396 Hs. 282177NM_012395	ENSG000004PIP5K1C	LCCS3 PIF phosphatidyl protein-coding	
chr2-218	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr2	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	20108 NR_106867	1.02E+08	NR_106867	ENSG000004MIR6809	hsa-mir-6809 microRNA ncRNA
chr16-295	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr16	1.16E+08	1.16E+08	0 NA	IntergeniIntergeni	33806 NM_00131C	728888 Hs. 720282NM_00131C	ENSG000004NPIP1	NPIP nuclear protein-coding	
chr7-1041	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.16E+08	1.16E+08	0 NA	intron (NMSTb LTR	10078 NM_002555	5001 Hs. 432945NM_002555	ENSG000004ORC5	ORC5 ORC origin protein-coding	
chr7-1484	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.16E+08	1.16E+08	0 NA	intron (NLINE LINE	75798 NM_00137C	8454 Hs. 146806NM_003592	ENSG000004CULL1	cullin 1 protein-coding	
chr14-556	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr14	1.16E+08	1.16E+08	0 NA	exon (NM_exon (NM	70148 NM_00107E	3895 Hs. 509414NM_004985	ENSG000004CTN1	CG1 KNT1 kinesin protein-coding	
chr6-1305	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr6	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	69778 NM_00135C	2037 Hs. 486477NM_001431	ENSG000004EPB41L2	4.1-G 4.1 erythrocy protein-coding	
chr5-4951	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr5	1.16E+08	1.16E+08	0 NA	IntergeniALR Alphe	92805 NM_198445	133418 Hs. 561411NM_198445	ENSG000004EMB	GP70 embigin protein-coding	
chr19-271	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	IntergeniALR Alphe	-646558 NR_14673E	1.02E+08 Hs. 567934NR_10687	ENSG000004LOC101927	uncharactncRNA	
chr14-815	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr14	1.16E+08	1.16E+08	0 NA	intron (NLTR12 LTR	20525 NM_00506E	6400 Hs. 18130C	ENSG000004SELLL	Hrd3 PRO1SELLL ade protein-coding	
chr3-4767	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr3	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-10982 NR_145791	1.1E+08	NR_145791	SNORD146	small nucsnoRNA
chr2-2308	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr2	1.16E+08	1.16E+08	0 NA	intron (NLIPA6 LIN	-59298 NM_001287	81618 Hs. 111577NM_030925	ENSG000004ITM2C	BRI3 BRIC integral protein-coding	
chr19-258	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	IntergeniALR Alphe	-1675038 NR_003603	1E+08 Hs. 149312NR_003603	ENSG000004HAVCR1P1	hepatitis pseudo	
chr7-3996	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.16E+08	1.16E+08	0 NA	intron (NLIPA4 LIN	11793 NM_031267	8621 Hs. 233552NM_003715	ENSG000004CDK13	CDCL2 CDC cyclin de protein-coding	
chr10-795	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr10	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-37473 NM_005725	10105 Hs. 381072NM_005725	ENSG000004PPIF	CYP3 CyP peptidyl protein-coding	
chr13-927	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr13	1.16E+08	1.16E+08	0 NA	IntergeniLIPA5 LIN	22022 NM_001071	440145 Hs. 28465	NR_001071	ENSG000004CMT1	C13orf37 mitotic s protein-coding
chr19-551	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	intron (NAluJr SIN	24621 NR_145733	1.1E+08	NR_145733	SNORD13G	small nucsnoRNA
chr19-924	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	intron (NLINE LINE	3424 NM_014222	5518 Hs. 467192NM_014222	ENSG000004PPP2R1A	MRD36 PP2 protein protein-coding	
chr2-2035	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr2	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	27812 NM_001282	10152 Hs. 471155NM_005755	ENSG000004ABI2	ABI-2 ABI1 inter protein-coding	
chr20-147	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr20	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	3662 NM_018835	55968 Hs. 12865	ENSG000004NSFL1C	P47 UBX1 NSFL1 cof protein-coding	
chr7-6176	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr7	1.16E+08	1.16E+08	0 NA	intron (Nintron (N	-5177 NM_001367	9265 Hs. 487475NM_004227	ENSG000004CYTH3	ARNO3 GRF cytohesin protein-coding	
chr9-6477	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr9	1.16E+08	1.16E+08	0 NA	non-codiron-codir	64608 NM_15289E	115426 Hs. 493401NM_15289E	ENSG000004UHRF2	NIRF RNFI ubiquitin protein-coding	
chr19-161	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA	3' UTR (N3' UTR (N	-6075 NM_00683C	10975 Hs. 8372	ENSG000004UCR11	0710008DC ubiquinol protein-coding	
chr1-175	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr1	1.16E+08	1.16E+08	0 NA	IntergeniIntergeni	-3249 NM_172071	149041 Hs. 30258	NR_172071	ENSG000004RC3H1	RNF198 RCR3 ing protein-coding
chr1-3176	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr1	1.16E+08	1.16E+08	0 NA	exon (NM_exon (NM	2193 NR_03621E	1E+08	NR_03621E	ENSG000004MIR4254	microRNA ncRNA
chr15-896	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr15	1.16E+08	1.16E+08	0 NA	intron (NSVA_F Ret	16530 NR_049807	1.01E+08	NR_049807	ENSG000004MIR5009	microRNA ncRNA
chr19-964	6.948252	0.891605	0.888095	1.003952	0.315402	0.981636	chr19	1.16E+08	1.16E+08	0 NA</						







chr6-1675	8.434131	-0.81278	0.824416	-0.98588	0.32419	0.981636	chr6	1.68E+08	1.68E+08	0	NA	intron (N)Tigger3b	32271	NM_001125	1E+08	Hs.448055	ENM_001129895	HGC6.3	-	uncharacterized protein-coding
chr10-10C	6.434098	0.944578	0.958313	0.985667	0.324297	0.981636	chr10	1E+08	1E+08	0	NA	intron (N)CRI_Mam L	12630	NM_001303	55280	Hs.215502	ENM_018294	ENSG00000CWF19L1	C19L1 SCA CWF19	lik protein-coding
chr11-10F	5.768354	0.965656	0.98008	0.985282	0.324486	0.981636	chr11	1.08E+08	1.08E+08	0	NA	intron (N)AluJo SIN	39624	NM_001321	4863	Hs.171061	ENM_002519	ENSG00000CNPAT	E14 E14 Nuclear	protein-coding
chr11-70C	3.428132	-1.26727	1.286309	-0.9852	0.324527	0.981636	chr11	76363672	76364528	0	NA	intron (N)intron (N)	16665	NM_130898	5612	Hs.50331	ENM_00470F	ENSG00000CTHAP12	DAP4 P52 THAP	dom protein-coding
chr15-407	3.428132	-1.26727	1.286309	-0.9852	0.324527	0.981636	chr15	40700830	40702727	0	NA	intron (N)AluSc SIN	6604	NM_001164	5888	Hs.63170	ENM_00287F	ENSG00000CRAD51	BRCC5 FAN RAD51	rec protein-coding
chr16-23C	3.428132	-1.26727	1.286309	-0.9852	0.324527	0.981636	chr16	23515085	23515961	0	NA	IntergeniAluSx SIN	-5029	NM_015044	23062	Hs.46033	ENM_015044	ENSG00000CGGA2	VEAR	golgi ass protein-coding
chr2-113C	3.428132	-1.26727	1.286309	-0.9852	0.324527	0.981636	chr2	1.13E+08	1.13E+08	0	NA	intron (N)intron (N)	7430	NR_015377	654433	Hs.65666	CNR_015377	ENSG00000CPAX8-AS1	PAX8	antincRNA
chr1-729E	8.836883	-0.78306	0.794827	-0.9852	0.324527	0.981636	chr1	729663	729936	0	NA	non-codiron-codir	552	NR_028327	1E+08	Hs.728864	NR_028327	LOC100133	-	uncharacterized
chr1-947I	8.836883	-0.78306	0.794827	-0.9852	0.324527	0.981636	chr1	947169	947523	0	NA	intron (N)intron (N)	11910	NM_015658	26155	Hs.405987	ENM_015658	ENSG00000CNO2L	NET15 NET10C2	like protein-coding
chr10-17C	7.12878	-0.87337	0.886724	-0.98495	0.324651	0.981636	chr10	73999734	74002274	0	NA	intron (N)intron (N)	2874	NM_003373	7414	Hs.64389	ENM_003373	ENSG00000CVCL	CMD1W CMF	vinculin protein-coding
chr4-74E	7.12878	-0.87337	0.886724	-0.98495	0.324651	0.981636	chr4	1942048	1944174	0	NA	TTS (NM_C)TTS (NM_C)	-31525	NR_003004	677770	Hs.676951	NR_003004	ENSG00000SCARNA22	ACA11	small CajncRNA
chr4-533A	7.12878	-0.87337	0.886724	-0.98495	0.324651	0.981636	chr4	53345180	53346029	0	NA	intron (N)LIPA6 LIN	20457	NM_15254C	152579	Hs.302287	ENM_15254C	ENSG00000SCFD2	STXPB1L1	secl fami protein-coding
chr16-294	11.86189	-0.6828	0.693289	-0.98487	0.324686	0.981636	chr16	29431987	29432773	0	NA	intron (N)AluJb SIN	14646	NR_135312	1E+08	Hs.55270	CNR_135312	ENSG00000CSMG1P6	SMG1	psedu
chr20-26	11.86189	-0.6828	0.693289	-0.98487	0.324686	0.981636	chr20	26949100	26949802	0	NA	IntergeniALR/Alphe	-74023	NR_04009E	284801	Hs.37069	NR_04009E	ENSG00000CMR663AHC	MIR663A	lncRNA
chr6-3737	5.195495	1.029606	1.045429	0.984865	0.324691	0.981636	chr6	37377892	37378282	0	NA	intron (N)AluSx SIN	24104	NR_046399	9025	Hs.48527	ENM_00395E	ENSG00000CRNF8	hRNF8	ring fing protein-coding
chr7-128E	5.195495	1.029606	1.045429	0.984865	0.324691	0.981636	chr7	1.29E+08	1.29E+08	0	NA	intron (N)intron (N)	16065	NM_001367	64753	Hs.52117	ENM_00274E	ENSG00000CCDC136	NAG6	coiled-cc protein-coding
chr9-350E	5.195495	1.029606	1.045429	0.984865	0.324691	0.981636	chr9	35090368	35090923	0	NA	exon (NM)exon (NM)	5904	NM_001201	84720	Hs.52209	ENM_003263	ENSG00000CPIGO	HPMRS2	phosphatiprotein-coding
chr1-429E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr1	42951770	42958101	0	NA	intron (N)intron (N)	3933	NM_00651E	6513	Hs.47372	ENM_00651E	ENSG00000SCLC2A1	CSE DYT17	solute c protein-coding
chr1-932E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr1	93260309	93261653	0	NA	intron (N)LIP47 LI	80265	NM_00130C	343099	Hs.48287	ENM_20688E	ENSG00000CCDC18	NY-SAR-41	coiled-cc protein-coding
chr1-181C	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr1	1.81E+08	1.81E+08	0	NA	intron (N)LTR12C LI	13152	NM_001531	3140	Hs.13500	ENM_001531	ENSG00000CMR1	HALMS	major his protein-coding
chr12-25E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr12	56417607	56418296	0	NA	exon (NM)exon (NM)	31475	NM_00133C	8914	Hs.118631	ENM_00392C	ENSG00000CTIMELESS	TIM1 TIM1	timeless protein-coding
chr13-44E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr13	44941774	44943063	0	NA	intron (N)intron (N)	47053	NM_01234E	26747	Hs.52500	ENM_01234E	ENSG00000CNF1P1	NUF1P baE	nuclear f protein-coding
chr14-21E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr14	21219508	21220447	0	NA	intron (N)L2a LINE	-13077	NR_03897I	283624	Hs.52521	CNR_03897C	ENSG00000CLNCO0641	-	long intencRNA
chr16-28E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr16	28729421	28730191	0	NA	intron (N)AluJb SIN	5554	NR_106922	1E+08	Hs.106922	ENSG00000CMR6862	hsa-mir-6	microRNA ncRNA	
chr17-16E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr17	16648648	16649365	0	NA	intron (N)intron (N)	4844	NM_020787	57547	Hs.12807	ENM_020787	ENSG00000CZNF624	-	zinc fing protein-coding
chr17-44E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr17	44938013	44939018	0	NA	intron (N)LIM5 LINE	-3834	NR_106841	1.02E+08	NR_106841	ENSG00000CMR6783	hsa-mir-6	microRNA ncRNA	
chr22-45E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr22	45600748	45601854	0	NA	TTS (NM_C)TTS (NM_C)	4346	NR_131244	1.01E+08	Hs.51769	NR_131244	ENSG00000CLNCO158E	TCONS_00C	long intencRNA
chr3-108I	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr3	1.08E+08	1.08E+08	0	NA	intron (N)LIMA4 LI	27092	NM_01801C	55081	Hs.41219	ENM_01801C	ENSG00000CIFT57	ESRRBL1 E	intraflag protein-coding
chr4-185A	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr4	1.85E+08	1.85E+08	0	NA	non-codiron-codir	11126	NM_18172E	353322	Hs.508154	ENM_18172E	ENSG00000CANRDR37	Lrp2bp	ankyrin r protein-coding
chr5-358E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr5	35861199	35861398	0	NA	intron (N)intron (N)	4407	NM_00218E	3575	Hs.59174	ENM_00218E	ENSG00000CIL7R	CD127 CDW	interleuk protein-coding
chr5-358E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr5	35871349	35871741	0	NA	intron (N)intron (N)	14654	NM_00218E	3575	Hs.59174	ENM_00218E	ENSG00000CIL7R	CD127 CDW	interleuk protein-coding
chr5-714E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr5	71479388	71480139	0	NA	intron (N)AluYk2 SI	24112	NM_01842E	55814	Hs.25827	ENM_01842E	ENSG00000BDP1	DFNB112 F	B double protein-coding
chr5-715E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr5	71567758	71567957	0	NA	TTS (NM_C)TTS (NM_C)	-19483	NR_002132	64087	Hs.60478	ENM_002132	ENSG00000CMCC2	MCCB	mythlcr protein-coding
chr6-10E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr6	1.08E+08	1.08E+08	0	NA	intron (N)intron (N)	46326	NM_00130C	8724	Hs.12102	ENM_00379E	ENSG00000CSNX3	Grd19 MC	sorting r protein-coding
chr7-124E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr7	1.25E+08	1.25E+08	0	NA	3' UTR (N)3' UTR (N)	20453	NM_005302	2861	Hs.406094	ENM_005302	ENSG00000GPR37	EDNRBL P	g protein-coding
chr8-588E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr8	58836100	58838959	0	NA	intron (N)intron (N)	-177676	NR_00358C	8439	Hs.37200	ENM_00358C	ENSG00000CSMAF	FAN GRAM	neutral s protein-coding
chr9-553E	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr9	5536678	5537792	0	NA	intron (N)Charlie2t	26704	NM_02523E	80380	Hs.53227	ENM_02523E	ENSG00000PCDC1L62	B7DC Btdc	programme protein-coding
chr9-860I	5.905708	-0.94966	0.964391	-0.98472	0.32476	0.981636	chr9	86010849	86011048	0	NA	intron (N)A-rich LC	69419	NM_001321	65660	Hs.43069	ENM_02192C	ENSG00000CNA35	EGAP MAK1N	(alpha)-protein-coding
chr14-761	10.15194	-0.73698	0.748535	-0.98456	0.324842	0.981636	chr14	76154207	76155363	0	NA	exon (NM)exon (NM)	431	NR_110314	55668	Hs.41203	ENM_01792E	ENSG00000CPATCH2L	C14orf11E	G-patch protein-coding
chr10-80C	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr10	806063	807376	0	NA	TTS (NM_C)TTS (NM_C)	-117051	NR_014974	22982	Hs.432397	ENM_014974	ENSG00000CIP2C	KIAA0934	disco int protein-coding
chr11-11I	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr11	1.12E+08	1.12E+08	0	NA	intron (N)intron (N)	49592	NM_00271E	5519	Hs.26912	ENM_00271E	ENSG00000PPP2R1B	PP2A-A	bet protein-coding
chr12-11I	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr12	1.12E+08	1.12E+08	0	NA	intron (N)L2a LINE	-77484	NR_001347	22895	Hs.21239	ENM_001347	ENSG00000CRP3A	-	rabphilin protein-coding
chr12-12C	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr12	1.23E+08	1.23E+08	0	NA	intron (N)AluSg SIN	70291	NM_01470E	9735	Hs.30055	ENM_01470E	ENSG00000CNKTC1	ROD	kinetoch protein-coding
chr15-44E	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr15	44507588	44509150	0	NA	intron (N)AluJb SIN	28531	NR_03417I	645212	Hs.594287	NR_03417I	EIF3J-DT	EIF3J-AS1 EIF3J	divncRNA
chr3-455E	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr3	45598765	45599887	0	NA	intron (N)LIMB5 LIN	4575	NM_01424C	8994	Hs.19337	CNR_01424C	ENSG00000CLMD1	-	LIM domain protein-coding
chr3-1597	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr3	1.6E+08	1.6E+08	0	NA	intron (N)AluY SINE	13435	NR_12166E	1.01E+08	Hs.60147	ENM_12166E	IQCJ-SCH1	IQCJ-SCH1	ncRNA
chr9-980E	6.674778	-1.06596	1.082794	-0.98446	0.324892	0.981636	chr9	98081862	98082707	0	NA	intron (N)intron (N)	25552	NM_01894E	54187	Hs.52231	CNR_01894E	ENSG00000CNANS	HEL-S-10C	N-acetyl r protein-coding
chr5-489A	29.06267	0.466636	0.474026	0.98441	0.324914	0.981636	chr5	48949810	48951019	0	NA	IntergeniALR/Alphe	1490874	NM_19844E	133418	Hs.56141	ENM_19844E	ENSG00000CEMB	GP70	embin protein-coding
chr19-384	8.870164	-0.77834	0.790816	-0.98422	0.325007	0.981636	chr19	3408394	3408704	0	NA	intron (N)AluJr SIN	41966	NM_00124E	4782	Hs.170131	ENM_00559E	ENSG00000CNFC	CTF CTF5	nuclear protein-coding
chr2-216I	8.870164	-0.77834	0.790816	-0.98422	0.325007	0.981636	chr2	2.16E+08	2.16E+08	0	NA	intron (N)L3 LINE C	24593	NM_021141	7520	Hs.38873	ENM_021141	ENSG00000CXRC5	KARP-1 KAX	ray re protein-coding





chrX-154:10.60554	-0.70577	0.726504	-0.97146	0.331318	0.981636	chrX	1.54E+08	1.54E+08	0	NA	promoter-promoter-	-658 NR_000011	26778 Hs. 534404NR_000011	ENSG000003SNORA70	DXS648E fsmall	nucsnRNA		
chr10-73:6.938544	0.880917	0.906917	0.971331	0.331383	0.981636	chr10	73392230	73392541	0	NA	intron (NLP1A5 LIN	21673 NM_001156	310 Hs. 631827NM_001156	ENSG000003ANXA7	ANX7 SNR anexin	protein-coding		
chr11-62:8.84659	-0.77423	0.797085	-0.97132	0.331386	0.981636	chr11	62515135	62515908	0	NA	TTS (NM_TTS (NM_C	30143 NM_001346	79026 Hs. 502755NM_00162C	ENSG000003AHNAK	AHNAKRS1 FAHNAK	nucprotein-coding		
chr2-2267:8.84659	-0.77423	0.797085	-0.97132	0.331386	0.981636	chr2	2.27E+08	2.27E+08	0	NA	intron (Nintron (N	30338 NM_005544	3667 Hs. 471505NM_005544	ENSG000003IRS1	HIRS-1	insulin	protein-coding	
chr6-1051:7.44484	0.83838	0.863451	0.970964	0.331566	0.981636	chr6	1.05E+08	1.05E+08	0	NA	intron (Nintron (N	20888 NM_147147	11149 Hs. 22166CNC_00707	ENSG000003BVES	CARIC HEB	lucod vesprotein-coding		
chr9-137:7.44484	0.83838	0.863451	0.970964	0.331566	0.981636	chr9	1.38E+08	1.38E+08	0	NA	3' UTR (N3' UTR (N	-3264 NR_030333	693187 NR_030333	ENSG000003MIR602	MIRN602 f	microRNA ncRNA		
chr19-131:8.607171	0.790921	0.814951	0.970513	0.331791	0.981636	chr19	13138489	13138711	0	NA	3' UTR (N3' UTR (N	11775 NM_001271	8677 Hs. 43812 NM_00376	ENSG000003STX10	SYN10 hsy	synsytaxin	protein-coding	
chr1-3206:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr1	32064231	32065420	0	NA	IntergeniAluSz6 SI	7206 NM_001316	55116 Hs. 25544 NM_01805	ENSG000003TMEM39B	-	transmem protein-coding		
chr12-28:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr12	2886524	2887078	0	NA	intron (Nintron (N	-4090 NM_003324	7289 Hs. 65533NM_003324	ENSG000003TULP3	TUBL3	TUB like	protein-coding	
chr16-71:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr16	71802501	71802926	0	NA	intron (NAluXs1 SI	6121 NM_00103C	164 Hs. 461255NM_00112	ENSG000003AP1G1	ADTG CLAF	adaptor	protein-coding	
chr19-38:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr19	38393146	38393657	0	NA	intron (NAluXs1 SI	3109 NR_073032	399473 Hs. 196011NM_00103	ENSG000003SPRED3	Eve-3 spr	sprouty	protein-coding	
chr3-274:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr3	27408553	27408937	0	NA	intron (Nintron (N	-39285 NM_152534	152110 Hs. 506115NM_152534	ENSG000003CNEK10	-	NIMA	rel	protein-coding
chr3-3704:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr3	37040956	37041462	0	NA	intron (Nintron (N	47859 NM_00125E	4292 Hs. 190536NM_00024	ENSG000003MLH1	COCA2 FCC	mtc	protein-coding	
chr3-729:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr3	72909669	72910011	0	NA	intron (Nintron (N	21794 NM_00108C	727936 Hs. 710275NM_00108	ENSG000003GXYLT2	GLT8D4	glucoside	protein-coding	
chr5-946:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr5	94654910	94656717	0	NA	intron (NLM2b LIN	37144 NM_03229C	84250 Hs. 657315NM_03229	ENSG000003SLF1	ANKRD32 E	SMC5-SMC6	protein-coding	
chr5-1264:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr5	1.26E+08	1.26E+08	0	NA	intron (NLM8B LIN	7086 NM_001345	65983 Hs. 363555NM_02392	ENSG000003GRAMD2B	GRAMD3 NS	gram dom	protein-coding	
chr7-729:5.931132	-0.94027	0.969064	-0.97029	0.331902	0.981636	chr7	72987991	72988682	0	NA	IntergeniAluSz LIN	17607 NR_04058E	442578 Hs. 63231CNC_001013739	STAG3L3	STAG3L1 S	stromal	pseudo	
chr15-49:5.864569	-0.95513	0.985445	-0.96923	0.332429	0.981636	chr15	49124125	49124419	0	NA	3' UTR (N3' UTR (N	31327 NM_00114Z	9318 Hs. 369614NM_00423	ENSG000003COPS2	ALIEN CSN	COP9	sig	protein-coding
chr3-638:5.864569	-0.95513	0.985445	-0.96923	0.332429	0.981636	chr3	63834679	63834908	0	NA	intron (Nintron (N	15494 NM_00135E	132200 Hs. 506386NM_00135	ENSG000003CORF49	-	chromosom	protein-coding	
chr3-1727:5.864569	-0.95513	0.985445	-0.96923	0.332429	0.981636	chr3	1.73E+08	1.73E+08	0	NA	intron (NAluJr SIN	33246 NM_00134E	1894 Hs. 518295NM_01809	ENSG000003ECT2	ARHGFEF31	epitheli	protein-coding	
chr6-247:5.864569	-0.95513	0.985445	-0.96923	0.332429	0.981636	chr6	24783462	24784903	0	NA	intron (Nintron (N	8769 NM_001251	51053 Hs. 234895NM_01589	ENSG000003GMN	MIR60R3	geminin	protein-coding	
chr15-64:4.633639	-1.07325	1.107821	-0.96879	0.332648	0.981636	chr15	64820868	64821455	0	NA	intron (Nintron (N	4486 NM_025045	80119 Hs. 11216CNC_02504	ENSG000003PIF1	C15orf20 PIF1	5'	protein-coding	
chr20-54:4.633639	-1.07325	1.107821	-0.96879	0.332648	0.981636	chr20	58393798	58394615	0	NA	intron (Nintron (N	4977 NR_036633	9217 Hs. 182625NM_00473	ENSG000003VAPB	ALS8 VAMF	VAMP	assoc	protein-coding
chr17-767:11.77961	-0.68762	0.709783	-0.96878	0.332657	0.981636	chr17	76735468	76736170	0	NA	promoter-promoter-	729 NR_03036E	693221 NR_03036E	ENSG000003MIR636	MIRN636 f	microRNA ncRNA		
chr1-2377:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr1	23770542	23772019	0	NA	intron (NAluJb SIN	7017 NR_03828C	1.01E+08 Hs. 592545NR_03828	ENSG000003ELOA-AS1	TCEB3-AS1	ELOA	antncRNA	
chr1-317:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr1	31729934	31732657	0	NA	exon (NM_exon (NM	-27278 NM_00185E	1307 Hs. 368921NM_00185	ENSG000003COL16A1	447AA FP1	collagen	protein-coding	
chr1-2042:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr1	2.04E+08	2.04E+08	0	NA	intron (NHERVL-int	-24233 NM_198447	127845 Hs. 532401NM_19844	ENSG000003GOLTI1A	CGI-141 C	golgi	protein-coding	
chr1-246:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr1	2.47E+08	2.47E+08	0	NA	intron (Nintron (N	77587 NM_15260E	163882 Hs. 368355NM_15260	ENSG000003CNST	Clorf71 f	consort	protein-coding	
chr10-90:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr10	97366513	97369761	0	NA	intron (NAluSz SIN	33203 NM_01517E	23223 Hs. 434251NM_01517	ENSG000003RRP12	KIAA0690	ribosomal	protein-coding	
chr15-97:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr15	90906257	90907057	0	NA	intron (Nintron (N	2467 NR_135504	4122 Hs. 116455NM_00961	ENSG000003MAN2A2	MANA2X	mannosid	protein-coding	
chr16-48:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr16	4886293	4886895	0	NA	intron (Nintron (N	38214 NM_00128E	29855 Hs. 440215NM_01693	ENSG000003CUBN1	VT VT4	ubinucl	protein-coding	
chr16-28:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr16	28908511	28909407	0	NA	intron (Nintron (N	16279 NM_02481E	79874 Hs. 555975NM_02481	ENSG000003RABEP2	FRA	rabatin	protein-coding	
chr17-76:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr17	76310972	76311781	0	NA	3' UTR (N3' UTR (N	-3696 NM_023134	84074 Hs. 252735NM_03213	ENSG000003QRICH2	SPGF35	glutamin	protein-coding	
chr20-62:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr20	62329743	62333961	0	NA	TTS (NR_TTS (NR_C	705 NR_03991E	1.01E+08 NR_03991E	ENSG000003MIR4758	-	microRNA ncRNA		
chr22-23:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr22	23668853	23870169	0	NA	intron (NAluJb SIN	11636 NM_001024	66035 Hs. 66191CNC_03080	ENSG000003SLC2A11	GLUT10 G	solute c	protein-coding	
chr3-75:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr3	75760107	75764857	0	NA	intron (NLM2B LIN	22520 NM_001324	1.0E+08 Hs. 556877NM_00112	ENSG000003ZNF17	OB1 X17 z	inc	protein-coding	
chr4-3021:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr4	3021531	3021888	0	NA	intron (Nintron (N	52805 NR_045414	1.01E+08 Hs. 575112NR_045414	HTT-AS	HTT-AS1 H	TTT	antisncRNA	
chr5-671:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr5	67154424	67155777	0	NA	intron (Nintron (N	41699 NM_00558E	4064 Hs. 87205 NM_00558	ENSG000003CD180	LY64 L	Y7CD180	mol	protein-coding
chr5-176:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr5	1.77E+08	1.77E+08	0	NA	intron (Nintron (N	23742 NM_01629C	51720 Hs. 116455NM_01629	ENSG000003UIMC1	RAP80 X2	f	ubiquit	protein-coding
chr6-311:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr6	31154613	31155415	0	NA	intron (Nintron (N	2775 NM_00110E	54535 Hs. 485075NM_01905	ENSG000003CCHCR1	C6orf18 f	coiled-c	protein-coding	
chr9-104:5.725365	0.949639	0.98034	0.968684	0.332703	0.981636	chr9	1.05E+08	1.05E+08	0	NA	intron (Nintron (N	42451 NM_00550E	19 Hs. 692974NM_00550	ENSG000003ABCA1	A1C ABC	ATP	bindi	protein-coding
chr10-14:10.62911	-0.70927	0.732423	-0.96838	0.332853	0.981636	chr10	14519819	14521837	0	NA	3' UTR (N3' UTR (N	11886 NM_00132C	83641 Hs. 446315NM_03145	ENSG000003FAM107B	ABC-1 ABC	ATP	bindi	protein-coding
chr3-195:9.211462	0.759384	0.784292	0.968242	0.332924	0.981636	chr3	1.96E+08	1.96E+08	0	NA	IntergeniLTR16C LI	31365 NR_003264	255812 Hs. 566872NR_00326	ENSG000003SDHAP1	SDHAL1 S	uccinat	pseudo	
chr2-613:14.19518	0.616397	0.636622	0.96823	0.332929	0.981636	chr2	61306391	61307161	0	NA	intron (NLP1A5 LIN	110601 NR_003707	1E+08 Hs. 675825NR_00370	ENSG000003SNORA702	-	small	nucsnRNA	
chr19-181:7.493837	0.83665	0.864179	0.968144	0.332972	0.981636	chr19	18130532	18134840	0	NA	intron (Nintron (N	-20477 NR_162071	5296 Hs. 371344NM_00502	ENSG000003PIK3R2	MPPP MPPI	phospho	protein-coding	
chr19-57:7.493837	0.83665	0.864179	0.968144	0.332972	0.981636	chr19	57512068	57517333	0	NA	3' UTR (N3' UTR (N	-12355 NM_153263	256051 Hs. 744285NM_15326	ENSG000003ZNF549	-	zinc	protein-coding	
chr2-105:7.493837	0.83665	0.864179	0.968144	0.332972	0.981636	chr2	1.05E+08	1.05E+08	0	NA	intron (NLMC5a LI	31789 NR_13732E	9392 Hs. 44635CNC_00425	ENSG000003TGFBAP1	TRAP-1 T	TF	transfor	protein-coding
chr12-911:10.59768	-0.7046	0.728072	-0.96776	0.333166	0.981636	chr12	91144657	91159398	0	NA	intron (Nintron (N	26619 NM_13350E	1634 Hs. 156315NM_00192	ENSG000003CCDCN	CSD DSPC	degrin	protein-coding	
chr1-841:8.410557	-0.80809	0.83502	-0.96774	0.333172	0.981636	chr1	8410304	8410572	0	NA								



chr12-297 5.923274	-0.93816	0.974951	-0.96226	0.335917	0.981636	chr12	29775488	29776274	+	0 NA	intron (NMER21C LI	8061 NM_001367	83857 Hs. 401954NM_03192C	ENSG00000TMTCT1	ARG99 OLF	transmembrane protein-coding	
chr20-384 5.923274	-0.93816	0.974951	-0.96226	0.335917	0.981636	chr20	38418447	38419588	+	0 NA	Intergeni Intergeni	6313 NR_00291C	26776 Hs. 40087ENR_00291C	ENSG00000SNORA71B	RNU7B U7small	nucsnRNA	
chr6-1366 5.923274	-0.93816	0.974951	-0.96226	0.335917	0.981636	chr6	1.37E+08	1.37E+08	+	0 NA	intron (AluS6 SI	35736 NR_12585E	1.02E+08 Hs. 66651ENR_12585E	LOC10192E-		uncharacterized RNA	
chr4-3195 7.419416	0.83323	0.866055	0.962098	0.336	0.981636	chr4	3199785	3200010	+	0 NA	exon (NM exon (NM	-44472 NM_00133C	345222 Hs. 442291NM_00101E	ENSG00000MSANTD1	C4orf44	Myb/SANT protein-coding	
chr11-300 8.921011	-0.76613	0.79641	-0.96198	0.33606	0.981636	chr11	3000240	3000439	+	0 NA	TTS (NM_CTS (NM_C	-8010 NM_00136E	4676 Hs. 731784NM_00596E	ENSG00000NAP1L4	NAP1L4 b	nucleoson protein-coding	
chr8-8978 7.598095	-0.8231	0.855684	-0.96192	0.336092	0.981636	chr8	89780168	89780509	+	0 NA	intron (intron (N	22522 NM_00382I	8767 Hs. 103755NM_00382I	ENSG00000CRIPK2	CARD3 CAF	receptor protein-coding	
chr10-125 5.962564	-0.94797	0.98551	-0.96191	0.336097	0.981636	chr10	12020963	12021964	+	0 NA	intron (AluJo SIN	21346 NM_01554Z	26019 Hs. 370688NM_01554Z	ENSG00000UPP2	HUPP2 REN	UPP2 reg protein-coding	
chr13-757 10.64668	-0.70302	0.730984	-0.96174	0.336178	0.981636	chr13	75796768	75797598	+	0 NA	intron (intron (N	36522 NM_01584Z	4008 Hs. 207631NM_00535E	ENSG00000LM07	FBX20 FBLIM	domain protein-coding	
chr2-2764 10.64668	-0.70302	0.730984	-0.96174	0.336178	0.981636	chr2	27645000	27645342	+	0 NA	intron (AluJr4 SI	16121 NM_00726E	11321 Hs. 18259 NM_00726E	ENSG00000CPN1	ATPBD1A GPN	loop protein-coding	
chr7-9904 10.64668	-0.70302	0.730984	-0.96174	0.336178	0.981636	chr7	99041235	99041924	+	0 NA	intron (intron (N	28614 NR_110102	1.02E+08 Hs. 63666E	NR_110102	LOC101927-		uncharacterized RNA
chr3-1572 8.838732	-0.77282	0.803867	-0.96138	0.336359	0.981636	chr3	15723543	15724269	+	0 NA	intron (intron (N	-26535 NR_03608E	1E+08 NR_03608E	ENSG00000MIR3134		microRNA ncRNA	
chr22-402 9.152757	0.752698	0.783392	0.960819	0.336643	0.981636	chr22	40286285	40287076	+	0 NA	intron (intron (N	-59820 NM_00136E	158 Hs. 75527 NM_00002E	ENSG00000ADSL	AMPS ASAS	adenylost protein-coding	
chr2-2398 8.656169	0.789274	0.821716	0.960519	0.336794	0.981636	chr2	23983253	23983953	+	0 NA	intron (intron (N	-26482 NM_00134E	388931 Hs. 407482NM_00108C	ENSG00000MPSD2B		major fac protein-coding	
chr1-9675 7.647092	-0.82072	0.854651	-0.9603	0.336903	0.981636	chr1	96755599	96757069	+	0 NA	intron (AluSp SIN	33696 NR_12535E	58155 Hs. 596061NM_02119C	ENSG00000PTPB2	PTBP1 brf	polyrribin protein-coding	
chr10-615 7.647092	-0.82072	0.854651	-0.9603	0.336903	0.981636	chr10	61924264	61925093	+	0 NA	intron (intron (N	22979 NM_03219E	84159 Hs. 535297NM_03219E	ENSG00000ARID5B	DESRT MRF	AT-rich protein-coding	
chr3-1218 7.647092	-0.82072	0.854651	-0.9603	0.336903	0.981636	chr3	1.22E+08	1.22E+08	+	0 NA	intron (intron (N	17480 NM_00102Z	9657 Hs. 60411C	NR_00102Z	ENSG00000IQCB1	NHPH5 PTG	IQ motif protein-coding
chr8-1404 7.647092	-0.82072	0.854651	-0.9603	0.336903	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	intron (intron (N	-84763 NR_02989E	442893 NR_02989E	ENSG00000MIR151A	MIR151 MI	microRNA ncRNA	
chr1-1971 4.692344	-1.05132	1.094789	-0.96029	0.336908	0.981636	chr1	1.97E+08	1.97E+08	+	0 NA	intron (Tiger1 I	30839 NM_01813C	259266 Hs. 121028NM_01813E	ENSG00000ASPM	ASP Calmt	abnormal protein-coding	
chr12-952 4.692344	-1.05132	1.094789	-0.96029	0.336908	0.981636	chr12	95272574	95273004	+	0 NA	intron (AluJb SIN	-35631 NR_02989E	442903 NR_02989E	ENSG00000MIR331	MIRN331 hm	microRNA ncRNA	
chr17-644 4.692344	-1.05132	1.094789	-0.96029	0.336908	0.981636	chr17	64485910	64486287	+	0 NA	intron (intron (N	10966 NM_00721E	11232 Hs. 43700E	NR_00721E	ENSG00000POLG2	HP55 MTPC	DNA polyn protein-coding
chr2-189 4.692344	-1.05132	1.094789	-0.96029	0.336908	0.981636	chr2	1.9E+08	1.9E+08	+	0 NA	non-codnon-codir	93004 NM_00132I	5378 Hs. 11174E	NR_00053A	ENSG00000PMS1	HNPC3 PMS1	homc protein-coding
chr2-6122 7.146346	-0.86368	0.89967	-0.95999	0.337058	0.981636	chr2	61226204	61226335	+	0 NA	intron (Tiger1 7c	48761 NR_15221I	130872 Hs. 65560E	NR_15239E	ENSG00000AHS2A2P	AHA1 AHS	activator pseudo
chr6-1113 7.146346	-0.86368	0.89967	-0.95999	0.337058	0.981636	chr6	1.11E+08	1.11E+08	+	0 NA	intron (intron (N	75511 NR_15336E	91749 Hs. 40057E	NR_15336E	ENSG00000MFS4B	KIAA1919 major	fac protein-coding
chr8-1235 7.146346	-0.86368	0.89967	-0.95999	0.337058	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (AluY SINE	-9951 NR_03751E	1.01E+08 NR_03751E	ENSG00000MIR548A1A		microRNA ncRNA	
chr1-9308 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr1	93084830	93085271	+	0 NA	intron (intron (N	5767 NM_00735E	22823 Hs. 31016 NM_00735E	ENSG00000MTF2	M96 PCL2 metal	res protein-coding	
chr12-45 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr12	45961752	45964004	+	0 NA	intron (LIMEd LIN	27698 NM_00471E	9169 Hs. 210367NM_00471E	ENSG00000SCAF11	CASP11 SFR	relate protein-coding	
chr12-105 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr12	1.05E+08	1.05E+08	+	0 NA	non-codnon-codir	37875 NM_15231E	121053 Hs. 29556E	NR_15231E	ENSG00000C12orf45		chromoson protein-coding
chr16-158 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr16	15872350	15873342	+	0 NA	intron (intron (N	15757 NM_00130A	123811 Hs. 51417E	NR_14460C	ENSG00000FOPNL	C16orf63 FGFR10P	protein-coding
chr17-371 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr17	37120732	37120972	+	0 NA	intron (intron (N	87107 NR_03605E	1E+08 NR_03605E	ENSG00000MIR2909		microRNA ncRNA	
chr18-587 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr18	58522362	58524763	+	0 NA	intron (LIP43 LIN	-27410 NR_03989E	1.01E+08 NR_03989E	ENSG00000MIR3591		microRNA ncRNA	
chr3-1962 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr3	1.96E+08	1.96E+08	+	0 NA	intron (intron (N	17995 NM_00131Z	5130 Hs. 135997NM_005017	ENSG00000PCYT1A	CCTA CTI	Cphosphate protein-coding	
chr6-5301 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr6	53013558	53013863	+	0 NA	exon (NM exon (NM	18090 NR_00144E	125050 NR_00144E	ENSG00000CRN7SK	7SK	RNA ncsnRNA	
chr8-131E 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr8	13153509	13153817	+	0 NA	intron (LTR12C LI	-20724 NM_00134E	10395 Hs. 13429E	NR_00609A	ENSG00000DLCL1	HNCGAP7 E	DLCL1 Rho protein-coding
chr9-218E 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr9	21834326	21834662	+	0 NA	intron (MLTID LTF	31858 NM_00245I	4507 Hs. 19326E	NR_00245I	ENSG00000MTAP	BDMF DMSF	methylthiprotein-coding
chr9-136E 7.623518	-0.81599	0.850027	-0.95995	0.337078	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (intron (N	2225 NM_00120C	26086 Hs. 23937C	NR_015597	ENSG00000GSPM1	AGS3	G protein protein-coding
chr1-123E 9.70805	0.726209	0.756552	0.959893	0.337109	0.981636	chr1	1.24E+08	1.24E+08	+	0 NA	Intergeni ALR/Alphe	2443198 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000EMBP1		embin pseudo
chr1-1717 9.70805	0.726209	0.756552	0.959893	0.337109	0.981636	chr1	1.72E+08	1.72E+08	+	0 NA	intron (AluJb SIN	27335 NR_03370A	8674 Hs. 6651 NM_00376E	ENSG00000CVAMP4	VAMP-4 V	vesicle protein-coding	
chr6-9054 9.70805	0.726209	0.756552	0.959893	0.337109	0.981636	chr6	90545789	90546081	+	0 NA	intron (MLTIJ LTF	41137 NM_00318E	6885 Hs. 59483E	NR_00318E	ENSG00000MAP3K7	CSCP FMD2	mitogen protein-coding
chr22-317 7.436982	0.840788	0.87605	0.959749	0.337182	0.981636	chr22	52364 NM_00136E	52364 NM_00136E	+	0 NA	intron (intron (N	52364 NM_00136E	9681 Hs. 435022NM_01466E	ENSG00000DEPDC5	DEP. 5 F	DEP domain protein-coding	
chr5-108E 7.436982	0.840788	0.87605	0.959749	0.337182	0.981636	chr5	1.08E+08	1.08E+08	+	0 NA	intron (LIM4 LINE	9504 NM_00116E	64839 Hs. 65722E	NR_02282A	ENSG00000FBXL17	FBXO13 F	box anc protein-coding
chr17-505 10.53112	-0.71249	0.742481	-0.95961	0.337253	0.981636	chr17	56910732	56910942	+	0 NA	intron (intron (N	3212 NM_00508E	7706 Hs. 52995E	NR_00508E	ENSG00000TRIM25	EFP RNFI4	tripartit protein-coding
chrX-246 9.270168	0.766903	0.799108	0.958685	0.337718	0.981636	chrX	2407107	2407483	+	0 NA	intron (LTR22C0 I	93244 NM_00117I	9189 Hs. 13145E	NR_00472E	ENSG00000ZBED1	ALTE DREF	zinc fing protein-coding
chr7-9962 6.971825	0.883672	0.921942	0.95849	0.337816	0.981636	chr7	99628248	99628734	+	0 NA	intron (intron (N	11545 NM_00135C	221785 Hs. 446297NM_14511E	ENSG00000ZSCAN25	ZNF498	zinc fing protein-coding	
chr11-78E 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr11	78220837	78221369	+	0 NA	intron (intron (N	32184 NM_02079E	57558 Hs. 53124E	NR_02079E	ENSG00000USP35		ubiquitin protein-coding
chr11-125 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr11	1.25E+08	1.25E+08	+	0 NA	3' UTR (3' UTR (N	-50457 NM_00130I	403312 Hs. 450611NM_20345E	LOC040331E-		putative protein-coding	
chr12-50E 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr12	50120934	50121226	+	0 NA	Intergeni Intergeni	9294 NM_001257	84987 Hs. 38864E	NR_03290I	ENSG00000COX14	C12orf62 cyto	chron protein-coding
chr15-41E 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr15	41573727	41575133	+	0 NA	intron (MIR SINE	14458 NM_00133C	7301 Hs. 38128E	NR_00629E	ENSG00000TYR03	BYK Dtk E	TYR03 prc protein-coding
chr16-16E 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr16	16260311	16260827	+	0 NA	intron (intron (N	62627 NM_00107E	368 Hs. 44218E	NR_00117I	ENSG00000ABC6C	ABC34 AR	ATP brd protein-coding
chr16-56E 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr16	56362339	56363247	+	0 NA	3' UTR (3' UTR (N	62196 NM_00132Z	267 Hs. 295137NM_00114E	ENSG00000AMFR	GP78 HNF4	autocrine protein-coding	
chr17-78E 5.699941	0.943075	0.984545	0.957879	0.338124	0.981636	chr17	78707604	78707896	+	0 NA	intron (AluSc SIN	9					

chr17-405.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr17	4099458	4099657	+	0	NA	intron (AluSq2 S)	43473	NM_015113	23140	Hs.277624NM_015113	ENSG000002ZEF1	ZZZA	zinc finger protein-coding
chr19-245.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr19	2430652	2431029	+	0	NA	3' UTR (N3' UTR (N	-3254	NM_012458	26517	Hs.75056	NM_012458	ENSG000002TIMM13	TIMM13 TIM translocase protein-coding
chr19-101.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr19	10171216	10173350	+	0	NA	intron (AluSx1 S)	22670	NM_001318	1786	Hs.202672NM_001318	ENSG000002DNMT1	ADCADN AIDNA methyltransferase protein-coding	
chr2-1731.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr2	1.73E+08	1.73E+08	+	0	NA	intron (NLIP47 L)	98517	NM_016652	51776	Hs.444451NM_016652	ENSG000002MAP3K20	AZK CNM6 mitogen-activated protein kinase-coding	
chr2-1865.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr2	1.87E+08	1.87E+08	+	0	NA	intron (AluS5 S)	14683	NM_018471	55854	Hs.74118CNC_018471	ENSG000002ZC3H15	HT010 LEF zinc finger protein-coding	
chr3-445.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr3	44506727	44506926	+	0	NA	intron (AluSx S)	3791	NM_001287	285346	Hs.648974NM_001287	ENSG000002ZNF852	zinc finger protein-coding	
chr3-1111.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr3	1.11E+08	1.11E+08	+	0	NA	intron (MER68 LTF)	23020	NM_001242	25945	Hs.293917NM_001242	ENSG000002NECTIN3	CDN13 CDNectin cell protein-coding	
chr5-3466.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr5	34661077	34661276	+	0	NA	intron (Tigger4 )	4685	NM_001145	26064	Hs.43140CNC_015577	ENSG000002RAI14	NR016 RAR retinoic acid protein-coding	
chr7-1305.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (intron (N	6691	NR_110472	378805	Hs.150556NM_001088	ENSG000002LINC-PIN1	LincRNA-F long intracncRNA	
chr7-1348.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (intron (N	26434	NM_033138	800	Hs.490203NM_004342	ENSG000002CALD1	CDM H-CAL caldesmon protein-coding	
chr9-6458.7.648942	-0.80894	0.850331	-0.95133	0.341438	0.981636	chr9	6458471	6458810	+	0	NA	intron (NLIP47 L)	45441	NM_152896	115426	Hs.493401NM_152896	ENSG000002UHRF7	NIRF RNFI ubiquitin protein-coding	
chr14-688.8.805451	-0.7777	0.817535	-0.95127	0.341467	0.981636	chr14	68976727	68977278	+	0	NA	intron (intron (N	2300	NM_001102	87	Hs.235755NM_001102	ENSG000002ACTN1	BDPLT15 actinin epsilon protein-coding	
chr1-3814.7.409708	0.823462	0.865918	0.95097	0.34162	0.981636	chr1	3814520	3815284	+	0	NA	3' UTR (N3' UTR (N	-18404	NM_02071C	57470	Hs.268488NM_02071C	ENSG000002RNF57	FAD104 PF fibronectin protein-coding	
chr14-202.7.409708	0.823462	0.865918	0.95097	0.34162	0.981636	chr14	20289342	20289773	+	0	NA	3' UTR (N3' UTR (N	16394	NM_028376	91875	Hs.98553	NM_138376	ENSG000002TTC5	Strap tetraatric protein-coding
chr6-3648.7.409708	0.823462	0.865918	0.95097	0.34162	0.981636	chr6	36485025	36485245	+	0	NA	intron (intron (N	42135	NM_173562	222658	Hs.188757NM_173562	ENSG000002KCTD20	C6orf69 cortactin protein-coding	
chr7-1117.7.409708	0.823462	0.865918	0.95097	0.34162	0.981636	chr7	1.12E+08	1.12E+08	+	0	NA	exon (NM exon (NM	-79793	NR_103800	1.01E+08	Hs.677512NR_103800	ENSG000002DOCK4-AS1	DOCK4 antncRNA	
chr9-8607.7.409708	0.823462	0.865918	0.95097	0.34162	0.981636	chr9	86007462	86007882	+	0	NA	intron (intron (N	66143	NM_001321	60560	Hs.436098NM_021925	ENSG000002NAA35	EGAP MAK1N(alpha)-protein-coding	
chr9-1312.7.409708	0.823462	0.865918	0.95097	0.34162	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (NMIR SINE)	13159	NM_001318	8021	Hs.65453CNC_005088	ENSG000002NUP214	CAN CAN nucleoporin protein-coding	
chr1-2251.7.990425	0.79081	0.831651	0.950892	0.341659	0.981636	chr1	22517338	22518190	+	0	NA	intron (intron (N	-45725	NM_001006	2046	Hs.283613NM_020526	ENSG000002EPH8A	EELK EK3 EPH receptor protein-coding	
chr2-1317.7.990425	0.79081	0.831651	0.950892	0.341659	0.981636	chr2	1.32E+08	1.32E+08	+	0	NA	intron (NLIPA5 L)	20196	NR_149014	29798	Hs.635289NM_013310	C2orf27A	C2orf27 chromosome protein-coding	
chr19-524.7.990425	0.79081	0.831651	0.950892	0.34171	0.981636	chr19	52465390	52466360	+	0	NA	intron (HERVK4-i	12322	NM_001099	147660	Hs.157287NM_152472	ENSG000002ZNF578	zinc finger protein-coding	
chr2-2308.7.990425	0.79081	0.831651	0.950892	0.34171	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	3' UTR (N3' UTR (N	-7415	NR_038238	151484	Hs.559309NR_038238	ENSG000002LOC151484	uncharacterized ncRNA	
chr22-352.7.990425	0.79081	0.831651	0.950892	0.34171	0.981636	chr22	35337362	35339063	+	0	NA	intron (intron (N	-1413	NR_106717	1.02E+08	NR_106717	ENSG000002MIR6069	hsa-mir-610 microRNA ncRNA	
chr3-1722.7.990425	0.79081	0.831651	0.950892	0.34171	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (intron (N	191873	NM_001133	64778	Hs.744888NM_022763	ENSG000002FND3B	FAD104 PF fibronectin protein-coding	
chr7-2314.7.990425	0.79081	0.831651	0.950892	0.34171	0.981636	chr7	23145525	23146445	+	0	NA	intron (AluJo S)	-36063	NM_00137C	11097	Hs.408241NM_007342	ENSG000002NUP42	CG1 NLP-1 nucleoporin protein-coding	
chr9-1377.7.990425	0.79081	0.831651	0.950892	0.34171	0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	intron (intron (N	-10312	NR_147508	651337	Hs.603195NR_147508	ENSG000002LOC651337	uncharacterized ncRNA	
chr1-2436.7.982567	0.79254	0.83415	0.950613	0.341801	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (NLIMEg L)	195604	NM_181696	10000	Hs.498292NM_005466	ENSG000002AKT3	MPPH MPPF AKT serine protein-coding	
chr3-1975.4.478904	1.052944	1.107677	0.950588	0.341814	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (Tigger9a )	37464	NR_02678E	89782	Hs.51854CNC_033025	ENSG000002LMLN	GP63 INV leishman protein-coding	
chr1-1195.7.564813	-0.82901	0.872113	-0.95058	0.341819	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	exon (NM exon (NM	-45041	NM_002179A	11085	Hs.283011NM_02179A	ENSG000002ADAM30	svf4 ADAM metalloprotein-coding	
chr5-167.7.564813	-0.82901	0.872113	-0.95058	0.341819	0.981636	chr5	16737928	16738144	+	0	NA	intron (intron (N	-120978	NM_001034	54463	Hs.481704NM_01900C	ENSG000002RETREG1	SM134B J reticulon protein-coding	
chr18-688.5.666659	0.939514	0.988427	0.950514	0.341851	0.981636	chr18	68879175	68879760	+	0	NA	intron (LTR12C L)	81387	NM_024781	79839	Hs.280781NM_024781	ENSG000002CCDC102B	ACYL1 AN coiled-coiled protein-coding	
chr20-635.5.666659	0.939514	0.988427	0.950514	0.341851	0.981636	chr20	63589168	63589619	+	0	NA	3' UTR (N3' UTR (N	-15154	NM_001037	85441	Hs.51718CNC_033405	ENSG000002HELZ2	PDIP1 PF helicase protein-coding	
chr7-1005.5.666659	0.939514	0.988427	0.950514	0.341851	0.981636	chr7	1E+08	1E+08	+	0	NA	TTS (NR_1TTS (NR_1	1833	NR_103728	1.02E+08	Hs.521072NR_103728	PVRIG2P	poliovirus pseudo	
chr9-8164.5.666659	0.939514	0.988427	0.950514	0.341851	0.981636	chr9	81642916	81643480	+	0	NA	intron (NLIMA9 L)	46337	NM_001303	7088	Hs.19732CNC_005077	ENSG000002CTLE1	ESG ESG1 TLE family protein-coding	
chr3-1278.9.341329	-0.73348	0.771705	-0.95046	0.341877	0.981636	chr3	1.28E+08	1.28E+08	+	0	NA	intron (MER91A D)	7108	NM_007283	11343	Hs.277033NM_007283	ENSG000002MGLL	HU-K5 HU homologous protein-coding	
chr13-984.5.915416	-0.93592	0.985152	-0.95002	0.3421	0.981636	chr13	98407029	98407228	+	0	NA	intron (intron (N	114997	NM_003576	8428	Hs.508514NM_003576	ENSG000002STK24	HEL-S-95 serine/threonine protein-coding	
chr3-1085.5.915416	-0.93592	0.985152	-0.95002	0.3421	0.981636	chr3	1.09E+08	1.09E+08	+	0	NA	intron (NLIME3A L)	15001	NM_02089C	57650	Hs.591308NM_02089C	ENSG000002CIP2A	KIAA1524 cell proliferation protein-coding	
chr6-1078.5.915416	-0.93592	0.985152	-0.95002	0.3421	0.981636	chr6	1.08E+08	1.08E+08	+	0	NA	intron (AluS6 S)	59995	NM_007214	11231	Hs.26904	NM_007214	ENSG000002SEC63	DNAJC23 ESE63 homoprotein-coding
chr17-701.11.93798	0.655271	0.689863	0.949856	0.342185	0.981636	chr17	70177082	70177731	+	0	NA	3' UTR (N3' UTR (N	6671	NM_000891	3759	Hs.1547	NM_000891	ENSG000002KCNJ2	ATFB9 HHE potassium protein-coding
chr19-576.11.93798	0.655271	0.689863	0.949856	0.342185	0.981636	chr19	57699959	57705128	+	0	NA	exon (NM exon (NM	6661	NR_110974	7710	Hs.646377NM_003444	ENSG000002ZNF154	pH2-92 zinc finger protein-coding	
chr15-1105.10.62726	-0.71822	0.756322	-0.94962	0.342303	0.981636	chr15	40954963	40955695	+	0	NA	intron (intron (N	1858	NM_001142	79094	Hs.155566NM_024111	ENSG000002CHAC1	ChaC glutathione protein-coding	
chr9-404.8.897438	-0.71822	0.756322	-0.94962	0.342303	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (AluJb S)	-90949	NM_00128E	255220	Hs.147064NM_00100C	ENSG000002TXND8	SPTRX-3 3-thioredoxin protein-coding	
chr3-1325.5.658801	0.942521	0.993456	0.94873	0.342758	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	intron (intron (N	-21307	NM_016557	51554	Hs.310512NM_016557	ENSG000002ACKR4	CC-CR-1 atypical protein-coding	
chr11-648.8.830874	-0.77138	0.813233	-0.94854	0.342856	0.981636	chr11	64857673	64857889	+	0	NA	intron (intron (N	-13128	NM_017522	55561	Hs.29359CNC_017522	ENSG000002CDC42BPG	DMPK2 HSM CDC42 binding protein-coding	
chr14-451.9.382468	-0.7304	0.770504	-0.94795	0.343155	0.981636	chr14	45105801	45106319	+	0	NA	intron (AluSx S)	-4795	NR_003691	1E+08	Hs.712501NR_003691	ENSG000002SNORD127	small nucleolar RNA	
chr15-635.9.382468	-0.7304	0.770504	-0.94795	0.343155	0.981636	chr15	63559902	63560220	+	0	NA	intron (intron (N	-37326	NM_001367	283807	Hs.631162NM_203377	ENSG000002FBXL22	Fb122 F-box ankyrin protein-coding	
chr5-624.5.831287	-0.96328	1.016183	-0.94793	0.343163	0.981636	chr5	62400905	62401442	+	0	NA	intron (LTR33 LTF)	2732	NM_00134E	27292	Hs.731666NM_014477	ENSG000002DITM1	DITM1 DITM1 rRNA protein-coding	
chr5-1342.4.684486	-1.04855	1.106171	-0.94791	0.343173	0.981636	chr5	1.34E												



chr6-1305 6.392588 -0.87241 0.924615 -0.94354 0.345407 0.981636 chr6 1.31E+08 1.31E+08 + 0 NA intron (NLIPA7|LIN 60267 NM\_00135C 2037 Hs. 48647C|NM\_001431|ENSG00000CEPB41L2 4.1-G|4.1erythrocyprotein-coding

chr8-1932 6.392588 -0.87241 0.924615 -0.94354 0.345407 0.981636 chr8 19320215 19320804 + 0 NA intron (NALuJr|SIN 6533 NM\_001174 63898 Hs. 30320E|NM\_022071|ENSG00000SH2D4A PPP1R38|SSH2 domainprotein-coding

chr8-4782 6.392588 -0.87241 0.924615 -0.94354 0.345407 0.981636 chr8 47822837 47824189 + 0 NA intron (NMSTB|LTR| 85349 NM\_00519E 1052 Hs. 44082E|NM\_00519E|ENSG00000CEBPD C/EBP-de|CCAAT enfprotein-coding

chr9-1347 6.392588 -0.87241 0.924615 -0.94354 0.345407 0.981636 chr9 1.35E+08 1.35E+08 + 0 NA intron (NTTS (NTTS ( 66484 NR\_039691 1.01E+08 NR\_039691|ENSG00000MIR3689C - microRNA ncRNA

chrX-7426 6.392588 -0.87241 0.924615 -0.94354 0.345407 0.981636 chrX 74284411 74289393 + 0 NA TTS (NR\_03025E 664614 NR\_03025E|ENSG00000MIR545 MIRN545|microRNA ncRNA

chr10-973 4.461338 1.040914 1.103414 0.943357 0.345498 0.981636 chr10 97359016 97360155 + 0 NA intron (Nintron (N -24856 NM\_01208E 23401 Hs. 14072C|NM\_01208E|ENSG00000FRAT2 FRAT-2 FRAT regt protein-coding

chr11-714 4.461338 1.040914 1.103414 0.943357 0.345498 0.981636 chr11 71436928 71438408 + 0 NA intron (Nintron (N 10725 NM\_00116E 1717 Hs. 503134|NM\_00136E|ENSG00000DHC7 FLOS 7-dehydroprotein-coding

chr7-1436 4.461338 1.040914 1.103414 0.943357 0.345498 0.981636 chr7 144E+08 1.44E+08 + 0 NA intron (Nintron (N -17779 NM\_00136E 285966 Hs. 17367E|NM\_00136E|ENSG00000TCAF2 SMI15C|FTRPM8 cheprotein-coding

chr9-6567 10.60739 -0.69701 0.738993 -0.94318 0.345587 0.981636 chr9 65679431 65680308 + 0 NA intron (Nintron (N 3941 NM\_00136E 220869 Hs. 35595C|NM\_001024|ENSG00000CBWD5 CBWD3|DC|COBW dome protein-coding

chr18-132 7.117366 -1.35605 1.437871 -0.9431 0.345632 0.981636 chr18 13707101 13707711 + 0 NA intron (NMER57-int 19152 NM\_15235E 125228 Hs. 13034 NM\_15235E|ENSG00000FAM210A C18orf19|family wiprotein-coding

chr11-468 11.00829 -0.68743 0.729286 -0.94261 0.345881 0.981636 chr11 46815937 46816254 + 0 NA intron (NMER1B|DNA 30185 NM\_00100E 7979 Hs. 20125E|NM\_01475E|ENSG00000CKAP5 CHTG0|MSF cytoskelcprotein-coding

chr1-2128 6.255234 0.883771 0.937582 0.942607 0.345882 0.981636 chr1 2.13E+08 2.13E+08 + 0 NA 3' UTR (N3' UTR (N 37382 NM\_01405E 28982 Hs. 7055 NM\_01405E|ENSG00000FLVCR1 AXPC1|FLVfeline lprotein-coding

chr19-282 6.255234 0.883771 0.937582 0.942607 0.345882 0.981636 chr19 2826583 2829322 + 0 NA intron (THE1B|LTF 8084 NM\_00110E 115196 Hs. 30704E|NM\_15230E|ENSG00000ZNF554 - zinc fingprotein-coding

chr1-4025 5.674517 0.936347 0.993362 0.942604 0.345883 0.981636 chr1 40294196 40294564 + 0 NA TTS (NM\_CTT (NM\_C 22906 NM\_00185E 1298 Hs. 41801E|NM\_00185E|ENSG00000COL9A2 DJ39G22.4|collagen protein-coding

chr8-4314 5.674517 0.936347 0.993362 0.942604 0.345883 0.981636 chr8 43147507 43148058 + 0 NA intron (NLIPA16|LI 7318 NM\_15241E 138050 Hs. 600384|NM\_15241E|ENSG00000HGSNAT HGNAT|MPS heparan-eprotein-coding

chr13-102 3.445698 -1.24561 1.32169 -0.94244 0.345968 0.981636 chr13 1.03E+08 1.03E+08 + 0 NA intron (Nintron (N 31504 NM\_00101C 196541 Hs. 50862E|NM\_00101C|ENSG00000METTL21C C13orf39 methyltrprotein-coding

chr1-1565 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr1 1.57E+08 1.57E+08 + 0 NA intron (Nintron (N -48503 NR\_030527 768220 NR\_030527|ENSG00000CMIR765 MIRN765|microRNA ncRNA

chr10-245 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr10 24532028 24534314 + 0 NA exon (NM exon (NM 66640 NM\_00128E 56243 Hs. 44588E|NM\_01959C|ENSG00000K1AA1217 ET14|SKT K1AA1217 protein-coding

chr12-665 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr12 6650185 6652955 + 0 NA intron (NALuSzl|SIN 4138 NM\_03248E 84519 Hs. 12323E|NM\_03248E|ENSG00000ACRBP CT23|OY-lactosin lprotein-coding

chr17-44 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr17 44082561 44083740 + 0 NA intron (NALuJb|SIN 12239 NR\_02858E 92579 Hs. 29400E|NM\_13838E|ENSG00000G6PC3 SCN4|UGRF glucose-tprotein-coding

chr19-111 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr19 11975210 11979715 + 0 NA intron (Nintron (N 10155 NR\_13493C 1.02E+08 Hs. 63164E|NR\_13492E|ENSG00000ZNF433-AS- C ZNF433 arncRNA

chr19-518 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr19 51874615 51880937 + 0 NA intron (NLIMB3|LIN 10160 NM\_00113E 84765 Hs. 72301E|NM\_03267E|ENSG00000ZNF577 - zinc fingprotein-coding

chr6-3728 7.972859 0.783853 0.832553 0.941505 0.346446 0.981636 chr6 37289823 37294760 + 0 NA intron (Nintron (N -34138 NM\_00128E 221468 Hs. 520101|NM\_14531E|ENSG00000TMEM217 C6orf128|transmemt protein-coding

chr11-517 7.117366 0.821039 0.872104 0.941447 0.346476 0.981636 chr11 1341526 NR\_024504 646813 Hs. 68417E|NR\_024504 L0C64681E DEXH-box pseudo

chr16-675 7.117366 0.821039 0.872104 0.941447 0.346476 0.981636 chr16 67908854 67909673 + 0 NA exon (NM exon (NM 16009 NM\_00674E 5681 Hs. 51368E|NM\_00674E|ENSG00000PSKH1 - protein sprotein-coding

chr2-4397 7.556595 -0.82736 0.87926 -0.9412 0.346604 0.981636 chr2 43991965 43992331 + 0 NA intron (NL2b|LINE| 3841 NM\_13325E 10128 Hs. 368084|NM\_13325E|ENSG00000LRPPRC CLONE-23E|leucine rprotein-coding

chr1-2597 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr1 25975194 25975227 + 0 NA intron (NL2a|LINE| 22303 NM\_000437 5051 Hs. 47708E|NM\_000437|ENSG00000PFAH2 HSD-PLA2 platelet protein-coding

chr1-2357 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr1 2.36E+08 2.36E+08 + 0 NA intron (NMSTL|LTR| 56260 NR\_03171E 1E+08 NR\_03171E|ENSG00000MIR1537 MIRN1537|microRNA ncRNA

chr17-395 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr17 39556552 39557424 + 0 NA Intergeni Intergeni 50932 NM\_00616E 4761 Hs. 322431|NM\_00616E|ENSG00000NEUROD2 EIEE72|N neuronal protein-coding

chr17-606 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr17 60649632 60655806 + 0 NA intron (Nintron (N -27632 NM\_00109E 54828 Hs. 65502E|NM\_01767E|ENSG00000BCAS3 GAOB1|MAFBCAS3 micprotein-coding

chr20-558 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr20 5588610 5589082 + 0 NA intron (NALuSzl|SIN 22160 NM\_01959E 56261 Hs. 63635E|NM\_01959E|ENSG00000GPCPD1 EDI3|GDEglyceropl protein-coding

chr3-1691 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr3 1.69E+08 1.69E+08 + 0 NA intron (Nintron (N 25182 NM\_00136E 2122 Hs. 65639E|NM\_004991|ENSG00000MECOM AML1-EV1-MDS1 and protein-coding

chr3-1702 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr3 1.7E+08 1.7E+08 + 0 NA intron (NALuSxl|SI 20327 NM\_00274C 5584 Hs. 47199E|NM\_00274C|ENSG00000PRKCI DXS1179E|protein lprotein-coding

chr4-7154 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr4 71546848 71547863 + 0 NA intron (Nintron (N 208302 NM\_00375E 8671 Hs. 5462 NM\_00375E|ENSG00000SLC4A4 HNBC1|KNE solute cprotein-coding

chr7-1398 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr7 1.4E+08 1.4E+08 + 0 NA intron (NALuJr|SIN 18721 NM\_00136E 6916 Hs. 520757|NM\_001061|ENSG00000TBXAS1 BDPLT14|C thromboxe protein-coding

chr7-1395 6.221953 0.880436 0.935532 0.941107 0.34665 0.981636 chr7 1.4E+08 1.4E+08 + 0 NA intron (Nintron (N 116234 NM\_00136E 6916 Hs. 520757|NM\_001061|ENSG00000TBXAS1 BDPLT14|C thromboxe protein-coding

chr22-214 10.2125 0.694792 0.738679 0.940588 0.346916 0.981636 chr22 21477511 21477946 + 0 NA intron (Nintron (N 10558 NM\_001207 645426 Hs. 376511|NM\_001207|ENSG00000TMEM191C - transmemt protein-coding

chr11-464 4.45348 1.0448 1.111023 0.940394 0.347015 0.981636 chr11 46441362 46442167 + 0 NA intron (NL3b|LINE| -10043 NR\_03611E 1E+08 NR\_03611E|ENSG00000MIR3160-Zmir-3160-microRNA ncRNA

chr16-896 4.45348 1.0448 1.111023 0.940394 0.347015 0.981636 chr16 89663889 89664674 + 0 NA intron (Nintron (N 6248 NR\_07351E 124045 Hs. 655171|NM\_15302E|ENSG00000SPATA33 C16orf55 spermatogprotein-coding

chr3-3737 4.45348 1.0448 1.111023 0.940394 0.347015 0.981636 chr3 37373590 37374317 + 0 NA IntergeniMER83B-ir -12316 NM\_178344 339883 Hs. 47594E|NM\_17833E|ENSG00000C3orf35 APRG1 chromosome protein-coding

chr7-9894 8.938577 -0.75831 0.80645 -0.9403 0.347062 0.981636 chr7 98942607 98942918 + 0 NA intron (Nintron (N 61065 NR\_132754 1.07E+08 NR\_132754 SCARNA28 ZL1 small Ca ncRNA

chr1-1628 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr1 47687 NM\_00618E 4921 Hs. 275757|NM\_00618E|ENSG00000DDR2 M1G20a|N1 discoidl protein-coding

chr11-332 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr11 33297803 33298493 + 0 NA intron (NTiger1|I 39817 NM\_00127E 10114 Hs. 20191E|NM\_005734|ENSG00000CHIPK3 DYRK6|FIS homeodome protein-coding

chr15-506 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr15 50607697 50607988 + 0 NA intron (NALuSx|SIN -61176 NM\_203494 373509 Hs. 67775E|NM\_203494|ENSG00000USP50 - ubiquitin protein-coding

chr16-155 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr16 15046981 15047659 + 0 NA intron (NL2a|LINE| 8754 NM\_173474 123803 Hs. 59204E|NM\_173474|ENSG00000CNTAN1 PNAAL|PNAI-N-termin protein-coding

chr17-305 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr17 30997005 30999971 + 0 NA intron (NLIMA5A|LI -9796 NM\_00135C 1.08E+08 Hs. 558901|NM\_001350575 L0C107984 - uncharacter protein-coding

chr19-965 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr19 9631900 9633684 + 0 NA intron (NHERV10|E 11310 NR\_12203E 284385 Hs. 651747|NM\_00124E|ENSG00000ZNF561-AS1 C19orf82 ZNF561 arncRNA

chr2-724 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr2 72460747 72465534 + 0 NA intron (NLIMD|LINE -315278 NM\_001277 56603 Hs. 91546 NM\_01988E|ENSG00000CYP26B1 CYP26A2|F cytochrom protein-coding

chr20-555 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr20 55594941 5604503 + 0 NA intron (Nintron (N 11011 NM\_01959E 56261 Hs. 63635E|NM\_01959E|ENSG00000GPCPD1 EDI3|GDEglyceropl protein-coding

chr6-1368 7.939578 0.78112 0.830712 0.940302 0.347063 0.981636 chr6 1.37E+08 1.37E+08 + 0 NA intron (NLIMC4|LIN 48542 NM\_00100E 340146 Hs. 36970E|NM\_00100E|ENSG00000SLC35D3 FRCL1 solute cprotein-coding

chr19-937 6.239518 0.88937 0.945853 0.940283 0.347072 0.981636 chr19 9371808 9372385 + 0 NA intron (NLIMEd|LIN -4220 NM\_00117E 7730 Hs. 728944|NM\_003451|ENSG00000ZNF177 PIGX zinc fingprotein-coding

chr11-108 8.394842 -0.80445 0.855572 -0.94025 0.347092 0.981636 chr11 1.01E+08 1.01E+08 + 0 NA intron (Nintron (N 28202 NR\_145747 1.1E+08 NR\_145747 SNORD131 - small nucsoRNA

chr2-9265 9.723766 0.722698 0.768651 0.940216 0.347107 0.981636 chr2 92654989 92655622 + 0 NA IntergeniALR|Alphe 714172 NR\_027714 440888 Hs. 73023E|NM\_001032412 ACTR3BP2 FKS673 ACTR3B ps pseudo

chr6-7367 7.93172 0.933228 0.833212 0.94001 0.347212 0.981636 chr6 73630586 73630879 + 0 NA intron (Nintron (N 23260 NM\_012434 26503 Hs. 59742E|NM\_012434|ENSG00000SLC17A5 AST|ISSD|solute cprotein-coding

chr1-3325 7.707799 0.789757 0.999736 0.939999 0.347218 0.981636 chr1 33276844 33277579 + 0 NA intron (Nintron (N 7518 NM\_00137C 149076 Hs. 74335E|NM\_15249E|ENSG00000ZNF362 RN|lin-2E zinc fingprotein-coding

chr11-725 7.707799 0.939751 0.999736 0.939999 0.347218 0.981636 chr11 72690043 72691299 + 0 NA intron (NALuJr|SIN -9803 NR\_14678C 1.01E+08 Hs. 50316E|NR\_14678C|ENSG00000ARAP1-AS2- ARAP1 antncRNA

chr1-1785 11.94584 0.653299 0.695646 0.939888 0.347275 0.981636 chr1 1.79E+08 1.79E+08 + 0 NA 3' UTR (N3' UTR (N -45494 NM\_00467E 9068 Hs. 591474|NM\_00467E|ENSG00000ANGPTL1 ANG3|ANGF angiopoie protein-coding

chr11-115 9.358894 -0.72646 0.773127 -0.93964 0.347403 0.981636 chr11 11942379 11943255 + 0 NA exon (NM exon (NM 65822 NM\_00101E 21722 Hs. 62925E|NM\_01325E|ENSG00000DKK3 REIC|RIG dickkopf protein-coding

chr17-47 9.358894 -0.72646 0.773127 -0.93964 0.347403 0.981636 chr17 47051266 47051503 + 0 NA Intergeni Intergeni -72131 NM\_20340C 388394 Hs. 36799E|NM\_20340C|ENSG00000RPRML - reprimol protein-coding

chr2-3259 9.358894 -0.72646 0.773127 -0.93964 0.347403 0.981636 chr2 32586451 32586974 + 0 NA intron (NALuJb|SIN -11894 NR\_12579E 1.04E+08 Hs. 66609E|NR\_12579E|ENSG00000BIRC6-AS2|linc-birc6BIRC6 antncRNA

chr2-1731 9.358894 -0.72646 0.773127 -0.93964 0.347403 0.981636 chr2 1.73E+08 1.73E+08 + 0 NA intron (Nintron (N 83198 NR\_03388E 339751 Hs. 57008E|NR\_03388E|ENSG00000MAP3K20-MLK7-AS1 MAP3K20 ncRNA

chr3-2738 9.358894 -0.72646 0.773127 -0.93964 0.347403 0.981636 chr3 27388892 27391047 + 0 NA non-codir non-codir -20509 NM\_152534 152110 Hs. 50611E|NM\_152534|ENSG00000CNEK10 - NIMA relcprotein-coding

chr11-882 8.36156 -0.80975 0.861838 -0.93956 0.347442 0.981636 chr11 88294332 88294545 + 0 NA exon (NM exon (NM 43298 NM\_14817C 1075 Hs. 12806E|NM\_001814|ENSG00000CTSC CPPI|DPP-cathepsir protein-coding

chr11-12 7.690802 -0.80489 0.856914 -0.93929 0.347582 0.981636 chr11 12500137 12500719 + 0 NA intron (Nintron (N 122857 NM\_01822E 55742 Hs. 432914|NM\_01822E|ENSG00000PARVA CH-ILKBP|parv in protein-coding

chr2-100 7.682224 -0.80334 0.855374 -0.93917 0.347642 0.981636 chr2 1E+08 1E+08 + 0 NA intron (N(GTGGTG)T 88863 NM\_00102E 3899 Hs. 444414|NM\_00228E|ENSG00000CAFF3 LAF4|MLL1AF4/FMR2 protein-coding

chr1-112 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr1 1.13E+08 1.13E+08 + 0 NA intron (Nintron (N 50814 NM\_138727 54879 Hs. 201921|NM\_017744|ENSG00000STL7 FAM4B|ST7 suppressir protein-coding

chr16-110 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr16 1.05E+08 1.05E+08 + 0 NA intron (NHUERS-P1- 5631 NM\_03330E 837 Hs. 13837E|NM\_00122E|ENSG00000CASPA ICE|RE1|Icaspase 4 protein-coding

chr17-182 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr17 11044514 11045075 + 0 NA intron (NALuSp|SIN 100230 NM\_01522E 23274 Hs. 35490 NM\_01522E|ENSG00000CLEC16A Gop-1|KIAC-type lprotein-coding

chr17-182 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr17 18265959 18266182 + 0 NA TTS (NM\_ITTS (NM\_3) 4956 NM\_14888E 125170 Hs. 65555E|NM\_13916E|ENSG00000MIEF2 MID49|SMC1 tochoch protein-coding

chr2-384 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr2 38479911 38481321 + 0 NA intron (NLIMYh3|SI 12520 NM\_00685E 11015 Hs. 74507E|NM\_00685E|ENSG00000KDELER3 EDYD2L3|KDEL endc protein-coding

chr9-6501 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr9 6501065 6501309 + 0 NA intron (Nintron (N 87988 NM\_15289E 115426 Hs. 493401|NM\_15289E|ENSG00000UHRF2 NIRP|RNF1ubiquitir protein-coding

chr9-2152 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chr9 21527685 21528510 + 0 NA intron (NLIPA13|LI -15912 NR\_02950E 407035 NR\_02950E|ENSG00000MIR31 MIRN31|hsmicroRNA ncRNA

chrX-7426 6.359307 -0.87915 0.936128 -0.93913 0.347662 0.981636 chrX 74261848 74262184 + 0 NA intron (NALuJo|SIN 25193 NR\_03025E 664614 NR\_03025E|ENSG00000MIR545 MIRN545|microRNA ncRNA

chr1-2772 6.229811 0.877714 0.935546 0.938183 0.34815 0.981636 chr1 27728357 27728997 + 0 NA intron (Nintron (N 2716 NM\_00114E 199870 Hs. 46935E|NM\_15266E|ENSG00000FAM76A - family wiprotein-coding

chr1-2077 6.229811 0.877714 0.935546 0.938183 0.34815 0.981636 chr1 2.08E+08 2.08E+08 + 0 NA intron (NMER44B|DI 10306 NR\_02983E 407026 NR\_02983E|ENSG00000MIR29C MIRN29C|hsmicroRNA ncRNA

chr10-116 6.229811 0.877714 0.935546 0.938183 0.34815 0.981636 chr10 1.11E+08 1.11E+08 + 0 NA intron (N(TAT)n|SI 12891 NM\_01445E 27250 Hs. 71149C|NM\_01445E|ENSG00000PCDC4 H731 programme protein-coding

chr11-764 6.229811 0.877714 0.935546 0.938183 0.34815 0.981636 chr11 76480346 76481002 + 0 NA intron (NLIP3|LINE 35649 NM\_02019E 56946 Hs. 35258E|NM\_02019E|ENSG00000EMSY C1orf303|EMSY trar protein-coding

chr11-116 6.229811 0.877714 0.935546 0.938183 0.34815 0.981636 chr11 1.17E+08 1.17E+08 + 0 NA intron (NMLT1D|LTF -86961 NM\_00003E 335 Hs. 93194 NM\_00003E|ENSG00000APOA1 apo(a) apolipoprotein-coding

chr15-727 6.229811 0.877714 0.935546 0.938183 0.34815 0.981636 chr15 30365 NM\_03302E 585 Hs. 208681|NM



chr6-1965	6.42587	-0.86583	0.924751	-0.93628	0.349129	0.981636	chr6	99502439	99503064	+	0	NA	intron (NMSTA LTR)	12625	NM_00134E	85015	Hs.14341CNM_03292E	ENSG00000C	USP45	-	ubiquitin protein-coding	
chr9-9795	6.42587	-0.86583	0.924751	-0.93628	0.349129	0.981636	chr9	97994884	97996539	+	0	NA	intron (NAIuSx6 SI)	12370	NM_006401	10541	Hs.730654NM_006401	ENSG00000C	ANP32B	-	APRIL PIH acidic n protein-coding	
chr9-113	3.998032	1.169493	1.249286	0.93613	0.349206	0.981636	chr9	1.13E+08	1.13E+08	+	0	NA	intron (NL2a LINE)	4581	NM_00128E	7539	Hs.15040E	ENSG00000C	ZFP37	-	ZNF906 zfZFP37 zir protein-coding	
chr12-111	12.40914	0.630715	0.673768	0.9361	0.349222	0.981636	chr12	1.13E+08	1.13E+08	+	0	NA	intron (Nintron)	7817	NM_001111	79039	Hs.506861NM_02407E	ENSG00000C	DDX54	-	DP97 DEAD-box protein-coding	
chr19-12	12.40914	0.630715	0.673768	0.9361	0.349222	0.981636	chr19	12012592	12021254	+	0	NA	intron (NAIuSx3 SI)	18818	NM_00130E	163059	Hs.66777E	ENSG00000C	ZNF433	-	zinc finger protein-coding	
chr13-48	10.18707	0.690911	0.738076	0.936097	0.349223	0.981636	chr13	48395174	48395413	+	0	NA	intron (NLIPA7 LIN)	17820	NM_00116E	10161	Hs.123464NM_00576E	ENSG00000C	CLPAR6	-	ARWH1 HYF lysophosph protein-coding	
chr7-661F	8.930719	-0.75684	0.808561	-0.93604	0.349254	0.981636	chr7	66153465	66153896	+	0	NA	non-codiron-codir	38833	NM_01447E	27297	Hs.300684NM_01447E	ENSG00000C	CRCP	-	CGRP-RCP CGRP receptor protein-coding	
chr9-135E	8.930719	-0.75684	0.808561	-0.93604	0.349254	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	TTS (NM TTS (NM_C	-25258	NM_01544E	157922	Hs.52249E	ENSG00000C	CAMSAP1	-	calmodulin protein-coding	
chr11-65C	6.214095	0.883233	0.943655	0.93597	0.349288	0.981636	chr11	65034769	65036247	+	0	NA	intron (Nintron)	-5425	NR_16002E	29901	Hs.23642	NM_01329E	ENSG00000C	SAC3D1	-	HSU79266 SAC3 dome protein-coding
chr11-68T	6.214095	0.883233	0.943655	0.93597	0.349288	0.981636	chr11	68796170	68796720	+	0	NA	intron (NAIuSq2 SI)	-44925	NM_00103E	9633	Hs.145932NM_00492E	ENSG00000C	TESMIN	-	CXCD2 CMT10 testis e protein-coding	
chr4-420T	6.674366	-0.80173	0.856621	-0.93593	0.349311	0.981636	chr4	42025350	42025801	+	0	NA	intron (Nintron)	35045	NM_00634E	10463	Hs.479634NM_00634E	ENSG00000C	SLC30A9	-	BILAPES Csolute e protein-coding	
chr6-135A	6.674366	-0.80173	0.856621	-0.93593	0.349311	0.981636	chr6	1.35E+08	1.35E+08	+	0	NA	intron (Nintron)	4728	NM_001134	54806	Hs.386684NM_01765E	ENSG00000C	AHI1	-	AHI-1 JBIAbelson l protein-coding	
chr2-861C	6.633226	-0.80563	0.861371	-0.93529	0.349637	0.981636	chr2	86102018	86102392	+	0	NA	intron (NLIMB3 LIN)	3681	NM_01542E	25885	Hs.53181E	ENSG00000C	POLR1A	-	A190 AFDCRNA poly protein-coding	
chr1-146E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr1	1.47E+08	1.47E+08	+	0	NA	intron (Nintron)	13432	NM_00127E	149013	Hs.666981NM_00127E	ENSG00000C	BNP1F2	-	COA1 K1/NBPFF mem protein-coding	
chr1-156E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (NLIMB7 LIN)	-39607	NR_03052E	768220	NR_03052E	ENSG00000C	MIR765	-	MIRN765 l microRNA ncRNA	
chr1-168E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr1	1.68E+08	1.68E+08	+	0	NA	intron (Nintron)	6517	NR_19934E	375035	Hs.64543E	ENSG00000C	SFT2D2	-	UNQ512 DJSF12 dome protein-coding	
chr12-11T	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (NAIuSx SIN)	-40770	NR_106921	1.02E+08	NR_106921	ENSG00000C	MIR6861	-	hsa-mir-6861 dome protein-coding	
chr13-11C	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (Nintron)	20572	NM_01821C	55739	Hs.408324NM_01821C	ENSG00000C	NAXD	-	CARRD LPC2(N)HX protein-coding	
chr15-40T	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr15	40749355	40749554	+	0	NA	intron (NAIuJr SIN)	5800	NM_01814E	55177	Hs.511067NM_01814E	ENSG00000C	RMDN3	-	FAM82A2 regulator protein-coding	
chr16-66E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr16	66809022	66810873	+	0	NA	intron (Nintron)	-8327	NM_00113E	283847	Hs.37650E	ENSG00000C	TERB1	-	CCDC79 telomere protein-coding	
chr16-66E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr16	66943136	66943466	+	0	NA	exon (NM exon (NM	7785	NM_00136E	8824	Hs.28297E	ENSG00000C	CES2	-	CE-2 CES2 carboxylc protein-coding	
chr17-29E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr17	29576577	29577650	+	0	NA	intron (Nintron)	8412	NM_00134E	90313	Hs.51405E	ENSG00000C	TP53I13	-	DSCP1 tumor prc protein-coding	
chr18-54E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr18	54936511	54944085	+	0	NA	intron (NL2 LINE I	17750	NM_00114E	80323	Hs.12079E	ENSG00000C	CCDC68	-	SE57-1 coiled-c protein-coding	
chr19-41E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr19	41897986	41899048	+	0	NA	exon (NM exon (NM	14074	NM_19900E	9138	Hs.63153E	ENSG00000C	ARHGEF1	-	GEP1 IMD6 Rho guaniprotein-coding	
chr21-33T	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr21	33794585	33794951	+	0	NA	intron (Nintron)	121036	NM_00169E	539	Hs.40914E	ENSG00000C	ATP5P0	-	ATP50 ATF ATP synt protein-coding	
chr5-326T	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr5	32262592	32263741	+	0	NA	exon (NM exon (NM	49773	NM_00104E	54545	Hs.48183E	ENSG00000C	MTMR12	-	3-PAP PIF myotubulc protein-coding	
chr6-106E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr6	1.06E+08	1.06E+08	+	0	NA	exon (NM exon (NM	6010	NM_18290E	639	Hs.43602E	ENSG00000C	PRDM1	-	BLIMP1 PFYPR/SET d protein-coding	
chr7-75E	6.947436	0.778992	0.833466	0.934641	0.349974	0.981636	chr7	75553266	75555312	+	0	NA	intron (Nintron)	-26166	NR_02805E	5387	Hs.659871NM_00539E	ENSG00000C	PMS2P3	-	PMS2L3 PWMS1 homc pseudo	
chr11-14E	6.433728	-0.86764	0.928407	-0.93455	0.350022	0.981636	chr11	14503809	14504307	+	0	NA	TTS (NM TTS (NM_I	-4163	NR_001144	1315	Hs.33927E	ENSG00000C	COPB1	-	COPB coator protein-coding	
chr19-49E	6.433728	-0.86764	0.928407	-0.93455	0.350022	0.981636	chr19	4942743	4943483	+	0	NA	intron (NAIuSx3 SI)	10426	NR_03990E	1.01E+08	NR_03990E	ENSG00000C	MIR4747	-	miR-4747 microRNA ncRNA	
chr2-157E	6.433728	-0.86764	0.928407	-0.93455	0.350022	0.981636	chr2	1.57E+08	1.57E+08	+	0	NA	intron (N75K RNA F	26972	NM_001304	57471	Hs.443894NM_02071E	ENSG00000C	CERNM	-	JN KIAA11ermin protein-coding	
chr1-131E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr1	1316094	1317900	+	0	NA	intron (NAIuJr SIN)	-4431	NR_10678E	1.02E+08	NR_10678E	ENSG00000C	MIR6727	-	hsa-mir-6727 microRNA ncRNA	
chr1-108E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr1	1.08E+08	1.08E+08	+	0	NA	TTS (NM TTS (NM_2	58813	NM_21365E	29957	Hs.65687E	ENSG00000C	SLC25A24	-	hpa1 SCAM solute e protein-coding	
chr11-12E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (Nintron)	45530	NM_001301	23365	Hs.24598	NM_01531E	ENSG00000C	CARHGEF12	-	LARG PRO2 Rho guaniprotein-coding
chr13-75E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr13	75798498	75799770	+	0	NA	intron (NL4_C_Mam)	38473	NM_01584E	4008	Hs.207631NM_00535E	ENSG00000C	LM07	-	FBX20 FBX LIM doma protein-coding	
chr15-58E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr15	58833316	58834209	+	0	NA	intron (NLTR5_Hs I	62460	NM_00104C	54629	Hs.59112E	ENSG00000C	MINDY2	-	FAM63B MINDY lys protein-coding	
chr16-70E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr16	70527915	70528607	+	0	NA	intron (NAIuSz SIN)	-1238	NR_03742E	1E+08	NR_03742E	ENSG00000C	SNORD111E	-	MIR3647 small nucsnoRNA	
chr2-36E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr2	36550000	36566734	+	0	NA	intron (NMER20 DNA	32284	NM_00104E	9637	Hs.25856E	ENSG00000C	FEZ2	-	HUM3CL fasciculc protein-coding	
chr20-50E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr20	50687008	50687239	+	0	NA	intron (Nintron)	4421	NR_11089E	140876	Hs.37257E	ENSG00000C	RIPOR3	-	C20orf17E RIPOR fan protein-coding	
chr4-420E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr4	42055404	42056345	+	0	NA	intron (Nintron)	65344	NM_00634E	10463	Hs.479634NM_00634E	ENSG00000C	SLC30A9	-	BILAPES Csolute e protein-coding	
chr4-139E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (NAIuMl SI)	24388	NM_01211E	25819	Hs.63984E	ENSG00000C	NOCT	-	CCR4L CCFnocturn protein-coding	
chr4-147E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr4	1.48E+08	1.48E+08	+	0	NA	intron (NLIMC1 LIN)	120842	NR_03996E	1.01E+08	NR_03996E	ENSG00000C	MIR4799	-	miRNA ncRNA	
chr5-146E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	3' UTR (N3' UTR (N	-7718	NR_00102E	153770	Hs.16236E	ENSG00000C	PLACL8L1	-	PLAC8 lll protein-coding	
chr6-714E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr6	71410004	71410273	+	0	NA	non-codiron-codir	-6517	NR_029504	407029	NR_029504	ENSG00000C	MIR30A	-	MIRN30A mi microRNA ncRNA	
chr7-6014E	6.418012	-0.86399	0.924654	-0.93439	0.350103	0.981636	chr7	6014974	6015578	+	0	NA	exon (NM exon (NM	-1601	NR_145771	1.1E+08	NR_145771	ENSG00000C	SNORA80D	-	small nucsnoRNA	
chr1-217E	6.698343	0.718576	0.769134	0.934267	0.350166	0.981636	chr1	2.18E+08	2.18E+08	+	0	NA	exon (NM exon (NM	10857	NM_001297	55105	Hs.36234E	ENSG00000C	PATCH2	-	CT110 GPAG-patch protein-coding	
chr12-48T	6.698343	0.718576	0.769134	0.934267	0.350166	0.981636	chr12	48770156	48774021	+	0	NA	promoter-promoter-	-51	NR_03985E	1.01E+08	NR_03985E	ENSG00000C	MIR4701	-	miRNA ncRNA	
chr21-371T	6.698343	0.718576	0.769134	0.934267	0.350166	0.981636	chr21	37121291	37121490	+	0	NA	intron (Nintron)	38443	NM_00331E	7267	Hs.368214NM_00331E	ENSG00000C	CTC3	-	DCRR1 RNf tetraic protein-coding	
chr21-464T	6.698343	0.718576	0.769134	0.934267	0.350166	0.981636	chr21	46402422	46403087	+	0	NA	intron (Nintron)	-56137	NM_20689E	23181	Hs.18958E	ENSG00000C	DIP2A	-	C21orf10E disco intr protein-coding	
chr19-25E	6.230593	1.213545	1.299362	0.933954	0.350327	0.981636	chr19	25814														

chr8-4286 6.204387	0.871655	0.937242	0.930022	0.35236	0.981636	chr8	42863119	42864280	+	0 NA	intron (AluSc SIN	-20368 NM_199003	55145 Hs. 7432 NM_01810f	ENSG000003THAP1	DYT6	THAP domain protein-coding	
chr17-427 7.906296	0.778343	0.836943	0.929984	0.352379	0.981636	chr17	42778798	42779351	+	0 NA	3' UTR (N3' UTR (N	-1536 NM_001321	65266 Hs. 10544f	ENSG000003WNK4	PHA2B PRKWNK	lysine protein-coding	
chr20-27 7.980717	0.781698	0.840805	0.929702	0.352526	0.981636	chr20	27366030	27366962	+	0 NA	IntergeniALR/Alpha	-1157263 NR_04009f	284801 Hs. 37069f	ENSG000003MIR663AHC	MIR663A	lncRNA	
chr4-723 7.980717	0.781698	0.840805	0.929702	0.352526	0.981636	chr4	722559	722558	+	0 NA	intron (Nintron (N	16626 NM_001317	10336 Hs. 14430f	ENSG000003PCGF3	DONG1 RNFL	polycomb protein-coding	
chr17-184 7.666508	-0.80005	0.860701	-0.92953	0.352615	0.981636	chr17	1843027	1843424	+	0 NA	intron (Nintron (N	13220 NM_00135f	6117 Hs. 46192f	ENSG000003RPA1	HSSB MSGC	replicator protein-coding	
chr6-117 7.666508	-0.80005	0.860701	-0.92953	0.352615	0.981636	chr6	1.18E+08	1.18E+08	+	0 NA	intron (LIME4b LI	58545 NM_00136f	285761 Hs. 658304	ENSG000003DCBLD1	dJ94G16.1	discoidin protein-coding	
chr18-508 6.441586	-0.86945	0.935771	-0.92913	0.352823	0.981636	chr18	58548503	58548921	+	0 NA	intron (Nintron (N	-51908 NR_13296f	1.07E+08	NR_13296f	SNORA108	small nucleolar RNA	
chr1-4008 8.118257	-0.76616	0.82461	-0.92912	0.352827	0.981636	chr1	40087853	40088374	+	0 NA	intron (Nintron (N	9139 NM_001142	5538 Hs. 3873	NR_00031f	ENSG000003PPT1	CLN1 INCL	lamitoy protein-coding
chr11-102 8.118257	-0.76616	0.82461	-0.92912	0.352827	0.981636	chr11	1.02E+08	1.02E+08	+	0 NA	TTS (NM_C TTS (NM_C	48637 NM_00125f	329 Hs. 69623f	ENSG000003BIRC2	API1 HIAF	baculovirus protein-coding	
chr5-967 8.118257	-0.76616	0.82461	-0.92912	0.352827	0.981636	chr5	96730580	96731989	+	0 NA	intron (Nintron (N	-12318 NR_14024f	831 Hs. 43618f	ENSG000003CAST	BS-17 PL7	calpastatin protein-coding	
chr5-109 8.118257	-0.76616	0.82461	-0.92912	0.352827	0.981636	chr5	-0.92E+08	1.09E+08	+	0 NA	intron (Nintron (N	-40444 NR_10498f	285638 Hs. 532104	ENSG000003LOC28563f		uncharacterized ncRNA	
chr8-1407 8.922861	-0.75529	0.813007	-0.92901	0.352884	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	promoter-promoter-	23 NR_02989f	442893	NR_02989f	ENSG000003MIR151A	MIR151	microRNA ncRNA
chr1-236 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr1	2.36E+08	2.36E+08	+	0 NA	intron (AluXs1 SI	42715 NM_00250f	4811 Hs. 356624	ENSG000003NID1	NID	nidogen 1 protein-coding	
chr11-104 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr11	1.05E+08	1.05E+08	+	0 NA	intron (L2a LINE	25024 NM_03330f	837 Hs. 13837f	ENSG000003CASP4	ICE (rel)	caspace 4 protein-coding	
chr12-48 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr12	48045333	48045560	+	0 NA	intron (Nintron (N	-40970 NM_03315f	1280 Hs. 40818f	ENSG000003COL2A1	ANFH AOM	collagen protein-coding	
chr13-467 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr13	46780263	46781980	+	0 NA	intron (Nintron (N	16040 NM_00198f	2098 Hs. 43249f	ENSG000003ESD	FGH	esterase protein-coding	
chr13-49 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr13	49914173	49914761	+	0 NA	non-coding-non-coding	21873 NM_02045f	57213 Hs. 44235	ENSG000003SPRYD7	C13orf1 CSRY	domain protein-coding	
chr15-67 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr15	67079020	67079616	+	0 NA	intron (Nintron (N	13716 NM_00590f	4088 Hs. 72798f	ENSG000003SMAD3	HSPC193 SMAD	fam protein-coding	
chr2-6111 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr2	61118875	61119438	+	0 NA	intron (Nintron (N	25819 NR_03649f	339803 Hs. 25243f	ENSG000003LOC33980f		uncharacterized ncRNA	
chr2-210 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr2	2.1E+08	2.1E+08	+	0 NA	intron (Nintron (N	6028 NM_00131f	6120 Hs. 28226f	ENSG000003CRPE	RPE2-1	ribulose protein-coding	
chr2-217 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr2	2.17E+08	2.17E+08	+	0 NA	intron (THE1B-int	108260 NR_13364f	1.05E+08	NR_13364f	DIRC3-AS1	DIRC3	antncRNA
chr2-224 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr2	2.25E+08	2.25E+08	+	0 NA	intron (AluSz SIN	17013 NM_00129f	55619 Hs. 46578	ENSG000003DOCK10	DRIP2 Nbl	dedicator protein-coding	
chr6-107 6.376873	-0.86871	0.935112	-0.929	0.352891	0.981636	chr6	1.08E+08	1.08E+08	+	0 NA	3' UTR (N3' UTR (N	-46765 NM_00128f	256380 Hs. 48610f	ENSG000003SCML4	dJ47M23.1	Scm polycomb protein-coding	
chr1-4294 6.410154	-0.8621	0.928118	-0.92887	0.352958	0.981636	chr1	42942245	42943547	+	0 NA	intron (MIRc SINE	15972 NM_00651f	6513 Hs. 47372f	ENSG000003SLC2A1	BSE DYTT1	solute carrier protein-coding	
chr12-705 6.410154	-0.8621	0.928118	-0.92887	0.352958	0.981636	chr12	7098469	7099218	+	0 NA	intron (LIMB7 LIN	-6398 NM_00173f	715 Hs. 52422f	ENSG000003CIR	EDSPD1	complement protein-coding	
chr17-37 6.410154	-0.8621	0.928118	-0.92887	0.352958	0.981636	chr17	37613573	37614602	+	0 NA	TTS (NR_C TTS (NR_C	952 NR_10674f	1.02E+08	NR_10674f	ENSG000003MIR378J	hsa-mir-5	microRNA ncRNA
chr2-3931 6.410154	-0.8621	0.928118	-0.92887	0.352958	0.981636	chr2	39318949	39319389	+	0 NA	intron (Nintron (N	-75186 NR_14452f	344387 Hs. 40320f	ENSG000003CDKL4		cyclin dependent protein-coding	
chr2-199 6.410154	-0.8621	0.928118	-0.92887	0.352958	0.981636	chr2	2E+08	2E+08	+	0 NA	non-coding-non-coding	18770 NM_15368f	205327 Hs. 15449f	ENSG000003C2orf69		chromosome protein-coding	
chr8-263 6.410154	-0.8621	0.928118	-0.92887	0.352958	0.981636	chr8	26397282	26397576	+	0 NA	intron (LIPA2 LIN	7016 NM_00133f	665 Hs. 13122f	ENSG000003BNIP3L	BNIP3a NBCL2	integrin protein-coding	
chr11-18 8.092833	-0.77287	0.83227	-0.92863	0.353079	0.981636	chr11	18352950	18353232	+	0 NA	intron (AluSq2 SI	30524 NM_00531f	2965 Hs. 57720f	ENSG000003GTF2H1	BTf2 P62	general protein-coding	
chr7-550 4.717768	-1.03811	1.118204	-0.92837	0.353213	0.981636	chr7	55083076	55083545	+	0 NA	intron (Nintron (N	-26529 NM_00134f	1956 Hs. 48829f	ENSG000003EGFR	ERBB ERBE	epidermal protein-coding	
chr1-203 6.668509	0.955119	1.029471	0.928165	0.353322	0.981636	chr1	2.04E+08	2.04E+08	+	0 NA	intron (AluJb SIN	-41286 NR_00301f	677843 Hs. 67613f	ENSG000003SNORA77	ACA63 SNC	small nucleolar RNA	
chr12-105 8.126114	-0.76768	0.827352	-0.92788	0.353469	0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	TTS (NM_C TTS (NM_C	29190 NR_13389f	339803 Hs. 25243f	ENSG000003LOC33980f		uncharacterized ncRNA	
chr1-153 6.188671	0.877133	0.945379	0.927811	0.353506	0.981636	chr1	1.54E+08	1.54E+08	+	0 NA	3' UTR (N3' UTR (N	14125 NR_12656f	343052 Hs. 51653f	ENSG000003LOC34305f		immunoglobulin pseudo	
chr16-864 6.188671	0.877133	0.945379	0.927811	0.353506	0.981636	chr16	8646318	8646891	+	0 NA	non-coding-non-coding	24906 NR_13460f	79091 Hs. 30638f	ENSG000003METTL22	C16orf68	methyltransferase protein-coding	
chr3-120 6.188671	0.877133	0.945379	0.927811	0.353506	0.981636	chr3	1.2E+08	1.2E+08	+	0 NA	intron (Nintron (N	4835 NM_00708f	11167 Hs. 26951f	ENSG000003PSTL1	FRP FSL1	follicle-stimulating protein-coding	
chr4-533 6.188671	0.877133	0.945379	0.927811	0.353506	0.981636	chr4	533062	533443	+	0 NA	intron (Nintron (N	34042 NM_00112f	54872 Hs. 7099	NR_01773f	ENSG000003PIGG	GP17 LAS2	phosphatidyl protein-coding
chr10-934 3.922871	-1.09485	1.180089	-0.92777	0.353526	0.981636	chr10	93473394	93474002	+	0 NA	intron (Nintron (N	8636 NM_01345f	26509 Hs. 60208f	ENSG000003MYOF	FERL13	myoferlin protein-coding	
chr2-177 3.922871	-1.09485	1.180089	-0.92777	0.353526	0.981636	chr2	1.8E+08	1.78E+08	+	0 NA	intron (LIPA16 LI	36751 NM_15251f	150737 Hs. 44765f	ENSG000003TTC30B	IFT70 IFT	tetralin protein-coding	
chr3-815 3.922871	-1.09485	1.180089	-0.92777	0.353526	0.981636	chr3	81525640	81526561	+	0 NA	intron (LIPA4 LIN	235545 NM_00015f	2632 Hs. 43606f	ENSG000003GBE1	APBD GBE1	1,4-alpha protein-coding	
chr3-1381 3.922871	-1.09485	1.180089	-0.92777	0.353526	0.981636	chr3	1.38E+08	1.38E+08	+	0 NA	intron (AluSq2 SI	5490 NM_00126f	25852 Hs. 74486f	ENSG000003ARMC8	GID5 HSPC	armadillo protein-coding	
chr6-144 3.922871	-1.09485	1.180089	-0.92777	0.353526	0.981636	chr6	1.45E+08	1.45E+08	+	0 NA	intron (Nintron (N	146679 NR_13277f	1.07E+08	NR_13277f	SNORA98	small nucleolar RNA	
chr1-2344 4.435914	1.032655	1.113063	0.92776	0.353532	0.981636	chr1	2.34E+08	2.34E+08	+	0 NA	intron (MER102b I	50700 NM_00564f	6894 Hs. 49811f	ENSG000003TARBP1	TRM3 TRMT	TAR (HIV-1) protein-coding	
chr7-154 5.177374	-0.96146	1.036579	-0.92753	0.353649	0.981636	chr7	1.55E+08	1.55E+08	+	0 NA	intron (Nintron (N	33160 NR_02447f	1E+08	ENSG000003PAX1P1-AS	PAX1P1OS	PAX1P1	lncRNA
chr1-183 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr1	1.84E+08	1.84E+08	+	0 NA	3' UTR (N3' UTR (N	9013 NM_00571f	10092 Hs. 51860f	ENSG000003ARPC5	ARPC16d J	lactin receptor protein-coding	
chr11-78 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr11	78067752	78068718	+	0 NA	TTS (NM_C TTS (NM_C	4374 NM_00325f	7069 Hs. 59196f	ENSG000003TRHP5	LRPG1 Lp	thyroid protein-coding	
chr14-911 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr14	91187898	91188657	+	0 NA	intron (MLT1J1 LI	56427 NM_00117f	8111 Hs. 8882	NR_00348f	ENSG000003GPR68	A12A6 GPF	G protein-coding
chr15-41 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr15	41899103	41901091	+	0 NA	3' UTR (N3' UTR (N	-6044 NM_01664f	51332 Hs. 70981f	ENSG000003SPTBN5	BSPECV H	spectrin protein-coding	
chr16-33 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr16	3302702	3303634	+	0 NA	intron (Nintron (N	-2238 NM_15302f	7627 Hs. 51329f	ENSG000003ZNF75A		zinc finger protein-coding	
chr2-724 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr2	72495491	72495996	+	0 NA	intron (LIME1 LIN	330290 NM_00132f	23233 Hs. 30345f	ENSG000003EXOC6B	SEC15B SE	exocyst protein-coding	
chr2-216 5.153801	-0.95467	1.029258	-0.92753	0.353651	0.981636	chr2	2.16E+08	2.16E+08	+	0 NA	intron (Nintron (N	-27693 NM_00099f	6168 Hs. 43370f	ENSG000003RPL37A	L37A	ribosomal protein-coding	
chr2-365 5.153801	-0.95467	1.029258	-0.92753	0.353651													



chr5-4881 37.78014	0.391905	0.425003	0.922123	0.356464	0.981636	chr5	48810888	48811807	+	0	NA	IntergeniALR/Alpha	1629941	NM_198444	133418	Hs.561411NM_198444	ENSG000000000000	GP70	emigin protein-coding
chr1-2237 8.135822	-0.75813	0.822231	-0.92204	0.356509	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (NLIMC3 LIN	10225	NM_001748	824	Hs.350899NM_001748	ENSG000000000000	CANP2	CAN calpain 2 protein-coding
chr11-865 8.135822	-0.75813	0.822231	-0.92204	0.356509	0.981636	chr11	86339010	86340873	+	0	NA	intron (NLIPA6 LIN	-34795	NM_021827	60494	Hs.144913NM_021827	ENSG000000000000	-	coiled-cc protein-coding
chr17-29 8.135822	-0.75813	0.822231	-0.92204	0.356509	0.981636	chr17	29080058	29080257	+	0	NA	intron (NCPG	-4548	NM_00474C	9220	Hs.462599NM_00474C	ENSG000000000000	MAJN	MAJN SPR2 TGFbeta1-inc protein-coding
chr5-5597 8.135822	-0.75813	0.822231	-0.92204	0.356509	0.981636	chr5	55972338	55972461	+	0	NA	intron (NMIR SINE	20064	NM_175767	3572	Hs.532082NM_002184	ENSG000000000000	CD130	CD130 CDW interluc protein-coding
chr6-7517 8.135822	-0.75813	0.822231	-0.92204	0.356509	0.981636	chr6	75175799	75184148	+	0	NA	intron (NLIMB3 LIN	26080	NM_08064E	1303	Hs.101302NM_00437C	ENSG000000000000	BA209D8	BA209D8 collagen protein-coding
chr8-2775 5.19494	-0.94858	1.028833	-0.922	0.35653	0.981636	chr8	27756365	27757002	+	0	NA	intron (Nintron (N	15957	NR_15643Z	55246	Hs.445512NM_01824C	ENSG000000000000	-	coiled-cc protein-coding
chr2-9361 5.187082	-0.94637	1.026442	-0.92199	0.356533	0.981636	chr2	9361958	9363398	+	0	NA	intron (NAluJo SIN	59913	NM_00131E	9270	Hs.467662NM_00476C	ENSG000000000000	ICAP-1A	ICAP-1A integin protein-coding
chr2-3302 5.187082	-0.94637	1.026442	-0.92199	0.356533	0.981636	chr2	33026782	33027767	+	0	NA	intron (NLIMA9 LIN	80321	NM_20694E	4052	Hs.619313NM_000627	ENSG000000000000	-	latent tr protein-coding
chr2-3324 5.187082	-0.94637	1.026442	-0.92199	0.356533	0.981636	chr2	33246904	33247657	+	0	NA	intron (NMIRb SINE	112683	NM_00116E	4052	Hs.619313NM_000627	ENSG000000000000	-	latent tr protein-coding
chr22-45 5.187082	-0.94637	1.026442	-0.92199	0.356533	0.981636	chr22	45541110	4555836	+	0	NA	intron (Nintron (N	50774	NR_131244	1.01E+08	Hs.517692NR_131244	ENSG000000000000	LINC01589	TCONS_00C long intncrRNA
chr19-291 12.91359	0.609947	0.661596	0.921933	0.356563	0.981636	chr19	2915647	2918752	+	0	NA	exon (NM exon (NM	10091	NM_00131E	126295	Hs.591373NM_17348C	ENSG000000000000	ZNF424	zinc fing protein-coding
chr8-5378 4.643346	-1.05547	1.145119	-0.92171	0.356678	0.981636	chr8	53788006	53788205	+	0	NA	intron (Nintron (N	54937	NM_21362C	51606	Hs.491737NM_015941	ENSG000000000000	CGI-11	MS ATPase H+ protein-coding
chr1-6261 9.802785	-0.70141	0.761114	-0.92156	0.356759	0.981636	chr1	62618090	62618477	+	0	NA	intron (Nintron (N	20763	NM_01449E	27329	Hs.209153NM_01449E	ENSG000000000000	ANG-5	ANG anagapoi protein-coding
chr5-934 9.802785	-0.70141	0.761114	-0.92156	0.356759	0.981636	chr5	93490666	93490865	+	0	NA	intron (N (GGT)n SI	80578	NR_10982E	441094	Hs.457407NR_01536E	ENSG000000000000	NR2F1	NR2F1 antncrRNA
chr5-129 9.86149	-0.69174	0.750767	-0.92137	0.356856	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (NMER58A DN	-11496	NM_001257	1E+08	Hs.582534NM_001257	ENSG000000000000	KIAA1024	membrane protein-coding
chr6-100 9.86149	-0.69174	0.750767	-0.92137	0.356856	0.981636	chr6	1.01E+08	1.01E+08	+	0	NA	intron (NLIPA3 LIN	-12270	NM_00506E	6492	Hs.520293NM_00506E	ENSG000000000000	bHLHe14	SI bHLH protein-coding
chr18-801 9.425457	-0.7175	0.778797	-0.92129	0.356899	0.981636	chr18	80133301	80133500	+	0	NA	intron (Nintron (N	-14524	NR_02833E	1E+08	Hs.352620NM_00114E	ENSG000000000000	PARD6	PARD6 arncrRNA
chr6-158 9.37646	-0.71928	0.780934	-0.92104	0.357027	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	3410	NM_00117E	8871	Hs.434494NM_00389E	ENSG000000000000	INPP5H	synaptoje protein-coding
chr7-777 9.37646	-0.71928	0.780934	-0.92104	0.357027	0.981636	chr7	7774310	7774603	+	0	NA	intron (NAluSx3 SI	23978	NM_03293E	85025	Hs.19025NM_03293E	ENSG000000000000	C7orf35	transmem protein-coding
chr1-241 7.65865	-0.79826	0.867745	-0.920986	0.357058	0.981636	chr1	77744682	77744972	+	0	NA	intron (NAluJr SIN	15025	NM_20162E	23032	Hs.480597NM_015017	ENSG000000000000	VDU1	inquitir protein-coding
chr15-727 6.171105	0.86827	0.942761	0.920986	0.357058	0.981636	chr15	72731508	72732863	+	0	NA	intron (Nintron (N	45978	NM_03302E	585	Hs.208681NM_03302E	ENSG000000000000	-	Bardet-Bi protein-coding
chr2-220 6.171105	0.86827	0.942761	0.920986	0.357058	0.981636	chr2	2.24E+08	2.24E+08	+	0	NA	intron (NAluSz6 SI	18487	NM_02083C	57590	Hs.368355NM_02083C	ENSG000000000000	WDFY1	FENS-1 FEWD repeat protein-coding
chr22-203 6.171105	0.86827	0.942761	0.920986	0.357058	0.981636	chr22	20044179	20044299	+	0	NA	intron (Nintron (N	10600	NR_02970E	406961	NR_02970E	ENSG000000000000	MIR185	nmicroRNA ncRNA
chr7-879 2.701649	-1.34751	1.463629	-0.92066	0.357228	0.981636	chr7	87907020	87907871	+	0	NA	exon (NM exon (NM	-26698	NM_021721	53616	Hs.25639E	ENSG000000000000	ADAM22	ADAM 22 ADAM meta protein-coding
chr2-332 12.42504	-0.64138	0.696953	-0.92027	0.357432	0.981636	chr2	33286580	33287018	+	0	NA	intron (NLIPA4 LIN	-131717	NR_03062E	1.01E+08	NR_03062E	ENSG000000000000	MIR4430	microRNA ncRNA
chr1-241 7.65865	-0.79826	0.867745	-0.91993	0.35761	0.981636	chr1	318	NM_00014E	2271	Hs.592429NM_00014E	ENSG000000000000	FMRD	HLRC fumarate protein-coding						
chr15-57 7.65865	-0.79826	0.867745	-0.91993	0.35761	0.981636	chr15	57276691	57277020	+	0	NA	intron (NAluSx SIN	1802	NR_14574E	1.1E+08	NR_14574E	ENSG000000000000	SNORD13D	small nucsnRNA
chr12-12 8.477305	0.742187	0.806824	0.919887	0.357632	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	42018	NM_000017	35	Hs.50707E	ENSG000000000000	ACADS	ACAD3 SCF acyl-CoA protein-coding
chr17-46 8.477305	0.742187	0.806824	0.919887	0.357632	0.981636	chr17	46351699	46352805	+	0	NA	intron (NAluSp SIN	9535	NM_00136E	1.01E+08	Hs.559255NM_00103E	ENSG000000000000	ARL17B	ARL17 ARI Arab protein-coding
chr8-9451 8.477305	0.742187	0.806824	0.919887	0.357632	0.981636	chr8	94518591	94519415	+	0	NA	exon (NM exon (NM	34466	NM_01549E	25962	Hs.202233NM_01549E	ENSG000000000000	VIKRA	KIAA1429 vir like protein-coding
chr18-58 8.46159	0.746177	0.811263	0.919773	0.357691	0.981636	chr18	58895854	58898989	+	0	NA	intron (Nintron (N	33842	NM_00135E	55205	Hs.529022NM_018181	ENSG000000000000	ZNF532	zinc fing protein-coding
chr11-894 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chr11	8949626	8950508	+	0	NA	intron (Nintron (N	-7034	NM_02064E	56676	Hs.501852NM_02064E	ENSG000000000000	ASCL3	HASH3 SG chaete- protein-coding
chr3-123 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (NLIM5 LINE	12963	NM_05302E	4638	Hs.47737E	ENSG000000000000	MYLK	AAT7 KRP myosin 1 protein-coding
chr4-183 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chr4	1.83E+08	1.83E+08	+	0	NA	intron (NLIM5 LINE	28002	NM_001111	53842	Hs.33317E	ENSG000000000000	CLDN22	CLDN21 claudin 2 protein-coding
chr6-182 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chr6	18238301	18241172	+	0	NA	intron (NTigger15e	24794	NM_001134	7913	Hs.48481E	ENSG000000000000	DEK	prot protein-coding
chr6-163 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chr6	1.64E+08	1.64E+08	+	0	NA	3' UTR (N3' UTR (N	101688	NR_13462C	1.03E+08	Hs.73818E	NR_134620	LOC102724	uncharactncrRNA
chr8-617 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chr8	61709518	61711713	+	0	NA	intron (Nintron (N	3977	NM_001164	444	Hs.332422NM_00431E	ENSG000000000000	ASPH	AAH BAH casparate protein-coding
chrX-738 3.915013	-1.09203	1.18731	-0.91975	0.357705	0.981636	chrX	73832883	73833504	+	0	NA	intron (Nintron (N	19560	NR_001564	7503	Hs.529901NR_001564	ENSG000000000000	XIST	DXS1089 X inactive ncRNA
chr19-44 12.92145	0.608666	0.661819	0.919686	0.357737	0.981636	chr19	44027742	44033536	+	0	NA	intron (NMER77B LI	5260	NM_00112E	7673	Hs.27984C	ENSG000000000000	ZNF222	zinc fing protein-coding
chr19-37 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr19	37350394	37350719	+	0	NA	intron (NLIMD2 LIN	15907	NM_00132E	284459	Hs.64024E	ENSG000000000000	ZNF875	HKR1 zinc fing protein-coding
chr21-17 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr21	17108280	17111420	+	0	NA	intron (Nintron (N	8506	NM_00110C	54149	Hs.239811NM_017447	ENSG000000000000	C21orf91	C21orf14 chromosom protein-coding
chr3-477 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr3	47726918	47727136	+	0	NA	intron (NAluSx SIN	54866	NM_003074	6599	Hs.47617E	ENSG000000000000	SMARCC1	BAF155 CF SWI/SNF i protein-coding
chr3-108 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr3	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	23069	NM_001777	961	Hs.446414NM_001777	ENSG000000000000	CD47	IAP MERG CD47 mole protein-coding
chr4-8294 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr4	82944963	82945352	+	0	NA	intron (Nintron (N	-44241	NR_034077	1E+08	Hs.72891E	ENSG000000000000	THAP9-AS1	THAP9 antncrRNA
chr4-8804 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr4	88047418	88047617	+	0	NA	intron (NAluJo SIN	39882	NR_15648E	5311	Hs.18127E	ENSG000000000000	PKD2	APKD2 PC2 polycyst protein-coding
chr4-159 6.402296	-0.86014	0.935304	-0.91963	0.357764	0.981636	chr4	1.59E+08	1.59E+08	+	0	NA	in							



chr17-48	7.88873	0.771257	0.841093	0.916969	0.359159	0.981636	chr17	4890647	4891128	+	0	NA	intron (Nintron (N	-8649 NM_001144	1E+08	Hs.57924	ENSG000001C7orf107	chromosonprotein-coding
chr20-315	7.88873	0.771257	0.841093	0.916969	0.359159	0.981636	chr20	31945731	31946423	+	0	NA	intron (Nintron (N	5969 NM_03081E	81572	Hs.43575E	ENSG00000PDRG1	C20orf12E p53 and Iprotein-coding
chr12-101	3.948294	-1.08071	1.178632	-0.91692	0.359184	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	exon (NM_exon (NM	41477 NM_01450E	27340	Hs.29573E	ENSG00000UTP20	1A6/DRIM UTP20 smε protein-coding
chr2-175	3.948294	-1.08071	1.178632	-0.91692	0.359184	0.981636	chr2	1.76E+08	1.76E+08	+	0	NA	intron (Nintron (N	65178 NM_03065E	80856	Hs.209561E	ENSG00000LNPK	K1AA1715 lunapark, protein-coding
chr20-37	3.948294	-1.08071	1.178632	-0.91692	0.359184	0.981636	chr20	37035042	37036082	+	0	NA	intron (Nintron (N	60435 NM_00132E	5933	Hs.20774E	ENSG00000RBL1	CPI07 PRE RB transcrprotein-coding
chr3-141	3.948294	-1.08071	1.178632	-0.91692	0.359184	0.981636	chr3	1.42E+08	1.42E+08	+	0	NA	intron (N(AT)n Sin	33680 NM_00130E	5922	Hs.98445	ENSG00000CRASA2	GAP1M RAS p21 fprotein-coding
chr5-807	3.948294	-1.08071	1.178632	-0.91692	0.359184	0.981636	chr5	80729208	80729765	+	0	NA	intron (Nintron (N	-74503 NM_000791	1719	Hs.592364E	ENSG00000DHR	DHFRP1 Dy dihydrofrc protein-coding
chr6-1754	3.948294	-1.08071	1.178632	-0.91692	0.359184	0.981636	chr6	17547802	17549461	+	0	NA	intron (N(LIME3Cz L	-37366 NR_110855	1.02E+08	Hs.62287E	ENSG00000LOC10192E	uncharactncRNA
chr12-62	7.880873	0.773372	0.843632	0.916718	0.359291	0.981636	chr12	6233315	6233777	+	0	NA	intron (Nintron (N	33146 NM_00176E	928	Hs.11428E	ENSG00000CCD9	BTCC-1 DFCD9 molecprotein-coding
chr9-598	10.68366	0.664315	0.72496	0.916346	0.359485	0.981636	chr9	5982467	5982756	+	0	NA	intron (NMSTC LTR	-25215 NM_039811	1.01E+08	NR_039811	ENSG00000MIR4665	mir-4665 microRNA ncRNA
chr5-4947	40.69938	0.394087	0.430122	0.916221	0.359551	0.981636	chr5	49479027	49479228	+	0	NA	IntergeniALR/Alphe	962161 NM_19844E	133418	Hs.561411E	ENSG00000EMB	GP70 embigin protein-coding
chr16-43	9.845775	-0.68923	0.752367	-0.91608	0.359623	0.981636	chr16	4301766	4301980	+	0	NA	IntergeniAluSc8 SI	-12888 NM_00131E	84662	Hs.592087E	ENSG00000GLIS2	NKL NHPH7GLIS fami protein-coding
chr19-76	8.039423	0.789434	0.862024	0.915791	0.359776	0.981636	chr19	7622252	7622568	+	0	NA	exon (NM_exon (NM	4971 NR_10685E	1.02E+08	NR_10685E	ENSG00000MIR6792	hsa-mir-ε microRNA ncRNA
chr3-1461	6.369015	-0.86681	0.946522	-0.91579	0.359777	0.981636	chr3	1.46E+08	1.46E+08	+	0	NA	intron (N(LIPAS LIN	-43057 NR_146297	1.1E+08	NR_146297	ENSG00000LNC5RRLR	lncRNA-ε lncRNA scncRNA
chr3-172	6.369015	-0.86681	0.946522	-0.91579	0.359777	0.981636	chr3	1.73E+08	1.73E+08	+	0	NA	intron (Nintron (N	54656 NM_00134E	1894	Hs.51829E	ENSG00000ECT2	ARHGFE31 epitheliε protein-coding
chr15-98	6.163247	0.870983	0.951134	0.915731	0.359808	0.981636	chr15	98834324	98834540	+	0	NA	intron (Nintron (N	50006 NR_039864	1.01E+08	NR_039864	ENSG00000MIR4714	uncharactncRNA
chr17-63	6.163247	0.870983	0.951134	0.915731	0.359808	0.981636	chr17	63086494	63086750	+	0	NA	intron (N(LIMCa LIN	120404 NM_02518E	26115	Hs.41088E	ENSG00000TANC2	ROLSA rol tetraatric protein-coding
chr22-21	6.163247	0.870983	0.951134	0.915731	0.359808	0.981636	chr22	21691658	21691866	+	0	NA	intron (Nintron (N	25750 NM_14817E	23759	Hs.438587E	ENSG00000PPL12	CYC4 CYPε peptidyl protein-coding
chr1-171	10.69938	0.661195	0.722154	0.915587	0.359884	0.981636	chr1	1.72E+08	1.72E+08	+	0	NA	exon (NM_exon (NM	47006 NM_01517E	23215	Hs.494641E	ENSG00000PRRC2C	BAT2-iso proline i protein-coding
chr19-121	10.69938	0.661195	0.722154	0.915587	0.359884	0.981636	chr19	12179842	12193133	+	0	NA	intron (Nintron (N	-8528 NR_10417E	1E+08	Hs.66260E	ENSG00000LOC10028E	uncharactncRNA
chr1-233	8.094683	-0.76172	0.831958	-0.91557	0.359892	0.981636	chr1	2.33E+08	2.33E+08	+	0	NA	intron (N(L2b LINE	43598 NM_00132E	80003	Hs.37060E	ENSG00000PCNX2	PCNXL2 pecanex 2 protein-coding
chr16-21	8.094683	-0.76172	0.831958	-0.91557	0.359892	0.981636	chr16	2152522	2154467	+	0	NA	3' UTR (N3' UTR (N	1611 NR_00273E	26788	NR_00273E	ENSG00000SNORD60	RNU60 U6C small nucsnRNA
chr17-14	8.094683	-0.76172	0.831958	-0.91557	0.359892	0.981636	chr17	1461950	1462219	+	0	NA	IntergeniAluSx4 SI	-5852 NM_00520E	1398	Hs.46189E	ENSG00000CCRK	CRK1I p3ε CRK protc protein-coding
chr3-532	8.094683	-0.76172	0.831958	-0.91557	0.359892	0.981636	chr3	53244093	53244292	+	0	NA	intron (Nintron (N	11830 NM_001064	7086	Hs.89643	ENSG00000TKT	HML-5-48 transketc protein-coding
chr3-150	8.094683	-0.76172	0.831958	-0.91557	0.359892	0.981636	chr3	1.51E+08	1.51E+08	+	0	NA	intron (NAluJb SIN	-27159 NM_01627E	51714	Hs.36905E	ENSG00000SELENOT	SELT selenoprc protein-coding
chr1-1457	10.17736	0.683668	0.746897	0.915344	0.360011	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	intron (N(SVA_D Ret	48279 NR_10384E	11126	Hs.488237E	ENSG00000CD160	BY55 NK1 CD160 mol protein-coding
chr2-190	8.069259	-0.76847	0.839695	-0.91518	0.360097	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (Nintron (N	9758 NM_01490E	2744	Hs.11644E	ENSG00000GLS	AAD20 CAS glutaminε protein-coding
chrX-103	8.069259	-0.76847	0.839695	-0.91518	0.360097	0.981636	chrX	1.03E+08	1.03E+08	+	0	NA	exon (NM_exon (NM	1338 NM_00100E	51186	Hs.533287E	ENSG00000TCEAL9	WBP5 WEXε transcrip protein-coding
chr5-1057	3.889589	-1.10683	1.209545	-0.91508	0.360149	0.981636	chr5	10573999	10574509	+	0	NA	intron (Nintron (N	10184 NM_001164	651746	Hs.26039	ENSG00000ANKRD33B	- ankryn i protein-coding
chr22-23	8.013999	0.784418	0.857254	0.915035	0.360173	0.981636	chr22	23261397	23262176	+	0	NA	promoter-promoter-	-981 NR_03340E	26226	Hs.72958E	ENSG00000FBXW4P1	FBW3 FBXW f-box anc pseudo
chr1-268	10.28692	0.697832	0.762711	0.914937	0.360225	0.981636	chr1	26888041	26888405	+	0	NA	intron (Nintron (N	2060 NM_01806E	54707	Hs.14333	ENSG00000GPN2	ATPBD1B GPN-loop protein-coding
chr10-73	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr10	73174276	73182877	+	0	NA	intron (Nintron (N	10682 NM_17334E	317662	Hs.408577E	ENSG00000FAM149B1	K1AA0974 family wiprotein-coding
chr12-507	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr12	50704568	50704982	+	0	NA	intron (NAluSx SIN	-59326 NM_005171	466	Hs.64856E	ENSG00000ATF1	EWS-ATF1 activat i protein-coding
chr13-11	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	3' UTR (N3' UTR (N	1164 NR_10704E	1.02E+08	NR_10704E	ENSG00000MIR8075	hsa-mir-ε microRNA ncRNA
chr16-27	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr16	2707447	2708801	+	0	NA	3' UTR (N3' UTR (N	12100 NM_00131E	83886	Hs.33287E	ENSG00000PRSS27	CAPH2 MPN serine i protein-coding
chr22-207	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr22	20763583	20765397	+	0	NA	intron (Nintron (N	-9623 NM_00018E	3053	Hs.47427E	ENSG00000SERPIND1	D22S673 ε serpin fε protein-coding
chr5-735	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr5	73559086	73562778	+	0	NA	intron (N(LIMA7 LIN	4707 NM_02303E	57763	Hs.239154E	ENSG00000ANKRA2	ANKRA ankryn i protein-coding
chr6-108	8.451882	0.737582	0.806312	0.91476	0.360318	0.981636	chr6	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	16278 NM_00119E	27244	Hs.59133E	ENSG00000SESNI	PA26 SES1ε sertrin i protein-coding
chr8-730	8.436166	0.741541	0.810752	0.914634	0.360384	0.981636	chr8	73055672	73055910	+	0	NA	IntergeniLIP6 LIN	37381 NR_15322E	157689	Hs.43904E	ENSG00000SBSPON	C8orf84 somatomec protein-coding
chr9-682	11.55573	-0.64133	0.701303	-0.91449	0.360459	0.981636	chr9	68259448	68259728	+	0	NA	intron (NAluSz SIN	17643 NM_20145E	445571	Hs.645337E	ENSG00000CBWD3	ba561023. COBW domε protein-coding
chr1-149	12.92931	0.607376	0.664413	0.914155	0.360636	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	25476 NM_001277	400818	Hs.44508E	ENSG00000NBPF9	AE01 NBPF memε protein-coding
chr18-29	9.284473	-0.73422	0.803446	-0.91384	0.360801	0.981636	chr18	2936563	2936796	+	0	NA	intron (NAluJb SIN	9944 NR_02665E	727896	Hs.67312E	ENSG00000LOC72789E	- cysteine pseudo
chr12-76	9.812493	-0.6934	0.759456	-0.91302	0.36123	0.981636	chr12	76856528	76857576	+	0	NA	IntergeniMLT1G3 LI	21967 NM_001321	1466	Hs.530904E	ENSG00000CSR2P	CRP2 LMOε cysteine protein-coding
chr15-64	7.92987	0.7718	0.845508	0.912823	0.361335	0.981636	chr15	64863407	64863633	+	0	NA	intron (N(TG)n Sin	21605 NM_025201	80301	Hs.709337E	ENSG00000PLEKH02	PLEKH01 Fpleckstr i protein-coding
chr15-65	7.92987	0.7718	0.845508	0.912823	0.361335	0.981636	chr15	65667535	65668222	+	0	NA	intron (Nintron (N	24999 NM_001254	9187	Hs.17309E	ENSG00000SLC24A1	CSNB21 Fshleckstr cε protein-coding
chr10-50	9.894772	-0.68761	0.753496	-0.91256	0.361473	0.981636	chr10	50095447	50095676	+	0	NA	intron (Nintron (N	27607 NM_00100E	387680	Hs.36528E	ENSG00000WASHC2A	PMA21A Fε WASH comε protein-coding
chr10-10	10.6661	0.659013	0.722264	0.912426	0.361544	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	17915 NM_01497E	22984	Hs.23949E	ENSG00000PDCD11	ALG-4 ALC programε protein-coding
chr19-12	10.6661	0.659013	0.722264	0.912426	0.361544	0.981636	chr19	12349425	12354224	+	0	NA	intron (Nintron (N	13859 NM_030824	79973	Hs.25319E	ENSG00000ZNF442	- zinc fing protein-coding
chr16-70	8.169104	-0.75304	0.825389	-0.91234	0.36159	0.981636	chr16	70028698	70029000	+	0	NA	intron (NAluSx SIN	-1497 NR_03626E	1E+08	NR_03626E	ENSG00000MIR1972-2	microRNA ncRNA
chr3-1421	8.169104	-0.75304	0.825389	-0.91234	0.36159	0.981636	chr3	1.42E+08	1.42E+08	+	0	NA	intron (Nintron (N	26885 NM_00103E	256356	Hs.135904E	ENSG00000CGK5	- glycerolε protein-coding
chr5-957	9.879056	-0.68512	0.751131	-0.91212	0.361706	0.981636	chr5	95755614	95756539	+	0	NA	intron (N(LIMB3 LIN	-23974 NM_00134E	83890	Hs.50499	ENSG00000SPATA9	NYD-SP16 spermatogε protein-coding
chr5-141	9.879056	-0.68512	0.751131	-0.91212	0.361706	0.981636	chr5	1.41E+08	1.41E+08	+	0	NA	TTS (NM_C TTS (NM_C	3284 NM_00564E	6879	Hs.43883E	ENSG00000TAF7	TAF2F TAF TATA-box protein-coding
chr19-217	6.435578	-0.85338	0.93627	-0.91147	0.362049	0.981636	chr19	21758570	21759304	+	0	NA	intron (Nintron (N	8192 NR_02452E	641367	Hs.68012E	ENSG00000LOC64136E	cyclin Y pseudo
chr16-37	7.896588	0.769053	0.843887	0.911323	0.362125	0.981636	chr16	375861	3762									

chr7-7697	6.91931	-0.79236	0.873754	-0.90684	0.364489	0.981636	chr7	76972579	76972819	+ 0 NA	Intergeni	Intergeni	-8123 NR_023388	441263 Hs. 675888NR_023388	ENS000000	DTX2P1-UF	PMS2L11	DTX2P1-UF	pseudo		
chr1-4395	8.45974	0.735585	0.811201	0.906785	0.36452	0.981636	chr1	43956343	43957113	+ 0 NA	intron (N	intron (N	9778 NM_014652	9670 Hs. 158497NM_014652	ENS000000	IPO13	IMP13	KAF	importin protein-coding		
chr11-944	8.45974	0.735585	0.811201	0.906785	0.36452	0.981636	chr11	94497129	94498438	+ 0 NA	intron (N	intron (N	3799 NM_017704	54851 Hs. 29052 NM_017704	ENS000000	CANKRD49	FGIF	GBIF	ankyrin r protein-coding		
chr14-507	8.45974	0.735585	0.811201	0.906785	0.36452	0.981636	chr14	50728891	50729768	+ 0 NA	intron (N	FAM SINE	-61023 NR_020181E	60485 Hs. 642842NM_020181E	ENS000000	SAV1	SAV	W45	salvador protein-coding		
chr22-355	8.45974	0.735585	0.811201	0.906785	0.36452	0.981636	chr22	35523426	35528162	+ 0 NA	intron (N	FAM SINE	-98426 NR_037471	1.01E+08	NR_037471	ENS000000	MIR3909	miR-3909	microRNA ncRNA		
chr3-524E	8.45974	0.735585	0.811201	0.906785	0.36452	0.981636	chr3	52489385	52490078	+ 0 NA	intron (N	intron (N	-5607 NM_01513E	23166 Hs. 301989NM_01513E	ENS000000	STAB1	miR-CLEVER-1	stabilin	protein-coding		
chr5-476E	8.45974	0.735585	0.811201	0.906785	0.36452	0.981636	chr5	47631951	47633692	+ 0 NA	Intergeni	ALR Alpha	-1936441 NM_021072	348980 Hs. 353177NM_021072	ENS000000	HCN1	BCNG-1	BC	hyperpolarized protein-coding		
chr1-434E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr1	43450883	43451211	+ 0 NA	TTS (NM_C	TTS (NM_C	-2403 NR_046744	1.01E+08	Hs. 619768NR_046744	ENS000000	SZT2-AS1	SZT2	antincRNA		
chr10-742	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr10	74242943	74243319	+ 0 NA	intron (N	LTR28B L1	66368 NM_00136E	132 Hs. 656588NM_00136E	ENS000000	CADK	AK	adenosine	protein-coding		
chr11-45E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr11	45947482	45949078	+ 0 NA	intron (N	intron (N	25624 NM_00130E	120071 Hs. 86543 NM_15231E	ENS000000	LARGE2	GYLLTLB1	FLARIGE	xlprotein-coding		
chr12-56E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr12	56034404	56035335	+ 0 NA	exon (NM	exon (NM	-7049 NM_00102E	6231 Hs. 447562NM_00102E	ENS000000	RPS26	DBA10	S2E	ribosomal protein-coding		
chr19-12E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr19	12605014	12605548	+ 0 NA	intron (N	AluJr SIN	5532 NM_020714	57474 Hs. 655866NM_020714	ENS000000	ZNF490			zinc finger protein-coding		
chr20-34E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr20	34500228	34501614	+ 0 NA	intron (N	L1M2 LINE	-15463 NM_00131E	83658 Hs. 59392NM_01418E	ENS000000	DYNLRB1	BITH	BLP	dynein I1 protein-coding		
chr12-56E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr12	56034404	56035335	+ 0 NA	exon (NM	exon (NM	11505 NM_01673E	3985 Hs. 474596NM_00556E	ENS000000	L1MK2			LIM domain protein-coding		
chr19-12E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr19	12605014	12605548	+ 0 NA	intron (N	AluJr SIN	5532 NM_020714	57474 Hs. 655866NM_020714	ENS000000	ZNF490			zinc finger protein-coding		
chr20-34E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr20	34500228	34501614	+ 0 NA	intron (N	L1M2 LINE	-15463 NM_00131E	83658 Hs. 59392NM_01418E	ENS000000	DYNLRB1	BITH	BLP	dynein I1 protein-coding		
chr12-56E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr12	56034404	56035335	+ 0 NA	exon (NM	exon (NM	11505 NM_01673E	3985 Hs. 474596NM_00556E	ENS000000	L1MK2			LIM domain protein-coding		
chr8-737E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr8	73737080	73737596	+ 0 NA	intron (N	AluSp SIN	9502 NM_001164	27067 Hs. 561815NM_01439E	ENS000000	STAU2	39K2	39K3	staufen c protein-coding		
chr9-999E	8.426458	0.73296	0.808376	0.906706	0.364562	0.981636	chr9	99922547	99922917	+ 0 NA	intron (N	intron (N	16078 NM_01791E	55014 Hs. 704031NM_01791E	ENS000000	STX17			syntactin protein-coding		
chr8-103E	6.394438	-0.85808	0.946559	-0.90652	0.36466	0.981636	chr8	1.03E+08	1.03E+08	+ 0 NA	intron (N	intron (N	6864 NM_01542E	25879 Hs. 532265NM_01542E	ENS000000	CCAF13	GM83	HSPC	DDB1 and protein-coding		
chr13-11E	6.153388	-0.75001	0.827654	-0.90618	0.364838	0.981636	chr13	1.14E+08	1.14E+08	+ 0 NA	intron (N	intron (N	5214 NM_00082C	2621 Hs. 646346NM_00082C	ENS000000	GAS6	AXLLG	AXS	growth ar protein-coding		
chr19-39E	6.153388	-0.75001	0.827654	-0.90618	0.364838	0.981636	chr19	3955850	3956436	+ 0 NA	Intergeni	Intergeni	5369 NR_030367	693222	NR_030367	ENS000000	MIR637	MIRN637	microRNA ncRNA		
chr4-802E	6.153388	-0.75001	0.827654	-0.90618	0.364838	0.981636	chr4	80268090	80268929	+ 0 NA	5' UTR (N	5' UTR (N	244 NM_001291	2250 Hs. 37055 NM_00446E	ENS000000	CGF5	HBGF-5	Sn	fibroblasts protein-coding		
chr3-186E	7.61751	-0.80201	0.885298	-0.90592	0.364978	0.981636	chr3	1.87E+08	1.87E+08	+ 0 NA	intron (N	AluSx SIN	-6059 NM_017541	1427 Hs. 376209NM_017541	ENS000000	CRYGS	CRYG8	CTF	crystallin protein-coding		
chr7-154E	7.61751	-0.80201	0.885298	-0.90592	0.364978	0.981636	chr7	1.55E+08	1.55E+08	+ 0 NA	TTS (NR_C	TTS (NR_C	21226 NR_02447E	1E+08	Hs. 586358NR_02447E	ENS000000	PAXIPI-AS	PAXIPI10S	PAXIPI	arcncRNA	
chr4-569E	3.907155	-1.08917	1.202454	-0.90579	0.365048	0.981636	chr4	56960533	56961112	+ 0 NA	Intergeni	AluSc SIN	16784 NM_03231E	84273 Hs. 8715 NM_03231E	ENS000000	NOA1	C4orf14	Wnitric	ox protein-coding		
chr6-147E	3.907155	-1.08917	1.202454	-0.90579	0.365048	0.981636	chr6	1.47E+08	1.47E+08	+ 0 NA	intron (N	L1MCI LIN	-15357 NR_03411E	729178 Hs. 557608NR_03411E	STXPB5-AS-	STXPB5	AS-	arcncRNA			
chr14-351E	6.138085	-0.95016	1.049345	-0.90548	0.365212	0.981636	chr14	35169140	35169572	+ 0 NA	intron (N	L1MEF LIN	46804 NM_00125E	9692 Hs. 458487NM_01467E	ENS000000	PRORP	K1AA0391		protein-coding		
chr2-240E	5.138085	-0.95016	1.049345	-0.90548	0.365212	0.981636	chr2	2.41E+08	2.41E+08	+ 0 NA	intron (N	LORI-int	13513 NM_01655E	51281 Hs. 656615NM_01655E	ENS000000	CANKMY1	ZMYND13		ankyrin r protein-coding		
chr5-695E	5.138085	-0.95016	1.049345	-0.90548	0.365212	0.981636	chr5	69589953	69591203	+ 0 NA	intron (N	intron (N	30333 NM_00109E	728340 Hs. 191356NM_00109E	ENS000000	GTF2P2C	GTF2P2C	ZTGT2H2	F protein-coding		
chr11-13E	6.086825	-0.76023	0.839853	-0.90519	0.365365	0.981636	chr11	1.34E+08	1.34E+08	+ 0 NA	intron (N	AluJb SIN	33838 NM_015261	23310 Hs. 438555NM_015261	ENS000000	CAPFD3	CAP-D3	C	non-SMC c protein-coding		
chr2-191E	6.086825	-0.76023	0.839853	-0.90519	0.365365	0.981636	chr2	1.92E+08	1.92E+08	+ 0 NA	non-codir	non-codir	-1682 NR_131917	1.06E+08	Hs. 104972NR_131917	LOC105747-				uncharacterncRNA	
chr16-53E	5.095095	-0.97512	1.077295	-0.90515	0.365384	0.981636	chr16	53443915	53444274	+ 0 NA	intron (N	AluSq2 SI	8475 NM_00132E	5934 Hs. 513605NM_005611	ENS000000	RBL2	P130	Rb2	RB	transcript protein-coding	
chr5-131E	5.095095	-0.97512	1.077295	-0.90515	0.365384	0.981636	chr5	1.31E+08	1.31E+08	+ 0 NA	3' UTR (N	3' UTR (N	129607 NM_00103E	56990 Hs. 508825NM_02024E	ENS000000	CDC42SE2	SPEC2		CDC42	sm protein-coding	
chr12-13E	4.999066	0.94409	1.043056	0.905119	0.365403	0.981636	chr12	1.33E+08	1.33E+08	+ 0 NA	3' UTR (N	3' UTR (N	34210 NM_18323E	1E+08	Hs. 29698 NM_18323E	ENS000000	ZNF605			zinc finger protein-coding	
chr17-50E	4.999066	0.94409	1.043056	0.905119	0.365403	0.981636	chr17	50461462	50463407	+ 0 NA	exon (NM	exon (NM	-5895 NR_11023E	80202 Hs. 288955NM_02514E	ENS000000	ACSF2	ACSMW	AV	acyl-CoA	protein-coding	
chr7-112E	4.999066	0.94409	1.043056	0.905119	0.365403	0.981636	chr7	1126382	1127009	+ 0 NA	intron (N	AluSz SIN	11552 NM_00131E	84310 Hs. 653255NM_03235E	ENS000000	C7orf50	YCRO16W		chromosom	protein-coding	
chr10-45E	6.887327	-0.80903	0.893875	-0.90508	0.365422	0.981636	chr10	45761483	45762034	+ 0 NA	intron (N	intron (N	34492 NM_001367	253725 Hs. 365286NM_01526E	ENS000000	WASHC2C	FAM21A1	FA	WASH	com protein-coding	
chr4-253E	6.887327	-0.80903	0.893875	-0.90508	0.365422	0.981636	chr4	25315291	25316108	+ 0 NA	intron (N	L1MB4 LIN	2925 NM_00131E	29063 Hs. 27894E	ENS000000	ZCHC4	FSPC052	Z	zinc finger protein-coding		
chr9-950E	6.887327	-0.80903	0.893875	-0.90508	0.365422	0.981636	chr9	95026616	95027093	+ 0 NA	intron (N	intron (N	-38496 NR_10672E	1.02E+08	NR_10672E	ENS000000	MIR6081	hsa-mir-6	microRNA ncRNA		
chrX-701E	6.887327	-0.80903	0.893875	-0.90508	0.365422	0.981636	chrX	70151876	70152869	+ 0 NA	intron (N	L1MEF LIN	18437 NM_00137E	3476 Hs. 496267NM_00155E	ENS000000	IGBP1	ALPHA-4	I	immunogl	protein-coding	
chr6-149E	5.112661	-0.96214	1.062188	-0.90496	0.365487	0.981636	chr6	1.5E+08	1.5E+08	+ 0 NA	intron (N	L1ME3F LI	-30208 NM_001204	11104 Hs. 45017E	NM_007044	ENS000000	KATNAL1			katanin	protein-coding
chr1-100E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr1	1.01E+08	1.01E+08	+ 0 NA	intron (N	AluJb SIN	16499 NM_001144	148867 Hs. 53390E	NM_13349E	ENS000000	SLC30A7	ZNT7	ZnT	solute c protein-coding	
chr12-28E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr12	2803548	2803923	+ 0 NA	3' UTR (N	3' UTR (N	8765 NM_002014	2288 Hs. 52418E	NM_002014	ENS000000	FKBP4	FKBP51	FK	FKBP	prol protein-coding
chr12-76E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr12	76043080	76044753	+ 0 NA	TTS (NM_C	TTS (NM_C	-12140 NM_00735E	22822 Hs. 62088E	NM_00735E	ENS000000	PHLDA1	IT1B11	I	pleckstrin	protein-coding
chr15-81E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr15	81002987	81004040	+ 0 NA	3' UTR (N	3' UTR (N	2590 NM_02256E	59274 Hs. 513071NM_02256E	ENS000000	TLNRD1	MESDC1		talin	ro protein-coding	
chr19-45E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr19	45084572	45085524	+ 0 NA	TTS (NR_C	TTS (NR_C	5343 NR_134887	1.05E+08	Hs. 66269E	NR_134887	ENS000000	GEM1NT-AS-	GEM1NT	arcncRNA	
chr2-111E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr2	1.11E+08	1.11E+08	+ 0 NA	intron (N	intron (N	1699 NR_03963E	1.01E+08	NR_03963E	ENS000000	MIR4435-2	mir-4435	microRNA ncRNA		
chr2-237E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr2	2.38E+08	2.38E+08	+ 0 NA	intron (N	intron (N	18242 NM_001137	9208 Hs. 47177E	NR_00473E	ENS000000	RFRFP1	FLAP-1	FL	LRR	bindi protein-coding
chr4-147E	6.879469	-0.80727	0.892128	-0.90488	0.365527	0.981636	chr4	1.48E+08	1.48E+08	+ 0 NA	intron (N	LTR12 LTF	67699 NR_03996E	1.01E+08	NR_03996E	ENS000000	MIR4799			microRNA ncRNA	
chr4-147E	6.879469	-0.80727	0.892128	-0.																	



chr5-7748	6.91275	-0.80127	0.890641	-0.89966	0.368302	0.981636	chr5	77487866	77488687	+	0	NA	intron (Nintron (N	4040	NM_01826E	55255	Hs.482572	NM_01826E	ENSG000000WDR41	MSTP048	WD repeatprotein-coding
chr6-7884	6.91275	-0.80127	0.890641	-0.89966	0.368302	0.981636	chr6	7884689	7885597	+	0	NA	intron (Nintron (N	24934	NM_001114F	81567	Hs.150837	NM_02208E	ENSG000000TXND5	ENDOPDI1	E thioredoxinprotein-coding
chr7-6507	6.91275	-0.80127	0.890641	-0.89966	0.368302	0.981636	chr7	65071632	65073054	+	0	NA	intron (Nintron (N	1805	NR_14571E	1.1E+08	NR_14571E	ENSG000000SNORA15B-		small nucsnRNA	
chr9-3364	6.91275	-0.80127	0.890641	-0.89966	0.368302	0.981636	chr9	33940727	33941523	+	0	NA	intron (Nintron (N	-6750	NR_10237C	1.01E+08	NR_10237C	ENSG000000SNORD121E		small nucsnRNA	
chr11-8678	6.112248	-0.75531	0.837588	-0.89962	0.368322	0.981636	chr11	86027518	86162764	+	0	NA	intron (NAluJr SIN	41443	NM_00716E	8301	Hs.16389E	NM_00716E	ENSG000000PICALM	CALM CLTF	phosphatidprotein-coding
chr1-1514	7.904446	0.766701	0.852266	0.899603	0.368332	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (NAluJb SIN	3389	NM_207171	23126	Hs.48987E	NM_01510C	ENSG000000POGZ	MRD37 WHS	pogo trar protein-coding
chr19-1576	6.16813	0.540514	0.600847	0.899587	0.36834	0.981636	chr19	57975854	57989843	+	0	NA	intron (NAluJr4 S1	-8314	NM_152474	147685	Hs.13420E	NM_152474	ENSG000000C19orf18		chromosomprotein-coding
chr11-175	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr11	17304972	17305789	+	0	NA	intron (NLM5 LINE	28410	NM_00135E	4925	Hs.65459E	NM_00501E	ENSG000000NUCB2	HEL-S-10E	nucleobir protein-coding
chr11-122	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	3' UTR (N3' UTR (N	-28447	NM_019604	56253	Hs.15952E	NM_019604	ENSG000000CCTAM	CD355	cytotoxicprotein-coding
chr15-806	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr15	80852846	80853610	+	0	NA	intron (NMLT10 LTF	-11155	NR_00303E	693132	NR_03039E	ENSG000000MIR549A	MIR549	miRNA ncRNA	
chr16-532	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr16	53222013	53222417	+	0	NA	intron (NAluSq2 S1	13764	NM_00135E	80205	Hs.59159	NR_01528E	ENSG000000CHD9	AD013 CHE	chromodnonprotein-coding
chr17-816	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr17	81862286	81863284	+	0	NA	IntergeniAluSx SIN	-2250	NM_00091E	5034	Hs.46433E	NM_00091E	ENSG000000CP4HB	CLCRP1 DS	prolyl 4-protein-coding
chr19-195	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr19	19915541	19920539	+	0	NA	intron (NLP1A5 LIN	17094	NM_03121E	81931	Hs.30105E	NM_03121E	ENSG000000ZNF93	HPF34 HTF	zinc fingprotein-coding
chr3-1544	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr3	15442675	15443002	+	0	NA	TTS (NM_C TTS (NM_C	15240	NM_03308E	85403	Hs.71673E	NM_03308E	ENSG000000EAF1		ELL assocprotein-coding
chr4-1223	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-50557	NM_13924E	132612	Hs.51895E	NM_13924E	ENSG000000ADAD1	Tenr	adenosineprotein-coding
chr4-1511	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr4	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	22249	NR_000007	8944	NR_000007	ENSG000000SNORD73A	RNU73 RNU	small nucsnRNA	
chr6-3746	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr6	37465357	37466816	+	0	NA	intron (NLM5E LIN	32865	NM_01505C	23070	Hs.52010E	NM_01505C	ENSG000000CMCR1	FTS JDS2 K1	cap nucsnRNA
chr7-840	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr7	84066704	84067618	+	0	NA	intron (NLP1A2 LIN	127628	NM_00608C	10371	Hs.252451	NM_00608C	ENSG000000SEMA3A	COLL1 HHI	semaphorinprotein-coding
chr7-1076	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr7	1.08E+08	1.08E+08	+	0	NA	intron (NLM1A4 LIN	20735	NM_00010E	1738	Hs.131711	NM_00010E	ENSG000000DLD	DLDD DLDF	dihydroliprotein-coding
chr8-2332	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr8	23320350	23323902	+	0	NA	intron (Nintron (N	-14082	NR_03832E	1.01E+08	Hs.66113C	NR_03832E	ENSG000000CLOC100507-		uncharactncRNA
chr9-3242	6.904892	-0.79955	0.8889	-0.89948	0.368398	0.981636	chr9	32420615	32425387	+	0	NA	intron (Nintron (N	38358	NM_00136E	48	Hs.56722E	NM_00219E	ENSG000000AC01	ACONS HEL	aconitaseprotein-coding
chr19-124	11.20382	0.635748	0.706931	0.899308	0.368489	0.981636	chr19	12428903	12432003	+	0	NA	exon (NM exon (NM	10568	NM_00581E	10224	Hs.63689E	NM_00581E	ENSG000000ZNF443	ZK1	zinc fingprotein-coding
chr1-1251	6.220103	0.86578	0.963219	0.89884	0.368738	0.981636	chr1	12576803	12577677	+	0	NA	intron (Nintron (N	1783	NR_10678E	1.02E+08	NR_10678E	ENSG000000MIR6730	hsa-mir-ε	microRNA ncRNA	
chr12-126	6.220103	0.86578	0.963219	0.89884	0.368738	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	exon (NM exon (NM	29975	NM_00127C	10645	Hs.29734E	NM_00654E	ENSG000000CAMK2C	CAMK2	CaM calcium/cprotein-coding
chr15-313	6.220103	0.86578	0.963219	0.89884	0.368738	0.981636	chr15	31380937	31381564	+	0	NA	intron (NMLT1D LTF	54415	NM_00130E	51621	Hs.37644E	NM_01599E	ENSG000000KLF13	BTEB3 FKI	Kruppel lprotein-coding
chr1-1235	8.434316	0.730925	0.813281	0.898736	0.368793	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniAluR/Alpha	2395909	NR_00395E	647211	Hs.69768E	NR_00395E	ENSG000000EMBPI1		embigin pseudo
chr19-140	8.434316	0.730925	0.813281	0.898736	0.368793	0.981636	chr19	40369893	40370927	+	0	NA	TTS (NR_1 TTS (NR_1	564	NR_10685E	1.02E+08	NR_10685E	ENSG000000MIR6796	hsa-mir-ε	microRNA ncRNA	
chr7-1288	8.434316	0.730925	0.813281	0.898736	0.368793	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	13642	NM_001367	64753	Hs.52117E	NM_02274E	ENSG000000CCDC136	NAG6	coiled-ccprotein-coding
chr16-743	8.14553	-0.74841	0.83274	-0.89873	0.368797	0.981636	chr16	74339017	74339216	+	0	NA	intron (NAluSp SIN	29139	NR_02695C	283922	Hs.55872E	NR_02695C	ENSG000000LOC283922		pyruvate pseudo
chr15-632	11.23895	0.646147	0.719077	0.898577	0.368878	0.981636	chr15	63303213	63303514	+	0	NA	intron (NLM1E3A LI	25758	NM_031301	83464	Hs.51170E	NM_031301	ENSG000000APH1B	APH-1B PF	aph-1 honprotein-coding
chr15-523	10.71509	0.658052	0.732353	0.898545	0.368895	0.981636	chr15	52374406	52375792	+	0	NA	intron (NAluJr SIN	-79295	NR_01872E	55930	Hs.48703E	NM_01872E	ENSG000000MY05C		myosin Vprotein-coding
chr3-1953	8.973894	0.707334	0.787327	0.8984	0.368972	0.981636	chr3	1.95E+08	1.95E+08	+	0	NA	intron (NAluV SINE	10123	NM_152531	152002	Hs.478741	NM_152531	ENSG000000XXYL11	C3orf21	lysidine protein-coding
chr1-3785	8.493021	0.733104	0.821746	0.898333	0.369008	0.981636	chr1	3785673	3787053	+	0	NA	intron (NAluSz SIN	-30135	NM_02071C	57470	Hs.26848E	NM_02071C	ENSG000000LRR4C7		leucine rprotein-coding
chr10-207	8.393176	0.730265	0.812947	0.898293	0.369029	0.981636	chr10	207384	207995	+	0	NA	intron (NLP1A3 LIN	27695	NM_00120E	10771	Hs.29226E	NM_00662E	ENSG000000ZMYND11	BRAM1 BS	zinc fingprotein-coding
chr4-159	8.393176	0.730265	0.812947	0.898293	0.369029	0.981636	chr4	1.59E+08	1.59E+08	+	0	NA	intron (NAluSx4 S1	56225	NM_001351	9693	Hs.74488E	NM_01424E	ENSG000000RAGPEF2	CNrasGEF Rap	guaniprotein-coding
chr18-585	8.981751	0.705455	0.785376	0.898243	0.369056	0.981636	chr18	58979233	58980157	+	0	NA	intron (Nintron (N	-55984	NR_024021	390858	Hs.71628E	NR_024021	OACVLP2		o-acetyl pseudo
chr10-101	4.973642	0.936658	1.043134	0.897927	0.369225	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	35640	NM_02203E	6468	Hs.50082E	NM_02203E	ENSG000000FBXW4	DAC FBW4 F	box ancprotein-coding
chr17-17	4.973642	0.936658	1.043134	0.897927	0.369225	0.981636	chr17	1732838	1734023	+	0	NA	intron (NMIR SINE	8599	NM_00116E	124997	Hs.23457E	NM_15234E	ENSG000000WDR81	CAMRQ2 HY	WD repeatprotein-coding
chr2-142	4.973642	0.936658	1.043134	0.897927	0.369225	0.981636	chr2	1.48E+08	1.48E+08	+	0	NA	intron (NHERVL18-1	-23212	NM_18174E	5000	Hs.55836E	NM_00255E	ENSG000000ORC4	ORC4 ORC	origin rprotein-coding
chr2-2322	4.973642	0.936658	1.043134	0.897927	0.369225	0.981636	chr2	2.32E+08	2.32E+08	+	0	NA	intron (Nintron (N	91786	NR_03028E	693147	NR_03028E	ENSG000000MIR562	MIRN562 f	microRNA ncRNA	
chr10-406	19.15579	0.530922	0.591938	0.896922	0.369761	0.981636	chr10	40683400	40683650	+	0	NA	IntergeniAluR/Alpha	1684520	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000000LOC441666-		zinc fingpseudo
chr5-7835	5.204648	-0.93315	1.040427	-0.89689	0.369777	0.981636	chr5	78357492	78358151	+	0	NA	TTS (NR_1 TTS (NR_1	2866	NR_105014	728769	Hs.58619E	NR_105014	ENSG000000SCAMP11A6E-		SCAMP1 arncRNA
chr5-1313	5.204648	-0.93315	1.040427	-0.89689	0.369777	0.981636	chr5	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	126018	NM_00103E	56990	Hs.50882E	NM_02024E	ENSG000000CDC42SE2	SPEC2	CDC42 smεprotein-coding
chr9-1107	9.753788	-0.70366	0.784759	-0.89665	0.369904	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	89084	NM_001351	1902	Hs.12666E	NM_001401	ENSG000000LPAR1	EDG2 GPR	ε lysophosphprotein-coding
chr12-718	6.05137	-0.72114	0.80435	-0.89655	0.369961	0.981636	chr12	71771993	71772375	+	0	NA	intron (NMLT1H LTF	17321	NM_01499E	23011	Hs.52459E	NM_01499E	ENSG000000RAB21		RAB21, mεprotein-coding
chr5-1110	10.31509	-0.66211	0.73856	-0.89649	0.36999	0.981636	chr5	1.11E+08	1.11E+08	+	0	NA	non-codiron-codir	3763	NM_138551	85480	Hs.38987E	NM_03303E	ENSG000000TSLP		thymic stprotein-coding
chr11-463	8.597279	-0.71969	0.802975	-0.89628	0.370103	0.981636	chr11	46321623	46322773	+	0	NA	TTS (NM_C TTS (NM_C	-10728	NM_20153E	8525	Hs.502461	NM_00364E	ENSG000000DGKZ	DAGK5 DAC	diacylglyprotein-coding
chr11-123	8.597279	-0.71969	0.802975	-0.89628	0.370103	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	42717	NM_001301	23365	Hs.24598	NM_01531E	ENSG000000ARHGEF12	ARG PRO2	Rho guaniprotein-coding
chr1-1024	6.716691	0.809181	0.902912	0.89619	0.370151	0.981636	chr1	1034912	1035579	+	0	NA	intron (Nintron (N	1252	NM_001364	375790	Hs.273331	NM_01985E	ENSG000000AGRN	LAGRN CMS	agrin protein-coding
chr1-17																					



chr7-1571	6.863753	-0.80384	0.898466	-0.89468	0.370958	0.981636	chr7	1.57E+08	1.57E+08	0	NA	intron (Nintron (N	31945	NM_014671	9690	Hs.118351NM_014671	ENSG000003CUBE3C	HECTH2	ubiquitin protein-coding					
chr8-1033	6.863753	-0.80384	0.898466	-0.89468	0.370958	0.981636	chr8	1.03E+08	1.03E+08	0	NA	intron (HAL LINE	6844	NR_145795	1.1E+08	NR_145795	SNORD173	-	small nucleolar RNA					
chr9-2186	6.863753	-0.80384	0.898466	-0.89468	0.370958	0.981636	chr9	21862022	21862548	+	0	NA	3' UTR (N3' UTR (N	59649	NM_002451	4507	Hs.193266NM_002451	ENSG000003MTAP	BDMF DMSF methyltransferase protein-coding					
chr1-155	8.956328	0.70106	0.783638	0.894622	0.370989	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (Nintron (N	-1161	NR_030282	693140	NR_030282	ENSG000003MIR555	Hsnr555 microRNA ncRNA					
chr17-427	8.956328	0.70106	0.783638	0.894622	0.370989	0.981636	chr17	42716303	42718633	+	0	NA	intron (Nintron (N	-9317	NR_106838	1.02E+08	NR_106838	ENSG000003MIR6780A	hsa-mir-6780a microRNA ncRNA					
chr17-64	8.956328	0.70106	0.783638	0.894622	0.370989	0.981636	chr17	64068710	64071231	+	0	NA	intron (MLT1H LTF	-49336	NM_001095	3384	Hs.431466NM_000872	ENSG000003ICAM2	CD102	intercellular protein-coding				
chr2-1098	8.956328	0.70106	0.783638	0.894622	0.370989	0.981636	chr2	1.1E+08	1.1E+08	+	0	NA	intron (NLIME1 LIN	-46840	NR_038099	1E+08	Hs.535619NM_001202	ENSG000003LIMS4	LIMS3L	LIM zinc finger protein-coding				
chr7-1587	8.956328	0.70106	0.783638	0.894622	0.370989	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	intron (Nintron (N	-32507	NR_104054	54892	Hs.18616	NR_017766	ENSG000003NCAPG3	K3S CAP-Conn-SMC	protein-coding			
chr2-1113	8.579713	-0.72754	0.813692	-0.89413	0.371254	0.981636	chr2	1.11E+08	1.11E+08	+	0	NA	intron (MLT1H LI	-43387	NR_039634	1.01E+08	NR_039634	ENSG000003MIR4435-1	mir-4435	microRNA ncRNA				
chr6-332	8.579713	-0.72754	0.813692	-0.89413	0.371254	0.981636	chr6	33257244	33257476	+	0	NA	intron (NLIME1 LIN	7824	NR_044997	414765	Hs.675862NR_044997	ENSG000003HCG25	d1J033B1 HLA	compncRNA				
chr4-1228	6.693117	0.816772	0.913517	0.894097	0.37127	0.981636	chr4	1.23E+08	1.23E+08	+	0	NA	intron (NLTR8A LTF	8464	NM_001361	2247	Hs.284244NM_002006	ENSG000003PGF2	BFGF FGF	fibroblast protein-coding				
chr6-1192	6.693117	0.816772	0.913517	0.894097	0.37127	0.981636	chr6	1.19E+08	1.19E+08	+	0	NA	intron (NTiger3b	-53558	NM_001288	79632	Hs.443788NM_024581	ENSG000003FAM184A	C6orf60	family wiprotein-coding				
chr9-344	4.45163	1.023933	1.145232	0.894084	0.371277	0.981636	chr9	34438113	34438647	+	0	NA	intron (NLTR12C LI	203259	NM_147202	203259	Hs.493771NM_147202	ENSG000003FAM219A	C9orf25	family wiprotein-coding				
chr17-295	10.30723	-0.66091	0.739302	-0.89397	0.371339	0.981636	chr17	29262010	29262353	+	0	NA	3' UTR (N3' UTR (N	15324	NM_005208	1411	Hs.46275	NM_005208	ENSG000003CRYBA1	CRYB1 CTF	crystallin protein-coding			
chr12-781	8.571855	-0.72606	0.812304	-0.89383	0.371411	0.981636	chr12	78140036	78140255	+	0	NA	intron (Nintron (N	219601	NR_135021	1.05E+08	Hs.156899NR_135021	ENSG000003LINC02424	-	long intencRNA				
chr1-8495	4.957926	0.943581	1.055658	0.893832	0.371412	0.981636	chr1	8499674	8500648	+	0	NA	intron (N(AAC)n SI	-5248	NR_132752	1.07E+08	NR_132752	SNORD128	ZL43	small nucleolar RNA				
chr10-68	8.63056	-0.71496	0.800094	-0.89359	0.371541	0.981636	chr10	68055462	68056607	+	0	NA	intron (NALuSx SIN	19249	NM_001278	26091	Hs.51891	NM_015601	ENSG000003CHERCA	-	HECT and protein-coding			
chr16-30	8.63056	-0.71496	0.800094	-0.89359	0.371541	0.981636	chr16	30059650	30060244	+	0	NA	intron (NMIRb SINE	-4332	NM_184043	226	Hs.513499NM_000034	ENSG000003ALDOA	ALDA GSDI	aldolase, protein-coding				
chr17-285	8.63056	-0.71496	0.800094	-0.89359	0.371541	0.981636	chr17	28583214	28583945	+	0	NA	exon (NM exon (NM	-6684	NM_005166	230	Hs.155247NM_005166	ENSG000003ALDOC	ALDC	aldolase, protein-coding				
chr12-661	10.28967	-0.66745	0.747079	-0.89341	0.371636	0.981636	chr12	66136735	66136934	+	0	NA	TTS (NM_TTS (NM_C	6083	NR_125724	1.04E+08	Hs.504822NR_125724	ENSG000003LLPH-DT	LLPH-AS1	LLPH divncRNA				
chr1-8393	8.622703	-0.71353	0.798725	-0.89334	0.371674	0.981636	chr1	83937464	83937710	+	0	NA	intron (NTiger3a	1645	NM_00135C	79739	Hs.445826NM_024688	ENSG000003TLL7	-	tubulin protein-coding				
chr11-657	8.622703	-0.71353	0.798725	-0.89334	0.371674	0.981636	chr11	65718545	65718752	+	0	NA	exon (NM exon (NM	2290	NM_032193	84153	Hs.718438NM_032193	ENSG000003RNA5E2C	AGS3 AYP1	ribonucleoprotein-coding				
chr13-48	8.622703	-0.71353	0.798725	-0.89334	0.371674	0.981636	chr13	48381385	48381924	+	0	NA	intron (Nintron (N	31459	NM_001162	10161	Hs.123464NM_005767	ENSG000003LPAR6	ARWH1 HYF	lysophosphatidase protein-coding				
chr17-281	8.622703	-0.71353	0.798725	-0.89334	0.371674	0.981636	chr17	28134734	28135024	+	0	NA	intron (Nintron (N	-91495	NR_003064	23615	Hs.157199NM_021093	ENSG000003PYY2	-	peptide lyase				
chr1-2065	8.989609	0.70362	0.787658	0.893307	0.371693	0.981636	chr1	2.07E+08	2.07E+08	+	0	NA	intron (Nintron (N	16764	NM_006893	1939	Hs.497581NM_006893	ENSG000003EIF2D	HCA56 LGI	eukaryotic protein-coding				
chr6-3357	8.989609	0.70362	0.787658	0.893307	0.371693	0.981636	chr6	33574406	33577720	+	0	NA	intron (NALuSp SIN	4213	NM_001188	578	Hs.485139NM_001188	ENSG000003BAK1	BAK BAK-1 BCL2	antiapoptotic protein-coding				
chr1-112	8.18667	-0.74473	0.833713	-0.89327	0.371715	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	7023	NM_001042	389	Hs.502656NM_001042	ENSG000003RHOC	ARH9 RHOC	Ras homolog protein-coding				
chr4-169	8.18667	-0.74473	0.833713	-0.89327	0.371715	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N	4798	NM_032783	84869	Hs.659311NM_032783	ENSG000003CBR4	SDR45C1	cardenolide protein-coding				
chr11-863	8.467598	0.733507	0.821236	0.893175	0.371763	0.981636	chr11	8635605	8636503	+	0	NA	intron (NLTR8A LTF	22782	NM_014818	9866	Hs.130833NM_014818	ENSG000003TRIM66	CTlorf29	tripartite protein-coding				
chr11-117	8.467598	0.733507	0.821236	0.893175	0.371763	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	9689	NM_00104C	51092	Hs.712144NM_015996	ENSG000003SIDT2	CGI-40	SID1	transcript protein-coding			
chr14-104	8.467598	0.733507	0.821236	0.893175	0.371763	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	12956	NR_162135	1.13E+08	NR_162135	MIR12121	-	microRNA ncRNA				
chr5-656	8.467598	0.733507	0.821236	0.893175	0.371763	0.981636	chr5	65687714	65688004	+	0	NA	intron (NALuSx SIN	34250	NM_019072	54557	Hs.482301NM_019072	ENSG000003SGTB	SGT2	small gtprotein-coding				
chr15-891	8.638329	-0.81185	0.909038	-0.89309	0.371808	0.981636	chr15	89179106	89179305	+	0	NA	intron (Nintron (N	42374	NM_00032E	6017	Hs.1933	NM_00032E	ENSG000003RLBP1	CRALBP	retinaldehyde protein-coding			
chr18-541	6.838329	-0.81185	0.909038	-0.89309	0.371808	0.981636	chr18	54182384	54182583	+	0	NA	intron (NL2c LINE	39929	NR_00297C	677819	Hs.655869NR_00297C	ENSG000003SNORA37	ACA37	small nucleolar RNA				
chr1-1244	24.91684	0.45302	0.509873	0.892971	0.371873	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alpha	291865	NR_003955	647121	Hs.697688NR_003955	ENSG000003EMBP1	23203	Hs.98041	NM_01534E	ENSG000003ZFVYE26	FYVE-CEN1	zinc finger protein-coding
chr14-705	6.683409	0.805992	0.902633	0.892934	0.371892	0.981636	chr14	70562379	70562664	+	0	NA	IntergeniMSTA-int	-27517	NM_003814	8748	Hs.177984NM_003814	ENSG000003ADAM20	-	ADAM metallopeptidase protein-coding				
chr19-796	6.683409	0.805992	0.902633	0.892934	0.371892	0.981636	chr19	7966537	7967002	+	0	NA	intron (NALuJr SIN	-23103	NM_006351	10469	Hs.465784NM_006351	ENSG000003TIMM44	TIMM44	translocase protein-coding				
chr3-9833	6.683409	0.805992	0.902633	0.892934	0.371892	0.981636	chr3	9833244	9833691	+	0	NA	intron (Nintron (N	10541	NM_001351	285367	Hs.33719	NM_17365E	ENSG000003RPSD3	-	RNA splicing protein-coding			
chr8-1334	6.683409	0.805992	0.902633	0.892934	0.371892	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	100001	NM_003033	6482	Hs.374257NM_003033	ENSG000003ST3GAL1	Gal-Nac6S	ST3 beta protein-coding				
chr9-127	6.683409	0.805992	0.902633	0.892934	0.371892	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	35349	NM_002283	64855	Hs.522401NM_002283	ENSG000003NIBAN2	C9orf88	Fniban apcprotein-coding				
chr9-129	6.683409	0.805992	0.902633	0.892934	0.371892	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	11320	NM_03280E	84895	Hs.632693NM_03280E	ENSG000003MIGAE2	C9orf54	Fmitoguanine protein-coding				
chr17-441	11.67129	-0.63285	0.708757	-0.89291	0.371908	0.981636	chr17	44197036	44197235	+	0	NA	intron (Nintron (N	1026	NM_00109E	56970	Hs.512651NM_02021E	ENSG000003ATXN7L3	-	ataxin 7 protein-coding				
chr2-927	16.17598	0.539477	0.604441	0.892522	0.372113	0.981636	chr2	92780060	92780372	+	0	NA	IntergeniALR/Alpha	839083	NR_027714	440888	Hs.730233NM_010324I2	ACTR3BP2	FKSG73	ACTR3B	psseudo			
chr1-2294	9.04057	0.712617	0.798483	0.892464	0.372144	0.981636	chr1	2.29E+08	2.29E+08	+	0	NA	intron (Nintron (N	18762	NM_01823C	55746	Hs.12457	NM_01823C	ENSG000003NUP133	GAMOS8	NF nucleoporin protein-coding			
chr1-376	6.75551	0.808482	0.906035	0.89233	0.372216	0.981636	chr1	37683414	37683801	+	0	NA	intron (Nintron (N	6922	NM_00135C	54955	Hs.272672NM_01785C	ENSG000003Crf109	-	chromosom protein-coding				
chr16-286	6.75551	0.808482	0.906035	0.89233	0.372216	0.981636	chr16	28837579	28838052	+	0	NA	TTS (NM_TTS (NM_1	6192	NR_039872	1.01E+08	NR_039872	ENSG000003MIR4721	-	microRNA ncRNA				
chr21-42	6.75551	0.808482	0.906035	0.89233	0.372216	0.981636	chr21	42854987	42856070	+	0	NA	intron (Nintron (N	23747	NM_00126E	10785	Hs.248819NM_01866E	ENSG000003WDR4	GAMOS6	M1WD	repeat protein-coding			
chr5-794	6.75551	0.808482	0.906035	0.89233	0.372216	0.981636	chr5	79491177	79490664	+	0	NA	intron (NALuSx SIN	104446	NM_001277	9456	Hs.591761NM_00427E	ENSG000003HOMER1	HOMER HOM	homeo sapien protein-coding				
chr9-101	6.75551	0.808482	0.906035	0.89233	0.372216	0.981636	chr9	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	20634	NM_019592	56254	Hs.729088NM_019592	ENSG000003RNF20	BRE1 BRE1	ring finger protein-coding				
chr2-849	16.04924	-0.5359	0.60082	-0.89194	0.372424	0.981636	chr2	84906074	84907327	+	0	NA	TTS (NM_TTS (NM_C	1044	NR_02110C	9								



chr2-2195	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr2	2.2E+08	2.2E+08	0	NA	intron (NL2c LINE	4948	NM_205847	29926	Hs. 27059	NM_013333	ENSG000006MPPA	AAMR	GDP-mannan-protein-coding		
chr20-256	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr20	25644067	25645800	+	0	NA	intron (NLIM3 LINE	20708	NR_126467	1.03E+08	Hs. 633621NR_126467	ENSG000002ZNF337-AS-	-	ZNF337	arcncRNA	
chr20-325	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr20	32309560	32310611	+	0	NA	exon (NM_exon (NM_	32434	NM_004798	9371	Hs. 369677	CNM_004798	ENSG000002KIF3B	FLA8 HHO	kinesin fprotein-coding	
chr21-334	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr21	33817277	33818067	+	0	NA	intron (NL2c LINE	98132	NM_001697	539	Hs. 40914	CNM_001697	ENSG000002ATP50	ATP50 ATF	ATP syntt protein-coding	
chr21-454	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr21	45474815	45475040	+	0	NA	intron (NCpG	-3339	NR_106877	1.02E+08	NR_106877	ENSG000002MIR6815	hsa-mir-6815	microRNA ncRNA		
chr21-464	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr21	46430646	46432425	+	0	NA	exon (NM_exon (NM_	-27356	NM_206891	23181	Hs. 189588	NM_015151	ENSG000002CIP2A	C21orf106	disco intprotein-coding	
chr22-236	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr22	23659537	23659870	+	0	NA	intron (Nintron (N	-27382	NM_016448	51233	Hs. 517466	NM_016448	ENSG000002DRICH1	C22orf43	aspartate-protein-coding	
chr3-4582	6.691267	0.803445	0.906155	0.886653	0.375266	0.981636	chr3	45833756	45834355	+	0	NA	intron (Nintron (N	8064	NM_020347	54585	Hs. 30824	NM_020347	ENSG000002LZTF1	BBS17	leucine zprotein-coding	
chr19-575	13.94606	0.569538	0.642689	0.886179	0.375521	0.981636	chr19	57571173	57577622	+	0	NA	intron (NMER74B LI	4514	NM_017878	55659	Hs. 247711	NM_017878	ENSG000002ZNF416	-	zinc fingprotein-coding	
chr11-74	4.948218	0.929151	1.048616	0.886073	0.375578	0.981636	chr11	77117253	77118118	+	0	NA	intron (NLMR SINE	-10311	NM_001127	4647	Hs. 370421	NM_000266	ENSG000002MY07A	DFNA11	DF myosin Vprotein-coding	
chr16-84	4.948218	0.929151	1.048616	0.886073	0.375578	0.981636	chr16	84071671	84072885	+	0	NA	intron (NLIMB7 LIN	-30121	NM_00108C	146167	NM_00108C	ENSG000002SLC38A8	FVH2	solute cprotein-coding		
chr19-388	4.948218	0.929151	1.048616	0.886073	0.375578	0.981636	chr19	38890083	38891353	+	0	NA	intron (NAluSx SIN	3437	NR_034148	22933	Hs. 466698	NM_012237	ENSG000002SIRT2	SIRT2 SIRT	zirtuin 2protein-coding	
chr6-1116	4.948218	0.929151	1.048616	0.886073	0.375578	0.981636	chr6	1.12E+08	1.12E+08	+	0	NA	intron (NL2b LINE	-66419	NM_001164	10758	Hs. 561514	NM_14720C	ENSG000002TRAF3IP2	ACT1 C6or	TRAF3 intprotein-coding	
chr5-4954	37.00299	0.378213	0.426852	0.886052	0.375589	0.981636	chr5	49545495	49547490	+	0	NA	IntergeniALR/Alphe	894795	NM_198445	133418	Hs. 561411	NM_198445	ENSG000002EMBP	GP70	embin protein-coding	
chr19-325	8.556139	-0.72327	0.816865	-0.88543	0.375926	0.981636	chr19	32382532	32383467	+	0	NA	exon (NM_exon (NM_	22540	NR_046201	400684	Hs. 438768	NR_046201	ENSG000002LOC400684	-	uncharactncRNA	
chr10-10C	8.648126	-0.70742	0.799177	-0.88519	0.376054	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (NAluSx3 SI	24897	NM_001138	55719	Hs. 447458	NM_018121	ENSG000002SLF2	C10orf6	F5MC5-SMC6 protein-coding	
chr12-48	6.648126	-0.70742	0.799177	-0.88519	0.376054	0.981636	chr12	48656711	48657412	+	0	NA	promoter-promoter-	-279	NR_002958	677793	Hs. 689722	NR_002958	ENSG000002SNORA2A	ACA2A	small nucsnoRNA	
chr13-75	6.648126	-0.70742	0.799177	-0.88519	0.376054	0.981636	chr13	75583741	75584313	+	0	NA	intron (NLIME6 LIN	34277	NM_006002	7347	Hs. 162241	NM_006002	ENSG000002UCHL3	UCH-L3	ubiquitin protein-coding	
chr16-881	6.648126	-0.70742	0.799177	-0.88519	0.376054	0.981636	chr16	8818097	8819098	+	0	NA	intron (Nintron (N	20758	NM_000303	5373	Hs. 625732	NM_000303	ENSG000002PMM2	CDG1 CDG1	phosphom protein-coding	
chr2-993	6.648126	-0.70742	0.799177	-0.88519	0.376054	0.981636	chr2	99398511	99400443	+	0	NA	TTS (NM_C TTS (NM_C	62088	NM_015904	9669	Hs. 158688	NM_015904	ENSG000002EIF5B	IF2	eukaryoti protein-coding	
chr6-8317	6.648126	-0.70742	0.799177	-0.88519	0.376054	0.981636	chr6	83177811	83179551	+	0	NA	intron (Nintron (N	14599	NM_001199	5238	Hs. 661666	NM_015599	ENSG000002PGM3	AGM1 IMD2	phosphog protein-coding	
chr22-208	8.442174	0.728778	0.823346	0.885142	0.37608	0.981636	chr22	20816567	20817696	+	0	NA	intron (Nintron (N	41680	NM_058004	5297	Hs. 529438	NM_002658	ENSG000002PI4KA	PI4K-ALPF	phosphatiprotein-coding	
chr6-1121	8.442174	0.728778	0.823346	0.885142	0.37608	0.981636	chr6	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	25121	NM_001033	619208	Hs. 59134C	NM_001033	ENSG000002FAM229B	C6orf225	family wiprotein-coding	
chr21-912	10.66425	0.650473	0.734893	0.885078	0.376115	0.981636	chr21	9126152	9126861	+	0	NA	intron (NLTR6A LTF	3255	NR_038328	1E+08	Hs. 487562	NM_17494E	ENSG000002TEKT4P2	MAFN12	TEktin 4 pseudo	
chr11-831	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr11	83164492	83171529	+	0	NA	intron (Nintron (N	10879	NM_001348	51585	Hs. 128958	NM_015888	ENSG000002PCF11	-	PCF11	clcprotein-coding
chr13-45	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr13	45028584	45028847	+	0	NA	3' UTR (N3' UTR (N	39177	NM_018558	55425	Hs. 731811	NM_018558	ENSG000002GPALPP1	AD029	KI GPALPP	mcprotein-coding
chr17-63	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr17	63361334	63361677	+	0	NA	intron (NMERS2A LI	78762	NM_001338	1534	Hs. 355264	NM_001918	ENSG000002CYB561	CYB561A1	cytochom protein-coding	
chr3-3851	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr3	38515451	38515828	+	0	NA	intron (Nintron (N	19299	NR_134938	9941	Hs. 517897	NM_005107	ENSG000002EXOQ	ENDOGL1	Exo/endor protein-coding	
chr5-511	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr5	1.11E+08	1.11E+08	+	0	NA	intron (NMSTC LTR	21817	NM_139281	134340	Hs. 533237	NM_139281	ENSG000002WDR36	GLTG1	TA-WD repeat protein-coding	
chr7-4823	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr7	45743796	45748235	+	0	NA	intron (Nintron (N	23003	NR_024271	641977	Hs. 723477	NR_024271	ENSG000002SEPTIN7P2	SEPTIN7	SE septin 7 pseudo	
chr9-1114	8.606987	-0.71069	0.803203	-0.88482	0.376251	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	62362	NM_001364	23392	Hs. 368258	NM_00108C	ENSG000002ECPAS	ECM29	KI Ecm29	prcprotein-coding
chr6-374	6.461002	-0.84403	0.953958	-0.88477	0.376281	0.981636	chr6	37458151	37458544	+	0	NA	intron (NAluSx SIN	25125	NM_015058	23070	Hs. 520102	NM_015058	ENSG000002CMTR1	FTSJ22	KI cp methyl protein-coding	
chr1-2201	3.899297	-1.08622	1.22792	-0.8846	0.376371	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (Nintron (N	-5117	NR_029711	406969	NR_029711	ENSG000002MIR194-1	MIRN194-1	microRNA ncRNA		
chr6-309	3.899297	-1.08622	1.22792	-0.8846	0.376371	0.981636	chr6	3098302	3098762	+	0	NA	intron (NLIM5 LINE	-19844	NR_026648	670	Hs. 10136	NM_004332	ENSG000002BPHL	BPH-RP	MC biphenyl protein-coding	
chr1-9871	6.667693	0.811005	0.916816	0.884589	0.376379	0.981636	chr1	98711818	98712259	+	0	NA	intron (NTigger1 E	50316	NM_001364	51375	Hs. 197018	NM_015978	ENSG000002SNX7	-	sorting rprotein-coding	
chr16-68	6.667693	0.811005	0.916816	0.884589	0.376379	0.981636	chr16	68060804	68061039	+	0	NA	intron (Nintron (N	-24449	NM_173163	4775	Hs. 436858	NM_004558	ENSG000002NFATC3	NF-AT4c	N nuclear fprotein-coding	
chr16-69	6.855895	-0.80212	0.906816	-0.88455	0.3764	0.981636	chr16	69575438	69575713	+	0	NA	intron (NAluJb SIN	9609	NM_138713	10725	Hs. 371987	NM_006598	ENSG000002NFAT5	NF-AT5	N nuclear fprotein-coding	
chr4-139	6.855895	-0.80212	0.906816	-0.88455	0.3764	0.981636	chr4	1.4E+08	1.4E+08	+	0	NA	intron (NTigger3a	29550	NM_001308	80854	Hs. 480792	NM_03064E	ENSG000002SETD7	DMK7	SET7SET domai protein-coding	
chr7-436	6.855895	-0.80212	0.906816	-0.88455	0.3764	0.981636	chr7	43603118	43603589	+	0	NA	intron (Nintron (N	20245	NM_004768	9263	Hs. 709488	NM_004768	ENSG000002STK17A	KRAT1	serine/t protein-coding	
chr1-3841	4.9815	0.933113	1.05523	0.884275	0.376548	0.981636	chr1	3841264	3842153	+	0	NA	intron (Nintron (N	15503	NM_014704	9731	Hs. 133088	NM_014704	ENSG000002CEP104	CFAP256	C centrosom protein-coding	
chr15-74	4.9815	0.933113	1.05523	0.884275	0.376548	0.981636	chr15	74633839	74634257	+	0	NA	intron (NMIR3 SINE	19054	NM_001138	1198	Hs. 51179C	NM_001298	ENSG000002CLK3	PHCLK3	PF CDC like protein-coding	
chr3-1291	4.9815	0.933113	1.05523	0.884275	0.376548	0.981636	chr3	12919866	12920740	+	0	NA	intron (Nintron (N	-35092	NR_136188	1.05E+08	Hs. 561178	NR_136188	ENSG000002LINC02022-	-	long intncRNA	
chr7-1177	6.710683	0.825445	0.933523	0.884226	0.376574	0.981636	chr7	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	115741	NM_001363	83992	Hs. 592288	NM_033427	ENSG000002CTTNBP2	C7orf8	C Cortactin protein-coding	
chr12-106	5.648539	-0.869	0.983147	-0.88389	0.376753	0.981636	chr12	1.06E+08	1.06E+08	+	0	NA	TTS (NM_C TTS (NM_C	10352	NM_006828	10970	Hs. 74368	NM_006828	ENSG000002CKAP4	CLIMP-63	cytoskele protein-coding	
chr12-11	5.648539	-0.869	0.983147	-0.88389	0.376753	0.981636	chr12	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	30487	NM_001032	4939	Hs. 414332	NM_002538	ENSG000002OAS2	-	2'-5'-oliprotein-coding	
chr2-232	5.648539	-0.869	0.983147	-0.88389	0.376753	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (NAluJo SIN	-24263	NM_001172	3769	Hs. 467338	NM_002242	ENSG000002KCNJ13	KIR1.4	K potassium protein-coding	
chr6-117	5.648539	-0.869	0.983147	-0.88389	0.376753	0.981636	chr6	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	29169	NM_138455	116150	Hs. 289008	NM_138455	ENSG000002NUS1	C6orf68	CNUS1 dehyprotein-coding	
chr17-75	6.922458	-0.79002	0.894001	-0.88369	0.376866	0.981636	chr17	75228912	75229360	+	0	NA	intron (Nintron (N	23457	NM_024844	79902	Hs. 362817	NM_024844	ENSG000002NUP85	FRONT1	NF nucleopor protein-coding	
chr20-38	6.922458	-0.79002	0.894001	-0.88369	0.376866	0.981636	chr20	389356	389609	+	0	NA										

chr14-10C.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	non-codiron-codir	-2343 NR_03052E	768222	NR_03052E	ENSG00000MIR770	MIRN770 l	microRNA	ncRNA		
chr17-394.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr17	39477761	39478734	+	0	NA	intron (Alu)Sx SIN	16761 NM_01508E	51755	Hs.34502E	NR_01508E	ENSG00000CDK12	CRK7 CRKf	cyclin	deprotein-coding	
chr2-3721.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr2	37219715	37220187	+	0	NA	intron (Nintron (N	11645 NM_00576C	10153	Hs.13540E	NR_00576C	ENSG00000CEBPZ	CBF CBF2 CCAAT	enl	protein-coding	
chr5-140F.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr5	1.41E+08	1.41E+08	+	0	NA	TTS (NM_C TTS (NM_C	1742 NM_00373Z	8637	Hs.594084	NR_00373Z	ENSG00000EIF4EBP3	4E-BP3 4E	eukaryot	protein-coding	
chr6-7567.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr6	75671810	75672459	+	0	NA	intron (Nintron (N	70254 NM_015571	26054	Hs.485784	NR_015571	ENSG00000SEN6P	SSP1 SUSF	smo	protein-coding	
chr6-133F.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr6	1.34E+08	1.34E+08	+	0	NA	3' UTR (N3' UTR (N	287469 NM_001301	2070	Hs.59668C	NR_001301	ENSG00000CEYA4	CMD1J DFNEYA	trans	protein-coding	
chr6-144F.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chr6	1.45E+08	1.45E+08	+	0	NA	intron (Nintron (N	166716 NR_132777	1.07E+08	NR_132777	SNORA98	small	nucsnRNA			
chrX-154F.5.673962	-0.85952	0.97805	-0.87881	0.379506	0.981636	chrX	1.54E+08	1.54E+08	+	0	NA	intron (Nintron (N	6275 NM_00111C	2316	Hs.195464	NR_00111C	ENSG00000FLNA	ABP-280 A	filamin	protein-coding	
chr1-230E.13.95391	0.568345	0.647155	0.87822	0.379824	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	intron (Nintron (N	2026 NM_00113E	84886	Hs.520494	NR_03280C	ENSG00000C1orf198		chromosom	protein-coding	
chr20-51F.5.615257	-0.8768	0.998511	-0.8781	0.379888	0.981636	chr20	5195254	5195698	+	0	NA	3' UTR (N3' UTR (N	68468 NM_00381E	8760	Hs.126857	NR_00381E	ENSG00000CDS2		CDP-diacy	protein-coding	
chr1-154F.11.6907	0.607712	0.692647	0.877376	0.380282	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	intron (Alu)Jr SIN	3605 NM_001367	57198	Hs.45370C	NR_02045E	ENSG00000ATP8B2	ATP1D	ATPase	protein-coding	
chr19-18F.7.246561	0.763684	0.870694	0.877098	0.380434	0.981636	chr19	18568522	18569221	+	0	NA	3' UTR (N3' UTR (N	-2859 NM_001321	7311	Hs.5308	NR_00333E	ENSG00000CUBA52	CEP52 HU	ubiquitin	protein-coding	
chr10-984.6.9146	-0.78817	0.89883	-0.87689	0.380547	0.981636	chr10	98402018	98403070	+	0	NA	intron (Nintron (N	-7237 NR_03161E	1E+08	NR_03161E	ENSG00000MIR1287	MIRN1287 micro	RNA	ncRNA		
chr10-11F.6.9146	-0.78817	0.89883	-0.87689	0.380547	0.981636	chr10	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	61139 NR_03982E	1.01E+08	NR_03982E	ENSG00000MIR4681		microRNA	ncRNA		
chr13-491.6.9146	-0.78817	0.89883	-0.87689	0.380547	0.981636	chr13	49115394	49116856	+	0	NA	intron (N2b LINE	5808 NM_01492Z	22862	Hs.50801C	NR_01492Z	ENSG00000FNDC3A	FNDC3 HUC	fibronect	protein-coding	
chr13-11F.6.9146	-0.78817	0.89883	-0.87689	0.380547	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	exon (NM exon (NM	29626 NM_00134E	55002	Hs.31759E	NR_01790E	ENSG00000TMC03	C13orf11	transment	protein-coding	
chr17-164.6.9146	-0.78817	0.89883	-0.87689	0.380547	0.981636	chr17	16432813	16433367	+	0	NA	intron (NAluSq2 SI	-5897 NR_04502E	125144	Hs.368934	NR_15235E	ENSG00000CENMG29	C17orf45 small	nucncRNA		
chr20-37F.6.9146	-0.78817	0.89883	-0.87689	0.380547	0.981636	chr20	37059386	37060665	+	0	NA	intron (Alu)Sp SIN	35972 NM_00132Z	5933	Hs.20774E	NR_00289E	ENSG00000RBL1	CP107 PRE	RB	transc	protein-coding
chr16-23F.9.486197	0.672854	0.767374	0.876827	0.38058	0.981636	chr16	23620633	23621287	+	0	NA	intron (NAluSzl SIN	20397 NM_02467E	79728	Hs.444664	NR_02467E	ENSG00000PALB2	FANCN PNC	partner	protein-coding	
chr22-21F.9.486197	0.672854	0.767374	0.876827	0.38058	0.981636	chr22	31845147	31845634	+	0	NA	intron (Nintron (N	91367 NM_00136E	9681	Hs.43502E	NR_01466E	ENSG00000DEPDC5	DEP.5 FFE	DEP	doma	protein-coding
chr1-279F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr1	27901215	27902155	+	0	NA	intron (Alu)Jr SIN	12709 NM_00294E	6118	Hs.79411	NR_00294E	ENSG00000CPA2	REPA2 RP-	replicat	protein-coding	
chr10-49F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr10	49960604	49962265	+	0	NA	intron (Nintron (N	7222 NR_14577E	1.1E+08	NR_14577E	SNORA74C-	small	nucsnRNA			
chr10-67F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr10	67959668	67961066	+	0	NA	intron (Nintron (N	50516 NR_131184	1E+08	NR_131184	POU5F1P5	Oct4-pg5	POU	class	pseudo	
chr10-68F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr10	68682949	68683771	+	0	NA	intron (NAlu)S SINE	-37879 NR_018237	55749	Hs.49853	NR_018237	ENSG00000CCAR1		cell	div	protein-coding
chr11-17F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr11	17311500	17312769	+	0	NA	intron (Nintron (N	35164 NM_00135E	4925	Hs.65459E	NR_00501E	ENSG00000NCUB2	HEL-S-10E	nucleobir	protein-coding	
chr12-781.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr12	78148996	78149949	+	0	NA	intron (Nintron (N	210274 NR_135021	1.05E+08	Hs.15689E	NR_135021	ENSG00000LINC02424-		long	intencRNA	
chr12-95F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr12	95027179	95029383	+	0	NA	intron (NLM87 LIN	-24568 NM_00125E	55967	Hs.506374	NR_01883E	ENSG00000NDUFA12	B17.2 DAF	NADH	ubiquitin	protein-coding
chr13-11F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	exon (NM exon (NM	5895 NM_001267	1E+08	Hs.64003E	NR_001267044	COL4A2-AS-	COL4A2	ar	protein-coding	
chr19-52F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr19	52771920	52772398	+	0	NA	intron (NAlu)Sp SIN	14632 NM_001321	162966	Hs.69684E	NR_19845E	ENSG00000ZNF600	KRE-ZNF1	zinc	finger	protein-coding
chr2-182F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr2	82378	82378	+	0	NA	intron (Nintron (N	-72273 NM_00146E	2487	Hs.12845E	NR_00146E	ENSG00000FRZB	FRF FRITZ	frizzled	protein-coding	
chr20-50F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr20	50682304	50684053	+	0	NA	intron (Nintron (N	8364 NR_11089C	140876	Hs.37257E	NR_08082E	ENSG00000CRIPOR3	C20orf17E	RIPOR	fan	protein-coding
chr5-369F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr5	36961672	36962730	+	0	NA	exon (NM exon (NM	8332 NM_015384	25836	Hs.481927	NR_015384	ENSG00000NIPBL	CDL3 CDL3N	NIPBL	col	protein-coding
chr7-143F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr7	1.43E+08	1.43E+08	+	0	NA	TTS (NR_C TTS (NR_C	7439 NR_10695E	1.02E+08	NR_10695E	ENSG00000MIR6892	hsa-mir-6	microRNA	ncRNA		
chr9-115F.5.666104	-0.85744	0.977999	-0.87673	0.380631	0.981636	chr9	1.15E+08	1.15E+08	+	0	NA	intron (N2a LINE	9148 NM_00216C	3371	Hs.14325C	NR_00216C	ENSG00000CTNC	150-225 I	tenascin	protein-coding	
chr1-378F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr1	37855340	37855539	+	0	NA	intron (N3 LINE C	4153 NM_00595E	4520	Hs.471991	NR_00595E	ENSG00000MTF1	MTF-1 ZRF	metal	reg	protein-coding
chr11-10F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr11	103550	103550	+	0	NA	intron (Nintron (N	12941 NM_001377	79659	Hs.503721	NR_001377	ENSG00000DYNC2H1	ATD3 DHC1	dynein	cy	protein-coding
chr12-46F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr12	46204829	46207575	+	0	NA	intron (Nintron (N	60314 NM_00127E	81539	Hs.53377C	NR_030674	ENSG00000SLC38A1	ATA1 NAT	z	solute	protein-coding
chr13-77F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr13	77009340	77010770	+	0	NA	intron (NLM1P7 LIN	17104 NM_01215E	26224	Hs.508284	NR_01215E	ENSG00000FBXL3	FBL3 FBL2	FB	anc	protein-coding
chr13-77F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr13	77087138	77087800	+	0	NA	intron (Nintron (N	11956 NR_04671E	1.01E+08	Hs.56928E	NR_04671E	ENSG00000MYCBP2-AS-		MYCBP2	ar	ncRNA
chr19-83F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr19	8322480	8324480	+	0	NA	TTS (NM_C TTS (NM_C	1984 NM_001031	6234	Hs.153177	NR_001031	ENSG00000CRPS28	DBA15 S2E	ribosomal	protein-coding	
chr2-234F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr2	2.35E+08	2.35E+08	+	0	NA	intron (NLM2B LI	5887 NM_001371302								
chr5-1674.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr5	16747574	16747803	+	0	NA	intron (NAlu)Sc8 SI	-130630 NM_001034	54463	Hs.481704	NR_01900C	ENSG00000RETREG1	FAMI34B J	reticulop	protein-coding	
chr5-529F.8.63241	-0.70453	0.803657	-0.87666	0.380674	0.981636	chr5	52927805	52928114	+	0	NA	intron (NMLT1A LI	-61393 NM_00220E	3673	Hs.482077	NR_00220E	ENSG00000ITGA2	BR CD49B	integrin	protein-coding	
chr2-173F.5.15565	-0.93658	1.068369	-0.87665	0.380678	0.981636	chr2	1.73E+08	1.73E+08	+	0	NA	intron (NMLT1L LTF	17998 NR_03388E	33975	Hs.57008E	NR_03388E	ENSG00000MAP3K20-	MLK7-AS1	MAP3K20	anc	ncRNA
chr14-311.8.599129	-0.70295	0.809177	-0.87651	0.380756	0.981636	chr14	31155596	31157393	+	0	NA	intron (NAlu)Sx SIN	51299 NM_01538E	25831	Hs.708017	NR_01538E	ENSG00000HECTD1	EULR	HECT	doma	protein-coding
chr5-4841.5.62855	-0.54688	0.624139	0.876216	0.380913	0.981636	chr5	48414003	48414324	+	0	NA	IntergeniALR/Alph	2027125 NR_19844E	133418	Hs.641411	NR_19844E	ENSG00000EMB	GP70	emigin	protein-coding	
chr1-2484.5.632823	-0.86487	0.987393	-0.87591	0.381079	0.981636	chr1	24844735	24845660	+	0	NA	TTS (NM_C TTS (NM_C	74219 NR_10678E	1.02E+08	NR_10678E	ENSG00000MIR6731	hsa-mir-6	microRNA	ncRNA		
chr1-5181.5.632823	-0.86487	0.987393	-0.87591	0.381079	0.981636	chr1	51817010	51817822	+	0	NA	intron (Nintron (N	18986 NR_03158E	1E+08	NR_03158E	ENSG00000MIR761	hsa-mir-7	microRNA	ncRNA		
chr10-11F.5.632823	-0.86487	0.987393	-0.87591	0.381079	0.981636	chr10	51856728	51857233	+	0	NA	intron (Nintron (N	52808 NM_00119E	8028	Hs.30385	NR_004641	ENSG00000MLLT10	AF10	MLLT10	hip	protein-coding
chr10-721.5.632823	-0.86487	0.987393	-0.87591	0.381079	0.981636	chr10	72183519	72184341	+	0	NA	intron (NAlu)Sx SIN	32026 NM_00136E	51008	Hs.500007	NR_01594E	ENSG00000ASCC1	ASCLP50 c	activat		



chr4-1541	4.956076	0.925478	1.060822	0.872416	0.382982	0.981636	chr4	154195	155969	+	0	NA	intron (THE1B-int	26961	NM_001288	255403	Hs.63663	ENSG000002ZNF718	-	zinc	finger	protein-coding	
chr5-1731	4.956076	0.925478	1.060822	0.872416	0.382982	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (intron (N	18486	NM_01398C	662	Hs.14572	ENSG000002BNIP1	-	NIP1 SEC2	BCL2	int	protein-coding
chr2-3684	7.205421	0.762973	0.874584	0.872384	0.382999	0.981636	chr2	36848746	36849807	+	0	NA	3' UTR (3' UTR (N	117260	NM_003162	6801	Hs.12748	ENSG000002CSTRN	-	PPP2R6A S	triatin	protein-coding	
chr3-1555	5.607399	-0.87478	1.002903	-0.87225	0.383072	0.981636	chr3	1.56E+08	1.56E+08	+	0	NA	intron (AluSj SIN	41160	NM_003875	8833	Hs.59131	ENSG000002GMPS	-	GATD7	guanine	n	protein-coding
chr9-1308	5.607399	-0.87478	1.002903	-0.87225	0.383072	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (intron (N	29747	NM_198188	347148	Hs.66070	ENSG000002QRFP	-	26RFa P51	pyru	glut	protein-coding
chr12-935	9.468632	0.66688	0.76474	0.872035	0.383189	0.981636	chr12	93574941	93575817	+	0	NA	3' UTR (3' UTR (N	2704	NM_00127C	8835	Hs.48557	ENSG000002SCS2	-	CIS2 Cis1	suppres	protein-coding	
chr16-288	4.686832	0.66688	0.76474	0.872035	0.383189	0.981636	chr16	28842590	28844775	+	0	NA	TTS (NR_C TTS (NR_C	325	NR_039872	1.01E+08	NR_039872	ENSG000002MIR4721	-	microRNA	ncRNA		
chr11-118	8.681408	-0.7026	0.80573	-0.87201	0.383205	0.981636	chr11	1.1E+08	1.1E+08	+	0	NA	intron (L1PA16 LI	7774	NM_004105	2230	Hs.744	ENSG000002FDX1	-	ADX FDX1	ferredoxin	protein-coding	
chr8-945	8.681408	-0.7026	0.80573	-0.87201	0.383205	0.981636	chr8	94533649	94534153	+	0	NA	intron (AluSz SIN	19568	NM_01549E	25962	Hs.20223	ENSG000002VIRMA	-	KIAA1429 vir	like	protein-coding	
chr2-1114	6.412004	-0.84665	0.971035	-0.87191	0.383259	0.981636	chr2	1.11E+08	1.11E+08	+	0	NA	intron (intron (N	20348	NR_136166	541471	Hs.56080	ENSG000002MIR4435	-	AGD2 LIN	MIR4435	znc	RNA
chr5-1764	6.412004	-0.84665	0.971035	-0.87191	0.383259	0.981636	chr5	1.76E+08	1.76E+08	+	0	NA	intron (intron (N	30728	NM_014613	23197	Hs.48424	ENSG000002FAF2	-	ETEA UBX1	Fas	assoc	protein-coding
chr19-345	8.67355	-0.7012	0.804352	-0.87176	0.383341	0.981636	chr19	34371531	34371730	+	0	NA	intron (AluSx3 SI	6434	NM_00132E	2821	Hs.46647	ENSG000002GPI	-	AMF GNP1	glucose- $\epsilon$	protein-coding	
chr6-1664	8.67355	-0.7012	0.804352	-0.87176	0.383341	0.981636	chr6	1.66E+08	1.66E+08	+	0	NA	intron (MER34A LI	35470	NR_040679	1.01E+08	Hs.57659	ENSG000002RPS6KA2-1	-	RPS6KA2	inc	RNA	
chr9-1254	8.67355	-0.7012	0.804352	-0.87176	0.383341	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (AluSz SIN	-76756	NM_002077	2800	Hs.59504	ENSG000002GOLGA1	-	golgin-97	golgin	Al	protein-coding
chr1-2038	11.69856	0.606302	0.695606	0.871617	0.383418	0.981636	chr1	2.04E+08	2.04E+08	+	0	NA	intron (intron (N	8176	NM_001174	1E+08	NM_001174	ENSG000002ZBED6	-	MGR	zinc	finger	protein-coding
chr19-374	11.69856	0.606302	0.695606	0.871617	0.383418	0.981636	chr19	37474322	37485331	+	0	NA	intron (L1MED LIN	10255	NM_001321	148268	Hs.12696	ENSG000002ZNF570	-	zinc	finger	protein-coding	
chr9-1110	10.30908	-0.65214	0.748374	-0.8714	0.383533	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (L1PA7 LI	11893	NM_001351	1902	Hs.12666	ENSG000002CLPAR1	-	EDG2 GPR2	lyso	phos	protein-coding
chr1-1757	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr1	75758164	75758727	+	0	NA	intron (MER21B LI	-13432	NR_13074E	1744	Hs.52545	ENSG000002DLSTP1	-	DLSTP	dihydro	lip	pseudo
chr10-794	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr10	79427915	79428742	+	0	NA	intron (L1MB3 LI	17296	NM_153367	219654	Hs.52308	ENSG000002ZCHC24	-	C10orf56 zinc	finger	protein-coding	
chr10-945	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr10	94340948	94342431	+	0	NA	exon (NM exon (NM	21250	NM_022451	64318	Hs.74899	ENSG000002NOC3L	-	AD24 C10	NOC3	like	protein-coding
chr10-995	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr10	99677844	99678454	+	0	NA	intron (L1ME3E LI	18520	NM_00134E	57089	Hs.28326	ENSG000002ENTPD7	-	LALP1	ectonuc	le	protein-coding
chr12-684	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr12	6841165	6841736	+	0	NA	intron (intron (N	525	NM_00207E	2784	Hs.63165	ENSG000002GNB3	-	CSNB1H	G	proteir	protein-coding
chr12-645	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr12	64064333	64066875	+	0	NA	intron (AluJr SIN	156692	NM_00130C	144577	Hs.44467	ENSG000002C12orf66	-	chromoson	protein-coding		
chr13-274	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr13	27433681	27434009	+	0	NA	intron (intron (N	9226	NM_002097	2971	Hs.44597	ENSG000002GTF3A	-	AP2 TFII	l	general	protein-coding
chr13-101	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr13	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	7599	NM_001271	9358	Hs.69655	ENSG000002ITGBL1	-	OSCP TIEE	integrin	protein-coding	
chr13-115	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	7937	NM_007111	7027	Hs.79353	ENSG000002TFDP1	-	DILC DP1	transcri	pt	protein-coding
chr13-115	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	11647	NM_00136E	1.01E+08	Hs.70426	ENSG000002C13orf46	-	chromoson	protein-coding		
chr13-115	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	6918	NM_00136E	1.01E+08	Hs.70426	ENSG000002C13orf46	-	chromoson	protein-coding		
chr14-528	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr14	52886355	52887234	+	0	NA	intron (intron (N	64256	NM_00683Z	10979	Hs.50934	ENSG000002FERMT2	-	KIND2 MIC	fermitin	protein-coding	
chr15-48	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr15	48732046	48732853	+	0	NA	IntergeniL1PA8A LI	78620	NM_01498E	22995	Hs.44300	ENSG000002CEP152	-	MCPH4 MCF	centrosom	protein-coding	
chr15-808	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr15	80840952	80842953	+	0	NA	TTS (NR_C TTS (NR_C	121	NR_03039E	693132	NR_03039E	ENSG000002MIR549A	-	MIR549	Mi	microRNA	ncRNA
chr2-155	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr2	15552228	15552632	+	0	NA	intron (Tigger2a	8904	NM_01590E	51594	Hs.46775	ENSG000002NBAS	-	L1P52 NAC	neurine	like	protein-coding
chr2-155	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (AluJr4 SI	5833	NM_00136E	27148	Hs.47140	ENSG000002STK36	-	FU	serine/t	protein-coding	
chr3-481	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr3	48166512	48168452	+	0	NA	intron (intron (N	20935	NM_00178E	993	Hs.43770	ENSG000002CDC25A	-	CDC25A2	cell	divi	protein-coding
chr3-136	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr3	1.36E+08	1.36E+08	+	0	NA	intron (L1MC4 LI	72552	NM_00053Z	5096	Hs.63788	ENSG000002PCCB	-	propionyl	protein-coding		
chr3-146	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr3	1.46E+08	1.46E+08	+	0	NA	intron (intron (N	-34828	NR_146297	1.1E+08	NR_146297	ENSG000002LNCsRLR	-	lncRNA-SF	lncRNA	sc	ncRNA
chr4-156	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr4	15684910	15685280	+	0	NA	intron (Tigger9a	3268	NM_00114E	285550	Hs.39998	ENSG000002FAM200B	-	C4orf53	family	wi	protein-coding
chr4-564	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr4	56458636	56463101	+	0	NA	3' UTR (3' UTR (N	-6749	NR_001267	6731	Hs.23782	ENSG000002SRP72	-	BMMF BMS	signal	re	protein-coding
chr4-823	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr4	82367020	82370919	+	0	NA	intron (intron (N	5022	NM_03137C	3184	Hs.48007	ENSG000002HNRNPD	-	AUF1 AUF1	heterog	er	protein-coding
chr4-1451	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr4	1.45E+08	1.45E+08	+	0	NA	intron (intron (N	-21130	NM_00125E	10393	Hs.48087	ENSG000002ANAPC10	-	APC10 DOC	anaphase	protein-coding	
chr4-186	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr4	1.87E+08	1.87E+08	+	0	NA	intron (intron (N	6151	NM_00524E	2195	Hs.48137	ENSG000002FAT1	-	CDHF7 CDF	FAT1	atyp	protein-coding
chr7-6731	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr7	67312490	67314316	+	0	NA	intron (Tigger1 E	10765	NR_04058E	64940	Hs.63201	ENSG000002STAG3L4	-	STAG3L4P	stromal	p	pseudo
chr7-127	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr7	1.27E+08	1.27E+08	+	0	NA	intron (intron (N	6877	NM_176814	168850	Hs.15900	ENSG000002ZNF800	-	-	zinc	finger	protein-coding
chr8-2544	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr8	25442181	25443929	+	0	NA	intron (HAL1M8 LI	15378	NM_017634	54793	Hs.72071	ENSG000002KCTD9	-	BTBD27	potassi	um	protein-coding
chr8-103	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr8	1.03E+08	1.03E+08	+	0	NA	intron (MIRb SINE	4223	NR_14579E	1.1E+08	NR_14579E	SNORD173	-	small	nuc	snoRNA	
chr8-103	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr8	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	27252	NM_01542C	25879	Hs.53226	ENSG000002DCAF13	-	GM83 HSPC	DBB1	and	protein-coding
chr8-133	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (intron (N	27552	NM_001161	10397	Hs.37291	ENSG000002NDRG1	-	CAP43 CM1	N-myc	do	protein-coding
chr9-100	5.658247	-0.85534	0.982257	-0.87079	0.383866	0.981636	chr9	1E+08	1E+08	+	0	NA	intron (L1MED LI	19677	NM_001161	54881	Hs.49464	ENSG000002TEX10	-	Ipi1 ba2C	testis	ex	protein-coding
chr7-640	5.658247	-0.85816	0.66978	-0.87067	0.383935	0.981636	chr7	6402782	6403031	+	0	NA	3' UTR (3' UTR (N	28379	NM_00690E	5879	Hs.41381	ENSG000002RAC1	-	MIG5 MRD4	Rac	ex	protein-coding
chr17-291	10.6721	0.648666																					

chr19-541 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr19	54148404	54151277	+	0	NA	intron (Nintron (N	9881 NM_024316	79165 Hs. 590974NM_024316	ENSG000001LENG1	-	leukocyte protein-coding	
chr2-3208 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr2	32089702	32090411	+	0	NA	intron (NAlu SINE	26445 NM_199436	6683 Hs. 468091NM_014946	ENSG000001SPAST	-	ADPSP FSF spastin protein-coding	
chr2-5554 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr2	55545309	55546118	+	0	NA	TTS (NM_C TTS (NM_C	26118 NM_080667	112942 Hs. 26420ENM_080667	ENSG000001CFAP36	-	BARTL1 CC cilia anc protein-coding	
chr20-93 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr20	9391440	9392073	+	0	NA	intron (NLR T6 C L	83956 NM_000993	5332 Hs. 472101NM_000993	ENSG000001PLCB4	-	ARCND2 P phospholip protein-coding	
chr22-312 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr22	31281155	31290028	+	0	NA	intron (NMR 3 SINE	6897 NM_052888	113791 Hs. 26670 NM_052888	ENSG000001PIK3IP1	-	HGNL7 TrIF phospho protein-coding	
chr22-404 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr22	40422415	40424184	+	0	NA	intron (Nintron (N	40141 NM_001282	57591 Hs. 65468ENM_020831	ENSG000001MRFTA	-	BSAC MAL myocardir protein-coding	
chr3-9651 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr3	9651901	9654654	+	0	NA	intron (Nintron (N	3772 NM_022486	64419 Hs. 475382NM_022486	ENSG000001MTRM14	-	C3orf29 myotubul protein-coding	
chr4-8672 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr4	86723280	86723541	+	0	NA	intron (NMR B DNA	125974 NM_197966	345274 Hs. 45299ENM_197966	ENSG000001SLC10A6	-	SOAT myotubul protein-coding	
chr6-472 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr6	47231831	47233070	+	0	NA	3' UTR (N3' UTR (N	77455 NM_014452	27242 Hs. 443577NM_014452	ENSG000001TNFRSF21	-	BM-018 TNF recepr protein-coding	
chr7-7546 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr7	754617	755194	+	0	NA	intron (NCPg-2525E	-27229 NM_001164	5575 Hs. 520851NM_00273E	ENSG000001PKRARI1B	-	PRKARI protein h protein-coding	
chr7-1346 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr7	135E+08	1.35E+08	+	0	NA	TTS (NM_C TTS (NM_C	33166 NM_0011724	669 Hs. 19836ENM_0011724	ENSG000001BPGM	-	DDGM ECY1bisphosp protein-coding	
chr9-1245 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	-53410 NM_002077	2800 Hs. 59504 NM_002077	ENSG000001GOLGA1	-	golgin-97 golgin A1 protein-coding	
chr9-1276 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	13628 NR_037473	1.01E+08	NR_037473	ENSG000001MIR3911	-	mir-3911 microRNA ncRNA
chr9-1367 7.195713	0.752972	0.869904	0.865581	0.38672	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (Nintron (N	11684 NR_039822	1.01E+08	NR_039822	ENSG000001MIR4673	-	mir-4673 microRNA ncRNA
chr1-1294 9.109583	-0.6741	0.778906	-0.86544	0.386798	0.981636	chr1	1294036	1294787	+	0	NA	exon (NM exon (NM	1759 NR_106784	1.02E+08	NR_106784	ENSG000001MIR6726	-	hsa-mir-6 microRNA ncRNA
chr14-607 9.109583	-0.6741	0.778906	-0.86544	0.386798	0.981636	chr14	60713461	60714819	+	0	NA	exon (NM exon (NM	10211 NM_01742C	51804 Hs. 97849 NM_01742C	ENSG000001SIX4	-	AREC3 SIX home protein-coding	
chr14-736 9.109583	-0.6741	0.778906	-0.86544	0.386798	0.981636	chr14	73900514	73900891	+	0	NA	intron (N Kanga2_a	13843 NR_040251	57862 Hs. 27086ENM_02118E	ENSG000001ZNF410	-	APA-1 AP2 zinc fing protein-coding	
chr1-1504 9.47649	0.665142	0.768788	0.865183	0.386938	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (NMR B SINE	1696 NR_106938	1.02E+08	NR_106938	ENSG000001MIR6878	-	hsa-mir-6 microRNA ncRNA
chr1-2143 9.47649	0.665142	0.768788	0.865183	0.386938	0.981636	chr1	2.14E+08	2.14E+08	+	0	NA	3' UTR (N3' UTR (N	76113 NM_020197	56950 Hs. 66170 NM_020197	ENSG000001SMYD2	-	HSKM-8 KMS2 and h protein-coding	
chr19-407 9.47649	0.665142	0.768788	0.865183	0.386938	0.981636	chr19	40729572	40731161	+	0	NA	intron (Nintron (N	13254 NM_025194	80271 Hs. 51541ENM_025194	ENSG000001ITPKC	-	IP3-3KCl inositol protein-coding	
chr4-4785 9.47649	0.665142	0.768788	0.865183	0.386938	0.981636	chr4	47859250	47897827	+	0	NA	TTS (NR_ITTS (NR_1	-16689 NR_125879	1.02E+08	NR_125879	ENSG000001LOC101927	-	uncharacterncRNA
chr5-1416 7.179997	0.757588	0.875823	0.865002	0.387038	0.981636	chr5	1.42E+08	1.42E+08	+	0	NA	intron (Nintron (N	4356 NR_149167	8841 Hs. 519632NM_00388E	ENSG000001HDAC3	-	HD3 KDAC histone c protein-coding	
chr6-8335 7.179997	0.757588	0.875823	0.865002	0.387038	0.981636	chr6	83359736	83360926	+	0	NA	intron (NHERV L-int	70720 NM_00239E	4199 Hs. 21160 NM_00239E	ENSG000001CEME1	-	HUMNDME kmalic enz protein-coding	
chr7-1333 7.179997	0.757588	0.875823	0.865002	0.387038	0.981636	chr7	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	15864 NR_10674E	1.02E+08	NR_10674E	ENSG000001MIR6133	-	hsa-mir-6 microRNA ncRNA
chr1-4121 5.699386	-0.85	0.982786	-0.86489	0.3871	0.981636	chr1	41219263	41220220	+	0	NA	intron (NAluSx S	22565 NM_00135C	22955 Hs. 571874NM_01223E	ENSG000001SCMH1	-	Scm13 Scm polyc protein-coding	
chr5-113 5.699386	-0.85	0.982786	-0.86489	0.3871	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	3' UTR (N3' UTR (N	48687 NM_152624	167227 Hs. 44387ENM_152624	ENSG000001DCP2	-	NUDT20 decapping protein-coding	
chr8-381 5.699386	-0.85	0.982786	-0.86489	0.3871	0.981636	chr8	38138272	38139218	+	0	NA	intron (Nintron (N	12207 NM_00034E	6770 Hs. 52153ENM_00034E	ENSG000001STAR	-	STARD1 steroidog protein-coding	
chr1-1675 11.63986	0.600766	0.694699	0.864787	0.387156	0.981636	chr1	1.68E+08	1.68E+08	+	0	NA	intron (NAluSx S	-16737 NM_001143	25874 Hs. 51776ENM_01541E	ENSG000001MPC2	-	BRP44 SLC mitochonc protein-coding	
chr18-68 7.399631	-0.74604	0.862734	-0.86474	0.387179	0.981636	chr18	68685593	68686281	+	0	NA	intron (N L2b LINE	29171 NM_00135C	54495 Hs. 440534NM_01902E	ENSG000001TMX3	-	PDAI3 T thioredo protein-coding	
chr20-199 7.399631	-0.74604	0.862734	-0.86474	0.387179	0.981636	chr20	19940941	19941566	+	0	NA	intron (N L2b LINE	51687 NM_01899E	54453 Hs. 472277NM_01899E	ENSG000001RIN2	-	MCA3 RSSAS and h protein-coding	
chr4-1505 7.399631	-0.74604	0.862734	-0.86474	0.387179	0.981636	chr4	1.51E+08	1.51E+08	+	0	NA	intron (N LIMB2 LIN	103200 NM_00119E	987 Hs. 48093ENM_00672E	ENSG000001LRBA	-	BGL CDC4L LPS resp protein-coding	
chr6-3214 9.552761	0.678075	0.784234	0.864633	0.38724	0.981636	chr6	32148675	32149185	+	0	NA	3' UTR (N3' UTR (N	3009 NM_030651	80863 Hs. 549204NM_030651	ENSG000001PRRT1	-	C6orf31 L proline i protein-coding	
chr6-4357 9.117441	-0.67548	0.81336	-0.86451	0.387305	0.981636	chr6	43578145	43578344	+	0	NA	intron (NAluSg2 S	2059 NM_001291	5429 Hs. 655467NM_00650E	ENSG000001POLH	-	RAD30 RAL DNA poly protein-coding	
chr1-183 8.921196	0.688392	0.796349	0.864435	0.387349	0.981636	chr1	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	102118 NM_001297	23179 Hs. 49714ENM_01514E	ENSG000001CRL1	-	RGL ral guaniprotein-coding	
chr5-1375 8.921196	0.688392	0.796349	0.864435	0.387349	0.981636	chr5	13793937	13793967	+	0	NA	exon (NM exon (NM	150933 NM_00136E	1767 Hs. 21236ENM_00136E	ENSG000001DNAH5	-	CILD3 DN dynein ax protein-coding	
chr10-94 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr10	94333498	94334521	+	0	NA	3' UTR (N3' UTR (N	28930 NM_022451	64318 Hs. 74899 NM_022451	ENSG000001NOC3L	-	AD24 C10c NOC3 like protein-coding	
chr10-127 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr10	1.27E+08	1.27E+08	+	0	NA	intron (N MLT1 L T	141215 NM_00103E	642938 Hs. 61388ENM_00103E	ENSG000001INSYN2A	-	C10orf141 inhibitor protein-coding	
chr12-502 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr12	50230078	50230358	+	0	NA	intron (NAluSx S	3994 NR_03162E	1E+08	NR_03162E	ENSG000001MIR1293	-	MIRN1293 microRNA ncRNA
chr16-314 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr16	31473328	31473535	+	0	NA	intron (NCPg-9530	3226 NM_0015927	7041 Hs. 51353CNM_015927	ENSG000001TGFB11	-	ARA55 HIC transforn protein-coding	
chr17-372 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr17	37237428	37237708	+	0	NA	intron (N LIME3D LI	-7233 NR_13277E	1.07E+08	SNORA90	-	small nucsnRNA	
chr3-227 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	intron (N LIME5 LIN	24426 NM_0017554	54625 Hs. 51820ENM_017554	ENSG000001PARP14	-	ARTD8 BAL poly (ADP- protein-coding	
chr4-149 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr4	24909908	24910190	+	0	NA	intron (N MLT1C L T	-2929 NM_00113C	91050 Hs. 52153ENM_17346E	ENSG000001CCDC149	-	coiled-c protein-coding	
chr5-804 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr5	80428091	80428449	+	0	NA	intron (N LIPA5 LIN	20206 NM_00110E	9765 Hs. 48266CNM_01473E	ENSG000001ZFYE16	-	PPP1R69 zinc fing protein-coding	
chr5-1158 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr5	1.16E+08	1.16E+08	+	0	NA	non-codir non-codir	11901 NM_004707	9140 Hs. 26448ENM_004707	ENSG000001ATG12	-	APG12 APC autophagy protein-coding	
chr5-1591 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr5	1.59E+08	1.59E+08	+	0	NA	intron (N LIME3F LI	41025 NM_00119E	153830 Hs. 34930ENM_14472E	ENSG000001CRNF145	-	ring fing protein-coding	
chr6-7505 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr6	75099963	75102730	+	0	NA	intron (Nintron (N	27436 NR_145788	1.1E+08	NR_145788	ENSG000001SNORD156	-	small nucsnRNA
chr7-1276 7.383915	-0.74275	0.859455	-0.86421	0.387471	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	5613 NM_01439C	27044 Hs. 12252ENM_01439C	ENSG000001SND1	-	TDRD11 T staphyloc protein-coding	
chr1-1565 7.228995	0.756006	0.874875	0.864131	0.387516	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	-26886 NR_030527	768220	NR_030527	ENSG000001MIR765	-	MIRN765 microRNA ncRNA
chr1-2357 7.228995	0.756006																	



chr14-685.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr14	68933813	68934559	+	0	NA	intron (intron (N	45116 NM_001102	87 Hs. 235755NM_001102	ENSG000000ACTN1	BDPLT15	actinin 1 protein-coding
chr15-636.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr15	63613856	63614372	+	0	NA	intron (intron (N	-13287 NR_03408C	1E+08 Hs. 631163NR_03408C	ENSG000000USP3-AS1	-	USP3 antincRNA
chr2-1874.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr2	1.87E+08	1.87E+08	+	0	NA	intron (intron (N	-33038 NM_001271	10203 Hs. 470882NM_005795	ENSG000000CALCRL	CGRPR CRI	calcitonin protein-coding
chr21-262.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr21	46292550	46293264	+	0	NA	TTS (NM_C	6565 NM_001314	54059 Hs. 474066NM_058181	ENSG000000YBIE	C21orf57	ybeY meta protein-coding
chr22-296.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr22	29327813	29328209	+	0	NA	3' UTR (3' UTR (N	5307 NR_00368E	1E+08 Hs. NR_00368E	ENSG000000SNORD125	-	small ncsnoRNA
chr3-1277.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr3	1.28E+08	1.28E+08	+	0	NA	intron (intron (N	26052 NM_007283	11343 Hs. 277035NM_007283	ENSG000000MGLL	HU-K5 HUK	monoglyc protein-coding
chr3-1286.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (intron (N	9751 NM_00295C	6184 Hs. 518244NM_00295C	ENSG000000RPN1	OST1 RBPI	ribophorin protein-coding
chr4-8805.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr4	88053015	88053449	+	0	NA	intron (MER3 DNA	45597 NR_15648E	5311 Hs. 181272NM_000297	ENSG000000PKD2	APKD2 PC2	polycystin protein-coding
chr8-2337.5.650389	-0.85318	0.991087	-0.86086	0.389317	0.981636	chr8	23374323	23375418	+	0	NA	intron (LIPA5 LIN	29250 NM_00231E	4017 Hs. 626637NM_00231E	ENSG000000CLOXL2	LOR LOR2 lysyl	oxiprotein-coding
chr6-111C.4.920268	-0.661966	0.769356	-0.860146	0.38956	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (ALuSx1 SI	21405 NM_032194	84154 Hs. 372262NM_032194	ENSG000000RPF2	BXDC1 ba3	ribosome protein-coding
chr1-1542.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	exon (NM exon (NM	-1130 NM_00101C	388701 Hs. 104967NM_00101C	ENSG000000C1orf189	-	chromosome protein-coding
chr12-123.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (intron (N	1247 NR_036187	1E+08 Hs. NR_036187	ENSG000000MIR4304	-	microRNA ncRNA
chr19-252.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr19	25299806	25300554	+	0	NA	IntergeniALR Alpha	-136733 NR_00360C	1E+08 Hs. 149312NR_00360C	ENSG000000HAVCR1P1	-	hepatitis pseudo
chr3-1134.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	intron (THE1 LTF	5802 NR_107043	1.02E+08 Hs. NR_107043	ENSG000000MIR8076	hsa-mir-5	microRNA ncRNA
chr5-179C.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr5	1.79E+08	1.79E+08	+	0	NA	intron (NLIME4a LI	6361 NM_001355	345462 Hs. 445744NM_001133	ENSG000000ZNF879	DKFZp686E	zinc finger protein-coding
chr9-351C.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr9	35105035	35107484	+	0	NA	non-codirnon-codir	-3063 NM_001287	30968 Hs. 3439 NM_013442	ENSG000000STOML2	HSPC108 Sst	tomatin protein-coding
chr9-927.9.451066	-0.660924	0.768214	-0.860338	0.389603	0.981636	chr9	92253524	92253389	+	0	NA	intron (intron (N	38861 NR_037424	1.01E+08 Hs. NR_037424	ENSG000000MIR3651	mir-3651	microRNA ncRNA
chr11-972.16.18187	-0.584716	0.679875	-0.860035	0.38977	0.981636	chr11	975370	975718	+	0	NA	intron (CPg	49674 NM_01230E	161 Hs. 19121 NM_01230E	ENSG000000AP2A2	ADTAP Ct	adaptor protein-coding
chr2-1275.9.093867	-0.67139	0.780794	-0.85988	0.389853	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (THE1B LTF	63484 NM_00114E	79595 Hs. 32995 NM_02454E	ENSG000000SAP130	-	Sin3A ass protein-coding
chr4-9832.9.093867	-0.67139	0.780794	-0.85988	0.389853	0.981636	chr4	98320618	98320817	+	0	NA	intron (NLIPA2 LIN	59333 NM_02115E	5910 Hs. 132855NM_02115E	ENSG000000CRAP1GDS1	GDS1 Smg	Crp1 GTPase protein-coding
chr5-141F.9.093867	-0.67139	0.780794	-0.85988	0.389853	0.981636	chr5	14157879	14158563	+	0	NA	intron (ALuSx1 SI	14879 NM_00711E	7204 Hs. 130031NM_00711E	ENSG000000TRIO	ARHGEP23 trio	Rho protein-coding
chr22-45E.9.135006	-0.66835	0.777309	-0.85983	0.389885	0.981636	chr22	45556911	45560828	+	0	NA	TTS (NM_C	46778 NR_131244	1.01E+08 Hs. 517692NR_131244	ENSG000000LINC0158E	TCOXS_OOC	long intencRNA
chr5-873C.9.135006	-0.66835	0.777309	-0.85983	0.389885	0.981636	chr5	87304674	87304600	+	0	NA	intron (NLIPA13 LI	18061 NR_13092E	644285 Hs. 709255NR_13092E	LOC64428E	-	uncharactercncRNA
chr7-839C.9.135006	-0.66835	0.777309	-0.85983	0.389885	0.981636	chr7	839001	839200	+	0	NA	intron (intron (N	-2274 NM_001367	23353 Hs. 438072NM_025154	ENSG000000SUN1	UNC84A	Sad1 protein-coding
chr9-279C.9.135006	-0.66835	0.777309	-0.85983	0.389885	0.981636	chr9	2790902	2792190	+	0	NA	IntergeniLTRB LTF	52549 NM_01487E	9933 Hs. 493305NM_01487E	ENSG000000PUM3	HA-8 HLA-	pumilio f protein-coding
chr1-230C.9.417784	-0.658476	0.765838	-0.859812	0.389893	0.981636	chr1	23059471	23059690	+	0	NA	intron (intron (N	15275 NR_036057	1E+08 Hs. NR_036057	ENSG000000MIR3115	mir-3115	microRNA ncRNA
chr1-226E.9.417784	-0.658476	0.765838	-0.859812	0.389893	0.981636	chr1	2262678	22626E+08	+	0	NA	intron (intron (N	28407 NM_00161E	142 Hs. 177766NM_00161E	ENSG000000PARP1	ADPRT ADF	poly (ADP- protein-coding
chr1-229E.9.417784	-0.658476	0.765838	-0.859812	0.389893	0.981636	chr1	22929E+08	229E+08	+	0	NA	promoter-promoter-	-617 NM_006542	10638 Hs. 296166NM_006542	ENSG000000SPHAR	-	S-phase r protein-coding
chr17-80E.9.417784	-0.658476	0.765838	-0.859812	0.389893	0.981636	chr17	80995959	80997843	+	0	NA	intron (N FLAM_A SI	5060 NM_024591	79643 Hs. 514566NM_024591	ENSG000000CHMP6	VPS20	charged n protein-coding
chr4-533E.9.417784	-0.658476	0.765838	-0.859812	0.389893	0.981636	chr4	53383311	53383808	+	0	NA	intron (ALuSx1 SI	5906 NM_001134	81608 Hs. 555105NM_030917	ENSG000000FIP1L1	FIP1 Rhe	factor r protein-coding
chr1-1717.12.20301	-0.58537	0.680973	-0.859608	0.390005	0.981636	chr1	1.72E+08	1.72E+08	+	0	NA	intron (intron (N	5500 NM_01495E	51603 Hs. 494705NM_01495E	ENSG000000EEF1AKNM1	5630401D2e	EF1A lys protein-coding
chr2-1192.3.196387	-1.11993	1.30305	-0.85947	0.390083	0.981636	chr2	1.19E+08	1.19E+08	+	0	NA	intron (MER113A I	-13188 NR_046721	1.01E+08 Hs. 704682NR_046721	ENSG000000STAP3-AC	-	STAP3 arncRNA
chr9-692E.3.196387	-1.11993	1.30305	-0.85947	0.390083	0.981636	chr9	69235003	69235693	+	0	NA	intron (ALu SINE	30193 NR_00136E	9414 Hs. 50382 NR_004817	ENSG000000TJP2	C9DUPq21.2	tight jur protein-coding
chr10-10C.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	-11640 NM_01789E	57715 Hs. 591922NM_01789E	ENSG000000SEMA4G	-	semaphorin protein-coding
chr11-754.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr11	75407264	75408768	+	0	NA	intron (intron (N	3554 NR_00002E	114599 Hs. 689089NR_00002E	ENSG000000SNORD15B	RNU15B U1	small ncsnoRNA
chr12-46E.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr12	46513545	46516068	+	0	NA	intron (NLIPA14 LI	131199 NR_125381	1E+08 Hs. 525922NR_125377	LOC100208E	-	uncharactercncRNA
chr18-28C.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr18	2800427	2800980	+	0	NA	intron (intron (N	-46303 NM_03204E	84034 Hs. 532815NM_03204E	ENSG000000CEMLIN2	EMILIN-2 e	elastin n protein-coding
chr2-874E.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr2	87469091	87470457	+	0	NA	promoter-promoter-	-176 NR_14646C	112597 Hs. 165216NR_024204	ENSG000000CYTOR	C2orf59 D	cytoskelcncRNA
chr3-998E.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr3	99852897	99856408	+	0	NA	intron (MER20 DNA	21521 NM_00137C	11259 Hs. 104672NM_01489C	ENSG000000FILIP1L	DOC-1 DOC	filament f protein-coding
chr3-1017.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr3	1.02E+08	1.02E+08	+	0	NA	intron (NLIPA7 LIN	10812 NM_02454E	79598 Hs. 444135NM_02454E	ENSG000000CEP97	2810403BC	centrosome protein-coding
chr3-1204.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr3	1.2E+08	1.2E+08	+	0	NA	intron (intron (N	16308 NM_00708E	11167 Hs. 269512NM_00708E	ENSG000000PSTL1	FRP FSL1	foolistat protein-coding
chr7-116E.7.376057	-0.74112	0.862318	-0.85945	0.390094	0.981636	chr7	1.17E+08	1.17E+08	+	0	NA	intron (ALuJo SIN	28916 NM_00117E	857 Hs. 74034 NM_00117E	ENSG000000CAV1	BSC3L CGI	collagen protein-coding
chr19-121.12.16973	-0.583368	0.678823	-0.85938	0.390131	0.981636	chr19	12110494	12113448	+	0	NA	exon (NM exon (NM	19674 NM_00134E	388507 Hs. 127475NM_001004314	ZNF788P	ZNF788	zinc finger protein-coding
chr5-495E.12.16973	-0.583368	0.678823	-0.85938	0.390131	0.981636	chr5	49535216	49537790	+	0	NA	IntergeniALR Alpha	904785 NM_19844E	133418 Hs. 561411NM_19844E	ENSG000000EMB	GN70	emigin protein-coding
chr1-1444.11.64771	-0.599318	0.697667	-0.859032	0.390323	0.981636	chr1	1.44E+08	1.44E+08	+	0	NA	exon (NM exon (NM	15256 NR_10407E	1.02E+08 Hs. NR_10407E	ENSG000000RNVU1-15	RNU1-121 RNA,	varisnRNA
chr14-737.9.142864	-0.6697	0.779735	-0.85888	0.390405	0.981636	chr14	73718809	73723324	+	0	NA	intron (NMIR SINE	-6882 NM_00602E	9240 Hs. 194705NR_00602E	ENSG000000PNMA1	MA1	PNMA famiprotein-coding
chr7-928E.9.142864	-0.6697	0.779735	-0.85888	0.390405	0.981636	chr7	92832644	92833526	+	0	NA	intron (CPg	874 NM_00125E	1021 Hs. 119882NM_00125E	ENSG000000CDK6	MCPI12 PI	cyclin d protein-coding
chr19-38E.8.954478	-0.69086	0.80479	-0.858435	0.390652	0.981636	chr19	38888369	38889509	+	0	NA	intron (intron (N	5446 NR_03414E	22933 Hs. 466695NM_012237	ENSG000000SIRT2	SIR2 SIR2	sirtuin 2 protein-coding
chr21-39E.5.25209	-0.75586	0.880621	-0.85832	0.390714	0.981636	chr21	39213791	39232318	+	0	NA	intron (intron (N					



chr11-573.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr11	57318773	57319392	+ 0 NA	intron (AluY SINE	5870 NM_03339E	85456 Hs. 53073CNM_03339E	ENSG000002TKNS1BP1	TAB182	tankyrase protein-coding	
chr12-781.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr12	78178360	78178993	+ 0 NA	intron (intron (N	181070 NR_135021	1.05E+08 Hs. 15689ENR_135021	ENSG000002LINC02424-		long intncRNA	
chr13-102.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr13	1.03E+08	1.03E+08	+ 0 NA	intron (MER31B LI	15941 NM_001204	1.01E+08 Hs. 25842ENM_001204	ENSG000002BIVM-ERCC	ERCC5-202BIVM-ERCC	protein-coding	
chr13-106.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr13	1.1E+08	1.1E+08	+ 0 NA	exon (NM exon (N	3058 NM_00374E	8660 Hs. 442344NM_00374E	ENSG000002IRS2	IRS-2	insulin 1 protein-coding	
chr14-50E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr14	50648584	50648982	+ 0 NA	intron (AluY SINE	19523 NM_02181E	60485 Hs. 64282ENM_02181E	ENSG000002SAV1	SAV WW45	salvador protein-coding	
chr15-712.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr15	71256719	71261142	+ 0 NA	intron (AluSp SIN	-69871 NR_12034E	1.02E+08 Hs. 68047ENR_12034E	THSD4-AS1-	THSD4	antncRNA	
chr16-54E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr16	549907	550106	+ 0 NA	intron (intron (N	6729 NR_036137	1E+08 NR_036137	ENSG000002MIR3176	mir-3176	microRNA ncRNA	
chr20-17E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr20	17667918	17669556	+ 0 NA	intron (L1MED LIN	13505 NM_00136E	6238 Hs. 47221ENM_004587	ENSG000002RRBP1	ES/130 E	ribosome protein-coding	
chr4-100E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr4	10095562	10095840	+ 0 NA	intron (intron (N	-17009 NR_03609C	1E+08 NR_03609C	ENSG000002MIR3138	mir-3138	microRNA ncRNA	
chr6-162E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr6	16247663	16247930	+ 0 NA	intron (NMIR SINE	9209 NM_006877	2766 Hs. 484741NM_006877	ENSG000002GMPR1	GMPR1 G	guanosine protein-coding	
chr6-130E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr6	1.31E+08	1.31E+08	+ 0 NA	TTS (NM_C TTS (NM_C	11640 NM_00119E	1.01E+08 Hs. 38871ENM_00119E	ENSG000002SMLR1		small leu protein-coding	
chr8-118E.7.409338	-0.73563	0.859743	-0.85564	0.392198	0.981636	chr8	1.18E+08	1.18E+08	+ 0 NA	intron (NL3 LINE C	38808 NM_000127	2131 Hs. 49261ENM_000127	ENSG000002EXT1	EXT L	GCRR protein-coding	
chr10-40E.9.998501	0.624024	0.750635	0.855332	0.392367	0.981636	chr10	40837518	40837916	+ 0 NA	IntergeniALR Alpha	1530298 NR_02438C	441666 Hs. 25572ENR_02438C	ENSG000002LOC44166E		zinc fingpseudo	
chr14-52E.9.133157	-0.67836	0.793196	-0.85522	0.392429	0.981636	chr14	52874279	52875179	+ 0 NA	intron (AluJr SIN	71626 NM_00683E	10979 Hs. 50934ENM_00683E	ENSG000002FERMT2	KIND2 MIC	fermitin protein-coding	
chr10-87E.10.86252	-0.61468	0.718983	-0.85494	0.392587	0.981636	chr10	87800473	87803977	+ 0 NA	intron (NMER4-int	16006 NM_001321	84896 Hs. 43594ENM_03281C	ENSG000002ATAD1	AFDC1 FNF	ATPase f2 protein-coding	
chr12-13E.10.86252	-0.61468	0.718983	-0.85494	0.392587	0.981636	chr12	1.33E+08	1.33E+08	+ 0 NA	intron (AluSp SIN	-17364 NM_015114	23141 Hs. 65462ENM_015114	ENSG000002ANKLE2	KIAA0692	ankyrin 1 protein-coding	
chr9-110E.10.86252	-0.61468	0.718983	-0.85494	0.392587	0.981636	chr9	1.11E+08	1.11E+08	+ 0 NA	3' UTR (N3' UTR (N	145883 NM_00136E	4593 Hs. 52165ENM_00559E	ENSG000002MUSK	CMS9 FADS	muscle as protein-coding	
chr1-94E.7.170289	0.747555	0.874437	0.854899	0.392607	0.981636	chr1	946308	947052	+ 0 NA	intron (intron (N	12576 NM_01565E	26155 Hs. 405987NM_01565E	ENSG000002NOC2L	CMT15 NEI	NOC2 like protein-coding	
chr10-10E.7.170289	0.747555	0.874437	0.854899	0.392607	0.981636	chr10	1093973	1094655	+ 0 NA	intron (NMER58A DN	-37610 NR_13430C	3422 Hs. 28365ENM_00450E	ENSG000002IDI1	IPPI IPPI	isoprenyl protein-coding	
chr2-262E.7.170289	0.747555	0.874437	0.854899	0.392607	0.981636	chr2	96252531	96253875	+ 0 NA	3' UTR (N3' UTR (N	12794 NM_00119E	55654 Hs. 16430ENM_01784E	ENSG000002MEM127		transmem protein-coding	
chr22-20E.7.170289	0.747555	0.874437	0.854899	0.392607	0.981636	chr22	20036690	20037116	+ 0 NA	non-codir-non-codir	3764 NR_02970E	406961 NR_02970E	ENSG000002MIR185	MIRN185 n	microRNA ncRNA	
chr6-387E.7.170289	0.747555	0.874437	0.854899	0.392607	0.981636	chr6	38700219	38700482	+ 0 NA	intron (intron (N	2795 NM_00670E	2739 Hs. 26884ENM_00670E	ENSG000002GLO1	GLOD1 GLY	glyoxalase protein-coding	
chr9-136E.7.170289	0.747555	0.874437	0.854899	0.392607	0.981636	chr9	1.37E+08	1.37E+08	+ 0 NA	3' UTR (N3' UTR (N	18662 NM_01899E	54461 Hs. 522507NM_01899E	ENSG000002FBXW5	Fbxw5	F-box anc protein-coding	
chr1-465E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr1	46561197	46567963	+ 0 NA	intron (AluSp SIN	-12923 NM_00132E	148930 Hs. 350764NM_18251E	ENSG000002KNCN	Kino L5	kinociliar protein-coding	
chr1-234E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr1	2.34E+08	2.34E+08	+ 0 NA	intron (L1MEF LIN	38976 NM_00564E	6894 Hs. 49811ENM_00564E	ENSG000002TARBP1	TRM3 TRM1	TAR (HIV- protein-coding	
chr11-64E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr11	6459466	6461361	+ 0 NA	intron (intron (N	13528 NM_03327E	10612 Hs. 59199ENM_00645E	ENSG000002TRIM3	BERP HAC1	tripartit protein-coding	
chr12-11E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr12	1.12E+08	1.12E+08	+ 0 NA	intron (intron (N	-92762 NR_106921	1.02E+08 NR_106921	ENSG000002MIR6861	HSA miR	microRNA ncRNA	
chr12-12E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr12	1.21E+08	1.21E+08	+ 0 NA	intron (AluSq2 SI	9979 NM_001037	8655 Hs. 5120 NR_00374E	ENSG000002YNLL1	DLCL1 DLCC	dynein 1 protein-coding	
chr13-11E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr13	1.13E+08	1.13E+08	+ 0 NA	intron (AluJb SIN	6734 NM_19916E	113622 Hs. 98669 NM_13843C	ENSG000002ADPRHL1	ARH2	ADP-ribos protein-coding	
chr15-30E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr15	30475640	30476364	+ 0 NA	intron (AluSp SIN	2019 NR_03665E	11E+08 Hs. 56262ENR_036650	WHAMMP1	WHDC1P1	W5 protepseudo	
chr18-12E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr18	12449032	12449527	+ 0 NA	3' UTR (N3' UTR (N	16505 NR_136514	1.05E+08 Hs. 51528ENR_136514	LOC105371-		uncharactncRNA	
chr19-29E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr19	29706945	29707325	+ 0 NA	intron (AluSx6 SI	7913 NM_00128E	83636 Hs. 529094NM_03144E	ENSG000002C19orf12	MPAN NBI	chromosome protein-coding	
chr4-561E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr4	5610592	5611124	+ 0 NA	intron (intron (N	85752 NR_126517	10141 Hs. 17792ENM_00575E	ENSG000002LINC01587	CAForf6 a	long intncRNA	
chr6-829E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr6	82930624	82932149	+ 0 NA	intron (THE1C-int	134455 NM_00135C	90025 Hs. 14860ENM_19892C	ENSG000002CUBE3D	C6orf157 u	ubiquitin protein-coding	
chr7-745E.5.452664	0.849467	0.993824	0.854746	0.392692	0.981636	chr7	74510846	74512868	+ 0 NA	intron (intron (N	57951 NM_01632E	9569 Hs. 64705ENM_00568E	ENSG000002GTF21RD1	BEN CREAM	GTF2I rep protein-coding	
chr1-221E.9.96522	0.639663	0.748441	0.854623	0.39276	0.981636	chr1	2.22E+08	2.22E+08	+ 0 NA	intron (intron (N	4929 NR_11193E	11221 Hs. 49782ENM_00720E	ENSG000002DUSP10	MKP-5 MKF	dual spec protein-coding	
chr19-10E.6.616846	0.799175	0.935131	0.854613	0.392765	0.981636	chr19	10454948	10455151	+ 0 NA	intron (intron (N	2117 NM_00620E	5141 Hs. 89901 NM_00620E	ENSG000002PDE4A	DPDE2 PDF	phosphodi protein-coding	
chr19-50E.7.154574	0.752167	0.880397	0.85435	0.392911	0.981636	chr19	50382025	50382266	+ 0 NA	exon (NM exon (N	-2178 NM_00125E	5424 Hs. 27941ENM_00269E	ENSG000002POLD1	CDC2 CRCS	DNA polyn protein-coding	
chr4-269E.7.342775	-0.74675	0.874114	-0.85429	0.392945	0.981636	chr4	26920401	26921025	+ 0 NA	intron (intron (N	59887 NM_02086C	57620 Hs. 74495ENM_02086C	ENSG000002STIM2		stromal protein-coding	
chr1-123E.42.13848	0.349653	0.409303	0.854266	0.392958	0.981636	chr1	1.24E+08	1.24E+08	+ 0 NA	IntergeniALR Alpha	2016633 NR_00395E	647121 Hs. 69768ENR_00395E	ENSG000002EMBPI1		embigin fpseudo	
chr15-40E.9.119291	-0.66563	0.779192	-0.85426	0.392961	0.981636	chr15	49131275	49131682	+ 0 NA	intron (intron (N	24121 NM_00114E	9318 Hs. 369614NM_00423E	ENSG000002COP5E	ALIEN CSN	COP9 sigr protein-coding	
chr4-109E.9.119291	-0.66563	0.779192	-0.85426	0.392961	0.981636	chr4	10072403	10075574	+ 0 NA	TTS (NM_C TTS (NM_C	4704 NR_03609C	ENSG000002MIR3138	1E+08 NR_03609C	ENSG000002MIR3138	ALIEN CSN	COP9 sigr protein-coding
chr4-113E.9.119291	-0.66563	0.779192	-0.85426	0.392961	0.981636	chr4	1.14E+08	1.14E+08	+ 0 NA	3' UTR (N3' UTR (N	77839 NM_00135A	79642 Hs. 22895 NM_02459C	ENSG000002CARSJ	ASJ	arylsulf protein-coding	
chr1-166E.14.91196	0.531373	0.622083	0.854183	0.393004	0.981636	chr1	16603810	16604399	+ 0 NA	intron (intron (N	9501 NM_01794C	55672 Hs. 467587NM_01794C	ENSG000002NBPF1	AB13 AB14	NBPF memt protein-coding	
chr16-39E.9.973078	0.637966	0.746877	0.854177	0.393007	0.981636	chr16	3965992	3966681	+ 0 NA	exon (NM exon (N	-15892 NR_120311	1.03E+08 Hs. 36473ENR_120311	ENSG000002LOC102724-		uncharactncRNA	
chr11-15E.5.444806	0.852527	0.998892	0.853473	0.393397	0.981636	chr11	15232763	15233814	+ 0 NA	intron (intron (N	84186 NM_00127E	387755 Hs. 591997NM_00103E	ENSG000002INSC		INSC spir protein-coding	
chr19-54E.5.444806	0.852527	0.998892	0.853473	0.393397	0.981636	chr19	54175674	54177473	+ 0 NA	intron (NMER20 DN	-3413 NM_00114E	147798 Hs. 35512ENM_14468E	ENSG000002TMC4		transmem protein-coding	
chr6-897E.5.444806	0.852527	0.998892	0.853473	0.393397	0.981636	chr6	89770478	89771746	+ 0 NA	intron (NLTR35B LI	48682 NM_014611	23195 Hs. 52994ENM_014611	ENSG000002MDM1	Real	midasin 1 protein-coding	
chr7-140E.5.444806	0.852527	0.998892	0.853473	0.393397	0.981636	chr7	1.4E+08	1.4E+08	+ 0 NA	intron (L1ME4b LI	44790 NM_00136E	84255 Hs. 446021NM_03229E	ENSG000002SLC37A3		solute c protein-coding	
chr3-152E.6.840179	-0.79859	0.935709	-0.85346	0.393406	0.981636	chr3	15224519	15224733	+ 0 NA	intron (L1ME4a LI	18380 NM_01429E	23473 Hs. 595234NM_01429E	ENSG000002CAPN7	CALPAINT	calpain 7 protein-coding	
chr3-12E.9.086009	-0.67004	0.785167	-0.85338	0.39345	0.981636	chr3	1.25E+08	1.25E+08								

chr16-317 5.460522	0.846349	0.998774	0.847388	0.396779	0.981636	chr16	31750939	31752384	+	0 NA	intron (NLIP4 LINE)	38432 NM_00113C	124411 Hs. 528822cNM_001004	ENSG000002ZNF720	-	zinc finger protein-coding	
chr16-68: 5.460522	0.846349	0.998774	0.847388	0.396779	0.981636	chr16	68322001	68322350	+	0 NA	intron (Nintron (N	11061 NM_00129C	54946 Hs. 64022cNM_01902c	ENSG000002PRM77	-	SBIDDS protein-coding	
chr19-12: 5.460522	0.846349	0.998774	0.847388	0.396779	0.981636	chr19	12236540	12237500	+	0 NA	IntergeniMER57E3 I	42005 NR_10417E	1E+08 Hs. 66260cNR_104179	LOC10028c	-	uncharacterized RNA	
chr19-35: 5.460522	0.846349	0.998774	0.847388	0.396779	0.981636	chr19	35941859	35942455	+	0 NA	intron (NALuYm S I	-4958 NR_13652E	1.05E+08 Hs. 64159cNR_136525	LOC10537c	-	uncharacterized RNA	
chr21-46: 5.460522	0.846349	0.998774	0.847388	0.396779	0.981636	chr21	46208062	46211257	+	0 NA	intron (Nintron (N	-15500 NR_147580	1.1E+08 NR_147580	SNORD159	-	small nucleolar RNA	
chr3-379: 5.460522	0.846349	0.998774	0.847388	0.396779	0.981636	chr3	37980554	37983258	+	0 NA	3' UTR (N3' UTR (N	-11681 NM_01587c	50853 Hs. 10366cNM_01587c	ENSG000002CIVL	-	villin liprotein-coding	
chr5-8147 11.31427	-0.59921	0.70732	-0.84716	0.396906	0.981636	chr5	81473208	81473738	+	0 NA	intron (NLIP4 LINE)	-79354 NM_130767	134526 Hs. 59175cNM_130767	ENSG000002ACOT12	-	CACH-1 Caelyl-CoA protein-coding	
chr12-301 6.932166	-0.77789	0.918265	-0.84713	0.396924	0.981636	chr12	301829	3021300	+	0 NA	intron (NLIP4 LINE)	-39106 NM_00119C	6540 Hs. 50439cNM_01661c	ENSG000002SLC6A13	-	GAT-2 GAI solute c protein-coding	
chr4-118: 6.932166	-0.77789	0.918265	-0.84713	0.396924	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (NL2c LINE )	8903 NM_01482c	9871 Hs. 189641cNM_01482c	ENSG000002SEC24D	-	CLCRP2 SEC24 hom protein-coding	
chr20-38: 7.735291	0.724064	0.854743	0.847112	0.396932	0.981636	chr20	38063902	38064539	+	0 NA	intron (Nintron (N	30474 NM_02121E	58490 Hs. 27883cNM_02121E	ENSG000002RPRD1B	-	C20orf77 regulator protein-coding	
chr9-1364 4.897371	0.913331	1.078433	0.846906	0.397047	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	-2675 NM_152571	158055 Hs. 21261cNM_152571	C9orf163	-	chromosome protein-coding	
chr15-307 5.675812	-0.84343	0.995921	-0.84689	0.397059	0.981636	chr15	30730979	30731367	+	0 NA	intron (Nintron (N	72456 NR_03825E	1E+08 Hs. 66895cNR_03825E	ENSG000002LOC10028E	-	OTU deubiquitinase	
chr16-24: 5.675812	-0.84343	0.995921	-0.84689	0.397059	0.981636	chr16	2446257	2447188	+	0 NA	intron (Nintron (N	1330 NR_10682E	1.02E+08 NR_10682E	ENSG000002MIR6767	-	hsa-mir-61 microRNA ncRNA	
chr4-880 5.675812	-0.84343	0.995921	-0.84689	0.397059	0.981636	chr4	88063355	88063833	+	0 NA	intron (Nintron (N	55958 NR_15648E	5311 Hs. 18127cNM_000297	ENSG000002PKD2	-	APKD2 PC2 polycystin protein-coding	
chr7-560: 5.675812	-0.84343	0.995921	-0.84689	0.397059	0.981636	chr7	56027849	56028347	+	0 NA	intron (Nintron (N	23346 NM_00137C	5723 Hs. 51265cNM_004577	ENSG000002PSPH	-	PSP PSPH phosphoprotein-coding	
chr17-75: 5.642531	-0.85093	1.005244	-0.84649	0.39728	0.981636	chr17	75680686	75680885	+	0 NA	intron (NALuYb S I	13447 NM_01326C	29115 Hs. 65508cNM_01326C	ENSG000002SAP30BP	-	HCGNG HITSAP30 bir protein-coding	
chr5-873: 5.642531	-0.85093	1.005244	-0.84649	0.39728	0.981636	chr5	87370504	87371207	+	0 NA	intron (Nintron (N	42049 NM_00119E	902 Hs. 292524cNM_00123E	ENSG000002CCNH	-	CAK CyclH cyclin H protein-coding	
chr7-121: 4.468456	-0.94187	1.112785	-0.8464	0.397327	0.981636	chr7	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	82165 NM_00110E	79974 Hs. 18965cNM_02491E	ENSG000002CPED1	-	C7orf58 cadherin protein-coding	
chr18-12: 4.460598	-0.93931	1.109807	-0.84638	0.397343	0.981636	chr18	12971346	12972088	+	0 NA	intron (NL2c LINE )	-19645 NM_03214E	55125 Hs. 100914cNM_01806E	ENSG000002CEP192	-	PPP1R62 centrosome protein-coding	
chr4-787: 4.460598	-0.93931	1.109807	-0.84638	0.397343	0.981636	chr4	78794730	78795369	+	0 NA	intron (Nintron (N	18671 NM_19898E	55589 Hs. 146551cNM_01759E	ENSG000002BMP2K	-	BIKE HRI BMP2 indt protein-coding	
chr9-137: 4.460598	-0.93931	1.109807	-0.84638	0.397343	0.981636	chr9	1.38E+08	1.38E+08	+	0 NA	intron (Nintron (N	35176 NR_14750E	651337 Hs. 60319cNR_14750E	ENSG000002LOC651337	-	uncharacterized RNA	
chr1-855: 21.97981	-0.44344	0.523942	-0.84636	0.397355	0.981636	chr1	85581111	85583536	+	0 NA	intron (Nintron (N	1562 NM_001554	3491 Hs. 8867	NR_001554	ENSG000002CCN1	-	CYR61 GIC cellular protein-coding
chr1-185: 9.955512	0.632293	0.747175	0.846245	0.397416	0.981636	chr1	1.85E+08	1.85E+08	+	0 NA	intron (NLIM7 LINE )	22105 NM_030934	81627 Hs. 10714cNM_030934	ENSG000002TRMT1L	-	Clorf25 tRNA met protein-coding	
chr1-207: 9.955512	0.632293	0.747175	0.846245	0.397416	0.981636	chr20	2.08E+08	2.08E+08	+	0 NA	intron (Nintron (N	9579 NM_17235E	4179 Hs. 51403cNM_00238E	ENSG000002CD46	-	AHUS2 MCFC46 mole protein-coding	
chr19-52: 9.955512	0.632293	0.747175	0.846245	0.397416	0.981636	chr19	52156855	52165237	+	0 NA	intron (NMIR SINE )	10575 NM_00110E	162962 Hs. 631584cNM_00110E	ENSG000002ZNF836	-	zinc finger protein-coding	
chr8-102: 9.955512	0.632293	0.747175	0.846245	0.397416	0.981636	chr8	1.02E+08	1.02E+08	+	0 NA	intron (Nintron (N	14226 NM_00117E	51034 Hs. 51259cNM_01571E	ENSG000002RRM2B	-	MTDPS8A ribonucleic protein-coding	
chr16-30: 9.955512	-0.56623	0.66913	-0.84622	0.397431	0.981636	chr20	30288275	30288614	+	0 NA	intron (NALuJo S I	-40031 NM_001321	60387 Hs. 58573cNM_001321	ENSG000002NPIP13	-	nuclear i protein-coding	
chr1-235: 12.67417	0.564203	0.666745	0.846205	0.397438	0.981636	chr1	23557487	23559335	+	0 NA	3' UTR (N3' UTR (N	1090 NM_002167	3399 Hs. 76884	NR_002167	ENSG000002ID3	-	HEIR-1 hb inhibitor protein-coding
chr16-34: 12.67417	0.564203	0.666745	0.846205	0.397438	0.981636	chr16	3403837	3409864	+	0 NA	TTS (NM_C TTS (NM_C	5635 NM_001347	7727 Hs. 155204cNM_00345E	ENSG000002ZNF174	-	ZSCAN8 zinc finger protein-coding	
chr7-64: 12.67417	0.564203	0.666745	0.846205	0.397438	0.981636	chr7	6445609	6448584	+	0 NA	intron (NALuSj S I	2263 NM_13917E	221955 Hs. 48749cNM_13917E	ENSG000002DAGLB	-	DAGLBETA diacylglycerol protein-coding	
chr1-114: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr1	11146406	11146951	+	0 NA	exon (NM_exon (NM_	2780 NR_04660C	1.01E+08 Hs. 67913cNR_04660C	ENSG000002MTOR-AS1	-	MTOR anticRNA	
chr1-204: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr1	20644185	20644700	+	0 NA	intron (Nintron (N	7751 NR_046507	1.01E+08 Hs. 71025cNR_046507	ENSG000002PINK1-AS	-	NAPINK1 PINK1 anticRNA	
chr11-66: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr11	64281228	64282717	+	0 NA	intron (NALuSc S I	-2367 NM_00117C	56834 Hs. 52376cNM_02015E	ENSG000002GPR137	-	CL1orf4 C protein-coding	
chr11-69: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr11	69055436	69055635	+	0 NA	intron (Nintron (N	6603 NM_13907E	219931 Hs. 131851cNM_13907E	ENSG000002TPCN2	-	SHEP10 Tf two pore protein-coding	
chr11-13: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr11	1.3E+08	1.3E+08	+	0 NA	TTS (NM_C TTS (NM_C	-14686 NM_02197E	6768 Hs. 50431cNM_02197E	ENSG000002ST14	-	ARCT11 H suppressin protein-coding	
chr14-10: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr14	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	21823 NM_14568E	2972 Hs. 424484cNM_00151E	ENSG000002BRF1	-	BRF1 BRF1 RNA protein-coding	
chr2-208: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr2	2.08E+08	2.08E+08	+	0 NA	intron (NALuJr4 S I	6540 NM_00128E	3417 Hs. 59342cNM_00589E	ENSG000002IDH1	-	HEL-216 E isocitrat protein-coding	
chr3-488: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr3	48858593	48859385	+	0 NA	intron (Nintron (N	11052 NR_10999E	1.01E+08 Hs. 63425cNR_10999E	ENSG000002PRKAR2A-1	-	PRKAR2A ncRNA	
chr8-143: 7.178147	0.745127	0.880686	0.846076	0.39751	0.981636	chr8	1.44E+08	1.44E+08	+	0 NA	3' UTR (N3' UTR (N	2390 NR_106904	1.02E+08 NR_106904	ENSG000002MIR6845	-	hsa-mir-61 microRNA ncRNA	
chr22-40: 12.11888	0.576649	0.682286	0.845172	0.398015	0.981636	chr22	40300708	40301607	+	0 NA	exon (NM_exon (NM_	-45343 NM_00136E	158 Hs. 75527	NR_00002E	ENSG000002ADSL	-	AMPS ASAs adenylost protein-coding
chr22-22: 11.33184	-0.59343	0.702455	-0.84479	0.398226	0.981636	chr22	37676457	37676804	+	0 NA	intron (NL2b LINE )	2534 NM_00230E	3956 Hs. 445351cNM_00230E	ENSG000002LGLS1	-	GALL GB galactin protein-coding	
chr5-37: 11.33184	-0.59343	0.702455	-0.84479	0.398226	0.981636	chr5	73767183	73767964	+	0 NA	intron (THE1B-int	-46153 NM_001244	64283 Hs. 482521cNM_00108E	ENSG000002ARHGFE28	-	RGNEF RIF Rho guaniprotein-coding	
chr1-179: 9.92223	0.629923	0.745685	0.844757	0.398246	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (Nintron (N	19305 NM_00134E	163590 Hs. 571797cNM_022347	ENSG000002TOR1AIP2	-	IFRG15 Ll torsin 1 protein-coding	
chr2-443: 9.92223	0.629923	0.745685	0.844757	0.398246	0.981636	chr2	44310032	44315241	+	0 NA	exon (NM_exon (NM_	37156 NM_000341	6519 Hs. 11291cNM_000341	ENSG000002SLC3A1	-	ATRI CSN solute c protein-coding	
chr1-146: 7.733441	0.712339	0.843414	0.84459	0.39834	0.981636	chr1	1.47E+08	1.47E+08	+	0 NA	intron (NLTR5_Hs I	10133 NM_00127E	149013 Hs. 666981cNM_00127E	ENSG000002CNBP12	-	COAS1 KI ANBP mem protein-coding	
chr15-77: 7.733441	0.712339	0.843414	0.84459	0.39834	0.981636	chr15	7798716	77999244	+	0 NA	intron (Nintron (N	-4755 NR_02699E	91450 Hs. 40676cNR_02699E	LOC91450	-	uncharacterized RNA	
chr16-15: 7.733441	0.712339	0.843414	0.84459	0.39834	0.981636	chr16	15616662	15617835	+	0 NA	intron (Nintron (N	-6153 NR_106761	1.02E+08 NR_106761	ENSG000002MIR6506	-	hsa-mir-61 microRNA ncRNA	
chr19-62: 7.733441	0.712339	0.843414	0.84459	0.39834	0.981636	chr19	628517	628890	+	0 NA	intron (NLIM4 LINE )	4834 NM_00503E	5442 Hs. 25411cNM_00503E	ENSG000002POLRMT	-	APOLMT MTRNA poly protein-coding	
chr22-50: 7.733441	0.712339	0.843414	0.84459	0.39834	0.981636	chr22	50453649	50457157	+	0 NA	exon (NM_exon (NM_	19632 NM_00297E	6305 Hs. 589924cNM_00297E	ENSG000002SBF1	-	CMT4B3 DE SET bindi protein-coding	
chr9-134: 7.733441	0.712339	0.843414	0.84459	0.39834	0.981636	chr9	1.33E+08	1.									



chr14-347 6. 127561	-0.79458	0.945886	-0.84004	0.400884	0.981636	chr14	34775474	34776839	+ 0 NA	exon (NM exon (NM	-61333 NR_02813C	1073 Hs. 180141NM_021914	ENSG00000CFL2	NEM7	cofilin 2 protein-coding		
chr15-487 6. 127561	-0.79458	0.945886	-0.84004	0.400884	0.981636	chr15	48741061	48741612	+ 0 NA	intron (HALIME LI	69733 NM_01498E	22995 Hs. 44300FNM_01498E	ENSG00000CEP152	MCPH4 MCFC	centrosome protein-coding		
chr16-184 6. 127561	-0.79458	0.945886	-0.84004	0.400884	0.981636	chr16	18499090	18499484	+ 0 NA	TTS (NM_TTS (NM_I	-4711 NR_03614E	1E+08	NR_03614E	ENSG00000CIR3179	microRNA ncRNA		
chr3-9484 6. 127561	-0.79458	0.945886	-0.84004	0.400884	0.981636	chr3	9484254	9485202	+ 0 NA	IntergeniLMC2 LI	69094 NM_19856E	375323 Hs. 56782E	NR_19856E	ENSG00000LHFP4	GARLH4	LHFP4 ltr protein-coding	
chr1-9444 15. 42426	0.51635	0.614785	0.839887	0.400972	0.981636	chr1	94449174	94450846	+ 0 NA	intron (HERVC2 IR	31621 NM_00285E	5825 Hs. 70057E	NR_00285E	ENSG00000ABCDC3	ABC43 CBATP	bindi protein-coding	
chr19-27C 15. 42426	0.51635	0.614785	0.839887	0.400972	0.981636	chr19	27076526	27077680	+ 0 NA	IntergeniALR Alpha	-716328 NR_14673E	1.02E+08	Hs. 567934NR_110687	ENSG00000CLOC101927	uncharacterized ncRNA		
chr5-4932 28. 87428	0.399333	0.475563	0.839707	0.401073	0.981636	chr5	49325611	49326176	+ 0 NA	IntergeniALR Alpha	1115395 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	emgbin protein-coding		
chr8-3875 5. 716952	-0.83786	0.997836	-0.83968	0.401088	0.981636	chr8	38794685	38795441	+ 0 NA	intron (intron (N	6957 NM_00135E	6867 Hs. 27924E	NR_00628E	ENSG00000TACC1	GA55	transform protein-coding	
chr9-703C 11. 36512	-0.58995	0.70267	-0.83959	0.40114	0.981636	chr9	70301421	70302922	+ 0 NA	intron (AluSx SIN	43193 NM_01511C	23137 Hs. 53418E	NR_01511C	ENSG00000CMC5	SMC5L1	structural protein-coding	
chr1-1234 18. 59652	0.471842	0.562018	0.83955	0.401161	0.981636	chr1	1.23E+08	1.23E+08	+ 0 NA	IntergeniALR Alpha	1904312 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000EMB51	emgbin ltr pseudo		
chr4-398 6. 370864	-0.85099	1.013966	-0.83927	0.401318	0.981636	chr4	39886377	39886576	+ 0 NA	intron (AluSp SIN	91435 NM_00110C	23244 Hs. 331431NM_01520C	ENSG00000PDS5A	PIG54 SCC	PDS5 cohesin protein-coding		
chr3-1237 11. 35726	-0.58884	0.701628	-0.83925	0.40133	0.981636	chr3	1.24E+08	1.24E+08	+ 0 NA	intron (intron (N	43925 NR_04662E	1.01E+08	Hs. 66731E	NR_04662E	ENSG00000MYLK-AS2	MYLK	antincRNA
chr1-123 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr1	12318148	12318579	+ 0 NA	intron (intron (N	88333 NM_01537E	55187 Hs. 439381NM_01537E	ENSG00000VPS13D	SCAR4	vacuolar protein-coding		
chr1-1924 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr1	19241935	19241879	+ 0 NA	intron (intron (N	8148 NM_001271	23065 Hs. 43920C	NR_015047	ENSG00000EMC1	CAV1PMR BER	membrane protein-coding	
chr1-1565 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr1	1.57E+08	1.57E+08	+ 0 NA	intron (AluJr SIN	-14311 NR_030527	768220	NR_030527	ENSG00000CIR765	MIRN765 f	microRNA ncRNA	
chr1-1656 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr1	1.66E+08	1.66E+08	+ 0 NA	intron (intron (N	21749 NM_00452E	4259 Hs. 191734NM_00452E	ENSG00000MGST3	GST-III	microsome protein-coding		
chr1-183 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr1	1.84E+08	1.84E+08	+ 0 NA	intron (LIMD3 LIN	94405 NM_001297	23179 Hs. 49714E	NR_01514E	ENSG00000CRL1	RGL	racal guanine protein-coding	
chr10-11 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr10	1.13E+08	1.13E+08	+ 0 NA	intron (intron (N	23963 NM_00134E	6934 Hs. 59399E	NR_03075E	ENSG00000CF7L2	TCF-4 TCF	transcription protein-coding	
chr11-714 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr11	71482874	71486899	+ 0 NA	intron (N (AGTGTG	11383 NR_10681E	1.02E+08	NR_10681E	ENSG00000MIR6754	hsa-mir-6	microRNA ncRNA	
chr12-122 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr12	1.22E+08	1.22E+08	+ 0 NA	3' UTR (N3' UTR (N	-4274 NM_019887	56616 Hs. 169611NM_019887	ENSG00000DIABLO	DFNA64 S	diablo 1 protein-coding		
chr14-677 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr14	67788126	67790794	+ 0 NA	exon (NM exon (NM	21730 NM_01534E	23503 Hs. 98041	NR_01534E	ENSG00000ZFVY26	FYVE-CEN1	zinc finger protein-coding	
chr15-52E 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr15	52609217	52612108	+ 0 NA	intron (intron (N	-41216 NM_00130E	10776 Hs. 51290E	NR_00662E	ENSG00000ARPP19	ARPP-16 A	cAMP regulated protein-coding	
chr15-72 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr15	72241068	72241470	+ 0 NA	TTS (NR_TTS (NR_I	-9645 NM_00120E	5315 Hs. 53477E	NR_00265E	ENSG00000CPKM	CTHBP HEL	pyruvate protein-coding	
chr16-864 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr16	8641854	8645685	+ 0 NA	intron (AluSx SIN	22071 NR_13460E	79091 Hs. 30638E	NR_02410E	ENSG00000METTL22	C16orf68	methyltransferase protein-coding	
chr17-121 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr17	12118287	12118486	+ 0 NA	intron (Tigger4 I	36487 NR_03061E	1E+08	NR_03061E	ENSG00000CIR744	MIRN744 f	microRNA ncRNA	
chr17-182 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr17	18263175	18265562	+ 0 NA	exon (NM exon (NM	3258 NM_14888E	125170 Hs. 65555E	NR_13916E	ENSG00000MIEF2	MID49 SMC	mitochondrial protein-coding	
chr17-29C 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr17	29085785	29089594	+ 0 NA	exon (NM exon (NM	-16760 NM_00474C	9220 Hs. 46259E	NR_00474C	ENSG00000TIAF1	MAJN SPR2	TGFBI-nc protein-coding	
chr19-237 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr19	23744153	23744755	+ 0 NA	exon (NM exon (NM	14437 NM_13828E	148213 Hs. 39995E	NR_13828E	ENSG00000ZNF681	zinc finger protein-coding		
chr19-40 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr19	40321902	40326795	+ 0 NA	intron (intron (N	24049 NR_04620E	126526 Hs. 631557NM_17883C	ENSG00000C19orf47	chromosom protein-coding			
chr2-702 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr2	70264858	70267778	+ 0 NA	intron (MLT1D LTF	8181 NM_016297	51449 Hs. 56750E	NR_016297	ENSG00000PCYOX1	PCL1	prenylation protein-coding	
chr2-1137 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr2	1.14E+08	1.14E+08	+ 0 NA	intron (THE1D LTF	-5699 NR_03994E	1.01E+08	NR_03994E	ENSG00000CIR4782	microRNA ncRNA		
chr2-504 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr2	50458534	50464586	+ 0 NA	exon (NM exon (NM	13475 NM_00297E	6305 Hs. 58992E	NR_00297E	ENSG00000SBF1	CMT4B3 DEF	SET domain protein-coding	
chr3-1965 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr3	1.97E+08	1.97E+08	+ 0 NA	3' UTR (N3' UTR (N	-8536 NR_04663C	1.01E+08	Hs. 591671NR_04663C	NCBP2-AS1	NCBP2	antincRNA	
chr4-323 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr4	3235435	3236486	+ 0 NA	intron (intron (N	-8409 NM_00133C	345222 Hs. 442291NM_00101E	ENSG00000CMSANTD1	C4orf44	Myb/SANT protein-coding		
chr6-352E 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr6	35289275	35293597	+ 0 NA	intron (intron (N	-6382 NM_022047	50619 Hs. 15476	NR_022047	ENSG00000DEF6	I6P SLAT DEF6	guar protein-coding	
chr6-441 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr6	44134734	44150081	+ 0 NA	intron (AluSx4 SI	14853 NM_01842E	55362 Hs. 41447E	NR_01842E	ENSG00000TMEM63B	Gor110	transmembrane protein-coding	
chr6-832 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr6	83292543	83292917	+ 0 NA	intron (LIPA7 LIN	-98830 NM_00119E	5238 Hs. 66166E	NR_01559E	ENSG00000PGM3	AGM1 IMD2	phosphoglycoprotein-coding	
chr7-259E 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr7	2598280	2599647	+ 0 NA	intron (intron (N	-33023 NM_02525E	80727 Hs. 44089E	NR_02525E	ENSG00000TTYH3	twinty 2 protein-coding		
chr7-1392 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr7	1.39E+08	1.39E+08	+ 0 NA	intron (AluSx SIN	28821 NM_17356E	254048 Hs. 15345E	NR_17356E	ENSG00000UBN2	ubiquitin-like protein-coding		
chr9-7171 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr9	71710937	71712754	+ 0 NA	intron (intron (N	56668 NM_00113E	23670 Hs. 49414E	NR_01339E	ENSG00000CEMP2	TMEM2	cell migration protein-coding	
chr9-9271 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr9	92715877	92716076	+ 0 NA	intron (intron (N	-45845 NM_002275E	64768 Hs. 45989E	NR_02275E	ENSG00000IPPK	C9orf12 L	inositol protein-coding	
chr9-9101 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr9	1.1E+08	1.1E+08	+ 0 NA	intron (MIRb SINE	-23457 NM_00113E	445815 Hs. 59190E	NR_00720E	ENSG00000PALM2-AK1	AKAP-2 AK	PALM2-AK1 protein-coding	
chr9-127E 7. 708017	0.707269	0.842964	0.839026	0.401454	0.981636	chr9	1.28E+08	1.28E+08	+ 0 NA	intron (intron (N	36969 NR_03747E	1.01E+08	NR_03747E	ENSG00000CIR3911	mir-3911	microRNA ncRNA	
chr17-821 7. 684443	0.713747	0.850822	0.838891	0.401531	0.981636	chr17	82197738	82198223	+ 0 NA	intron (MLT2B1 LI	14862 NM_00131E	284001 Hs. 631724NM_15267E	ENSG00000CCDC57	coiled-coil protein-coding			
chr19-374 7. 684443	0.713747	0.850822	0.838891	0.401531	0.981636	chr19	37444229	37444633	+ 0 NA	intron (LIME3 LI	22978 NM_00133C	148266 Hs. 51184E	NR_15248E	ENSG00000ZNF569	ZAP1 ZNF	zinc finger protein-coding	
chr20-33 7. 684443	0.713747	0.850822	0.838891	0.401531	0.981636	chr20	33091429	33091623	+ 0 NA	intron (MERC3 DNA	10187 NM_01640E	51654 Hs. 43595E	NR_01608E	ENSG00000CDK5RAP1	C20orf34 CDK5	regulatory protein-coding	
chr17-637 9. 103575	-0.66281	0.790329	-0.83865	0.401667	0.981636	chr17	63776664	63777016	+ 0 NA	intron (MIR SINE	2651 NM_00737E	11325 Hs. 70201C	NR_00737E	ENSG00000DDX42	DDX42P RF	DEAD-box protein-coding	
chr21-451 9. 103575	-0.66281	0.790329	-0.83865	0.401667	0.981636	chr21	45185158	45189974	+ 0 NA	intron (LIME3Cz I	35036 NM_00134E	104 Hs. 47401E	NR_00111E	ENSG00000ADARB1	ADAR2 DRP	adenosine protein-coding	
chr1-1121 8. 934234	1.065201	1.270318	0.83851	0.401733	0.981636	chr1	11216088	11216425	+ 0 NA	intron (intron (N	26901 NM_02114E	10218 Hs. 14655E	NR_02114E	ENSG00000ANGPTL7	AngX CDTc	angiopoietin protein-coding	
chr10-115 6. 160843	-0.78785	0.939572	-0.83852	0.401741	0.981636	chr10	1.2E+08	1.2E+08	+ 0 NA	intron (intron (N	5631 NM_004281	9531 Hs. 52330					



chr7-1006 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr6	1.01E+08	0 NA	intron (Nintron (N	-191851 NM_005066	6492 Hs. 5202929	NR_005066	ENSG00000CSIM1	bHLHe14	SIM	bHLH protein-coding			
chr7-9256 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr7	92561056	92562314	0 NA	non-codiron-codir	28364 NM_001288	257415 Hs. 18564	NR_152789	ENSG00000FAM133B	-	family wiprotein-coding			
chr7-1006 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr7	1E+08	1E+08	0 NA	non-codiron-codir	-12142 NM_001362	7589 Hs. 632294	NR_145914	ENSG00000ZSCAN21	NY-REN-21	zinc fingprotein-coding			
chr7-1276 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr7	1.28E+08	1.28E+08	0 NA	intron (Nintron (N	-20448 NR_027333	27099 Hs. 657377	NR_014411	ENSG00000SND1-TT1	C7orf54	SNB1 intrncRNA			
chr8-6727 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr8	67275642	67276049	0 NA	intron (Nintron (N	67936 NM_006421	10565 Hs. 656902	NR_006421	ENSG00000ARFGEF1	ARFGEF1	EADP ribotncRNA			
chr8-9486 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr8	94882115	94883329	0 NA	TTS (NM_C	12532 NM_057745	9134 Hs. 521695	NR_004702	ENSG00000CCNE2	CYCE2	cyclin E2 protein-coding			
chr9-1096 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chr9	1.09E+08	1.09E+08	0 NA	intron (Nintron (N	3516 NR_029506	407036	NR_029506	ENSG00000MIR32	MIRN32	hsimicroRNA ncRNA			
chrX-7226 6.145127	-0.78396	0.939407	-0.83453	0.403981	0.981636	chrX	72267793	72269571	0 NA	Intergeni	8566 NM_001007	6191 Hs. 118076	NR_001007	ENSG00000RPS43	CCG2	DXS ribosomal protein-coding			
chr7-1495 10.52837	0.619974	0.743028	0.834388	0.404062	0.981636	chr7	1.5E+08	1.5E+08	0 NA	non-codiron-codir	-51057 NM_152557	155061 Hs. 24643	NR_152557	ENSG00000ZNF746	PARIS	zinc fingprotein-coding			
chr14-104 5.435099	0.839297	1.006061	0.83424	0.404146	0.981636	chr14	1.05E+08	1.05E+08	0 NA	intron (Nintron (N	6212 NM_001364	122616 Hs. 27183	NR_174891	ENSG00000CLBA1	C14orf79	clathrin protein-coding			
chr16-151 5.435099	0.839297	1.006061	0.83424	0.404146	0.981636	chr16	15135300	15136187	0 NA	non-codiron-codir	1216 NR_123721	1.05E+08 Hs. 634612	NR_123721	ENSG00000PKD1P6-NF	-	PKD1P6-NF pseudo			
chr19-20C 5.435099	0.839297	1.006061	0.83424	0.404146	0.981636	chr19	20009718	20012660	0 NA	intron (N	28066 NM_001077	91120 Hs. 306299	NR_033196	ENSG00000ZNF682	BC39498	zinc fingprotein-coding			
chr2-2637 5.435099	0.839297	1.006061	0.83424	0.404146	0.981636	chr2	26371812	26372232	0 NA	intron (N	-25233 NM_001321	165082 Hs. 631878	NR_153836	ENSG00000ADGRF3	APR113	PCadhesion protein-coding			
chr5-3225 5.435099	0.839297	1.006061	0.83424	0.404146	0.981636	chr5	32254242	32254466	0 NA	intron (N	55855 NM_001040	54545 Hs. 481838	NR_019061	ENSG00000MTMR12	3-PAP	PIF myotubul protein-coding			
chr6-4285 5.435099	0.839297	1.006061	0.83424	0.404146	0.981636	chr6	42858365	42861347	0 NA	intron (N	-19760 NR_134562	285855 Hs. 520133	NR_198488	ENSG00000RPL7L1	dJ475N16	ribosomal protein-coding			
chr19-494 13.5541	-0.53969	0.647074	-0.83405	0.404255	0.981636	chr19	49488328	49493075	0 NA	promoter-promoter-	84 NR_00002C	26818	NR_00002C	ENSG00000SNORD33	RNU33	U3c small nucsnRNA			
chr14-917 7.845371	-0.70186	0.841526	-0.83403	0.404265	0.981636	chr14	91867841	91868184	0 NA	promoter-promoter-	-476 NM_001128	123036 Hs. 510262	NR_152332	ENSG00000CTC2N	C14orf47	tandem C2 protein-coding			
chr2-333 7.845371	-0.70186	0.841526	-0.83403	0.404265	0.981636	chr2	33339691	33340012	0 NA	intron (N	-78665 NR_039628	1.01E+08	NR_039628	ENSG00000MIR4430	-	microRNA ncRNA			
chr3-5662 7.845371	-0.70186	0.841526	-0.83403	0.404265	0.981636	chr3	56626267	56626760	0 NA	intron (N	37533 NM_015224	23272 Hs. 116877	NR_015224	ENSG00000TASOR	C3orf63	F transcriptin protein-coding			
chr12-534 7.878653	-0.69665	0.835287	-0.83402	0.404269	0.981636	chr12	53063064	53064243	0 NA	intron (N	5359 NR_10681E	1.02E+08	NR_10681E	ENSG00000MIR6757	hsa-mir-6	microRNA ncRNA			
chr17-774 7.878653	-0.69665	0.835287	-0.83402	0.404269	0.981636	chr17	77499000	77500777	0 NA	3' UTR (3' UTR (N	24645 NM_001113	10801 Hs. 440932	NR_00664C	ENSG00000SEPTIN9	AF17q25	septin 9 protein-coding			
chr2-1825 7.878653	-0.69665	0.835287	-0.83402	0.404269	0.981636	chr2	1.83E+08	1.83E+08	0 NA	intron (N	-67634 NM_001463	2487 Hs. 128455	NR_001463	ENSG00000FRZB	FRE	FRT17 frizzled protein-coding			
chr7-272C 7.878653	-0.69665	0.835287	-0.83402	0.404269	0.981636	chr7	2726957	2727293	0 NA	TTS (NM_C	36015 NM_001282	2768 Hs. 487341	NR_007353	ENSG00000GNA12	NNX3	RMP G protein-coding			
chr15-494 10.4521	0.608079	0.729152	0.833954	0.404307	0.981636	chr15	49423717	49427471	0 NA	intron (N	2352 NM_002009	2252 Hs. 567268	NR_002009	ENSG00000FGF7	HBGF-7	KC fibroblas protein-coding			
chr21-332 10.4521	0.608079	0.729152	0.833954	0.404307	0.981636	chr21	33278398	33280364	0 NA	intron (N	13014 NM_000628	3588 Hs. 654593	NR_000628	ENSG00000LL10RB	CDW210B	C interleuk protein-coding			
chr9-3944 10.4521	0.608079	0.729152	0.833954	0.404307	0.981636	chr9	39447415	39448087	0 NA	intron (N	16775 NR_003528	401509 Hs. 449445	NR_001032297	ZNF658B	-	zinc fingpseudo			
chr1-1558 12.66446	-0.583775	0.66966	0.833818	0.404384	0.981636	chr1	1.56E+08	1.56E+08	0 NA	exon (NM exon (NM	3786 NM_032292	54856 Hs. 656361	NR_032292	ENSG00000GON4L	GON-4	GON gon-4 lik protein-coding			
chr1-252C 7.741299	0.710184	0.851775	0.833769	0.404411	0.981636	chr1	2520663	2521632	0 NA	exon (NM exon (NM	5449 NM_01821E	55229 Hs. 26156	NR_01821E	ENSG00000PANK4	-	panthoether protein-coding			
chr1-151 7.741299	0.710184	0.851775	0.833769	0.404411	0.981636	chr1	1.52E+08	1.52E+08	0 NA	3' UTR (3' UTR (N	-20449 NM_182578	284488 Hs. 132648	NR_182578	ENSG00000THEM5	ACOT15	thioester protein-coding			
chr2-1592 7.741299	0.710184	0.851775	0.833769	0.404411	0.981636	chr2	1.59E+08	1.59E+08	0 NA	intron (N	28163 NR_10694E	1.02E+08	NR_10694E	ENSG00000MIR6888	hsa-mir-6	microRNA ncRNA			
chr8-144 7.741299	0.710184	0.851775	0.833769	0.404411	0.981636	chr8	1.44E+08	1.44E+08	0 NA	intron (N	6811 NM_174922	203054 Hs. 283374	NR_174922	ENSG00000ADCK5	-	aarF dom protein-coding			
chr1-9362 5.709094	-0.83559	1.002217	-0.83374	0.404429	0.981636	chr1	93621924	93622322	0 NA	intron (N	-8026 NM_001261	8412 Hs. 36958	NR_003567	ENSG00000BCAR3	AND-34	NSBCAR3 ad protein-coding			
chr1-1102 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr1	11024270	11025297	0 NA	3' UTR (3' UTR (N	12386 NM_007375	23435 Hs. 300624	NR_007375	ENSG00000TARDBP	ALD10	TDNF DNA t protein-coding			
chr12-297 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr12	29765778	29766811	0 NA	intron (N	17648 NM_001367	83857 Hs. 401954	NR_03192C	ENSG00000TMTCT1	ARG99	OLF transmemt protein-coding			
chr12-462 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr12	46253360	46255205	0 NA	intron (N	12234 NR_0010278	81539 Hs. 53377C	NR_030674	ENSG00000SLC38A1	ATA1	NAT2 solute c protein-coding			
chr12-112 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr12	1.12E+08	1.12E+08	0 NA	intron (N	-17071 NR_03743C	1.01E+08	NR_03743C	ENSG00000MIR3657	-	microRNA ncRNA			
chr14-505 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr14	50502841	50504492	0 NA	intron (N	28903 NM_198794	11183 Hs. 130491	NR_00657E	ENSG00000MAP4K5	GCKR	KHS mitogen- protein-coding			
chr17-281 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr17	28195500	28198318	0 NA	TTS (NM_C	-29453 NR_003064	23615 Hs. 15719E	NR_021093	ENSG00000PY2	-	peptide lypseudo			
chr19-344 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr19	3425520	3427370	0 NA	intron (N	5480 Hs. 130714	NR_00113E	ENSG00000SMIM24	284422	Hs. 150714	NR_00113E	ENSG00000SMIM24	C19orf77	small intrnprotein-coding
chr19-111 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr19	11062375	11062574	0 NA	TTS (NM_C	-26888 NM_000527	3949 Hs. 21328E	NR_000527	ENSG00000CLDLR	FH	FHC LI low densiprotein-coding			
chr19-577 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr19	57771048	57772507	0 NA	intron (N	2101 NM_017652	54807 Hs. 625133	NR_017652	ENSG00000ZNF586	-	zinc fingprotein-coding			
chr5-143 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr5	14350059	14350742	0 NA	intron (N	-113883 NR_14581E	1.01E+08	NR_14581E	ENSG00000SNORD170	-	small nucsnRNA			
chr5-144 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr5	14435733	14436761	0 NA	intron (N	-27736 NR_14581E	1.1E+08	NR_14581E	SNORD170	-	small nucsnRNA			
chr5-141 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr5	1.42E+08	1.42E+08	0 NA	Intergeni	13722 NM_005471	10007 Hs. 633855	NR_005471	ENSG00000GNPDA1	GNP1	GNP1 glucosamin protein-coding			
chr8-1197 7.870795	-0.69508	0.833747	-0.83368	0.404462	0.981636	chr8	1.2E+08	1.2E+08	0 NA	intron (N	41842 NM_003184	6873 Hs. 122752	NR_003184	ENSG00000CTAF2	CIF150	MF TATA-box protein-coding			
chr7-9195 4.905229	0.909329	1.090947	0.833522	0.40455	0.981636	chr7	91996197	91996396	0 NA	intron (N	55421 NM_005751	10142 Hs. 651221	NR_005751	ENSG00000AKAP9	AKAP-9	AK A-kinase protein-coding			
chr1-1197 4.411601	-0.94357	1.132488	-0.83318	0.404741	0.981636	chr1	1.2E+08	1.2E+08	0 NA	intron (N	22673 NM_006622	26227 Hs. 48729E	NR_006622	ENSG00000PHGDH	3-PGDH	3F phosphog protein-coding			
chr15-74C 4.411601	-0.94357	1.132488	-0.83318	0.404741	0.981636	chr15	74041203	74041961	0 NA	intron (N	40968 NM_001038	342096 Hs. 54640E	NR_001038	ENSG00000GOLGA6A	GLP	GOLGA6 golgin A protein-coding			
chrX-1014 4.411601	-0.94357	1.132488	-0.83318	0.404741	0.981636	chrX	10141731	10142322	0 NA	3' UTR (3' UTR (N	-14919 NM_001256	1183 Hs. 495674	NR_00183C	ENSG00000CLCN4	CLC4	C10C-chloride protein-coding			
chr1-3931 9.629745	-0.63483	0.762173	-0.83293	0.404886	0.981636	chr1	39313897	39314385	0 NA	intron (N	-94932 NM_015038	643314 Hs. 65876C	NR_015038	ENSG00000KIAA0754	-	KIAA0754 protein-coding			
chr10-69 6.629745	-0.63483	0.762173	-0.83293	0.404886	0.981636	chr10	69384636	69386587	0 NA	intron (N	31307 NM_001057	6865 Hs. 88372	NR_001057	ENSG00000TACR2	NKR2	NKN2 tachykinin protein-coding			
chr5-736 5.667954	-0.84096	1.009982	-0.83265	0.405044	0.981636	chr5	73681190	73681787	0 NA	intron (N	55330 NM_00108C	64283 Hs. 482521	NR_00108C	ENSG00000ARHGEF28	RGNEF	RIF Rho guaniprotein-coding			
chr1-2262 6.152724	0.739504	0.8888	0.832025	0.405395	0.981636	chr1	2.26E+08	2.26E+08	0 NA	intron (N	37455 NM_00161E	142 Hs. 17776E	NR_00161E	ENSG00000PARP1	ADPRT	ADP poly (ADP- protein-coding			
chr15-65 7.152724	0.739504	0.8888	0.832025	0.405395	0.981636	chr15	65906902	65908271	0 NA	intron (N	38095 NR_00120E	8766 Hs. 321541	NR_004663	ENSG00000RAB11A	YL8	RAB11A, n protein-coding			
chr6-170 7.152724	0.739504	0.8888	0.832025	0.405395	0.981636	chr6	1.7E+08	1.7E+08	0 NA	intron (N	2812								

chr14-21:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr14	21371719	21372974	+ 0 NA	intron (Nintron (N	11673 NM_007192	11198 Hs. 213724NM_007192	ENSG000003UPT16H	CDC68 FACSP16	honprotein-coding	
chr15-50:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr15	50617005	50618105	+ 0 NA	intron (Nintron (N	69242 NR_149154	54822 Hs. 512894NM_017672	ENSG000003TRPM7	ALSPDC CF	transientprotein-coding	
chr15-74:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr15	74029446	74031076	+ 0 NA	intron (Nintron (N	35545 NM_033244	5371 Hs. 526464NM_002675	ENSG000003PML	MYL PP867	promyelocprotein-coding	
chr19-211:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr19	21143982	21144907	+ 0 NA	intron (NAluS2 S1	2404 NM_133473	170959 Hs. 156256NM_133473	ENSG000003ZNF431	-	zinc fingprotein-coding	
chr3-580:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr3	58094325	58095234	+ 0 NA	intron (Nintron (N	58094325	1.05E+08 Hs. 613914NR_135534	ENSG000003FLNB-AS1	-	FLNB antncRNA	
chr3-130:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr3	1.31E+08	1.31E+08	+ 0 NA	intron (Nintron (N	48199 NM_001001	27032 Hs. 584884NM_014382	ENSG000003ATP2C1	ATP2C1A EATPase	seprotein-coding	
chr4-182:6.178408	-0.77735	0.937706	-0.82899	0.407112	0.981636	chr4	1.83E+08	1.83E+08	+ 0 NA	IntergeniIntergeni	31414 NM_001351	1635 Hs. 183856NM_001921	ENSG000003DCTD	-	dCMP deacprotein-coding	
chr16-50:3.213952	-1.09836	1.324941	-0.82898	0.407113	0.981636	chr16	50028656	50029469	+ 0 NA	intron (Nintron (N	3856 NR_104042	255919 Hs. 591134 NM_153261	ENSG000003CNEP1R1	C16orf69 CTD	neulprotein-coding	
chr9-366:3.213952	-1.09836	1.324941	-0.82898	0.407113	0.981636	chr9	36639409	36640042	+ 0 NA	intron (Nintron (N	66830 NM_014791	9833 Hs. 184336NM_014791	ENSG000003MELK	HPK38	maternal protein-coding	
chr1-155:10.54594	0.625872	0.754994	0.828976	0.407118	0.981636	chr1	1.56E+08	1.56E+08	+ 0 NA	intron (NAluSp SIN	-1595 NR_024117	1E+08 Hs. 656361NR_024117	MSTO2P	MSTO2	misato fepseudo	
chr3-9157:53.32945	0.323654	0.390539	0.828739	0.407252	0.981636	chr3	91572763	91572986	+ 0 NA	IntergeniALR/Alpha	2401207 NM_001314	5627 Hs. 64016 NM_000315	ENSG000003PROS1	PROS PS21	protein fepseudo-coding	
chr6-227:9.996652	0.633008	0.763842	0.828716	0.407265	0.981636	chr6	2272196	2272691	+ 0 NA	intron (Nintron (N	26690 NR_046225	1.01E+08 Hs. 188825NR_046229	GMDS-DT	GMDS-AS1	GMDS divncRNA	
chr2-205:8.255453	0.681152	0.822054	0.828597	0.407333	0.981636	chr2	2.01E+08	2.01E+08	+ 0 NA	intron (NAluS2 SIN	22937 NR_03391E	4999 Hs. 444877NM_00619C	ENSG000003ORC2	ORC2L	origin reprotein-coding	
chr11-40:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr11	45952761	45953541	+ 0 NA	intron (NCharlie2E	30495 NM_00130C	120071 Hs. 86543 NM_152312	ENSG000003LARGE2	ORCLTL L1	FLARGE2 xylprotein-coding	
chr16-84:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr16	84180099	84181721	+ 0 NA	5' UTR (N5' UTR (N	6147 NM_00567E	9013 Hs. 153022NM_00567E	ENSG000003TAF1C	MGC:3997E	TATA-box protein-coding	
chr17-291:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr17	29101615	29101958	+ 0 NA	intron (Nintron (N	-26177 NM_00474C	9220 Hs. 46259C	ENSG000003TAF1A	MAJN SPR2	TGFB1-incprotein-coding	
chr17-80:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr17	80249015	80250313	+ 0 NA	intron (NAluSx1 S1	-11188 NM_00125E	57674 Hs. 195642NM_020914	ENSG000003CRNF213	AL017 Cl17	ring fingprotein-coding	
chr19-57:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr19	57790669	57791404	+ 0 NA	IntergeniIntergeni	21374 NM_017652	54807 Hs. 625133NM_017652	ENSG000003ZNF586	-	zinc fingprotein-coding	
chr20-26:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr20	26517932	26518917	+ 0 NA	IntergeniALR/Alpha	-309191 NR_04009E	284801 Hs. 370699NR_04009E	ENSG000003MIR663AHC	-	MIR663A lncRNA	
chr4-886:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr4	88655661	88656494	+ 0 NA	3' UTR (N3' UTR (N	41752 NM_153757	266812 Hs. 12554 NM_153757	ENSG000003NAP1L5	DRLM	nucleosonprotein-coding	
chr7-1117:5.990392	0.787749	0.950756	0.82855	0.407359	0.981636	chr7	1.12E+08	1.12E+08	+ 0 NA	intron (NHUERS-P3-	-11503 NR_10380E	1.01E+08 Hs. 67751NR_10380E	ENSG000003DOCK4-AS1	DOCK4	antncRNA	
chr20-501:13.19433	0.54408	0.656783	0.828401	0.407443	0.981636	chr20	50192051	50194646	+ 0 NA	TTS (NM_C	-1279 NR_12573E	1.02E+08 Hs. 442486NR_12573E	ENSG000003CEBPB-AS1	-	CEBPB antncRNA	
chr15-101:9.128998	-0.65688	0.792977	-0.82837	0.407462	0.981636	chr15	1.02E+08	1.02E+08	+ 0 NA	intron (NLINE I	10933 NM_152334	132833 Hs. 657166NM_152334	ENSG000003TARSL2	-	threonyl-protein-coding	
chr13-321:7.419046	-0.72481	0.875001	-0.82835	0.407471	0.981636	chr13	32180544	32180775	+ 0 NA	intron (Nintron (N	131295 NM_00113E	646799 Hs. 569254NM_00113E	ENSG000003ZARIL2	Z3CXXC7 Z	zygote arprotein-coding	
chr6-897:7.419046	-0.72481	0.875001	-0.82835	0.407471	0.981636	chr6	89753932	89754134	+ 0 NA	intron (Nintron (N	65761 NM_014611	23195 Hs. 52994E	ENSG000003MDN1	Real	midasin fprotein-coding	
chr9-1101:7.419046	-0.72481	0.875001	-0.82835	0.407471	0.981636	chr9	1.1E+08	1.1E+08	+ 0 NA	intron (NFLAM_C S1	24241 NM_00113E	445815 Hs. 59190E	ENSG000003PALM2-AK1	AKAP-2 AK	PAK2-AK1 protein-coding	
chr5-485:18.11565	0.479151	0.57852	0.828236	0.407537	0.981636	chr5	48505107	48506150	+ 0 NA	IntergeniALR/Alpha	1935705 NM_19844E	133418 Hs. 561411NM_19844E	ENSG000003EMB	GP70	embin protein-coding	
chr1-272:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr1	27287654	27288167	+ 0 NA	intron (Nintron (N	-34235 NM_03212E	84065 Hs. 469171NM_03212E	ENSG000003TMEM222	Clorf160	transmem protein-coding	
chr1-2057:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr1	2.06E+08	2.06E+08	+ 0 NA	intron (NLM2 LIN	-18617 NM_00113E	8934 Hs. 11532E	ENSG000003RAB29	RAB7L RAE	RAB29, meprotein-coding	
chr11-65:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr11	65624434	65626705	+ 0 NA	intron (Nintron (N	9257 NM_03222E	399909 Hs. 380801NM_03222E	ENSG000003PCNX3	PCNXL3	pecanex fprotein-coding	
chr16-87:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr16	87343203	87343699	+ 0 NA	intron (Nintron (N	25942 NR_13518C	1.02E+08 Hs. 66745NR_13518C	ENSG000003LOC10192E	-	uncharactncRNA	
chr17-71:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr17	7191964	7197771	+ 0 NA	intron (NAluYc SIN	10320 NM_001321	1742 Hs. 46392E	ENSG000003DLG4	PSD95 SAF	discs larprotein-coding	
chr19-55:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr19	55500357	55501739	+ 0 NA	exon (NM_exon (NM	12612 NM_001144	284927 Hs. 554182NM_182571	ENSG000003SCSD	S5D-SRRE	scavengerprotein-coding	
chr2-217:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr2	2.18E+08	2.18E+08	+ 0 NA	intron (Nintron (N	4866 NR_106867	1.02E+08	NR_106867	ENSG000003MIR6809	hsa-mir-6	microRNA ncRNA
chr2-22:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr2	22291032	22292142	+ 0 NA	IntergeniG-rich Lc	-6511 NR_02729E	96610 Hs. 449601NM_08092E	BMS1P20	IGL IGLV BMS1	psetpseudo	
chr3-1291:7.715875	0.705059	0.851326	0.82819	0.407563	0.981636	chr3	1.29E+08	1.29E+08	+ 0 NA	intron (NAluS2 S1	9125 NM_020701	57461 Hs. 512661NM_020701	ENSG000003ISY1	FSAP33	ISY1 spliprotein-coding	
chr1-1114:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr1	11144064	11144382	+ 0 NA	intron (NMER5B DNA	325 NR_04660C	1.01E+08 Hs. 679133NR_04660C	ENSG000003MTOR-AS1	-	MTOR antncRNA	
chr10-32:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr10	32697553	32898646	+ 0 NA	IntergeniIntergeni	3373 NR_13276E	1.07E+08	NR_13276E	SNORA86	-	small nucsnRNA
chr11-10:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr11	10208291	10604055	+ 0 NA	intron (NMER1B DNA	-34808 NR_006691	10894 Hs. 655332NM_006691	ENSG000003LYVE1	CRSBP-1 E	lymphatic protein-coding	
chr16-30:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr16	30263116	30263591	+ 0 NA	IntergeniAluS2 SIN	-14940 NM_001321	613037 Hs. 58573E	ENSG000003NPIP3	-	nuclear fprotein-coding	
chr2-1331:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr2	1.33E+08	1.33E+08	+ 0 NA	intron (NAluS8 S1	-163901 NR_110294	1.02E+08 Hs. 661917NR_110294	ENSG000003NCKAP5-AS	-	NCKAP5 arncRNA	
chr2-22:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr2	35812752	35814253	+ 0 NA	intron (Nintron (N	26962 NM_00134E	23543 Hs. 628299NM_01430E	ENSG000003RBF0X2	FOX2 Fox-	N bndiprotein-coding	
chr4-1134:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr4	1.13E+08	1.13E+08	+ 0 NA	intron (NLIPA2 LIN	201915 NM_001354	287 Hs. 620557NM_00114E	ENSG000003ANK2	ANK-2 LQ	ankyrin f2protein-coding	
chr5-883:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr5	883067	883887	+ 0 NA	intron (Nintron (N	9045 NR_13429E	65980 Hs. 44927E	ENSG000003BRD9	LAVS3040 bromodome	protein-coding	
chr6-565:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr6	5658757	56589670	+ 0 NA	intron (Nintron (N	54067 NM_01554E	667 Hs. 60491E	ENSG000003COST	BP240 BP4	dystonin protein-coding	
chr9-981:7.896219	-0.68846	0.831482	-0.82799	0.407677	0.981636	chr9	98199442	98200236	+ 0 NA	intron (NLINE I	-7202 NM_05282E	7464 Hs. 113094NM_00338E	ENSG000003CORA2A	CLIP1NB I	cononin f2protein-coding	
chr3-425:5.634673	-0.84854	1.02536	-0.82756	0.407922	0.981636	chr3	42551412	42551611	+ 0 NA	3' UTR (N3' UTR (N	-18905 NR_046654	1.01E+08 Hs. 600642NR_046654	VIPR1-AS1	-	VIPR1 antncRNA	
chr1-180:8.230029	0.676266	0.817387	0.827351	0.408038	0.981636	chr1	1.81E+08	1.81E+08	+ 0 NA	intron (NLIPA7 LIN	-79747 NM_02095E	57710 Hs. 73481E	ENSG000003KIAA1614	-	KIAA1614 protein-coding	
chr3-1224:8.230029	0.676266	0.817387	0.827351	0.408038	0.981636	chr3	1.22E+08	1.22E+08	+ 0 NA	intron (NAluY6 S1	22941 NR_02669E	3836 Hs. 16100E	ENSG000003KPN1A	IPOA5 NP1	karyopher protein-coding	
chr6-5794:8.230029	0.676266	0.817387	0.827351	0.408038	0.981636	chr6	57946512	57947300	+ 0 NA	non-codirnon-codir	-9977 NR_13299E	375513 Hs. 56153E	ENSG000003GUSBP4	G6orf216 GUSB	psetpseudo	
chr1-1794:6.137269	-0.78202	0.945243	-0.82732	0.408054	0.981636	chr1	77949861	77950851	+ 0 NA	intron (NAluJb SIN	28716 NR_13015E	8880 Hs. 56738C	ENSG000003FUBP1	FBP FUBP	far upstr protein-coding	



chr4-397	7.855079	-0.69199	0.839025	-0.82476	0.409507	0.981636	chr4	39702433	39702988	+	0	NA	intron (Nintron (N	4574	NM_001111	3093	Hs. 50308	NM_005333	ENSG00000	UBE2K	E2-25K	H	ubiquitin protein-coding		
chr7-134	7.855079	-0.69199	0.839025	-0.82476	0.409507	0.981636	chr7	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	-43677	NR_160299	340351	Hs. 64861	ENM_178563	ENSG00000	AGBL3	CCP3	ATP/GTP	protein-coding		
chr9-127	7.855079	-0.69199	0.839025	-0.82476	0.409507	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	15749	NM_022833	64855	Hs. 522401	NM_022833	ENSG00000	CNIBAN2	C9orf88	F	ribonucleoprotein-coding		
chrX-710	7.855079	-0.69199	0.839025	-0.82476	0.409507	0.981636	chrX	7105456	7105655	+	0	NA	intron (Nintron (N	-41735	NM_00132C	412	Hs. 522578	NM_000351	ENSG00000	STS	ARSC	ARSC	steroid	protein-coding	
chr20-275	26.58565	0.40018	0.485607	0.824573	0.409614	0.981636	chr20	27350665	27351284	+	0	NA	IntergeniALR/Alpha	-1141741	NR_04009E	284801	Hs. 370699	NM_04009E	ENSG00000	MIR663AHC	MIR663A	lincRNA			
chr4-7794	7.641454	0.701324	0.850946	0.82417	0.409843	0.981636	chr4	77945470	77945875	+	0	NA	intron (MER11A LI	82842	NM_02023E	65008	Hs. 53201	NM_02023E	ENSG00000	MRPL1	BM022	L	mitochondrial protein-coding		
chr2-2267	9.631595	-0.6255	0.758983	-0.82413	0.409863	0.981636	chr2	2.27E+08	2.27E+08	+	0	NA	exon (NM exon (NM	1189	NM_005544	3667	Hs. 47150E	NM_005544	ENSG00000	TRS1	HIRS-1	I	insulin protein-coding		
chr1-1844	8.204605	0.671452	0.815514	0.823348	0.41031	0.981636	chr1	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	90232	NM_03080E	81563	Hs. 49715E	NM_03080E	ENSG00000	C1orf21	PIG13	C	chromosome protein-coding		
chr1-2242	8.204605	0.671452	0.815514	0.823348	0.41031	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (AluJb SIN	10517	NR_11066E	1.02E+08	Hs. 71012E	NR_11066E	ENSG00000	LOC101927-			uncharacterized ncRNA		
chr11-98	8.204605	0.671452	0.815514	0.823348	0.41031	0.981636	chr11	985231	985289	+	0	NA	exon (NM exon (NM	51143	NM_005961	4588	Hs. 52843E	NM_005961	ENSG00000	MUC6	MUC-6	M	mucin 6, protein-coding		
chr6-3731	8.204605	0.671452	0.815514	0.823348	0.41031	0.981636	chr6	37316749	37319033	+	0	NA	intron (L2a LINE	-36092	NM_18307E	9025	Hs. 48527E	NM_00395E	ENSG00000	CNRF8	hRNF8	R	ring finger protein-coding		
chr7-299	8.204605	0.671452	0.815514	0.823348	0.41031	0.981636	chr7	29954357	29955658	+	0	NA	intron (LIMB8 LIN	34794	NM_01476E	9805	Hs. 52074	CNM_01476E	ENSG00000	SCRN1	SES1	S	secretory protein-coding		
chr9-1047	8.204605	0.671452	0.815514	0.823348	0.41031	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (AluSc SIN	20673	NR_13076E	55335	Hs. 429294	NM_01837E	ENSG00000	NIPSNAP3E	PP944	NIP	nipsnap 3 protein-coding		
chr16-48	7.119442	0.736246	0.894436	0.82314	0.410428	0.981636	chr16	4869147	4869367	+	0	NA	intron (Nintron (N	20877	NR_00128E	29855	Hs. 44021	NM_01693E	ENSG00000	UBN1	VT VT4	V	ubiquitin protein-coding		
chr1-1557	10.40125	0.600362	0.729899	0.822528	0.410777	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (AluJr4 SI	-9838	NR_132767	1.07E+08		NR_132767		SCARNA26E				small Ca <sub>v</sub> ncRNA	
chr3-4912	10.40125	0.600362	0.729899	0.822528	0.410777	0.981636	chr3	49124291	49125309	+	0	NA	exon (NM exon (NM	-3862	NM_001351	10869	Hs. 25559E	NM_006677	ENSG00000	USP19	ZMYND9	Z	ubiquitin protein-coding		
chr19-271	25.6179	0.412214	0.50138	0.822159	0.410987	0.981636	chr19	27156007	27157002	+	0	NA	IntergeniALR/Alpha	-636297	NR_14673E	1.02E+08	Hs. 567934	NR_110687	ENSG00000	LOC1019127-			uncharacterized ncRNA		
chr1-429	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr1	42982490	42981967	+	0	NA	intron (Nintron (N	22049	NR_033967	440584	Hs. 26092E	NR_033967	ENSG00000	SLC2A1-AC				SLC2A1	arncRNA
chr1-1844	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr1	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	85544	NM_03080E	81563	Hs. 49715E	NM_03080E	ENSG00000	C1orf21	PIG13	C	chromosome protein-coding		
chr1-2191	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr1	2.19E+08	2.19E+08	+	0	NA	intron (Nintron (N	7951	NM_00130C	127018	Hs. 657617	NM_138794	ENSG00000	LYPLAL1	Q96AV0	L	lysophosphatidyl protein-coding		
chr12-47	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr12	4790265	4791045	+	0	NA	intron (Nintron (N	17417	NM_01784E	55652	Hs. 438867	NM_01784E	ENSG00000	SLC48A1	H8G-1	HRC	solute carrier protein-coding		
chr12-12	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	10179	NM_00131E	353116	Hs. 53031E	NM_178314	ENSG00000	RILPL1	GOSPFL	R	Rab interprotein-coding		
chr12-13	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	3' UTR (N3' UTR (N	-20093	NM_00130C	7699	Hs. 18155E	NM_00344E	ENSG00000	ZNF140	pHZ-39	Z	zinc finger protein-coding		
chr13-20	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr13	20511192	20512449	+	0	NA	intron (Nintron (N	51084	Hs. 37070E	NM_015974	ENSG00000	CRYL1	GDH HEL3C	C	crystallin protein-coding				
chr15-52	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr15	52668999	52672365	+	0	NA	intron (Nintron (N	7952	NM_01960C	56204	Hs. 15238E	NM_01960C	ENSG00000	FAM214A	KIAA1370	F	family wiprotein-coding		
chr16-18	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr16	1807418	1810757	+	0	NA	TTS (NM_C	-14179	NR_02738E	3483	Hs. 839	NM_00497E	ENSG00000	IGFALS	ACLSLD	A	insulin I protein-coding		
chr16-68	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr16	68352411	68354822	+	0	NA	intron (Nintron (N	42502	NM_00129C	54946	Hs. 64022E	NM_01902E	ENSG00000	PRMT7	SBIDS	S	protein arginine-coding		
chr17-80	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr17	80951045	80952102	+	0	NA	intron (Nintron (N	19640	NR_14896E	400627	Hs. 591201	NR_14896E	ENSG00000	LOC400627-				uncharacterized ncRNA	
chr19-29	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr19	29674558	29675634	+	0	NA	3' UTR (N3' UTR (N	9635	NM_02431C	79156	Hs. 46638E	NM_02431C	ENSG00000	PLEKHF1	APPD	L	LAPF complex protein-coding		
chr19-49	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr19	49176125	49179543	+	0	NA	intron (MIRb SINE	20042	NM_01763E	54795	Hs. 467101	NM_01763E	ENSG00000	TRPM4	L1TrpC4	P	transient receptor protein-coding		
chr19-54	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr19	54120704	54121723	+	0	NA	intron (AluSj SIN	5459	NM_01562E	26121	Hs. 51559E	NM_01562E	ENSG00000	PRPF31	NY-BR-99	P	pre-mRNA protein-coding		
chr2-238	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	intron (Nintron (N	12514	NM_0022817	8864	Hs. 58756	NM_003894	ENSG00000	PER2	FASPS	F	fast period 2 protein-coding		
chr20-24	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr20	24963242	24964331	+	0	NA	3' UTR (N3' UTR (N	14517	NM_00365C	8530	Hs. 14321E	NM_00365C	ENSG00000	CST7	CMAP	C	cystatin protein-coding		
chr20-33	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr20	33629838	33631463	+	0	NA	intron (Nintron (N	-31677	NM_08082E	128864	Hs. 324104	NM_08082E	ENSG00000	C2orf144	dJ63M2.6	C	chromosome protein-coding		
chr22-29	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr22	29795297	29795766	+	0	NA	intron (Nintron (N	28117	NM_013387	29796	Hs. 28429E	NM_013387	ENSG00000	UQCRL0	HSPC051	F	ubiquitin protein-coding		
chr3-144	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr3	14443542	14444385	+	0	NA	intron (Nintron (N	41357	NM_001134	6533	Hs. 52948E	NM_00304E	ENSG00000	SLC6A6	TAU6	T	solute carrier protein-coding		
chr3-44	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr3	44932136	44933633	+	0	NA	intron (Nintron (N	43290	NM_00134E	51304	Hs. 61430	NM_01659E	ENSG00000	ZDHH3	DHHC-3	D	zinc finger protein-coding		
chr3-48	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr3	48538342	48540444	+	0	NA	intron (Nintron (N	10628	NR_106881	1.02E+08		NR_106881	ENSG00000	MIR6823	hsa-mir-6823	M	microRNA ncRNA		
chr3-48	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr3	48746021	48746220	+	0	NA	TTS (NM_C	-28842	NM_00114E	51447	Hs. 59598E	NM_016291	ENSG00000	IP6K2	IHPK2	I	inositol protein-coding		
chr3-53	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr3	53245323	53248378	+	0	NA	intron (AluSp SIN	9172	NM_001064	7086	Hs. 89643	NM_001064	ENSG00000	TKT	HEL-S-48	T	transketolase protein-coding		
chr4-87	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr4	874952	882414	+	0	NA	intron (LIMEc LIN	-52554	NM_006651	10815	Hs. 47893E	NM_006651	ENSG00000	CPLX1	CPX-1	C	complexin protein-coding		
chr5-34	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr5	348021	348999	+	0	NA	intron (LIMEl LIN	44334	NM_020731	57491	Hs. 80E23	NM_020731	ENSG00000	AHRR	AHH AHR	A	aryl hydrocarbon receptor protein-coding		
chr7-14	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr7	1479924	1481288	+	0	NA	intron (Nintron (N	-21136	NM_182924	79778	Hs. 376617	NM_02472E	ENSG00000	MICAL2	JRAB	J	MICAL like protein-coding		
chr7-22	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr7	2212483	2213336	+	0	NA	intron (Nintron (N	20036	NM_001304	8379	Hs. 65483E	NM_00355E	ENSG00000	MADL1	MAD1	P	mitotic 1 protein-coding		
chr7-23	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr7	23128732	23129892	+	0	NA	intron (Nintron (N	22651	NM_01884E	55975	Hs. 654817	NM_01884E	ENSG00000	KLHL7	CISS3	K	kelch like protein-coding		
chr9-13	5.964968	0.78136	0.950562	0.821998	0.411078	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	exon (NM exon (NM	5913	NM_014811	9858	Hs. 53326E	NM_014811	ENSG00000	PPP1R26	KIAA0649	P	protein phosphatase 1 protein-coding		
chr19-47	7.468044	-0.72234	0.879375	-0.82142	0.411405	0.981636	chr19	47153749	47154219	+	0	NA	intron (AluSj SIN	23149	NM_00114E	10055	Hs. 51550E	NM_00550C	ENSG00000	SAE1	AOS1	H	HSPC SUMO1 act protein-coding		
chr1-17	10.44239	0.601083	0.732172	0.820959																					



chrX-1295 7.377907	-0.72851	0.890912	-0.81772	0.41352	0.981636	chrX	1.3E+08	1.3E+08	0 NA	intron (AluSz SIN	13874 NM_006649	10813 Hs. 458598NM_006649	ENSG00000000000	UTP14A	NYCO16 SI	UTP14A	snprotein-coding	
chr8-9375 9.514184	-0.64536	0.789434	-0.8175	0.413642	0.981636	chr8	93738505	93738742	0 NA	intron (AluJb SIN	-1488 NR_027255	55472 Hs. 192788NM_018608	ENSG00000000000	RBM12B-AS1	CSorF39 FRBM12B	arncRNA		
chr1-6815 8.245745	0.672292	0.822481	0.817395	0.413703	0.981636	chr1	68153062	68153850	0 NA	intron (intron (	30154 NR_031664	1E+08	NR_031664	ENSG00000000000	MIRN1262	microRNA ncRNA		
chr10-457 8.245745	0.672292	0.822481	0.817395	0.413703	0.981636	chr10	45776050	45776729	0 NA	intron (intron (	40935 NM_001351	643479 Hs. 522900NM_001351	FAM25E	FAM25E	family wiprotein-coding			
chr10-875 8.245745	0.672292	0.822481	0.817395	0.413703	0.981636	chr10	87530518	87530938	0 NA	intron (L1P45 LIN	22895 NM_001178	95672 Hs. 121262NM_004897	ENSG00000000000	M1NP1	H1PERI MI	miuiprotein-coding		
chr1-5475 7.411188	-0.72288	0.884372	-0.81739	0.413705	0.981636	chr1	54733160	54733588	0 NA	intron (AluJb SIN	17513 NM_004623	7268 Hs. 412482NM_004623	ENSG00000000000	CTTC4	CNS1	tetratricprotein-coding		
chr12-246 7.411188	-0.72288	0.884372	-0.81739	0.413705	0.981636	chr12	24892350	24892757	0 NA	intron (intron (	9669 NM_001178	586 Hs. 438993NM_005504	ENSG00000000000	BCAT1	BCATC BC1	branched protein-coding		
chr17-666 7.9295	-0.68334	0.836041	-0.81735	0.413729	0.981636	chr17	66641862	66642416	0 NA	intron (AluY SINE	-144933 NR_030364	693219	NR_030364	ENSG00000000000	MIR634	tmicroRNA ncRNA		
chr10-406 26.09692	0.404693	0.495166	0.817288	0.413764	0.981636	chr10	40633542	40633977	0 NA	IntergeniALR/Alpha	1734286 NR_02438C	441666 Hs. 255725NR_02438C	ENSG00000000000	LOC441666		zinc fingpseudo		
chr2-1327 11.35911	-0.58075	0.710727	-0.81712	0.413861	0.981636	chr2	1.33E+08	1.33E+08	0 NA	intron (intron (	-101919 NM_001077	116372 Hs. 432395NM_14458E	ENSG00000000000	LYPD1	LYPDC1 PF	LYF/PLAUF	protein-coding	
chr14-954 4.221919	0.919094	1.124831	0.817095	0.413874	0.981636	chr14	95411797	95411874	0 NA	3' UTR (3' UTR (	58300 NM_001363	161176 Hs. 41502 NM_024653	ENSG00000000000	SYNE3	C14orf135	spectrin protein-coding		
chr7-1474 4.221919	0.919094	1.124831	0.817095	0.413874	0.981636	chr7	1474716	1475647	0 NA	intron (AluJb SIN	-15711 NM_182924	79778 Hs. 376617NM_024723	ENSG00000000000	MICAL2	JRAB MIC MICAL	11k	protein-coding	
chr1-5275 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr1	52797566	52798005	0 NA	intron (AluY SINE	-44975 NM_001307	440590 Hs. 658455NM_001004	ENSG00000000000	ZYG11A	ZYG11	zyg-11	protein-coding	
chr13-215 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr13	21509487	21509737	0 NA	intron (MLT1H LTF	-05242 NM_00128E	253832 Hs. 564611NM_153251	ENSG00000000000	ZDHHC20	4933421L1L	zinc fingprotein-coding		
chr16-882 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr16	8829879	8830345	0 NA	intron (HERV351-i	-19357 NR_14790E	1E+08 Hs. 735515NR_14790E	LOC10013C			uncharactercRNA		
chr2-1357 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr2	1.36E+08	1.36E+08	0 NA	intron (LA_C_Mam	-20880 NR_16347E	1.08E+08 Hs. 591242NM_001365	239	LOC10798E		uncharactercRNA		
chr3-7145 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr3	71490831	71491416	0 NA	intron (AluXs1 SI	50966 NR_031697	1E+08	NR_031697	ENSG00000000000	MIRN1284	tmicroRNA ncRNA		
chr7-5338 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr7	5338957	5340151	0 NA	intron (T(G)n Sin	56611 NM_00104C	222962 Hs. 4302 NM_153247	ENSG00000000000	SLC29A4	ENT4 PMA1	solute cprotein-coding		
chr9-1347 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chr9	1.35E+08	1.35E+08	0 NA	intron (intron (	75797 NR_039691	1.01E+08	NR_039691	ENSG00000000000	MIR3689C		microRNA ncRNA	
chrX-1685 7.921642	-0.6818	0.834499	-0.81702	0.413917	0.981636	chrX	16855503	16855736	0 NA	intron (intron (	14244 NM_00119E	5931 Hs. 495755NM_002893	ENSG00000000000	RBBP7	RbAp46	RB	bindir protein-coding	
chr9-1217 7.749157	0.707935	0.866561	0.816947	0.413958	0.981636	chr9	1.22E+08	1.22E+08	0 NA	intron (intron (	33137 NM_13870E	153090 Hs. 522378NM_032552	ENSG00000000000	DAB2IP	AF9Q34 A1	DAB2	intcprotein-coding	
chr7-1056 7.160582	0.736781	0.902001	0.81683	0.414026	0.981636	chr7	1.06E+08	1.06E+08	0 NA	intron (intron (	-34640 NM_00135E	1E+08 Hs. 719432NM_00135E	ENSG00000000000	EFCAB10		EF-hand	cprotein-coding	
chr7-6728 4.437024	-0.93064	1.139428	-0.81676	0.414063	0.981636	chr7	67286899	67287098	0 NA	TTS (NR_C TTS (NR_C	15444 NR_046297	5382 Hs. 712714NR_022007	ENSG00000000000	PMS2P4	PMS2L4 P	PMS1	homc	pseudo
chr8-9865 7.821797	-0.69732	0.853923	-0.81661	0.41415	0.981636	chr8	98699589	98699794	0 NA	intron (L1P43 LIN	125980 NM_00125E	6788 Hs. 492333NM_006281	ENSG00000000000	STK3	KRS1 MS12	serine/t	protein-coding	
chr1-2276 10.9644	0.583202	0.71418	0.816604	0.414155	0.981636	chr1	2.28E+08	2.28E+08	0 NA	exon (NM exon (NM	43215 NR_036753	401983 Hs. 681815NR_036753	ZNF847P		gml27	zinc fingpseudo		
chr1-123 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr1	12308691	12309003	0 NA	intron (AluXs SIN	78817 NM_01537E	55187 Hs. 439381NM_01537E	ENSG00000000000	VPS13D	SCAR4	vacuolar	protein-coding	
chr13-102 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr13	1.03E+08	1.03E+08	0 NA	intron (AluXs SIN	26239 NM_003291	7174 Hs. 432424NM_003291	ENSG00000000000	PPP2	PPP2	tripeptic	protein-coding	
chr17-405 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr17	4054940	4055139	0 NA	intron (L2c LINE	77936 NR_146884	1.05E+08 Hs. 579235NR_146884	LINC0197E			long intcncRNA		
chr19-111 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr19	11359546	11360145	0 NA	exon (NM exon (NM	4413 NM_00117E	64748 Hs. 6846 NM_022737	ENSG00000000000	PLPPR2	LPPR2 PRC	phospholip	protein-coding	
chr2-8621 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr2	86210861	86211060	0 NA	3' UTR (3' UTR (	11503 NM_016622	51318 Hs. 434335NM_016622	ENSG00000000000	MRPL35	L35mt MR1	mitochonc	protein-coding	
chr20-582 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr20	58246857	58248462	0 NA	intron (intron (	-19006 NM_001304	140731 Hs. 266571NM_080674	ENSG00000000000	ANKRD60	C20orf86	ankyrin r	protein-coding	
chr4-3578 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr4	357885	360025	0 NA	3' UTR (3' UTR (	8798 NR_030297	693156	NR_030297	ENSG00000000000	MIR571	tmicroRNA ncRNA		
chr5-1802 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr5	1.8E+08	1.8E+08	0 NA	intron (L1M3B LI	6815 NM_00130E	5601 Hs. 484371NM_002752	ENSG00000000000	MAPK9	JNK-55 J	mitogen-e	protein-coding	
chr9-1215 8.179182	0.666655	0.816398	0.816581	0.414168	0.981636	chr9	1.21E+08	1.21E+08	0 NA	intron (HAL1 LINE	11587 NM_198194	2040 Hs. 253903NM_00409E	ENSG00000000000	STOM	BND7 EPB7	stomatin	protein-coding	
chr1-214 6.129411	-0.78004	0.955542	-0.81633	0.41431	0.981636	chr1	21447344	21446737	0 NA	intron (L1M2C LI	7353 NM_00125E	84224 Hs. 325422NM_032264	ENSG00000000000	NBPF3	AE2	NBPF	meat	protein-coding
chr19-577 6.129411	-0.78004	0.955542	-0.81633	0.41431	0.981636	chr19	57761071	57761200	0 NA	IntergeniALR/Alpha	-8482 NM_001204	54807 Hs. 625133NM_017652	ENSG00000000000	ZNF586		zinc fingprotein-coding		
chr2-1514 6.129411	-0.78004	0.955542	-0.81633	0.41431	0.981636	chr2	1.51E+08	1.51E+08	0 NA	intron (intron (	21972 NM_001177	55183 Hs. 536537NM_018151	ENSG00000000000	CRIF1		replicatiprotein-coding		
chr2-202 6.129411	-0.78004	0.955542	-0.81633	0.41431	0.981636	chr2	2.02E+08	2.02E+08	0 NA	IntergeniIntergeni	13842 NR_003031	692058	NR_003031	ENSG00000000000	SNORD11	HB11-95	small nucsnRNA	
chr6-1582 6.129411	-0.78004	0.955542	-0.81633	0.41431	0.981636	chr6	1.58E+08	1.58E+08	0 NA	intron (intron (	73874 NM_00117E	8871 Hs. 434494NM_00389E	ENSG00000000000	SYNJ2	INPF5H	synaptoe	protein-coding	
chr11-654 7.847221	-0.69045	0.846022	-0.81611	0.414437	0.981636	chr11	65436819	65438182	0 NA	non-codirnon-codir	-6958 NR_030343	693197	NR_030343	ENSG00000000000	MIR612	tmicroRNA ncRNA		
chr2-5557 7.847221	-0.69045	0.846022	-0.81611	0.414437	0.981636	chr2	55570500	55577153	0 NA	intron (AluSc8 SI	41021 NM_001122	57223 Hs. 516182NM_020463	ENSG00000000000	PPP4R3B	CNLF2 PP4	phospholip	protein-coding	
chr4-159 7.847221	-0.69045	0.846022	-0.81611	0.414437	0.981636	chr4	1.59E+08	1.59E+08	0 NA	intron (L1P64 LIN	37424 NM_001351	9693 Hs. 744884NM_014247	ENSG00000000000	RAPGEF2	FRAS GEP	Rap	guaniprotein-coding	
chr9-137 7.847221	-0.69045	0.846022	-0.81611	0.414437	0.981636	chr9	1.38E+08	1.38E+08	0 NA	intron (L1R13 LTF	7694 NM_032477	64975 Hs. 44017 NM_032477	ENSG00000000000	MRPL41	BMRP MRP-	mitochonc	protein-coding	
chr18-492 10.97411	0.590072	0.723221	0.815894	0.414561	0.981636	chr18	49281673	49281891	0 NA	intron (L1P44 LIN	178663 NM_00135E	54808 Hs. 162996NM_017652	ENSG00000000000	DYM	DMC SMC	dymeclin	protein-coding	
chr17-408 9.672734	-0.62259	0.763775	-0.81515	0.414986	0.981636	chr17	40817345	40818159	0 NA	TTS (NM_C TTS (NM_C	-1393 NR_160887	147184 Hs. 353163NM_145274	ENSG00000000000	TMEM99		transmemncRNA		
chr11-124 7.452328	-0.71889	0.882166	-0.81491	0.415124	0.981636	chr11	1.24E+08	1.24E+08	0 NA	intron (AluSg SIN	11132 NM_00113C	4013 Hs. 152944NM_014622	ENSG00000000000	VWA5A	BCSC-1 B	von Wille	protein-coding	
chr19-255 27.3591	0.411485	0.505111	0.814643	0.415277	0.981636	chr19	25552364	25552870	0 NA	IntergeniALR/Alpha	-1389170 NR_003603	1E+08 Hs. 149312NR_003603	ENSG00000000000	HAVCR1P1		hepatitis	pseudo	
chr16-88 5.931687	0.777711	0.954675	0.814634	0.415282	0.981636	chr16	88606413	88606923	0 NA	intron (AluJo SIN	-31904 NM_01327E	27189 Hs. 278911NM_01327E	ENSG00000000000	IL17C	CX2 IL-17	interleu	protein-coding	
chr17-600 5.931687	0.777711	0.954675	0.814634	0.415282	0.981636	chr17	60043221											

chr19-458.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr19	45895765	45896738	+	0	NA	intron (AluSx SIN	6362	NM_001012	339344	Hs.51547ENM_001012	ENSG000005MPOP	P42pop	Myb	relatprotein-coding		
chr20-585.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr20	58998810	59000152	+	0	NA	intron (intron (N	7773	NM_001336	1522	Hs.25254ENM_001336	ENSG000005CTS	CTSX	cathepsin	protein-coding		
chr22-317.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr22	31776425	31778888	+	0	NA	intron (intron (N	23633	NM_001366	9681	Hs.435022NM_014662	ENSG000005DEPDC5	DEP.5	FFDEP	domainprotein-coding		
chr5-1735.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr5	1.74E+08	1.74E+08	+	0	NA	intron (intron (N	18783	NM_001308	80315	Hs.12712ENM_030627	ENSG000005CPEBA	CPBE-BP4	cytochrome	protein-coding		
chr7-7504.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr7	75043822	75044287	+	0	NA	intron (intron (N	29748	NM_001362	81554	Hs.52962ENM_030798	ENSG000005RCC1L	WBCSCR16	RCC1	likeprotein-coding		
chr7-1395.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (intron (N	107074	NM_001366	6916	Hs.520757NM_001061	ENSG000005TBXAS1	BDPLT14	thromboxane	protein-coding		
chr9-1132.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr9	1.13E+08	1.13E+08	+	0	NA	intron (MLT2A2 L1	10620	NM_015258	23307	Hs.522351NM_015258	ENSG000005FKBP15	FKBP133	FKBP	protein-coding		
chr9-1315.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (intron (N	4725	NM_031432	83547	Hs.9597	NM_031432	ENSG000005UCK1	URK1	uridine	protein-coding	
chr9-1365.5.939545	0.774921	0.954679	0.811708	0.416959	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (intron (N	-7741	NM_052813	64170	Hs.694071NM_052813	ENSG000005CARD9	CANDF2	h caspase	protein-coding		
chr8-3046.0.106763	-0.60498	0.745454	-0.81155	0.417047	0.981636	chr8	30465386	30465782	+	0	NA	intron (AluSx1 S1	-80183	NR_046205	1E+08	Hs.12681ENR_046205	ENSG000005RBPMS-AS1	RBPMS	antncRNA			
chr1-4051.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr1	40510008	40512757	+	0	NA	intron (intron (N	2663	NM_001346	64789	Hs.59584	NM_022774	ENSG000005EXO5	Clorf176	exonucle	protein-coding	
chr1-1693.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr1	1.69E+08	1.69E+08	+	0	NA	intron (intron (N	15933	NM_001320	8548	Hs.13074ENM_003666	ENSG000005BLZF1	GOLGIN-4	basic	protein-coding		
chr11-83.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr11	83074824	83075553	+	0	NA	Intergeni (GGAGA)n	3122	NR_038903	1.01E+08	Hs.50342ENR_038903	ENSG000005RAB30-DT	RAB30-AS1	RAB30	divncRNA		
chr12-248.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr12	24869267	24870967	+	0	NA	intron (intron (N	32105	NM_001178	586	Hs.43899ENM_005504	ENSG000005CBAT1	BCATC	BC1	branched	protein-coding	
chr13-195.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr13	19972510	19973190	+	0	NA	intron (intron (N	13036	NR_148365	7750	Hs.50743ENM_003455	ENSG000005ZMYM2	FIM	MYM	finger	protein-coding	
chr14-994.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr14	99455290	99456249	+	0	NA	intron (MER20 DN	25090	NM_199122	84193	Hs.510407NM_032233	ENSG000005SETD3	C1orf154	SET	domain	protein-coding	
chr2-1281.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr2	11810115	11810983	+	0	NA	3' UTR (A3' UTR (N	25081	NM_001282	130814	Hs.27441ENM_152391	ENSG000005CLC66A3	C2orf22	F	solute	protein-coding	
chr2-2185.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (intron (N	52643	NR_027671	56886	Hs.74330ENM_020120	ENSG000005UGGT1	HUGT1	UGC	UDP-gluc	protein-coding	
chr3-3821.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr3	32509	NM_020935	+	0	NA	intron (AluY SIN	32509	NM_020935	57695	Hs.16606ENM_020935	ENSG000005USP37	-	ubiquitin	protein-coding		
chr3-1965.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr3	1.98216812	38218295	+	0	NA	intron (AluS6 S1	-48259	NM_004256	9390	Hs.225941NM_004256	ENSG000005SLC22A13	OAT10	OC	solute	protein-coding	
chr6-2054.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr6	20545887	20546764	+	0	NA	intron (NLIP3 LINE	-30244	NR_046633	1.01E+08	Hs.591671NR_046630	NCBP2-AS1	NCBP2	antncRNA			
chr7-9948.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr7	99481345	99483614	+	0	NA	intron (intron (N	11868	NM_017774	54901	Hs.657604NM_017774	ENSG000005CDKAL1	-	CDK5	regu	protein-coding	
chr7-1305.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	TTS (NR_1TTS (NR_1	9587	NM_001351	285989	Hs.440384NM_213605	ENSG000005ZNF789	-	zinc	finger	protein-coding	
chrX-1014.4.914197	-0.84886	1.046034	-0.81155	0.417076	0.981636	chrX	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	62628	NR_109780	1.01E+08	Hs.63501ENR_109780	LINC00515	-	long	intncRNA		
chr19-101.7.796374	-0.70453	0.868204	-0.81148	0.41709	0.981636	chr19	10169950	10170378	+	0	NA	exon (NM exon (NM	3860	NM_019597	3188	Hs.43248ENM_019597	ENSG000005HNRNP2	FTP3	HNRF	heterog	protein-coding	
chr22-305.7.723733	0.702718	0.866117	0.811343	0.417169	0.981636	chr22	30583081	30585063	+	0	NA	intron (AluSx1 S1	24789	NM_001318	1786	Hs.202672NM_001318	ENSG000005DNMT1	ADCADN	A1DNA	methyl	protein-coding	
chr6-431.7.723733	0.702718	0.866117	0.811343	0.417169	0.981636	chr6	43139135	43139934	+	0	NA	intron (intron (N	7838	NM_001243	23481	Hs.51754ENM_014305	ENSG000005NPT7	NPT7	pes	protein-coding		
chr7-4387.7.723733	0.702718	0.866117	0.811343	0.417169	0.981636	chr7	43804052	43804370	+	0	NA	intron (AluSx SIN	-31735	NM_003131	6722	Hs.52014ENM_003131	ENSG000005SRF	MCM1	serum	res	protein-coding	
chr5-1687.10.10091	-0.60103	0.740913	-0.81122	0.417252	0.981636	chr5	16872796	16876985	+	0	NA	intron (THEIA1 LTF	45531	NM_000712	644	Hs.48814ENM_000712	ENSG000005BLVRA	BLVR	BVR	biliverdin	protein-coding	
chr2-2312.10.45025	0.599462	0.739013	0.811166	0.417271	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (intron (N	61398	NM_012334	4651	Hs.48172ENM_012334	ENSG000005MYO10	-	myosin	X	protein-coding	
chr12-504.10.10877	-0.60229	0.743092	-0.81052	0.417641	0.981636	chr12	50463264	50464849	+	0	NA	intron (NMSTA-int	37493	NM_001352	80210	Hs.162411NM_025135	ENSG000005ARMC9	ARM	JBTS	armadill	protein-coding	
chr15-735.10.10877	-0.60229	0.743092	-0.81052	0.417641	0.981636	chr15	73919240	73920089	+	0	NA	intron (intron (N	7485	NR_132753	1.07E+08	NR_132753	SNORD133	L102	ZLA	small	nuc	snoRNA
chr6-1385.10.10877	-0.60229	0.743092	-0.81052	0.417641	0.981636	chr6	1.39E+08	1.39E+08	+	0	NA	TTS (NM_TTS (NM_C	85102	NM_001128	85021	Hs.33460ENM_031922	ENSG000005CREP5	NBIA7	RAL	BLBP1	as	protein-coding
chr1-9227.7.872645	-0.6837	0.843718	-0.81034	0.417747	0.981636	chr1	92284980	92286113	+	0	NA	intron (NLIP6 L1	13441	NM_053274	11146	Hs.49105	NR_007070	ENSG000005GLMN	FAP	FAP4	glomulin	protein-coding
chr15-777.7.872645	-0.6837	0.843718	-0.81034	0.417747	0.981636	chr15	7751241	7751588	+	0	NA	intron (AluSg2 S1	19695	NM_001168	10099	Hs.74486ENM_005724	ENSG000005TSPAN3	TM4-A	TM4	transp	protein-coding	
chr22-408.7.872645	-0.6837	0.843718	-0.81034	0.417747	0.981636	chr22	40828874	40829112	+	0	NA	intron (intron (N	-9594	NM_001282	10478	Hs.47493ENM_006358	ENSG000005SLC25A17	PMP34	solute	protein-coding		
chr3-1414.7.872645	-0.6837	0.843718	-0.81034	0.417747	0.981636	chr3	1.41E+08	1.41E+08	+	0	NA	intron (intron (N	5724	NM_001355	253461	Hs.518301NM_152535	ENSG000005ZBTB38	CIBZ	PPP1	zinc	finger	protein-coding
chr9-1657.7.872645	-0.6837	0.843718	-0.81034	0.417747	0.981636	chr9	16551737	16551940	+	0	NA	intron (intron (N	-174976	NR_151723	1.11E+08	Hs.60921ENR_151723	ENSG000005BNC2-AS1	-	BNC2	antncRNA		
chr14-775.5.923829	0.78048	0.963193	0.810305	0.417765	0.981636	chr14	77534869	77535095	+	0	NA	intron (AluSp SIN	-36166	NM_199299	145501	Hs.29742	NM_182505	ENSG000005ISM2	TAIL1	THS	isthmin	protein-coding
chr16-125.5.923829	0.78048	0.963193	0.810305	0.417765	0.981636	chr16	12084101	12084412	+	0	NA	intron (AluSg4 S1	107525	NM_032167	92017	Hs.458401NM_032167	ENSG000005SNX29	A-388D4	Isort	ing	protein-coding	
chr3-1635.5.923829	0.78048	0.963193	0.810305	0.417765	0.981636	chr3	16351062	16351397	+	0	NA	3' UTR (A3' UTR (N	86017	NM_001352	92106	Hs.65544ENM_001352	ENSG000005OXNAD1	-	oxidore	protein-coding		
chr8-6162.10.09305	-0.59978	0.740717	-0.80973	0.418094	0.981636	chr8	61639585	61643762	+	0	NA	intron (intron (N	48138	NM_001164	444	Hs.332422NM_004318	ENSG000005ASPH	AAH	BAH	oxaspartate	protein-coding	
chrX-4455.6.219548	-0.77233	0.954049	-0.80953	0.418212	0.981636	chrX	44535706	44536560	+	0	NA	intron (AluSg4 S1	6726	NM_173794	139341	Hs.7549	NM_173794	ENSG000005FUND1	-	FUN14	don	protein-coding
chr12-117.6.589572	0.778455	0.961668	0.809484	0.418237	0.981636	chr12	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	20707	NM_016196	9904	Hs.7482	NM_016196	ENSG000005RBM19	Mrd1	RNA	bind	protein-coding
chr16-115.7.61603	0.696045	0.859971	0.809382	0.418295	0.981636	chr16	11724719	11724932	+	0	NA	intron (AluSx3 S1	18032	NM_001303	51061	Hs.313847NM_015914	ENSG000005TXND11	EFP1	thioredo	protein-coding		
chr17-500.7.61603	0.6960																					



chr7-2996	8.357675	-0.6534	0.812208	-0.80448	0.421122	0.981636	chr7	29965280	29965627	+	0	NA	intron (Nintron (N	2438 NM_014766	9805 Hs. 52074CNM_014766	ENSG000003SCRN1	SES1	secernin protein-coding
chr1-3974	8.161616	0.659811	0.820232	0.804421	0.421154	0.981636	chr1	39741593	39741966	+	0	NA	intron (Nintron (N	2934 NR_036543	10450 Hs. 52469CNM_006112	ENSG000003PPIE	CYP-33 C	peptidyl protein-coding
chr13-302	8.161616	0.659811	0.820232	0.804421	0.421154	0.981636	chr13	30224739	30225639	+	0	NA	intron (NMLT2F LTF	-72115 NR_138041	1.02E+08 Hs. 63987ENR_138041	LINC00384	-	long intencRNA
chr20-411	8.161616	0.659811	0.820232	0.804421	0.421154	0.981636	chr20	41164800	41165490	+	0	NA	intron (Nintron (N	-3876 NR_106931	1.02E+08 Hs. NR_106931	ENSG000003MIR6871	hsa-mir-6	microRNA ncRNA
chr3-1701	8.161616	0.659811	0.820232	0.804421	0.421154	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (NAluJb SIN	22795 NM_024947	80012 Hs. 525952NM_024947	ENSG000003PHC3	EDR3 HPHE	polyhome protein-coding
chr5-9716	8.161616	0.659811	0.820232	0.804421	0.421154	0.981636	chr5	97163841	97164498	+	0	NA	intron (NAluJo SIN	19078 NM_001155	55781 Hs. 27021 NM_01834	ENSG000003CROK2	RIO2	RIO kinase protein-coding
chr7-5624	8.161616	0.659811	0.820232	0.804421	0.421154	0.981636	chr7	5624119	56245409	+	0	NA	intron (Nintron (N	31518 NM_003038	6624 Hs. 11840CNM_003038	ENSG000003FSCN1	FAN1 HSM	fascin acprotein-coding
chr1-2405	10.42483	0.59553	0.740395	0.80434	0.4212	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (NAluSx3 SI	254432 NM_022465	64388 Hs. 98206 NM_022465	ENSG000003GREM2	CKTSF1B2 gremlin	protein-coding
chr10-315	10.11847	-0.59466	0.739557	-0.80408	0.421351	0.981636	chr10	31518422	31521659	+	0	NA	intron (Nintron (N	-120285 NM_001368	1.01E+08 Hs. 730227NM_001368	169 LOC100505	-	putative protein-coding
chr11-128	10.11847	-0.59466	0.739557	-0.80408	0.421351	0.981636	chr11	1.28E+08	1.28E+08	+	0	NA	Intergeni Intergeni	64937 NM_005238	2113 Hs. 369432NM_005238	ENSG000003ETS1	ETS-1 EWS	ETS protc protein-coding
chr13-115	10.11847	-0.59466	0.739557	-0.80408	0.421351	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (NAluYc SIN	12450 NR_044995	650669 Hs. 369201NM_01039799	GAS6-AS1	-	GAS6 antincRNA
chr19-520	10.11847	-0.59466	0.739557	-0.80408	0.421351	0.981636	chr19	52090856	52093443	+	0	NA	intron (NLIAMA9 LIN	2122 NM_001352	284371 Hs. 665751NM_001133	ENSG000003ZNF841	-	zinc fing protein-coding
chr3-1238	10.11847	-0.59466	0.739557	-0.80408	0.421351	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (NLIIME1 LIN	9972 NM_05302E	4638 Hs. 47737ENM_00596	ENSG000003MYLK	AAT7 KRP	myosin I protein-coding
chr22-495	4.196496	0.910283	0.132283	0.803936	0.421434	0.981636	chr22	49908041	49908692	+	0	NA	intron (NAluSc5 SI	10072 NM_02401E	79087 Hs. 526711NM_02410E	ENSG000003ALG12	CDG1G ECM	ALG1 protein-coding
chr2-2334	4.947479	-0.84049	1.045518	-0.80389	0.421458	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (Nintron (N	62204 NM_00364E	8527 Hs. 47167ENM_00364E	ENSG000003DGKD	DGKdelta diacylgly	protein-coding
chr20-344	4.947479	-0.84049	1.045518	-0.80389	0.421458	0.981636	chr20	34404385	34404909	+	0	NA	intron (NAluSq2 SI	41374 NM_001324	83737 Hs. 632227NM_03148E	ENSG000003ITCH	ADMPD AIF	itchy E3 protein-coding
chr20-365	4.947479	-0.84049	1.045518	-0.80389	0.421458	0.981636	chr20	36937709	36938388	+	0	NA	intron (NAluJb SIN	13660 NM_00136E	25939 Hs. 580681NM_01547E	ENSG000003SAMHD1	CHBL2 DCISAM	and I protein-coding
chr3-119	4.947479	-0.84049	1.045518	-0.80389	0.421458	0.981636	chr3	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	69975 NR_07350E	55254 Hs. 594171NM_01826E	ENSG000003TMEM39A	-	transmem protein-coding
chr3-1725	4.947479	-0.84049	1.045518	-0.80389	0.421458	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	175294 NM_00113E	64778 Hs. 744888NM_02276E	ENSG000003FND3C3B	FAD104 PF	fibronect protein-coding
chr15-101	6.096129	-0.78707	0.979109	-0.80386	0.421478	0.981636	chr15	1.01E+08	1.01E+08	+	0	NA	TTS (NM_C TTS (NM_C	77205 NM_01491E	22856 Hs. 110488NM_01491E	ENSG000003CHSY1	CHSY CSS1	chondroit protein-coding
chr8-389	6.096129	-0.78707	0.979109	-0.80386	0.421478	0.981636	chr8	9831113	9831351	+	0	NA	intron (NAluSx SIN	29886 NM_02162E	59339 Hs. 36912E2NM_02162E	ENSG000003PLEKHA2	TAPP2	pleckstr protein-coding
chr12-692	11.84599	-0.55651	0.692835	-0.80323	0.421842	0.981636	chr12	69261760	69263049	+	0	NA	exon (NM exon (NM	10814 NR_03169E	1E+08 Hs. NR_03169E	ENSG000003MIR1279	MIRN1279 microRNA	ncRNA
chr3-514	7.40333	-0.72081	0.897572	-0.80306	0.421938	0.981636	chr3	51430907	51431106	+	0	NA	intron (NAluJb SIN	39721 NM_01328E	29890 Hs. 11873ENM_01328E	ENSG000003RBM15B	HUMAGCGB RNA	bindi protein-coding
chr1-435	7.698309	0.69745	0.868755	0.802816	0.422081	0.981636	chr1	43592683	43593294	+	0	NA	intron (Nintron (N	-57161 NM_01466E	9682 Hs. 15598ENM_01466E	ENSG000003KDM4A	JHDM3A JM	lysine de protein-coding
chr16-301	7.698309	0.69745	0.868755	0.802816	0.422081	0.981636	chr16	30115400	30116034	+	0	NA	intron (Nintron (N	-2180 NM_024307	79153 Hs. 28901ENM_024307	ENSG000003GDPD3	GDE7	glycerol protein-coding
chr9-104	7.698309	0.69745	0.868755	0.802816	0.422081	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	42477 NR_13076E	55335 Hs. 429294NM_01837E	ENSG000003NIPSNAP3E	FP944 NIF	napsnap I protein-coding
chr2-3327	8.349817	-0.65192	0.812041	-0.80281	0.422082	0.981636	chr2	33273616	33275561	+	0	NA	intron (NLI3 LINE C	139991 NM_00116E	4052 Hs. 61931ENM_00062E	ENSG000003LTBP1	-	latent tr protein-coding
chr3-113	8.349817	-0.65192	0.812041	-0.80281	0.422082	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	TTS (NM_C TTS (NM_C	11947 NM_01417C	29083 Hs. 12749E9NM_01417C	ENSG000003GTPBP8	HSPC135	GTP bindi protein-coding
chr1-112	8.709051	0.63894	0.79488	0.802755	0.422116	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (NLIIMB7 LIN	29710 NM_138727	54879 Hs. 201921NM_01774E	ENSG000003STL7	FAM4B ST7	suppressi protein-coding
chr11-708	6.512404	0.741736	0.924253	0.802525	0.422249	0.981636	chr11	70888922	70889729	+	0	NA	intron (NMLT1C LTF	-16957 NR_037437	1.01E+08 Hs. NR_037437	ENSG000003MIR3664	mir-3664	microRNA ncRNA
chr1-282	8.716909	0.636208	0.792905	0.802376	0.422336	0.981636	chr1	28238004	28238559	+	0	NA	TTS (NM_C TTS (NM_C	2157 NM_17819C	93974 Hs. 744914NM_016311	ENSG000003ATP5IF1	ATP1 ATP1ATP	syntf protein-coding
chr1-150	8.716909	0.636208	0.792905	0.802376	0.422336	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	2761 NM_018997	57402 Hs. 40588CNM_018997	ENSG000003MRP52	MDSO16 MF	mitochon protein-coding
chr1-153	8.716909	0.636208	0.792905	0.802376	0.422336	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	intron (NAluSx1 SI	-4930 NM_02067E	57402 Hs. 28899E9NM_02067E	ENSG000003S100A14	84284 S1	S100 calc protein-coding
chr4-714	8.716909	0.636208	0.792905	0.802376	0.422336	0.981636	chr4	71408295	71410444	+	0	NA	intron (NTHE1A-int	70316 NM_00375E	8671 Hs. 5462 NM_00375E	ENSG000003SLC4A4	HNBC1 KNE	solute c protein-coding
chr6-3147	8.716909	0.636208	0.792905	0.802376	0.422336	0.981636	chr6	3147282	3148397	+	0	NA	intron (NMLT2B4 LI	9705 NM_00131C	7280 Hs. 65454E3NM_00106E	ENSG000003TUBB2A	CDCBMS TU	tubulin t protein-coding
chr22-429	9.187704	-0.64598	0.805131	-0.80233	0.422365	0.981636	chr22	428212750	428212988	+	0	NA	intron (NLI3 LINE C	44404 NM_01457C	26286 Hs. 68522E2NM_01457C	ENSG000003ARFGAP3	ARFGAP1	ARF ribos protein-coding
chr18-63	10.05191	-0.60253	0.751087	-0.80222	0.422427	0.981636	chr18	63340674	63340959	+	0	NA	intron (Nintron (N	-21436 NM_000657	596 Hs. 15074ENM_00065E	ENSG000003BCL2	Bcl-2 PPF	BCL2 apof protein-coding
chr15-297	6.639865	-0.72581	0.904854	-0.80213	0.422477	0.981636	chr15	29767662	29768310	+	0	NA	intron (Nintron (N	53078 NM_00135E	7082 Hs. 74399CNM_00325E	ENSG000003TJP1	ZO-1	tight jur protein-coding
chr8-301	6.639865	-0.72581	0.904854	-0.80213	0.422477	0.981636	chr8	30105065	30106480	+	0	NA	intron (Nintron (N	10314 NM_00112E	23484 Hs. 14658ENM_01534E	ENSG000003LEPROTL1	HSPC112 V	leptin r protein-coding
chr8-129	4.955336	-0.84283	1.050898	-0.80201	0.42255	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-57214 NM_03141E	56169 Hs. 133244NM_03141E	ENSG000003GSDMC	MLZE	gasdermir protein-coding
chr5-109	4.955336	-0.84283	1.050898	-0.80201	0.42255	0.981636	chr5	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	-12781 NR_14904C	285638 Hs. 532104NR_14904C	ENSG000003LOC28563E	-	uncharacterncRNA
chr1-1657	17.3912	0.464039	0.578829	0.801686	0.422735	0.981636	chr1	16576305	16577088	+	0	NA	intron (Nintron (N	27882 NR_03744E	1.01E+08 Hs. NR_03744E	ENSG000003MIR3675	-	microRNA ncRNA
chr1-285	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr1	28534678	28535413	+	0	NA	intron (Nintron (N	16819 NM_00104E	1104 Hs. 46972E2NM_00126E	ENSG000003RCC1	CHC1 RCC1	regulator protein-coding
chr10-35	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr10	35013004	35014341	+	0	NA	intron (Nintron (N	60611 NM_00119E	8453 Hs. 82919 NM_003591	ENSG000003CUL2	-	cullin 2 protein-coding
chr10-12	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (Nintron (N	25178 NM_07846E	56647 Hs. 37029E2NM_01656E	ENSG000003BCC1P	TOK-1 TOB	BRCA2 anc protein-coding
chr11-651	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr11	65116165	65116861	+	0	NA	TTS (NM_C TTS (NM_C	1188 NM_01420E	741 Hs. 12102E2NM_01420E	ENSG000003ZNHT2	Clorf5 F	zinc fing protein-coding
chr12-27	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr12	27745053	27745787	+	0	NA	intron (Nintron (N	26162 NM_00114E	1E+08 Hs. NM_00114E	ENSG000003MANS4	-	MANS4 don protein-coding
chr15-52	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr15	52033191	52034079	+	0	NA	intron (NLIIMEF LIN	14716 NM_00274E	5597 Hs. 411847NM_00274E	ENSG000003MAPK6	ERK3 HsT	mitogen-ε protein-coding
chr16-70	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr16	70239963	70241020	+	0	NA	Intergeni AluJb SIN	11449 NM_05821E	118460 Hs. 66063ENM_005821E	ENSG000003EXOSC6	EAP4 MTRE	exosome c protein-coding
chr17-83	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr17	83045928	83047208	+	0	NA	intron (NLIIMB5 LIN	5202 NR_13546E	146712 Hs. 607824NM_00100E	ENSG000003B3GNTL1	3-Gn-T8 E	UDDP-GlcN protein-coding
chr19-217	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr19	21764449	21765569	+	0	NA	intron (Nintron (N	2570 NM_00135E	163227 Hs. 365142NM_173531	ENSG000003ZNF100	-	zinc fing protein-coding
chr19-37	4.939621	-0.8381	1.045534	-0.8016	0.422782	0.981636	chr19	3										



chr11-282 5.915971	0.683348	0.981369	0.79822	0.424743	0.981636	chr11	28216910	28217363	+	0 NA	intron (NLIPA5 LIN	108748 NM_152636	196074 Hs. 243326NM_152636	ENSG000003METTL15	METT5D1	methyltransferase protein-coding	
chr1-2066 8.724767	0.634347	0.795204	0.797715	0.425036	0.981636	chr1	2.07E+08	2.07E+08	+	0 NA	intron (intron (N	7486 NM_001004	8444 Hs. 164267NM_003582	ENSG000003DYRK3	DYRK5	RE dual specific protein-coding	
chr17-392 8.724767	0.634347	0.795204	0.797715	0.425036	0.981636	chr17	39298435	39298801	+	0 NA	intron (NAluJr SIN	1218 NR_162098	1.14E+08	NR_162098	MIR548BC	microRNA ncRNA	
chr19-105 8.724767	0.634347	0.795204	0.797715	0.425036	0.981636	chr19	10907705	10909842	+	0 NA	intron (NMTIRb SINE	20316 NM_024025	78992 Hs. 164026NM_024025	ENSG000003YIPF2	FinGER2	Yip1 domain protein-coding	
chr2-3246 8.724767	0.634347	0.795204	0.797715	0.425036	0.981636	chr2	32462757	32463429	+	0 NA	intron (intron (N	-69066 NR_030285	69343 Hs. 164026NM_024025	ENSG000003MIR558	MIRN558	microRNA ncRNA	
chr3-1958 8.724767	0.634347	0.795204	0.797715	0.425036	0.981636	chr3	1.96E+08	1.96E+08	+	0 NA	intron (intron (N	-1454 NR_106887	1.02E+08	NR_106887	ENSG000003MIR6829	hsa-mir-6829	microRNA ncRNA
chr12-326 5.914121	0.768329	0.963379	0.797535	0.42514	0.981636	chr12	32611275	32611947	+	0 NA	intron (intron (N	-67589 NM_00133C	10059 Hs. 556299NM_005699	ENSG000003DNM1L	DLM1	DRP1 domain protein-coding	
chr2-2178 5.914121	0.768329	0.963379	0.797535	0.42514	0.981636	chr2	1.28E+08	2.18E+08	+	0 NA	exon (NM exon (NM	15033 NR_145792	1.1E+08	NR_145792	SNORA115	small nucleolar RNA	
chr20-322 5.914121	0.768329	0.963379	0.797535	0.42514	0.981636	chr20	32219553	32219752	+	0 NA	intron (NAluY SINE	11772 NM_015352	23509 Hs. 472409NM_015352	ENSG000003POFUT1	DDD2	FUT1 protein (protein-coding	
chr7-5435 5.914121	0.768329	0.963379	0.797535	0.42514	0.981636	chr7	5435701	5435929	+	0 NA	IntergeniIntergeni	-6888 NM_001354	1E+08	Hs. 147507NM_001354	8886	LOC100122	uncharacterized protein-coding
chr1-1507 8.683628	0.633517	0.794348	0.797531	0.425142	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	exon (NM exon (NM	9047 NM_000396	1513 Hs. 632466NM_000396	ENSG000003CTS	CTS02	CTS cathepsin protein-coding	
chr1-1513 8.683628	0.633517	0.794348	0.797531	0.425142	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	exon (NM exon (NM	-3142 NR_131972	1.02E+08	Hs. 634042NR_131972	GBAT2	glioblastin protein-coding	
chr1-1613 8.683628	0.633517	0.794348	0.797531	0.425142	0.981636	chr1	1.61E+08	1.61E+08	+	0 NA	intron (intron (N	20663 NM_001013	257177 Hs. 534593NM_001013	ENSG000003CFAP126	Clorf192	cilia and protein-coding	
chr11-15 8.683628	0.633517	0.794348	0.797531	0.425142	0.981636	chr11	51308315	51309505	+	0 NA	IntergeniALR/Alphe	899763 NR_024504	646813 Hs. 684175NR_024504	LOC646813	DEXH-box pseudo		
chr12-452 8.683628	0.633517	0.794348	0.797531	0.425142	0.981636	chr12	4523561	4523827	+	0 NA	intron (NLIPA5 LIN	14775 NM_020374	57102 Hs. 302977NM_020374	ENSG000003C12orf4	chromosome protein-coding		
chr6-302 8.683628	0.633517	0.794348	0.797531	0.425142	0.981636	chr6	30200624	30200827	+	0 NA	intron (NMTIRb SINE	12681 NM_001242	7726 Hs. 485041NM_003444	ENSG000003TRIM26	AFP	RNF99 tripartite protein-coding	
chr15-907 6.939208	-0.67331	0.844315	-0.79747	0.425181	0.981636	chr15	90614548	90614761	+	0 NA	intron (intron (N	-45580 NR_120371	1.02E+08	Hs. 615346NR_120371	ENSG000003LINC01585	long intronic RNA	
chr1-2200 10.45811	0.597767	0.74961	0.797438	0.425197	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	3' UTR (3' UTR (N	-12168 NM_004444	2058 Hs. 497788NM_004444	ENSG000003EPRS	EARS	GLUF glutamyl protein-coding	
chr1-3538 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr1	35381441	35381992	+	0 NA	exon (NM exon (NM	-15639 NR_046655	1.01E+08	Hs. 585397NR_046655	ENSG000003ZMYM4-AS1	ZMYM4	antncRNA
chr1-1507 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr1	1.55E+08	1.55E+08	+	0 NA	intron (intron (N	3648 NM_198883	4580 Hs. 490874NM_002455	ENSG000003MTX1	MTX	MTXN metaxin 1 protein-coding	
chr1-1707 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr1	1.71E+08	1.71E+08	+	0 NA	intron (intron (N	56468 NM_006902	5396 Hs. 283413NM_006902	ENSG000003PRR1	AGOTC	PHC related protein-coding	
chr1-1796 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	promoter-promoter-	-702 NM_001345	163590 Hs. 571797NM_022347	ENSG000003TOR1AIP2	IFRG15	LIU torsin 1 protein-coding	
chr19-119 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr19	11250222	11252421	+	0 NA	intron (intron (N	11203 NM_020812	57572 Hs. 591002NM_020812	ENSG000003DOCK6	AOS2	ZIR1 dedicator protein-coding	
chr19-112 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr19	19632527	19635368	+	0 NA	exon (NM exon (NM	-5727 NM_00472C	9170 Hs. 122577NM_00472C	ENSG000003LPAR2	EDG-4	EDC lysophospholipase protein-coding	
chr2-6981 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr2	69819297	69822388	+	0 NA	intron (intron (N	-8818 NM_178435	64395 Hs. 293971NM_178435	ENSG000003GMCL1	BTD13	GC germ cell protein-coding	
chr2-154 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr2	1.34E+08	1.34E+08	+	0 NA	exon (NM exon (NM	194752 NM_00241C	4249 Hs. 4988 NM_00241C	ENSG000003MGAT5	GNT-V	GNT1 alpha-1, epsilon protein-coding	
chr20-556 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr20	5560600	5581177	+	0 NA	intron (intron (N	40388 NM_019593	56261 Hs. 636355NM_019593	ENSG000003GPCPD1	ED13	GDEE glycerol protein-coding	
chr4-1361 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr4	13612726	13616012	+	0 NA	exon (NM exon (NM	13356 NM_148894	259282 Hs. 744933NM_148894	ENSG000003BOD1L1	BOD1L	FAM biont protein-coding	
chr5-3131 8.691485	0.631646	0.792372	0.797158	0.425359	0.981636	chr5	31312397	31313916	+	0 NA	intron (intron (N	119470 NM_004932	1004 Hs. 124777NM_004932	ENSG000003CDH6	CAD6	KCAI cadherin protein-coding	
chr10-457 8.169474	0.657727	0.825206	0.797045	0.425425	0.981636	chr10	45793618	45793817	+	0 NA	TTS (NR_TTS (NR_1	23607 NM_001351	643479 Hs. 522909NM_001351	23434	FAM25E	FAM25 family wiprotein-coding	
chr10-92 8.169474	0.657727	0.825206	0.797045	0.425425	0.981636	chr10	92014657	92015058	+	0 NA	intron (NTiger3a	91087 NM_003972	9044 Hs. 500522NM_003972	ENSG000003BTAF1	MOT1	TAF(B-TFIID 1 protein-coding	
chr11-111 8.169474	0.657727	0.825206	0.797045	0.425425	0.981636	chr11	1.12E+08	1.12E+08	+	0 NA	intron (intron (N	62793 NM_00271E	5519 Hs. 269128NM_00271E	ENSG000003PPP2R1B	PP2A	Abet protein protein-coding	
chr20-635 8.169474	0.657727	0.825206	0.797045	0.425425	0.981636	chr20	63531323	63534175	+	0 NA	3' UTR (3' UTR (N	8294 NR_031735	1E+08	NR_031735	ENSG000003MIR1914	MIRN1914	microRNA ncRNA
chr14-495 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr14	49576768	49577784	+	0 NA	3' UTR (3' UTR (N	9104 NM_00103C	6235 Hs. 156367NM_00103C	ENSG000003RPS29	DBA13	S29 ribosomal protein-coding	
chr16-234 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr16	23484271	23488049	+	0 NA	intron (intron (N	24334 NM_015044	23062 Hs. 460333NM_015044	ENSG000003GGA2	VEAR	golgi ass protein-coding	
chr2-2164 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr2	2.16E+08	2.16E+08	+	0 NA	intron (intron (N	-30487 NM_00099E	6168 Hs. 437011NM_00099E	ENSG000003RPL37A	L37A	ribosomal protein-coding	
chr20-385 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr20	38568281	38569178	+	0 NA	intron (intron (N	-12468 NR_130907	149685 Hs. 368028NM_174900	ENSG000003ADIG	SMAF1	adipogenin protein-coding	
chr22-312 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr22	31814484	31815467	+	0 NA	intron (intron (N	60952 NM_00136E	9681 Hs. 435022NM_014662	ENSG000003DEPDC5	DEP.5	FFDEP domain protein-coding	
chr5-1501 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr5	1.5E+08	1.5E+08	+	0 NA	intron (NL2a LINE	-20801 NM_005211	1436 Hs. 586211NM_005211	ENSG000003CSF1R	C-FMS	CD1 colony st protein-coding	
chr7-1495 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr7	1.5E+08	1.5E+08	+	0 NA	intron (MLT2D LTF	36156 NR_02778E	79970 Hs. 520785NM_02491C	ENSG000003ZNF767P	ZNF767	zinc finger pseudo	
chr8-8655 6.469414	0.727033	0.91223	0.796984	0.42546	0.981636	chr8	86530942	86531544	+	0 NA	intron (intron (N	16808 NM_00390E	8895 Hs. 191215NM_00390E	ENSG000003CPNE3	CPN3	PRO1 copine 3 protein-coding	
chr15-328 6.52812	0.736586	0.924362	0.796859	0.425533	0.981636	chr15	32893207	32893880	+	0 NA	intron (intron (N	174631 NM_001103	342184 Hs. 657645NM_001103	ENSG000003FNM1	FNM1	LDL formin 1 protein-coding	
chr14-705 11.45128	0.557009	0.699043	0.796817	0.425557	0.981636	chr14	70978015	70978840	+	0 NA	exon (NM exon (NM	70968 NM_00130E	22990 Hs. 446555NM_014982	ENSG000003PCNX1	PCNX1	PCNX1 pectanex 1 protein-coding	
chr20-356 6.461556	0.729583	0.915822	0.796643	0.425658	0.981636	chr20	35939637	35940072	+	0 NA	intron (intron (N	14772 NM_00336C	51282 Hs. 584905NM_016555	ENSG000003SCAND1	RAC1	SDP1 domain protein-coding	
chr5-3942 6.461556	0.729583	0.915822	0.796643	0.425658	0.981636	chr5	39421426	39424017	+	0 NA	intron (intron (N	2259 NM_001343	1601 Hs. 696631NM_001343	ENSG000003DAB2	DOC2	DOC2AB domain protein-coding	
chrX-1356 6.461556	0.729583	0.915822	0.796643	0.425658	0.981636	chrX	13581166	1359420	+	0 NA	intron (intron (N	22008 NM_002183	3563 Hs. 632793NM_002183	ENSG000003IL3RA	CD123	IL3 interleukin protein-coding	
chr1-4627 6.665289	-0.71796	0.901544	-0.79637	0.425818	0.981636	chr1	46278211	46278775	+	0 NA	TTS (NM_TTS (NM_C	24873 NM_00636E	10489 Hs. 144941NM_00636E	ENSG000003LRRC41	MUF1	PP77 leucine protein-coding	
chr10-583 6.665289	-0.71796	0.901544	-0.79637	0.425818	0.981636	chr10	58388660	58389109	+	0 NA	intron (intron (N	3474 NM_003201	7019 Hs. 594255NM_003201	ENSG000003TFAM	NTPC-15	transcript protein-coding	
chr16-836 6.665289	-0.71796	0.901544	-0.79637	0.425818	0.981636	chr16	83811389	83813497	+	0 NA	3' UTR (3' UTR (N	4465 NM_001537	3281 Hs. 250899NM_001537	ENSG000003HSBP1	PP3A-A	13 heat shock protein-coding	
chr16-895 6.665289	-0.71796	0.901544	-0.79637	0.425818	0.981636	chr16	89909002	89911486	+	0 NA	intron (intron (N	-7635 NM_00238E	4157 Hs. 51382				

chr15-626 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr15	62649959	62654326	+	0	NA	intron (Nintron (N	4831 NM_01505E	83660 Hs. 56943ENR_01505E	ENSG00000CLTN2	ILWEQ	talin 2 protein-coding		
chr17-376 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr17	37510207	37514700	+	0	NA	exon (NM exon (NM	22562 NM_00702E	11072 Hs. 91448 NM_00702E	ENSG00000DUSP14	MKP-1 MKF dual spec	protein-coding		
chr19-144 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr19	14400150	14401764	+	0	NA	intron (NAluJb SIN	18384 NM_00580A	10212 Hs. 31160ENR_00580A	ENSG00000CDDX39A	BAT1 BAT1DExD-box	protein-coding		
chr19-236 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr19	23238619	23239320	+	0	NA	intron (Nintron (N	11425 NM_00135E	440519 Hs. 675811NM_00135E	ENSG00000ZNF724	ZNF724P	zinc finger protein-coding		
chr19-406 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr19	40616135	40616235	+	0	NA	intron (NAluSz SIN	15316 NM_00104E	8425 Hs. 466766NM_00357E	ENSG00000LTBP4	ARCL1C L1latent t	protein-coding		
chr2-8746 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr2	87466339	87468172	+	0	NA	intron (Nintron (N	-2695 NR_14646C	112597 Hs. 65216ENR_02420A	ENSG00000CCYTOR	C2orf59 l	cytoskeleton RNA		
chr2-1276 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr2	1.27E+08	1.27E+08	+	0	NA	intron (NMIR SINE	36121 NM_00130C	2071 Hs. 469872NM_00012E	ENSG00000ERCC3	BTf2 GTfE	ERCC exciprotein-coding		
chr2-1332 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (NLM5 LINE	11677 NR_110294	1.02E+08 Hs. 661917NR_110294	ENSG00000NCKAP5-AS-	NCKAP5	arcncRNA		
chr2-2016 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (Nintron (N	9639 NM_15238E	65062 Hs. 12319 NM_15238E	ENSG00000TMEM237	ALS2CR4 J	transmemt protein-coding		
chr2-232 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr22	30841 NM_00247E	30841 NM_00247E	+	0	NA	intron (NL2b LINE	4627 Hs. 474751NM_00247E	ENSG00000MYH9	BDPLT6 DF	myosin h protein-coding			
chr2-466 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr22	46088899	46091162	+	0	NA	intron (Nintron (N	-1014 NR_03741E	1.01E+08 NR_03741E	ENSG00000MIR3619	NCKAP5	arcncRNA		
chr4-1393 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	-73703 NM_001184	4717 Hs. 84549 NM_00249A	ENSG00000NDUF1C	KFYI	NADH:ubiq	protein-coding	
chr4-1854 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr4	1.85E+08	1.85E+08	+	0	NA	intron (Nintron (N	6409 NM_18172E	353322 Hs. 508154NM_18172E	ENSG00000ANKRD37	Lrp2bp	ankyrin r	protein-coding	
chr5-7826 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr5	78264375	78265943	+	0	NA	intron (NAluJr SIN	29539 NM_00127I	8546 Hs. 532091NM_00366A	ENSG00000CAP3B1	ADTB3 AD1	adaptor l	protein-coding	
chr6-8547 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr6	85471886	85478321	+	0	NA	intron (Nintron (N	25020 NM_00252E	4907 Hs. 153952NM_00252E	ENSG00000CNT5E	CALJA CD75	-nuclec	protein-coding	
chr6-1334 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr6	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	215862 NM_00130I	2070 Hs. 596688NM_00410C	ENSG00000EYA4	CMDJ1 JFN	EYA trans	protein-coding	
chr7-668 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr7	66802323	66803532	+	0	NA	intron (NA-rich Lc	41899 NR_00393A	729156 Hs. 70987ENR_00393A	ENSG00000GTF2IRD1F-	GTF2I	repseude		
chr8-615 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr8	61558928	61561898	+	0	NA	intron (NA-rich Lc	129398 NM_001164	444 Hs. 332422NM_00431E	ENSG00000ASPH	AAH BAH	Caspate	protein-coding	
chr8-7696 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr8	76982048	76983705	+	0	NA	3' UTR (N3' UTR (N	-16026 NR_13046C	1E+08 NR_13046C	ENSG00000MIR3149		microRNA	ncRNA	
chr8-1301 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (NAluJb SIN	-86043 NR_04538E	1.01E+08 Hs. 10601ENR_04538E	ENSG00000ASAP1-IT2-	ASAP1	intncRNA		
chr9-982 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr9	98204909	98205698	+	0	NA	intron (Nintron (N	8248 NM_001267	55357 Hs. 37101ENR_01842I	ENSG00000TBC1D2	PARIS-1 F	TBC1	protein-coding	
chr9-1096 6.657431	-0.71614	0.901432	-0.79445	0.426932	0.981636	chr9	1.09E+08	1.09E+08	+	0	NA	intron (NAluSx SIN	13489 NR_02950E	407036 NR_02950E	ENSG00000MIR32	MIRN32 hs	microRNA	ncRNA	
chr1-2846 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr1	28464178	28464720	+	0	NA	intron (NAluJo SIN	26299 NM_02392E	65979 Hs. 225641NM_02392E	ENSG00000PHACTR4	PPP1R124	phosfat	protein-coding	
chr12-572 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr12	57325679	57325660	+	0	NA	intron (Nigger1 I	13398 NM_00135I	22864 Hs. 44367E	ENSG00000R3HDM2	CAG6 PRO1R3H	doma	protein-coding	
chr12-654 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr12	65841923	65842766	+	0	NA	intron (NMIR SINE	-15370 NR_02682E	204010 Hs. 55868ENR_02682E	ENSG00000RPSAP52	RPSA_17	ribosoma	pseudo	
chr14-693 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr14	69375299	69377584	+	0	NA	IntergeniLTR87 LTF	21543 NM_00445E	2079 Hs. 509791NM_00445E	ENSG00000CERH	DROER	ERH	mRNA	protein-coding
chr2-1995 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr2	19952929	19952508	+	0	NA	intron (NMIRb SINE	-9277 NM_00136E	79568 Hs. 154494NM_02452C	ENSG00000MAIP1	C2orf47	matrix A	protein-coding	
chr2-2185 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (Nintron (N	6473 NM_02093E	57695 Hs. 166066NM_02093E	ENSG00000CUSP37		ubiquiti	protein-coding	
chr3-1081 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr3	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	40021 NR_11002E	1.02E+08 Hs. 57065E	NR_11002E	ENSG00000LINC0121E-		long	intncRNA
chr3-1794 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr3	1.8E+08	1.8E+08	+	0	NA	intron (NAluSx1 SI	15301 NM_00430I	86 Hs. 435322NM_00430I	ENSG00000ACTL6A	ACTL6 ARF	actin	lik	protein-coding
chr4-1684 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (NAluJb SIN	23436 NM_00129I	91351 Hs. 535011NM_00101E	ENSG00000CDDX60L		DEXD/H-bc	protein-coding	
chrX-7394 4.898481	-0.84408	1.062733	-0.79426	0.427046	0.981636	chrX	73949842	73950644	+	0	NA	intron (NLM5B LIN	5918 NR_02458E	554203 Hs. 64831ENR_02458E	ENSG00000JPX	DCBALD06 JPX	transc	ncRNA	
chr1-3294 8.202755	-0.660484	0.831652	-0.794183	0.427089	0.981636	chr1	32944378	32944683	+	0	NA	intron (Nintron (N	20574 NM_001127	127544 Hs. 591504NM_15334I	ENSG00000RNF19B	IBRD03 NR	ring	protein-coding	
chr15-898 8.202755	-0.660484	0.831652	-0.794183	0.427089	0.981636	chr15	89868855	89869242	+	0	NA	intron (NSVA F Ret	14982 NR_049807	1.01E+08 NR_049807	ENSG00000MIR5009		microRNA	ncRNA	
chr19-105 8.202755	-0.660484	0.831652	-0.794183	0.427089	0.981636	chr19	10376503	10377219	+	0	NA	intron (NAluSz SIN	3711 NM_00333I	7297 Hs. 75516 NM_00333I	ENSG00000TYK2	IMD35 JF	tyrosine	protein-coding	
chr19-258 8.202755	-0.660484	0.831652	-0.794183	0.427089	0.981636	chr19	25848034	25850213	+	0	NA	IntergeniALR/Alpha	-1685676 NR_00360E	1E+08 Hs. 149312NR_00360E	ENSG00000HACR1P1		hepatitis	pseudo	
chr19-403 8.202755	-0.660484	0.831652	-0.794183	0.427089	0.981636	chr19	40374331	40375229	+	0	NA	intron (Nintron (N	4934 NR_106854	1.02E+08 NR_106854	ENSG00000MIR6796	hsa-mir-	microRNA	ncRNA	
chr6-4304 8.202755	-0.660484	0.831652	-0.794183	0.427089	0.981636	chr6	43043923	43045784	+	0	NA	exon (NM exon (NM	9092 NM_00116E	9820 Hs. 52013ENR_01478C	ENSG00000CUL7	3M1 CUL-	7-cullin 7	protein-coding	
chr19-514 5.980684	-0.775488	0.977133	-0.793636	0.427407	0.981636	chr19	51426208	51426800	+	0	NA	intron (NCpG	173241 NM_001137C	23030 Hs. 65481ENR_01501E	ENSG00000KDM4B	JMJ2B2 TI	lysine	de	protein-coding
chr7-2591 5.980684	-0.775488	0.977133	-0.793636	0.427407	0.981636	chr7	2591669	2594569	+	0	NA	exon (NM exon (NM	34140 NM_15255E	23288 Hs. 520627NM_15255E	ENSG00000IQCE	1700028P	IQ motif	protein-coding	
chr1-1714 8.675777	-0.63543	0.800744	-0.79355	0.427458	0.981636	chr1	1.71E+08	1.71E+08	+	0	NA	intron (NAluSg SIN	4632 NM_01517E	2261 Hs. 494611NM_01517E	ENSG00000PRRC2C	BAT2-iso	proline	r	protein-coding
chr6-5657 8.408523	-0.64099	0.808331	-0.79297	0.427793	0.981636	chr6	56578281	56578652	+	0	NA	intron (Nintron (N	64423 NM_00103I	6675 Hs. 60491ENR_00117E	ENSG00000CST	BP20 BP	dystonin	protein-coding	
chr1-1122 8.699343	-0.629772	0.794671	-0.792493	0.428073	0.981636	chr1	11228694	11232997	+	0	NA	intron (Nintron (N	31706 NM_00495E	2475 Hs. 338207NM_00495E	ENSG00000MTOR	FRAP FRAF	mechanist	protein-coding	
chr1-2688 8.699343	-0.629772	0.794671	-0.792493	0.428073	0.981636	chr1	26883256	26883619	+	0	NA	intron (NMIRb SINE	7679 NM_03228E	84243 Hs. 52371ENR_03228E	ENSG00000ZDHH18	DHHC-18 Z	zinc	finger	protein-coding
chr1-1204 8.699343	-0.629772	0.794671	-0.792493	0.428073	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	-69414 NR_00324E	767846 Hs. 65718ENR_00324E	ENSG00000PFN1P2	CHRC152 P	profilin	pseudo	
chr1-168 8.699343	-0.629772	0.794671	-0.792493	0.428073	0.981636	chr1	1.68E+08	1.68E+08	+	0	NA	intron (NMER58A DN	65187 NM_001267	23432 Hs. 27180ENR_00736E	ENSG00000GPR161	RE2	G	protein	protein-coding
chr1-2128 8.699343	-0.629772	0.794671	-0.792493	0.428073	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	intron (Nintron (N	15484 NM_01405E	28982 Hs. 7055 NM_01405E	ENSG00000FLVCR1	AXPC1 FLV	feline	l	protein-coding
chr1-2294 8.699343	-0.629772	0.794671	-0.792493	0.428073	0.981636	chr1	2.29E+08	2.29E+08	+	0	NA	intron (NLTR33 LTF							



chr8-125c.666062	0.627071	0.79441	0.789355	0.429905	0.981636	chr8	1.25E+08	1.25E+08	0	NA	intron (AluSp SIN	40015 NM_01484E	9897 Hs. 27004E	ENSG00000WASHC5	KIAA0196 WASH	comp	protein-coding		
chr1-197c.3.675409	-0.95585	1.210944	-0.78934	0.429914	0.981636	chr1	1.9750777	1.9752311	+	NA	intron (AluJb SIN	47805 NM_001345	255104 Hs. 46672E	ENSG00000TMC04	-	-	transment protein-coding		
chr10-167c.675409	-0.95585	1.210944	-0.78934	0.429914	0.981636	chr10	16752880	16753834	+	NA	intron (intron (N	64067 NM_01242E	6251 Hs. 524161NM	01242E	ENSG00000CRS1U	RSP-1	Ras suppr	protein-coding	
chr10-27c.675409	-0.95585	1.210944	-0.78934	0.429914	0.981636	chr10	107540290	27540666	+	NA	non-codiron-codir	36174 NR_04617E	22931 Hs. 406799NM	02125E	ENSG00000RAB18	RAB18L11	RAB18, me	protein-coding	
chr12-102c.675409	-0.95585	1.210944	-0.78934	0.429914	0.981636	chr12	2.02E+08	1.02E+08	+	NA	intron (Mam SINE1	51019 Hs. 40569E	ENSG00000WASHC3	CCDC53	CCWASH	comp	protein-coding		
chr13-11c.675409	-0.95585	1.210944	-0.78934	0.429914	0.981636	chr13	1.11E+08	1.11E+08	+	NA	intron (LIMC5 LIN	41512 NM_01821C	55739 Hs. 408324NM	01821C	ENSG00000CNAXD	CARKD LP:	NAD(P)HX	protein-coding	
chr3-138c.675409	-0.95585	1.210944	-0.78934	0.429914	0.981636	chr3	1.38E+08	1.38E+08	+	NA	intron (NMIRb SINE	58737 NM_001345	347736 Hs. 660992NM	17813C	ENSG00000NME9	NP23-H9	TNME NM23	protein-coding	
chr1-971c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr1	9715644	9716107	+	NA	exon (NM exon (NM	24408 NM_00135C	5293 Hs. 518451NM	00502E	ENSG00000PIK3CD	AMDS IMD1	phosphatiprotein-coding		
chr1-103c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr1	10364898	10367965	+	NA	intron (intron (N	-32633 NM_001304	5226 Hs. 464071NM	00263I	ENSG00000CPGD	6PGD	phosphogl	protein-coding	
chr1-212c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr1	2.12E+08	2.12E+08	+	NA	intron (NLIM4a LIN	17753 NM_01825E	55248 Hs. 44538E	ENSG00000PACC1	Clorf75	Fproton ac	protein-coding		
chr1-247c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr1	2.47E+08	2.47E+08	+	NA	intron (MLT1B LTF	28855 NM_00132E	84838 Hs. 168677NM	03275E	ENSG00000ZNF496	N1ZP1 ZFF	zinc fing	protein-coding	
chr12-66c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr12	6656909	6658483	+	NA	intron (AluSg SIN	5423 NM_001127	51147 Hs. 52421C	ENSG00000ING4	my036 p2E	inhibitor	protein-coding		
chr12-101c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr12	1.01E+08	1.01E+08	+	NA	intron (NLIP47 LIN	-76150 NR_04983E	1.01E+08	NR_04983E	ENSG00000MIR5484Q	-	microRNA	ncRNA	
chr13-100c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr13	1E+08	1E+08	+	NA	intron (MER61 int	72840 NR_04768E	1.01E+08	Hs. 662554NR	04768E	PCCA-AS1	-	PCCA	anticrRNA
chr14-34c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr14	34956122	34957480	+	NA	intron (AluSq2 SI	16879 NR_002937	280655 Hs. 639271NR	002937	IGBP1P1	C14orf19	immunogl	pseudo	
chr15-991c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr15	99151149	99151805	+	NA	intron (intron (N	46397 NM_01528E	23336 Hs. 20710E	ENSG00000SYNM	DMN SYN	synemin	protein-coding		
chr16-311c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr16	3119755	3120973	+	NA	3' UTR (N3' UTR (N	-4766 NR_02416E	81854 Hs. 66949C	NR_02416E	ZNF205-AS-	ZNF205	arnRNA		
chr17-27c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr17	27591457	27594099	+	NA	intron (intron (N	-38410 NM_00230E	3965 Hs. 81337	NR_00230E	ENSG00000LIGALS9	HUAT L	LGALectin	protein-coding	
chr17-454c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr17	45477088	45479358	+	NA	intron (intron (N	-2788 NR_03619E	1E+08	NR_03619E	ENSG00000MIR4315-	-	microRNA	ncRNA	
chr17-70c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr17	60683816	60685444	+	NA	intron (intron (N	6779 NM_00132C	54828 Hs. 65502E	ENSG00000BCAS3	GAOB1 MA:	BCAS3	mic	protein-coding	
chr17-66c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr17	77336840	77337984	+	NA	intron (NLIMEf LIN	17897 NM_00664C	10801 Hs. 44093E	ENSG00000SEPTIN9	AF17q25	septin	9	protein-coding	
chr17-805c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr17	80998684	80999906	+	NA	3' UTR (N3' UTR (N	7454 NM_02459I	79643 Hs. 51456C	ENSG00000CHMP6	VPS20	charged	n	protein-coding	
chr19-12c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr19	12043210	12045078	+	NA	exon (NM exon (NM	-8403 NM_00108E	163059 Hs. 66777E	ENSG00000ZNF433	-	zinc fing	protein-coding		
chr19-422c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr19	37108181	37117044	+	NA	intron (HERYK int	34179 NM_00132E	147923 Hs. 44499E	ENSG00000ZNF420	APAK	zinc fing	protein-coding		
chr22-17c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr22	17863954	17864450	+	NA	3' UTR (N3' UTR (N	42684 NM_00112E	57553 Hs. 528024NM	01524I	ENSG00000MICAL3	MICAL-3	microtub	protein-coding	
chr3-9937c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr3	9937154	9938176	+	NA	exon (NM exon (NM	3831 NM_01551E	78987 Hs. 9383	NR_01551E	ENSG00000CRELD1	AVSD2 C1F	cysteine	protein-coding	
chr6-422c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr6	42299799	42300537	+	NA	intron (NL3 LINE C	-82307 NM_01814I	55173 Hs. 380887NM	01814I	ENSG00000MRP50	MRP-S10	Fmitochon	protein-coding	
chr7-5504c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr7	5504083	5505778	+	NA	intron (AluY SINE	8879 NM_00136E	80028 Hs. 623974NM	02496E	ENSG00000FBXL18	Fb118	F-box	anc	protein-coding
chr7-121c.6.443991	0.721061	0.913875	0.789015	0.430103	0.981636	chr7	1.21E+08	1.21E+08	+	NA	intron (NMSTA LTR	-135991 NR_01608E	51384 Hs. 27237E	ENSG00000WNT16	-	Wnt	family	protein-coding	
chr13-951c.6.432625	0.632467	0.801934	0.788677	0.430301	0.981636	chr13	95219672	95219911	+	NA	intron (AluJo SIN	9447 NR_14573E	1.1E+08	NR_14573E	SNORD13G	-	small	nucsnRNA	
chr16-46c.6.432625	0.632467	0.801934	0.788677	0.430301	0.981636	chr16	4699830	4700756	+	NA	intron (AluSx3 SI	6575 NM_00137C	84309 Hs. 51331E	ENSG00000NUDT16L1	SDOS TIR:	nudix	hyc	protein-coding	
chr16-11c.6.432625	0.632467	0.801934	0.788677	0.430301	0.981636	chr16	1125236	11272442	+	NA	intron (NLIMEc LIN	81775 NM_01522E	23274 Hs. 35490	ENSG00000CLEC16A	Gop-1 K1A	C-type	l	protein-coding	
chr9-126c.6.432625	0.632467	0.801934	0.788677	0.430301	0.981636	chr9	1.27E+08	1.27E+08	+	NA	intron (Tigger L	15326 NM_01400E	23099 Hs. 355581NM	01400E	ENSG00000ZBTB43	ZBTB22B z	zinc fing	protein-coding	
chr1-310c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr1	31055147	31055916	+	NA	intron (MamRTE L	10186 NM_00102C	9698 Hs. 281707NM	01467E	ENSG00000PUM1	HSPUM PUM	pumilio	f	protein-coding
chr1-1851c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr1	1.85E+08	1.85E+08	+	NA	intron (NLIMC5 LIN	13926 NM_03093A	81627 Hs. 10714E	ENSG00000TRMT1L	Clorf25	trna	met	protein-coding	
chr12-881c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr12	88129030	88129777	+	NA	intron (intron (N	12813 NM_025114	80184 Hs. 150444NM	025114	ENSG00000CEP290	3H11Ag E	chromatin	protein-coding	
chr2-170c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr2	1.7E+08	1.7E+08	+	NA	intron (NLIME3 LIN	-107721 NR_04568E	140469 Hs. 67190C	ENSG00000MYO3B	-	myosin	II	protein-coding	
chr3-3714c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr3	3714737	37147939	+	NA	intron (intron (N	26919 NM_00630E	9209 Hs. 74052E	ENSG00000LRRFP2	HUF1-2	LRR	bindip	protein-coding	
chr3-1224c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr3	1.22E+08	1.22E+08	+	NA	intron (intron (N	8244 NM_01906E	54554 Hs. 56751E	ENSG00000WDR5B	-	WD	repeat	protein-coding	
chr4-420c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr4	42062818	42064206	+	NA	intron (LTR78 LTF	72982 NM_00634E	10463 Hs. 479634NM	00634E	ENSG00000SLC30A9	BILAPES	colute	protein-coding	
chr9-231c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr9	23196188	23197141	+	NA	intron (LOR1b LTF	28438 NM_00384A	8797 Hs. 213467NM	00384A	ENSG00000TNFRSF10A	AP02 CD2E	TNF	rece	protein-coding
chr9-1907c.6.436133	0.723591	0.917478	0.788674	0.430303	0.981636	chr9	19075185	19076086	+	NA	intron (NLIMB5 LIN	-11849 NR_00300E	677776 Hs. 68963E	ENSG00000SCARN8A	U92	small	Ca_	ncRNA	
chr10-68c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr10	68068757	68073161	+	NA	intron (intron (N	4324 NM_00127E	26091 Hs. 51891	NR_01560I	ENSG00000CHERC4	-	HECT	and	protein-coding
chr16-85c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr16	85435	85930	+	NA	TTS (NM_C	7457 NM_00101E	4350 Hs. 45959E	ENSG00000MCPG	AAG ADP	C-N-methyl	l	protein-coding	
chr2-179c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr2	1.8E+08	1.8E+08	+	NA	intron (HelitronE	23490 NM_02094E	57703 Hs. 31136E	ENSG00000CWC22	E1F4A	NC	C22	spl	protein-coding
chr20-21c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr20	21332627	21334382	+	NA	intron (intron (N	30006 NM_001317	22803 Hs. 25593E	ENSG00000XRN2	-	5'-3'	exc	protein-coding	
chr6-405c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr6	4056927	4058306	+	NA	intron (intron (N	21521 NM_17356E	222826 Hs. 65734E	ENSG00000FAM217A	C6orf146	general	wip	protein-coding	
chr6-110c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr6	1.11E+08	1.11E+08	+	NA	TTS (NM_C	9450 NM_13840E	112495 Hs. 41852C	ENSG00000GTF3C6	C6orf51	general	t	protein-coding	
chr6-133c.6.359525	-0.64273	0.815192	-0.78843	0.430443	0.981636	chr6	1.34E+08	1.34E+08	+	NA	intron (NLIP47 LIN</								



chr11-618	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr11	61807835	61810759	+	0	NA	intron (Nintron (N	5943	NR_031725	1E+08	NR_031725	ENSG00000MIR1908	MIRN1908	microRNA	ncRNA	
chr11-714	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr11	71472734	71477086	+	0	NA	intron (NLTR53 LTF	1407	NR_106812	1.02E+08	NR_106812	ENSG00000MIR6754	hsa-mir-61	microRNA	ncRNA	
chr11-13C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr11	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-22457	NM_021978	6768	Hs.50431	ENSG00000CT14	ARCT11	H1 suppressor	protein-coding	
chr12-43C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr12	4324551	4325234	+	0	NA	intron (Nintron (N	3679	NM_020375	57103	Hs.50454	ENSG00000TIGAR	C12orf5	FTP53	ind protein-coding	
chr12-10C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr12	1E+08	1E+08	+	0	NA	intron (Nintron (N	-39503	NM_001145	246123	Hs.116871	ENSG00000SLC17A8	DFNA25	VC solute c	protein-coding	
chr12-124	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr12	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	20434	NM_032656	57647	Hs.107382	ENSG00000DXH37	DDX37	DhrDEAH-box	protein-coding	
chr13-46C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr13	46000195	46001179	+	0	NA	intron (NTigger1 E	52059	NM_00133C	23091	Hs.136102	ENSG00000ZC3H13	KIAA0853	zinc finger	protein-coding	
chr13-77C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr13	77099840	77099813	+	0	NA	intron (Nintron (N	23607	NR_046716	1.01E+08	Hs.56928	ENSG00000MYPB2-AS	MYPB2	arncRNA		
chr16-82C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr16	82094178	82096459	+	0	NA	intron (Nintron (N	60065	NM_002153	3294	Hs.16279	ENSG00000HSD17B2	EDH17B2	F hydroxyst	protein-coding	
chr16-85C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr16	85079699	85078962	+	0	NA	intron (Nintron (N	14753	NM_00128E	9764	Hs.30165	ENSG00000KIAA0513	KIAA0513	protein-coding		
chr19-374	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr19	37438564	37439598	+	0	NA	intron (NAluSq SIN	28363	NM_00133C	148266	Hs.51184	ENSG00000ZNF569	ZNF569	ZNF zinc	protein-coding	
chr2-273C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr2	27326094	27327622	+	0	NA	exon (NM exon (NM	-3761	NM_002437	4358	Hs.75659	ENSG00000MYPV17	CMT2E	MI mitochond	protein-coding	
chr2-427C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr2	42703397	42704321	+	0	NA	intron (NAluSc8 S	60402	NM_148962	165140	Hs.16843	ENSG00000OXER1	GPCR	GPR1 oxoecis	protein-coding	
chr2-196C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr2	1.97E+08	1.97E+08	+	0	NA	intron (NLMIME3B L	8507	NM_001321	80055	Hs.22998	ENSG00000PGAP1	Bst1	ISFP post-GPI	protein-coding	
chr2-219C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr2	2.2E+08	2.2E+08	+	0	NA	intron (Nintron (N	7994	NM_052902	114790	Hs.22410	ENSG00000STK111P	LIP1	LKB1 serine/tl	protein-coding	
chr20-34C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr20	34851312	34851995	+	0	NA	intron (Nintron (N	-17191	NR_002165	128872	Hs.55862	ENSG00000HMG3P1	HMG4L	HMC high	mobipseudo	
chr22-31C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr22	31265331	31266584	+	0	NA	intron (NAluSg SIN	16573	NM_016733	3985	Hs.47459	ENSG00000CLIMK2		LIM domain	protein-coding	
chr3-195C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	exon (NM exon (NM	-7356	NR_134939	1.02E+08	Hs.55175	ENSG00000LINC01983		long intencRNA		
chr4-408C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr4	40821788	40823048	+	0	NA	intron (Nintron (N	34737	NM_00116E	323	Hs.47960	ENSG00000APB2	FEF5L	FEF amyloid t	protein-coding	
chr6-1421	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr6	1.42E+08	1.42E+08	+	0	NA	intron (NMSTB-int	27289	NM_016485	51534	Hs.431367	ENSG00000CVTA1	C6orf55	l vesicle t	protein-coding	
chr7-7451	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr7	74513677	74516410	+	0	NA	intron (NAluSx1 S	61137	NM_01632E	9569	Hs.64705	ENSG00000GTF21RD1	BEN	CREAM GTP2I	reprotein-coding	
chr8-1181	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr8	11811437	11812583	+	0	NA	intron (NMamSINE1	2866	NM_001287	2222	Hs.59329	ENSG00000FDFT1	DGPT	ERCC farnesyl-	protein-coding	
chr8-287C	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr8	28738325	28738715	+	0	NA	intron (NMER33 DN	37019	NR_07346E	2137	Hs.49135	ENSG00000EXTL3	BOTV	EXT1 exostosyl	protein-coding	
chr9-1377	6.451849	0.718493	0.917582	0.783029	0.43361	0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	intron (NLMIM2 L	67704	NR_14750E	651337	Hs.60319	ENSG00000LOC651337		uncharactcRNA		
chr3-184C	10.17718	-0.58548	0.748021	-0.7827	0.433802	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (NAluJb SIN	2266	NM_00127E	5437	Hs.43257	ENSG00000POLR2H	RPABC3	RF RNA	polynprotein-coding	
chr1-1708	9.213497	0.608566	0.777535	0.782866	0.433812	0.981636	chr1	77864048	77864310	+	0	NA	intron (NAluSq2 S	-24336	NM_144573	91624	Hs.61238	ENSG00000CNEXN	CMH20	NEI nexilin	F protein-coding	
chr2-160C	8.326243	-0.64757	0.827462	-0.7826	0.433864	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	TTS (NM_CTS (NM_C	137	NR_10377E	1.01E+08	Hs.10377	ENSG00000LINC0247E		long intencRNA		
chr1-3167	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr1	31676630	31677192	+	0	NA	intron (Nintron (N	27106	NM_00185E	1307	Hs.36892	ENSG00000COL16A1	447AA	FP1 collagen	protein-coding	
chr13-951	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr13	95180211	95180578	+	0	NA	intron (NAluSq2 S	-29950	NR_145733	1.1E+08	NR_145733	SNORD13G		small nucsnoRNA		
chr18-35C	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr18	35341732	35341931	+	0	NA	intron (NAluJo SIN	2589	NM_00130E	7572	Hs.51480	ENSG00000ZNF24	KOX17	RSC zinc	protein-coding	
chr20-58C	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr20	58663225	58664109	+	0	NA	intron (Nintron (N	12384	NM_001134	8675	Hs.30791	ENSG00000CSTX16	SYN16	syntaxin	protein-coding	
chr4-8494	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr4	84941011	84941830	+	0	NA	intron (NLMIM5 L	-21496	NR_152774	404201	Hs.46730	ENSG00000WDFY3-AS2	C4orf12	WDFY3	antcncRNA	
chr4-139C	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr4	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	21474	NM_001354	287	Hs.62057	ENSG00000ANK2	ANK2	-LQ1 tankyrin	protein-coding	
chr5-7151	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr5	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	-68651	NM_001184	4717	Hs.84549	ENSG00000NDUF1	KFY1	NADH:ubiq	protein-coding	
chr5-1791	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr5	17151940	17152102	+	0	NA	intron (NLMIM4 L	64578	NM_01842E	55814	Hs.25827	ENSG00000BDP1	KDNB112	F B double	protein-coding	
chr9-380C	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chr9	1.99E+08	1.99E+08	+	0	NA	intron (Nintron (N	118947	NM_014594	30832	Hs.27232	ENSG00000ZNF354C	IDF3	zinc	protein-coding	
chrX-1667	6.682854	-0.70826	0.905061	-0.78255	0.433891	0.981636	chrX	38060785	38061506	+	0	NA	intron (NAluJb SIN	8082	NM_00302E	6461	Hs.52148	ENSG00000CSHB	ba3J10.2	SH2	domaiprotein-coding	
chr6-333C	6.113695	-0.77585	0.991487	-0.78251	0.433915	0.981636	chr6	33308759	33309342	+	0	NA	intron (Nintron (N	3348	NM_001011	6399	Hs.59223	ENSG00000TRAPP2C	MIP2A	SEE trafficki	protein-coding	
chr16-67C	6.428275	0.726177	0.928427	0.782158	0.434122	0.981636	chr16	67828452	67828911	+	0	NA	TTS (NM_CTS (NM_C	20090	NM_004057	7395	Hs.639	ENSG00000S100G	CABP	CABF S100	calcprotein-coding	
chr18-23C	6.428275	0.726177	0.928427	0.782158	0.434122	0.981636	chr18	23205684	23206517	+	0	NA	intron (NMLTIC L	50275	NM_13837E	91768	Hs.11108	ENSG00000CABLES1	CABL1	CAF Cdk5	and	protein-coding
chr19-136	6.428275	0.726177	0.928427	0.782158	0.434122	0.981636	chr19	1388881	1389853	+	0	NA	intron (Nintron (N	5460	NM_00136E	374291	Hs.21194	ENSG00000NDUF57	CI-20	CI-NADH:ubiq	protein-coding	
chr15-61C	9.229213	0.604988	0.77398	0.781658	0.434416	0.981636	chr15	61964292	61964969	+	0	NA	intron (Nintron (N	95817	NM_017684	54832	Hs.51166	ENSG00000VPS13C	PARK23	vacuolar	protein-coding	
chr1-6637	10.5975	-0.56562	0.723663	-0.78161	0.434446	0.981636	chr1	66372196	66374081	+	0	NA	3' UTR (N3' UTR (N	18603	NM_001297	5142	Hs.19807	ENSG00000PDE4B	DPDE4	PDE phosphodi	protein-coding	
chr8-3901	10.5975	-0.56562	0.723663	-0.78161	0.434446	0.981636	chr8	39011835	39013962	+	0	NA	intron (NLMIP5 L	5787	NR_14598E	1.1E+08	NR_145733	ENSG00000SNORD38D		small nucsnoRNA		
chr1-1561	11.92245	0.535758	0.685529	0.781524	0.434494	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	3' UTR (N3' UTR (N	-15982	NM_00314E	6746	Hs.74564	ENSG00000SSR2	HSD25	TLA signal	protein-coding	
chr19-264	11.92245	0.535758	0.685529	0.781524	0.434494	0.981636	chr19	26437272	26438043	+	0	NA	IntergeniALR/Alph	-1355774	NR_146733	1.02E+08	Hs.56793	ENSG00000LOC101927		uncharactcRNA		
chr16-894	8.30082	-0.65412	0.837091	-0.78142	0.434557	0.981636	chr16	89498784	89499010	+	0	NA	IntergeniL2a L	-8336	NR_04583E	29123	Hs.33500	ENSG00000ANKRD11	ANCO-1	AN ankyrin	r protein-coding	
chr7-134C	10.16932	-0.58422	0.747825	-0.78123	0.434666	0.981636	chr7	1.35E+08	1.35E+08	+	0	NA	intron (N(TCTT)n S	42321	NM_03313E	800	Hs.49020	ENSG00000CALD1	CDM	H-CAL	caldesmor	protein-coding
chr12-437	6.471264	0.741369	0.949052	0.781168	0.434704	0.981636	chr12	43784418	43784796	+	0	NA	intron (Nintron (N	21710	NM_00124E	5756	Hs.18907	ENSG00000TWF1	A6 PTK9	twinfilin	protein-coding	
chr1-2147	6.641715	-0.71242	0.91204	-0.78113	0.434727	0.981636	chr1	21475286	21475607	+	0	NA	intron (NLMIP2 L	-33538	NM_00136E	249	Hs.75431	ENSG00000ALPL	AF-TNAP	alkaline	protein-coding	
chr11-58C	6.641715	-0.71242	0.91204	-0.78113	0.434727	0.981636	chr11	58623824	58624647	+	0											

chr17-38c	6.410709	0.717538	0.92313	0.777287	0.436989	0.981636	chr17	38399447	38400431	+	0	NA	3' UTR (N3' UTR (N	-28525 NM_001199	57636 Hs. 37444cNM_02087c	ENSG00000CARHGAP23	-	Rho	GTPase protein-coding
chr2-117c	6.410709	0.717538	0.92313	0.777287	0.436989	0.981636	chr2	11788919	11789475	+	0	NA	intron (Nintron (N	21753 NR_036071	1E+08	NR_036071	ENSG00000MIR548S	-	microRNA ncRNA
chr2-177c	10.12032	-0.58555	0.753412	-0.77719	0.437044	0.981636	chr2	1.77E+08	1.77E+08	+	0	NA	non-coding non-coding	8036 NR_13847c	220988 Hs. 51653cNM_194247	ENSG00000HNRNP3	2610510D1	hetero protein-coding	
chr2-332c	10.58964	-0.56442	0.726275	-0.77714	0.437075	0.981636	chr2	33262804	33267122	+	0	NA	intron (NMLT2B1 LI	130366 NM_001166	4052 Hs. 61931cNM_000627	ENSG00000LTBP1	-	latent t protein-coding	
chr3-197c	10.58964	-0.56442	0.726275	-0.77714	0.437075	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (NMLT1A1 LI	12601 NR_03996c	1.01E+08	NR_03996c	ENSG00000MIR4797	-	microRNA ncRNA
chr1-1247	11.93816	0.533042	0.685965	0.777069	0.437118	0.981636	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alpha	3248669 NR_00395c	647121 Hs. 69768cNR_00395c	ENSG00000CEMBP1	-	embigin p pseudo	
chr15-40c	10.63078	-0.56195	0.723546	-0.77666	0.437357	0.981636	chr15	40009936	40001841	+	0	NA	intron (NCharlie4c	37793 NM_003134	6127 Hs. 53373cNM_003134	ENSG00000SRP14	ALURBP	signal r protein-coding	
chr20-19c	10.63078	-0.56195	0.723546	-0.77666	0.437357	0.981636	chr20	19965756	19965955	+	0	NA	intron (NAluX1 SI	-51435 NM_18152c	5726 Hs. 36878cNM_01610c	ENSG00000NAA20	NAT3 NAT3N(alpha)	protein-coding	
chr2-100c	10.08704	-0.58947	0.759191	-0.77644	0.437488	0.981636	chr2	1E+08	1E+08	+	0	NA	intron (NLM14 LINE	17664 NM_00102c	3899 Hs. 44441cNM_00228c	ENSG00000CAFF3	LAF4 MLL1AF4/FMR2	protein-coding	
chr16-47c	8.210613	0.658192	0.847948	0.776217	0.437621	0.981636	chr16	47505408	47505250	+	0	NA	intron (NLSU-rRNA	43953 NM_001031	5257 Hs. 78060cNM_00029c	ENSG00000PKHB	-	phosphory protein-coding	
chr1-986c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr1	98690008	9870385	+	0	NA	intron (Nintron (N	40573 NM_02024c	56998 Hs. 46375cNM_02024c	ENSG00000CTNNBP1	ICAT	catenin t protein-coding	
chr16-397c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr16	3978509	3979481	+	0	NA	intron (NAluSc SIN	-28551 NR_120311	1.03E+08	Hs. 36473cNR_120311	ENSG00000LOC102724	-	uncharacter ncRNA
chr19-50c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr19	5052049	5052840	+	0	NA	intron (Nintron (N	83331 NM_00137c	23030 Hs. 65481cNM_01501c	ENSG00000KDM4B	JMJD2B T	lysine d protein-coding	
chr2-478c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr2	47829654	47830442	+	0	NA	intron (Nintron (N	46093 NM_001281	2956 Hs. 44505cNM_00017c	ENSG00000MSH6	GTBP GTME	mtS homc protein-coding	
chr2-933c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr2	93340659	93342363	+	0	NA	IntergeniALR/Alpha	866908 NR_14610c	728034	NR_14610c	BMS1P14	-	BMS1 p set pseudo
chr21-33c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr21	33253679	33254969	+	0	NA	intron (NMER4D1 LI	11936 NR_038974	1E+08	Hs. 70979cNR_038974	IL10RB-D1	IFNAR2-AS	IL10RB dincRNA
chr4-526c	4.734223	0.824827	1.062985	0.775954	0.437776	0.981636	chr4	526506	528764	+	0	NA	intron (Nintron (N	28425 NM_001127	54872 Hs. 7099	NM_01773c	ENSG00000PIGG	GP17 LAS2	phosphatid protein-coding
chr1-1541	6.1724	-0.75969	0.97923	-0.7758	0.437865	0.981636	chr1	1541106	1541383	+	0	NA	promoter-promoter-	-620 NM_001114	339453 Hs. 66865cNM_001114	ENSG00000TMM240	CLorf70 S	transmem protein-coding	
chr12-92c	8.681778	0.623205	0.803466	0.775646	0.437958	0.981636	chr12	92895779	92896244	+	0	NA	intron (NAluSc SIN	33284 NM_00356c	8411 Hs. 56736cNM_00356c	ENSG00000EEA1	MST105 MS	early enc protein-coding	
chr22-19c	8.681778	0.623205	0.803466	0.775646	0.437958	0.981636	chr22	19913416	19915564	+	0	NA	intron (NLM8B LIN	18063 NM_00135c	10587 Hs. 44343cNM_00644c	ENSG00000TXNRD2	GCCD5 SEI	thioredo protein-coding	
chr15-39c	6.608433	-0.71857	0.926675	-0.77543	0.438087	0.981636	chr15	39959784	39959987	+	0	NA	intron (NAluU SINE	25770 NM_00101c	440275 Hs. 65667cNM_00101c	ENSG00000EIF2AK4	GCN2 PVOL	eukaryot protein-coding	
chr3-491c	6.608433	-0.71857	0.926675	-0.77543	0.438087	0.981636	chr3	49108274	49108552	+	0	NA	TTS (NM_C	-3656 NM_00127c	5859 Hs. 79322	NM_00505c	ENSG00000QARS	GLNRS MSC	glutamin protein-coding
chr3-62c	6.608433	-0.71857	0.926675	-0.77543	0.438087	0.981636	chr3	69087251	69087450	+	0	NA	intron (Nintron (N	2413 NM_006407	10550 Hs. 51806cNM_006407	ENSG00000CARL6IP5	DERP11 G	ADP ribos protein-coding	
chr10-49c	9.237071	0.603241	0.778067	0.775307	0.438158	0.981636	chr10	42520355	42521911	+	0	NA	intron (Nintron (N	31737 NR_026777	1E+08	Hs. 27806cNR_026777	ENSG00000ZNF37BP	KOXY21 ZNF	zinc fng pseudo
chr2-426c	9.237071	0.603241	0.778067	0.775307	0.438158	0.981636	chr2	42643723	42646854	+	0	NA	intron (NAluSz SIN	76656 NM_00133c	57504 Hs. 43541cNM_02074c	ENSG00000MTA3	-	metastasis protein-coding	
chr3-183c	9.237071	0.603241	0.778067	0.775307	0.438158	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	58563 NR_03965c	1.01E+08	NR_03965c	ENSG00000MIR4448	-	microRNA ncRNA
chr6-154c	6.58301	-0.72687	0.937657	-0.77519	0.438225	0.981636	chr6	1.51E+08	1.51E+08	+	0	NA	3' UTR (N3' UTR (N	-13446 NM_020861	57621 Hs. 52007cNM_020861	ENSG00000ZBTB2	ZNF437	-	zinc fng protein-coding
chr1-144c	8.869979	-0.61074	0.788039	-0.77501	0.438331	0.981636	chr1	1.44E+08	1.44E+08	+	0	NA	intron (NLM1Ec LIN	6984 NR_027354	645166 Hs. 74418cNR_027354	LSP1P5	-	LSP1 p set pseudo	
chr17-30c	8.869979	-0.61074	0.788039	-0.77501	0.438331	0.981636	chr17	30764901	30765249	+	0	NA	intron (NAluSp SIN	55467 NR_14439c	440423 Hs. 62888cNR_024187	SUZ12P1	SUZ12	p set pseudo	
chr2-188c	8.869979	-0.61074	0.788039	-0.77501	0.438331	0.981636	chr2	1.88E+08	1.88E+08	+	0	NA	intron (NTHE1B-int	87914 NR_030287	693146	NR_030287	ENSG00000MIR561	MIRN561 t	microRNA ncRNA
chr11-65c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr11	65434443	65436017	+	0	NA	non-coding non-coding	-9228 NR_03034c	693197	NR_03034c	ENSG00000MIR612	MIRN612 t	microRNA ncRNA
chr16-33c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr16	3398409	3399205	+	0	NA	intron (Nintron (N	2197 NM_001284	54925 Hs. 59207cNM_01781c	ENSG00000ZSCAN32	HCCS-5 Zn	zinc fng protein-coding	
chr2-134c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr2	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	169055 NM_00241c	4249 Hs. 4988	NM_00241c	ENSG00000MGAT5	GCN2 PVOL	eukaryot protein-coding
chr22-27c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr22	27908474	27911226	+	0	NA	intron (NAluJo SIN	9364 NM_001284	23760 Hs. 70532cNM_01239c	ENSG00000PITPNB	PI-TP-beta	phosphatid protein-coding	
chr7-840c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr7	84004777	84006094	+	0	NA	exon (NM exon (NM	189354 NM_00608c	10371 Hs. 25245cNM_00608c	ENSG00000SEMA3A	COLL1 HHH	semaphor protein-coding	
chr9-271c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr9	27168571	27170978	+	0	NA	intron (Nintron (N	60633 NM_00045c	7010 Hs. 89640	NM_00045c	ENSG00000CTEK	CD202B GLTEK	recep protein-coding
chr9-134c	8.862121	-0.60932	0.786663	-0.77457	0.438596	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	87182 NR_039691	1.01E+08	NR_039691	ENSG00000MIR3689C	-	microRNA ncRNA
chr1-186c	8.648496	0.620507	0.801417	0.774623	0.438775	0.981636	chr1	1.86E+08	1.86E+08	+	0	NA	intron (Nintron (N	31445 NM_001127	10216 Hs. 64772cNM_005807	ENSG00000PRG4	CACP HAPC	proteogly protein-coding	
chr21-44c	9.170508	0.598027	0.772678	0.773967	0.43895	0.981636	chr21	44854138	44859297	+	0	NA	intron (Nintron (N	18658 NM_00433c	754 Hs. 44101cNM_00433c	ENSG00000PTTG1P1	C1orf11 CTTG1	intron protein-coding	
chr3-459c	9.170508	0.598027	0.772678	0.773967	0.43895	0.981636	chr3	45979303	45980593	+	0	NA	intron (Nintron (N	15876 NM_02451c	79443 Hs. 20022cNM_02451c	ENSG00000FYCO1	CATC2 CTFF	YVE and protein-coding	
chr8-1441	9.170508	0.598027	0.772678	0.773967	0.43895	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	promoter-promoter-	-902 NM_00131c	340390 Hs. 98723	NM_03252c	ENSG00000WDR97	KIAA1875	WD repeat protein-coding
chr11-52c	24.69977	0.388646	0.502233	0.773835	0.439028	0.981636	chr11	52320907	52321152	+	0	NA	IntergeniALR/Alpha	1911882 NR_024504	646813 Hs. 68417cNR_024504	LOC646811	-	DEXH-box pseudo	
chr12-277	8.82884	-0.61383	0.793708	-0.77337	0.439305	0.981636	chr12	27791730	27793381	+	0	NA	intron (NAluSx SIN	12322 NM_02078c	57542 Hs. 50510cNM_02078c	ENSG00000KLHL42	Ctb9 KLHE	kelch lik protein-coding	
chr11-524	4.718507	0.831948	1.075884	0.773269	0.439363	0.981636	chr11	52414247	52415191	+	0	NA	IntergeniALR/Alpha	2005572 NR_024504	646813 Hs. 68417cNR_024504	LOC646811	-	DEXH-box pseudo	
chr10-10c	6.991426	0.689096	0.891251	0.773179	0.439416	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (Nintron (N	-12640 NR_002954	677800 Hs. 66216cNR_002954	ENSG00000SNORA12	U108	small nucsnoRNA	
chr5-157c	6.991426	0.689096	0.891251	0.773179	0.439416	0.981636	chr5	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	-21666 NR_13620c	1.03E+08	Hs. 57088cNR_13620c	LOC102724	-	uncharacter ncRNA
chr9-686c	7.007142	0.684285	0.885215	0.773015	0.439513	0.981636	chr9	6863467	6864087	+	0	NA	intron (NAluU SINE	106427 NR_130707	23081 Hs. 70942cNM_015061	ENSG00000KDM4C	GASC1 JHE	lysine d protein-coding	
chr15-407	7.882353	-0.67315	0.870827	-0.773	0.439522	0.981636	chr15	40744605	40744861	+	0	NA	intron (Nintron (N	10521 NM_01814c	55177 Hs. 51106cNM_01814c	ENSG00000RMDN3	FAM82A2 F	regulator protein-coding	
chr1-168c	6.97386	0.680961	0.881216	0.772752	0.439669	0.981636	chr1	61350681	61350945	+	0	NA	promoter-promoter-	68 NR_026844	84832 Hs. 53706cNR_026844	ENSG00000ANKRD36B	ANKRD26 lankyrin	pseudo	
chr11-61c	6.97386	0.680961	0.881216	0.772752	0.439669	0.981636	chr11	97690602	97692634	+	0	NA	intron (NAluSj SIN	6501 NM_001161	220002 Hs. 22546	NM_15361c	ENSG00000CYB561A3	CYBASC3 c	cytochron protein-coding
chr11-95c	6.97386	0.680961	0.881216	0.772752	0.439669	0.981636	chr11	97690602	97692634	+	0	NA	intron (NAluSj SIN	5791 NR_149094	7507 Hs. 65436cNM_00038c	ENSG00000XPA	XPI XPAC	XPA, DNA protein-coding	
chr11-97c	11.91274	0.529593	0.68614	0.771844	0.440207	0.981636	chr19	95835166	95835397	+	0								



chr4-504	8.887545	-0.60352	0.785035	-0.76878	0.442022	0.981636	chr14	50433034	50441371	+	0	NA	intron (Nintron (N	-39904	NR_001367	8814	Hs.280881	NR_00419	ENSG00000	CDKL1	KKIALRE F	cyclin d	protein-coding	
chr2-5496	8.887545	-0.60352	0.785035	-0.76878	0.442022	0.981636	chr2	54969731	54974557	+	0	NA	TTS (NM_TTS (NM_1	38128	NR_007008	57142	Hs.63785	NR_00700	ENSG00000	RTN4	ASY NI22C	reticular protein-coding	AS	
chr4-1126	8.887545	-0.60352	0.785035	-0.76878	0.442022	0.981636	chr4	1.13E+08	1.13E+08	+	0	NA	intron (NAluSp SIN	-3577	NR_146092	1.1E+08	Hs.64297	NR_14609	ENSG00000	MIR302CHC	-	mir-302/2	ncRNA	
chr20-504	4.916047	-0.83027	1.080571	-0.76836	0.442271	0.981636	chr20	5945674	5945873	+	0	NA	intron (Nintron (N	4760	NR_015939	51605	Hs.12879	NR_01593	ENSG00000	TRMT6	CGI-09 GC	RNA methyl protein-coding	CGI-09	
chr11-305	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr11	3097590	3097919	+	0	NA	intron (NLMed LIN	-40331	NR_001194	833	Hs.27487	NR_00175	ENSG00000	CARS	CARS1 CYS	cysteine ly protein-coding	CARS1	
chr12-248	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr12	24815914	24817763	+	0	NA	3' UTR (N3' UTR (N	85384	NR_001178	586	Hs.43899	NR_00550	ENSG00000	BCAT1	BCATC BC1	branched protein-coding	BCATC	
chr15-447	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr15	44539286	44541282	+	0	NA	intron (NAluSz SIN	3137	NR_003758	8669	Hs.40405	NR_00375	ENSG00000	E1F3J	E1F3S1 E	eukaryot protein-coding	E1F3S1	
chr2-207	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr2	2.07E+08	2.07E+08	+	0	NA	intron (Nintron (N	23528	NR_036227	1E+08	NR_03622	ENSG00000	MIR2355	-	mir-2355	microRNA	ncRNA	
chr5-1591	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr5	1.59E+08	1.59E+08	+	0	NA	intron (Nintron (N	19728	NR_001199	153830	Hs.34930	NR_14472	ENSG00000	CRNF145	-	ring finger protein-coding	CRNF145	
chr6-158	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	62597	NR_001178	8871	Hs.43449	NR_00389	ENSG00000	SYNJ2	INPP5F	synapto protein-coding	INPP5F	
chr8-479	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr8	47902559	47904735	+	0	NA	intron (Nintron (N	56489	NR_001081	5591	Hs.49168	NR_00690	ENSG00000	PRKDC	DNA-PKC I	protein-coding	DNA-PKC	
chr8-1198	7.118887	-0.67288	0.876008	-0.76806	0.442453	0.981636	chr8	1.2E+08	1.2E+08	+	0	NA	intron (NTHE1B-int	7538	NR_003184	6873	Hs.12275	NR_00318	ENSG00000	TAF2	CIF150 M	TATA-box protein-coding	CIF150	
chr3-123	10.11247	-0.58411	0.761561	-0.767	0.443084	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	-14554	NR_153032	4638	Hs.47737	NR_00596	ENSG00000	MYLK	AAR7 KR	myosin I protein-coding	AAR7	
chr6-734	8.343809	-0.63963	0.833988	-0.76695	0.443112	0.981636	chr6	73425058	73425267	+	0	NA	3' UTR (N3' UTR (N	27135	NR_138441	115004	Hs.65840	NR_13844	ENSG00000	CGAS	CAAT7 F150	cyclic G protein-coding	CAAT7	
chr1-120	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr1	12009475	12012038	+	0	NA	intron (NMIRb SINE	-8742	NR_021933	60672	Hs.8595	NR_02193	ENSG00000	MIIP	IIP45	migrator protein-coding	IIP45	
chr1-286	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr1	28603759	28608093	+	0	NA	intron (NAluSq2 SI	13431	NR_001199	115273	Hs.65232	NR_15230	ENSG00000	RAB42	-	RAB42	protein-coding	RAB42
chr1-313	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr1	31316662	31317245	+	0	NA	intron (Nintron (N	19971	NR_016505	51538	Hs.52409	NR_01650	ENSG00000	ZCCHC17	HSPC251 F	zinc finger protein-coding	HSPC251	
chr1-110	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	exon (NM exon (NM	12084	NR_001201	9122	Hs.35130	NR_00469	ENSG00000	SLC16A4	MCT4 MCT	solute carrier protein-coding	MCT4	
chr1-217	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr1	2.18E+08	2.18E+08	+	0	NA	intron (NAluSq2 SI	117951	NR_001297	55105	Hs.36234	NR_01804	ENSG00000	GPATCH2	CT110 G	PAG-patch protein-coding	GPATCH2	
chr1-229	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr1	2.29E+08	2.29E+08	+	0	NA	intron (NAluSx SIN	24800	NR_018232	55746	Hs.12457	NR_01823	ENSG00000	CNUP133	GAMOS8 N	neucleoporin-coding	GAMOS8	
chr14-754	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr14	75036503	75036733	+	0	NA	intron (NAluSx1 SI	14849	NR_014381	27030	Hs.43665	NR_01438	ENSG00000	MLH3	HNPCC7	mutL	hom protein-coding	HNPCC7
chr16-234	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr16	23443899	23444911	+	0	NA	intron (Nintron (N	8784	NR_153603	91949	Hs.18580	NR_15360	ENSG00000	COG7	CDG2E	component protein-coding	COG7	
chr2-690	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr2	69058191	69061093	+	0	NA	intron (NTiger1 I	-4490	NR_036073	1E+08	NR_03607	ENSG00000	MIR3126	-	mir-3126	microRNA	ncRNA	
chr7-231	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr7	23125379	23125939	+	0	NA	intron (Nintron (N	18998	NR_01884	55975	Hs.65481	NR_01884	ENSG00000	KLHL7	CISS3 KLF	kelch like protein-coding	CISS3	
chr8-97	6.948437	0.675349	0.880851	0.766701	0.443259	0.981636	chr8	9776824	9777885	+	0	NA	3' UTR (N3' UTR (N	35682	NR_030327	693182	NR_03032	ENSG00000	MIR597	-	mir-597	microRNA	ncRNA	
chr1-841	8.846405	-0.60652	0.791133	-0.76665	0.443289	0.981636	chr1	8418091	8418789	+	0	NA	intron (Nintron (N	5392	NR_001042	473	Hs.46304	NR_01210	ENSG00000	RCERE	ARG ARP	arginine protein-coding	ARG	
chr3-470	11.06681	-0.54264	0.712517	-0.76664	0.443295	0.981636	chr3	47056733	47057403	+	0	NA	exon (NM exon (NM	45526	NR_02404	1E+08	NR_02152	NR_02404	ENSG00000	NRADDP	-	neurotroph pseudo	NRADDP	
chr5-326	7.101322	-0.6823	0.890549	-0.76616	0.443584	0.981636	chr5	32600833	32601307	+	0	NA	exon (NM exon (NM	15513	NR_006711	10923	Hs.22964	NR_00671	ENSG00000	SUB1	P15 PC41	rSUB1 reg protein-coding	P15	
chr19-10	7.134603	-0.67646	0.882933	-0.76615	0.443584	0.981636	chr19	10321013	10321337	+	0	NA	intron (Nintron (N	-5126	NR_001031	112812	Hs.65486	NR_08066	ENSG00000	FDX2	FDX1L ME	ferredoxin protein-coding	FDX1L	
chr1-8507	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr1	85076114	85076888	+	0	NA	intron (NTHE1B LTF	126820	NR_059933	126820	Hs.97933	NR_14517	ENSG00000	WDR63	DIC3 NYD	WD repeat protein-coding	DIC3	
chr14-10	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	-15190	NR_001199	647310	Hs.72949	NR_00119	ENSG00000	TEX22	-	testis ex protein-coding	TEX22	
chr15-73	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr15	73250134	73251170	+	0	NA	intron (NLMC4 LIN	-49258	NR_162148	1.13E+08	NR_16214	NR_16214	ENSG00000	MIR12135	-	mir-12135	microRNA	ncRNA
chr17-19	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr17	19799756	19801895	+	0	NA	intron (Nintron (N	-52527	NR_000691	218	Hs.53168	NR_00069	ENSG00000	ALDH3A1	ALDH3	AL	aldehyde protein-coding	ALDH3
chr18-231	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr18	23181821	23183312	+	0	NA	intron (NMER5B DNA	26741	NR_138375	91768	Hs.11108	NR_13837	ENSG00000	CABLES1	CABL1 CAE	Cdk5 and protein-coding	CABL1	
chr18-62	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr18	62300775	62301182	+	0	NA	intron (NLC2 LINE	-24309	NR_001272	8792	Hs.20404	NR_00383	ENSG00000	TNFRSF11	CD265 FEC	TNF receptor protein-coding	TNFRSF11	
chr19-19	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr19	19883318	19884573	+	0	NA	intron (NAluSp SIN	-17001	NR_031218	81931	Hs.30105	NR_03121	ENSG00000	ZNF93	HPF34 HTF	zinc finger protein-coding	HPF34	
chr2-238	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	IntergeniLIMDa LIN	42269	NR_00104	51665	Hs.51678	NR_01611	ENSG00000	CASB1	ASB-1	ankyrin I protein-coding	ASB-1	
chr2-52	4.7088	0.816842	1.066192	0.76613	0.443599	0.981636	chr2	50253620	50254191	+	0	NA	intron (Nintron (N	-2640	NR_032019	83933	Hs.26593	NR_03201	ENSG00000	HDAC10	HD10	histone c protein-coding	HD10	
chr14-507	7.849071	-0.67838	0.885587	-0.76602	0.443661	0.981636	chr14	52769295	52769511	+	0	NA	intron (Nintron (N	22204	NR_19806	64841	Hs.47802	NR_19806	ENSG00000	GPNPAT1	GNA1 GNP	glucosamin protein-coding	GNA1	
chr10-67	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr10	67989771	67996986	+	0	NA	intron (NFAM SINE	17505	NR_131184	1E+08	NR_13118	NR_13118	ENSG00000	POU5F1P5	Oct4-pg5	POU class pseudo	POU5F1P5	
chr10-10	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr10	87164091	87164523	+	0	NA	intron (NAluJb SIN	-61141	NR_001099	728118	Hs.71056	NR_00109	ENSG00000	NTM2A	FAM22A	NUT	famil protein-coding	FAM22A
chr11-85	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr11	65894117	65897246	+	0	NA	intron (Nintron (N	4707	NR_00130	8061	Hs.28356	NR_00543	ENSG00000	FOSL1	FRA FRA1	FOS like protein-coding	FOSL1	
chr12-69	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr12	6939265	6940999	+	0	NA	intron (NAluSc SIN	-3306	NR_001301	113246	Hs.40591	NR_13842	ENSG00000	C12orf57	C10 GRCC1	chromosome protein-coding	C12orf57	
chr15-57	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr15	57231394	57235778	+	0	NA	intron (NAluS6 SI	14156	NR_001306	6938	Hs.51150	NR_00320	ENSG00000	TCF12	CRS3 HEB	transcrip protein-coding	CRS3	
chr15-71	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr15	71858238	71858576	+	0	NA	intron (NLIPIA5 LIN	47853	NR_01424	10002	Hs.18735	NR_01424	ENSG00000	NR2E3	ESCS PNR	nuclear I protein-coding	NR2E3	
chr2-171	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr2	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	3575	NR_00132	1781	Hs.54675	NR_00137	ENSG00000	DYNC1I2	DIC74 DNC	dynein cy protein-coding	DYNC1I2	
chr2-174	8.879687	-0.60211	0.786052	-0.766	0.443679	0.981636	chr2	1.75E+08	1.75E+08	+	0	NA	TTS (NM_TTS (NM_C	-34896	NR_001039	1134	Hs.43447	NR_00007	ENSG00000	CHRNA1	ACHRA AC	cholinergic protein-coding	CHRNA1	
chr3-425																								



chr7-1665 6.434359	-0.7611	0.99618	-0.76402	0.444854	0.981636	chr7	16634603	16635347	+	0	NA	intron (NLIMEc LIN	10779	NM_02031E	57037	Hs.15737ENM_02031E	ENSG00000ANKMY2	ZMYND20	ankyrin1 protein-coding	
chr1-8496 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	8496666	8497158	+	0	NA	intron (NLIPA8 LIN	-1999	NR_132752	1.07E+08	NR_132752	SNORD128	ZLY43	small nucsnoRNA	
chr1-1457 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	intron (NSVA_C Ret	44659	NR_10384E	1.1126	Hs.488237NM_00705E	ENSG00000CD160	BY55 NK1 CD160	molprotein-coding	
chr1-1504 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	1.5E+08	1.51E+08	+	0	NA	intron (NALuSx SIN	7227	NR_10693E	1.02E+08	NR_10693E	ENSG00000MIR6878	hsa-mir-εmicroRNA	ncRNA	
chr1-1786 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (NALuJb SIN	56450	NM_00467E	9068	Hs.591474NM_00467E	ENSG00000ANGPTL1	ANG3 mir-angiopoietin	protein-coding	
chr1-213C 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	intron (NALuJb SIN	29449	NM_012424	26750	Hs.59141ENM_012424	ENSG00000CRPS6KC1	RPK118 RS	ribosomal protein-coding	
chr1-222C 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (Nintron (N	19831	NM_022831	64853	Hs.15662ENM_022831	ENSG00000AIDA	Clorf80	axin intcprotein-coding	
chr1-225E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (Nintron (N	25823	NM_01469E	9725	Hs.119387NM_01469E	ENSG00000TMEM63A	KIAA0792	transment protein-coding	
chr1-229E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr1	2.3E+08	2.3E+08	+	0	NA	intron (Nintron (N	20049	NM_01208E	23456	Hs.17614	NM_01208E	ENSG00000ABC10	EST20237 ATP	bindiprotein-coding
chr10-124 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	exon (NM exon (NM	-21985	NR_12063C	1.02E+08	Hs.43744ENR_120630	FAM53B-AS-	FAM53B	arncRNA	
chr10-125 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (N (TTTTTC)r	14998	NM_01818C	55760	Hs.370292NM_01818C	ENSG00000DHX32	DDX32 DHL	DEAH-box protein-coding	
chr11-64E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr11	6454170	6455653	+	0	NA	intron (Nintron (N	-13924	NM_00061E	3263	Hs.42648ENM_00061E	ENSG00000CHPX	HX	hemopexin protein-coding	
chr13-19C 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr13	19649611	19651423	+	0	NA	intron (Nintron (N	16858	NM_01752E	54737	Hs.269654NM_01752E	ENSG00000MPHOSPH8	HSPMP8 TWM	phase protein-coding	
chr14-96E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr14	96215242	96216140	+	0	NA	intron (Nintron (N	10893	NM_00062E	624	Hs.654542NM_00062E	ENSG00000BKDKR2	B2R BK-2 bradykinin	protein-coding	
chr14-101 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	3689	NM_00135E	5527	Hs.368264NM_00271E	ENSG00000PPP2R5C	B56G B56E	protein protein-coding	
chr15-28E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr15	28667377	28670244	+	0	NA	intron (Nintron (N	14368	NR_03644E	440248	Hs.53150ENM_19904E	ENSG00000HERC2P9	-	hect dom pseudo	
chr16-29E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr16	2932489	2935452	+	0	NA	exon (NM exon (NM	21991	NM_00130E	84256	Hs.655321NM_02091E	ENSG00000FLYWCH1	-	FLYWCH-typ protein-coding	
chr17-18C 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr17	18045199	18048198	+	0	NA	intron (NALuS2 SI	7290	NM_02405E	79018	Hs.187422NM_02405E	ENSG00000GTD4	C1orf80	GID complprotein-coding	
chr17-18E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr17	18928841	18931759	+	0	NA	intron (NALuY SIN	-20376	NM_00128E	125206	Hs.46241ENM_152351	ENSG00000SLCSA10	SGLT-5 SC	solute cprotein-coding	
chr17-427 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr17	42724608	42725320	+	0	NA	intron (NALuSc SIN	-16913	NR_10683E	1.02E+08	NR_10683E	ENSG00000MIR6780A	hsa-mir-εmicroRNA	ncRNA	
chr17-427 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr17	42726547	42730824	+	0	NA	intron (NALuY SIN	16305	NM_001321	2145	Hs.19466ENM_001991	ENSG00000EZHI	KMT6B	enhancer protein-coding	
chr19-11E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr19	11936221	11936638	+	0	NA	intron (NLIPA6 LIN	11322	NM_14456E	90592	Hs.52848ENM_14456E	ENSG00000ZNF700	-	zinc fingprotein-coding	
chr19-36E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr19	36560836	36562407	+	0	NA	intron (NMLTIA1-ir	-11449	NR_11070E	1.02E+08	Hs.51537ENR_11070E	ENSG00000ZNF529-AS-	-	ZNF529	arncRNA
chr19-46E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr19	46705950	46710986	+	0	NA	TTS (NR_C TTS (NR_C	886	NR_03615E	1E+08	NR_03615E	ENSG00000MIR320E	mir-320e	microRNA	ncRNA
chr19-47E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr19	47673710	47675259	+	0	NA	intron (NMLTIF1 LI	-38938	NM_014601	30846	Hs.74496ENM_014601	ENSG00000EHD2	PAST2	EH domain protein-coding	
chr20-35E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr20	35927422	35933064	+	0	NA	intron (NL2a LINE	24383	NM_03363C	51282	Hs.58490ENM_01655E	ENSG00000SCAND1	RAV1 SDP1	SCAN dom protein-coding	
chr22-37E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr22	37399227	373943209	+	0	NA	3' UTR (N3' UTR (N	12383	NM_032561	84645	Hs.51761ENM_032561	ENSG00000C22orf23	EVG1 dJ1C	chromoson protein-coding	
chr22-39E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr22	39418694	39424988	+	0	NA	exon (NM exon (NM	-10319	NR_04053E	1.01E+08	Hs.72908ENR_040535	LOC10050E-	-	uncharactncRNA	
chr3-316E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr3	36833475	36833923	+	0	NA	exon (NM exon (NM	-11199	NR_147141	1.05E+08	Hs.33386ENR_147141	ENSG00000LINC0203E-	-	long intcncRNA	
chr3-114E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr3	1.14E+08	1.14E+08	+	0	NA	exon (NM exon (NM	-1010	NR_03899E	1E+08	Hs.122417NR_03899E	ENSG00000ZBTB20-AS-	-	ZBTB20	arncRNA
chr3-128E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	31279	NM_01404E	28976	Hs.56748ENM_01404E	ENSG00000ACAD9	MC1DN20 Nacyl-CoA	protein-coding	
chr3-129E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr3	1.73E+08	1.73E+08	+	0	NA	intron (NLIME1 LIN	42116	NM_00134E	1894	Hs.51829ENM_01809E	ENSG00000ECT2	ARHGEP31	epitheli protein-coding	
chr5-127E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-82709	NM_012574	1.04E+08	Hs.62863ENR_12574E	ENSG00000ADAMTS19-	-	ADAMTS19	ncRNA
chr5-134E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (NMIRc SINE	16996	NM_032151	84105	Hs.710014NM_032151	ENSG00000PCBD2	DCOH2 DCC	pterin-4 protein-coding	
chr7-166E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr7	16623507	16624989	+	0	NA	intron (Nintron (N	21506	NM_002031	57037	Hs.15737ENM_02031E	ENSG00000ANKMY2	ZMYND20	ankyrin1 protein-coding	
chr7-101E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr7	1.01E+08	1.01E+08	+	0	NA	TTS (NM_C TTS (NM_C	6544	NM_00634E	10467	Hs.21107ENM_00634E	ENSG00000ZNH1T	CG11 ZNF	zinc fingprotein-coding	
chr7-138E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (NTigger3a	91978	NM_01590E	8805	Hs.490287NM_00385E	ENSG00000TRIM24	PTC6 RNFE	tripartit protein-coding	
chr7-149E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	17213	NR_16390E	-	-	-	-	-	-
chr7-149E 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	11362	NM_015694	27153	Hs.38512	NM_015694	ENSG00000ZNF777	-	zinc fingprotein-coding
chr9-130C 6.956295	0.673017	0.880938	0.763977	0.444881	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (NALuSz SIN	27386	NM_02096C	57720	Hs.512461NM_02096C	ENSG00000GPR107	GCDRP LUSG	protein protein-coding	
chr1-2261 9.137226	0.595398	0.779479	0.763841	0.444962	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (NALuJb SIN	13820	NM_00227E	64746	Hs.520207NM_0227E	ENSG00000ACBD3	GCP60 GOC	acyl-CoA protein-coding	
chr10-155E 4.26501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr10	45945522	45946672	+	0	NA	exon (NM exon (NM	23441	NM_00130C	120071	Hs.862543NM_15231E	ENSG00000LARGE2	GLYTL1B FLARGE	acyl protein-coding	
chr10-22E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr10	22572341	22573188	+	0	NA	intron (NL2a LINE	-134835	NR_03653E	1E+08	Hs.7444	NR_03653E	LOC10049E-	-	uncharactncRNA
chr10-63E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr10	63598262	63599631	+	0	NA	intron (NALuJr4 SI	-77056	NM_00131E	221037	Hs.41341ENM_004241	ENSG00000JMJD1C	KDM3C TRI	jumonji cprotein-coding	
chr10-86E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr10	86463342	86463852	+	0	NA	intron (NTigger3 I	58187	NM_00131E	23063	Hs.20309ENM_01504E	ENSG00000WAPL	F0E KIAAC	WAPL cohe protein-coding	
chr13-39E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr13	39027389	39028584	+	0	NA	intron (Nintron (N	10089	NM_17071E	80209	Hs.31852ENM_02513E	ENSG00000PROSER1	C1orf323	proline ε protein-coding	
chr15-74E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr15	74868475	74869044	+	0	NA	intron (NALuS6 SI	4608	NM_00132C	10066	Hs.458917NM_00569E	ENSG00000SCAMP2	-	secretory protein-coding	
chr17-75E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr17	75897656	75898454	+	0	NA	TTS (NM_C TTS (NM_C	-1104	NM_00125E	20192	Hs.18982ENM_17354E	ENSG00000TRIM65	4732463G1	tripartit protein-coding	
chr19-21E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr19	21166373	21169219	+	0	NA	intron (Nintron (N	25757	NM_13347E	170959	Hs.15625ENM_13347E	ENSG00000ZNF431	-	zinc fingprotein-coding	
chr19-21E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr19	21736516	21737474	+	0	NA	intron (NLIPA10 LI	-13749	NR_02452E	641367	Hs.68012ENR_02452E	ENSG00000LOC64136E-	-	cyclin Y pseudo	
chr19-44E 5.426501	-0.75891	0.993771	-0.76367	0.445067	0.981636	chr19	44272525	442												

chr11-345 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr11	34974197	34974894	+ 0 NA	intron (NLM1B3 LIN	32708 NR_039836	1.01E+08	NR_039836	ENSG000003MIR1343	-	microRNA ncRNA
chr11-937 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr11	93723671	93725468	+ 0 NA	intron (NALuS6 SI	3055 NR_002566	619383	Hs.660666	NR_002566	ENSG000003SCARNA9	Z32 mgU2- small CajncRNA
chr11-122 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr11	1.22E+08	1.22E+08	+ 0 NA	intron (NCRI-3_Crc	-12351 NM_001001	414899	Hs.686105	NR_001001	ENSG000003BLID	BRCC2 BH3-like protein-coding
chr11-124 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr11	1.26E+08	1.26E+08	+ 0 NA	intron (Nintron (N	13941 NM_003139	6734	Hs.368376	NR_003139	ENSG000003SRPA	DP SRPR SRRP receptor protein-coding
chr11-134 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr11	1.34E+08	1.34E+08	+ 0 NA	exon (NM_exon (NM	31718 NM_015261	23310	Hs.438555	NR_015261	ENSG000003NCAPD3	CAP-D3 Cano-SMC protein-coding
chr12-637 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr12	63782132	63783014	+ 0 NA	intron (NMLTID-int	2447 NM_001278	10329	Hs.216388	NR_014254	ENSG000003CRXYLT1	HP10481 ribitol protein-coding
chr12-64 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr12	64044904	64045739	+ 0 NA	intron (Nintron (N	176975 NM_001300	144577	Hs.444671	NR_152440	ENSG000003C12orf66	- chromosom protein-coding
chr12-111 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr12	1.1E+08	1.1E+08	+ 0 NA	exon (NM_exon (NM	16272 NM_013300	29902	Hs.436618	NR_013300	ENSG000003FAM216A	C12orf24 family wiprotein-coding
chr15-435 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr15	43050068	43050702	+ 0 NA	intron (NLIPA13 LI	55653 NM_174916	197131	Hs.591121	NR_174916	ENSG000003CUBR1	JBS ubiquitin protein-coding
chr15-587 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr15	58778791	58779479	+ 0 NA	intron (NFLAM_C SI	7833 NR_001040	54629	Hs.591122	NR_019092	ENSG000003MINDY2	FAM63B MINDY lysprotein-coding
chr16-292 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr16	29214471	29215885	+ 0 NA	Intergeni AluY SINE	-87109 NR_002935	440352	Hs.658145	NR_002939	SNX29P2	RUND2C2 sorting rpsudo
chr16-564 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr16	56445080	56445596	+ 0 NA	intron (NLIMA2 LIN	5994 NM_007006	11051	Hs.528834	NR_007006	ENSG000003NUDT21	CFIM25 CFnudix hycprotein-coding
chr17-632 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr17	63286992	63287681	+ 0 NA	intron (NLIMEc LIN	152931 NM_001330	1534	Hs.355264	NR_001915	ENSG000003CYB561	CYB561A1 cytochrom protein-coding
chr2-8758 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr2	87580035	87590979	+ 0 NA	Intergeni LIME2z LI	-41248 NR_039634	1.01E+08	NR_039634	ENSG000003MIR4435-1	mir-4435-microRNA ncRNA	
chr2-1611 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr2	1.61E+08	1.61E+08	+ 0 NA	intron (NLIPA2 LI	25350 NM_001199	10010	Hs.132257	NR_004180	ENSG000003TANK	I-TRAF ITRAF famiprotein-coding
chr2-1975 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr2	1.98E+08	1.98E+08	+ 0 NA	Intergeni LIPA6 LI	46415 NM_001204	25843	Hs.633165	NR_015387	ENSG000003MOB4	2C40 CGI-MOB famil protein-coding
chr20-365 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr20	36897129	36897840	+ 0 NA	intron (Nintron (N	21346 NM_080628	140711	Hs.472633	NR_080628	ENSG000003TLD2C	C20orf11E TBC/LysM protein-coding
chr3-476 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr3	47657908	47659275	+ 0 NA	intron (NLM1B7 LIN	3103 NR_145791	1.1E+08	NR_145791	SNORD146	- small nucsnRNA	
chr3-1112 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr3	1.11E+08	1.11E+08	+ 0 NA	Intergeni Intergeni	131483 NM_001242	25945	Hs.293917	NR_015480	ENSG000003NECTIN3	CD113 CDWnectin cprotein-coding
chr3-1247 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr3	1.25E+08	1.25E+08	+ 0 NA	intron (Nintron (N	41192 NR_036088	1E+08	NR_036088	ENSG000003MIR544B	- microRNA ncRNA	
chr3-149 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr3	1.49E+08	1.49E+08	+ 0 NA	intron (NALuY SINE	41477 NM_004130	2992	Hs.477892	NR_004130	ENSG000003GYG1	GSD15 GYCglycogeniprotein-coding
chr4-554 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr4	55434230	55435682	+ 0 NA	3' UTR (N3' UTR (N	38999 NM_018475	55858	Hs.479766	NR_018475	ENSG000003TMEM165	CDG2K FT2 transment protein-coding
chr4-9421 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr4	94217682	94218529	+ 0 NA	intron (Nintron (N	10021 NR_045644	56916	Hs.410406	NR_020155	ENSG000003SMARCAD1	ADERM BAS SWI/SNF-1 protein-coding
chr5-5542 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr5	55428096	55429262	+ 0 NA	intron (Nintron (N	80247 NR_049866	1.01E+08	NR_049866	ENSG000003MIR5687	- microRNA ncRNA	
chr7-2315 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr7	23198289	23198961	+ 0 NA	intron (Nintron (N	16577 NM_001370	11097	Hs.408241	NR_007342	ENSG000003NUP42	CG1 NLP-1nucleopor protein-coding
chr7-1276 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr7	1.28E+08	1.28E+08	+ 0 NA	intron (Nl2b LINE	38129 NM_014390	27044	Hs.122522	NR_014390	ENSG000003SND1	TDRD11 Tt staphyloc protein-coding
chr7-139 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr7	1.4E+08	1.4E+08	+ 0 NA	3' UTR (N3' UTR (N	41172 NM_001080	154790	Hs.57806	NR_001080	ENSG000003CLEC2L	- C-type lprotein-coding
chr9-9742 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr9	97429475	97430427	+ 0 NA	intron (NLIME4c LI	17855 NM_014290	23424	Hs.193842	NR_014290	ENSG000003TDRD7	CATC4 PCI tudor don protein-coding
chr9-1047 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chr9	1.05E+08	1.05E+08	+ 0 NA	intron (Nintron (N	-6623 NR_130755	55335	Hs.429294	NR_018375	ENSG000003NIPSNAP3E	FP944 NIP nipsnap l protein-coding
chrX-1005 5.418643	-0.7567	0.996118	-0.75965	0.447465	0.981636	chrX	10091159	10091944	+ 0 NA	intron (NMLT1C LTF	-65394 NM_001255	1183	Hs.495694	NR_001830	ENSG000003CLCN4	CCN10 Cl chloride protein-coding
chr18-242 6.434283	0.709595	0.934381	0.759428	0.447597	0.981636	chr18	24235686	24236562	+ 0 NA	intron (NMLT1D LTF	36108 NM_018030	114876	Hs.370722	NR_018030	ENSG000003OSBPL1A	ORP-1 ORF oxysterol protein-coding
chr19-15 6.434283	0.709595	0.934381	0.759428	0.447597	0.981636	chr19	1555619	1556081	+ 0 NA	exon (NM_exon (NM	12208 NM_203304	399664	Hs.436495	NR_203304	ENSG000003MEX3D	MEX-3D Mex-3 RN protein-coding
chr19-75 6.434283	0.709595	0.934381	0.759428	0.447597	0.981636	chr19	7562047	7562060	+ 0 NA	exon (NM_exon (NM	25336 NM_001166	10908	Hs.631863	NR_006702	ENSG000003PNPLA	BNHS LNMSPatatin l protein-coding
chr22-43 6.434283	0.709595	0.934381	0.759428	0.447597	0.981636	chr22	43929885	43930359	+ 0 NA	intron (Nintron (N	6317 NM_025225	80339	Hs.654800	NR_025225	ENSG000003PNPLA3	ADPN C22cpatatin l protein-coding
chr7-994 6.434283	0.709595	0.934381	0.759428	0.447597	0.981636	chr7	99456442	99456963	+ 0 NA	3' UTR (N3' UTR (N	9460 NM_001198	1.01E+08	NR_001198	ENSG000003ATP5MF-P1	ATP5J2-2 ATP5MF-P1 protein-coding	
chrX-168 6.434283	0.709595	0.934381	0.759428	0.447597	0.981636	chrX	16820963	16821651	+ 0 NA	intron (NALuS6 SI	34841 NM_018360	55787	Hs.555961	NR_018360	ENSG000003TXLNG	Xorf15 E taxilin g protein-coding
chr11-106 8.920826	-0.59908	0.789037	-0.75926	0.447698	0.981636	chr11	10612072	10618159	+ 0 NA	intron (NLIPA5 LIN	37186 NM_001098	10335	Hs.501895	NR_130388	ENSG000003MRV11	IRAG JAWI murine rprotein-coding
chr5-143 8.920826	-0.59908	0.789037	-0.75926	0.447698	0.981636	chr5	1.43E+08	1.43E+08	+ 0 NA	exon (NM_exon (NM	3328 NM_001364	2908	Hs.122927	NR_000175	ENSG000003NR3C1	GCRC GCR1 nuclear l protein-coding
chr19-38 8.920826	-0.59908	0.789037	-0.75926	0.447698	0.981636	chr19	38825491	38825995	+ 0 NA	intron (NHERV9NC-i	6051 NM_001398	1891	Hs.196176	NR_001398	ENSG000003ECH1	HCCCL enoyl-CoA protein-coding
chr17-548 8.920826	-0.60511	0.797107	-0.75914	0.447769	0.981636	chr17	5488272	5490040	+ 0 NA	exon (NM_exon (NM	2263 NM_024035	79003	Hs.267194	NR_024035	ENSG000003MIS12	2510025 FMCIS12 kir protein-coding
chr4-311 8.920826	-0.69807	0.919622	-0.75909	0.447800	0.981636	chr4	31135644	31136507	+ 0 NA	intron (Nintron (N	71718 NM_015382	25831	Hs.708017	NR_015382	ENSG000003HECTD1	EULIR HECT dom protein-coding
chr19-148 8.920826	-0.69807	0.919622	-0.75909	0.447800	0.981636	chr19	14825491	14825995	+ 0 NA	intron (Nintron (N	-6694 NM_001105	221545	Hs.159122	NR_145025	ENSG000003C6orf136	- chromosom protein-coding
chr10-10 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr10	1E+08	1E+08	+ 0 NA	intron (Nintron (N	12082 NM_001347	10613	Hs.150087	NR_006455	ENSG000003ERLIN1	C10orf69 ER lipid protein-coding
chr12-12 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr12	1.22E+08	1.22E+08	+ 0 NA	intron (NALuSx SIN	-57289 NR_045382	1.01E+08	NR_045382	CLIP1-AS1	CLIP1 antncRNA	
chr19-101 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr19	10156042	10157794	+ 0 NA	intron (Nintron (N	-37019 NR_003755	8666	Hs.529055	NR_003755	ENSG000003EIF3G	EIF3-P42 eukaryot protein-coding
chr2-690 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr2	69066166	69066430	+ 0 NA	intron (NALuSp SIN	-37384 NR_036073	1E+08	NR_036073	ENSG000003MIR3126	mif-3126 microRNA ncRNA	
chr4-770 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr4	77053365	77053803	+ 0 NA	intron (Nintron (N	21326 NM_001348	10983	Hs.518827	NR_006835	ENSG000003CCN1	CCN1 CYC cyclin I protein-coding
chr5-168 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr5	16829266	16829554	+ 0 NA	intron (Nintron (N	106878 NM_012334	4651	Hs.481722	NR_012334	ENSG000003MYO10	- myosin X protein-coding
chr9-154 8.920826	-0.66959	0.882419	-0.75871	0.448024	0.981636	chr9	15466241	15466669	+ 0 NA	non-codirnon-codir	43579 NR_161442	6619	Hs.546299	NR_003084	ENSG000003SNAPC3	PTFbeta S small nuc protein-coding
chr2-301 9.716093	0.572945	0.755244	0.758622	0.448079	0.981636	chr2	30156661	30158340	+ 0 NA	intron (NMamRep60E	10493 NM_016061	51646	Hs.515890	NR_016061	ENSG000003YPEL5	CGI-127 yippee l protein-coding



chr22-215	6.964152	0.670642	0.887225	0.755888	0.449717	0.981636	chr22	21973407	21975159	+	0	NA	intron (Nintron (N	8504 NM_001345	8940 Hs. 436401NM_003935	ENSG000003TOP3B	TOP3B1	DNA topoisomerase protein-coding
chr4-106	6.964152	0.670642	0.887225	0.755888	0.449717	0.981636	chr4	1.06E+08	1.06E+08	+	0	NA	intron (NLR12C L1	-69225 NR_125928	1.02E+08 Hs. 631131NR_125928	ENSG000001LOC101925	-	uncharactericRNA
chr6-529	6.964152	0.670642	0.887225	0.755888	0.449717	0.981636	chr6	52982787	52983873	+	0	NA	intron (Nintron (N	11954 NM_001512	2941 Hs. 485557NM_001512	ENSG000003GSTA4	GSTA4-4 Cglutathione S-transferase gamma 4 protein-coding	
chr7-143	6.964152	0.670642	0.887225	0.755888	0.449717	0.981636	chr7	1435577	1438658	+	0	NA	intron (Nintron (N	22353 NM_182924	79778 Hs. 376617NM_024722	ENSG000003MICALL2	JRAB MICACICAL1 lik protein-coding	
chr9-133	6.964152	0.670642	0.887225	0.755888	0.449717	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	2821 NR_106937	1.02E+08	NR_106937	ENSG000003MIR6877	hsa-mir-6877 microRNA ncRNA
chr4-714	5.359938	-0.77435	1.024736	-0.75566	0.449855	0.981636	chr4	71455515	71455755	+	0	NA	intron (Nintron (N	116582 NM_003755	8671 Hs. 5462	NR_003755	ENSG000003SLC44A	HNBC1 KNE solute carrier protein-coding
chr2-372	9.667096	0.573802	0.759489	0.755511	0.449942	0.981636	chr2	37247553	37249272	+	0	NA	non-codiron-codir	16754 NR_146408	55471 Hs. 433466NM_018607	ENSG000003NDUFAF7	C2orf56 NADH:ubiquinone oxidoreductase 7 protein-coding	
chr11-47	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr11	47370327	47370783	+	0	NA	intron (Nintron (N	-35490 NR_120566	1.02E+08 Hs. 664956NR_120566	ENSG000003LOC101925	-	uncharactericRNA
chr15-38	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr15	38323089	38323525	+	0	NA	intron (Nintron (N	70471 NM_152594	161742 Hs. 525781NM_152594	ENSG000003SPRED1	LGSS NFLS sprouty 1 protein-coding	
chr17-70	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr17	7003159	7003851	+	0	NA	intron (NAluJo SIN	7456 NM_000697	239 Hs. 654431NM_000697	ENSG000003ALOX12	12-LOX 12arachidonic acid oxidase protein-coding	
chr2-664	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr2	66466320	66466556	+	0	NA	intron (Nintron (N	-26108 NR_046622	1.01E+08 Hs. 734696NR_046622	ENSG000003MEI51-AS2	MEI51-AS1 MEI51 antncRNA	
chr2-202	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	promoter-promoter-	-345 NR_003031	692058	NR_003031	ENSG000003SNORD11	HBII1-95 small nucleolar RNA
chr4-101	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr4	1.01E+08	1.01E+08	+	0	NA	intron (Nintron (N	195626 NR_107033	1.02E+08	NR_107033	ENSG000003MIR8066	hsa-mir-8066 microRNA ncRNA
chr4-13	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	-57088 NM_001184	4717 Hs. 84549	NR_002494	ENSG000003NDUFC1	KFYI NADH:ubiquinone oxidoreductase 1 protein-coding
chr7-139	7.128595	-0.66216	0.876506	-0.75545	0.44998	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	1930 NM_080660	92092 Hs. 512833NM_080660	ENSG000003ZC3HAV1L	C7orf39 zinc finger protein-coding	
chr1-243	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (Nintron (N	165255 NR_039824	1.01E+08	NR_039824	ENSG000003MIR4677	mir-4677 microRNA ncRNA
chr10-10	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	47066 NM_024541	79591 Hs. 16004	NR_024541	ENSG000003ARMH3	C10orf76 armadillo protein-coding
chr14-35	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr14	35611650	35612695	+	0	NA	intron (NAluJo SIN	78008 NM_032594	84684 Hs. 62813	NR_032594	ENSG000003INSM2	IA-6 IAG INSM trar protein-coding
chr19-57	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr19	57883074	57883667	+	0	NA	intron (NAluYe6 S1	5667 NM_001144	730051 Hs. 634142NM_001144	ENSG000003ZNF814	-	zinc finger protein-coding
chr21-37	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr21	37182858	37184292	+	0	NA	intron (NMLT1H LTF	10349 NR_046651	1.01E+08 Hs. 570411NR_046651	ENSG000003TTC3-AS1	-	TTC3 antncRNA
chr3-129	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr3	12922033	12922232	+	0	NA	exon (NM exon (NM	-36921 NR_136188	1.05E+08 Hs. 561179NR_136188	ENSG000003LINC02022	-	long intncRNA
chr3-196	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (N(TG)n Sin	-63402 NM_001308	205564 Hs. 240777NM_152699	ENSG000003SEN5	-	SUMO spec protein-coding
chr5-138	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (NHUERS-P3-	-31223 NR_073445	51308 Hs. 416099NM_016606	ENSG000003REEP2	C5orf19 Sreceptor protein-coding	
chr8-287	6.915155	0.672046	0.890172	0.754962	0.450271	0.981636	chr8	28737581	28738052	+	0	NA	intron (Nintron (N	36315 NR_073469	2137 Hs. 491354NM_001440	ENSG000003EXTL3	BOTV EXTL3 exostosin protein-coding	
chr3-102	4.186788	0.891943	1.181489	0.754931	0.45029	0.981636	chr3	10286207	10286797	+	0	NA	TTS (NR_C TTS (NR_C	2083 NR_026825	84657 Hs. 302131NM_001035	ENSG000003LINC00852	C3orf42 C long intncRNA	
chr19-43	4.675518	0.812244	1.075926	0.754925	0.450294	0.981636	chr19	43477982	43479039	+	0	NA	intron (NMR1b SINE	-12902 NM_014400	227076 Hs. 631594NM_014400	ENSG000003LYPD3	C4.4A LY6/PLAUF protein-coding	
chr9-357	4.675518	0.812244	1.075926	0.754925	0.450294	0.981636	chr9	35754474	35755231	+	0	NA	promoter-promoter-	-576 NM_001044	692094 Hs. 571601NM_001044	ENSG000003MSPM	PSPM	microsemin protein-coding
chr1-116	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr1	11659105	11661095	+	0	NA	intron (NMER3 DNA	-4100 NM_018438	26270 Hs. 464415NM_018438	ENSG000003FBX06	FBG2 FBX2 F-box protein-coding	
chr1-333	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr1	33354534	33355204	+	0	NA	exon (NM exon (NM	4517 NR_125978	1.02E+08 Hs. 568627NR_125978	ENSG000003LOC101925	-	uncharactericRNA
chr1-439	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr1	43960186	43960990	+	0	NA	intron (Nintron (N	-9422 NM_001315	1802 Hs. 632369NM_001384	ENSG000003DPH2	DPH2L2	diphthamide protein-coding
chr1-157	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (Nintron (N	-7614 NR_132767	1.07E+08	NR_132767	SCARNA26E	small Cajal box RNA
chr1-164	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr1	1.65E+08	1.65E+08	+	0	NA	intron (Nintron (N	-25533 NR_038072	1.01E+08 Hs. 661035NR_038072	ENSG000003LOC100505E	-	uncharactericRNA
chr1-225	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	exon (NM exon (NM	21228 NM_014698	9725 Hs. 119387NM_014698	ENSG000003TMEM63A	KIAA0792 transmembrane protein-coding	
chr15-32	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr15	32798722	32798921	+	0	NA	exon (NM exon (NM	-79956 NR_109767	1E+08 Hs. 610545NR_109767	ENSG000003LOC100131	-	uncharactericRNA
chr16-22	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr16	22260128	22261555	+	0	NA	intron (Nintron (N	-36534 NM_001258	55718 Hs. 460298NM_018115	ENSG000003POLR3E	RPC5 SIN RNA polymerase protein-coding	
chr16-85	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr16	85778163	85778637	+	0	NA	TTS (NM_C TTS (NM_C	-14015 NR_001195	1.02E+08 Hs. 662217NR_135195	ENSG000003LOC101925	-	uncharactericRNA
chr17-50	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr17	50105536	50106206	+	0	NA	intron (Nintron (N	10176 NM_001195	5164 Hs. 256667NM_002611	ENSG000003CPDK2	PDHK2 PK pyruvate dehydrogenase kinase 2 protein-coding	
chr19-15	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr19	1505654	1506219	+	0	NA	3' UTR (N3' UTR (N	7083 NM_001367	339366 Hs. 371674NM_213604	ENSG000003ADAMTSL5	THSD6	ADAMTSL5 protein-coding
chr2-685	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr2	68508823	68509216	+	0	NA	intron (N(LIP45 LIN	41434 NM_173545	200558 Hs. 173545	NR_173545	ENSG000003APL	APLF C2orf42 apoptosis-inducing factor 1 protein-coding
chr2-121	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr2	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	-86447 NR_023343	1E+08 Hs. 689635NR_023343	ENSG000003RNU4ATAC	MOPD1 RFWRNA, U4atsnRNA	
chr20-34	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr20	34292017	34292756	+	0	NA	exon (NM exon (NM	10604 NM_001322	191 Hs. 388004NM_000687	ENSG000003AHCY	SAHH adof adenosyl protein-coding	
chr20-41	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr20	41443157	41444133	+	0	NA	intron (Nintron (N	-76827 NM_052846	90187 Hs. 726525NM_052846	ENSG000003EMILIN3	C2orf13 elastin protein-coding	
chr22-37	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr22	37373275	37373640	+	0	NA	exon (NM exon (NM	-18618 NR_110515	1.01E+08 Hs. 220555NR_110515	ENSG000003LOC100505E	-	uncharactericRNA
chr3-49	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr3	49680644	49682256	+	0	NA	intron (Nintron (N	7099 NM_001640	327 Hs. 517966NM_001640	ENSG000003APEH	AARE ACPF acylaminic protein-coding	
chr4-168	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	Intergeni(L2b LINE	23701 NM_032783	84869 Hs. 659311NM_032783	ENSG000003CBR4	SDR45C1 dibenzoyl protein-coding	
chr5-13	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr5	13863141	13866308	+	0	NA	intron (Nintron (N	79756 NM_001386	1767 Hs. 212368NM_001386	ENSG000003DNAH5	C1LD3 DN <sup>2</sup> dynein alpha protein-coding	
chr6-11	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr6	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	70787 NM_001033	619208 Hs. 591340NM_001033	ENSG000003FAM229B	C6orf225 family wiprotein-coding	
chr7-14	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	non-codiron-codir	47078 NM_001363	84255 Hs. 446021NM_032295	ENSG000003SLC37A3	-	solute carrier protein-coding
chr7-149	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr7	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	-52861 NR_152557	155061 Hs. 24643	NR_152557	ENSG000003ZNF746	PARIS zinc finger protein-coding
chr8-47	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr8	47280500	47280800	+	0	NA	intron (NAluSx SIN	19712 NM_001080	23514 Hs. 381055NM_001080	ENSG000003SPIDR	KIAA0146 scaffold protein-coding	
chr9-33	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chr9	33133091	33133200	+	0	NA	intron (Nintron (N	24768 NR_162131	1.13E+08	NR_162131	MIR12117	microRNA ncRNA
chrX-40	6.930871	0.667371	0.884125	0.754839	0.450346	0.981636	chrX	40631171	40632829	+	0	NA	intron (NAluS6 S1	8019 NM_001195</				



chr6-1175 5.410785	-0.75444	1.003388	-0.75189	0.452117	0.981636	chr6	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	57218 NM_001017	57120 Hs. 191535NM_020399	ENSG00000G0PC	CAL FIG C golgi ass	protein-coding
chr6-1334 5.410785	-0.75444	1.003388	-0.75189	0.452117	0.981636	chr6	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	233718 NM_001301	2070 Hs. 596688NM_004100	ENSG00000EY4A	CMD1J DFN EYA	transprotein-coding
chr8-7865 5.410785	-0.75444	1.003388	-0.75189	0.452117	0.981636	chr8	78681779	78683490	+	0	NA	intron (NTHE1B LTF	16545 NR_156423	51101 Hs. 271878NM_016010	ENSG00000CZ2HC1A	C8orf70 C zinc fing	protein-coding
chr8-1255 5.410785	-0.75444	1.003388	-0.75189	0.452117	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	33236 NM_003125	6713 Hs. 71465 NM_003125	ENSG00000SQLE	-	squalene protein-coding
chr9-8597 5.410785	-0.75444	1.003388	-0.75189	0.452117	0.981636	chr9	85976288	85976645	+	0	NA	intron (Nintron (N	34937 NM_001321	60560 Hs. 436098NM_021925	ENSG00000NAA35	EGAP MAK1N alpha-	protein-coding
chr9-1225 5.410785	-0.75444	1.003388	-0.75189	0.452117	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	IntergeniL2 LINE I	-2753 NM_012197	23637 Hs. 271341NM_012197	ENSG00000CRABGAP1	GAPCENA TRAB	GTPas protein-coding
chr6-1006 9.127518	0.587397	0.78148	0.751647	0.452263	0.981636	chr6	1.01E+08	1.01E+08	+	0	NA	intron (NMLTL LTF	-181128 NM_005066	6492 Hs. 520293NM_005066	ENSG00000S1M1	bHLHe14 SIM	bHLH protein-coding
chr14-102 8.664212	0.616306	0.819952	0.751637	0.45227	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	intron (NAluJo SIN	14297 NM_014844	9895 Hs. 195667NM_014844	ENSG00000TECPR2	KIAA0329 t	ectonin protein-coding
chr19-581 12.39962	0.507668	0.675578	0.751457	0.452377	0.981636	chr19	58127035	58143891	+	0	NA	intron (NAluSq2 SI	15326 NM_024620	79673 Hs. 458377NM_024620	ENSG00000ZNF329	-	zinc fing protein-coding
chr16-884 6.467564	0.712873	0.948879	0.751279	0.452485	0.981636	chr16	88069705	88070107	+	0	NA	intron (NTigger2 I	31079 NR_12031C	400553 Hs. 592071NR_12031C	ENSG00000LOC400553	-	uncharactcrRNA
chr18-124 6.467564	0.712873	0.948879	0.751279	0.452485	0.981636	chr18	12432315	12433324	+	0	NA	promoter-promoter-	45 NR_136514	1.05E+08 Hs. 515283NR_136514	LOC105371	-	uncharactcrRNA
chr3-1971 6.467564	0.712873	0.948879	0.751279	0.452485	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (NLM4c LIN	28701 NM_001366	1739 Hs. 292545NM_004087	ENSG00000CDLGI	DLGH1 SAF	discs lar protein-coding
chr3-1805 8.897253	-0.59479	0.792131	-0.75088	0.452727	0.981636	chr3	1.81E+08	1.81E+08	+	0	NA	intron (Nintron (N	20829 NM_00119C	131118 Hs. 230601NM_145261	ENSG00000DNAJ19	PAM18 TIM	DnaJ heat protein-coding
chr4-744 8.897253	-0.59479	0.792131	-0.75088	0.452727	0.981636	chr4	74475	744863	+	0	NA	intron (NCpG	37129 NR_036511	1E+08 Hs. 731755NR_036511	ENSG00000LOC100129	-	uncharactcrRNA
chr5-6617 8.897253	-0.59479	0.792131	-0.75088	0.452727	0.981636	chr5	6617510	6617974	+	0	NA	intron (Nintron (N	15302 NR_037947	54888 Hs. 481522NM_017755	ENSG00000NSUN2	MISU MRT	E NOP2/Sun protein-coding
chr11-115 6.692562	-0.69597	0.926906	-0.75086	0.452739	0.981636	chr11	11929971	11930729	+	0	NA	intron (NMER58A DN	78289 NM_00101E	27122 Hs. 292155NM_013255	ENSG00000DKK3	REIC RIG	dickkopf protein-coding
chr6-152 6.692562	-0.69597	0.926906	-0.75086	0.452739	0.981636	chr6	1.52E+08	1.52E+08	+	0	NA	exon (NM exon (NM	-25654 NR_120501	1.01E+08 Hs. 571203NR_120501	SYNE1-AS1	SYNE1	antncRNA
chr11-125 9.723951	0.571276	0.760837	0.750853	0.452741	0.981636	chr11	1.3E+08	1.3E+08	+	0	NA	exon (NM exon (NM	23282 NM_00616E	4798 Hs. 530535NM_00616E	ENSG00000FRFRK	INO80G	nuclear f protein-coding
chr2-9255 9.723951	0.571276	0.760837	0.750853	0.452741	0.981636	chr2	92533517	92534424	+	0	NA	IntergeniALR Alpha	592837 NR_027714	440888 Hs. 730235NM_001032412	ACTR3BP2	FKSG73	ACTR3B ps
chr9-1296 9.723951	0.571276	0.760837	0.750853	0.452741	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (NMER5A1 DN	5769 NM_000113	1861 Hs. 534312NM_000113	ENSG00000TORIA	DQ2 DYT1	torsin f protein-coding
chr1-2008 12.35848	0.506423	0.675257	0.75074	0.452809	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	exon (NM exon (NM	-23758 NM_00529E	2841 Hs. 534312NM_00529E	ENSG00000GPR25	-	G protein protein-coding
chr1-2265 9.657388	0.56627	0.754349	0.750673	0.452849	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (NMER33 DNA	32350 NM_00161E	142 Hs. 177766NM_00161E	ENSG00000PARP1	ADPRT ADF	poly (ADP- protein-coding
chr15-55 5.459782	-0.75139	1.001004	-0.75064	0.452872	0.981636	chr15	55949751	55950759	+	0	NA	intron (Nintron (N	-33124 NM_001284	4734 Hs. 1565 NM_006154	ENSG00000CNEDD4	NEDD4-1 FNEDD4	E3 protein-coding
chr3-1324 5.459782	-0.75139	1.001004	-0.75064	0.452872	0.981636	chr3	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	70280 NM_00132E	23317 Hs. 12707 NM_015268	ENSG00000DNAJ13	PARK21 RM	DnaJ heat protein-coding
chr12-297 9.349001	-0.577	0.768815	-0.7505	0.452952	0.981636	chr12	29704054	29705174	+	0	NA	intron (N L3 LINE C	79328 NM_001367	83857 Hs. 401954NM_031920	ENSG00000TMTCI	ARG99 OLF	transmemt protein-coding
chr10-924 8.581933	0.614667	0.819204	0.750322	0.453061	0.981636	chr10	92463455	92463797	+	0	NA	intron (Nintron (N	34140 NM_001322	3416 Hs. 500545NM_004965	ENSG00000IDE	INSULYSIN	insulin c protein-coding
chr1-4101 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr1	41016603	41017224	+	0	NA	non-codiron-codir	2323 NR_03786E	1.01E+08 Hs. 660055NR_03786E	ENSG00000SLFNL1-AS-	SLFNL1	arncRNA
chr13-115 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	15015 NM_007111	7027 Hs. 79353 NM_007111	ENSG00000TFDP1	DILC DP1 transcrip	protein-coding
chr2-161 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr2	1.61E+08	1.61E+08	+	0	NA	intron (N L2c LINE I	-15478 NR_110163	1.01E+08 Hs. 660925NR_110163	ENSG00000LINC0180E-	-	long intncRNA
chr20-455 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr20	45368354	45368770	+	0	NA	3' UTR (N3' UTR (N	5393 NR_00318E	677557 Hs. 730645NR_00318E	ENSG00000SYS1-DBN1	C20orf166	SYS1-DBN1
chr22-462 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr22	46208347	46209214	+	0	NA	intron (N LIMA7 LIN	41513 NM_207327	150383 Hs. 103111NM_207327	ENSG00000CDPF1	C22orf40	cysteine protein-coding
chr5-554 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr5	55405503	55406085	+	0	NA	intron (Nintron (N	97805 NM_01536C	23517 Hs. 274531NM_01536C	ENSG00000MTRFX	Dob1 KIA	Mtr4 exos protein-coding
chr6-8317 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr6	83179880	83176814	+	0	NA	intron (NMER58A DN	16868 NM_00119E	5238 Hs. 661665NM_015595	ENSG00000PGM3	AGM1 LMD2	phosphog protein-coding
chr8-3105 5.451925	-0.74922	0.998575	-0.75029	0.453081	0.981636	chr8	31090150	31091150	+	0	NA	intron (Nintron (N	-57294 NM_00101E	29942 Hs. 373778NM_013357	ENSG00000PURG	PURG-A PL	purine r protein-coding
chr5-4957 18.36311	0.432949	0.577065	0.75026	0.453098	0.981636	chr5	49573966	49579432	+	0	NA	IntergeniALR Alpha	866839 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	emigin protein-coding
chr16-295 11.14308	-0.53228	0.709936	-0.74975	0.453403	0.981636	chr16	29521019	29521242	+	0	NA	IntergeniLTR7B LTF	-12526 NM_00135E	440353 NM_001355400	NPIPB12	-	nuclein protein-coding
chr6-158 7.095314	-0.66784	0.890785	-0.74972	0.453425	0.981636	chr6	1.59E+08	1.59E+08	+	0	NA	3' UTR (N3' UTR (N	11246 NM_001291	6993 Hs. 445995NM_006515	ENSG00000DYNLT1	CW-1 TCTF	dynein l protein-coding
chr11-87 7.478306	0.641414	0.855586	0.749678	0.453449	0.981636	chr11	87043179	87043645	+	0	NA	intron (Nintron (N	5478 NM_00116E	65084 Hs. 188591NM_02291E	ENSG00000KMT135	PMP52	transmemt protein-coding
chr20-181 7.478306	0.641414	0.855586	0.749678	0.453449	0.981636	chr20	18179817	18180365	+	0	NA	intron (NTHE1A-int	35098 NR_028402	57325 Hs. 488051NM_02053E	ENSG00000KAT14	ATAC2 CRF	lyase ac protein-coding
chr6-494 7.478306	0.641414	0.855586	0.749678	0.453449	0.981636	chr6	49438794	49440207	+	0	NA	intron (NHERVL-int	23753 NM_00025E	4594 Hs. 485527NM_00025E	ENSG00000MMUT	MCM MUT	methylmal protein-coding
chr17-757 18.27131	-0.4244	0.566239	-0.7495	0.453556	0.981636	chr17	7577547	75779341	+	0	NA	3' UTR (N3' UTR (N	1335 NM_005324	3021 Hs. 180877NM_005324	ENSG00000H3F3B	H3.3B	H3 histor protein-coding
chr19-105 7.486164	0.639214	0.853005	0.749368	0.453636	0.981636	chr19	10550413	10551145	+	0	NA	intron (NAluY SINE	-1343 NR_031603	1E+08 NR_031603	ENSG00000MIR1238	MIRN1238	microRNA ncRNA
chr2-240 7.486164	0.639214	0.853005	0.749368	0.453636	0.981636	chr2	2.4E+08	2.4E+08	+	0	NA	exon (NM exon (NM	10553 NR_136157	4705 Hs. 277677NM_004544	ENSG00000NDUFA10	CI-42KD C	NADH:ubiq protein-coding
chr1-8393 8.830689	-0.60368	0.805773	-0.7492	0.453739	0.981636	chr1	8393050	8393498	+	0	NA	intron (Nintron (N	30558 NM_00104C	473 Hs. 463041NM_012102	ENSG00000RERE	ARG ARP	arginine- protein-coding
chr17-437 8.830689	-0.60368	0.805773	-0.7492	0.453739	0.981636	chr17	43776645	43777570	+	0	NA	intron (NAluSq2 SI	1870 NM_00409C	1845 Hs. 181045NM_00409C	ENSG00000DUSP3	VHR	dual spec protein-coding
chr16-305 4.94147	-0.81851	1.092624	-0.74912	0.453782	0.981636	chr16	30928715	30929000	+	0	NA	intron (Nintron (N	4282 NM_00109E	54620 Hs. 152145NM_01908E	ENSG00000FBXL19	CXXC11 FE	F-box an protein-coding
chr19-507 4.94147	-0.81851	1.092624	-0.74912	0.453782	0.981636	chr19	5071876	5072075	+	0	NA	intron (Nintron (N	102862 NM_00137C	23030 Hs. 654815NM_01501E	ENSG00000KDM4B	JMJD2B TT	lysine de protein-coding
chr16-845 11.86975	0.521158	0.695711	0.749101	0.453796	0.981636	chr16	84990165	84990420	+	0	NA	intron (Nintron (N	21243 NM_00114E	55625 Hs. 461615NM_01774C	ENSG00000ZDIHC7	DHHC7 SEF	zinc fing protein-coding
chr3-1235 9.341143	-0.57565	0.768628	-0.74893	0.453901	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	6				

chr14-746 5.238669	0.753046	1.010211	0.745434	0.456009	0.981636	chr14	74687434	74688410	+	0	NA	intron (NLMC5a LI	25158 NM_001039	9870 Hs. 497417NM_014821	ENSG000004AREL1	FIEL1 KI apoptosis protein-coding
chr17-195 5.238669	0.753046	1.010211	0.745434	0.456009	0.981636	chr17	19913118	19914194	+	0	NA	intron (Nintron (N	-45720 NM_014688	9706 Hs. 168762NM_014688	ENSG000004ULK2	ATG1B Unc-51 liprotein-coding
chr6-1334 5.238669	0.753046	1.010211	0.745434	0.456009	0.981636	chr6	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	240525 NM_001301	2070 Hs. 596688NM_00410C	ENSG000004CEYA4	CMD1J DFNEYA transprotein-coding
chrX-1567 5.238669	0.753046	1.010211	0.745434	0.456009	0.981636	chrX	15678773	15679370	+	0	NA	intron (NMLT2D LTF	3579 NR_160542	340591 Hs. 732244NM_026551	ENSG000004CA5BP1	CAB7L CAE carbonic pseudo
chr5-4836 10.22054	0.549667	0.737436	0.745376	0.456044	0.981636	chr5	48364399	48365273	+	0	NA	IntergeniALR/Alphe	20764524	561411NM_198444	ENSG000004EMB	CP50 embigin protein-coding
chr7-7347 10.22054	0.549667	0.737436	0.745376	0.456044	0.981636	chr7	73476716	73478288	+	0	NA	exon (NM_exon (NM	43724 NM_003508	8326 Hs. 647029NM_003508	ENSG000004CFZD9	CD349 FZI frizzled protein-coding
chr12-716 6.897589	0.663985	0.890944	0.745261	0.456114	0.981636	chr12	71907869	71908697	+	0	NA	intron (Nintron (N	-30562 NM_173355	121278 Hs. 736577NM_173355	ENSG000004TPH2	ADHD7 NTF tryptophan protein-coding
chr9-1291 6.897589	0.663985	0.890944	0.745261	0.456114	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (N2b LINE	3144 NM_004003	1384 Hs. 12068 NM_000758	ENSG000004CRAT	CD7 CAT1 carnitine protein-coding
chr1-1174 7.452883	0.636086	0.853541	0.745232	0.456131	0.981636	chr1	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	57760 NM_006699	10905 Hs. 435938NM_006699	ENSG000004MANIA2	MAN1B mannosidase protein-coding
chr11-681 7.452883	0.636086	0.853541	0.745232	0.456131	0.981636	chr11	68184249	68184692	+	0	NA	intron (Nintron (N	28826 NM_001366	51111 Hs. 63212CNM_016028	ENSG000004KMT5B	CI8-85 CC lysine meprotein-coding
chr2-702 7.452883	0.636086	0.853541	0.745232	0.456131	0.981636	chr2	70262850	70263995	+	0	NA	intron (N2a LINE	5285 NM_016297	51449 Hs. 567502NM_016297	ENSG000004PCYOX1	PCL1 prenylcys protein-coding
chr22-412 7.452883	0.636086	0.853541	0.745232	0.456131	0.981636	chr22	41210146	41211239	+	0	NA	intron (NAluSx1 SI	5380 NM_031488	83746 Hs. 517641NM_031488	ENSG000004L3MBTL2	H-1(3) mbtL3MBTL2 hiprotein-coding
chr4-3924 7.452883	0.636086	0.853541	0.745232	0.456131	0.981636	chr4	39246784	39247332	+	0	NA	intron (NLIpA4 LIN	64529 NM_025132	57728 Hs. 438482NM_025132	ENSG000004WDR19	ATD5 CED4D repeat protein-coding
chr4-8807 7.452883	0.636086	0.853541	0.745232	0.456131	0.981636	chr4	88071660	88072707	+	0	NA	intron (NLIuJb SIN	64548 NR_156488	5311 Hs. 181272NM_000297	ENSG000004PKD2	APKD2 PC2 polycystiprotein-coding
chr5-1325 9.333286	-0.57432	0.770695	-0.74519	0.456155	0.981636	chr5	1.33E+08	1.33E+08	+	0	NA	intron (NLIpA5 LIN	27184 NM_005732	10111 Hs. 633509NM_005732	ENSG000004RAD50	NBSLD RAI RAD50 dot protein-coding
chr1-3284 11.12737	-0.52995	0.711292	-0.74505	0.456239	0.981636	chr1	32845725	32847059	+	0	NA	intron (NLMIE1 LIN	21079 NR_135106	64766 Hs. 440888NM_022755	ENSG000004S100BP	S100BPBP S100P b2 protein-coding
chr11-958 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr11	9587756	9589384	+	0	NA	exon (NM_exon (NM	13883 NM_001143	7465 Hs. 249441NM_00339C	ENSG000004WEE1	WEE1A WEE1E G2 cprotein-coding
chr12-686 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr12	6869181	6871177	+	0	NA	TTS (NM_C TTS (NM_C	2065 NM_001258	7167 Hs. 524219NM_00036E	ENSG000004TP11	HEL-5-49 triosephc protein-coding
chr19-206 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr19	20656961	20658414	+	0	NA	intron (NAluSp SIN	3884 NM_001076	199777 Hs. 657001NM_145297	ENSG000004ZNF626	- zinc fingprotein-coding
chr2-1361 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (NAluSq2 SI	-112071 NR_110294	1.02E+08 Hs. 661917NR_110294	ENSG000004NCKAP5-AS-	NCKAP5 arn crNA
chr3-1461 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr3	1.46E+08	1.46E+08	+	0	NA	intron (NLIpA4 LIN	40673 NM_182943	5352 Hs. 477866NM_00093E	ENSG000004PLOD2	BRK52 LH2 procollag protein-coding
chr4-5702 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr4	57028623	57033861	+	0	NA	TTS (NM_C TTS (NM_C	52346 NM_000938	5431 Hs. 602757NM_000938	ENSG000004POLR2B	POL2R2B RF RNA polynprotein-coding
chr4-823 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr4	82353830	82359650	+	0	NA	intron (Nintron (N	17521 NM_03137C	3184 Hs. 480072NM_00213E	ENSG000004HNRNP	AUF1 AUF1 heterog protein-coding
chr4-1025 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr4	1.03E+08	1.03E+08	+	0	NA	intron (NAluYc SIN	96549 NM_005908	4126 Hs. 480411NM_00590E	ENSG000004MANBA	MANB1 mannosidase protein-coding
chr8-3908 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr8	39086892	39087988	+	0	NA	intron (NLMIE4c LI	-20089 NM_001313	203102 Hs. 52154E NM_145004	ENSG000004ADAM32	ADAM ADAM metc protein-coding
chr9-3608 9.366567	-0.57015	0.765287	-0.74502	0.456259	0.981636	chr9	36089291	36087517	+	0	NA	3' UTR (N3' UTR (N	48306 NM_001316	8434 Hs. 388918NM_021111	ENSG000004RECK	ST15 reversio protein-coding
chr19-284 16.15075	-0.44753	0.601013	-0.74498	0.456273	0.981636	chr19	2849857	28495724	+	0	NA	exon (NM_exon (NM	11815 NM_152791	148254 Hs. 47712 NM_152791	ENSG000004ZNF555	- zinc fingprotein-coding
chr9-3785 8.94625	-0.59309	0.79609	-0.745	0.456273	0.981636	chr9	37824998	37825762	+	0	NA	intron (NLIpA13 LI	24583 NM_02434E	79269 Hs. 118394NM_02434E	ENSG000004CAF10	WDR32 DBD1 and protein-coding
chr1-1232 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr1	12333506	12334737	+	0	NA	intron (Nintron (N	104091 NM_01537E	55187 Hs. 439381NM_01537E	ENSG000004VPS13D	SCAR4 vacuolar protein-coding
chr1-3925 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr1	39254387	39256619	+	0	NA	intron (Nintron (N	-153570 NM_015038	643314 Hs. 658766NM_01503E	ENSG000004KIAA0754	- KIAA0754 protein-coding
chr11-354 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr11	35434010	35440909	+	0	NA	intron (Nintron (N	-17401 NM_00119E	6506 Hs. 50233E NM_004171	ENSG000004SLC1A2	EAA2T EIF solute c protein-coding
chr13-492 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr13	49259263	49261593	+	0	NA	intron (NMLT1J2 LI	12503 NM_030911	81602 Hs. 38822C NM_030911	ENSG000004CDADC1	NYD-SP15 cytidine protein-coding
chr15-495 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr15	49319030	49321442	+	0	NA	intron (Nintron (N	-103006 NM_00200E	2252 Hs. 56726E NM_00200E	ENSG000004PGF7	PHZ-7 KC fibroblas protein-coding
chr17-767 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr17	76754334	76755142	+	0	NA	intron (Nintron (N	17237 NM_024311	79157 Hs. 73965 NM_024311	ENSG000004MFSD11	ET major fac protein-coding
chr18-461 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr18	46002722	46003297	+	0	NA	intron (NLMIMD LI	-35680 NM_020964	57724 Hs. 51484E NM_020964	ENSG000004EPG5	HEEW1 KI ectopic f protein-coding
chr19-121 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr19	12172201	12174119	+	0	NA	intron (NMERSA LI	10064 NM_003437	7695 Hs. 479874NM_003437	ENSG000004ZNF136	pH2-20 zinc fing protein-coding
chr19-435 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr19	43598698	43599883	+	0	NA	3' UTR (N3' UTR (N	2695 NM_00114E	79177 Hs. 11110 NM_024327	ENSG000004ZNF576	- zinc fing protein-coding
chr20-176 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr20	17600981	17601524	+	0	NA	intron (Nintron (N	31177 NM_00687C	11034 Hs. 304192NM_00687C	ENSG000004DSTN	ACTDP ADF destrin, protein-coding
chr22-467 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr22	46694281	46701966	+	0	NA	intron (NMERSA DNA	40129 NM_00276E	64781 Hs. 20066E NM_02276E	ENSG000004CERK	LK4 dA59E ceramide protein-coding
chr6-248 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr6	24806990	24811087	+	0	NA	intron (NAluS2 SIN	-10121 NM_00128E	1.02E+08 Hs. 63513E NM_00128E	ENSG000004ARMH2	C6orf229 armadillc protein-coding
chr9-193 7.460741	0.633911	0.850963	0.744934	0.456312	0.981636	chr9	19352720	19353646	+	0	NA	intron (Nintron (N	27053 NM_00101C	6194 Hs. 48087E NM_00101C	ENSG000004RPS6	S6 ribosomal protein-coding
chr1-1225 18.3044	0.429098	0.576285	-0.744592	0.456518	0.981636	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1006006 NR_00395E	647121 Hs. 69768E NR_00395E	ENSG000004EMB1P	- embigin pseudo
chr17-481 6.408859	0.703192	0.944482	0.744527	0.456558	0.981636	chr17	48115465	48115789	+	0	NA	intron (Nintron (N	8042 NM_01332E	29916 Hs. 15827 NM_01332E	ENSG000004SNX11	- sorting r protein-coding
chr3-485 6.408859	0.703192	0.944482	0.744527	0.456558	0.981636	chr3	48500082	48500561	+	0	NA	intron (Nintron (N	3729 NM_00127E	51246 Hs. 41457E NM_01647E	ENSG000004SHISA5	SCOTIN shisa fan protein-coding
chr8-377 6.408859	0.703192	0.944482	0.744527	0.456558	0.981636	chr8	3775281	37775480	+	0	NA	exon (NM_exon (NM	12735 NM_00134E	11212 Hs. 30479E NM_00719E	ENSG000004PLPBP	EPVB6D PF pibic protein-coding
chr10-102 7.494022	0.637065	0.855823	0.744389	0.456641	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	19812 NM_02478E	79847 Hs. 30906E NM_02478E	ENSG000004MPSD13A	CTP107 f7 major fac protein-coding
chr13-416 7.494022	0.637065	0.855823	0.744389	0.456641	0.981636	chr13	41683609	41684076	+	0	NA	intron (N2c LINE	-15444 NR_04980C	1.01E+08 NR_04980C	ENSG000004MIR5006	- microRNA ncRNA
chr14-735 7.494022	0.637065	0.855823	0.744389	0.456641	0.981636	chr14	73955301	73956220	+	0	NA	intron (Nintron (N	5461 NM_18247E	51004 Hs. 13155E NM_18247E	ENSG000004COQ6	CGI-10 CC coenzyme protein-coding
chr7-102 7.494022	0.637065	0.855823	0.744389	0.456641	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	exon (NM_exon (NM	-83421 NM_02097E	10603 Hs. 48944E NM_02097E	ENSG000004SH2B2	APS SH2B adap protein-coding
chr9-124 7.494022	0.63706															



chr15-204 9.300004	-0.57867	0.782584	-0.73944	0.459642	0.981636	chr15	20453763	20453996	+	0 NA	non-codirnon-codir	-13392 NR_036444	440248 Hs. 531509NM_199044	ENSG000003HERC2P9	-	hct domε pseudo		
chr11-102 9.325428	-0.57299	0.77507	-0.73928	0.459737	0.981636	chr11	1.02E+08	1.02E+08	+	0 NA	intron (Alu)S2 SI	-101944 NM_001116E	330 Hs. 127799NM_00116E	ENSG000003BTRC3	AIP1 AP12	baculovir protein-coding		
chr4-122 9.325428	-0.57299	0.77507	-0.73928	0.459737	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (intron)	-47278 NM_139243	132612 Hs. 518957NM_139243	ENSG000003CADAD1	Tenr	adenosine protein-coding		
chr18-927 7.1873	-0.64924	0.878409	-0.73911	0.459838	0.981636	chr18	92717750	92722100	+	0 NA	intron (intron)	-62781 NM_02064E	57045 Hs. 514688NM_02064E	ENSG000003TWSG1	TSG	torked ε protein-coding		
chr7-4727 7.1873	-0.64924	0.878409	-0.73911	0.459838	0.981636	chr7	4727900	4728193	+	0 NA	intron (intron)	-45751 NM_001037	221937 Hs. 487393NM_001037	ENSG000003FOXK1	FOXK1L	forkhead protein-coding		
chr7-649E 7.1873	-0.64924	0.878409	-0.73911	0.459838	0.981636	chr7	64991995	64992598	+	0 NA	exon (NM_exon)	-1260 NM_01585E	51351 Hs. 250699NM_01585E	ENSG000003ZNF117	H-p1k HPF	zinc fing protein-coding		
chr2-4631 11.53012	-0.51975	0.703243	-0.73908	0.459857	0.981636	chr2	46317137	46317813	+	0 NA	intron (Tigger1) E	20068 NM_00143C	2034 Hs. 468411NM_00143C	ENSG000003EPAS1	ECYT4 HIF	endothelin protein-coding		
chr1-2434 9.086379	-0.58636	0.793384	-0.739061	0.45987	0.981636	chr1	46317137	46317813	+	0 NA	intron (MLTB) SINE	80846 NR_039824	1.01E+08	NR_039824	ENSG000003MIR4677	mir-4677	microRNA ncRNA	
chr5-172E 8.101061	-0.639657	0.865654	-0.73893	0.45995	0.981636	chr5	1.73E+08	1.73E+08	+	0 NA	intron (MLT1L) LTF	9243 NM_001317	51121 Hs. 546399NM_01609E	ENSG000003RPL26L1	RPL26P1	ribosomal protein-coding		
chr13-491 9.399849	-0.56603	0.766015	-0.73893	0.459951	0.981636	chr13	49148285	49149259	+	0 NA	intron (L1M2) LINE	38455 NM_01492E	22862 Hs. 508011NM_01492E	ENSG000003FNDC3A	FNDC3 HUC	fibronectin protein-coding		
chr15-61E 9.616248	-0.565364	0.765139	-0.738904	0.459965	0.981636	chr15	61961609	61961838	+	0 NA	exon (NM_exon)	98724 NM_017684	54832 Hs. 51166E	NR_017684	ENSG000003VPS13C	PARK23	vacuolar protein-coding	
chr11-72E 5.246527	-0.749937	1.01509	-0.738789	0.460035	0.981636	chr11	72888844	72888947	+	0 NA	intron (intron)	74934 NM_00131E	89849 Hs. 65318E	NR_03338E	ENSG000003ATG16L2	ATG16B WI	autophagy protein-coding	
chr19-26E 5.246527	-0.749937	1.01509	-0.738789	0.460035	0.981636	chr19	26600854	26602304	+	0 NA	IntergeniALR Alpha	-1191852 NR_14673E	1.02E+08	Hs. 567934NR_110687	ENSG000003LOC101927-	uncharactncRNA		
chr10-71 9.673104	-0.562846	0.761915	-0.738726	0.460073	0.981636	chr10	73156164	73156479	+	0 NA	exon (NM_exon)	11687 NM_00726E	11319 Hs. 63182E	NR_00726E	ENSG000003CECD	GCR2 HSG1	ecdysone protein-coding	
chr10-11 5.436209	-0.74458	1.008264	-0.73848	0.460225	0.981636	chr10	1.14E+08	1.14E+08	+	0 NA	intron (intron)	49217 NM_198514	374354 Hs. 369924NM_198514	ENSG000003NHLRC2	FINCA	NHL repeat protein-coding		
chr14-34E 5.436209	-0.74458	1.008264	-0.73848	0.460225	0.981636	chr14	34843991	34844323	+	0 NA	intron (AluY) SINE	-30034 NR_16077E	1.12E+08	Hs. 50914CNR_16077E	LOC11226E	uncharactncRNA		
chr3-447 5.436209	-0.74458	1.008264	-0.73848	0.460225	0.981636	chr3	44748514	44748993	+	0 NA	TTS (NM_CTTT)	12866 NM_00132C	57456 Hs. 74495E	NR_02069E	ENSG000003KIAA1143	-	KIAA1143 protein-coding	
chr8-230 5.436209	-0.74458	1.008264	-0.73848	0.460225	0.981636	chr8	230037	230689	+	0 NA	intron (intron)	-1774 NM_001287	169270 Hs. 59138E	NR_17353E	ENSG000003ZNF596	-	zinc fing protein-coding	
chr8-897E 5.436209	-0.74458	1.008264	-0.73848	0.460225	0.981636	chr8	89788116	89788828	+	0 NA	intron (L2b) LINE	30656 NM_003821	8767 Hs. 10375E	NR_003821	ENSG000003R1PK2	CARD3 CAF	receptor protein-coding	
chr8-1301 5.436209	-0.74458	1.008264	-0.73848	0.460225	0.981636	chr8	1.3E+08	1.3E+08	+	0 NA	intron (intron)	-67916 NR_04538E	1.01E+08	Hs. 10601E	NR_04538E	ENSG000003ASAP1-IT2	ASAP1	intncRNA
chr1-328E 9.407707	-0.56736	0.768446	-0.73832	0.46032	0.981636	chr1	32855995	32856340	+	0 NA	non-codirnon-codir	14646 NM_001171	252995 Hs. 524234NM_15375E	ENSG000003FNDC5	FRCP2 iri	fibronectin protein-coding		
chr10-87 9.407707	-0.56736	0.768446	-0.73832	0.46032	0.981636	chr10	87745103	87745947	+	0 NA	intron (intron)	72706 NM_001321	84896 Hs. 43594E	NR_03281E	ENSG000003ATAD1	AFDC1 FNF	ATPase ε protein-coding	
chr4-174E 9.407707	-0.56736	0.768446	-0.73832	0.46032	0.981636	chr4	17491891	17492199	+	0 NA	intron (MLT1A) LI	20045 NM_00032C	5860 Hs. 75438	NR_00032C	ENSG000003QDPR	DHPR HDHF	quinoid ε protein-coding	
chr1-921E 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr1	92159073	92160213	+	0 NA	IntergeniL1MB1 LI	92159073	21554 Hs. 015237	ENSG000003KIAA1107-	-	KIAA1107 protein-coding		
chr10-29E 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr10	29666797	29667362	+	0 NA	intron (L1ME1) LI	-32108 NM_02173E	6840 Hs. 49920E	NR_003174	ENSG000003SVIL	-	supervill protein-coding	
chr10-71 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr10	72101332	72103496	+	0 NA	intron (intron)	-13382 NM_001134	9806 Hs. 52300E	NR_014767	ENSG000003SPOCK2	testican-SPARC	(os) protein-coding	
chr10-121 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr10	1.32E+08	1.32E+08	+	0 NA	intron (intron)	37771 NM_001291	55844 Hs. 38037E	NR_018461	ENSG000003PPP2R2D	B55D B55E	protein ε protein-coding	
chr11-664 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr11	66491579	66493805	+	0 NA	intron (intron)	12258 NM_13044E	10072 Hs. 502914NM_00570C	ENSG000003DPP3	DPP11I	dipeptidyl protein-coding		
chr12-10E 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	intron (NLIPA3) LI	9881 NM_000431	4598 Hs. 130607NM_000431	ENSG000003MVK	LRBP MK	lyveal on protein-coding		
chr19-13 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr19	13089904	13087610	+	0 NA	intron (intron)	15601 NM_00558E	4066 Hs. 46446	NR_00558E	ENSG000003LYL1	bHLHa18	LYL1 basiprotein-coding	
chr20-11E 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr20	1168215	1169689	+	0 NA	3' UTR (3' UTR)	15521 NM_018354	55321 Hs. 516834NM_018354	ENSG000003TMEM74B	C20orf46	transmem protein-coding		
chr3-196 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr3	1.96E+08	1.96E+08	+	0 NA	intron (Alu)S2 SI	-12901 NM_005017	5130 Hs. 135997NM_005017	ENSG000003PCYT1A	CCTA CTC	phosphatε protein-coding		
chr7-396 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr7	39635046	39635820	+	0 NA	intron (L1MB7) LI	11861 NM_00540E	5898 Hs. 6906	NR_00540E	ENSG000003RALA	RAL	RAS like protein-coding	
chr7-149E 5.213246	-0.745739	1.010211	-0.738201	0.460392	0.981636	chr7	1.5E+08	1.5E+08	+	0 NA	intron (intron)	31988 NR_02778E	79970 Hs. 52078E	NR_02491E	ENSG000003ZNF767P	ZNF767	zinc fing pseudo	
chr10-11 10.16183	-0.543256	0.736019	-0.7381	0.460454	0.981636	chr10	1.2E+08	1.2E+08	+	0 NA	3' UTR (3' UTR)	26029 NM_004281	9531 Hs. 52330E	NR_004281	ENSG000003BAG3	BAG-3 BTS	BCL2 assoc protein-coding	
chr2-395 10.16183	-0.543256	0.736019	-0.7381	0.460454	0.981636	chr2	39518556	39522629	+	0 NA	intron (L1MC4a) LI	39518556	39522629	ENSG000003MAP4K3-D1-	MAP4K3	dincRNA		
chr1-218E 7.427459	-0.630782	0.854735	-0.737985	0.460524	0.981636	chr1	21866723	21866936	+	0 NA	intron (intron)	54564 NM_00101E	401944 Hs. 74515E	NR_00101E	ENSG000003DLRAD2	-	low densiprotein-coding	
chr2-22E 7.427459	-0.630782	0.854735	-0.737985	0.460524	0.981636	chr2	42576136	42577782	+	0 NA	intron (intron)	5152 NR_002184	91695 Hs. 534041NR_002184	ENSG000003RRP7BP	RRP7B dJ2	ribosomal pseudo		
chr5-50E 7.427459	-0.630782	0.854735	-0.737985	0.460524	0.981636	chr5	20091353	20091758	+	0 NA	IntergeniL1TR41 LTF	42042 NM_001297	6606 Hs. 53575E	NR_000344	ENSG000003SMN1	BCD541 GE	survival protein-coding	
chr7-106E 7.427459	-0.630782	0.854735	-0.737985	0.460524	0.981636	chr7	1.06E+08	1.06E+08	+	0 NA	IntergeniAluS2 SI	23489 NM_18271E	6856 Hs. 80919	NR_006754	ENSG000003SYPL1	H-SP1 SYF	synaptopl protein-coding	
chr9-127 7.427459	-0.630782	0.854735	-0.737985	0.460524	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	intron (intron)	-1626 NR_03981E	1.01E+08	NR_03981E	ENSG000003MIR4672	-	microRNA ncRNA	
chr9-128 7.427459	-0.630782	0.854735	-0.737985	0.460524	0.981636	chr9	1.29E+08	1.29E+08	+	0 NA	exon (NM_exon)	15636 NR_04624C	1.01E+08	Hs. 62946	NR_04624C	ENSG000003LOC10050E	uncharactncRNA	
chr1-2201 9.102095	-0.582791	0.789751	-0.737942	0.46055	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (Alu)S4 SIN	-40442 NR_029711	406969	NR_029711	ENSG000003MIR194-1	MIRN194-1	microRNA ncRNA	
chr10-14E 7.605768	-0.62882	0.852253	-0.73784	0.460614	0.981636	chr10	14509034	14509596	+	0 NA	IntergeniIntergeni	23399 NM_00132C	83641 Hs. 44631E	NR_03145E	ENSG000003FAM107B	C10orf45	family wiprotein-coding	
chr5-156 7.605768	-0.62882	0.852253	-0.73784	0.460614	0.981636	chr5	1.55E+08	1.55E+08	+	0 NA	intron (Alu)S2 SI	33034 NM_01546E	25929 Hs. 483921NM_01546E	ENSG000003GEMIN5	GEMIN-5	gen nucle protein-coding		
chr9-134 7.605768	-0.62882	0.852253	-0.73784	0.460614	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (intron)	-8811 NM_00114E	26086 Hs. 23937E	NR_015597	ENSG000003GSPM1	AGS3	G protein protein-coding	
chr10-271 7.146161	-0.653	0.885082	-0.73779	0.460643	0.981636	chr10	27164076	27164434	+	0 NA	intron (Alu)Jr SIN	9431 NM_00117E	84930 Hs. 27690E	NR_032844	ENSG000003MASTL	GREATWALL	microtub protein-coding	
chr15-857 7.146161	-0.653	0.885082	-0.73779	0.460643	0.981636	chr15	85723672	85723912	+	0 NA	intron (intron)	34933 NR_12036E	1.02E+08	Hs. 51311E	NR_12036E	LOC10192E-	uncharactncRNA	
chr17-61 7.146161	-0.653	0.885082	-0.73779	0.460643	0.981636	chr17	61917468	61917721	+	0 NA	intron (NLIPA16) LI	10388 NM_02074E	57508 Hs. 27964E	NR_02074E	ENSG000003INTS2	INT2 KIA	integract protein-coding	
chr19-101 7.146161	-0.653	0.885082	-0.73779	0.460643	0.981636													



chr12-705	7.50188	0.634909	0.864299	0.734594	0.462587	0.981636	chr12	7099616	7100559	+	0	NA	intron (NMER102b I	-7642 NM_001733	715 Hs. 524224NM_001733:ENSG00000C1R	EDSPD1	complemer protein-coding	
chr19-402	7.50188	0.634909	0.864299	0.734594	0.462587	0.981636	chr19	4024411	4025288	+	0	NA	intron (NAIuS SIN	17113 NM_015897	51588 Hs. 105775NM_015897:ENSG00000PIA54	PIAS-gamm	protein-coding	
chr19-11C	7.50188	0.634909	0.864299	0.734594	0.462587	0.981636	chr19	11019407	11020115	+	0	NA	intron (Nintron (N	35609 NM_001128	6597 Hs. 327527NM_003072:ENSG00000CMARCA4	BAF190 BA SWI/SNF	protein-coding	
chr7-7504	7.50188	0.634909	0.864299	0.734594	0.462587	0.981636	chr7	75042296	75043020	+	0	NA	3' UTR (N3' UTR (N	31144 NM_001363	81554 Hs. 529622NM_030798:ENSG00000RCC1L	WBSRC16	RCC1 like protein-coding	
chr1-1002	6.913305	0.659108	0.897402	0.734463	0.462667	0.981636	chr1	1E+08	1E+08	+	0	NA	promoter-promoter-	-416 NR_030275	693138 NR_030275:ENSG00000MIR553	MIRN5533	microRNA ncRNA	
chr10-115	6.913305	0.659108	0.897402	0.734463	0.462667	0.981636	chr10	1.14E+08	1.14E+08	+	0	NA	3' UTR (N3' UTR (N	20306 NM_001267	840 Hs. 9216 NM_001227:ENSG00000CASP7	CASP-7 C	caspase 7 protein-coding	
chr21-332	6.913305	0.659108	0.897402	0.734463	0.462667	0.981636	chr21	33251834	33252243	+	0	NA	intron (NAIuSx S	14222 NR_038974	1E+08 Hs. 709799NR_038974	IL10RB-D1	IFNAR2-AS IL10RB dincRNA	
chr4-6296	6.913305	0.659108	0.897402	0.734463	0.462667	0.981636	chr4	6290702	6292254	+	0	NA	intron (Nintron (N	21628 NM_001145	7466 Hs. 518602NM_006006:ENSG00000WFS1	CTRCT41	WU framing protein-coding	
chr15-718	7.112879	-0.65859	0.896997	-0.73422	0.462815	0.981636	chr15	71817522	71817766	+	0	NA	exon (NM exon (NM	7090 NM_014245	10002 Hs. 187354NM_014245:ENSG00000CNR2E3	ESCS PNR nuclear	protein-coding	
chr10-112	4.195571	-0.82746	1.127334	-0.734	0.462949	0.981636	chr10	1.14E+08	1.14E+08	+	0	NA	intron (N(GTAT)n S	7457 NM_001227	840 Hs. 9216 NM_001227:ENSG00000CASP7	CASP-7 C	caspase 7 protein-coding	
chr17-287	4.195571	-0.82746	1.127334	-0.734	0.462949	0.981636	chr17	28756344	28757217	+	0	NA	3' UTR (N3' UTR (N	12769 NM_004295	9618 Hs. 8375 NM_004295:ENSG00000CTRAF4	CART1 MLN TNF receptor	protein-coding	
chr11-625	11.58097	-0.51079	0.696169	-0.73371	0.463126	0.981636	chr11	62557634	62560473	+	0	NA	TTS (NM_C TTS (NM_C	1253 NR_037427	1.01E+08 NR_037427:ENSG00000CIR3654	-	microRNA ncRNA	
chr11-962	9.384133	-0.56332	0.767886	-0.7336	0.463193	0.981636	chr11	96364183	96364730	+	0	NA	intron (Nintron (N	-21261 NM_032427	84441 Hs. 428214NM_032427:ENSG00000MAML2	MAM-3 MAW	termin protein-coding	
chr12-625	9.384133	-0.56332	0.767886	-0.7336	0.463193	0.981636	chr12	62303069	62306016	+	0	NA	TTS (NM_C TTS (NM_C	44138 NR_147088	9958 Hs. 434951NM_006313:ENSG00000CUSP15	UNPH-2 UN	ubiquitin protein-coding	
chr3-1414	9.384133	-0.56332	0.767886	-0.7336	0.463193	0.981636	chr3	1.41E+08	1.41E+08	+	0	NA	intron (Nintron (N	4050 NM_001355	253461 Hs. 518301NM_152533:ENSG00000ZBTB38	CIBZ PPP1zinc	finger protein-coding	
chr3-1501	7.419601	0.632979	0.862972	0.733488	0.463261	0.981636	chr3	15014270	15015204	+	0	NA	intron (NLIMB3 LIN	50578 NM_002249	64432 Hs. 657764NM_022497:ENSG00000MRP525	MRP-S25 Fmi	topon protein-coding	
chr15-286	10.74255	0.534127	0.728218	0.733471	0.463271	0.981636	chr15	28636754	28637006	+	0	NA	Intergeni Intergeni	-17562 NR_036443	440248 Hs. 531505NM_199045:ENSG00000CHERC2P9	-	hect dom pseudo	
chr17-147	7.588202	-0.63785	0.869809	-0.73332	0.463362	0.981636	chr17	1452427	1452698	+	0	NA	intron (NAIuSx S	3670 NM_016822	1398 Hs. 461896NM_005206:ENSG00000CRK	CRK11 p38 CRK	protc protein-coding	
chr5-1434	11.15279	-0.52517	0.716457	-0.73301	0.463555	0.981636	chr5	14343503	14344520	+	0	NA	intron (Nintron (N	-119972 NR_145815	1.1E+08 NR_145815	SNORD170	-	small nucsnoRNA
chr12-987	7.179443	-0.64739	0.883244	-0.73297	0.463577	0.981636	chr12	98723752	98724106	+	0	NA	intron (Nintron (N	78299 NM_181868	317 Hs. 552567NM_001166:ENSG00000CAPAF1	APAF-1 C	apoptotic protein-coding	
chr13-951	7.179443	-0.64739	0.883244	-0.73297	0.463577	0.981636	chr13	95118407	95118467	+	0	NA	intron (Nintron (N	-92191 NR_145733	1.1E+08 NR_145733	SNORD13G	-	small nucsnoRNA
chr19-488	7.179443	-0.64739	0.883244	-0.73297	0.463577	0.981636	chr19	48847688	48847962	+	0	NA	intron (Nintron (N	-11334 NM_016246	51171 Hs. 18788 NM_016246:ENSG00000HSD17B14	DHR510 SE	hydroxyst protein-coding	
chr21-415	7.179443	-0.64739	0.883244	-0.73297	0.463577	0.981636	chr21	41917935	41918204	+	0	NA	intron (Nintron (N	8634 NM_19905C	25966 Hs. 473894NM_01550C:ENSG00000C2CD2	C21orf25 C2	calcit protein-coding	
chr1-3628	6.946587	0.662339	0.903704	0.732916	0.46361	0.981636	chr1	3628707	3629890	+	0	NA	3' UTR (N3' UTR (N	4283 NM_182752	127262 Hs. 20529 NM_182752:ENSG00000TPRG1L	FAM79A b	tumor prc protein-coding	
chr12-714	6.946587	0.662339	0.903704	0.732916	0.46361	0.981636	chr12	7149197	7151501	+	0	NA	intron (Nintron (N	19978 NM_014718	9746 Hs. 535378NM_014718:ENSG00000CLSTN3	CDHR14 CS	calynter protein-coding	
chr4-2508	6.946587	0.662339	0.903704	0.732916	0.46361	0.981636	chr4	2508693	2508982	+	0	NA	intron (NAIuSp SIN	-26583 NM_001366	8603 Hs. 652364NM_003704:ENSG00000FAM193A	C4orf38 RF	family wiprotein-coding	
chr1-1216	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr1	1216164	1218798	+	0	NA	3' UTR (N3' UTR (N	-3328 NM_003327	7293 Hs. 12978CNM_003327:ENSG00000TNFRSF4	A3orf35 CD1TNF	recep protein-coding	
chr1-7836	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr1	7836425	7839082	+	0	NA	intron (Nintron (N	15312 NM_00678E	10911 Hs. 715862NM_00678E:ENSG00000UTS2	PRO1068 turo	tsinr protein-coding	
chr1-1814	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	intron (NMIRb SINE	2801 NM_00377E	8703 Hs. 321231NM_00377E:ENSG00000B4GALT3	beta4GAL-beta-1,4-	protein-coding	
chr1-1604	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (NLIPA14 L	-23890 NR_036067	NR_036067:ENSG00000MIR3121	mir-3121	microRNA ncRNA	
chr10-92C	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr10	92032193	92033243	+	0	NA	Intergeni Intergeni	108948 NM_003972	9044 Hs. 500526NM_003972:ENSG00000BTAF1	MOT1 TAF	(B-TFIID) protein-coding	
chr11-647	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr11	647630	648533	+	0	NA	intron (Nintron (N	10812 NM_000797	1815 Hs. 99922 NM_000797:ENSG00000DRD4	D4DR	dopamine protein-coding	
chr12-105	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	5279 NM_03230C	84260 Hs. 410924NM_03230C:ENSG00000TCHP	Tpms	trichople protein-coding	
chr14-677	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr14	67771203	67781748	+	0	NA	intron (NMER58A DN	40115 NM_01534E	23503 Hs. 98041 NM_01534E:ENSG00000ZFVYE26	FVYE-CEN1zinc	finger protein-coding	
chr14-735	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr14	73984928	73987574	+	0	NA	intron (Nintron (N	33037 NM_001321	957 Hs. 655077NM_00124E:ENSG00000ENTPD5	CD39L4 N	ectonucle protein-coding	
chr14-915	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr14	91936280	91938155	+	0	NA	intron (Nintron (N	10485 NM_00632E	10516 Hs. 33270E NM_00632E:ENSG00000FBLN5	ADCL2 ARC	fibulin 5 protein-coding	
chr16-222	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr16	22256911	22259312	+	0	NA	intron (Nintron (N	-39264 NM_00125E	55718 Hs. 46029E NM_01811E:ENSG00000POLR3E	RPC5 SIN	RNA polyn protein-coding	
chr17-397	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr17	39714148	39718141	+	0	NA	intron (Nintron (N	-10351 NR_039881	1.01E+08 NR_039881:ENSG00000MIR4728	-	microRNA ncRNA	
chr17-507	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr17	50352403	50355357	+	0	NA	exon (NM exon (NM	7754 NR_11001C	64132 Hs. 46341E NM_022167:ENSG00000XYLT2	PXYLT2 SC	xlyosltr protein-coding	
chr17-82C	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr17	82078495	82082596	+	0	NA	exon (NM exon (NM	9595 NR_132755	1.07E+08 NR_132755	SNORD134	-	small nucsnoRNA
chr19-147	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr19	14095898	14107672	+	0	NA	intron (NAIuSp SIN	6605 NM_001304	5566 Hs. 63163C NM_00273C:ENSG00000PRKACA	PACA PPN	protein k protein-coding	
chr19-374	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr19	37419618	37427849	+	0	NA	intron (NLIME4B L	43711 NM_00133C	148266 Hs. 51184E NM_15248A:ENSG00000ZNF569	ZNF569	ZNF zinc finger protein-coding	
chr19-394	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr19	39451684	39453984	+	0	NA	intron (NAIuSx SIN	7186 NM_00316E	6829 Hs. 631604NM_00316E:ENSG00000SUPT5H	SPT5 SPT5	SPT5 homc protein-coding	
chr2-5552	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr2	55523679	55527384	+	0	NA	intron (Nintron (N	5936 NM_080667	112942 Hs. 26420E NM_080667:ENSG00000CFAP36	BARTL1 CC	ilicilia ancp protein-coding	
chr20-11E	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr20	1163206	1166234	+	0	NA	intron (Nintron (N	19753 NM_018354	55321 Hs. 516834NM_018354:ENSG00000TMEM74B	C20orf46	transment protein-coding	
chr21-462	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr21	46249050	46250090	+	0	NA	intron (Nintron (N	20339 NR_11056E	114044 Hs. 65509E NR_00277E:ENSG00000MCM3AP-AS	C21orf85 MCM3AP	ancRNA	
chr3-1291	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	exon (NM exon (NM	-14989 NM_001204	339122 Hs. 381132NM_19849C:ENSG00000RAB43	RAB11B RAB43,	nc protein-coding	
chr4-107E	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr4	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	26764 NM_005443	9061 Hs. 36861C NM_005443:ENSG00000PAPSS1	ATPSK1 P3'	-phosp protein-coding	
chr7-1404	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (NAIu SINE	10222 NM_01344E	23608 Hs. 74488C NM_01344E:ENSG00000MKRN1	RNF61	makorin 1 protein-coding	
chr9-457E	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr9	4576268	4577298	+	0	NA	intron (Nintron (N	85440 NR_14844E	55064 Hs. 17961E NM_01798E:ENSG00000SPAT6L	C9orf68 t	spermatog protein-coding	
chr9-893	7.443175	0.626435	0.85497	0.732699	0.463742	0.981636	chr9	89338989	89339630	+	0	NA	intron (Nintron (N	20458 NM_00128E	79048 Hs. 59804 NM_024077:ENSG00000SECS1BP2	SBP2	SECS1 bir protein-coding	
chr14-55C	10.75041	0.532582	0.72692	0.732655	0.463769	0.981636	chr14	55035226	55035425	+	0	NA	intron (NTiger10	8089 NM_080867	122809 Hs. 744302NM_080867:ENSG00000SOC5A	SOC5	suppress protein-coding	
chr1-162E	10.26168	0.550606	0.751599	0.732579	0.463815	0.981636	chr1	1.63E+08	1.63E+08	+								

chr19-117	17.13421	0.425306	0.582804	0.729758	0.465538	0.981636	chr19	11776444	11783195	+	0 NA	intron (AluJb SIN	12819	NM_152355	126068	Hs.675132NM_152355	ENSG000002CNF441	-	zinc finger protein-coding
chr1-1008	9.64768	0.558557	0.765896	0.729285	0.465827	0.981636	chr1	1.01E+08	1.01E+08	+	0 NA	intron (intron (N	17397	NM_001003	2135	Hs.357637NM_001003	ENSG000002EXTL2	-	EXTR2 exostosin protein-coding
chr12-827	9.64768	0.558557	0.765896	0.729285	0.465827	0.981636	chr12	827425	827698	+	0 NA	intron (AluSz SIN	74638	NM_213655	65125	Hs.744906NM_014822	ENSG000002WNK1	-	HSAN2 HSA WNK lysin protein-coding
chr15-636	7.99061	0.605006	0.829606	0.729269	0.465837	0.981636	chr15	63631761	63633871	+	0 NA	intron (intron (N	-31989	NR_034088	1E+08	Hs.631162NR_034088	ENSG000002USP3-AS1	-	USP3 antinucRNA
chr16-468	7.99061	0.605006	0.829606	0.729269	0.465837	0.981636	chr16	4681505	4681861	+	0 NA	exon (NM exon (NM	10365	NM_106827	1.02E+08	NR_106827	ENSG000002MIR6769A	-	hsa-mir-6769 microRNA ncRNA
chr3-1946	7.99061	0.605006	0.829606	0.729269	0.465837	0.981636	chr3	1.95E+08	1.95E+08	+	0 NA	intron (L2a LINE	5269	NM_138399	93109	Hs.478722NM_138399	ENSG000002MEM44	-	transmembrane protein-coding
chr1-1111	10.69956	0.524801	0.719709	0.729184	0.465889	0.981636	chr1	1.11E+08	1.11E+08	+	0 NA	intron (intron (N	8067	NR_138483	10390	Hs.363572NM_006099	ENSG000002CEPT1	-	choline esterase protein-coding
chr12-125	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr12	1.24E+08	1.24E+08	+	0 NA	intron (AluSx SIN	18044	NM_012462	23545	Hs.25786 NM_012462	ENSG000002ATP6VOA2	A2 ARCL AATPase H protein-coding	
chr14-751	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr14	75119771	75120368	+	0 NA	intron (intron (N	6979	NM_001325	91754	Hs.7200 NM_033116	ENSG000002CNEK9	-	APUG LCCS NIMA release protein-coding
chr17-315	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr17	61970726	61971349	+	0 NA	intron (AluJb SIN	-43055	NM_001332	57508	Hs.279646NM_020748	ENSG000002INTS2	-	INT2 KIAA integrator protein-coding
chr19-681	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr19	38154250	38154654	+	0 NA	intron (AluSq2 SI	-8644	NR_145800	1.1E+08	NR_145800	SNORD152	-	small nucleolar RNA
chr19-508	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr19	50801383	50802098	+	0 NA	TTS (NR_C TTS (NR_C	681	NR_003066	692204	NR_003066	ENSG000002SNORD88C	-	HBIT-180C small nucleolar RNA
chr5-171	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr5	1.71E+08	1.71E+08	+	0 NA	intron (MER41 int	193261	NM_022897	64901	Hs.410811NM_022897	ENSG000002RANBP17	-	RAN binding protein-coding
chr6-1498	5.880099	-0.70063	0.961159	-0.72895	0.466034	0.981636	chr6	1.5E+08	1.5E+08	+	0 NA	intron (AluJr4 SI	55257	NM_001360	5110	Hs.279257NM_005389	ENSG000002PCMT1	-	PIMT protein-ligase protein-coding
chr10-962	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr10	96543416	96544783	+	0 NA	exon (NM exon (NM	-30173	NM_012465	7093	Hs.154299NM_012465	ENSG000002TLL2	-	toll-like receptor protein-coding
chr11-276	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr11	27661600	27662136	+	0 NA	intron (intron (N	-2219	NM_001143	627	Hs.502182NM_001143	ENSG000002BDNF	-	ANON2 BUB brain derived protein-coding
chr12-477	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr12	47695907	47696544	+	0 NA	intron (intron (N	9805	NM_024604	79657	Hs.437855NM_024604	ENSG000002CRPAP3	-	Tah1 hSpa RNA polymerase protein-coding
chr15-576	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr15	57281450	57284460	+	0 NA	intron (intron (N	-4298	NR_145748	1.1E+08	NR_145748	ENSG000002SNORD13D	-	small nucleolar RNA
chr2-372	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr2	37208867	37214562	+	0 NA	intron (intron (N	15218	NM_001322	1.01E+08	Hs.666956NM_001322	ENSG000002CEBPZOS	-	CEBPZ-AS1 CEBPZ opf protein-coding
chr2-556	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr2	55654056	55654426	+	0 NA	intron (AluSx4 SI	-36619	NM_020465	57223	Hs.516182NM_020465	ENSG000002PPP4R3B	-	FLFL2 PP4 protein tyrosine kinase protein-coding
chr2-652	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr2	65268043	65272884	+	0 NA	3' UTR (3' UTR (N	42768	NM_001100	10097	Hs.643727NM_005722	ENSG000002ACTR2	-	ARP2 actin regulator protein-coding
chr2-2377	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr2	2.38E+08	2.38E+08	+	0 NA	intron (intron (N	-39758	NM_001080	375316	Hs.607266NM_198855	ENSG000002RBM44	-	RNA binding protein-coding
chr21-293	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr21	29362211	29363408	+	0 NA	TTS (NR_C TTS (NR_C	-9692	NR_046564	1.01E+08	Hs.326404NR_046564	BACH1-IT2	-	BACH1 intron ncRNA
chr3-5261	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr3	52615418	52617271	+	0 NA	intron (intron (N	69255	NM_001350	55193	Hs.189922NM_018166	ENSG000002PBRM1	-	BAF180 PF polycomb protein-coding
chr4-754	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr4	75498470	75500742	+	0 NA	intron (L1MA4 LIN	9690	NR_103725	25898	Hs.48297 NM_015436	ENSG000002RCHY1	-	ARNIP CH ring finger protein-coding
chr5-278	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr5	72879069	72880228	+	0 NA	TTS (NR_C TTS (NR_C	1057	NR_039966	1.01E+08	NR_039966	ENSG000002MIR4804	-	microRNA ncRNA
chr5-1518	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr5	1.52E+08	1.52E+08	+	0 NA	intron (AluSx3 SI	-31127	NR_132345	1.01E+08	Hs.587054NM_001278082	LOC100652	-	uncharacterized ncRNA
chr5-177	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr5	1.78E+08	1.78E+08	+	0 NA	intron (intron (N	-18284	NM_016222	51428	Hs.484288NM_016222	ENSG000002DDX41	-	ABS MLP PF DEAD-box protein-coding
chr6-875	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr6	87567371	87568670	+	0 NA	intron (AluSc8 SI	21967	NM_020322	57038	Hs.485911NM_020322	ENSG000002RARS2	-	ArgRS DAL arginyl-tRNA-protein-coding
chr6-1444	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr6	14447631	14448408	+	0 NA	intron (AluSx SIN	83780	NR_132778	1.07E+08	NR_132778	SNORA98	-	small nucleolar RNA
chr6-151	7.648757	-0.61362	0.84188	-0.72887	0.466082	0.981636	chr6	1.51E+08	1.51E+08	+	0 NA	exon (NM exon (NM	23936	NM_001370	9590	Hs.371242NM_005100	ENSG000002AKAP12	-	AKAP250 SA-kinase protein-coding
chr14-30	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr14	30597702	30598273	+	0 NA	intron (intron (N	-20630	NR_151723	1.05E+08	Hs.603989NR_151723	ENSG000002G2E3-AS1	-	CAT1647 G2E3 antinucRNA
chr14-905	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr14	90315645	90316744	+	0 NA	intron (intron (N	15747	NM_001797	55051	Hs.528131NM_001797	ENSG000002NRDE2	-	C14orf102 NRDE-2, r protein-coding
chr17-366	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr17	3661454	3662949	+	0 NA	TTS (NM_C TTS (NM_C	6377	NM_014604	30851	Hs.12956 NM_014604	ENSG000002TAX1BP3	-	TIP-1 TIF Tax1 binc protein-coding
chr17-161	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr17	16107593	16108129	+	0 NA	intron (AluY SINE	46235	NR_145787	1.1E+08	NR_145787	SNORD163	-	small nucleolar RNA
chr19-115	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr19	11599367	11601208	+	0 NA	intron (AluY SINE	2804	NM_145295	199692	Hs.526666NM_145295	ENSG000002ZNF627	-	zinc finger protein-coding
chr19-525	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr19	52592194	52595094	+	0 NA	Intergeni SVA_D Ret	-3040	NR_023311	7696	Hs.373646NM_003438	ZNF137P	-	ZNF137 pf zinc finger pseudo
chr2-691	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr2	69165530	69166717	+	0 NA	intron (NL4_A_Mam	62441	NR_036073	1E+08	NR_036073	ENSG000002MIR3126	-	mir-3126 microRNA ncRNA
chr2-1137	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr2	1.14E+08	1.14E+08	+	0 NA	exon (NM exon (NM	-1758	NR_039944	1.01E+08	NR_039944	ENSG000002MIR4782	-	microRNA ncRNA
chr5-1474	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr5	1.47E+08	1.47E+08	+	0 NA	intron (intron (N	52564	NM_001387	1809	Hs.519655NM_001387	ENSG000002DPYSL3	-	CRMP-4 CF dihydropyridine protein-coding
chr8-132	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr8	1.32E+08	1.32E+08	+	0 NA	non-coding-non-coding	46657	NM_001088	729330	Hs.653174NM_001088	ENSG000002OC90	-	PLA2L otoconin protein-coding
chr8-140	5.913381	-0.69385	0.952681	-0.72831	0.466422	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	intron (AluJr SIN	56431	NM_001164	27161	Hs.660189NM_001164	ENSG000002AG02	-	CASC7 EIF argonaute protein-coding
chr1-193	7.402035	0.625434	0.859241	0.727891	0.466681	0.981636	chr1	19382498	19382738	+	0 NA	intron (intron (N	70292	NM_001040	54896	Hs.647622NM_017766	ENSG000002SLC66A1	-	LAAT-1 L soluble cytochrome protein-coding
chr17-161	7.402035	0.625434	0.859241	0.727891	0.466681	0.981636	chr17	16198456	16198661	+	0 NA	intron (AluSp SIN	-3919	NM_001190	9611	Hs.462322NM_006311	ENSG000002NCOR1	-	N-CoR N-C nuclear receptor protein-coding
chr19-19	7.402035	0.625434	0.859241	0.727891	0.466681	0.981636	chr19	19648989	19649819	+	0 NA	intron (intron (N	-5747	NM_016573	51291	Hs.49427 NM_016573	ENSG000002GMIP	-	ARHGAP46 GEM interprotein-coding
chr3-566	7.402035	0.625434	0.859241	0.727891	0.466681	0.981636	chr3	56638209	56639142	+	0 NA	intron (intron (N	25371	NM_015224	23272	Hs.116877NM_015224	ENSG000002TASOR	-	C3orf63 F transcriptase protein-coding
chr7-924	7.402035	0.625434	0.859241	0.727891	0.466681	0.981636	chr7	92490799	92491616	+	0 NA	intron (intron (N	-13246	NM_001133	30816	NR_014590	ENSG000002ERVW-1	-	ENV ENVW endogenous protein-coding
chr7-129	7.402035	0.625434	0.859241	0.727891	0.466681	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (FAM SINE	13785	NM_003344	7328	Hs.643546NM_003344	ENSG000002CUBE2H	-	E2-20K G tubiquitin protein-coding
chr2-6124	11.57131	-0.50966	0.700198	-0.72787	0.466691	0.981636	chr2	61240692	61241370	+	0 NA	intron (intron (N	63613	NR_152211	130872	Hs.655602NM_152392	ENSG000002AHS2P	-	AHA1 AHS activator pseudo
chr1-184	10.68385	0.527865	0.725344	0.72745	0.46677	0.981636	chr1	1.85E+08	1.85E+08	+	0 NA	exon (NM exon (NM	48163	NM_001315	80267	Hs.523811NM_025191	ENSG000002EDEM3	-	Clorf22 ER degrad protein-coding
chr16-447	7.982752	0.60712	0.834334	0.72767	0.466816	0.981636	chr16	47503077	47504058	+	0 NA	intron (AluSc SIN	42236	NM_001031	5257	Hs.78060 NM_000295	ENSG000002PKHK	-	phosphorylation protein-coding
chr11-43	7.409893	0.623274	0.85664	0.72758	0														



chr1-1514 7.957329	0.602018	0.830856	0.724576	0.468712	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	950 NM_207171	23126 Hs. 489875	NR_01510C	ENSG000003POGZ	MRD37 WHS	pogo trar protein-coding
chr16-507 7.957329	0.602018	0.830856	0.724576	0.468712	0.981636	chr16	50783336	50784012	+	0 NA	intron (NAluSx SIN	-22998 NR_146575	1.05E+08	NR_146575	ENSG000003LINC02166	-	long intncRNA
chr16-748 7.957329	0.602018	0.830856	0.724576	0.468712	0.981636	chr16	74884433	74885047	+	0 NA	intron (Nl2c LINE	100383 NM_030581	79726 Hs. 280951	NM_030581	ENSG000003WDR59	CDW12 FPF	WD repeat protein-coding
chr18-361 7.957329	0.602018	0.830856	0.724576	0.468712	0.981636	chr18	36115938	36116710	+	0 NA	intron (NLMC4 LIN	13016 NM_012319	25800 Hs. 79136	NM_012319	ENSG000003SLC39A6	LIV-1 ZIF	solute c protein-coding
chr1-1481 10.67414	0.520972	0.719081	0.724497	0.468761	0.981636	chr1	1.48E+08	1.48E+08	+	0 NA	intron (Nl1P2 LINE	22359 NM_001101	20030 Hs. 721558	NR_183372	ENSG000003NBPF1	NBPF24	NBPF mem protein-coding
chr1-1514 10.67414	0.520972	0.719081	0.724497	0.468761	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	exon (NM exon (NM	7434 NM_002796	5692 Hs. 89545	NM_002796	ENSG000003PSMB4	HN3 HsN3	proteasome protein-coding
chr1-1567 10.67414	0.520972	0.719081	0.724497	0.468761	0.981636	chr1	1.57E+08	1.57E+08	+	0 NA	intron (Nintron (N	-21465 NM_001007	4914 Hs. 406293	NR_002525	ENSG000003NTRK1	MTC TRK	neurotrophin protein-coding
chr1-2226 10.67414	0.520972	0.719081	0.724497	0.468761	0.981636	chr1	2.23E+08	2.23E+08	+	0 NA	intron (Nintron (N	8572 NM_001300	375056 Hs. 118474	NR_198551	ENSG000003MIA3	ARNT D3C2MIA	SH3 c protein-coding
chr1-2578 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr1	25783379	25783902	+	0 NA	intron (Nintron (N	-16553 NM_206926	57190 Hs. 32339	NR_020451	ENSG000003SELENON	CFTD MDR5	selenoprotein-coding
chr10-145 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr10	45975421	45978514	+	0 NA	intron (NLMB8 LIN	4478 NM_006327	1E+08 Hs. 52430	NR_006327	ENSG000003TIMM23	TIM23	translocase protein-coding
chr10-127 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr10	69689 NM_001035	642938 Hs. 61388	NR_001035	ENSG000003INSY2A	642938 Hs. 61388	NR_001035	ENSG000003INSY2A	C10orf14	inhibitor protein-coding		
chr11-103 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr11	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	14685 NM_001318	84259 Hs. 50371	NR_032299	ENSG000003DCUN1D5	SCCR05	defective protein-coding
chr11-106 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr11	1.06E+08	1.06E+08	+	0 NA	intron (Nintron (N	-2620 NM_001330	143879 Hs. 10194	NR_152433	ENSG000003KBTBD3	BKLBH3	kelch repeat protein-coding
chr14-305 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr14	30904142	30906837	+	0 NA	exon (NM exon (NM	-15681 NR_038356	1.01E+08 Hs. 72919	NR_038356	ENSG000003LOC1005006	-	uncharacterized ncRNA
chr15-226 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr15	22672168	22675652	+	0 NA	intron (NMLT1A LTF	9171 NR_003521	339005 Hs. 21267	NR_003521	WHAMMP3	WHAMML1 WAS	proteasome pseudo
chr17-307 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr17	30759357	30762019	+	0 NA	intron (Nintron (N	51080 NR_144399	440423 Hs. 62888	NR_024187	SUZ12P1	SUZ12P	SUZ12 pseudo
chr18-363 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr18	36227362	36228255	+	0 NA	intron (Nl1PA13 LI	40311 NM_017947	55034 Hs. 40502	NR_017947	ENSG000003MOCOS	HMC5 MCS	molybdenum protein-coding
chr19-344 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr19	34351867	34352091	+	0 NA	intron (NAluJr4 SI	-12761 NM_001184	2821 Hs. 46647	NR_000177	ENSG000003GPI	AMF GNP1	glucose-6-phosphate protein-coding
chr2-3858 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr2	38580166	38581643	+	0 NA	intron (Nintron (N	22024 NM_138394	92906 Hs. 44549	NR_138394	ENSG000003HNRNPLL	HNRNPLL SF	heterogeneous protein-coding
chr3-9965 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr3	99691909	99692231	+	0 NA	intron (Nintron (N	53476 NM_003551	1295 Hs. 65454	NR_001850	ENSG000003COL8A1	C3orf7	collagen protein-coding
chr3-1207 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr3	1.21E+08	1.21E+08	+	0 NA	intron (Nl1PA3 LIN	4992 NM_005513	2960 Hs. 44527	NR_005513	ENSG000003GTF2E1	FE TF2E1	general transcription factor-coding
chr3-1237 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (NAluJo SIN	40390 NR_046625	1.01E+08 Hs. 66731	NR_046625	ENSG000003MYLK-AS2	-	MYLK antncRNA
chr3-1884 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr3	1.88E+08	1.88E+08	+	0 NA	intron (Nl1PA7 LIN	123587 NR_046625	1.01E+08 Hs. 67499	NR_046625	ENSG000003LPP-AS1	-	LPP antisense ncRNA
chr5-3618 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr5	36182555	36185248	+	0 NA	exon (NM exon (NM	31790 NM_032637	6502 Hs. 52348	NR_005983	ENSG000003SKP2	FBL1 FBX1	S-phase kinase protein-coding
chr5-1135 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr5	1.14E+08	1.14E+08	+	0 NA	intron (Nl1PA11 LI	59827 NM_001345	64848 Hs. 23194	NR_022828	ENSG000003YTHDC2	CAHL HYTH	YTH domain protein-coding
chr7-1027 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr7	1.03E+08	1.03E+08	+	0 NA	intron (Nl1PA4 LIN	32279 NM_001145	22234 Hs. 20254	NR_147194	ENSG000003FAM185A	-	family wiprotein-coding
chr7-1212 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr7	1.21E+08	1.21E+08	+	0 NA	intron (Nl2b LINE	-56615 NM_016087	51384 Hs. 27237	NR_016087	ENSG000003WNT16	-	Wnt family protein-coding
chr9-6015 7.640899	-0.61198	0.844727	-0.72447	0.468774	0.981636	chr9	6013672	6014338	+	0 NA	exon (NM exon (NM	1619 NM_001243	26953 Hs. 16749	NR_012411	ENSG000003RANBP6	-	RAN binding protein-coding
chr21-348 9.853447	-0.54154	0.747598	-0.72437	0.46884	0.981636	chr21	34848183	34848687	+	0 NA	intron (Nintron (N	40264 NM_001001	861 Hs. 14926	NR_001754	ENSG000003RUNX1	AML1 AML1	RUNX family protein-coding
chr5-9552 9.853447	-0.54154	0.747598	-0.72437	0.46884	0.981636	chr5	95528149	95529686	+	0 NA	intron (Nintron (N	26088 NM_014638	9652 Hs. 48286	NR_014638	ENSG000003TTC37	KIAA0372	tetratricopeptide protein-coding
chr8-131 9.853447	-0.54154	0.747598	-0.72437	0.46884	0.981636	chr8	13105860	13108328	+	0 NA	intron (Nintron (N	9150 NM_001164	10395 Hs. 13429	NR_006094	ENSG000003DLCL1	ARHGAP7 DLCL1	Rho protein-coding
chr1-1565 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr1	15695662	15695365	+	0 NA	intron (NAluJb SIN	11688 NM_015164	23207 Hs. 64677	NR_015164	ENSG000003PLEKHM2	SKPIN	pleckstrin protein-coding
chr13-326 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr13	32653155	32655455	+	0 NA	intron (Nintron (N	67858 NM_015032	23047 Hs. 74490	NR_015032	ENSG000003PDS5B	ARLIP ASE	PDS5 cohesin protein-coding
chr16-435 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr16	4396952	4397769	+	0 NA	intron (NAluSz SIN	18537 NM_001351	79585 Hs. 43795	NR_024533	ENSG000003COR07	O61001 B1	coronin 7 protein-coding
chr17-355 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr17	35354661	35355141	+	0 NA	intron (Nintron (N	18720 NM_001104	91607 Hs. 74505	NR_152270	ENSG000003SLFN11	SLFN8/9	schlafen protein-coding
chr2-1774 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr2	17729667	17773956	+	0 NA	intron (Nintron (N	19323 NM_001130	34854 Hs. 50499	NR_017855	ENSG000003GEN1	Gen	GEN1 Holliday junction protein-coding
chr2-3055 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr2	30550844	30552750	+	0 NA	intron (NMLT1D LTF	104551 NM_001304	253558 Hs. 46804	NR_182551	ENSG000003CLAT1	1AGPAT8 A	lysocardiolipin protein-coding
chr2-281 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr2	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	73149 NR_0027671	56886 Hs. 74330	NR_020120	ENSG000003UGGT1	HUGT1 UGR	UDP-glucuronosyltransferase-coding
chr20-635 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr20	63505227	63509805	+	0 NA	intron (Nintron (N	671 NM_001199	54963 Hs. 50499	NR_017855	ENSG000003UCKL1	UCKL1 URK	uridine-5-phosphate protein-coding
chr4-8481 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr4	84816184	84817525	+	0 NA	intron (NMIRb SINE	-148762 NR_152774	404201 Hs. 46730	NR_205857	ENSG000003WDFY3-AS2	C4orf12 F	WDFY3 antisense ncRNA
chr6-149 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr6	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	-8246 NR_077247	645958 Hs. 63261	NR_077247	RPS18P9	RPS18	ribosomal pseudo
chr6-1571 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr6	1.57E+08	1.57E+08	+	0 NA	intron (Nintron (N	130987 NR_001363	57492 Hs. 29158	NR_017511	ENSG000003ARID1B	GAG3-5 BAF	AT-ribosome protein-coding
chr8-3844 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr8	38449759	38450575	+	0 NA	intron (Nintron (N	17557 NM_001174	2260 Hs. 26488	NR_015850	ENSG000003FGFR1	BFGFR CD	fibroblast growth factor-coding
chr8-1233 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (NAluJr4 SI	-26126 NR_037511	1.01E+08 Hs. NR_037511	ENSG000003MIR548A1	-	microRNA ncRNA	
chrX-1475 4.179855	-0.82183	1.134615	-0.72432	0.468868	0.981636	chrX	1.48E+08	1.48E+08	+	0 NA	intron (NmamTip2 S	32095 NM_001185	2332 Hs. 10318	NR_020204	ENSG000003FMR1	FMRP FRA	fragile X protein-coding
chr17-804 5.254385	-0.746747	1.031022	-0.72429	0.468895	0.981636	chr17	80419551	80420085	+	0 NA	TTS (NR_TTS (NR_C	400 NR_039883	1.01E+08 Hs. NR_039883	ENSG000003MIR4730	-	microRNA ncRNA	
chr2-2082 5.254385	-0.746747	1.031022	-0.72429	0.468895	0.981636	chr2	2.08E+08	2.08E+08	+	0 NA	intron (NMIRb SINE	11920 NM_001282	3417 Hs. 59342	NR_005899	ENSG000003IDH1	HEL-216 E	isocitrate dehydrogenase-coding
chr19-597 7.171585	-0.64542	0.891607	-0.72389	0.469136	0.981636	chr19	57931652	57931851	+	0 NA	intron (NAluJr SINE	3651 NM_001317	147686 Hs. 66072	NR_133460	ENSG000003ZNF418	-	zinc finger protein-coding
chr4-190 7.171585	-0.64542	0.891607	-0.72389	0.469136	0.981636	chr4	19										



chr2-3333	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr2	33335366	33336173	+	0 NA	intron (Nintron (N	-82747 NR_039628	1.01E+08	NR_039628	ENSG00000MIR4430	-	microRNA ncRNA
chr2-1444	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr2	1.44E+08	1.44E+08	+	0 NA	intron (NMIR SINE	-86050 NM_001354	79712	Hs. 44780	NR_024656	ENSG00000GTD1C1	Hmat-Xa nglycosyl protein-coding
chr2-171	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr2	1.71E+08	1.71E+08	+	0 NA	intron (Nintron (N	-12020 NM_001136	9874	Hs. 744917NM_01229C	ENSG00000CTLK1	PKU-beta tousled lprotein-coding	
chr2-182	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr2	1.83E+08	1.83E+08	+	0 NA	intron (Nintron (N	49063 NM_013436	10787	Hs. 603732NM_01343C	ENSG00000NCKAP1	HEM2 NAP NCK assoc protein-coding	
chr21-29	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr21	29037248	29040933	+	0 NA	exon (NM exon (NM	14422 NM_006447	10600	Hs. 99819	NR_006447	ENSG00000USP16	UBP-MUB ubiquitin protein-coding
chr3-239	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr3	23954880	23956083	+	0 NA	intron (Nintron (N	9360 NM_001145	9975	Hs. 37288	NR_00512C	ENSG00000CNR1D2	BD73 EAR-nuclear rprotein-coding
chr4-564	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr4	56450897	56454541	+	0 NA	intron (Nintron (N	-14898 NM_001267	6731	Hs. 237822NM_006947	ENSG00000SRP72	BMFF EMFS signal rprotein-coding	
chr4-942	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr4	94285059	94286376	+	0 NA	intron (Nintron (N	32408 NM_001254	56916	Hs. 414006NM_02015C	ENSG00000SMARCAD1	ADERM BAS SWI SNF-1 protein-coding	
chr4-105	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr4	1.06E+08	1.06E+08	+	0 NA	intron (NAluSz SIN	16246 NM_020395	57117	Hs. 480454NM_02039C	ENSG00000INTS12	INT12 PHF integrat protein-coding	
chr5-6917	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr5	69172135	69178131	+	0 NA	intron (Nintron (N	7983 NM_031966	891	Hs. 23960	NR_031966	ENSG00000CCNB1	CCNB cyclin B protein-coding
chr5-874	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr5	87402317	87403741	+	0 NA	intron (Nintron (N	9875 NM_001195	902	Hs. 292524NM_00123C	ENSG00000CCNH	CAK CycH cyclin H protein-coding	
chr5-177	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	3' UTR (N3' UTR (N	6626 NM_001031	53917	Hs. 16258	NR_130781	ENSG00000CRAB24	- RAB24, m protein-coding
chr6-333	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr6	33300475	33301571	+	0 NA	3' UTR (N3' UTR (N	-1635 NM_001243	5863	Hs. 509622NM_004761	ENSG00000RGL2	HKE1.5 KFR sol guanine protein-coding	
chr8-645	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr8	23544098	23544591	+	0 NA	intron (Nintron (N	15571 NM_001317	51312	Hs. 596022NM_01661C	ENSG00000SLC25A37	HTO15 MF soluble c protein-coding	
chr9-6487	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chr9	6487996	6488507	+	0 NA	intron (NAluJb SIN	75052 NM_15289C	115426	Hs. 493401NM_15289C	ENSG00000UHRP2	NIRP RNF ubiquitin protein-coding	
chrX-123	5.897665	-0.68976	0.956857	-0.72086	0.470996	0.981636	chrX	1.24E+08	1.24E+08	+	0 NA	intron (NAluSj SIN	32227 NM_001167	331	Hs. 356077NM_001167	ENSG00000XIAP	AP13 BIRC-X-linked protein-coding	
chr11-68	9.309712	-0.57032	0.791247	-0.72079	0.471041	0.981636	chr11	68034257	68034599	+	0 NA	TTS (NR_C TTS (NR_C	531 NR_03984C	NR_03984C	ENSG00000MIR4691	mir-4691 microRNA ncRNA		
chr1-155	10.682	0.51947	0.720781	0.720704	0.471092	0.981636	chr1	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	3071 NR_024117	1E+08	Hs. 656361NR_024117	MSTO2P	MSTO2 misato f pseudo	
chr1-155	10.682	0.51947	0.720781	0.720704	0.471092	0.981636	chr1	1.56E+08	1.56E+08	+	0 NA	intron (Nintron (N	9510 NR_132762	1.07E+08	NR_132762	SCARNA26A	- small CA ncRNA	
chr1-2051	10.682	0.51947	0.720781	0.720704	0.471092	0.981636	chr1	2.05E+08	2.05E+08	+	0 NA	intron (Nintron (N	-36113 NM_001193	5929	Hs. 519232NM_005057	ENSG00000RBBP5	RBQ3 SWD1RB bindir protein-coding	
chr12-132	10.682	0.51947	0.720781	0.720704	0.471092	0.981636	chr12	1.33E+08	1.33E+08	+	0 NA	intron (NLA_A Mam	11449 NM_183238	1E+08	Hs. 29698	NR_183238	ENSG00000ZNF605	1E+08 Hs. 29698
chr19-44	10.682	0.51947	0.720781	0.720704	0.471092	0.981636	chr19	44061063	44067853	+	0 NA	intron (Nintron (N	-7701 NM_001037	342909	Hs. 445395NM_001037	ENSG00000ZNF284	ZNF284L zinc fing protein-coding	
chr14-10	6.921163	0.656394	0.910775	0.720698	0.471095	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	53701 NM_006035	9578	Hs. 654634NM_00603C	ENSG00000CDC42BPB	MRCBK CDC42 bir protein-coding	
chr1-169	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr1	1.7E+08	1.7E+08	+	0 NA	intron (Nintron (N	24636 NM_020423	57147	Hs. 435566NM_02042C	ENSG00000SCYL3	PACE-1 PASCY1 like protein-coding	
chr11-104	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr11	10462144	10465204	+	0 NA	intron (Nintron (N	2543 NM_001172	272	Hs. 501896NM_00048C	ENSG00000AMPD3	- adenosine protein-coding	
chr11-45	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr11	45880622	45889091	+	0 NA	intron (Nintron (N	-4845 NM_005456	9479	Hs. 234245NM_00545C	ENSG00000MAPK8IP1	IB1 JIP-1 mitogen- protein-coding	
chr11-12	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr11	1.3E+08	1.3E+08	+	0 NA	intron (NLA_A Mam	17771 NM_00616E	4798	Hs. 530525NM_00616C	ENSG00000FRBK	IN080G nuclear f protein-coding	
chr17-29	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr17	29655288	29656108	+	0 NA	intron (Nintron (N	-34275 NM_032854	84940	Hs. 143045NM_03285C	ENSG00000COR06	- coronin f protein-coding	
chr18-70	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr18	70102876	70103177	+	0 NA	intron (NSVA_A Ret	102661 NM_001318	25914	Hs. 654809NM_17363C	ENSG00000RTTN	MSSP rotatin protein-coding	
chr19-39	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr19	39369486	39370741	+	0 NA	exon (NM exon (NM	20993 NM_00125E	54623	Hs. 466714NM_01908C	ENSG00000PAF1	PAF1 hom protein-coding	
chr6-30	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr6	30329884	30331591	+	0 NA	intron (Nintron (N	1426 NM_001195	202658	Hs. 413493NM_001195	ENSG00000TRIM39-RF	TRIM39R TRIM39-RF protein-coding	
chr6-37	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr6	37473878	37475767	+	0 NA	intron (Nintron (N	25071 NM_138499	154647	Hs. 284207NM_13849C	ENSG00000CCDC167	G6orf129 coiled-c protein-coding	
chr7-12	7.939763	0.594938	0.825666	0.720555	0.471183	0.981636	chr7	1.29E+08	1.29E+08	+	0 NA	IntergeniAluSz SIN	-30964 NR_024368	402483	Hs. 722355NM_001039682	LINC0100C	long intcncRNA	
chr1-16	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr1	16393741	16394625	+	0 NA	intron (NCR1_Mam I	26941 NR_073501	26099	Hs. 252967NM_001114	ENSG00000CZRDI	C1orf144 SUZ RNA t protein-coding	
chr1-19	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr1	19324003	19324959	+	0 NA	intron (Nintron (N	12155 NM_00104C	54896	Hs. 647622NM_01776C	ENSG00000SLC66A1	LAAT-1 L soluble c protein-coding	
chr1-22	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr1	2.24E+08	2.24E+08	+	0 NA	intron (NAluSg SIN	17096 NR_031574	1E+08	NR_031574	ENSG00000MIR320B2	MIR320B-2 microRNA ncRNA	
chr11-87	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr11	8784601	8784800	+	0 NA	intron (NAluSx SIN	15922 NR_12059C	1.03E+08	Hs. 613277NR_120590	LOC102724	- uncharact ncRNA	
chr11-64	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr11	64789456	64789955	+	0 NA	intron (Nintron (N	-10882 NM_20199E	7536	Hs. 502825NM_00463C	ENSG00000SF1	BBP D115E splicing protein-coding	
chr11-7	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr11	78218632	78219251	+	0 NA	3' UTR (N3' UTR (N	30022 NM_02079E	5758	Hs. 531245NM_02079C	ENSG00000USP35	- ubiquitin protein-coding	
chr12-11	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr12	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	16552 NM_00684C	10993	Hs. 439022NM_00684C	ENSG00000SDS	SDH serine d protein-coding	
chr13-11	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr13	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	21836 NM_005561	3916	Hs. 494415NM_005561	ENSG00000LAMP1	CDI07a L lysosomal protein-coding	
chr16-34	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr16	3448033	3449144	+	0 NA	intron (Nintron (N	4908 NM_00108C	79903	Hs. 513292NM_02484C	ENSG00000NA60	HAT4 NAT1N(alpha)- protein-coding	
chr19-56	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr19	56605727	56606117	+	0 NA	intron (Nintron (N	10620 NM_00137C	58491	Hs. 301431NM_02121C	ENSG00000ZNF71	EZF1T zinc fing protein-coding	
chr2-13	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr2	1.32E+08	1.32E+08	+	0 NA	intron (Nintron (N	-8186 NM_00125E	90557	Hs. 351461NM_13877C	ENSG00000CCDC74A	- coiled-c protein-coding	
chr9-10	5.19568	0.735154	1.020517	0.720374	0.471295	0.981636	chr9	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	59697 NM_00550C	19	Hs. 659274NM_00550C	ENSG00000ABCA1	ABC-1 ABCAT bindir protein-coding	
chr2-42	7.682039	-0.6085	0.845067	-0.72006	0.471488	0.981636	chr2	42316247	42319282	+	0 NA	intron (Nintron (N	42274 NR_13494F	9167	Hs. 339635NM_00471C	ENSG00000COX7A2L	COX7AR C cytochrome protein-coding	
chr2-61	7.682039	-0.6085	0.845067	-0.72006	0.471488	0.981636	chr2	61280687	61282242	+	0 NA	intron (NAluSz6 SI	104046 NR_152211	130872	Hs. 655602NM_15239C	ENSG00000AHSAP2P	AHA1 AHS activator pseudo	
chr22-42	7.682039	-0.6085	0.845067	-0.72006	0.471488	0.981636	chr22	42578232	42580288	+	0 NA	intron (Nintron (N	2751 NR_002184	91695	Hs. 534041NR_002184	ENSG00000RRP7BP	RRP7B dJ2 ribosomal pseudo	
chr3-51	7.682039	-0.6085	0.845067	-0.72006	0.471488	0.981636	chr3	43569	43569	+	0 NA	intron (NLI PA4 LIN	43569 NM_001171	9730	Hs. 716622NM_01470C	ENSG00000DCAF1	RIP VPRB DBD1 and protein-coding	

chr9-1217.7.947621	0.592923	0.825806	0.717993	0.472761	0.981636	chr9	1.22E+08	1.22E+08	0	NA	intron (NLM5 LINE	24212 NM_138709	153090 Hs. 52237ENR_032552	ENSG000003DAB2IP	AF9Q34 AIDAB2	intcprotein-coding	
chrX-3115.7.947621	0.592923	0.825806	0.717993	0.472761	0.981636	chrX	311951	313009	0	NA	intron (Nintron (N	6339 NM_012227	8225 Hs. 43714ENR_012227	ENSG000003GTPBP6	PGPL	GTP bindi protein-coding	
chrX-4063.7.947621	0.592923	0.825806	0.717993	0.472761	0.981636	chrX	40634116	40639680	0	NA	intron (Nintron (N	10663 NM_14497C	159013 Hs. 495961NM_14497C	ENSG000003CXorf38	-	chromoson protein-coding	
chr7-1248.4.146573	-0.81382	1.15874	-0.71787	0.47284	0.981636	chr7	1.25E+08	1.25E+08	0	NA	intron (Nintron (N	-60582 NM_001024	154872 Hs. 44416ENR_001024	ENSG000003C7orf77	-	chromoson protein-coding	
chr2-9855.10.64871	0.517138	0.720427	0.717821	0.472868	0.981636	chr2	9855054	9851087	0	NA	intron (Nintron (N	7321 NM_005688	9014 Hs. 58483ENR_005688	ENSG000003TAF1B	MGC:9349 TATA-box	protein-coding	
chr9-1228.10.64871	0.517138	0.720427	0.717821	0.472868	0.981636	chr9	1.23E+08	1.23E+08	0	NA	3' UTR (N3' UTR (N	-18610 NM_005388	5082 Hs. 27174ENR_005388	ENSG000003PDCL	PhLP	phosducin protein-coding	
chr21-437.9.655538	0.556662	0.775498	0.717812	0.472873	0.981636	chr21	43724209	43724470	0	NA	intron (Nintron (N	5210 NM_003681	8566 Hs. 284491NM_003681	ENSG000003PDXK	C2orf124 pyridoxal	protein-coding	
chr9-1208.9.655538	0.556662	0.775498	0.717812	0.472873	0.981636	chr9	1.23E+08	1.23E+08	0	NA	intron (Nintron (N	11104 NM_001325	26995 Hs. 63268ENR_001325	ENSG000003TRUB2	CLONE2492 Trub	psen protein-coding	
chr11-978.8.580083	0.603325	0.840513	0.717805	0.472878	0.981636	chr11	9787160	9787359	0	NA	intron (Nintron (N	-27726 NR_033972	440028 Hs. 677541NR_033972	ENSG000003LINC02705	-	long intcncRNA	
chr15-297.9.894587	-0.53894	0.751022	-0.71761	0.472999	0.981636	chr15	29769460	29770360	0	NA	intron (Ntigger 3b	50764 NM_001355	7082 Hs. 74399ENR_003257	ENSG000003TJPI	ZO-1	tight jur protein-coding	
chr4-1688.9.894587	-0.53894	0.751022	-0.71761	0.472999	0.981636	chr4	1.69E+08	1.69E+08	0	NA	intron (Nintron (N	23370 NM_001367	23022 Hs. 15122ENR_016081	ENSG000003PALLD	CGI-151 C	calladin, protein-coding	
chr13-454.7.633041	-0.61031	0.850679	-0.71744	0.473105	0.981636	chr13	45483294	45484887	0	NA	intron (Nintron (N	19151 NM_031431	83548 Hs. 50794ENR_031431	ENSG000003COG3	SEC34	component protein-coding	
chr14-92.7.633041	-0.61031	0.850679	-0.71744	0.473105	0.981636	chr14	92005118	92005614	0	NA	exon (NM exon (NM	34693 NM_004235	9321 Hs. 63233ENR_004235	ENSG000003TRIP11	ACG1A CEV	thyroid l protein-coding	
chr15-671.7.633041	-0.61031	0.850679	-0.71744	0.473105	0.981636	chr15	67129020	67129924	0	NA	intron (NMER44 DN	3756 NM_001145	4088 Hs. 72798ENR_005902	ENSG000003SMAD3	HSP193 F	MSTF fami protein-coding	
chr16-898.7.633041	-0.61031	0.850679	-0.71744	0.473105	0.981636	chr16	89895973	89896433	0	NA	intron (Nintron (N	-21676 NM_002388	4157 Hs. 51382ENR_002388	ENSG000003CMCIR	CMM5 MSH	melanocor protein-coding	
chr3-1204.7.633041	-0.61031	0.850679	-0.71744	0.473105	0.981636	chr3	1.2E+08	1.2E+08	0	NA	intron (Nintron (N	12894 NM_007078	11167 Hs. 26951ENR_007078	ENSG000003PSTL1	FRP FSL1 F	ollistat protein-coding	
chr9-958.7.633041	-0.61031	0.850679	-0.71744	0.473105	0.981636	chr9	95892937	95892640	0	NA	intron (NAluS SIN	16510 NM_00101C	375748 Hs. 432364NM_020207	ENSG000003ERCC6L2	BMP52 C9c	ERCC exciprotein-coding	
chr3-1578.9.837732	-0.53897	0.751437	-0.71725	0.473218	0.981636	chr3	15789973	15793965	0	NA	intron (NLM1A LIN	6010 NM_001349	23243 Hs. 33523ENR_001519	ENSG000003ANKRD28	P1TK PPP	lankyrin r protein-coding	
chr1-1568.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr1	1.57E+08	1.57E+08	0	NA	Intergeni Intergeni	-13577 NM_001007	4914 Hs. 40629ENR_002525	ENSG000003NTRK1	MTC TRK1 neurotro	protein-coding	
chr1-240.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr1	2.4E+08	2.4E+08	0	NA	intron (Nintron (N	2524 NM_020066	56776 Hs. 24889 NM_020066	ENSG000003FMN2	-	formin 2 protein-coding	
chr10-685.9.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr10	68921413	68923725	0	NA	intron (NAluJo SIN	21254 NM_024045	79009 Hs. 522984NM_024045	ENSG000003DDX50	GU2 GUB F	DEd-box protein-coding	
chr11-125.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr11	1.26E+08	1.26E+08	0	NA	intron (NAluJb SIN	8020 NM_001274	1111 Hs. 24529 NM_001274	ENSG000003CHEK1	CHK1	checkpoir protein-coding	
chr12-128.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr12	12831137	12832901	0	NA	Intergeni Intergeni	18673 NM_016355	51202 Hs. 71993ENR_016355	ENSG000003DDX47	E4-DBP H	DEAD-box protein-coding	
chr14-547.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr14	54791902	54792662	0	NA	3' UTR (N3' UTR (N	37449 NM_001161	23034 Hs. 98259 NM_015588	ENSG000003SAMD4A	SAMD4 SMP	sterile ε protein-coding	
chr14-103.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr14	1.04E+08	1.04E+08	0	NA	Intergeni Intergeni	11371 NM_001823	1152 Hs. 173724NM_001823	ENSG000003CKB	B-CK BCK c	reatine protein-coding	
chr16-234.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr16	23671294	23672709	0	NA	non-codiron-codir	-6888 NM_00503C	5347 Hs. 59204ENR_00503C	ENSG000003PLK1	PLK STPK	polo like protein-coding	
chr17-37.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr17	37443405	37444775	0	NA	intron (NAluJo SIN	36865 NM_001488	6871 Hs. 50066ENR_001488	ENSG000003TADA2A	ADA2 ADA2	transcrip protein-coding	
chr17-471.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr17	47122702	47123554	0	NA	intron (Nintron (N	60637 NM_001256	996 Hs. 46329ENR_001256	ENSG000003CDC27	ANAPC3 AF	cell divi protein-coding	
chr17-60.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr17	60371544	60332008	0	NA	intron (NAluJb SIN	60351 NM_032582	84669 Hs. 13286ENR_032582	ENSG000003USP32	NY-REN-6	ubiquitir protein-coding	
chr18-587.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr18	58701913	58710744	0	NA	intron (Nintron (N	-38355 NM_001288	1.02E+08 Hs. 64487ENR_001289	ENSG000003LOC101927	-	uncharact protein-coding	
chr2-2784.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr2	278475	279618	0	NA	TTS (NR_C TTS (NR_C	9045 NM_001002	285016 Hs. 355207NM_001002	ENSG000003ALKAL2	AUGA FAM	1ALK and l protein-coding	
chr2-6644.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr2	66454024	66455492	0	NA	intron (Nintron (N	-14428 NR_046622	1.01E+08 Hs. 73469ENR_046622	ENSG000003MEI51-AS2	MEI51-AS1 MEI51	atncRNA	
chr2-1005.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr2	1.05E+08	1.05E+08	0	NA	intron (NAluS SIN	39527 NR_137325	9392 Hs. 44635ENR_004257	ENSG000003TGFBRAP1	TRAP-1 T	TF transfn protein-coding	
chr2-1774.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr2	1.77E+08	1.77E+08	0	NA	intron (Nintron (N	50103 NM_003655	8540 Hs. 51654ENR_003655	ENSG000003AGPS	ADAP-S A	E alkylglyc protein-coding	
chr2-1814.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr2	1.81E+08	1.81E+08	0	NA	intron (NLa LINE	26744 NM_000888	3676 Hs. 72981 NM_000888	ENSG000003ITGA4	CD49D IA	integrin protein-coding	
chr2-2004.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr2	2E+08	2E+08	0	NA	intron (Nintron (N	96446 NM_001321	130535 Hs. 60577ENR_001321	ENSG000003CKTD18	6530404F1	potassium protein-coding	
chr20-137.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr20	13770292	13771779	0	NA	intron (Nintron (N	13851 NM_016645	51575 Hs. 369284NM_016645	ENSG000003ESF1	ABTAP C2C	ESF1 nucl protein-coding	
chr21-36.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr21	36073569	36073987	0	NA	TTS (NM_C TTS (NM_C	3754 NM_001757	873 Hs. 88778 NM_001757	ENSG000003CBR1	CBR1 SDR2	carbonyl protein-coding	
chr22-31.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr22	31837444	31837805	0	NA	intron (NAluJb SIN	83601 NM_001365	9681 Hs. 435022NM_014662	ENSG000003DEPDC5	DEP. 5 F	DEP domain protein-coding	
chr3-1232.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr3	1.23E+08	1.23E+08	0	NA	intron (Nintron (N	45731 NM_01243C	26984 Hs. 477361NM_01243C	ENSG000003SEC22A	SEC22L2	SEC22 hon protein-coding	
chr4-741.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr4	76119369	76119602	0	NA	intron (NAluJb SIN	28912 NM_017422	53371 Hs. 43043ENR_017422	ENSG000003NUP54	-	nucleoson protein-coding	
chr5-615.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr5	61496439	61497096	0	NA	intron (Nintron (N	-140993 NR_161251	285668 Hs. 68386ENR_126525	ENSG000003C5orf64	-	chromoson ncRNA	
chr5-6601.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr5	66012942	66015472	0	NA	intron (Nintron (N	-68634 NR_028474	1E+08 Hs. 60806ENR_028474	LOC100305	-	LSM3 homc pseudo	
chr5-7704.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr5	77040501	77041786	0	NA	intron (Nintron (N	10739 NM_018046	55109 Hs. 63484ENR_018046	ENSG000003AGGF1	GPATCT G	F angiogeni protein-coding	
chr6-154.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr6	1.55E+08	1.55E+08	0	NA	intron (NLM4 LINE	-22604 NM_152405	134553 Hs. 70853ENR_152405	ENSG000003C5orf24	-	chromoson protein-coding	
chr6-1514.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr6	1.51E+08	1.51E+08	0	NA	intron (Nintron (N	-20252 NM_020861	57621 Hs. 52007ENR_020861	ENSG000003ZBTB2	ZNF437	zinc fing protein-coding	
chr7-105.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr7	1.05E+08	1.05E+08	0	NA	intron (Nintron (N	3316 NR_182692	6733 Hs. 285197NM_182691	ENSG000003SRPK2	SFRSK2	SRSF prot protein-coding	
chr7-1368.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr7	1.37E+08	1.37E+08	0	NA	intron (NAluSx SIN	-8585 NR_030165	574443	NR_030165	ENSG000003MIR490	MIRNA90 t	microRNA ncRNA
chr8-5855.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr8	58598989	58599466	0	NA	intron (Nintron (N	45921 NM_005622	6386 Hs. 200804NM_005622	ENSG000003SDCBP	MDA-9 MD	syndecan protein-coding	
chr8-1301.5.930947	-0.6831	0.952591	-0.7171	0.473312	0.981636	chr8	1.3E+08	1.3E+08	0	NA	intron (Nintron (N	-88148 NR_045388	1.01				



chr19-473.7.914339	0.589917	0.828181	0.712304	0.476277	0.981636	chr19	47380419	47380987	+	0	NA	intron (NMLT1K LTF	31388	NM_014681	9704	Hs.151706NM_014681	ENSG000003DHX34	DDX34 HRE	DEH-box protein-coding
chr21-332.7.914339	0.589917	0.828181	0.712304	0.476277	0.981636	chr21	33276354	33277365	+	0	NA	intron (NMLT1K LTF	10492	NM_000628	3588	Hs.654593NM_000628	ENSG000003IL10RB	CDW210B C	interleukin protein-coding
chr22-497.7.914339	0.589917	0.828181	0.712304	0.476277	0.981636	chr22	49787128	49788082	+	0	NA	exon (NM_exon NM	36726	NR_146334	23774	Hs.127953NM_014577	ENSG000003BRD1	BRL BRPF1	bromodomain protein-coding
chr5-1707.7.914339	0.589917	0.828181	0.712304	0.476277	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (NALuSp SIN	19187	NM_00104C	80230	Hs.306766NM_025158	ENSG000003RUFY1	RAB1P4 ZF	RUN and F protein-coding
chr7-1476.7.914339	0.589917	0.828181	0.712304	0.476277	0.981636	chr7	1.41E+08	1.41E+08	+	0	NA	intron (NTiger4a	-82458	NR_024454	1E+08	Hs.534141NR_024454	ENSG000003NDUFB2-AS-	NDUFB2	ancRNA
chr9-1281.7.914339	0.589917	0.828181	0.712304	0.476277	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	TTS (NM_C TTS (NM_C	3652	NM_024112	79095	Hs.522412NM_024112	ENSG000003C9orf16	ESTO0098	chromosom protein-coding
chr12-101.4.171997	-0.81887	1.149665	-0.71227	0.4763	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (Nintron (N	108959	NM_00128E	121601	Hs.58785 NM_17882E	ENSG000003AN04	TMEM16D	anoctamin protein-coding
chr18-215.4.171997	-0.81887	1.149665	-0.71227	0.4763	0.981636	chr18	21564245	21564935	+	0	NA	intron (NALu SINE	36114	NM_052911	114799	Hs.464733NM_052911	ENSG000003ESCO1	A9300141	establis protein-coding
chr2-1781.4.171997	-0.81887	1.149665	-0.71227	0.4763	0.981636	chr2	1.78E+08	1.78E+08	+	0	NA	intron (Nintron (N	7443	NM_15294E	129831	Hs.377257NM_15294E	ENSG000003CRBM45	DRB1 RB-1	RNA bindi protein-coding
chr21-464.4.171997	-0.81887	1.149665	-0.71227	0.4763	0.981636	chr21	46443858	46444344	+	0	NA	intron (Nintron (N	-14790	NM_206891	14790	Hs.189588NM_015151	ENSG000003DIP2A	C21orf106	disco intncRNA
chr5-5781.4.171997	-0.81887	1.149665	-0.71227	0.4763	0.981636	chr5	57819439	57820178	+	0	NA	Intergeni LIMEc LIN	79354	NR_109900	1.02E+08	Hs.63938E NR_109900	ENSG000003LINC0222E-	long intncRNA	
chr6-1597.4.171997	-0.81887	1.149665	-0.71227	0.4763	0.981636	chr6	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	3361	NM_00127C	9589	Hs.446091NM_00490E	ENSG000003WTAP	Mum2	WT1 assoc protein-coding
chr1-2397.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr1	23976577	23977589	+	0	NA	intron (Nintron (N	3244	NM_001191	10772	Hs.3530 NM_00662E	ENSG000003SRSF1	FUS1P1 FU	serine ar protein-coding
chr11-737.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr11	73720523	73721174	+	0	NA	exon (NM_exon NM	39245	NM_001243	5870	Hs.530222NM_00286E	ENSG000003RAB6A	RAB6	RAB6, me protein-coding
chr12-462.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr12	46241211	46242056	+	0	NA	intron (Nintron (N	24883	NM_00127E	81539	Hs.533777NM_030674	ENSG000003SLC38A1	ATA1 NAT2	solute c protein-coding
chr14-100.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	promoter-promoter-	-166	NR_00321E	767603	NR_00321E	ENSG000003SNORD114-	14q (II-22	small nucsnRNA
chr17-493.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr17	4935958	4936308	+	0	NA	TTS (NM_C TTS (NM_C	3856	NM_00017E	2811	Hs.1472 NM_00017E	ENSG000003GP1B4	BDPLT1 BL	glycoprot protein-coding
chr2-333.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr2	33138400	33139328	+	0	NA	intron (NALu SINE	4267	NM_00116E	4052	Hs.61931E NM_00062E	ENSG000003LTBP1	-	latent tr protein-coding
chr22-296.5.889807	-0.68768	0.965675	-0.71213	0.476385	0.981636	chr22	29688193	29688459	+	0	NA	intron (Nintron (N	-31677	NM_182527	164633	Hs.64360E NM_182527	ENSG000003CABP7	CALN2	calcium t protein-coding
chr14-996.5.829252	-0.72034	1.011542	-0.71213	0.476387	0.981636	chr14	99878733	99879067	+	0	NA	intron (Nintron (N	85487	NM_004434	2009	Hs.12451 NM_004434	ENSG000003EML1	BH ELP79 EMAP	like protein-coding
chr1-159.10.1267	0.531908	0.747015	0.712044	0.476438	0.981636	chr1	1.59E+08	1.59E+08	+	0	NA	intron (Nintron (N	27150	NM_00120E	3428	Hs.38025E NM_005531	ENSG000003IF116	IFNGIP1 IF	interfer protein-coding
chr1-1736.10.1267	0.531908	0.747015	0.712044	0.476438	0.981636	chr1	1.74E+08	1.74E+08	+	0	NA	3' UTR (N3' UTR (N	-7634	NR_152521	60674	Hs.53185E NR_00257E	ENSG000003GAS5	NCRNA000E	growth ancRNA
chr1-1703.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr1	17037793	17038536	+	0	NA	intron (NALuJo SIN	16006	NM_00300C	6390	Hs.465924NM_00300C	ENSG000003SDHB	CWS2 IP F	succinate protein-coding
chr10-112.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr10	1.12E+08	1.12E+08	+	0	NA	exon (NM_exon NM	15329	NM_02091E	57678	Hs.42586 NM_02091E	ENSG000003GPAM	GPAT GPA	glycerol-protein-coding
chr12-456.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr12	45944745	45945659	+	0	NA	intron (Nintron (N	45372	NM_00471E	9169	Hs.210367NM_00471E	ENSG000003SCAF11	CASP11 SF	SR-related protein-coding
chr17-821.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr17	82183571	82184996	+	0	NA	intron (N2b LINE	28559	NM_00131E	284001	Hs.631724NM_15267E	ENSG000003CCDC57	-	coiled-c protein-coding
chr19-556.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr19	55688528	55690191	+	0	NA	exon (NM_exon NM	12734	NM_00113C	29924	Hs.27995E NM_01333E	ENSG000003EPN1	-	epsin I protein-coding
chr3-4733.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr3	47333575	47334367	+	0	NA	intron (Nintron (N	-47050	NM_01546E	25930	Hs.25524 NM_01546E	ENSG000003PTPN23	HD-PTP HE	protein t protein-coding
chr5-1492.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr5	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	-19467	NM_100132E	134265	Hs.62930 NM_15240E	ENSG000003AFAP111	-	actin fil protein-coding
chr7-1734.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr7	17342326	17343197	+	0	NA	intron (Nintron (N	-32156	NR_11001E	1.03E+08	Hs.55948E NR_110014	KCCAT333	-	retin clncRNA
chr7-2761.5.717692	0.687783	0.96614	0.711887	0.476535	0.981636	chr7	27619325	27620551	+	0	NA	intron (NLM2 LINE	3964	NR_12212E	790953	Hs.57133E NR_122122	TSL	-	testis-ancRNA
chr15-484.7.163727	-0.64332	0.903862	-0.71174	0.476625	0.981636	chr15	49463339	49466375	+	0	NA	intron (N2 LINE I	40361	NM_00200E	2252	Hs.56726E NM_00200E	ENSG000003PGF7	HBGF-7 KC	fibroblas protein-coding
chr15-589.7.163727	-0.64332	0.903862	-0.71174	0.476625	0.981636	chr15	58991370	58991884	+	0	NA	intron (N2a LINE	3481	NM_00127C	54778	Hs.40442E NM_01761E	ENSG000003RNF111	hRNF111	ring fing protein-coding
chr2-5567.7.163727	-0.64332	0.903862	-0.71174	0.476625	0.981636	chr2	55655676	55655909	+	0	NA	intron (Nintron (N	38052	NM_03310E	87178	Hs.38873E NM_03310E	ENSG000003PNPT1	COXPDI3 P	polyribor protein-coding
chr3-1441.7.163727	-0.64332	0.903862	-0.71174	0.476625	0.981636	chr3	14418659	14418959	+	0	NA	intron (NMR SINE	16203	NM_001134	6533	Hs.52948E NM_00304E	ENSG000003SLC6A6	TAUT	solute c protein-coding
chr1-8466.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr1	84664999	84666099	+	0	NA	intron (Nintron (N	24912	NM_00116E	117178	Hs.22587 NM_014021	ENSG000003SSX2IP	ADIP hMSC	SSX fami protein-coding
chr10-943.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr10	94343296	94346671	+	0	NA	intron (NLM3Cz I	17956	NM_022451	64318	Hs.74899 NM_022451	ENSG000003CNO3L	AD24 C10c	NOC3 like protein-coding
chr10-994.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr10	99419397	99419815	+	0	NA	intron (NMERSB DNA	11018	NM_00207E	2805	Hs.50075E NM_00207E	ENSG000003GOT1	AST1 AST	glutamic protein-coding
chr11-20.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr11	20093328	20093328	+	0	NA	intron (Nintron (N	-42768	NR_04667E	1.01E+08	Hs.55791E NR_04667E	ENSG000003NAV2-AS2	-	NAV2 antncRNA
chr12-106.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr12	10606055	10607979	+	0	NA	intron (NLM4c LI	5961	NM_00130C	55110	Hs.10465E NM_01804E	ENSG000003MAGOHB	MGN2 mag	mago homc protein-coding
chr12-248.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr12	24825446	24826947	+	0	NA	intron (NALuJb SIN	76026	NM_00117E	586	Hs.43899E NM_005504	ENSG000003BCAT1	BCATC BC	branched protein-coding
chr13-758.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr13	75809979	75809983	+	0	NA	exon (NM_exon NM	47320	NM_01584E	4008	Hs.207631NM_00535E	ENSG000003LCM7	FBX20 FB	LIM domain protein-coding
chr15-588.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr15	58825585	58826578	+	0	NA	intron (Nintron (N	54779	NM_00104C	54629	Hs.59112E NM_01909E	ENSG000003MINDY2	FAM63B	MINDY lys protein-coding
chr15-101.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr15	1.01E+08	1.01E+08	+	0	NA	intron (NMSTA LTR	37278	NM_01491E	22856	Hs.11048E NM_01491E	ENSG000003CHSY1	CHSY CSS1	chondroit protein-coding
chr18-232.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr18	23247697	23248040	+	0	NA	intron (Nintron (N	92043	NM_13837E	91768	Hs.11108 NM_13837E	ENSG000003CABLES1	CABL1 CAE	Cdk5 and protein-coding
chr2-6137.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr2	61379311	61379822	+	0	NA	intron (NMER102b I	37811	NR_0033707	1E+08	Hs.67582E NR_0033707	ENSG000003SNORA70B	-	small nucsnRNA
chr2-1118.5.923089	-0.681	0.956834	-0.71172	0.476638	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	50180	NM_02266E					

chr11-102	8.08479	-0.58886	0.830756	-0.70883	0.478433	0.981636	chr11	1.02E+08	1.02E+08	+	0 NA	intron (NAluSp SIN	52312 NM_00119E	10413 Hs. 503692NM_00610f	ENSG00000CYP1	COB1 YAP Yes assoc	protein-coding		
chr15-586	8.08479	-0.58886	0.830756	-0.70883	0.478433	0.981636	chr15	58657778	58658413	+	0 NA	intron (NLIMA2 LIN	35512 NR_07341E	664618 Hs. 670224NR_002927	HSP90A HSP90B	heat shock	pseudo		
chr7-129	8.014184	0.598984	0.845048	0.708816	0.478438	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (Nintron (N	24124 NM_003344	7328 Hs. 643544NM_003344	ENSG00000CUBE2H	E2-20K Gubiquitin	protein-coding		
chr2-939	2.923501	-0.96618	1.36319	-0.70876	0.478473	0.981636	chr2	9399856	93999474	+	0 NA	intron (N (TCCTC N	23375 NM_00131E	9270 Hs. 467662NM_00476E	ENSG00000ITGB1BP1	ICAP-1A Integrin	protein-coding		
chr21-415	12.14227	-0.48476	0.683975	-0.70874	0.478485	0.981636	chr21	41995737	41995936	+	0 NA	intron (THE1B int	-13558 NR_119384	150142 Hs. 143833NM_119384	ENSG00000ZNF295-AS2	Clorf121 ZNF295	arncRNA		
chr14-35	5.709834	0.690678	0.974779	0.708548	0.478605	0.981636	chr14	35072301	35073155	+	0 NA	intron (NTiger2 I	-8353 NR_11041E	1.02E+08 Hs. 617135NR_11041E	ENSG00000CLOC101927-		uncharacterncRNA		
chr14-88	5.709834	0.690678	0.974779	0.708548	0.478605	0.981636	chr14	88882722	88883366	+	0 NA	Intergeni THE1D-int	58393 NM_00136E	123016 Hs. 303055NM_14459E	ENSG00000CTTC8	BBS8 RP51	tetratric	protein-coding	
chr16-68	5.709834	0.690678	0.974779	0.708548	0.478605	0.981636	chr16	68919209	68920167	+	0 NA	intron (Nintron (N	76157 NM_02456E	79613 Hs. 13526 NM_02456E	ENSG00000TANG06	TMC07	transport	protein-coding	
chr17-78	5.709834	0.690678	0.974779	0.708548	0.478605	0.981636	chr17	78100571	78101502	+	0 NA	intron (NAluSq2 SI	10763 NR_040071	1E+08 Hs. 635442NR_040071	ENSG00000TNR6C-AS	TMC6 Inc	TNR6C	arncRNA	
chr19-19	3.444773	0.883329	1.246758	0.708501	0.478634	0.981636	chr19	1946420	1947056	+	0 NA	intron (NAluY SINE	5566 NM_00131E	1455 Hs. 65190E NM_00131E	ENSG00000CSNK1G2	CK1g2	casein	protein-coding	
chr7-116	9.920011	-0.53371	0.753373	-0.70843	0.478679	0.981636	chr7	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	1346 NM_00120E	858 Hs. 212332NM_00123E	ENSG00000CAV2	CAV	caveolin	protein-coding	
chr6-128	1.393841	-0.55475	0.783504	-0.70803	0.478924	0.981636	chr6	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	156296 NR_12584E	1.02E+08 Hs. 65677E NR_125849	LLOC10192E-		uncharacterncRNA		
chr15-25	7.458891	0.621741	0.878449	0.707771	0.479088	0.981636	chr15	25103890	25104673	+	0 NA	promoter-promoter-	-360 NR_003361	ENSG00000SNORD116-	HBI1-85-2	small	nucsnRNA		
chr15-48	7.625183	-0.60857	0.859962	-0.70768	0.479146	0.981636	chr15	48423357	48424079	+	0 NA	intron (Nintron (N	91521 NM_00194E	1854 Hs. 527928NM_00194E	ENSG00000CDUT	dUTPase	deoxyribonucleic acid	protein-coding	
chr7-121	7.625183	-0.60857	0.859962	-0.70768	0.479146	0.981636	chr7	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	21933 NM_05716E	51384 Hs. 27237E NM_01608E	ENSG00000WNT16	-	Wnt	family	protein-coding
chr12-437	11.15316	0.498499	0.704703	0.707388	0.479325	0.981636	chr12	43796796	43796995	+	0 NA	intron (Nintron (N	9422 NM_00124E	5756 Hs. 18907E NM_00282E	ENSG00000TWF1	A6 PTK9	twintin	protein-coding	
chr1-520	8.47749	0.568279	0.803424	0.707321	0.479367	0.981636	chr1	52023638	52024718	+	0 NA	intron (NAluJb SIN	9632 NM_138417	112970 Hs. 47603E NM_138417	ENSG00000CKTI12	SBB181 TKCT112	chr	protein-coding	
chr1-168	8.47749	0.568279	0.803424	0.707321	0.479367	0.981636	chr1	1.68E+08	1.68E+08	+	0 NA	intron (Nintron (N	24649 NR_03170E	1E+08 NR_03170E	ENSG00000MIR1255B2	MIR1255B	microRNA	ncRNA	
chr14-21	8.47749	0.568279	0.803424	0.707321	0.479367	0.981636	chr14	21387433	21387632	+	0 NA	intron (NAluSp SIN	-3513 NM_00719E	11198 Hs. 213724NM_00719E	ENSG00000SUPT16H	CDC68 FAC	SPT16	hom	protein-coding
chr17-4	8.47749	0.568279	0.803424	0.707321	0.479367	0.981636	chr17	47477271	47479323	+	0 NA	intron (NMLT1A0 LI	14323 NR_033934	653479 Hs. 53727E NR_033934	MRPL45P2	-	mitochondrion	pseudo	
chr19-26	14.37442	0.444556	0.628894	0.706886	0.479638	0.981636	chr19	26675521	26676488	+	0 NA	Intergeni ALR Alpha	-117427 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG00000CLOC101927-		uncharacterncRNA		
chr5-113	9.896437	-0.52987	0.749613	-0.70686	0.479652	0.981636	chr5	1.14E+08	1.14E+08	+	0 NA	intron (NLR22B1 I	17644 NM_00134E	64848 Hs. 23194E NM_02282E	ENSG00000YTHDC2	CAHL HYTH	YTH	domain	protein-coding
chr1-95	7.658465	-0.60345	0.853747	-0.70683	0.479675	0.981636	chr1	95024834	95025555	+	0 NA	intron (NTiger1 I	-36402 NR_13278E	1.02E+08 Hs. 73009E NR_13278E	ENSG00000CLOC10192E-		uncharacterncRNA		
chr15-65	7.658465	-0.60345	0.853747	-0.70683	0.479675	0.981636	chr15	65023771	65024291	+	0 NA	intron (Nintron (N	5608 NM_13924E	123263 Hs. 53161E NM_13924E	ENSG00000MTFM	COXPDI5	F	mitochondrion	protein-coding
chr18-13	7.658465	-0.60345	0.853747	-0.70683	0.479675	0.981636	chr18	13107914	13108510	+	0 NA	intron (NLIPA16 LI	-110548 NM_18148E	753 Hs. 697787NM_00433E	ENSG00000LDLRAD4	C18orf1	low	density	protein-coding
chr2-159	7.658465	-0.60345	0.853747	-0.70683	0.479675	0.981636	chr2	1.6E+08	1.6E+08	+	0 NA	intron (Nintron (N	31168 NM_01488E	9936 Hs. 130014NM_01488E	ENSG00000CD302	B1MLEC CI	CD302	mol	protein-coding
chr4-168	7.658465	-0.60345	0.853747	-0.70683	0.479675	0.981636	chr4	1.69E+08	1.69E+08	+	0 NA	Intergeni LM2c LIN	79350 NM_03278E	84869 Hs. 65931NM_03278E	ENSG00000CBR4	SDR45C1	carboxyl	protein-coding	
chr8-14	7.658465	-0.60345	0.853747	-0.70683	0.479675	0.981636	chr8	1.44E+08	1.44E+08	+	0 NA	TTS (NM_C TTS (NM_C	1155 NR_10690E	1.02E+08 NR_10690E	ENSG00000MIR6847	hsa-mir-6	microRNA	ncRNA	
chr1-21	8.102356	-0.58082	0.822392	-0.70625	0.48003	0.981636	chr1	2.13E+08	2.13E+08	+	0 NA	intron (NMSTA LTR	-41589 NM_018664	55509 Hs. 62919 NM_018664	ENSG00000BATF3	JDP1 JUN	basic	let	protein-coding
chr10-87	8.102356	-0.58082	0.822392	-0.70625	0.48003	0.981636	chr10	87957655	87958924	+	0 NA	intron (Nintron (N	94664 NM_000314	5728 Hs. 50046E NM_000314	ENSG00000PTEN	10q23del1	phosphate	protein-coding	
chr14-9	8.102356	-0.58082	0.822392	-0.70625	0.48003	0.981636	chr14	92131146	92132111	+	0 NA	intron (NAluSj SIN	9659 NM_00132E	53981 Hs. 65763E NM_01743E	ENSG00000CPSF2	CPSF100	cleavage	protein-coding	
chr4-18	8.102356	-0.58082	0.822392	-0.70625	0.48003	0.981636	chr4	1.83E+08	1.83E+08	+	0 NA	3' UTR (N3' UTR (N	3697 NM_001317	55602 Hs. 59250E NM_01763E	ENSG00000CDKN2AIP	CARG	CDKN2A	ir	protein-coding
chr5-115	8.102356	-0.58082	0.822392	-0.70625	0.48003	0.981636	chr5	1.15E+08	1.15E+08	+	0 NA	intron (Nintron (N	-12331 NM_00502E	5229 Hs. 25400E NM_00502E	ENSG00000PGT81	BGG1 GGT1	grip	protein-coding	
chr2-23	11.076932	-0.58732	0.831998	-0.70592	0.480238	0.981636	chr2	2.31E+08	2.31E+08	+	0 NA	intron (NAluJo SIN	-29550 NM_000867	3357 Hs. 42164E NM_000867	ENSG00000CHTR2B	5-HT (2B) 5	-hydroxy	protein-coding	
chr16-16	5.203538	0.731678	1.036589	0.705851	0.480281	0.981636	chr16	16188954	16189908	+	0 NA	intron (NAluXj SI	33995 NM_00107E	368 Hs. 44218E NM_001171	ENSG00000ABCC6	ABC34 ARAF	bindi	protein-coding	
chr6-16	5.203538	0.731678	1.036589	0.705851	0.480281	0.981636	chr6	1.7E+08	1.7E+08	+	0 NA	non-codir-non-codir	33914 NM_00135E	253769 Hs. 13190E NM_18255E	ENSG00000WDR27	-	WD	repeat	protein-coding
chr9-39	5.203538	0.731678	1.036589	0.705851	0.480281	0.981636	chr9	39456121	39456586	+	0 NA	intron (NMER2 DNA	8173 NR_00352E	401509 Hs. 44944E NM_001032297	ZNF658B	-	zinc	finger	pseudo
chr11-10	8.143495	-0.57759	0.818322	-0.70582	0.480297	0.981636	chr11	1.02E+08	1.02E+08	+	0 NA	intron (Nintron (N	98925 NM_00119E	10413 Hs. 503692NM_00610E	ENSG00000CYP1	COB1 YAP Yes	assoc	protein-coding	
chr12-10	8.143495	-0.57759	0.818322	-0.70582	0.480297	0.981636	chr12	1.05E+08	1.05E+08	+	0 NA	intron (NMLRb SINE	36204 NM_001034	160428 Hs. 42572 NM_001034	ENSG00000ALDH1L2	mtFBH	aldehyde	protein-coding	
chr15-8	8.143495	-0.57759	0.818322	-0.70582	0.480297	0.981636	chr15	80944416	80949706	+	0 NA	exon (NM_exon (NM	42758 NR_12632E	23184 Hs. 57845E NM_015154	ENSG00000MESD	BOCA MES	mesoderm	protein-coding	
chr17-3	8.143495	-0.57759	0.818322	-0.70582	0.480297	0.981636	chr17	38883031	38884343	+	0 NA	intron (NAluXj SIN	12309 NM_00614E	3927 Hs. 74115E NM_00614E	ENSG00000LASP1	Lasp-1 ML	LIM and S	protein-coding	
chr19-4	8.143495	-0.57759	0.818322	-0.70582	0.480297	0.981636	chr19	47788299	47788299	+	0 NA	intron (NAluJo SIN	29271 NM_014681	9704 Hs. 15170E NM_014681	ENSG00000DHX34	DDX34 HRE	DEX-h	box	protein-coding
chr7-5	8.143495	-0.57759	0.818322	-0.70582	0.480297	0.981636	chr7	55169012	55169681	+	0 NA	TTS (NM_C TTS (NM_C	19603 NR_047551	1.01E+08 Hs. 72048E NR_047551	ENSG00000EGFR-AS1	-	EGFR	antincRNA	
chr19-8	7.98876	0.59386	0.84154	0.705683	0.480386	0.981636	chr19	899293	899701	+	0 NA	intron (Nintron (N	5828 NR_12573E	1.04E+08 NR_12573E	ENSG00000RNU6-2	U6-2	RNA, U6	snRNA	
chr2-4	7.98876	0.59386	0.84154	0.705683	0.480386	0.981636	chr2	46159536	46160966	+	0 NA	intron (Nintron (N	-137156 NM_00143E	2034 Hs. 46841NM_00143E	ENSG00000CEPAS1	ECYT4 HIF	endothelin	protein-coding	
chr19-8	11.1943	0.49932	0.707624	0.705629	0.480419	0.981636	chr19	8809871	8821427	+	0 NA	intron (NAluJr SIN	6414 NM_001304	148156 Hs. 349444NM_014469E	ENSG00000ZNF558	-	zinc	finger	protein-coding
chr9-1	11.1943	0.49932	0.707624	0.705629	0.480419	0.981636	chr9	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	9581 NM_00128E	7539 Hs. 15040E NM_00340E	ENSG00000ZFP37	ZNF906 zf	ZFP37	zir	protein-coding
chr11-4	5.453774	-0.7314	1.036973	-0.70533	0.480608	0.981636	chr11	44108902	44109557	+	0 NA	exon (NM_exon (NM	13032 NM_000401	2132 Hs. 368404NM_000401	ENSG00000EXT2	SOTV SSM	exostosin	protein-coding	
chr10-7	5.453774	-0.7314	1.036973	-0.70533	0.480641	0.981636	chr10	70216038	70218884	+	0 NA	intron (NMLRc SINE	15968 NM_02112E	5464 Hs. 43740E NM_02112E	ENSG00000PPA1	HEL-5-6	pyrophosph	protein-coding	
chr11-3	5.453774	-0.7314	1.036973	-0.70533	0.480641	0.981636	chr11	34882896	34883095	+	0 NA	intron (Nintron (N	-33135 NM_00116E	8050 Hs. 50231E NM_00347E	ENSG00000PDHX	DLDBP E3E	pyruvate	protein-coding	
chr11-8	5.453774	-0.7314	1.036973	-0.70533	0.480641	0.981636	chr11	88303207	88311003	+	0 NA	intron (Nintron (N	30631 NM_14817E	1075 Hs. 12806E NM_001814	ENSG00000CTSC	CPPI DPP	cathepsin	protein-coding	
chr12-1	5.453774	-0.7314	1.036973	-0.70533	0.480641	0.981636	chr12	21651813	21654675	+	0 NA	intron (NLMC4 LIN	4550 NM_001174	3945 Hs. 44614E NM_00230E	ENSG00000LDHB	HEL-5-28	lactate		



chr16-305.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr16	30979749	30981627	+	0	NA	intron (NCpG)	-4519	NM_001142	80270	Hs.46061ENM_02519:ENSG00000CHSD3B7	CBAS1 PFI hydroxy-c-protein-coding	
chr2-3202.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr2	32028136	32029088	+	0	NA	intron (NAuSc SIN)	11193	NM_001321	84661	Hs.51788NM_032574:ENSG00000DPY30	Cps25 HDF pdy-30 hiprotein-coding	
chr5-180C.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (NLIMB7 LIN)	-20730	NR_02988E	442908	NR_02988E:ENSG00000CIR340	MIRN340 l-microRNA ncRNA	
chr6-1164.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr6	1.16E+08	1.16E+08	+	0	NA	intron (NLIPA16 LI)	-27594	NM_00127E	441168	Hs.38122C:NM_00101C:ENSG00000CALHM6	C6orf187 calcium I-protein-coding	
chr6-1697.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (NALuSg SIN)	6879	NM_13332E	55274	Hs.43593:NM_01828E:ENSG00000PHF10	BAF454 XAPH finger protein-coding	
chr7-130C.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (NALuY SINE)	10875	NM_00136E	51530	Hs.194157:NM_01647E:ENSG00000CZ3HC1	HSPC216 zinc finger protein-coding	
chr9-209C.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr9	20990232	20990786	+	0	NA	intron (Nintron (N))	41131	NM_00101C	401494	Hs.71667E:NM_00101C:ENSG00000HACD4	PTPLAD2 3-hydroxyprotein-coding	
chr1-229C.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr1	2.3E+08	2.3E+08	+	0	NA	intron (Nintron (N))	20394	NR_11063C	1.02E+08	Hs.80208:NR_11063C:ENSG00000LOC101927	LOC101927-1	
chr2-922C.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr2	92296775	92297631	+	0	NA	IntergeniALR/Alpha	356070	NR_027714	440888	Hs.73023E:NM_001032412	ACTR3BP2 FKGSG73 ACTR3B ps-pseudo	
chr7-442C.7.930055	0.585803	0.833335	0.702962	0.482079	0.981636	chr7	64523802	64524841	+	0	NA	TTS (NM_CTS (NM_C))	38750	NM_17855E	340252	Hs.52088E:NM_17855E:ENSG00000ZNF680	- zinc finger protein-coding	
chr4-4427.11.71631	0.487262	0.693192	0.702924	0.482103	0.981636	chr4	442772	442525	+	0	NA	exon (NM exon (NM))	30197	NR_002451	79963	Hs.67749E:NM_02490E:ENSG00000ABCA11P	ABCA11 ES ATP bindipseudo	
chr10-145.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr10	14924649	14925133	+	0	NA	intron (Nintron (N))	29205	NM_00135C	64421	Hs.65593E:NM_02248E:ENSG00000DCLRE1C	A-SCID DCDNA cross protein-coding	
chr11-614.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr11	614960	615467	+	0	NA	exon (NM exon (NM))	737	NM_00402E	3665	Hs.16612C:NM_00157E:ENSG00000IRF7	IMD39 IRF interferon protein-coding	
chr12-681.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr12	6817395	6818067	+	0	NA	intron (N (CA)n Sin)	-4090	NM_01985E	27239	Hs.631654:NM_01444E:ENSG00000GPR162	A-2 GRCA G protein protein-coding	
chr13-111.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N))	-69039	NR_046661	1.01E+08	Hs.65869E:NR_046661:ENSG00000ATP11A-AS	ATP11A arn-cRNA	
chr16-587.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr16	58711504	58711703	+	0	NA	intron (NMER102a LI)	22713	NM_00128C	2806	Hs.59947C:NM_00208C:ENSG00000GOT2	KAT4 KAT glutamic-protein-coding	
chr17-35C.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr17	35655305	35655790	+	0	NA	intron (NLIME3 LI)	68225	NM_00103C	163	Hs.51481E:NM_00128E:ENSG00000CAP2B1	ADTB2 AP1 adaptor protein-coding	
chr20-36C.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr20	36994981	36995762	+	0	NA	TTS (NM_CTS (NM_C))	-43528	NM_015474	25939	Hs.580681:NM_015474:ENSG00000SAMHD1	CHBL2 DC15AM and I-protein-coding	
chr5-8394.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr5	83943317	83943830	+	0	NA	intron (Nintron (N))	-222718	NM_001884	1404	Hs.2799	NM_001884:ENSG00000HAPLN1	CRT1 CRT hyaluronan protein-coding
chr7-139C.5.915231	-0.6788	0.965813	-0.70283	0.482165	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N))	89509	NM_00111E	28996	Hs.731417:NM_02274C:ENSG00000CHIPK2	SGO0593 homeodomain protein-coding	
chr13-252.7.699604	-0.5999	0.85358	-0.70281	0.482175	0.981636	chr13	52662735	52663010	+	0	NA	intron (Nintron (N))	10036	NM_00132C	10910	Hs.28190E:NM_00670C:ENSG00000SUGT1	SGT1 SGT1 home protein-coding	
chr6-265C.7.699604	-0.5999	0.85358	-0.70281	0.482175	0.981636	chr6	26598992	26599220	+	0	NA	3' UTR (3' UTR (N))	2153	NM_01337E	29777	Hs.25440E:NM_01337E:ENSG00000ABT1	Esf2 HAB1 activator protein-coding	
chr2-104.10.33247	-0.51454	0.732277	-0.70265	0.482273	0.981636	chr2	10643800	10644202	+	0	NA	intron (NALuSz SIN)	45974	NM_024894	79954	Hs.222494:NM_024894:ENSG00000NOL10	PQB55 nucleolar protein-coding	
chr1-2454.5.972086	-0.67822	0.96566	-0.70238	0.482442	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	IntergeniIntergeni	135915	NM_02246E	64388	Hs.98206	NM_02246E:ENSG00000GREM2	CKTSF1B2 gremlin 2 protein-coding
chr1-176C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr1	1762083	1762305	+	0	NA	intron (Nintron (N))	-3552	NM_00119E	65220	Hs.65479E:NM_02301E:ENSG00000NADK	dJ28E3E.1 NAD kinase protein-coding	
chr1-4054.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr1	40543193	40543899	+	0	NA	intron (NALuY SINE)	11909	NM_15237E	127396	Hs.524767:NM_15237E:ENSG00000ZNF684	- zinc finger protein-coding	
chr10-151.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr10	15117399	15120635	+	0	NA	intron (NCharlie a)	21662	NM_006414	10557	Hs.94986	NM_006414:ENSG00000RPP38	ribonucleoprotein-coding
chr10-605.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr10	60934863	60936414	+	0	NA	intron (NMER63C DN)	8547	NM_00135C	9886	Hs.737374:NM_01483E:ENSG00000RHOBTB1	Rho relat protein-coding	
chr10-88C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr10	68015615	68017876	+	0	NA	intron (Nintron (N))	-5862	NR_131184	1E+08	NR_131184:POU5F1P5	Oct4-pg5 POU class-pseudo	
chr10-87C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr10	87047353	87049556	+	0	NA	IntergeniNALuY SINE	28160	NM_00114E	643161	Hs.72994E:NM_00114E:ENSG00000FAM25A	bA96C23.E family wiprotein-coding	
chr11-65C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr11	65891229	65893153	+	0	NA	TTS (NR_1TTS (NR_1))	1518	NM_00684E	11007	Hs.66713	NM_00684E:ENSG00000CCDC85B	DIPA coiled-cc protein-coding
chr11-106.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr11	1.06E+08	1.06E+08	+	0	NA	intron (Nintron (N))	-5038	NM_00133C	143879	Hs.10194E:NM_15243E:ENSG00000KBTBD3	BKLHD3 kelch repeat protein-coding	
chr13-98C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr13	98000853	98003698	+	0	NA	intron (NALuYk2 SI)	48600	NM_002271	3843	Hs.1259E:NM_002271:ENSG00000IPO5	IMB3 JNK importin protein-coding	
chr14-61C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr14	61004246	61006061	+	0	NA	intron (NLIPA3 LIN)	-23463	NM_00135C	57570	Hs.38015E:NM_02081C:ENSG00000TRMT5	COXP26 k-tRNA met protein-coding	
chr2-2114.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr2	1.11E+08	1.11E+08	+	0	NA	intron (NMLT1C LTF)	15092	NR_13616E	54147	Hs.56080E:NR_01539E:ENSG00000MIR4435-2	AGD2 LIN MIR4435-2 ncRNA	
chr2-237C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	TTS (NM_CTS (NM_C))	-16738	NM_00108C	375316	Hs.60726E:NM_19885E:ENSG00000RBM44	- RNA bindi protein-coding	
chr20-37C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr20	37216129	37218291	+	0	NA	intron (NALuJb SIN)	-37662	NM_21363E	140699	Hs.34912E:NM_15250E:ENSG00000CMROH8	C20orf131 maestro protein-coding	
chr20-41C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr20	41078887	41082674	+	0	NA	intron (Nintron (N))	51958	NM_00328E	7150	Hs.47273C:NM_00328E:ENSG00000TOP1	TOPI DNA topoi protein-coding	
chr21-34C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr21	34840724	34841351	+	0	NA	intron (Nintron (N))	47662	NM_001001	861	Hs.149261:NM_001754:ENSG00000RUNK1	AML1 AML1 RUNX family protein-coding	
chr3-575C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr3	57559662	57560530	+	0	NA	3' UTR (3' UTR (N))	3822	NM_00132E	201626	Hs.57299E:NM_17796E:ENSG00000PDE12	2'-PDE 2-phosphodi protein-coding	
chr3-122C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N))	18601	NM_00114E	83666	Hs.51820C:NM_03145E:ENSG00000PARP9	ARTD9 BAL poly (ADP- protein-coding	
chr5-637C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr5	6375524	6376648	+	0	NA	intron (Nintron (N))	2461	NM_03228E	84246	Hs.13885	NM_03228E:ENSG00000MED10	L61 NUT72 mediator protein-coding
chr5-6604.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr5	66046392	66046880	+	0	NA	intron (Nintron (N))	-97664	NM_00132E	140890	Hs.49367	NM_13916E:ENSG00000SREK1	SFRS12 SF splicing protein-coding
chr5-1107.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr5	1.11E+08	1.11E+08	+	0	NA	intron (NLIPA17 LI)	9339	NM_00130E	91137	Hs.75639	NM_13877E:ENSG00000SLC25A46	HMSN6B solute c protein-coding
chr5-1461.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (NMIRb SINE)	-20116	NM_00102E	153770	Hs.16236E:NM_00102E:ENSG00000PLAC8L1	- PLAC8 lik protein-coding	
chr6-1437.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N))	76149	NM_00110C	9749	Hs.102471:NM_014721:ENSG00000PHACTR2	C6orf56 phosphatase protein-coding	
chr7-436C.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr7	43624521	43626275	+	0	NA	3' UTR (3' UTR (N))	42290	NM_00476E	9263	Hs.70948E:NM_00476E:ENSG00000STK17A	DRAK1 serine/th protein-coding	
chr8-2337.8.127779	-0.57452	0.817997	-0.70235	0.482464	0.981636	chr8	23378032	23378245	+	0	NA	intron (NLIPA5 LIN)	25708	NM_00231E	4017	Hs.626637:NM_00231E:ENSG00000CLOX2	LOR LOR2 lysyl oxiprotein-coding	
chr8-103C.8.127779	-0.																	



chr1-2254	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr1	2.28E+08	2.28E+08	+	0	NA	intron (AluSg SIN	5426 NM_00101C	149603 Hs.356377NM_00101C ENSG00000CRNF187	RACO-1 P ring protein-coding
chr1-2351	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	intron (AluSg2 SI	-13459 NM_01476E	9804 Hs.533192NM_01476E ENSG00000TOMM20	MAS20 MOV translocase protein-coding
chr10-114	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr10	1.15E+08	1.15E+08	+	0	NA	IntergeniAluSx1 SI	-11910 NR_120677	1.03E+08 NR_120677 ENSG00000CLINCO262C-	long intencRNA
chr11-681	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr11	681838	689205	+	0	NA	intron (AluSx SIN	-10070 NM_001217E	283232 Hs.448664NM_17494C ENSG00000TMEM80	- transmem protein-coding
chr11-651	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr11	65394294	65398416	+	0	NA	intron (intron (N	9718 NM_00130C	83786 Hs.578433NM_031904 ENSG00000FRMD8	FKSG44 1 FERM domain protein-coding
chr11-703	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr11	70338571	70340018	+	0	NA	exon (NM exon (NM	55339 NR_031624	1E+08 NR_031624 ENSG00000MIR548K	MIRN548K microRNA ncRNA
chr16-84	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr16	84066235	84069648	+	0	NA	intron (intron (N	-25784 NM_00108C	146167 Hs.00108C ENSG00000SLC38A8	FVH2 solute carrier protein-coding
chr18-12	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr18	12340739	12344329	+	0	NA	intron (LIME1 LIN	34293 NM_00130C	84617 Hs.193491NM_03252E ENSG00000TUBB6	FPVEPD Hs tubulin beta protein-coding
chr19-435	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr19	43551922	43552393	+	0	NA	exon (NM exon (NM	18969 NM_17494E	284346 Hs.213534NM_17494E ENSG00000ZNF575	- zinc finger protein-coding
chr19-444	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr19	44441632	44443077	+	0	NA	intron (intron (N	6118 NR_103551	7772 Hs.70934E ENSG00000ZNF229	- zinc finger protein-coding
chr19-466	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr19	46678087	46704533	+	0	NA	intron (intron (N	18044 NR_036157	1E+08 NR_036157 ENSG00000MIR320E	mir-320e microRNA ncRNA
chr20-325	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr20	3254660	3256245	+	0	NA	intron (intron (N	-16262 NM_001174	83959 Hs.105607NM_032034 ENSG00000SLC4A11	BTRI CDPI solute carrier protein-coding
chr3-1237	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (NL2a LINE	37403 NR_046625	1.01E+08 Hs.66731E NR_046625 ENSG00000MYLK-AS2	- MYLK antincRNA
chr9-135	8.459925	0.561627	0.803849	0.698672	0.484757	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (AluSx3 SI	24099 NM_016172	10422 Hs.9194 NM_016172 ENSG00000UBAC1	GBDR1 KPCUBA domain protein-coding
chr16-885	10.63901	0.510133	0.730288	0.698536	0.484842	0.981636	chr16	88577508	88577735	+	0	NA	exon (NM exon (NM	7218 NM_144604	124245 Hs.93670 NM_144604 ENSG00000ZC3H18	NHN1 zinc finger protein-coding
chr2-1125	10.63901	0.510133	0.730288	0.698536	0.484842	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	intron (AluJb SIN	35973 NM_005054	84220 Hs.46963C NM_005054 ENSG00000RGPD5	BS-63 BSF RNBP2.1 protein-coding
chr5-7234	10.63901	0.510133	0.730288	0.698536	0.484842	0.981636	chr5	72343284	72343499	+	0	NA	intron (intron (N	23018 NM_001284	79810 Hs.12690E NM_024754 ENSG00000CTCD2	- pentatric protein-coding
chr14-962	10.35789	-0.50961	0.729636	-0.69845	0.484895	0.981636	chr14	96261339	96265537	+	0	NA	intron (MER58A DN	7228 NM_00071C	623 Hs.52557E NM_00071C ENSG00000BDRKB1	B1BKR B1F bradykinin protein-coding
chr22-356	10.35789	-0.50961	0.729636	-0.69845	0.484895	0.981636	chr22	35655252	35660329	+	0	NA	intron (intron (N	9344 NM_030641	80830 Hs.25735E NM_030641 ENSG00000APOL6	APOL-VII apolipoprotein-coding
chr3-123	10.35789	-0.50961	0.729636	-0.69845	0.484895	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (AluJo SIN	5601 NM_053031	4638 Hs.47737E NM_00596E ENSG00000MYLK	AAT7 KRP myosin I protein-coding
chr1-1195	7.691746	-0.59818	0.856466	-0.69842	0.484912	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (intron (N	-67670 NM_021794	11085 Hs.283011NM_021794 ENSG00000ADAM30	svph4 ADAM metal protein-coding
chr2-6077	7.691746	-0.59818	0.856466	-0.69842	0.484912	0.981636	chr2	60778130	60778509	+	0	NA	intron (N (ATTTT) n	22051 NM_022894	64895 Hs.387471NM_022894 ENSG00000PAPOLG	- poly (A) protein-coding
chr2-8746	12.61158	-0.47108	0.674897	-0.69801	0.485173	0.981636	chr2	87460331	87460703	+	0	NA	intron (intron (N	5090 NR_02420E	112597 Hs.65216E NR_02420E ENSG00000CYTOR	C2orf59 l cytoskeleton ncRNA
chr1-2205	8.168919	-0.57133	0.818752	-0.6978	0.485301	0.981636	chr1	22096960	22099427	+	0	NA	3' UTR (N3' UTR (N	44904 NM_030761	54361 Hs.25766 NM_030761 ENSG00000WNT4	SERKAL W Wnt family protein-coding
chr2-3927	8.168919	-0.57133	0.818752	-0.6978	0.485301	0.981636	chr2	39274337	39275353	+	0	NA	intron (MIR SINE	-30862 NR_144521	344387 Hs.403201NM_00100E ENSG00000CDKL4	- cyclin dependent protein-coding
chr2-112	8.168919	-0.57133	0.818752	-0.6978	0.485301	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	intron (intron (N	5216 NM_032824	84910 Hs.65629E NM_032824 ENSG00000TMEM87B	- transmem protein-coding
chr4-6641	8.168919	-0.57133	0.818752	-0.6978	0.485301	0.981636	chr4	6641937	6643225	+	0	NA	3' UTR (N3' UTR (N	2490 NM_001272	93621 Hs.406594NM_03329E ENSG00000MRFP1	PAM14 PGF Morf4 fan protein-coding
chr1-1037	7.433467	0.61617	0.883048	0.697776	0.485317	0.981636	chr1	10375018	10375596	+	0	NA	exon (NM exon (NM	-23757 NM_001304	5226 Hs.464071NM_002631 ENSG00000PGD	6PGD phosphoglycoprotein-coding
chr17-456	7.433467	0.61617	0.883048	0.697776	0.485317	0.981636	chr17	45630622	45630843	+	0	NA	intron (AluS6 SI	8824 NM_00130C	1.05E+08 NM_00125E ENSG00000LINC0221C	CRHR1-IT1 LINC0221C protein-coding
chr3-4708	11.20216	0.497862	0.713157	0.697758	0.485329	0.981636	chr3	47080221	47080981	+	0	NA	intron (intron (N	69050 NR_02404E	1E+08 Hs.201522NR_02404E	NRADDP microRNA pseudo
chr1-1244	11.13559	0.493362	0.707076	0.69775	0.485334	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alph	2902300 NR_00395E	647121 Hs.69768E NR_00395E ENSG00000EMBPI	- embigin pseudo
chr1-7781	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr1	7789731	77897830	+	0	NA	intron (NLIP4 LIN	-7741 NR_10353E	374987 Hs.632414NM_19934E ENSG00000NEXN-AS1	Clorf118 NEXN antincRNA
chr1-1568	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (AluJb SIN	2856 NM_170707	4000 Hs.00557E NM_00557E ENSG00000LMNA	CCDC1 CDE lamin A/C protein-coding
chr10-74	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr10	74016950	74017389	+	0	NA	intron (AluYa5 SI	19053 NM_00337E	7414 Hs.64389E NM_00337E ENSG00000CVCL	CMD1W CM vinculin protein-coding
chr11-108	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr11	1.09E+08	1.09E+08	+	0	NA	intron (AluSx SIN	46417 NM_00439E	1662 Hs.591931NM_00439E ENSG00000DDX10	Dbx4 HRH-DEAD-box protein-coding
chr17-82	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr17	82641421	82644364	+	0	NA	intron (N (Charlie E	5552 NM_01961E	56270 Hs.132161NM_01961E ENSG00000WDR45B	NEDSBA3 WWD repeat protein-coding
chr2-2244	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr2	2.24E+08	2.24E+08	+	0	NA	intron (LIME1 LIN	74438 NM_001257	8452 Hs.37228E NM_00359C ENSG00000CUL3	CUL-3 PH cullin 3 protein-coding
chr5-9347	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr5	93478937	93480256	+	0	NA	intron (NLIME5 LI	91747 NR_10982E	441094 Hs.457407NR_01536E ENSG00000NR2F1-AS1	NR2F1 antincRNA
chr6-176	8.161061	-0.5698	0.817208	-0.69725	0.485643	0.981636	chr6	17631733	17632608	+	0	NA	intron (N (MamRep 187	3216 NM_00095E	5732 Hs.2090 NM_00095E ENSG00000PTGER2	EP2 prostaglandin protein-coding
chr3-4771	7.650607	-0.60161	0.863057	-0.69706	0.485762	0.981636	chr3	47714106	47714368	+	0	NA	intron (AluSx SIN	-52543 NR_145791	1.1E+08 NR_145791	SNORD146 - small nucleolar RNA
chr8-1033	7.650607	-0.60161	0.863057	-0.69706	0.485762	0.981636	chr8	18200 NR_14579E	1.1E+08 NR_14579E	+	0	NA	intron (LIME4b LI	-1365 NR_00307C	692205 Hs.65650E NR_00307C ENSG00000SNORD89	HBIT-289 small nucleolar RNA
chr2-1012	8.119921	-0.57297	0.82202	-0.69703	0.485785	0.981636	chr2	50352104	50352303	+	0	NA	intron (AluSx1 SI	8876 NM_001351	9701 Hs.44909E NM_01467E ENSG00000PPP6R2	KIAA0685 protein protein-coding
chr5-3615	8.119921	-0.57297	0.82202	-0.69703	0.485785	0.981636	chr5	36154273	36155103	+	0	NA	intron (AluJo SIN	2577 NM_032637	6502 Hs.23348 NM_00598E ENSG00000SKP2	FBL1 FBX S-phase kinase protein-coding
chr8-4794	8.119921	-0.57297	0.82202	-0.69703	0.485785	0.981636	chr8	47949535	47950563	+	0	NA	intron (AluSx2 SI	10087 NM_001081	5591 Hs.49168E NM_006904 ENSG00000PRKDC	DNA-PKC I protein kinase protein-coding
chr1-3782	8.418785	0.56065	0.804395	0.696984	0.485813	0.981636	chr1	37821588	37823431	+	0	NA	exon (NM exon (NM	-14301 NM_02464C	79693 Hs.301564NM_02464C ENSG00000YRDC	DRIP3 IRI yrdc N6-t protein-coding
chr1-1451	8.418785	0.56065	0.804395	0.696984	0.485813	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	non-codnon-codir	-1338 NM_00130E	8515 Hs.158237NM_003637 ENSG00000ITGA10	PRO827 integrin protein-coding
chr1-1768	8.418785	0.56065	0.804395	0.696984	0.485813	0.981636	chr1	1.76E+08	1.76E+08	+	0	NA	intron (NLIMEF LI	48904 NM_001001	64326 Hs.523744NM_022457 ENSG00000COP1	RFWD2 RFNF E3 ubiquitin-coding
chr7-745	8.418785	0.56065	0.804395	0.696984	0.485813	0.981636	chr7	74509826	74510031	+	0	NA	intron (AluSc SIN	56022 NM_01632E	9569 Hs.64705E NM_00568E ENSG00000GTF2IRD1	BEN CREAM GTF2I repeat protein-coding
chr10-131	11.69875	0.482326	0.692282	0.696718	0.485979	0.981636	chr10	13111207	13114424	+	0	NA	intron (intron (N	12652 NM_00100E	10133 Hs.33270E NM_02198C ENSG00000COPTN	ALS12 FIF optineurin protein-coding
chr10-381	11.69875	0.482326	0.692282	0.696718	0.485979	0.981636	chr10	38113072	38119262	+	0	NA	TTS (NM_TTS (NM_C	21830 NM_001324	7587 Hs.29257E NM_003421 ENSG00000ZNF37A	KOX21 ZNF zinc finger protein-coding



chr3-4896	7.904631	0.580633	0.838989	0.692062	0.488898	0.981636	chr3	48981441	48982128	+	0	NA	intron (Nintron (N	-8124 NM_17793E	54681	Hs. 654944NM_01773E	ENSG0000CP4HTM	EGLN4 HIF	prolyl 4-protein-coding	
chr11-591	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr11	59182496	59182939	+	0	NA	intron (Nintron (N	10585 NM_015177	23220	Hs. 523696NM_015177	ENSG000000DTX4	RNF155	deltex E protein-coding	
chr17-738	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr17	7389387	7392968	+	0	NA	intron (Nintron (N	3348 NM_001201	57048	Hs. 534591NM_02036E	ENSG000000PLSCR3	-	phospholiprotein-coding	
chr17-812	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr17	81269150	81270215	+	0	NA	intron (Nintron (N	25625 NM_001037	124565	Hs. 352242NM_13857E	ENSG000000SLC38A10	PP1744	solute c protein-coding	
chr2-4225	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr2	42258678	42259109	+	0	NA	intron (Nintron (N	-88662 NR_110584	1.03E+08	Hs. 63982E	NR_110584	LOC10272E	uncharactercna	
chr22-394	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr22	39432176	39432438	+	0	NA	TTS (NM_C	147 NR_04053E	1.01E+08	Hs. 72908CN	_040535	LOC10050E	uncharactercna	
chr3-112	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	intron (N2a LINE	-13587 NM_00134F	55032	Hs. 23748CN	_01794E	ENSG000000SLC35A5	-	solute c protein-coding
chr3-1567	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	26714 NM_001184	25976	Hs. 74405CN	_01550E	ENSG000000TIPARP	ARTD14 PATCD	ind protein-coding
chr5-348	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr5	34832644	34833175	+	0	NA	TTS (NM_C	-6255 NM_14472E	153657	Hs. 435742NM_14472E	ENSG000000TTC23L	MC25-1	tetratric protein-coding	
chr6-177	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr6	17763191	17765253	+	0	NA	exon (NM_exon (NM	57179 NR_13461E	1.05E+08	Hs. 71801CN	_13461E	ENSG000000LOC105374	-	uncharactercna
chr6-4367	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr6	43676858	43677425	+	0	NA	intron (Nintron (N	10671 NM_01813E	55168	Hs. 520145NM_01813E	ENSG000000MRPS18A	HumanS18	mitochondrion protein-coding	
chr8-307	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr8	30701938	30709747	+	0	NA	intron (Nintron (N	22004 NM_000637	2936	Hs. 27151CN	_000637	ENSG000000GSR	GR HEL-7E	glutathic protein-coding
chr9-920	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr9	92054189	92055341	+	0	NA	intron (NAluSc SIN	60648 NM_00641E	10558	Hs. 90458	NM_00641E	ENSG000000SPTLC1	HSAN1 HSN	serine p protein-coding
chr9-116	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr9	1.16E+08	1.16E+08	+	0	NA	TTS (NR_C	3261 NR_103711	493913	Hs. 728832NR_103711	ENSG000000PAPPA-AS1	DP1AS NCF	PAPPA antncRNA	
chr9-125	8.434501	0.556857	0.804711	0.691996	0.48894	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	6595 NM_001174	10244	Hs. 19012	NM_00583E	ENSG000000CRABEPK	RAB9P40 t	Rab9 effe protein-coding
chr13-51	10.57429	0.51378	0.742648	0.691821	0.48905	0.981636	chr13	51387184	51382124	+	0	NA	intron (NAluSq4 SI	-33315 NR_04987E	1.01E+08	NR_04987E	ENSG000000MIR5693	-	microRNA ncRNA	
chr1-150	7.937913	0.5836	0.843632	0.691771	0.489081	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	TTS (NR_C	2994 NR_14574E	1.1E+08	NR_14574E	SNORD13C	-	small nucsnoRNA	
chr11-66	7.937913	0.5836	0.843632	0.691771	0.489081	0.981636	chr11	66341723	66341973	+	0	NA	intron (N(TGTC)A r	3256 NM_001024	25855	Hs. 10042e	NM_01539E	ENSG000000BRMS1	BRMS1	tr protein-coding
chr5-169	2.941067	-0.94376	1.364786	-0.69151	0.489248	0.981636	chr5	1.7E+08	1.7E+08	+	0	NA	intron (NMER1 3 DN	102118 NM_00134E	1E+08	Hs. 721917NM_00112E	ENSG000000INSYN2B	C5orf57 F	inhibitor protein-coding	
chr16-294	7.683889	-0.59634	0.862492	-0.69142	0.489301	0.981636	chr16	29430450	29431154	+	0	NA	intron (Nintron (N	16224 NR_13531E	1E+08	Hs. 55270CN	_13531E	ENSG000000SMG1P6	-	SMG1 pset pseudo
chr1-280	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr1	28040821	28041020	+	0	NA	intron (N2 LINE I	47690 NM_00128E	2140	Hs. 185774NM_00119E	ENSG000000EYA3	-	EMY trans protein-coding	
chr1-565	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr1	56545508	56547371	+	0	NA	intron (Nintron (N	33124 NM_00371E	8613	Hs. 40515E	NM_00371E	ENSG000000PLPP3	Dri42 LPF	phospholiprotein-coding
chr11-90	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr11	90209578	90210893	+	0	NA	intron (N2a LINE	12814 NM_012124	26973	Hs. 22857	NM_012124	ENSG000000CHORDC1	CHP1	cysteine protein-coding
chr12-48	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr12	48679954	48680912	+	0	NA	intron (NAluJr4 SI	1805 NM_01782E	54934	Hs. 50541E	NM_01782E	ENSG000000KANSL2	C12orf41 KAT8	reg protein-coding
chr2-549	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr2	54979263	54979665	+	0	NA	intron (Nintron (N	30808 NM_00700E	57142	Hs. 63785CN	_00700E	ENSG000000RTN4	ASY N122C	reticulor protein-coding
chr2-128	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	69732 NR_027671	56886	Hs. 74330e	NM_02012E	ENSG000000UGGT1	HUGT1 UGUDP	glucc protein-coding
chr20-19	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr20	19853247	19853857	+	0	NA	IntergeniLIP45 LIN	-32969 NM_00124E	54453	Hs. 47227CN	_01899E	ENSG000000RIN2	MACS RASS	Ras and F protein-coding
chr20-49	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr20	49245361	49246912	+	0	NA	3' UTR (N3' UTR (N	26841 NM_01789E	55661	Hs. 65234	NM_01789E	ENSG000000DDX27	DRS1 Drs1	DEAD-box protein-coding
chr3-58	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr3	58167113	58169255	+	0	NA	intron (Nintron (N	2451 NR_135534	1.05E+08	Hs. 613914NR_135534	ENSG000000FLNB-AS1	-	FLNB antncRNA	
chr3-186	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr3	1.87E+08	1.87E+08	+	0	NA	intron (Nintron (N	12312 NM_01630E	51726	Hs. 31719E	NM_01630E	ENSG000000DNAJB11	ABBP-2 A	Flna heat protein-coding
chr4-47	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr4	47453001	47453402	+	0	NA	exon (NM_exon (NM	10501 NM_01784E	54951	Hs. 23956	NM_01784E	ENSG000000COMM8	-	COMM dome protein-coding
chr5-31	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr5	31208696	31209108	+	0	NA	intron (NMaamRTEI I	15216 NM_00493E	1004	Hs. 12477e	NM_00493E	ENSG000000CDH6	CAD6 KCAL	cadherin protein-coding
chr5-43	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr5	43145150	43145517	+	0	NA	intron (Nintron (N	23768 NM_00133C	7690	Hs. 535804NM_00343E	ENSG000000ZNF131	ZBTB35 p	zinc fing protein-coding	
chr5-17	6.384545	-0.63561	0.919361	-0.69137	0.489336	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	IntergeniMIRc SINE	15947 NR_00298E	67784	Hs. 69272CN	_00298E	ENSG000000SNORA74B	U19-2	small nucsnoRNA
chr12-4	6.4917	-0.74589	1.078962	-0.69131	0.489373	0.981636	chr12	4503996	4504599	+	0	NA	intron (Nintron (N	34175 NM_020374	57102	Hs. 302977NM_020374	ENSG000000C12orf4	-	chromosom protein-coding	
chr14-49	10.38332	-0.50471	0.730244	-0.69115	0.489469	0.981636	chr14	49583305	49584736	+	0	NA	intron (Nintron (N	2482 NM_00103C	6235	Hs. 51367NM_00103E	ENSG000000RPS29	-	chromosom protein-coding	
chr7-7	10.38332	-0.50471	0.730244	-0.69115	0.489469	0.981636	chr7	74181682	74181942	+	0	NA	intron (NAluSq4 SI	7456 NM_03199E	7458	Hs. 52094e	NM_02217E	ENSG000000EIF4H	WBCSR1 W	eukaryoti protein-coding
chr1-9	6.5707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr1	91262337	91262963	+	0	NA	intron (Nintron (N	22753 NM_00128E	9563	Hs. 463511NM_00428E	ENSG000000H6PD	CORTRD1 C	hexose-6- protein-coding	
chr11-6	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr11	61785686	61786746	+	0	NA	3' UTR (N3' UTR (N	6345 NR_03034E	693196	NR_03034E	ENSG000000MIR611	MIRN611 ch	xros ncRNA	
chr11-6	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr11	64897857	64898871	+	0	NA	promoter-promoter-	73 NR_10680E	1.02E+08	NR_10680E	ENSG000000MIR6750	hsa-mir-6	microRNA ncRNA	
chr11-6	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr11	67495257	67496509	+	0	NA	intron (Nintron (N	5638 NR_10681E	1.02E+08	NR_10681E	ENSG000000MIR6752	hsa-mir-6	microRNA ncRNA	
chr11-6	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr11	68410514	68412142	+	0	NA	intron (Nintron (N	-49424 NM_00135E	55291	Hs. 503022NM_01831E	ENSG000000PPP6R3	Hsaorf23 p	rotein protein-coding	
chr12-4	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr12	49655958	49657814	+	0	NA	exon (NM_exon (NM	26342 NM_00136E	25766	Hs. 706827NM_01227E	ENSG000000PRPF40B	HYPIC	pre-mRNA protein-coding	
chr12-5	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr12	52011436	52014955	+	0	NA	intron (NAlu SINE	2703 NM_00127E	160622	Hs. 407202NM_18171E	ENSG000000GRASP	TAMALIN	general i protein-coding	
chr12-1	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr12	1.25E+08	1.25E+08	+	0	NA	intron (N2a LINE	18385 NM_03265E	57647	Hs. 10738E	NM_03265E	ENSG000000DHX37	DDX37 Dhr	DEAH-box protein-coding
chr14-10	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	-18573 NR_07308E	1397	Hs. 53430e	NM_00131E	ENSG000000CRIP2	CRIP1 CRP2	cysteine protein-coding
chr15-5	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr15	50974288	50975359	+	0	NA	intron (NLIMB1 LIN	30694 NR_02764E	1E+08	Hs. 73049E	NR_02764E	DCAF13P3	-	DDB1 and pseudo
chr15-7	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr15	71846173	71847355	+	0	NA	intron (Nintron (N	36210 NM_01424E	10002	Hs. 187354NM_01424E	ENSG000000NR2E3	ESCS PNR	nuclear i protein-coding	
chr20-1	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr20	18569984	18570536	+	0	NA	TTS (NM_C	2840 NM_00134F	388789	Hs. 349092NM_00134E	ENSG000000SMIM26	LINC0049E	small intron protein-coding	
chr20-5	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr20	50199462	50199835	+	0	NA	IntergeniMLT1 LITF	-7579 NR_12573E	1.02E+08	Hs. 44248e	NR_12573E	ENSG000000CEBPB-AS1	-	CEBPB antncRNA
chr22-4	5.707984	0.675242	0.977032	0.691116	0.489492	0.981636	chr22	42870401	42871643	+	0									

chr2-1874 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr2	1.87E+08	1.87E+08	+	0 NA	intron (Nintron (N	-19932 NM_001271	12023 Hs. 470882NM_005799	ENSG00000CALCRL	CGRPR CRI	calcitriol protein-coding
chr2-463 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr22	46340430	46341082	+	0 NA	intron (NMIR3 SINE	5042 NM_001282	55687 Hs. 439524NM_018006	ENSG00000TRMU	LCAL3 MT	LCAL3 5-mecp protein-coding
chr3-1025 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr3	10298795	10301917	+	0 NA	TTS (NM_TTS (NM_1	-7409 NM_001134	51738 Hs. 59008CNM_016362	ENSG00000GHRL	MTLPR	ghrelin protein-coding
chr3-108 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr3	1.08E+08	1.08E+08	+	0 NA	intron (NLM2 LINE	13093 NM_001777	961 Hs. 446414NM_001777	ENSG00000CD47	IAP MER6	CD47 mole protein-coding
chr3-1605 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr3	1.61E+08	1.61E+08	+	0 NA	intron (NAluJ SINE	4026 NR_003001	677767 Hs. 675955NR_003001	ENSG00000SCARNA7	U90	small Ca <sub>v</sub> ncRNA
chr4-675 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr4	67508434	67508824	+	0 NA	intron (NMIRb SINE	36874 NM_001812	1060 Hs. 479867NM_001812	ENSG00000CENPC	CENP-C CF	centromere protein-coding
chr4-1684 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr4	1.68E+08	1.68E+08	+	0 NA	intron (NLI2A LINE	34824 NM_001291	91351 Hs. 535011NM_001291	ENSG00000DDX60L		DEXD/H-bc protein-coding
chr4-1855 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr4	1.85E+08	1.85E+08	+	0 NA	TTS (NM_TTS (NM_1	3448 NM_181726	353322 Hs. 508154NM_181726	ENSG00000ANKRD37	Lrp2bp	ankyrin protein-coding
chr5-7968 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr5	79680698	79682413	+	0 NA	intron (Nintron (N	-8281 NM_15361C	202333 Hs. 482622NM_15361C	ENSG00000CMTA5	C5orf10 S	cardiomy protein-coding
chr5-9352 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr5	93525254	93527522	+	0 NA	intron (NLI2A LINE	44955 NR_109822	441094 Hs. 457407NR_109822	ENSG00000NR2F1-AS1	NR2F1	antncRNA
chr5-1461 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr5	1.46E+08	1.46E+08	+	0 NA	intron (Nintron (N	5563 NM_020117	51520 Hs. 432674NM_01646C	ENSG00000LARS	HSPC192 I	lucyl-tf protein-coding
chr5-1762 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr5	1.76E+08	1.76E+08	+	0 NA	intron (Nintron (N	2790 NM_001317	51491 Hs. 696282NM_016391	ENSG00000CNP16	HSPC111 F	NOP16 nuc protein-coding
chr6-1005 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr6	1.01E+08	1.01E+08	+	0 NA	intron (NLI2a LINE	-133685 NM_005068	6492 Hs. 520292NM_005068	ENSG00000SIM1	bHLHe14	SIM bHLH protein-coding
chr6-1365 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr6	1.37E+08	1.37E+08	+	0 NA	intron (NLI2b LINE	-27537 NM_00398C	9053 Hs. 486549NM_00398C	ENSG00000MAP7	E-MAP-11E	microtub protein-coding
chr7-2993 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr7	29933115	29934514	+	0 NA	intron (Nintron (N	55987 NM_014766	9805 Hs. 520744NM_014766	ENSG00000SCRN1	SES1	secernin protein-coding
chr7-423 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr7	47323027	47324608	+	0 NA	intron (NLMda LINE	140986 NR_14581E	1.1E+08 NR_14581E	SNORD151		small nucsnoRNA
chr7-171 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr7	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	76797 NM_001105	79774 Hs. 189652NM_024913	ENSG00000CPED1	C7orf58	cadherin protein-coding
chr7-135 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr7	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	-23782 NM_00113C	647087 Hs. 200022NM_00113C	ENSG00000STMP1	C7orf73 F	short tr protein-coding
chr8-378 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr8	37868833	37869545	+	0 NA	intron (NAluJb SINE	-19328 NM_01831C	55290 Hs. 709301NM_01831C	ENSG00000BRF2	BRFU TF11	BRF2 RNA protein-coding
chr9-114 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chr9	1.14E+08	1.14E+08	+	0 NA	TTS (NR_TTS (NR_C	608 NR_03025E	619556 NR_03025E	ENSG00000MIR455	MIRN455 I	microRNA ncRNA
chr9-1092 6.417827	-0.62956	0.913975	-0.68881	0.49094	0.981636	chrX	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	-48717 NM_012282	23630 Hs. 522752NM_012282	ENSG00000CKNE5	KCNE1	potassium protein-coding
chr1-279 6.674702	0.67127	0.975535	0.688105	0.491387	0.981636	chr1	27964011	27965190	+	0 NA	intron (NLI2b LINE	5138 NM_01805E	55113 Hs. 55024 NM_01805E	ENSG00000XKR8	XRG8 HXK	HK relate protein-coding
chr2-121 6.674702	0.67127	0.975535	0.688105	0.491387	0.981636	chr2	1.22E+08	1.22E+08	+	0 NA	intron (NAluY SINE	10223 NM_001142	23332 Hs. 469844NM_01528E	ENSG00000CLASP1	MAST1	cytoplasm protein-coding
chr20-324 6.674702	0.67127	0.975535	0.688105	0.491387	0.981636	chr20	32462409	32462628	+	0 NA	intron (Nintron (N	20972 NM_001351	140688 Hs. 516978NM_08061E	ENSG00000NOL4F	C20orf12	nucleolar protein-coding
chr21-464 6.674702	0.67127	0.975535	0.688105	0.491387	0.981636	chr21	46463816	46464321	+	0 NA	intron (Nintron (N	1597 NR_04640C	1.01E+08 Hs. 737163NR_04640C	ENSG00000DIP2A-IT1	DIP2A	intncRNA
chr16-251 8.956513	0.53752	0.781162	0.688103	0.491388	0.981636	chr16	25166855	25167054	+	0 NA	intron (Nintron (N	-17922 NR_03999E	1.01E+08 Hs. 657576NR_03999E	ENSG00000LCMT1-AS2	LCMT1	antncRNA
chr19-325 8.956513	0.53752	0.781162	0.688103	0.491388	0.981636	chr19	32592591	32592821	+	0 NA	intron (NAluJr SINE	19252 NM_00108C	84902 Hs. 59970E	ENSG00000CEP89	CCDC123 C	centromer protein-coding
chr8-472 8.956513	0.53752	0.781162	0.688103	0.491388	0.981636	chr8	47291283	47291861	+	0 NA	intron (NMIRb SINE	30634 NM_00108C	23514 Hs. 38105E	ENSG00000SPIDR	KIAA0146	scaffold protein-coding
chr16-89 10.61358	0.506117	0.73579	0.68755	0.491544	0.981636	chr16	89906425	89907210	+	0 NA	intron (Nintron (N	-11062 NM_00238E	4157 Hs. 51382E	ENSG00000CMCIR	CM55 MSH	melanocor protein-coding
chr12-297 10.37546	-0.50346	0.732023	-0.68776	0.491604	0.981636	chr12	29757469	29758249	+	0 NA	intron (Nintron (N	29575469	29575469	ENSG00000TMT1C	25883 OLH	transmem protein-coding
chr5-102 10.37546	-0.50346	0.732023	-0.68776	0.491604	0.981636	chr5	10262000	10264463	+	0 NA	exon (NM_exon (NM_	12694 NM_00130E	22948 Hs. 1600 NM_01207E	ENSG00000CCT5	CCT-epsil	chaperon protein-coding
chr11-68 7.863492	0.579581	0.842757	0.68772	0.491629	0.981636	chr11	68526306	68526552	+	0 NA	intron (NAluJb SINE	65727 NM_00135E	55291 Hs. 503022NM_01831E	ENSG00000PPP6R3	C11orf23 P	protein protein-coding
chr19-452 7.863492	0.579581	0.842757	0.68772	0.491629	0.981636	chr19	45695619	45695916	+	0 NA	intron (Nintron (N	3101 NM_01765E	54814 Hs. 63155E	ENSG00000QPCTL	gQC	glutamin protein-coding
chr5-770 7.863492	0.579581	0.842757	0.68772	0.491629	0.981636	chr5	77055755	77056345	+	0 NA	intron (NLMEL LINE	24521 NR_003014	677828 Hs. 69324E	ENSG00000SNORA47	HBI-115	small nucsnoRNA
chr12-26 5.940655	-0.66965	0.974306	-0.68731	0.491886	0.981636	chr12	26931708	26931680	+	0 NA	intron (NAluSc8 SINE	6602 NM_018164	55726 Hs. 505077NM_018164	ENSG00000INTS13	ASOD C12c	integrat protein-coding
chr16-71 5.940655	-0.66965	0.974306	-0.68731	0.491886	0.981636	chr16	71665059	71665578	+	0 NA	intron (NAluSc8 SINE	33383 NR_033337	51708 Hs. 72511E	ENSG00000SNORA70D	UT0D	small nucsnoRNA
chr2-388 5.940655	-0.66965	0.974306	-0.68731	0.491886	0.981636	chr2	38850310	38851047	+	0 NA	intron (Nintron (N	25256 NM_19896E	90957 Hs. 46822E	ENSG00000DXH57	DDX57	DEXH-box protein-coding
chr20-25 5.940655	-0.66965	0.974306	-0.68731	0.491886	0.981636	chr20	25427129	25427456	+	0 NA	intron (NAluSg2 SINE	19607 NR_134574	9837 Hs. 658464NM_021067	ENSG00000GINS1	INM57 PSF	GINS comp protein-coding
chr19-404 8.401219	0.553967	0.806046	0.687265	0.491915	0.981636	chr19	40036305	40037562	+	0 NA	exon (NM_exon (NM_	19701 NM_00100E	163131 Hs. 10113E	ENSG00000ZNF780B	ZNF779	zinc finger protein-coding
chr19-49 8.401219	0.553967	0.806046	0.687265	0.491915	0.981636	chr19	49015445	49015682	+	0 NA	TTS (NM_TTS (NM_C	1527 NM_000894	3972 Hs. 154704NM_000894	ENSG00000LHB	CGB4 HH2	luteinizer protein-coding
chr1-129 6.222138	0.639656	0.930865	0.687163	0.49198	0.981636	chr1	1293194	1293694	+	0 NA	3' UTR (N3' UTR (N	2726 NR_106784	1.02E+08 NR_106784	ENSG00000MIR6726	hsa-mir-6	microRNA ncRNA
chr17-174 6.222138	0.639656	0.930865	0.687163	0.49198	0.981636	chr17	17486573	17487390	+	0 NA	intron (NLTR12C LINE	9414 NM_016084	51655 Hs. 25829 NM_016084	ENSG00000CRASD1	AGS1 LTXF	ras relat protein-coding
chr8-2631 6.222138	0.639656	0.930865	0.687163	0.49198	0.981636	chr8	26316290	26316800	+	0 NA	intron (Nintron (N	23329 NM_001177	5520 Hs. 14633E	ENSG00000PPP2R2A	B55A B55	protein protein-coding
chr11-117 8.948655	0.539339	0.784931	0.687117	0.492009	0.981636	chr11	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	34331 NM_01495E	22897 Hs. 50400E	ENSG00000CEP164	NPHP15	syntaxon protein-coding
chr1-2774 6.229996	0.637048	0.927193	0.687072	0.492038	0.981636	chr1	27749060	27750631	+	0 NA	intron (Nintron (N	-23734 NM_177424	23673 Hs. 52385E	ENSG00000CSTX12	STX13 ST	syntxin protein-coding
chr12-10 6.229996	0.637048	0.927193	0.687072	0.492038	0.981636	chr12	1.06E+08	1.06E+08	+	0 NA	intron (NIGger17a	70321 NM_01484C	9891 Hs. 52469E	ENSG00000NUAK1	ARK5	NUAK fami protein-coding
chr12-11 6.229996	0.637048	0.927193	0.687072	0.492038	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	intron (NERV3-16A3	58020 NM_001347	28981 Hs. 52838E	ENSG00000IFT81	CDV-1 CDV	intraflag protein-coding
chr2-203 6.229996	0.637048	0.927193	0.687072	0.492038	0.981636	chr2	1.62E+08	1.62E+08	+	0 NA	intron (Nintron (N	8590 NM_00193E	1803 Hs. 36891E	ENSG00000DPP4	ADABP ADC	dipteryd protein-coding
chr2-1621 6.229996	0.637048	0.927193	0.687072	0.492038	0.981636	chr2	2.03E+08	2.03E+08	+	0 NA	intron (NAluS6 SINE	-60155 NM_177538	57404 Hs. 44606E	ENSG00000CYP20A1	CYP-M	cytochrome protein-coding
chr20-34 6.229996	0.637048	0.927193	0.687072	0.492038	0.981636	chr20	34287184	34288125	+	0 NA	intron (NAluS2 SINE	15336 NM_001322	191 Hs. 388004NM_000687	ENSG00000AHCY	SAHH ado	adenosyl protein-coding
chr22-17 6.229996	0.637048	0.927193	0.687072	0.492												



chr10-744	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr10	74003791	74005843	+	0	NA	intron (AluSx SIN	6701 NM_003373	7414 Hs. 643899NM_003373	ENSG000000CVCL	CMD1W CMF vinculin protein-coding
chr11-204	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr11	20408872	20409354	+	0	NA	intron (intron (N	21397 NM_005788	10196 Hs. 152337NM_005788	ENSG000000PRMT3	HRMT1L3 protein εprotein-coding
chr11-668	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr11	66858494	66860345	+	0	NA	intron (intron (N	2355 NM_001363	78999 Hs. 209979NM_024033	ENSG000000LRFN4	FIGLER6 S leucine rprotein-coding
chr11-857	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr11	85730724	85732429	+	0	NA	intron (NLIP47 LIN	-12226 NM_001298	54843 Hs. 369522NM_032373	ENSG000000SYTL2	CHR115Y7 synaptotagmin protein-coding
chr12-494	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr12	49987603	49997331	+	0	NA	intron (intron (N	19520 NM_001652	363 Hs. 54505 NM_001652	ENSG000000AQP6	AQP2L KII aquaporin protein-coding
chr13-482	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr13	48321411	48322194	+	0	NA	intron (AluSq2 SI	18055 NM_000321	5925 Hs. 408522NM_000321	ENSG000000CRB1	OSRC PPP1R3B transcr protein-coding
chr13-111	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (intron (N	16558 NM_001352	79587 Hs. 508722NM_024537	ENSG000000CAR52	COXP227 cysteinyln protein-coding
chr17-124	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr17	12081395	12082598	+	0	NA	promoter-promoter-	197 NR_030611	NR_030611	ENSG000000MIR744	MIRN744 microRNA ncRNA
chr17-424	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr17	42008836	42009860	+	0	NA	intron (intron (N	7817 NM_001144	7266 Hs. 500156NM_003311	ENSG000000DNAJC7	DJ11 DJC7DnaJ heatprotein-coding
chr19-374	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr19	37760133	37760593	+	0	NA	intron (NLIM4a LI	19227 NM_001172	126231 Hs. 531262NM_152366	ENSG000000ZNF573	- zinc fing protein-coding
chr19-521	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr19	52195923	52198219	+	0	NA	intron (Charlie4e	-4125 NM_001136	5518 Hs. 467192NM_014222	ENSG000000PPP2R1A	MRD36 PP2 protein i protein-coding
chr2-4042	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr2	40428702	40430295	+	0	NA	exon (NM exon (NM	806 NM_001112	6546 Hs. 31961 NM_021097	ENSG000000SLC8A1	NCX1 solute cεprotein-coding
chr2-201C	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	IntergeniAluSx1 SI	15208 NM_001257	4709 Hs. 109766NM_002491	ENSG000000DNDFB3	B12 CI-B1NADH:ubiquinone-protein-coding
chr2-224	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (intron (N	-29380 NM_001172	3769 Hs. 467363NM_002242	ENSG000000KCNJ1	KIR1.4 K1potassium protein-coding
chr22-328	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr22	32808684	32810138	+	0	NA	intron (intron (N	8595 NM_000362	7078 Hs. 644633NM_000362	ENSG000000TIMP3	HSMRK222 TIMP metεprotein-coding
chr3-4862	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr3	48622020	48622840	+	0	NA	promoter-promoter-	-661 NM_001008	440955 Hs. 631922NM_001008	ENSG000000TMEM89	- transment protein-coding
chr4-195	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr4	1950317	1951374	+	0	NA	intron (intron (N	23609 NR_003004	67770 Hs. 676951NM_003004	ENSG000000SCARN22	ACA11 small Ca_ncRNA
chr4-1682	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (intron (N	42036 NM_017631	55601 Hs. 591711NM_017631	ENSG000000DDX60	- Dexd/H-bcprotein-coding
chr6-1547	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr6	1.55E+08	1.55E+08	+	0	NA	intron (AluS6 SI	45322 NM_00128E	22828 Hs. 591325NM_014892	ENSG000000SCAF8	RBM16 SR-relate protein-coding
chr7-9234	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr7	92386181	92387295	+	0	NA	intron (intron (N	50576 NR_145992	1.05E+08 NM_001317	ENSG000000TMB17P	- transment pseudo
chr9-339	4.666735	-0.7321	1.068789	-0.68498	0.493353	0.981636	chr9	33937152	33938296	+	0	NA	intron (AluSq SIN	-13349 NR_102377	1.01E+08 NR_102377	ENSG000000SNORD121E	- small nucsnRNA
chr1-1135	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr1	1.14E+08	1.14E+08	+	0	NA	exon (NM exon (NM	6214 NM_001363	64858 Hs. 591412NM_022833	ENSG000000DCLRE1B	APOLLO SN DNA crossprotein-coding
chr11-13C	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr11	1.31E+08	1.31E+08	+	0	NA	intron (intron (N	-19276 NR_125382	1.04E+08 Hs. 430303NR_125382	ENSG000000LOC103611	- uncharactncRNA
chr12-957	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr12	95727723	95729069	+	0	NA	intron (NLIMB7 LIN	61799 NM_001325	59277 Hs. 201034NM_021222	ENSG000000NTN4	PRO3091 netrin 4 protein-coding
chr12-101	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (AluSp SIN	11300 NM_014503	27340 Hs. 295732NM_014503	ENSG000000UTP20	IAG DRIM UTP20 smεprotein-coding
chr19-471	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr19	47146648	47148241	+	0	NA	intron (AluJb SIN	16609 NM_001145	10055 Hs. 515500NM_005500	ENSG000000SAE1	AOS1 HSPC SUMO1 actεprotein-coding
chr2-181	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr2	1.82E+08	1.82E+08	+	0	NA	intron (NL2c LINE	20479 NM_001287	6744 Hs. 196983NM_006751	ENSG000000ITPRID2	CS-1 CSI1 ITPR intεprotein-coding
chr3-5264	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr3	52646691	52647070	+	0	NA	intron (NLIMB8 LIN	38719 NM_00135C	55193 Hs. 189922NM_018161	ENSG000000PBRM1	BAF180 PE polybrom protein-coding
chr3-1111	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr3	1.11E+08	1.11E+08	+	0	NA	intron (intron (N	93094 NM_001243	25945 Hs. 293917NM_015483	ENSG000000NECTIN3	CD113 CDWnectin cεprotein-coding
chr4-5644	6.376688	-0.63372	0.925201	-0.68496	0.493371	0.981636	chr4	56448300	56449528	+	0	NA	intron (intron (N	12654 NM_001075	10606 Hs. 518774NM_006452	ENSG000000PAICS	ADE2 ADE2 phosphor i protein-coding
chr4-102f	8.597094	-0.54896	0.801768	-0.68469	0.493541	0.981636	chr4	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	-108939 NR_136202	1.05E+08 Hs. 15833 NR_136202	LOC105377-	- uncharactncRNA
chr2-206	8.526488	0.567512	0.829049	0.685433	0.493639	0.981636	chr2	2.06E+08	2.06E+08	+	0	NA	intron (THE1B-int	69801 NM_017755	54891 Hs. 445033NM_017755	ENSG000000IN080D	- IN080 conprotein-coding
chr16-701	12.17777	0.463337	0.677607	0.683784	0.494111	0.981636	chr16	1.54E+08	1.54E+08	+	0	NA	3' UTR (3' UTR (N	15922 NR_126007	400541 Hs. 461183NR_126007	ENSG000000LOC400541	- uncharactncRNA
chr19-581	12.17777	0.463337	0.677607	0.683784	0.494111	0.981636	chr19	58184823	58214192	+	0	NA	intron (AluSz SIN	16446 NM_133502	10782 Hs. 83761 NM_016324	ENSG000000ZNF274	HFB101 Z zinc fing protein-coding
chr1-4344	8.442359	0.55489	0.811516	0.683769	0.494121	0.981636	chr1	43446307	43449293	+	0	NA	promoter-promoter-	-739 NR_106793	1.02E+08 NR_106793	ENSG000000MIR6735	hwa-mir-εmicroRNA ncRNA
chr1-1537	8.442359	0.55489	0.811516	0.683769	0.494121	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	intron (intron (N	-2554 NR_14582E	11000 Hs. 438722NM_024333	ENSG000000SLC27A3	ACSVL3 Fεsolute cεprotein-coding
chr12-121	8.442359	0.55489	0.811516	0.683769	0.494121	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (intron (N	48714 NM_001178	144406 Hs. 709837NM_144668	ENSG000000WDR66	CFAP251 CWD repeatprotein-coding
chr5-1484	8.442359	0.55489	0.811516	0.683769	0.494121	0.981636	chr5	1.48E+08	1.48E+08	+	0	NA	intron (intron (N	43999 NM_003079	81545 Hs. 483772NM_030792	ENSG000000FBX038	Fbx38 HMM F-box prcprotein-coding
chr17-175	7.41265	0.679101	0.993189	0.683758	0.494128	0.981636	chr17	17861401	17862354	+	0	NA	intron (intron (N	-24866 NM_00417E	6720 Hs. 592122NM_00417E	ENSG000000SREBF1	SREBF1 βsterol rεprotein-coding
chr19-191	5.741265	0.679101	0.993189	0.683758	0.494128	0.981636	chr19	19182193	19183039	+	0	NA	non-codiron-codir	9536 NR_027308	4207 Hs. 153622NM_005911	ENSG000000BORCS8-MF	LOC729991 BORCS8-MF protein-coding
chr7-5205	5.741265	0.679101	0.993189	0.683758	0.494128	0.981636	chr7	5205811	5206895	+	0	NA	intron (intron (N	-7916 NM_001033	26100 Hs. 122263NM_015611	ENSG000000WIP12	ATG18B AtWD repeatprotein-coding
chr9-9808	5.874091	-0.68331	0.999924	-0.68336	0.494377	0.981636	chr9	98084330	98084971	+	0	NA	3' UTR (3' UTR (N	27918 NM_001894	54187 Hs. 522331NM_018944	ENSG000000CNANS	HEL-S-10CN-acetyl r protein-coding
chr17-374	10.83507	-0.49373	0.722557	-0.68331	0.494412	0.981636	chr17	37440559	37440979	+	0	NA	intron (intron (N	33544 NM_001488	6871 Hs. 500666NM_001488	ENSG000000TADA2A	ADA2 ADA2 transcriεprotein-coding
chr8-2874	3.982501	0.785909	1.150301	0.683221	0.494467	0.981636	chr8	28749794	28750587	+	0	NA	intron (intron (N	48689 NR_07346E	2137 Hs. 491354NM_00144C	ENSG000000EXTL3	BOTV EXTL exostosin r protein-coding
chr10-35	6.962303	0.656237	0.960565	0.683178	0.494495	0.981636	chr10	35530098	35530348	+	0	NA	exon (NM exon (NM	-75118 NM_15336E	219770 Hs. 638922NM_15336E	ENSG000000CGJD4	CX40.1 gap junct protein-coding
chr22-394	6.962303	0.656237	0.960565	0.683178	0.494495	0.981636	chr22	39415602	39415805	+	0	NA	intron (intron (N	15923 NM_00611E	10454 Hs. 507681NM_00611E	ENSG000000TAB1	3'-Tab1 MTGF-beta protein-coding
chr9-218	8.078782	-0.57628	0.84364	-0.68309	0.494551	0.981636	chr9	21864619	21864900	+	0	NA	3' UTR (3' UTR (N	62123 NM_002451	4507 Hs. 193266NM_002451	ENSG000000MTAP	BDMF DMSF methylthi protein-coding
chr1-218	8.409077	0.552034	0.808378	0.682891	0.494676	0.981636	chr1	21883657	21886783	+	0	NA	intron (intron (N	59290 NM_001291	3339 Hs. 562227NM_005521	ENSG000000HSPG2	HSPG PLC heparan sεprotein-coding
chr11-77	8.409077	0.552034	0.808378	0.682891	0.494676	0.981636	chr11	77696945	77697207	+	0	NA	intron (MIR SINE	-52970 NM_001311	1207 Hs. 430733NM_001291	ENSG000000CLNS1A	CLC1 CLNC chloride protein-coding
chr16-56	8.409077	0.552034	0.808378	0.682891	0.494676	0.981636	chr16	56500356	56503220	+	0	NA	intron (intron (N	18236 NM_03188E	5883 Hs. 333733NM_03188E	ENSG000000BBS2	BBS RP74 Bardet-Bi protein-coding
chr19-212	8.409077	0.552034	0.808378	0.682891	0.494676	0.981636	chr19	2120708	2121811	+	0	NA	exon (NM exon (NM	24344 NM_001035	113177 Hs. 424045NM_052871	ENSG000000IZUM04	C19orf36 IZUM0 fan protein-coding
chr4-1697	8.409077	0.552034	0.808378	0.682891	0.494676	0.981636	chr4	1.7E+08	1.7E+08	+	0	NA	intron (intron (N	44522 NM_017867	54969 Hs. 406756NM_017867	ENSG000000HPP1	C4orf27 histone F protein-coding
chr5-119	8.409077	0.552034	0.808378	0.682891	0.494676	0.981636	chr5	1.2E+08	1.2E+08	+	0	NA	intron (NLIM4				

chr14-214.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr14	21466394	21467431	+	0	NA	intron (AluSx4 SI	9762	NM_001163	84932	Hs.22399	NM_03284 ENSG0000CRAB2B	-	RAB2B, mc	protein-coding	
chr14-751.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr14	75100662	75101122	+	0	NA	intron (intron (N	26156	NM_001325	91754	Hs.7200	NM_03311 ENSG0000NEK9	-	APUG LCCSNIMA	rel protein-coding	
chr14-921.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr14	92129002	92129833	+	0	NA	intron (NL2a LINE	7448	NM_001322	53981	Hs.657632	NM_017437 ENSG0000CPSF2	-	CPSF100	cleavage protein-coding	
chr14-102.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	TTS (NM_CTS (NM_C	18908	NM_03263C	51550	Hs.129634	NM_03263C ENSG0000CINP	-	CINP	cyclin d protein-coding	
chr15-48.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr15	48848156	48850076	+	0	NA	intron (intron (N	-29018	NM_01433E	23741	Hs.255977	NM_01433E ENSG0000CED1	-	C15orf3 CEP300	intron protein-coding	
chr15-657.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr15	65783885	65785051	+	0	NA	intron (LIMC3 LIN	7825	NM_00132C	10260	Hs.654567	NM_00584E ENSG0000CENND4A	-	ENND4A	domain protein-coding	
chr16-19.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr16	19630509	19633436	+	0	NA	intron (AluSx SIN	76269	NM_00136E	57020	Hs.654964	NM_020314 ENSG0000CVPS35L	-	VP35	encl protein-coding	
chr17-196.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr17	19652696	19653845	+	0	NA	intron (AluSx SIN	4519	NM_001031	224	Hs.49988E	NM_00038E ENSG0000ALDH3A2	-	ALDH10F FALDH	aldehyde protein-coding	
chr17-295.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr17	29514151	29516265	+	0	NA	intron (intron (N	51829	NM_198147	116236	Hs.10651	CNM_198147 ENSG0000CABHD15	-	ABHD15	abhydrolase protein-coding	
chr17-31.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr17	31002256	31027603	+	0	NA	IntergeniAluS	-5855	NM_00135C	1.08E+08	Hs.558901	NM_001350575	LOC107984	-	LOC107984	uncharacter protein-coding
chr18-17.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr18	172429	1727107	+	0	NA	intron (Tigger L	14016	NM_005151	9097	Hs.64441	CNM_005151 ENSG0000CUSP14	-	CUSP14	ubiquitin protein-coding	
chr18-95.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr18	9501853	9503265	+	0	NA	intron (AluY SINE	27046	NM_00678E	10928	Hs.52899	CNM_00678E ENSG0000CRALBP1	-	RALBP1	bin protein-coding	
chr19-957.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr19	9574280	9575305	+	0	NA	intron (LTR OCL L	9712	NM_00130E	7675	Hs.501537	NM_00100E ENSG0000CNZF121	-	ZNF121	zinc finger protein-coding	
chr19-164.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr19	16420296	16422740	+	0	NA	intron (intron (N	50452	NM_00125E	58513	Hs.65463E	NM_02123E ENSG0000CEPS15L1	-	EPS15R	epidermal protein-coding	
chr2-2441.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr2	244177	245170	+	0	NA	intron (MIR SINE	11667	NM_00128E	26751	Hs.515951	NM_015677 ENSG0000CSH3YL1	-	SH3YL1	SH3 and protein-coding	
chr2-174.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr2	1.74E+08	1.74E+08	+	0	NA	intron (THE1C-int	5866	NM_00488E	9541	Hs.632531	NM_00488E ENSG0000CIR1	-	CIR	corepress protein-coding	
chr20-114.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr20	1145894	1147100	+	0	NA	intron (intron (N	27895	NM_00132E	9491	Hs.471917	NM_006814 ENSG0000CPSMF1	-	P131	proteasome protein-coding	
chr21-392.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr21	39273581	39276828	+	0	NA	intron (intron (N	38428	NM_01896E	54014	Hs.62713E	NM_01896E ENSG0000CBRDW1	-	BRDW1	C21orf107 bromodome protein-coding	
chr22-232.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr22	23292521	23294188	+	0	NA	intron (MIR3 SINE	30587	NR_03340E	26226	Hs.72958E	NR_03340E ENSG0000CFBXW4P1	-	FBXW4	FBXW-box an pseudo	
chr22-504.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr22	50449868	50451000	+	0	NA	intron (AluSx1 SI	24601	NM_00297E	6305	Hs.589924	NM_00297E ENSG0000CSBF1	-	SBF1	CMT4B3 DESET	bind protein-coding
chr3-185.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr3	1.85E+08	1.85E+08	+	0	NA	intron (intron (N	152056	NM_00102E	285382	Hs.24579E	NM_00102E ENSG0000C3orf70	-	C3orf70	chromosome protein-coding	
chr7-1491.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr7	1491474	1492389	+	0	NA	intron (LIMB8 LIN	12458	NM_00108C	26173	Hs.53218E	NM_00108C ENSG0000CNTS1	-	INTS1	INT1 NET2	integrat protein-coding
chr7-1392.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (AluJr SIN	38693	NM_17356E	250408	Hs.15345E	NM_17356E ENSG0000CUBN2	-	CUBN2	ubiquitin protein-coding	
chr8-423.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr8	42302724	42310475	+	0	NA	intron (intron (N	-29620	NM_00269C	5423	Hs.654484	NM_00269C ENSG0000CPOLB	-	POLB	DNA polyn protein-coding	
chr8-1442.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	TTS (NM_CTS (NM_C	48908	NR_107057	1.02E+08	NR_107057	ENSG0000CIR1712	-	MIR1712	l-microRNA ncRNA	
chrX-474.6.204572.0.630747.0.926949.0.680455.0.496216.0.981636	chrX	47451742	47454676	+	0	NA	intron (AluJr SIN	14460	NM_001324	7592	Hs.496074	NM_00713C ENSG0000CZNF41	-	ZNF41	zinc finger protein-coding	
chr1-1182.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr1	11828500	11830175	+	0	NA	intron (intron (N	-10982	NR_03780E	1E+08	Hs.71001E	NR_03780E	NPPA-AS1	NPPA	antincRNA	
chr1-1504.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (AluSp SIN	-39914	NM_001271	80222	Hs.288974	NM_02515E ENSG0000CARS2	-	COXP211	l-threonyl-protein-coding	
chr1-1508.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr1	1.58E+08	1.58E+08	+	0	NA	intron (intron (N	53790	NR_03394E	642628	Hs.50690E	NR_03394E ENSG0000CLINCO170A	-	LINC0170A	long intncRNA	
chr1-1602.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr1	1.6E+08	1.6E+08	+	0	NA	intron (intron (N	-14523	NR_12372E	729867	Hs.674191	NR_12372E ENSG0000CLOC29867	-	CLOC29867	uncharactercna	
chr1-220C.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (AluS6 SI	36648	NM_00444E	2058	Hs.49778E	NM_00444E ENSG0000CEPRS	-	CEPRS	EARS GLUF	glutamyl-protein-coding
chr10-274.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr10	29485775	29494500	+	0	NA	intron (intron (N	54959	NR_03033E	693189	NR_03033E ENSG0000CMIR604	-	MIR604	l-microRNA ncRNA		
chr10-395.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr10	3951755	3957570	+	0	NA	intron (intron (N	21253	NR_13806E	219749	Hs.49942E	NM_145011 ENSG0000CNZF25	-	ZNF25	zinc finger protein-coding	
chr13-302.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr13	30248735	30249898	+	0	NA	intron (LIME3A LI	57695	NM_001014	84056	Hs.24359E	NM_03211E ENSG0000CKATNAL1	-	KATNAL1	katanin c protein-coding	
chr16-15.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr16	15634971	15639100	+	0	NA	intron (intron (N	6114	NM_014647	9665	Hs.173524	NM_014647 ENSG0000CMARF1	-	MARF1	KIAA0430 meiosis	l-protein-coding
chr17-48E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr17	48862442	48864897	+	0	NA	3' UTR (3' UTR (N	-29118	NM_00100E	516	Hs.80956	NM_00517E ENSG0000CATP5MC1	-	ATP5MC1	ATP synth protein-coding	
chr19-53E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr19	535361	539338	+	0	NA	intron (intron (N	5589	NM_00435E	997	Hs.514997	NM_00435E ENSG0000CCDC34	-	CDC34	cell divi protein-coding	
chr2-952.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr2	95209501	95217792	+	0	NA	IntergeniIntergeni	47862	NM_001291	7549	Hs.59091E	NM_02108E ENSG0000CNZF2	-	ZNF2	ZNF2 zinc	finger protein-coding
chr2-218E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr2	2.18E+08	2.18E+08	+	0	NA	intron (MIRB SINE	1866	NR_10676E	1.02E+08	NR_10676E ENSG0000CMIR6513	-	MIR6513	mir-ε microRNA ncRNA		
chr20-35E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr20	35669782	35674147	+	0	NA	intron (N (GTTTTT)r	-7064	NM_00119E	10137	Hs.70018E	NM_006047 ENSG0000CRBM12	-	RBM12	HRIHF20E RNA	bind protein-coding
chr20-214.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr20	41452073	41452600	+	0	NA	intron (intron (N	-85522	NM_05284E	90187	Hs.7652E	NM_05284E ENSG0000CEMILIN3	-	EMILIN3	C20orf13 elastin	n protein-coding
chr22-41E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr22	24541436	24543493	+	0	NA	non-codir non-codir	12674	NM_001284	8306	Hs.72855	NM_031444 ENSG0000CUCD1	-	CUCD1	C20orf13 guanylyl	protein-coding
chr3-1841.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	exon (NM exon (NM	2874	NM_001351	55324	Hs.36132E	NM_01835E ENSG0000CABC3F	-	ABC3F	EST201864 ATP	bind protein-coding
chr5-372E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr5	37223410	37223987	+	0	NA	intron (intron (N	-25348	NR_13426E	1.05E+08	Hs.17099E	NR_13426E ENSG0000CLOC105374	-	CLOC105374	uncharactercna	
chr7-138E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (LTR4 LTR	96632	NM_01590E	8805	Hs.490287	NM_00385E ENSG0000CTRIM24	-	TRIM24	PTC6 RNFE	tripartit protein-coding
chr8-102E.8.938947.0.531216.0.780782.0.680364.0.496274.0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (AluJb SIN	27716	NM_00117E	50484	Hs.51259E	NM_01571E ENSG0000CRMB2B	-	MB2B	MTDPS8A ribonucle	protein-coding
chr14-761.4.707875.0.72619.1.068123.0.67987.0.496586.0.981636	chr14	76174753	76175640	+	0	NA	3' UTR (3' UTR (N	20842	NR_110314	55668	Hs.410231	NM_01792E ENSG0000CPATCH2L	-	PATCH2L	C14orf11E G-patch	c protein-coding
chr15-591.4.707875.0.72619.1.068123.0.67987.0.496586.0.981636	chr15	59144058	59144631	+	0	NA	intron (AluSx1 SI	26918	NR_03175E	1E+08	NR_03175E ENSG0000CMIR2116	-	MIR2116	mir-2116	microRNA ncRNA	
chr1-2064.8.972229.0.533971.0.785453.0.679825.0.496615.0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (MERSB DNA	-15032	NM_18266E	83593	Hs.49757E	NM_031437 ENSG0000CRASSF5	-	RASSF5	Maxp1 NOF	RAS assoc protein-coding
chr1-212E.8.972229.0.533971.0.785453.0.679825.0.496615.0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	intron (AluY SINE	27371								



chr17-756	4.658877	-0.72955	1.078219	-0.67662	0.498646	0.981636	chr17	75684593	75685808	+	0	NA	intron (Nintron (N	17862	NM_01326C	29115	Hs. 65508ENM_01326C	ENSG000003AP30BP	HCNGP HTF	SAP30	bir	protein-coding	
chr2-1696	4.658877	-0.72955	1.078219	-0.67662	0.498646	0.981636	chr2	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	20414	NM_024622	79675	Hs. 52927ENM_024622	ENSG000003FASTKD1	-	FAST	kin	protein-coding	
chr21-436	7.441325	-0.61336	0.906565	-0.676575	0.498676	0.981636	chr21	43672026	43672558	+	0	NA	intron (Nintron (N	12732	NM_01505E	23076	Hs. 56572ENM_01505E	ENSG000003RRP1B	KIAA0179	ribosomal	protein-coding		
chr1-8906	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr1	89051041	89060366	+	0	NA	intron (Nintron (N	9505	NM_00205E	2633	Hs. 62661	NM_00205E	ENSG000003GBP1	-	guanylate	protein-coding	
chr1-1501	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	-3494	NR_135098	1.05E+08	Hs. 59936ENR_135098	LOC105371-	-	uncharact	ncRNA		
chr11-876	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr11	8730218	8731285	+	0	NA	exon (NM_exon (NM	-38027	NR_12059C	1.03E+08	Hs. 61327ENR_120590	LOC102724-	-	uncharact	ncRNA		
chr12-952	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr12	95255365	95256681	+	0	NA	intron (Nintron (N	38216	NM_01759E	55591	Hs. 24135	NM_01759E	ENSG000003VEZT	VEZATIN	vezatin	protein-coding	
chr13-758	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr13	75848280	75853958	+	0	NA	intron (NMLTIH2 LI	-19919	NM_001257	729420	Hs. 58682ENM_001257	75995	LM07DN	LM07	dowr	protein-coding	
chr13-110	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	3' UTR (N3' UTR (N	-4675	NR_04658E	1.01E+08	Hs. 50871ENR_04658E	ENSG000003COL4A2-AS-	-	COL4A2	ar	ncRNA	
chr18-882	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr18	8821551	8827398	+	0	NA	intron (Nintron (N	107093	NM_01521C	23255	Hs. 70792ENM_01521C	ENSG000003MTCL1	CCDC165	microtub	protein-coding		
chr19-108	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr19	10832820	10833158	+	0	NA	non-codiron-codir	2751	NR_10401E	11018	Hs. 21146ENM_00685E	ENSG000003TMED1	IL1RL1 LG	transmem	protein-coding		
chr8-6058	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr8	60584484	60586204	+	0	NA	intron (NAluJb SIN	68357	NM_00286E	5862	Hs. 369017NM_00286E	ENSG000003CRAB2A	LHX RAB2	RAB2A	me	protein-coding	
chr9-1322	8.647941	-0.53711	0.794007	-0.67646	0.498749	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (NMER104 DN	88574	NM_00135E	23064	Hs. 460317NM_01504E	ENSG000003SETX	ALS4 AOA2	senataxir	protein-coding		
chr22-222	6.343406	-0.64018	0.946488	-0.67637	0.498805	0.981636	chr22	22288122	22288355	+	0	NA	IntergeniFLAM_C SI	-9860	NR_02729E	96610	Hs. 449601NM_080926	BMS1P20	IGL IGLV BMS1	pset	pseudo		
chr19-267	15.38146	-0.416563	0.615899	-0.67635	0.498819	0.981636	chr19	26785712	26786021	+	0	NA	IntergeniALR/Alpha	-1007565	NR_14673E	1.02E+08	Hs. 567934NR_110687	ENSG000003LOC101927-	-	uncharact	ncRNA		
chr15-732	8.367938	-0.550968	0.814677	-0.676302	0.498849	0.981636	chr15	73266753	73267243	+	0	NA	intron (NAluY SINE	-32912	NR_16214E	1.13E+08	Hs. 16214E	MIR12135	-	microRNA	ncRNA		
chr14-211	8.655799	-0.53857	0.796752	-0.67596	0.499066	0.981636	chr14	21073219	21073518	+	0	NA	intron (Nintron (N	-2496	NM_00128E	57447	Hs. 52520ENM_01625C	ENSG000003NDRG2	SYLD	NDRG	fami	protein-coding	
chr3-1118	8.655799	-0.53857	0.796752	-0.67596	0.499066	0.981636	chr3	1.11E+08	1.11E+08	+	0	NA	TTS (NM_C TTS (NM_C	122444	NM_00124C	25445	Hs. 293917NM_01548C	ENSG000003NECTIN3	CD113 CDW	nectin	ce	protein-coding	
chr5-9356	8.655799	-0.53857	0.796752	-0.67596	0.499066	0.981636	chr5	93561060	93563493	+	0	NA	intron (Nintron (N	9067	NR_10982E	441094	Hs. 457407NR_01536E	ENSG000003NR2F1-AS1	NR2F1	ant	ncRNA		
chr8-134	8.655799	-0.53857	0.796752	-0.67596	0.499066	0.981636	chr8	13499532	13499760	+	0	NA	exon (NM_exon (NM	15205	NM_18264E	10395	Hs. 13429ENM_00609E	ENSG000003DLC1	ARHGAP7 DLC1	Rho	protein-coding		
chr5-747	10.8706	-0.48307	0.71477	-0.67584	0.49914	0.981636	chr5	74705251	74707566	+	0	NA	intron (NLIAPA3 LIN	21160	NM_000521	3074	Hs. 69293	NM_000521	ENSG000003HEXB	ELC-1AS F	hexosamir	protein-coding	
chr6-152	7.945771	-0.581223	0.860138	-0.675733	0.49921	0.981636	chr6	1.52E+08	1.52E+08	+	0	NA	exon (NM_exon (NM	-43671	NR_120501	1.01E+08	Hs. 57120ENR_120501	SYNE1-AS1	-	SYNE1	ant	ncRNA	
chr1-2368	8.375796	-0.549072	0.812643	-0.675663	0.499255	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (NTigger3a	43743	NM_001291	4548	Hs. 498187NM_00025E	ENSG000003MTR	HMAG MS c	5-methylt	protein-coding		
chr16-182	6.36883	-0.63182	0.935345	-0.67549	0.499365	0.981636	chr16	1675501	1675894	+	0	NA	3' UTR (N3' UTR (N	-2582	NM_14457C	90861	Hs. 513261NM_14457C	ENSG000003JPT2	C16orf34 J	Jupiter	n	protein-coding	
chr2-1541	6.36883	-0.63182	0.935345	-0.67549	0.499365	0.981636	chr2	15410373	15410709	+	0	NA	intron (Nintron (N	150793	NM_01590E	51594	Hs. 46775ENM_01590E	ENSG000003NBAS	ILF52 NAC	neuroblas	protein-coding		
chr9-1208	6.36883	-0.63182	0.935345	-0.67549	0.499365	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	TTS (NM_C TTS (NM_C	22550	NR_02744E	1E+08	Hs. 70681ENR_02744E	B3GNT10	-	UDP-GlcNA	pseudo		
chr16-676	6.188856	-0.635983	0.941749	-0.675322	0.499471	0.981636	chr16	67684482	67685771	+	0	NA	3' UTR (N3' UTR (N	18312	NM_00101E	388284	Hs. 63220ENM_00101E	ENSG000003C16orf86	-	chromoson	protein-coding		
chr18-422	6.188856	-0.635983	0.941749	-0.675322	0.499471	0.981636	chr18	42009684	42010710	+	0	NA	intron (NTigger1 E	54963	NM_002647	5289	Hs. 464971NM_002647	ENSG000003PIK3C3	VPS34 Vps	phosphat	protein-coding		
chr19-417	3.990359	-0.781805	1.157774	-0.675265	0.499507	0.981636	chr19	4175329	4176159	+	0	NA	exon (NM_exon (NM	6562	NM_001321	51548	Hs. 42375ENM_01653E	ENSG000003SIRT6	SIRT6	sirtuin	f	protein-coding	
chr1-8855	10.8702	-0.48189	0.713634	-0.67526	0.49951	0.981636	chr1	8859384	8877825	+	0	NA	intron (NMARNA DNA	-2014	NR_10678E	1.02E+08	Hs. 10678E	ENSG000003MIR6728	hsa-mir-6	microRNA	ncRNA		
chr12-124	10.8702	-0.48189	0.713634	-0.67526	0.49951	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	3' UTR (N3' UTR (N	12516	NR_10694C	1.02E+08	Hs. 10694C	ENSG000003MIR6880	hsa-mir-6	microRNA	ncRNA		
chr1-1557	8.905665	-0.528458	0.782625	-0.675237	0.499525	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (NMIR SINE	21506	NM_033657	7818	Hs. 51674ENM_00463E	ENSG000003DAP3	DAP-3 MR	death	as	protein-coding	
chr22-292	8.905665	-0.528458	0.782625	-0.675237	0.499525	0.981636	chr22	29279899	29280111	+	0	NA	intron (Nintron (N	-27499	NR_10687E	1.02E+08	Hs. 10687E	ENSG000003MIR6818	hsa-mir-6	microRNA	ncRNA		
chr5-1772	8.905665	-0.528458	0.782625	-0.675237	0.499525	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	37598	NM_001031	53917	Hs. 16258	NM_130781	ENSG000003CRAB2	-	RAB24	me	protein-coding
chr19-106	5.715842	-0.67208	0.995526	-0.6751	0.499612	0.981636	chr19	10913745	10914165	+	0	NA	exon (NM_exon (NM	14684	NM_02402E	78992	Hs. 16402ENM_02402E	ENSG000003YIPF2	FinGer2	Yip1	dom	protein-coding	
chr22-386	5.715842	-0.67208	0.995526	-0.6751	0.499612	0.981636	chr22	38618448	38619546	+	0	NA	intron (Nintron (N	37395	NM_00101E	646851	Hs. 542707NM_00101E	ENSG000003FAM227A	-	family	wi	protein-coding	
chr1-351	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr1	35102949	35103579	+	0	NA	intron (NLMBS LIN	23879	NM_02477E	79830	Hs. 47124ENM_02477E	ENSG000003ZMYM1	MYM	zinc	fin	protein-coding	
chr1-4212	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr1	4219782	42197297	+	0	NA	intron (NLMBS LINE	-32294	NM_03355E	2980	Hs. 778	NM_03355E	ENSG000003GUC2A	GCAP-1 G	uanyl	at	protein-coding
chr10-11	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr10	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	4765	NM_198514	374354	Hs. 369924NM_198514	ENSG000003NHLRC2	FINCA	NHL	repe	protein-coding	
chr11-466	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr11	46960062	46961295	+	0	NA	intron (NAluSq SIN	23917	NM_00100E	79096	Hs. 36829ENM_02411E	ENSG000003C11orf49	-	chromoson	protein-coding		
chr12-112	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	9032	NM_02495E	80018	Hs. 530941NM_02495E	ENSG000003NAA25	C12orf30 N	(alpha)-	protein-coding		
chr19-314	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr19	31458027	32460300	+	0	NA	intron (Nintron (N	53038	NM_20732E	147991	Hs. 194392NM_20732E	ENSG000003YIP19L3	-	dpy-19	lip	protein-coding	
chr2-3512	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr2	3512208	3512852	+	0	NA	intron (NMSTA-int	5217	NM_00130E	55256	Hs. 50277ENM_01826E	ENSG000003ADI1	APL1 ARD	acireduct	protein-coding		
chr2-1756	4.692159	-0.72107	1.068218	-0.67502	0.499661	0.981636	chr2	1.76E+08	1.76E+08	+	0	NA	intron (NMER2 DNA	23998	NM_03065E	80856	Hs. 209561NM_03065E	ENSG000003LNPK	KIAA1715	lunapark	protein-coding		
chr20-937	4.692159	-0.72107	1.068218	-0.67502	0.4																		



chr12-952.8.416935	0.550011	0.815215	0.674682	0.499878	0.981636	chr12	95283571	95284346	+	0	NA	intron (NL2) LINE I	-24462 NR_029899	442903	NR_029899 ENSG000002MIR331	MIRN331 l microRNA ncRNA
chr2-1715.8.416935	0.550011	0.815215	0.674682	0.499878	0.981636	chr2	1.72E+08	1.72E+08	+	0	NA	3' UTR (N3' UTR (N	32639 NM_001127	79901 Hs. 221941NM_024844 ENSG000002CYBRD1	CYB561A2 cytochrome protein-coding	
chrX-2435.8.416935	0.550011	0.815215	0.674682	0.499878	0.981636	chrX	2439684	2439962	+	0	NA	intron (MER1A) DNA	60716 NM_001171	9189 Hs. 131452NM_004725 ENSG000002ZBED1	ALTE DRE zinc finger protein-coding	
chr3-4865.9.49424	0.517087	0.766561	0.674554	0.499959	0.981636	chr3	48698857	48699933	+	0	NA	intron (AluSp) SIN	-13480 NM_016455	51517 Hs. 655006NM_016455 ENSG000002NCK1P5D	AF3P21 DNCK1 interprotein-coding	
chr15-694.10.82906	-0.48418	0.717826	-0.67454	0.499985	0.981636	chr15	69453643	69456659	+	0	NA	intron (intron (N	2333 NM_213725	6176 Hs. 356502NM_001000 ENSG000002RPLP1	LPI1 P1 RF ribosomal protein-coding	
chr1-1657.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr1	1.66E+08	1.66E+08	+	0	NA	intron (AluJo) SIN	15118 NM_001366	54499 Hs. 31498 NM_019025 ENSG000002TCMO1	HP10122 F transmembrane protein-coding	
chr1-1864.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr1	1.86E+08	1.86E+08	+	0	NA	exon (NM exon (NM	5556 NM_022375	10896 Hs. 679232NM_022375 ENSG000002OCLM	TISR oculomedial protein-coding	
chr1-2011.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (intron (N	8328 NM_001288	252839 Hs. 181444NM_016455 ENSG000002TMEM9	DERM4 TME transmembrane protein-coding	
chr11-354.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr11	35430720	35433502	+	0	NA	3' UTR (N3' UTR (N	-12053 NM_001195	6506 Hs. 502335NM_004171 ENSG000002SLC1A2	EAA2T2 EIF solute carrier protein-coding	
chr14-102.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	35210 NM_030943	81693 Hs. 534494NM_030943 ENSG000002AMN	PR1028 amionin alpha protein-coding	
chr15-555.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr15	5379770	5379969	+	0	NA	intron (AluSq2) SI	-6835 NR_030358	693213	NR_030358 ENSG000002MIR628	MIRN628 l microRNA ncRNA
chr16-161.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr16	16158382	16159526	+	0	NA	intron (intron (N	64517 NM_001075	368 Hs. 442182NM_001171 ENSG000002ABCC6	ABC34 ARF ATP binding protein-coding	
chr16-678.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr16	67876321	67881666	+	0	NA	exon (NM exon (NM	-5892 NM_198444	123904 Hs. 435464NM_198444 ENSG000002NRN1L	MRC2246 neurotin protein-coding	
chr17-535.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr17	5358619	5358866	+	0	NA	intron (intron (N	-60899 NM_001166	84268 Hs. 462085NM_032305 ENSG000002RPL1	HRIP IRIP RPA interprotein-coding	
chr17-755.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr17	75953173	75956541	+	0	NA	intron (AluSg) SIN	-16625 NM_001315	85302 Hs. 720065NM_001080 ENSG000002PBF1	Alb FBF-1 Fas binding protein-coding	
chr19-495.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr19	49879684	49885819	+	0	NA	intron (intron (N	-4395 NM_001278	84335 Hs. 515542NM_032375 ENSG000002AKT1S1	Lobe PRAS AKT1 subunit protein-coding	
chr22-193.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr22	19381527	19383820	+	0	NA	intron (intron (N	49060 NM_003325	7290 Hs. 474205NM_003325 ENSG000002CHIRA	DGCR1 TUF histone core protein-coding	
chr22-215.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr22	21932675	21933700	+	0	NA	intron (intron (N	-5050 NR_147622	1E+08 Hs. 659182NR_147622	LOC100208E-1	uncharacterized ncRNA
chr3-4867.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr3	48671060	48672141	+	0	NA	Intergeni Intergeni	7832 NR_111921	1.03E+08 Hs. 663571NR_111921 ENSG000002LINC02258	CELSR3-AS long intergenic ncRNA	
chr4-1181.8.946805	0.529419	0.784901	0.674504	0.499991	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (intron (N	-5835 NR_109983	729218 Hs. 448515NR_103825	LOC729218E-1	uncharacterized pseudo
chr15-591.8.646091	-0.5476	0.812011	-0.67437	0.500075	0.981636	chr15	59194602	59195492	+	0	NA	intron (intron (N	11796 NM_033195	92483 Hs. 307052NM_033195 ENSG000002LDHAL6B	LDHB LD lactate dehydrogenase protein-coding	
chr6-1697.8.646091	-0.5476	0.812011	-0.67437	0.500075	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (THE1A) LTF	5529 NM_001278	55780 Hs. 47546 NM_018341 ENSG000002ERMARD	G6orf70 FER membrane protein-coding	
chr11-111.8.897807	0.530233	0.786407	0.674247	0.500154	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (LIMA9) LIN	77502 NM_002716	5519 Hs. 269125NM_002716 ENSG000002PPP2R1B	PP2A Abet protein-coding	
chr9-3305.11.15917	0.488747	0.725049	0.674089	0.500255	0.981636	chr9	33052460	33052744	+	0	NA	intron (intron (N	24072 NM_018222	55234 Hs. 655351NM_018222 ENSG000002SMU1	BWD SMU-1 SMU1 DNA protein-coding	
chr22-245.5.899515	-0.67398	0.999843	-0.67408	0.500258	0.981636	chr22	24576339	24576617	+	0	NA	Intergeni AluSq2 SI	-7272 NM_013430	2678 Hs. 595805NM_005265 ENSG000002GGT1	CD224 D22 gamma-glutamate protein-coding	
chr5-1097.5.899515	-0.67398	0.999843	-0.67408	0.500258	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (HAL1) LINE	16831 NM_014757	9794 Hs. 631951NM_014757 ENSG000002MAML1	Mam-1 Man mastermind protein-coding	
chr10-175.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (AluJb) SIN	25281 NM_015915	51063 Hs. 241545NM_015915 ENSG000002CALHM2	FAM26B calcium protein-coding	
chr12-121.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr12	12199951	12200577	+	0	NA	intron (intron (N	66780 NM_002335	4040 Hs. 584775NM_002335 ENSG000002LRP6	ADCAD2 SLDL receptor protein-coding	
chr15-297.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr15	29793155	29794947	+	0	NA	intron (LIMA3) LIN	26624 NM_001355	7082 Hs. 743995NM_003257 ENSG000002TJP1	ZO-1 tight junction protein-coding	
chr15-341.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr15	34142185	34143207	+	0	NA	intron (intron (N	40613 NM_152595	161779 Hs. 156317NM_152595 ENSG000002PGBD4	- piggyback protein-coding	
chr2-2894.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr2	28940205	28940721	+	0	NA	intron (AluSp) SIN	12480 NR_145755	1.1E+08 NR_145755 ENSG000002SNORD53B	- small nucleolar RNA	
chr2-131.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr2	1.31E+08	1.31E+08	+	0	NA	intron (MERS) DNA	6456 NM_001321	130074 Hs. 534675NM_001005 ENSG000002FAM168B	MANI family wiprotein-coding	
chr20-436.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr20	43621972	43623083	+	0	NA	intron (AluY) SINE	31590 NM_001322	51098 Hs. 444332NM_016004 ENSG000002IFT52	C20orf9 C intracellular protein-coding	
chr4-1955.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr4	1959230	1961352	+	0	NA	intron (intron (N	-14345 NR_003004	677770 Hs. 676951NR_003004 ENSG000002SCARNA22	ACA11 small Ca <sup>2+</sup> ncRNA	
chr6-3217.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr6	32171468	32171667	+	0	NA	intron (intron (N	-1451 NR_106775	1.02E+08 NR_106775 ENSG000002MIR6721	hsa-mir-6721 microRNA ncRNA	
chr7-1732.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr7	17323881	17324271	+	0	NA	intron (intron (N	25649 NM_001621	196 Hs. 171185NM_001621 ENSG000002AHR	RP85 bHLH aryl hydrocarbon receptor protein-coding	
chr8-9765.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chr8	97690121	97691565	+	0	NA	intron (intron (N	46659 NM_001365	92140 Hs. 377155NM_178812 ENSG000002MTDH	3D3 AEG-1 metadherin protein-coding	
chrX-5481.6.435393	-0.61961	0.919622	-0.67376	0.500461	0.981636	chrX	54814015	54814444	+	0	NA	promoter-promoter	-139 NR_002955	677799 Hs. 679785NR_002955 ENSG000002SNORA11	SNORA11 small nucleolar RNA	
chr19-551.9.00551	0.536785	0.796914	0.67358	0.500578	0.981636	chr19	55101537	55101813	+	0	NA	intron (intron (N	15962 NM_0017607	54776 Hs. 631575NM_017607 ENSG000002PPP1R2C	AAVS1 LEN protein-coding	
chr17-823.9.460959	0.5144	0.763983	0.673313	0.500748	0.981636	chr17	8231542	8232855	+	0	NA	exon (NM exon (NM	-8155 NR_026951	284029 Hs. 121692NM_173621 ENSG000002LINC00324	C17orf44 long intergenic ncRNA	
chr3-5325.8.57352	-0.54626	0.809109	-0.67311	0.500875	0.981636	chr3	53286519	53286758	+	0	NA	3' UTR (N3' UTR (N	-30524 NR_047588	7086 Hs. 89643 NM_001064 ENSG000002TKT	HEL-5-48 transketolase protein-coding	
chr8-4455.42.96377	0.273628	0.406515	0.673107	0.500879	0.981636	chr8	44594451	44594671	+	0	NA	Intergeni ALR Alphe	1302119 NM_001002	340441 Hs. 631575NM_001002 ENSG000002POTEA	A26A1 CT1POTE ankyrin protein-coding	
chr10-125.7.894554	0.939092	1.395454	0.672965	0.500969	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (MER44B) DN	7042 NR_120633	1.02E+08 Hs. 634265NR_120633 ENSG000002EDRF1-AS1	EDRF1 antinuclear RNA	
chr11-352.10.86234	-0.4807	0.714359	-0.67291	0.501004	0.981636	chr11	35214779	35226617	+	0	NA	intron (intron (N	57748 NR_145794	1.1E+08 NR_145794	SNORD164	small nucleolar RNA
chr15-605.10.86234	-0.4807	0.714359	-0.67291	0.501004	0.981636	chr15	60394238	60397060	+	0	NA	intron (intron (N	2337 NM_001002	302 Hs. 511605NM_004035 ENSG000002ANXA2	ANX2 ANX annexin I protein-coding	
chr4-1187.10.86234	-0.4807	0.714359	-0.67291	0.501004	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (LIPA6) LIN	53473 NM_014822	9871 Hs. 189641NM_014822 ENSG000002SEC24D	CLCRP2 SEC24 homoprotein-coding	
chr7-7405.10.86234	-0.4807	0.714359	-0.67291	0.501004	0.981636	chr7	74096057	74097911	+	0	NA	intron (intron (N	3767 NM_001204	3984 Hs. 647035NM_002314 ENSG000002LIMK1	LIMK LIM LIM domain protein-coding	
chr1-1657.8.913523	0.526673	0.782798	0.672809	0.501069	0.981636	chr1	1.66E+08	1.66E+08	+	0	NA	intron (AluJb) SIN	26518 NM_001366	54499 Hs. 31498 NM_019025 ENSG000002TCMO1	HP10122 F transmembrane protein-coding	
chr1-2355.8.913523	0.526673	0.782798	0.672809	0.501069	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	intron (AluJb) SIN	-38178 NR_039905	1.01E+08 NR_039905 ENSG000002MIR4753	mir-4753 microRNA ncRNA	
chr1-2367.8.913523	0.526673	0.782798	0.672809	0.501069	0.981636	chr1	2.36E+08	2.36E+08	+	0	NA	intron (intron (N	40517 NM_002505	4811 Hs. 356624NM_002505 ENSG000002NID1	NID nidogen 1 protein-coding	
chr10-111.8.913523	0.526673	0.782798	0.672809	0.501069	0.981636	chr10	1.2E+08	1								



chr16-207 6.394253 -0.62365 0.931869 -0.66925 0.503339 0.981636 chr16 20797457 20798004 + 0 NA TTS (NM\_CTTT (NM\_C 8742 NM\_001142 112479 Hs. 248437NM\_080665:ENSG000000CER12 EXOD1|ZGFER1|exor|protein-coding







chr5-148: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr5	1.48E+08	1.48E+08	0	NA	intron (NLIME4c LI	11867 NM_030793	81545 Hs. 483772NM_030793:ENSG00000PFBX038	Fbx38 HMF-box prcprotein-coding	
chr5-157: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr5	1.58E+08	1.58E+08	0	NA	intron (Nintron (N	56026 NM_014666	9685 Hs. 64400CNM_014666:ENSG00000CLINT1	CLINT ENT clathrin protein-coding	
chr5-157: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr5	1.58E+08	1.58E+08	0	NA	intron (NAluSx1 SI	11701 NM_014666	9685 Hs. 64400CNM_014666:ENSG00000CLINT1	CLINT ENT clathrin protein-coding	
chr5-175: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr5	1.75E+08	1.75E+08	0	NA	intron (NLIME3 LI	16458 NM_022754	94081 Hs. 36944CNM_022754:ENSG00000SFXX1	SLC56A1 Siderofilin protein-coding	
chr6-7401: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr6	7401914	7405437	0	NA	intron (NMER104 DN	13456 NM_001346	83732 Hs. 437474NM_03148C:ENSG00000C10K1	AD034 RICR10 kinaseprotein-coding	
chr6-169: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr6	1.7E+08	1.7E+08	0	NA	intron (NLIME3A LI	14563 NM_00135C	253769 Hs. 13190ENM_182552:ENSG00000WDR27	-WD repeatprotein-coding	
chr7-4574: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr7	45741146	45742368	0	NA	intron (Nintron (N	27261 NR_024271	641977 Hs. 723477NR_024271:ENSG00000SEPTIN7P2	SEPTIN3 SEPTIN7 pseudo	
chr7-4736: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr7	47363452	47364620	0	NA	intron (Nintron (N	100767 NR_145811	1.1E+08 NR_145813	SNORD151	small nucleosRNA
chr7-120: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr7	1.21E+08	1.21E+08	0	NA	intron (Nintron (N	-14397 NM_024913	79974 Hs. 189652NM_024913:ENSG00000CCPEDI	C7orf58	cadherin protein-coding
chr8-232: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr8	23293884	23300326	0	NA	TTS (NM_CTS (NM_C	8997 NM_001136	203069 Hs. 458644NM_001136:ENSG00000R3HCC1	-R3H domaiprotein-coding	
chr9-375: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr9	37583661	37586712	0	NA	Intergeni LIMEH LI	7411 NM_001001	401505 Hs. 130774NM_001001:ENSG00000TOMM5	C9orf105 translocprotein-coding	
chr9-980: 6.896849	-0.58225	0.882455	-0.6598	0.50938	0.981636	chr9	98007894	98009101	0	NA	intron (NCharlie3	25156 NM_006401	10541 Hs. 730654NM_006401:ENSG00000ANP32B	APRIL PH acidic m protein-coding	
chr1-356: 9.10154	-0.51225	0.776432	-0.65975	0.509417	0.981636	chr1	35602074	35603435	0	NA	3' UTR (N3' UTR (N	28783 NM_001199	5690 Hs. 471441NM_002794:ENSG00000PSMB2	HC7-1	proteasomprotein-coding
chr6-354: 9.10154	-0.51225	0.776432	-0.65975	0.509417	0.981636	chr6	35424115	35425060	0	NA	exon (NM exon (NM	-27744 NM_021922	2178 Hs. 30200CNM_021922:ENSG00000FANCE	FACE FAE FA complprotein-coding	
chr8-2641: 11.67147	0.470783	0.713706	0.659631	0.509491	0.981636	chr8	26413190	26413887	0	NA	TTS (NM_CTS (NM_C	23125 NM_00133C	665 Hs. 131222NM_004331:ENSG00000BNIP3L	BNIP3a NBCL2 inte protein-coding	
chr4-800: 11.35708	-0.46111	0.699339	-0.65936	0.509667	0.981636	chr4	80007583	80008230	0	NA	intron (NMLT1D LTF	65323 NM_00128E	118429 Hs. 162966NM_058172:ENSG00000ANTXR2	CMG-2 CMC ANTXR cel protein-coding	
chr13-33: 6.70116	0.593097	0.899717	0.659203	0.509765	0.981636	chr13	33232867	33233657	0	NA	intron (NLTR28 LTF	-27212 NM_00124E	90627 Hs. 156551NM_052851:ENSG00000STARD13	ARHGAP37 Star rel protein-coding	
chr2-196: 6.70116	0.593097	0.899717	0.659203	0.509765	0.981636	chr2	1.97E+08	1.97E+08	0	NA	intron (NLIPA7 LIN	-56796 NM_01236E	410207 Hs. 245666NM_21360E:ENSG00000C2orf66	L1DS6411 chromosomprotein-coding	
chr1-323: 6.863568	-0.58787	0.891893	-0.65913	0.509814	0.981636	chr1	32329668	32330005	0	NA	intron (NL2c LINE	6397 NM_02300E	65108 Hs. 75061 NM_02300E:ENSG00000MARCKSL1	F52 MACM MARCKS liprotein-coding	
chr11-764: 6.863568	-0.58787	0.891893	-0.65913	0.509814	0.981636	chr11	76452510	76453300	0	NA	intron (NL3 LINE C	7930 NM_02019E	56946 Hs. 352588NM_02019E:ENSG00000CEMSY	C11orf30 EMSY trarp protein-coding	
chr12-58: 6.863568	-0.58787	0.891893	-0.65913	0.509814	0.981636	chr12	58881930	58882696	0	NA	intron (NMTRe SINE	37233 NM_001136	112227 Hs. 253732NM_153377:ENSG00000LRIG3	LIG3	leucine iprotein-coding
chr17-59: 6.334656	0.547786	0.83112	0.659094	0.509835	0.981636	chr17	59056166	59056432	0	NA	intron (NFLAM_A SI	50581 NR_148347	4591 Hs. 579075NM_015294:ENSG00000TRIM37	MUL POBI tripartit protein-coding	
chr13-143: 6.15503	-0.55665	0.844939	-0.6588	0.510022	0.981636	chr13	1.43E+08	1.43E+08	0	NA	intron (NLMIB3 LIN	25997 NM_00132C	23350 Hs. 596572NM_00108C:ENSG00000U2SURP	SR140 fsA U2 snRNP protein-coding	
chr10-42: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr10	42819884	42821254	0	NA	exon (NM exon (NM	37771 NM_01475E	9790 Hs. 10848 NM_01475E:ENSG00000BMS1	ACCBMS1 BMS1 rib protein-coding	
chr15-65: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr15	65700560	65704088	0	NA	exon (NM exon (NM	-5388 NR_14575C	1.1E+08 NR_14575C	ENSG00000SNORD13E	-small nucleosRNA
chr16-29: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr16	2920693	2923967	0	NA	intron (Nintron (N	10351 NM_00130E	84756 Hs. 655321NM_020912:ENSG00000FLYWCH1	-FLYWCH-typ protein-coding	
chr17-79: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr17	7908366	7911927	0	NA	intron (N(TCTT) n S	677763 NR_00300C	677763 NR_00300C	SCARN21	ACA68 SCA small Ca ncRNA
chr19-18: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr19	18361450	18362455	0	NA	intron (NLIME3G LI	21354 NM_00132E	54858 Hs. 131776NM_017712:ENSG00000PGPEP1	PAP-1 PG pyrog lut protein-coding	
chr19-32: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr19	32893559	32894282	0	NA	intron (NLM2 LINE	-24153 NM_00124E	11136 Hs. 743345NM_01427C:ENSG00000SLC7A9	BAT1 CSN solute c protein-coding	
chr2-117: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr2	11794718	11797683	0	NA	intron (Nintron (N	28756 NR_036071	1E+08 NR_036071	ENSG00000MIR548S	ncRNA
chr2-470: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr2	47012468	47013082	0	NA	intron (Nintron (N	-70920 NM_001171	90411 Hs. 662152NM_13927E:ENSG00000CMCFD2	F5F8D F5F multiple protein-coding	
chr21-46: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr21	46204584	46207145	0	NA	exon (NM exon (NM	-11705 NR_14578C	1.1E+08 NR_145780	SNORD159	-small nucleosRNA
chr21-46: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr21	46204584	46207145	0	NA	intron (Nintron (N	44720 NM_00627E	6285 Hs. 422181NM_00627E:ENSG00000S100B	NEF S100 S100 calc protein-coding	
chr3-17: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr3	1.72E+08	1.72E+08	0	NA	intron (Nintron (N	148672 NM_00266E	5337 Hs. 382865NM_00266E:ENSG00000PLD1	CVDD	phospholip protein-coding
chr3-17: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr3	1.72E+08	1.72E+08	0	NA	intron (NLMIB7 LIN	86425 NM_00266E	5337 Hs. 382865NM_00266E:ENSG00000PLD1	CVDD	phospholip protein-coding
chr3-19: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr3	1.98E+08	1.98E+08	0	NA	intron (NMTRe SINE	-1659 NR_030627	1E+08 NR_030627	ENSG00000MIR922	MIRN922 microRNA ncRNA
chr4-135: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr4	1356778	1358961	0	NA	intron (Nintron (N	10313 NM_001317	57654 Hs. 380475NM_020894:ENSG00000UVSSA	KIAA1530 UV stimul protein-coding	
chr6-30: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr6	30640618	30641757	0	NA	intron (NMTRe 19E	-5946 NM_001109	221545 Hs. 591787NM_14502E:ENSG00000C6orf136	-chromosom protein-coding	
chr7-129: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr7	1.3E+08	1.3E+08	0	NA	intron (NMER2 DNA	72772 NM_003344	7328 Hs. 643545NM_003344:ENSG00000UBEZH	E2-20K G ubiquit it protein-coding	
chr9-81: 6.716876	0.588316	0.893596	0.65837	0.510301	0.981636	chr9	81650749	81651822	0	NA	intron (Nintron (N	38250 NM_00130E	7088 Hs. 197322NM_005077:ENSG00000TLE1	ESG ESG1 TLE famil protein-coding	
chr1-180: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr1	1.81E+08	1.81E+08	0	NA	intron (NMER33 DN	-13366 NR_145481	1.03E+08 Hs. 665315NR_145481:ENSG00000KIAA1614-	KIAA1614 ncRNA	
chr10-85: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr10	853484	855801	0	NA	intron (NTigger1 E	77063 NR_001351	23185 Hs. 159066NM_01515E:ENSG00000LARP4B	KIAA0217 La ribon protein-coding	
chr10-12: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr10	1.26E+08	1.26E+08	0	NA	intron (Nintron (N	-2418 NR_12063E	1.02E+08 Hs. 63426E NR_12063E:ENSG00000EDRF1-AS1	EDRF1 ant ncRNA	
chr12-4: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr12	49524896	49526185	0	NA	intron (Nintron (N	-13490 NM_001314	23416 Hs. 64064 NM_012284:ENSG00000KCNI3	BEC1 ELK2 potassi um protein-coding	
chr12-7: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr12	1.23E+08	1.23E+08	0	NA	intron (Nintron (N	43518 NR_10703E	1.02E+08 NR_10703E:ENSG00000MIR8072	hsa-mir-8 microRNA ncRNA	
chr16-12: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr16	74330669	74337015	0	NA	intron (Nintron (N	34413 NR_02695E	283922 Hs. 558722NR_02695E:ENSG00000LOC283922	pyruvate pseudo	
chr19-37: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr19	37696655	37700508	0	NA	exon (NM exon (NM	-6266 NM_15260E	163115 Hs. 722657NM_15260E:ENSG00000ZNF781	-zinc fing protein-coding	
chr2-230: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr2	2.3E+08	2.3E+08	0	NA	intron (Nintron (N	11439 NM_00450E	3431 Hs. 14515CNM_00450E:ENSG00000CSP110	IFI411 IFI5P110 nuc protein-coding	
chr3-48: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr3	48585953	48593011	0	NA	intron (Nintron (N	5678 NM_000094	1294 Hs. 47621E NM_000094:ENSG00000C6orf71	EBB1 EBDC collagen protein-coding	
chr5-31: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr5	31314527	31319257	0	NA	intron (Nintron (N	123206 NM_00493E	1004 Hs. 124776NM_00493E:ENSG00000CDH6	CAD6 KCAL cadherin protein-coding	
chr5-95: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr5	95917628	95919780	0	NA	intron (Nintron (N	43147 NM_012081	22936 Hs. 192221NM_012081:ENSG00000CELL2	MRCRAT1 elongat ic protein-coding	
chr6-30: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr6	30624873	30625324	0	NA	intron (Nintron (N	-1776 NR_03382E	79969 Hs. 654798NM_02490E:ENSG00000ATAT1	C6orf134 alpha tub protein-coding	
chr8-67: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr8	67298238	67300006	0	NA	intron (Nintron (N	44659 NM_006421	10565 Hs. 656902NM_006421:ENSG00000ARFGEF1	ARFGEF1 EADP ribos protein-coding	
chr9-13: 9.425827	0.50236	0.763193	0.658234	0.510388	0.981636	chr9	1.31E+08	1.31E+08	0	NA	exon (NM exon (NM	21997 NM_00131E	8021 Hs. 65453CNM_00508E:ENSG00000CNP214	CAIN CAN nucleop rotein-coding	
chr16-8: 6.716876	0.588316	0.893596	0.65821	0.510401	0.981636	chr16	57788496	57788945	0	NA	intron (Nintron (N	-6351 NM_00131E	3801 Hs. 23131 NM_00555C:ENSG00000KIFC3	-kinesin f protein-coding	
chr20-3: 6.716876	0.588316	0.893596	0.65821	0.510401	0.981636	chr20	36915094	3							

chr17-295.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr17	29573172	29573781	+	0 NA	TTS (NM_C TTS (NM_C	4775 NM_001346	90313 Hs. 51405CNM_13834	ENS00000TP53I13	DSCP1	tumor prcprotein-coding
chr17-356.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr17	35629851	35630051	+	0 NA	intron (N intron (N	42629 NM_00103C	163 Hs. 51481ENM_00128	ENS00000CAP2B1	ADTB2	AP1 adaptor rprotein-coding
chr19-431.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr19	4310620	4311046	+	0 NA	intron (N intron (N	6235 NM_02433	79187 Hs. 28144 NM_02433	ENS00000CFSD1	GLFND	MIF fibronect protein-coding
chr2-138.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr2	1.33E+08	1.33E+08	+	0 NA	intron (N LTR84a LI	-20653 NR_135572	1.02E+08 Hs. 680114NR_13557	ENS00000NCKAP5-AS	NCKAP5	arncRNA
chr2-212.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr2	2.19E+08	2.19E+08	+	0 NA	intron (N intron (N	143503 NM_00129C	55619 Hs. 46578 NM_01468	ENS00000DOCK10	DRIP2	Nbl dedicator protein-coding
chr2-224.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr2	44752906	46153768	+	0 NA	intron (N AluSq2 SI	2542 NM_001362	5465 Hs. 10311CNM_00503	ENS00000PPARA	NR1C1	PPPeroxin protein-coding
chr3-4947.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr3	49477306	49477991	+	0 NA	intron (N intron (N	7516 NM_001177	1605 Hs. 76111 NM_00439	ENS00000DAG1	156DAG	AAcystrogly protein-coding
chr5-1764.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr5	1.76E+08	1.76E+08	+	0 NA	intron (N intron (N	4790 NM_01461	23197 Hs. 484242NM_01461	ENS00000CFAP2	ETEA	UBX1 Fas assoc protein-coding
chr6-149.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr6	1.49E+08	1.49E+08	+	0 NA	intron (N intron (N	-14331 NM_001002	387802 Hs. 657168NM_00100	ENS00000SUC0	IDD55	SMI small ubi protein-coding
chr7-5312.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr7	5312369	5312781	+	0 NA	exon (NM_exon (NM	29632 NM_00104C	222962 Hs. 4302 NM_15324	ENS00000SLC29A4	ENT4	PM1 solute cprotein-coding
chr7-8734.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr7	87340568	87341315	+	0 NA	intron (N intron (N	4551 NR_015381	11257 Hs. 27432ENM_00723	ENS00000TP53TG1	LINC0009	TP53 targetncRNA
chr7-1277.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr7	1.28E+08	1.28E+08	+	0 NA	intron (N HAL1 LINE	59537 NM_00149C	27044 Hs. 12252ENM_01439	ENS00000SND1	TDRD11	Tustaphyloc protein-coding
chr8-1302.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr8	1.3E+08	1.3E+08	+	0 NA	intron (N MR1B SINE	61535 NR_00276E	29065 Hs. 63931ENR_00276	ENS00000ASAP1-IT1	ASAP1-IT1	ASAP1 intrncRNA
chr9-1134.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr9	1.13E+08	1.13E+08	+	0 NA	non-codirnon-codir	2609 NM_01744	54107 Hs. 10811ENM_01744	ENS00000POLE3	CHARAC17	DNA polyn protein-coding
chr9-125.6.888991	-0.58045	0.885885	-0.65522	0.512327	0.981636	chr9	1.25E+08	1.25E+08	+	0 NA	intron (N THE1B LTF	60397 NM_17369C	286205 Hs. 59504 NM_17369	ENS00000SCAI	C9orf126	suppress protein-coding
chr11-118.6.888991	-0.52669	0.803931	-0.65514	0.512379	0.981636	chr11	1.19E+08	1.19E+08	+	0 NA	exon (NM_exon (NM	6950 NM_001144	23187 Hs. 54046ENM_01515	ENS00000PHLDB1	LL5a	pleckstri protein-coding
chr2-862.8.888991	-0.52669	0.803931	-0.65514	0.512379	0.981636	chr2	86206122	86206342	+	0 NA	exon (NM_exon (NM	6775 NM_016622	51318 Hs. 43343ENM_01662	ENS00000MRPL35	L35mt	MRF1 tochohc protein-coding
chr13-114.11.34136	-0.45883	0.700683	-0.65483	0.512579	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	intron (N CpG	18881 NM_00736E	22821 Hs. 59307ENM_00736	ENS00000CRASA3	GAP1IP4	BFAS p21 rprotein-coding
chr10-69.9.142679	-0.50951	0.778221	-0.65471	0.512651	0.981636	chr10	69050598	69006254	+	0 NA	intron (N AluSg7 SI	16873 NM_015634	26128 Hs. 27958CNM_01563	ENS00000KIF1BP	KBP	KIAA1K1F1 binc protein-coding
chr12-53.9.142679	-0.50951	0.778221	-0.65471	0.512651	0.981636	chr12	53053846	53054361	+	0 NA	intron (N intron (N	335 NR_033854	283335 Hs. 65706CNR_03385	ENS00000LOC28333	uncharactncRNA	
chr2-2327.9.384688	0.501378	0.765858	0.654663	0.512685	0.981636	chr2	2.33E+08	2.33E+08	+	0 NA	exon (NM_exon (NM	-14789 NM_001172	3769 Hs. 46733ENM_00224	ENS00000KCNJ13	KIR1.4	KIpotassium protein-coding
chr1-7021.8.557804	-0.54179	0.828013	-0.65433	0.51291	0.981636	chr1	70215671	70216097	+	0 NA	intron (N AluSp SIN	-5496 NM_00135C	9295 Hs. 47969ENM_00476	ENS00000SRSP11	NET2	SFRS serine ar protein-coding
chr1-2042.6.194864	0.618978	0.946067	0.654265	0.512941	0.981636	chr1	2.04E+08	2.04E+08	+	0 NA	intron (N intron (N	-52905 NM_198447	127845 Hs. 532401NM_19844	ENS00000GOLTI1A	CG1-141	Cglogi tr protein-coding
chr12-118.6.194864	0.618978	0.946067	0.654265	0.512941	0.981636	chr12	1.18E+08	1.18E+08	+	0 NA	intron (N intron (N	13312 NM_022491	64426 Hs. 41663CNM_02249	ENS00000SUD53	SAP45	SDS SDS3 homc protein-coding
chr20-332.6.194864	0.618978	0.946067	0.654265	0.512941	0.981636	chr20	33384721	33386060	+	0 NA	intron (N MR1B SINE	16129 NM_01640E	51654 Hs. 43595ENM_01608	ENS00000CDK5RAP1	C20orf34	CDK5 regt protein-coding
chr5-173.6.194864	0.618978	0.946067	0.654265	0.512941	0.981636	chr5	1.72E+08	1.72E+08	+	0 NA	intron (N intron (N	-42443 NM_03364E	23291 Hs. 48413ENM_01230	ENS00000FBXW11	BTRC2	BTFF-box an protein-coding
chr1-153.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr1	1.54E+08	1.54E+08	+	0 NA	TTS (NM_C TTS (NM_C	2551 NM_006694	10899 Hs. 6396 NM_00669	ENS00000JTB	HJTB	HSPC jumping tprotein-coding
chr1-248.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr1	2.47E+08	2.47E+08	+	0 NA	intron (N AluSq4 SI	69002 NR_015422	149134 Hs. 720494NM_207326	LINC01341	long intncRNA	
chr14-226.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr14	22840128	22847207	+	0 NA	intron (N intron (N	7082 NM_00499E	4323 Hs. 2399 NM_00499	ENS00000MMP14	MMP-14	MM matrix m protein-coding
chr2-206.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr2	2.06E+08	2.06E+08	+	0 NA	exon (NM_exon (NM	29778 NM_01775E	54891 Hs. 44503ENM_01775	ENS00000IN080D	IN080	con protein-coding
chr7-2994.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr7	29942460	29944316	+	0 NA	intron (N intron (N	46413 NM_01476E	9805 Hs. 52074CNM_01476	ENS00000SCRNI	SES1	secernin protein-coding
chr9-121.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr9	2.11E+08	2.11E+08	+	0 NA	intron (N MR1A Am	4339 NM_0010177	2934 Hs. 52237ENM_00017	ENS00000GSN	AGEL	AGEL gelsoin protein-coding
chr11-77.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr11	77853445	77857378	+	0 NA	intron (N AluY SINE	14273 NM_00136E	28971 Hs. 74504CNM_02468	ENS00000CAAMD	C11orf67	adipogene protein-coding
chr6-147.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr6	1.47E+08	1.47E+08	+	0 NA	intron (N LM2 LINE	-92755 NR_03411E	729178 Hs. 55760ENR_03411	ENS00000STXBP5-AS	STXBP5	arncRNA
chr8-263.9.955697	0.486308	0.743712	0.653894	0.51318	0.981636	chr8	26308783	26309427	+	0 NA	intron (N AluJb SIN	15890 NM_001177	5520 Hs. 14633ENM_00271	ENS00000PPP2R2A	B55A	B55a protein-coding
chr15-80.6.683594	-0.71547	1.094583	-0.65364	0.513342	0.981636	chr15	80597717	80598083	+	0 NA	TTS (NM_C TTS (NM_C	16797 NR_049837	1.01E+08 NR_04983	ENS00000MIR5572	microRNA	ncRNA
chr9-136.6.683594	0.629139	0.962684	0.653252	0.513418	0.981636	chr9	1.37E+08	1.37E+08	+	0 NA	intron (N intron (N	28042 NM_01899E	54461 Hs. 522507ENM_01899	ENS00000FBXW5	Fbw5	F-box an protein-coding
chr7-106.8.683594	-0.52517	0.803746	-0.6534	0.513499	0.981636	chr7	1.06E+08	1.06E+08	+	0 NA	Intergeni LINE	38064 NM_00574E	10135 Hs. 48961ENM_00574	ENS00000NAMPT	11100350	nicotinacn protein-coding
chr12-50.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr12	50674919	50676209	+	0 NA	intron (N L2c LINE	-88537 NM_005171	466 Hs. 64856ENM_00517	ENS00000ATF1	EWS-ATF1	activatir protein-coding
chr12-55.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr12	55901977	55903369	+	0 NA	intron (N AluXs1 SI	24452 NM_001143	84305 Hs. 50568ENM_03234	ENS00000PYM1	PYM	WIBG PYM homol protein-coding
chr14-64.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr14	64498041	64498487	+	0 NA	promoter-promoter	-272 NM_001354	7597 Hs. 654571NM_00697	ENS00000ZBTB25	C14orf51	zinc fing protein-coding
chr14-10.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (N HAL1 LINE	60093 NM_00603E	9578 Hs. 654634NM_00603	ENS00000CDC42BPB	MCRKB	CDC42 bir protein-coding
chr14-10.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (N intron (N	55079 NM_00603E	9578 Hs. 654634NM_00603	ENS00000CDC42BPB	MCRKB	CDC42 bir protein-coding
chr15-42.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr15	42720011	42720614	+	0 NA	3' UTR (N3' UTR (N	16816 NM_138477	146059 Hs. 59923ENM_13847	ENS00000CDANI	CDAI	CDAI cadin l protein-coding
chr17-19.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr17	19925989	19927006	+	0 NA	intron (N LIMB7 LIN	51331 NM_007202	11216 Hs. 613424NM_00720	ENS00000AKAP10	AKAP-10	IA-kinase protein-coding
chr17-64.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr17	64053029	64053276	+	0 NA	intron (N intron (N	-32518 NM_00109E	3384 Hs. 43146CNM_00087	ENS00000ICAM2	CD102	intercell protein-coding
chr19-79.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr19	7939510	7941289	+	0 NA	intron (N intron (N	3267 NM_006351	10469 Hs. 465784NM_00635	ENS00000TIMM44	TIM44	transloc protein-coding
chr19-44.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr19	44324654	44325368	+	0 NA	Intergeni LMCC LIN	-19986 NM_004234	9310 Hs. 613424NM_00423	ENS00000ZNF235	ANF270	HZ zinc fing protein-coding
chr2-17.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr2	1.77E+08	1.77E+08	+	0 NA	intron (N intron (N	1675 NM_00114E	4780 Hs. 74400ENM_00616	ENS00000NFE2L2	HEBP1	IME nuclear f protein-coding
chr2-186.6.683594	0.584774	0.895117	0.653293	0.513567	0.981636	chr2	1.87E+08	1.87E+08	+	0 NA	intron (N L2b LINE	23387 NM_001144	3685 Hs. 43687ENM_00221	ENS00000ITGAV	CD51	MSK integrin protein-coding
chr20-4																



chr3-3147.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr3	3147894	2150916	+	0	NA	TTS (NM_C	22465	NR_15994C	51095	Hs.73272ENM_01600	ENSG00000	TRNT1	CCA1 CGI-	tRNA	nucl	protein-coding	
chr3-1506.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr3	1.51E+08	1.51E+08	+	0	NA	intron (N	-20158	NR_016277	51714	Hs.369052NM_016277	ENSG00000	SELENOT	SELT	selenoprotein-coding			
chr3-196C.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	intron (N	13888	NR_001128	7037	Hs.52961ENM_003234	ENSG00000	TFRC	CD71 IMD4	transferrin	protein-coding		
chr4-1086.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr4	1.09E+08	1.09E+08	+	0	NA	Intergeni	13609	NR_001319	6164	Hs.438227NM_000995	ENSG00000	RPL34	L34	ribosomal	protein-coding		
chr5-3701.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr5	37015465	37017135	+	0	NA	intron (N	139531	NR_015384	25836	Hs.481927NM_015384	ENSG00000	NIPBL	CDLS CDLS	NIPBL	col	protein-coding	
chr5-5686.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr5	56885211	56886362	+	0	NA	intron (N	-23474	NR_136556	133383	Hs.85950	NR_153706	ENSG00000	SETD9	C5orf35	SET	domain	protein-coding
chr5-7156.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr5	71558613	71560489	+	0	NA	intron (N	-27789	NR_022132	64087	Hs.604789NM_022132	ENSG00000	MCCC2	MCCB	methylcr	protein-coding		
chr6-2645.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr6	26431515	26433050	+	0	NA	Intergeni	26431515	NR_001242	10384	Hs.167741NM_006994	ENSG00000	BTN3A3	BTF3 BTN3	butyryl	protein-coding		
chr6-7564.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr6	75640722	75642278	+	0	NA	intron (N	39620	NR_015571	26054	Hs.485784NM_015571	ENSG00000	SENP6	SSP1 SUSF	SUMO	spec	protein-coding	
chr7-5516.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr7	55194129	55195508	+	0	NA	intron (N	-5869	NR_047551	1.01E+08	Hs.720489NR_047551	ENSG00000	EGFR-AS1	EGFR	antincRNA			
chr7-7424.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr7	74241463	74241824	+	0	NA	intron (N	12756	NR_181471	5982	Hs.647062NM_002914	ENSG00000	RFC2	RFC40	replicat	protein-coding		
chr8-4787.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr8	47873450	47874825	+	0	NA	intron (N	85999	NR_001081	5591	Hs.491682NM_006904	ENSG00000	PRKDC	DNA-PKC I	protein	protein-coding		
chr8-6157.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr8	61578226	61582279	+	0	NA	intron (N	109559	NR_001164	444	Hs.332422NM_004318	ENSG00000	ASPH	AAH BAH	Casp	protein-coding		
chr8-1254.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	intron (N	17287	NR_003126	6713	Hs.71465	NR_003126	ENSG00000	SQLE	-	squalene	protein-coding	
chr9-3245.6.922273	-0.57493	0.882702	-0.65133	0.514835	0.981636	chr9	32452084	32452463	+	0	NA	3' UTR (N	67630	NR_001362	48	Hs.567222NM_002197	ENSG00000	AC01	ACONS HEL	aconitase	protein-coding		
chr3-103C.9.150537	-0.51096	0.784529	-0.65133	0.514855	0.981636	chr3	10306356	10308838	+	0	NA	intron (N	13444	NR_001136	6396	Hs.166924NM_030675	ENSG00000	SEC13	D3S1231E SEC13	hnc	protein-coding		
chr12-644.9.922415	0.483765	0.742913	0.651173	0.514935	0.981636	chr12	64464289	64465752	+	0	NA	intron (N	12900	NR_013254	29110	Hs.505874NM_013254	ENSG00000	TBK1	FTDALS4 ITANK	hnc	protein-coding		
chr12-122.9.922415	0.483765	0.742913	0.651173	0.514935	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (N	37573	NR_107038	0.02E+08	NR_107038	ENSG00000	MR18072	hsa-mir-5	microRNA	ncRNA		
chr6-1304.9.922415	0.483765	0.742913	0.651173	0.514935	0.981636	chr6	1.3E+08	1.3E+08	+	0	NA	exon (NM	4591	NR_052912	114801	Hs.591341NM_052912	ENSG00000	TMEM200A	K1AA1913	transmem	protein-coding		
chr1-8469.9.492391	0.507658	0.77962	0.651161	0.514942	0.981636	chr1	84657554	84659475	+	0	NA	intron (N	-23494	NR_027375	439927	Hs.407054NM_001035	ENSG00000	LINC01555	C1orf180	long	intcncRNA		
chr1-3591.9.433685	0.500623	0.768836	0.651144	0.514953	0.981636	chr1	35913585	35914401	+	0	NA	exon (NM	-17112	NR_177422	192669	Hs.657659NM_024852	ENSG00000	AG03	E1P2C3	argonaut	protein-coding		
chr10-718.9.433685	0.500623	0.768836	0.651144	0.514953	0.981636	chr10	71817893	71821965	+	0	NA	intron (N	8046	NR_001171	64072	Hs.656032NM_022124	ENSG00000	CDH23	CDHR23 P1	cadherin	protein-coding		
chr1-1702.6.830286	-0.59389	0.912164	-0.65108	0.514993	0.981636	chr1	1.73E+08	1.73E+08	+	0	NA	intron (N	40478	NR_014285	51430	Hs.204555NM_014285	ENSG00000	SUCO	C1orf9 C1U	SN	domain	protein-coding	
chr1-1821.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (N	17215	NR_002822	5768	Hs.719176NM_002822	ENSG00000	CSOX1	Q6 Q5CN6	quiescin	protein-coding		
chr11-29C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr11	2905363	2906331	+	0	NA	intron (N	-2272	NR_001302	5003	Hs.300076NM_007105	ENSG00000	SLC22A18A	BWR1B BWS	solute	carrier	protein-coding	
chr14-20C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr14	20395594	20396514	+	0	NA	intron (N	17447	NR_007110	7011	Hs.508833NM_007110	ENSG00000	TEP1	TLP1 TP1	telomeras	protein-coding		
chr17-37C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr17	37563643	37566121	+	0	NA	intron (N	44536	NR_080555	11276	Hs.594647NM_007247	ENSG00000	SYNRG	API6BP1 S	ynnerg	protein-coding		
chr18-46C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr18	46008140	46010869	+	0	NA	intron (N	-42175	NR_020964	57724	Hs.514842NM_020964	ENSG00000	EPG5	HEEW1 K1	ectopic	protein-coding		
chr19-176.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr19	2760684	2767705	+	0	NA	intron (N	19079	NR_003021	6449	Hs.203911NM_003021	ENSG00000	SGTA	SGT alpha	SM	glut	protein-coding	
chr19-29C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr19	19639435	19640204	+	0	NA	intron (N	3838	NR_001288	51291	Hs.49427	NR_016575	ENSG00000	GMP1P	ARHGAP46	GEM	inter	protein-coding
chr19-49C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr19	49831179	49836241	+	0	NA	intron (N	1692	NR_106855	1.02E+08	NR_106855	ENSG00000	MIR6800	hsa-mir-5	microRNA	ncRNA		
chr2-8756.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr2	8758422	8759114	+	0	NA	intron (N	76712	NR_002166	3398	Hs.180915NM_002166	ENSG00000	ID2	G1G8 ID2	inhibitor	protein-coding		
chr2-182.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (N	4197	NR_001366	27148	Hs.471404NM_015690	ENSG00000	STK36	FU	serine/thr	protein-coding		
chr2-240C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr2	2.4E+08	2.4E+08	+	0	NA	intron (N	18540	NR_136157	4705	Hs.277677NM_004544	ENSG00000	CNDUFA10	CI-42KD C	NADH:ubiq	protein-coding		
chr21-414.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr21	41440976	41441902	+	0	NA	intron (N	9389	NR_001282	4599	Hs.517307NM_002462	ENSG00000	MX1	IF1-78K IMX	dynam	protein-coding		
chr22-37C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr22	37644956	37648191	+	0	NA	intron (N	6904	NR_018957	23616	Hs.601143NM_018957	ENSG00000	SH3BP1	ARHGAP43	SH3	doma	protein-coding	
chr22-38C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr22	38247083	38247814	+	0	NA	intron (N	-22728	NR_132774	1.07E+08	NR_132774	ENSG00000	SNORA92	-	small	nuc	snoRNA	
chr5-176C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (N	7724	NR_014901	22838	Hs.434888NM_014901	ENSG00000	RNF44	-	ring	finger	protein-coding	
chr7-222C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr7	2225107	2227085	+	0	NA	intron (N	6849	NR_001304	8379	Hs.654832NM_003550	ENSG00000	MAD1L1	MAD1 PIG5	mitotic	protein-coding		
chr9-120C.6.724734	0.585932	0.899964	0.651061	0.515007	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (N	-27844	NR_001272	55755	Hs.269566NM_018245	ENSG00000	CDK5RAP2	C48 Cep21	CDK5	reg	protein-coding	
chr10-141.13.15153	0.427261	0.656296	0.651018	0.515035	0.981636	chr10	1.15E+08	1.15E+08	+	0	NA	Intergeni	415775889	NR_024388	441666	Hs.255725NR_024388	ENSG00000	LOC441666	-	zinc	finger	pseudo	
chr5-136.11.37464	-0.45552	0.699782	-0.65095	0.515081	0.981636	chr5	1.36E+08	1.36E+08	+	0	NA	exon (NM	24863	NR_030583	1E+08	NR_030583	ENSG00000	VTRNA2-1	CBL-3 CBL	vault	RNA	ncRNA	
chr19-345.13.11039	0.426481	0.655302	0.650816	0.515165	0.981636	chr19	34955650	34960508	+	0	NA	exon (NM	6150	NR_175872	126375	Hs.50405	NR_175872	ENSG00000	ZNF792	-	zinc	finger	protein-coding
chr19-541.8.862676	0.517334	0.794926	0.650795	0.515179	0.981636	chr19	54127854	54128067	+	0	NA	intron (N	-9802	NR_014515	4849	Hs.343571NM_014515	ENSG00000	CNOT3	LENG2 NOT	CCR4-NOT	protein-coding		
chr1-5954.6.486947	0.707086	1.086702	0.650762	0.515258	0.981636	chr1	59558366	59559049	+	0	NA	intron (N	43077	NR_001278	55277	Hs.444301NM_018291	ENSG00000	PCGY	-	FGGY	cart	protein-coding	
chr1-1594																							

chr17-49c 9.160245	-0.50257	0.774957	-0.64851	0.516655	0.981636	chr17	49036974	49037425	+	0 NA	intron (Nintron (N	39814 NM_00116C	10642 Hs. 14493cNM_00654c	ENSG000001IGF2BP1	CRD-BP CF insulin I protein-coding
chr5-1341 9.160245	-0.50257	0.774957	-0.64851	0.516655	0.981636	chr5	1.34E+08	1.34E+08	+	0 NA	intron (Nintron (N	14240 NM_170675	6500 Hs. 17162cNM_00693c	ENSG00000SKP1	EMC19 OCF5-phase I protein-coding
chr5-487c 31.09488	0.302188	0.465999	0.648475	0.516678	0.981636	chr5	48791310	48792133	+	0 NA	IntergeniALR/Alpha	1649567 NM_19844c	133418 Hs. 561411NM_19844c	ENSG00000CEMB	GP70 embigin protein-coding
chr19-441 13.64812	0.41664	0.625227	0.64844	0.5167	0.981636	chr19	44100561	44108688	+	0 NA	TTS (NR_C TTS (NR_C	8559 NR_033341	1E+08 Hs. 58585cNR_033341	ENSG00000LOC10037c	uncharacterizedncRNA
chr17-565 4.709725	-0.70676	1.089953	-0.64844	0.516703	0.981636	chr17	56909146	56909672	+	0 NA	intron (NAluJb SIN	4640 NM_005082	7706 Hs. 52895cNM_005082	ENSG00000TRIM25	EFP RNFI14 tripartite protein-coding
chr12-88c 9.111248	-0.5039	0.777487	-0.64812	0.516909	0.981636	chr12	88087406	88087653	+	0 NA	intron (NAluY SINE	51993 NM_001005	91298 Hs. 59100cNM_001005	ENSG00000C12orf29	chromosom protein-coding
chr3-1137 9.111248	-0.5039	0.777487	-0.64812	0.516909	0.981636	chr3	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	22875 NM_001308	80218 Hs. 37237cNM_02514c	ENSG00000NAA50	MAK3 NAT1N(alpha)-protein-coding
chr8-1411 9.111248	-0.5039	0.777487	-0.64812	0.516909	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	IntergeniMLT1C LTF	31050 NM_00108C	57210 Hs. 37249cNM_00108C	ENSG00000SLC4544	solute c protein-coding
chr1-992c 6.881134	-0.57863	0.89303	-0.64793	0.517027	0.981636	chr1	9928331	9928802	+	0 NA	3' UTR (N3' UTR (N	-14357 NM_001297	64802 Hs. 63376cNM_02278c	ENSG00000NMNAT1	LCA9 NMNp nicotinan protein-coding
chr13-23c 6.881134	-0.57863	0.89303	-0.64793	0.517027	0.981636	chr13	23522291	23523569	+	0 NA	intron (Nintron (N	22564 NM_001278	26278 Hs. 15949cNM_01436c	ENSG00000SACS	ARSACS DN saccin m protein-coding
chr16-16c 6.881134	-0.57863	0.89303	-0.64793	0.517027	0.981636	chr16	16242744	16243458	+	0 NA	intron (Nintron (N	10511 NM_173614	28320 Hs. 460141NM_173614	ENSG00000NOM02	NOM0 PM5 NODAL m protein-coding
chr2-1114 6.881134	-0.57863	0.89303	-0.64793	0.517027	0.981636	chr2	1.11E+08	1.11E+08	+	0 NA	intron (N L3 LINE C	11337 NR_13616c	541471 Hs. 56080cNR_01539c	ENSG00000MIR4435-2	AGD2 LINCMIR4435-2ncRNA
chr2-1514 6.881134	-0.57863	0.89303	-0.64793	0.517027	0.981636	chr2	1.51E+08	1.51E+08	+	0 NA	3' UTR (N3' UTR (N	65330 NM_001177	55183 Hs. 53653cNM_01815c	ENSG00000RIF1	replicat protein-coding
chr20-35c 6.881134	-0.57863	0.89303	-0.64793	0.517027	0.981636	chr20	35282291	35283186	+	0 NA	intron (NAluSp SIN	1979 NM_001267	3692 Hs. 70925cNM_02221c	ENSG00000EIF6	CAB EIF3a eukaryot protein-coding
chr2-173c 9.152387	-0.50118	0.773577	-0.64788	0.517065	0.981636	chr2	1.73E+08	1.73E+08	+	0 NA	intron (Nintron (N	77449 NR_033882	339751 Hs. 57008cNR_033882	ENSG00000MAP3K20-1	MLK7-AS1 MAP3K20 ncRNA
chr5-873c 9.152387	-0.50118	0.773577	-0.64788	0.517065	0.981636	chr5	87338270	87340066	+	0 NA	intron (Nintron (N	-15540 NR_130925	644285 Hs. 70925cNR_130929	LOC64428c	uncharacterizedncRNA
chr6-1004 9.152387	-0.50118	0.773577	-0.64788	0.517065	0.981636	chr6	1.01E+08	1.01E+08	+	0 NA	intron (Nintron (N	20893 NM_00682c	10973 Hs. 486031NM_00682c	ENSG00000CASC3	ASC1p200 activat protein-coding
chr9-1114 9.152387	-0.50118	0.773577	-0.64788	0.517065	0.981636	chr9	1.11E+08	1.11E+08	+	0 NA	intron (Nintron (N	72310 NM_001364	23392 Hs. 36825cNM_00108C	ENSG00000CEPAS	ECM29 K1 Ecm29 prc protein-coding
chr20-38c 11.36679	-0.45436	0.701336	-0.64785	0.517082	0.981636	chr20	38017325	38018812	+	0 NA	intron (N LIMEg LIN	15388 NM_00130c	9675 Hs. 655481NM_01465c	ENSG00000TTI1	KIAA0406 TEL02 intr protein-coding
chr15-904 8.683073	-0.52215	0.805993	-0.64783	0.517095	0.981636	chr15	90466893	90467382	+	0 NA	intron (Nintron (N	-62786 NM_02276c	64784 Hs. 56757cNM_02276c	ENSG00000CRTC3	TORC-3 TCREB regt protein-coding
chr8-377c 6.683073	-0.52215	0.805993	-0.64783	0.517095	0.981636	chr8	37754600	37755050	+	0 NA	3' UTR (N3' UTR (N	-6779 NR_003671	728024 Hs. 64713cNR_003671	LOC728024	chromosom pseudo
chr17-44c 8.903816	0.51821	0.799992	0.647769	0.517134	0.981636	chr17	44351532	44351863	+	0 NA	exon (NM exon (NM	6611 NM_002087	2896 Hs. 51422cNM_002087	ENSG00000GRN	CLN11 GEF granulin protein-coding
chr1-234c 9.466967	0.503237	0.777831	0.646976	0.517648	0.981636	chr1	23436893	23437333	+	0 NA	intron (N CpG-648	-12365 NM_00319c	6920 Hs. 446354NM_00319c	ENSG00000TCEA3	TFIIS TFI transcript protein-coding
chr13-23c 6.686967	0.503237	0.777831	0.646976	0.517648	0.981636	chr13	23883301	23885900	+	0 NA	intron (N MR SINE I	-4267 NM_001014	542767 Hs. 642624NM_001014442	PCOTH	C1QTNF9B-Pro-X-Gly protein-coding
chr19-11c 6.228146	0.622574	0.962459	0.646857	0.517724	0.981636	chr19	11225815	11226523	+	0 NA	intron (N Charlie8	-13450 NM_018687	55908 Hs. 534467NM_018687	ENSG00000ANGPTL8	C19orf80 angiopoic protein-coding
chr1-1616 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr1	1.62E+08	1.62E+08	+	0 NA	intron (N LIM5 LINE	20072 NM_00734c	22926 Hs. 49274cNM_00734c	ENSG00000ATF6	AChM7 ATF activat protein-coding
chr10-11c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr10	1.2E+08	1.2E+08	+	0 NA	intron (Nintron (N	16175 NM_024834	79892 Hs. 12424cNM_024834	ENSG00000CMBP	C10orf115 minichron protein-coding
chr12-24c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr12	24860467	24860766	+	0 NA	intron (N MER41-int	41606 NM_00117c	586 Hs. 43899cNM_005504	ENSG00000BCAT1	BCATC BC1 branched protein-coding
chr12-69c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr12	69562337	69563097	+	0 NA	intron (N AluJo SIN	-22006 NR_03747c	201163 Hs. 51618cNR_03747c	ENSG00000MIR3913-2	mir-3913-microRNA ncRNA
chr17-17c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr17	17245628	17246688	+	0 NA	TTS (NM_C TTS (NM_C	-8990 NM_14460c	201163 Hs. 31652 NM_14460c	ENSG00000FLNC	BHD DENN1 follicul protein-coding
chr17-37c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr17	37528974	37529258	+	0 NA	intron (Nintron (N	39225 NM_00702c	11072 Hs. 91448 NM_00702c	ENSG00000DUSP14	MKP-L MKF dual spec protein-coding
chr2-248c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr2	24820425	24820958	+	0 NA	non-codiron-codir	27266 NM_00119c	79172 Hs. 73156cNM_02432c	ENSG00000CENP0	CENP-0 1 centromer protein-coding
chr2-3331c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr2	33317821	33319328	+	0 NA	intron (Nintron (N	-99942 NR_03962c	1.01E+08 NR_03962c	ENSG00000MIR4430	microRNA ncRNA
chr2-5557 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr2	55578540	55579484	+	0 NA	intron (N Tiger13c	38610 NM_00112c	57223 Hs. 51618cNM_02046c	ENSG00000PPP4R3B	FLFL2 PP4 protein f protein-coding
chr20-467 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr20	46728993	46730268	+	0 NA	intron (N AluYc3 S1	19981 NM_030777	81031 Hs. 305971NM_030777	ENSG00000SLC2A10	ATORS ATS solute c protein-coding
chr22-314 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr22	31446501	31447145	+	0 NA	intron (Nintron (N	42733 NM_001164	56478 Hs. 51755cNM_01984c	ENSG00000EIF4ENIF14E-T	Clas eukaryot protein-coding
chr3-1054 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr3	1.05E+08	1.05E+08	+	0 NA	intron (N THE1C-int	124460 NM_001627	214 Hs. 59129cNM_001627	ENSG00000CALCAM	CD166 MEV activatc protein-coding
chr3-187c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr3	1.87E+08	1.87E+08	+	0 NA	intron (N MLT1H-int	-21709 NR_135551	1.02E+08 NR_135551	ENSG00000LOC10192c	uncharacterizedncRNA
chr4-564c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr4	56498667	56502995	+	0 NA	intron (Nintron (N	-4378 NM_20691c	132946 Hs. 44444cNM_20691c	ENSG00000ARL9	ADP ribosom protein-coding
chr5-5444 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr5	5444264	5444928	+	0 NA	intron (Nintron (N	21919 NM_01532c	23379 Hs. 44929cNM_01532c	ENSG00000ICE1	KIAA0947 interactc protein-coding
chr5-9357 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr5	93570898	93573067	+	0 NA	promoter-promoter-	-639 NR_10982c	441094 Hs. 457407NR_01536c	ENSG00000NR2F1-AS1	NR2F1 antncRNA
chr5-137c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr5	1.38E+08	1.38E+08	+	0 NA	TTS (NM_C TTS (NM_C	47822 NM_01438c	27039 Hs. 716884NM_01438c	ENSG00000PKD2L2	TRPP5 polycyst protein-coding
chr5-177c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (N MER50 LTF	7020 NM_00130c	23567 Hs. 48425cNM_01227c	ENSG00000ZNF346	JAZ Zfp34 zinc fing protein-coding
chr6-1324 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr6	1.32E+08	1.32E+08	+	0 NA	intron (Nintron (N	43788 NM_00132c	8417 Hs. 59314cNM_00356c	ENSG00000STX7	syntaxin protein-coding
chr6-1514 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr6	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	21942 NM_01790c	55005 Hs. 48683cNM_01790c	ENSG00000CRMND1	C6orf96 Crequired protein-coding
chr7-154c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr7	1541898	1543222	+	0 NA	3' UTR (N3' UTR (N	-7680 NR_14903c	1E+08 Hs. 65698cNR_14903c	LOC10012c	uncharacterizedncRNA
chr7-248c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr7	24860184	24861486	+	0 NA	intron (N LIMD2 LIN	31786 NR_104111	26031 Hs. 52025cNM_01555c	ENSG00000OSBPL3	ORP-3 ORF oxysterol protein-coding
chr7-4751 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr7	47511307	47512222	+	0 NA	intron (Nintron (N	-46961 NR_14581c	1.1E+08 NR_14581c	SNORD151	small nucsnRNA
chr8-5897 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chr8	58976455	58977332	+	0 NA	intron (N Tiger1 I	142254 NM_01472c	9760 Hs. 49180cNM_01472c	ENSG00000TOX	TOX1 thymocyte protein-coding
chrX-136c 6.914415	-0.57309	0.886132	-0.64673	0.517808	0.981636	chrX	1.37E+08	1.37E+08	+	0 NA	intron (N AluY SINE	7875 NR_00273c	26787 NR_00273c	ENSG00000SNORD61	HBI1-342 small nucsnRNA
chr1-9454 14.08378	-0.41027	0.634458	-0.64665	0.517857	0.981636	chr1	94529544	94541609	+	0 NA	intron (Nintron (N	6183 NM_00199c	2152 Hs. 62192 NM_00199c	ENSG00000CF3	CD142 TF coagulat protein-coding
chr19-26c 37.3331	0.281166	0.434945	0.646441	0.517993	0.981636	chr19	26919544	26920304	+	0 NA	IntergeniALR/Alpha	-873057 NR_146733c	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927	uncharacterizedncRNA
chr10-14c 11.82639	-0.44759	0.692973	-0.6459	0.518344	0.981636	chr10	14914586	14914785	+	0 NA	intron (N AluSx SIN	35785 NM_02467c	79723 Hs. 55488cNM_02467c	ENSG00000SUV39H2	KMT1B suppressc protein-coding
chr2-182c 9.077966	-0.50811	0.786868	-0.64573	0.518452	0.981636	chr2	1.83E+08	1.83E+08	+	0 NA	intron (Nintron (N	-60127 NM_00146c	2487 Hs. 12845cNM_00146c	ENSG00000FRZB	FRE FRITZ frizzled protein-coding
chr2-552c 8.608652	-0.52949	0.820025	-0.6457	0.518471	0.981636	chr2	55203584	55203907	+	0 NA	intron (N LIM43 LIN	-28158 NM_00113c	6233 Hs. 3116		



chr10-27 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr10	27089513	27091883	+	0 NA	intron (Nintron (N	9800 NM_001256	22852 Hs.	361041NM_014911	ENSG000000ANKRD26	THC2 ba14	ankyrin 1 protein-coding
chr10-745 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr10	74997381	74998545	+	0 NA	intron (NAluSx1 SI	-23770 NR_145812	1.1E+08	NR_145812	SNORD172	-	small nucsnoRNA
chr10-864 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr10	86489084	86490050	+	0 NA	intron (NMER20 DNA	32217 NM_001318	23063 Hs.	203099NM_015044	ENSG000000WAPL	FOE KIAAC	WAPL cohesin protein-coding
chr10-134 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr10	133E+08	1.33E+08	+	0 NA	intron (NCpG	10679 NM_001321	3632 Hs.	523366NM_005539	ENSG000000INPP5A	5PTASE	inositol protein-coding
chr11-103 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr11	10485845	10486453	+	0 NA	intron (NL3 LINE C	22177 NR_039705	1.01E+08	NR_039705	ENSG000000MIR4485	mir-4485	microRNA ncRNA
chr13-451 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr13	45175118	45176029	+	0 NA	intron (NLIMEg LIN	25472 NM_198404	386618 Hs.	23406 NM_198404	ENSG000000CKTD4	ba321C24	potassium protein-coding
chr14-526 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr14	52642926	52644553	+	0 NA	intron (Nintron (N	51819 NM_014584	30001 Hs.	525339NM_014584	ENSG000000ER01A	ER01-L EF	endoplasmic protein-coding
chr15-756 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr15	75919045	75919939	+	0 NA	intron (NMIRb SINE	15614 NM_147188	26263 Hs.	591111NM_012170	ENSG000000FBX022	FBX22 FISF-box	prc protein-coding
chr15-943 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr15	94357289	94358306	+	0 NA	intron (Nintron (N	1867 NM_001155	55784 Hs.	33368 NM_018349	ENSG000000MCTP2	-	multiple protein-coding
chr16-507 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr16	50744744	50746549	+	0 NA	intron (NAluJo SIN	3341 NR_130462	84306 Hs.	515344NM_032346	ENSG000000PDCD2L	-	microRNA ncRNA
chr19-344 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr19	34414071	34414829	+	0 NA	intron (NAluSx1 SI	10051 NM_032346	1E+08	NR_130462	ENSG000000MIR3181	-	programme protein-coding
chr2-5463 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr2	54636762	54637882	+	0 NA	intron (Nintron (N	78928 NM_178313	6711 Hs.	503177NM_003128	ENSG000000SPTBN1	ELF HELIC	spectrin protein-coding
chr2-101 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr2	1.01E+08	1.01E+08	+	0 NA	TTS (NM_C TTS (NM_C	15520 NM_000993	6160 Hs.	469473NM_000993	ENSG000000RPL31	L31	ribosomal protein-coding
chr3-1242 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr3	12428320	12429505	+	0 NA	intron (NMIR3 SINE	-55520 NM_001145	80746 Hs.	335555NM_025266	ENSG000000TSEN2	PCH2B SEN	tRNA spliprotein-coding
chr3-9882 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr3	98821207	98823144	+	0 NA	intron (Nintron (N	58868 NM_001323	10402 Hs.	148716NM_006100	ENSG000000ST3GAL6	SIAT10 S1T3	beta protein-coding
chr3-1721 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr3	1.72E+08	1.72E+08	+	0 NA	intron (Nintron (N	96595 NM_001133	64778 Hs.	744888NM_022763	ENSG000000FNDC3B	FAD104 PF	fibronectin protein-coding
chr3-1997 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr3	1.95E+08	1.95E+08	+	0 NA	3' UTR (N3' UTR (N	-7357 NM_152531	152002 Hs.	478741NM_152531	ENSG000000XXYL1T	C3orf21	xyloside protein-coding
chr4-3997 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr4	39971816	39972441	+	0 NA	intron (Nintron (N	5783 NM_001100	23244 Hs.	331431NM_015200	ENSG000000PDS5A	PI654 SCC	PDS5 cohesin protein-coding
chr4-4752 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr4	47522756	47524709	+	0 NA	intron (Nintron (N	38138 NM_020453	57205 Hs.	437241NM_020453	ENSG000000ATP10D	ATPVD	ATPase 10 protein-coding
chr5-1683 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr5	16836476	16837401	+	0 NA	intron (NLIMB7 LIN	99346 NM_012334	4651 Hs.	481722NM_012334	ENSG000000MYO10	6	myosin X protein-coding
chr5-1117 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr5	1.12E+08	1.12E+08	+	0 NA	3' UTR (N3' UTR (N	26388 NM_001142	9315 Hs.	36053 NM_004477	ENSG000000NREP	C5orf13 Ine	uronic protein-coding
chr5-1514 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr5	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	30580 NM_001308	206358 Hs.	269004NM_078483	ENSG000000SLC36A1	Dct1 LYAA	solute carrier protein-coding
chr5-154 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr5	1.54E+08	1.54E+08	+	0 NA	exon (NM exon (NM	12441 NM_001317	10827 Hs.	166551NM_018691	ENSG000000FAM114A2	133K02 C3	family wiprotein-coding
chr7-2344 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr7	23409481	23415093	+	0 NA	intron (N (TACTTAT)	15841 NR_145734	1.1E+08	NR_145734	ENSG000000SNORD65C	-	small nucsnoRNA
chr7-4805 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr7	48096012	48097346	+	0 NA	intron (Nintron (N	7414 NM_003364	7378 Hs.	488242NM_003364	ENSG000000UPP1	UDRPASE U	ridine 1 protein-coding
chr7-1487 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr7	1.49E+08	1.49E+08	+	0 NA	intron (Nintron (N	84697 NM_001370	8454 Hs.	146806NM_003592	ENSG000000CUL1	-	culin 1 protein-coding
chr8-2655 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr8	26594039	26595262	+	0 NA	intron (N (ATCT)n S	16245 NM_001244	1808 Hs.	593187NM_001386	ENSG000000DPYSL2	CRMP-2 CF	dihydropyridin protein-coding
chr8-4296 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr8	42969451	42971490	+	0 NA	intron (NLIME3Cz L	73492 NM_032411	84376 Hs.	162852NM_032411	ENSG000000H00K3	HK3	hook micr protein-coding
chr8-6318 5.179039	-0.65078	1.012227	-0.64292	0.520276	0.981636	chr8	63181601	63182192	+	0 NA	intron (Nintron (N	12893 NM_001277	253943 Hs.	491861NM_152758	ENSG000000YTHDF3	-	YTH N6-me
chr1-1225 9.408262	0.496207	0.771891	0.642846	0.520324	0.981636	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR Alpha	998723 NR_003955	647121 Hs.	697682NR_003955	ENSG000000EMBP1	-	ethin pseude
chr1-1512 6.658171	0.578798	0.900669	0.642617	0.520473	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	IntergeniIntergeni	-8876 NM_001304	57592 Hs.	186755NM_020832	ENSG000000ZNF687	PDB6	zinc fing protein-coding
chr1-13 6.658171	0.578798	0.900669	0.642617	0.520473	0.981636	chr1	1.3E+08	1.3E+08	+	0 NA	exon (NM exon (NM	24842 NM_139055	170689 Hs.	534221NM_139055	ENSG000000ADAMTS15	-	ADAM tetr protein-coding
chr12-293 6.658171	0.578798	0.900669	0.642617	0.520473	0.981636	chr12	2935992	2936324	+	0 NA	intron (NAluSx1 SI	-23239 NM_003213	7004 Hs.	949855NM_003213	ENSG000000TEAD4	EFTR-2 RT	TEA doma protein-coding
chr14-932 6.658171	0.578798	0.900669	0.642617	0.520473	0.981636	chr14	93247771	93248541	+	0 NA	intron (Nintron (N	40900 NM_175748	55148 Hs.	648806NM_175748	ENSG000000CUBR7	C14orf13C	ubiquitin protein-coding
chr7-9202 6.658171	0.578798	0.900669	0.642617	0.520473	0.981636	chr7	92023539	92023974	+	0 NA	intron (NL2a LINE	82881 NM_005751	10142 Hs.	651221NM_005751	ENSG000000AKAP9	AKAP-9 AK	-kinase protein-coding
chr7-1556 6.658171	0.578798	0.900669	0.642617	0.520473	0.981636	chr7	1.56E+08	1.56E+08	+	0 NA	intron (NAluSx1 SI	34421 NM_053043	155435 Hs.	591815NM_053043	ENSG000000RBM33	PRR8	RNA bindi protein-coding
chr16-467 4.461523	0.698515	1.087004	0.642606	0.52048	0.981636	chr16	4675979	4676562	+	0 NA	intron (Nintron (N	4952 NR_106827	1.02E+08	NR_106827	ENSG000000MIR6769A	hsa-mir-6	microRNA ncRNA
chr21-372 4.461523	0.698515	1.087004	0.642606	0.52048	0.981636	chr21	37235379	37236151	+	0 NA	intron (Nintron (N	27262 NR_026716	257203 Hs.	515155NM_148673	ENSG000000DSCR9	NCRNA0000	Down syncncRNA
chr4-2641 4.461523	0.698515	1.087004	0.642606	0.52048	0.981636	chr4	26413259	26413992	+	0 NA	intron (Nintron (N	76859 NR_000730	886 Hs.	129 NM_000730	ENSG000000CCKAR	CCK-A CCK	cholecyst protein-coding
chr1-109 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr1	1.09E+08	1.09E+08	+	0 NA	intron (NLIMEb LIN	25238 NM_001142	22911 Hs.	570055NM_014963	ENSG000000WDR47	-	WD repeat protein-coding
chr15-184 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr15	18497649	18498173	+	0 NA	intron (Nintron (N	9109 NM_001127	51324 Hs.	242455NM_016630	ENSG000000SPG21	ABHD21 AC	SPG21 abt protein-coding
chr17-64 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr17	6492420	6494043	+	0 NA	intron (Nintron (N	14439 NM_001355	6117 Hs.	461922NM_002949	ENSG000000RPA1	HBSB MSTC	replicat protein-coding
chr17-171 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr17	17161860	17163079	+	0 NA	intron (Nintron (N	43864 NM_178833	201164 Hs.	729075NM_178833	ENSG000000PLD6	ZUC	phospholip protein-coding
chr17-21 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr17	21305987	21307201	+	0 NA	intron (NAluSx6 SI	18558 NM_002755	5606 Hs.	514012NM_002755	ENSG000000MAP2K3	MAPKK3 ME	mitten protein-coding
chr17-47 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr17	47923058	47923542	+	0 NA	intron (Nintron (N	18104 NR_103855	1.01E+08	NR_103855	ENSG000000SP2-AS1	-	SP2 antiscRNA
chr20-554 7.213464	0.556414	0.865933	0.64256	0.520509	0.981636	chr20	5940016	5941467	+	0 NA	intron (NAluJb SIN	9792 NM_015933	51605 Hs.	128791NM_015933	ENSG000000TRMT6	CGI-09 CG	tRNA meti protein-coding
chr2-175 3.402524	-0.81776	1.27383	-0.64197	0.520892	0.981636	chr2	1.76E+08	1.76E+08	+	0 NA	intron (NAluSx1 SI	26379 NM_030653	80856 Hs.	209561NM_030653	ENSG000000LNPK	KIAA1715 I	unapark, protein-coding
chr2-1791 3.402524	-0.81776	1.27383	-0.64197	0.520892	0.981636	chr2	1.79E+08	1.79E+08	+	0 NA	intron (Nintron (N	-99045 NM_173648	285025 Hs.	324341NM_173648	ENSG000000CCDC141	CAMD1	coiled-ec protein-coding
chr12-953 4.427947	-0.80203	1.249343	-0.64196	0.5209	0.981636	chr12	95772241	95773422	+	0 NA	intron (NL2a LINE	17364 NM_001322	59277 Hs.	201034NM_021			

chr8-558k 6.906557	-0.57118	0.893277	-0.63942	0.522552	0.981636	chr8	55802523	55802836	+	0	NA	intron (NLMC4 LIN	29233	NM_001363	96764	Hs.335066NM_024831	ENSG000007TGS1	NCOA6IP F	trimethylprotein-coding	
chr9-980k 6.906557	-0.57118	0.893277	-0.63942	0.522552	0.981636	chr9	98098556	98099317	+	0	NA	intron (NALuS26 SI	20286	NM_014788	9830	Hs.575631NM_014788	ENSG000007TRIM14	-	tripartitprotein-coding	
chrX-5361k 6.906557	-0.57118	0.893277	-0.63942	0.522552	0.981636	chrX	53613511	53613982	+	0	NA	intron (N(AAC)n Si	-56472	NR_029484	406889	NR_029484	ENSG000007MIRLET7F2	LET7F2 M	microRNA ncRNA	
chr1-224k 14.16042	0.404539	0.632838	0.639247	0.522663	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (Nintron (N	14016	NM_025166	80232	Hs.497872NM_025166	ENSG000007WDR26	CDW2 G	1D7WD repeatprotein-coding	
chr19-584k 14.16042	0.404539	0.632838	0.639247	0.522663	0.981636	chr19	58431034	58438871	+	0	NA	exon (NM exon (NM	5201	NM_003433	7691	Hs.156166NM_003433	ENSG000007ZNF132	pH2-12	zinc fingerprotein-coding	
chr1-150k 10.43472	0.463972	0.726012	0.639069	0.522778	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	TTS (NR_1TTS (NR_1	-10046	NM_001297	23248	Hs.213666NM_015203	ENSG000007CPRD2	HSPC099 K	regulatoryprotein-coding	
chr1-155k 10.43472	0.463972	0.726012	0.639069	0.522778	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (NMIRb SINE	3713	NR_030282	693140	NR_030282	ENSG000007MIR555	MIRN555 H	microRNA ncRNA	
chr22-41k 6.732592	0.583452	0.913347	0.638806	0.522949	0.981636	chr22	41870973	41872397	+	0	NA	intron (NALuSx SIN	-29259	NR_029507	407039	NR_029507	ENSG000007MIR33A	MIRN33A M	microRNA ncRNA	
chr3-482k 6.732592	0.583452	0.913347	0.638806	0.522949	0.981636	chr3	48297105	48298446	+	0	NA	intron (NMLT1E2 LI	3636	NM_001308	10201	Hs.465558NM_005793	ENSG000007NME6	IPIA-ALP	NME/NM23 protein-coding	
chr7-1301k 8.57537	-0.53404	0.83602	-0.63879	0.522957	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (NALuJo SIN	-24072	NR_149033	1E+08	Hs.105944NR_149033	ENSG000007LOC100128	-	uncharactericncRNA	
chr2-166k 3.461229	-0.79038	1.237482	-0.6387	0.523018	0.981636	chr2	1.66E+08	1.66E+08	+	0	NA	intron (Nintron (N	99253	NM_001365	6335	Hs.439145NM_002977	ENSG000007SCN9A	ETHA FEB	sodium vcpprotein-coding	
chr5-1404k 3.461229	-0.79038	1.237482	-0.6387	0.523018	0.981636	chr5	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N	64013	NM_017978	54882	Hs.594084NM_017747	ENSG000007ANKHD1	MASK MAS	ankyrin rprotein-coding	
chr11-10k 6.947697	-0.56745	0.889191	-0.63817	0.523364	0.981636	chr11	10578173	10578741	+	0	NA	intron (Nintron (N	-9792	NM_006691	10894	Hs.655332NM_006691	ENSG000007LYVE1	CRSBP-1 F	lymphaticprotein-coding	
chr11-62k 6.947697	-0.56745	0.889191	-0.63817	0.523364	0.981636	chr11	62649631	62649830	+	0	NA	exon (NM exon (NM	-3004	NM_001278	23193	Hs.595071NM_014611	ENSG000007GANAB	G2AN G1A	glucosidaseprotein-coding	
chr5-132k 6.947697	-0.56745	0.889191	-0.63817	0.523364	0.981636	chr5	1.33E+08	1.33E+08	+	0	NA	intron (NMLT1E2 LI	15982	NM_005732	10111	Hs.633509NM_005732	ENSG000007RAD50	NBSLD RAI	RAD50 dotprotein-coding	
chr16-13k 5.698276	0.66109	1.035988	0.638126	0.523392	0.981636	chr16	1399227	1399711	+	0	NA	exon (NM exon (NM	15232	NM_001193	64718	Hs.643536NM_001037	ENSG000007UNKL	C16orf28 u	unk like protein-coding	
chr13-50k 0.044684	-0.51254	0.803228	-0.6381	0.523407	0.981636	chr13	50047686	50047885	+	0	NA	intron (NALuS2 SI	1276	NR_029486	406950	NR_029486	ENSG000007MIR16-1	MIRN16-1	microRNA ncRNA	
chr1-243k 11.86938	-0.43787	0.686397	-0.63793	0.523521	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (NLMIB7 LIN	216152	NR_039824	1.01E+08	NR_039824	ENSG000007MIR4677	mir-4677	microRNA ncRNA	
chr1-7781k 6.873276	-0.57675	0.904237	-0.63783	0.523584	0.981636	chr1	77811306	77811789	+	0	NA	intron (Nintron (N	31742	NM_001363	374986	Hs.437755NM_198545	ENSG000007MIGA1	FAM73A	mitochondrialprotein-coding	
chr16-69k 6.873276	-0.57675	0.904237	-0.63783	0.523584	0.981636	chr16	69569063	69570768	+	0	NA	intron (Nintron (N	3949	NM_138713	10725	Hs.371987NM_006595	ENSG000007NFAT5	NF-AT5 N	nuclear fprotein-coding	
chr2-187k 6.873276	-0.57675	0.904237	-0.63783	0.523584	0.981636	chr2	28113554	28123227	+	0	NA	intron (NMLT1B LTF	25083	NM_001325	7035	Hs.516578NM_006287	ENSG000007TFP1	EPI LACI	tissue fprotein-coding	
chr21-334k 6.873276	-0.57675	0.904237	-0.63783	0.523584	0.981636	chr21	33430044	33430471	+	0	NA	intron (Nintron (N	27361	NM_001325	3460	Hs.634632NM_005534	ENSG000007IFNGR2	AF-1 IFG	interfercprotein-coding	
chr8-424k 6.873276	-0.57675	0.904237	-0.63783	0.523584	0.981636	chr8	42462475	42464588	+	0	NA	intron (Nintron (N	36800	NM_001257	6575	Hs.653172NM_006745	ENSG000007SLC20A2	GLVR-2 G	solute cprotein-coding	
chr9-2811k 6.873276	-0.57675	0.904237	-0.63783	0.523584	0.981636	chr9	32155	32155	+	0	NA	intron (Nintron (N	32155	NM_014878	9933	Hs.493095NM_014878	ENSG000007PUM3	HA-8 HLA	pulmo fprotein-coding	
chr7-143k 9.555138	-0.49025	0.768815	-0.63767	0.523686	0.981636	chr7	1.43E+08	1.43E+08	+	0	NA	intron (Nintron (N	5286	NM_001224	835	Hs.368982NM_001224	ENSG000007CASP2	CASP-2 C	caspase 2protein-coding	
chr3-485k 7.358306	-0.55013	0.862764	-0.63764	0.523707	0.981636	chr3	48564830	48565228	+	0	NA	intron (Nintron (N	-1248	NM_033199	90226	Hs.631914NM_033199	ENSG000007UCN2	SRP UCN	urocortin protein-coding	
chr5-348k 7.358306	-0.55013	0.862764	-0.63764	0.523707	0.981636	chr5	34833194	34834024	+	0	NA	TTS (NM_CTS (NM_C	-5555	NM_144722	136527	Hs.435742NM_144722	ENSG000007TTC23L	MC25-1	tetratricprotein-coding	
chr11-127k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr11	1276155	1277245	+	0	NA	3' UTR (3' UTR (N	20095	NR_106802	1.02E+08	NR_106802	ENSG000007MIR6744	hsa-mir-6	microRNA ncRNA	
chr11-58k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr11	58531851	58533039	+	0	NA	intron (NLTR12C LI	-24340	NM_001005	219968	Hs.553647NM_001005	ENSG000007OR5B21	-	olfactoryprotein-coding	
chr13-36k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr13	36852989	36854138	+	0	NA	exon (NM exon (NM	34361	NM_000538	5994	Hs.24422	NR_000538	ENSG000007RFXAP	-	regulatorprotein-coding
chr19-20k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr19	20659239	20659856	+	0	NA	intron (NMER92B LI	2024	NM_001076	199777	Hs.657001NM_145297	ENSG000007ZNF626	-	zinc fingerprotein-coding	
chr19-45k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr19	45287482	45293711	+	0	NA	intron (Nintron (N	32279	NM_001824	1158	Hs.334347NM_001824	ENSG000007CKM	CKMM CPK	creatine protein-coding	
chr20-48k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr20	485559	486057	+	0	NA	intron (Nintron (N	-23275	NM_144622	128637	Hs.590876NM_144622	ENSG000007TBC1D20	C20orf4 C	TBC1 domeprotein-coding	
chr5-136k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr5	1.36E+08	1.36E+08	+	0	NA	3' UTR (3' UTR (N	14007	NM_001355	389332	Hs.127688NM_001355	ENSG000007SMIM32	-	small intprotein-coding	
chr6-352k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr6	35283470	35286685	+	0	NA	intron (Nintron (N	-12741	NM_0022047	50619	Hs.15476	NR_0022047	ENSG000007DEF6	IBP SLAT	DEP6 guarprotein-coding
chr7-782k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chr7	782334	783242	+	0	NA	intron (NCPg	-32769	NM_001171	23535	Hs.438072NM_025154	ENSG000007SUNI	UNC84A	Sadl and protein-coding	
chrX-411k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chrX	41184487	41185477	+	0	NA	intron (Nintron (N	-90757	NR_135616	1.05E+08	Hs.546119NR_135616	ENSG000007LINC02601	-	long intncRNA	
chrX-714k 7.22918	0.552017	0.866156	0.637319	0.523917	0.981636	chrX	71407888	71408269	+	0	NA	exon (NM exon (NM	41721	NR_104387	6872	Hs.158566NM_004605	ENSG000007TAF1	BA2R CCG	TATA-box protein-coding	
chr7-747k 11.86152	-0.43677	0.68535	-0.6373	0.52393	0.981636	chr7	74751680	74756242	+	0	NA	exon (NM exon (NM	-20001	NM_000265	653361	Hs.647047NM_000265	ENSG000007NCF1	NCF1A NO	nucleothriprotein-coding	
chr1-331k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr1	33125156	33125955	+	0	NA	IntergeniL2a LINE	43377	NM_001301	113451	Hs.101807NM_052998	ENSG000007AZIN2	ADC AZI2	antizyme protein-coding	
chr12-145k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr12	45392214	45393217	+	0	NA	intron (NLIAP6 LIN	10025	NM_001142	196527	Hs.505332NM_001022	ENSG000007ANOG	BDPLT7 S	canactamir protein-coding	
chr12-131k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr12	9.12E+08	9.12E+08	+	0	NA	intron (NALuY SINE	28615	NM_004459	6433	Hs.381871NM_004459	ENSG000007SFSWAF	SFR58 SW	splicing protein-coding	
chr13-49k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr13	49532104	49534223	+	0	NA	non-codiron-codir	36107	NM_001045	51131	Hs.369033NM_001045	ENSG000007PHF11	APY BCAP	PHD fingerprotein-coding	
chr17-46k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr17	46041419	46042284	+	0	NA	intron (Nintron (N	42601	NM_001007	246744	Hs.661831NM_001007	ENSG000007STH	MAPTIT	saitohin protein-coding	
chr18-26k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr18	2692229	2693350	+	0	NA	intron (NML2c LINE	36992	NM_015295	23347	Hs.8118	NR_015295	ENSG000007SMCHD1	BAMS FSH	structure protein-coding
chr2-260k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr2	26099881	26100771	+	0	NA	intron (Nintron (N	66242	NM_016131	10890	Hs.467966NM_016131	ENSG000007RAB10	-	RAB10, meprotein-coding	
chr2-757k 5.171181	-0.6484	1.017602	-0.63719	0.524003	0.981636	chr2	75700783	75702635	+	0	NA									



chr4-152:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr4	1.52E+08	1.52E+08	0	NA	intron (Nintron (N	-14499 NR_104273	1.02E+08	Hs. 712524NR_104273	ENSG00000FBXW7-AS1	DEAR DESF	FBXW7	antncRNA
chr5-1805:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr5	1.809209	1.809937	+	NA	intron (Nintron (N	8166 NM_004555	4726	Hs. 408285NR_004555	ENSG00000NDUFS6	CI-13kA CNADH	ubic protein-coding	
chr5-7805:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr5	78097728	78098045	+	NA	intron (NSVA_D Ret	139639 NR_105012	1.02E+08	Hs. 252895NR_105012	LOC101925	-	uncharactncRNA	
chr5-1684:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr5	1.68E+08	1.69E+08	0	NA	intron (Nintron (N	13886 NM_002887	5917	Hs. 654907NM_002887	ENSG00000CARRS	ArgRS DAL	arginyl-t-protein-coding	
chr6-619:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr6	41907890	41909572	+	0	NA	intron (Nintron (N	12212 NM_001305	9477	Hs. 278483NM_004277	ENSG00000MED20	PROG213 Smediator	protein-coding
chr6-5712:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr6	57121863	57123181	+	0	NA	intron (NLIPA17 LI	32334 NM_001031	26036	Hs. 485628NM_015555	ENSG00000ZNF451	COASTER ezinc	finfprotein-coding
chr6-111:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr6	1.11E+08	1.11E+08	0	NA	intron (Nintron (N	95401 NM_153366	91749	Hs. 400572NM_153366	ENSG00000MPSD4B	KIAA1919 major	fagprotein-coding	
chr7-6496:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr7	64983604	64988919	+	0	NA	intron (NPRIMA4_L1	4775 NM_015852	51351	Hs. 250699NM_015852	ENSG00000ZNF117	H-plk HPF	zinc finfprotein-coding
chr7-130C:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (NLM14 LINE	19514 NM_001363	51530	Hs. 194157NM_016478	ENSG00000ZC3HC1	HSPC216 zinc	finfprotein-coding
chr8-3057:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr8	30572374	30578993	+	0	NA	TTS (NM_CTS (NM_C	-60397 NR_001206	1.01E+08	Hs. 659493NM_001206	ENSG00000SMIM18	-	small intronprotein-coding
chr8-672C:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr8	67208242	67212471	+	0	NA	intron (NALuJb SIN	126508 NM_001291	79848	Hs. 370147NM_02479C	ENSG00000CSPP1	CSPP JBTs	centrosomprotein-coding
chr9-9364:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr9	93649530	93651811	+	0	NA	intron (Nintron (N	55829 NR_049855	1.01E+08	NR_049855	ENSG00000MIR548AU	-	microRNA ncRNA
chr9-971C:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr9	97196733	97198974	+	0	NA	intron (Nintron (N	-40573 NR_03652C	1E+08	Hs. 435625NR_03652C	ENSG00000SUGTIP4-5	-	SUGTIP4-5pseudo
chr9-137C:7.195898	0.548652	0.862911	0.635815	0.524897	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (Nintron (N	3926 NR_04572C	11253	Hs. 279881NM_016215	ENSG00000CMAN1B1	ERMANN EF	mannoside protein-coding
chr6-319C:8.301375	0.54436	0.856435	0.635611	0.52503	0.981636	chr6	31966869	31967523	+	0	NA	intron (Nintron (N	-3979 NR_026717	8859	Hs. 654371NM_004197	ENSG00000STK19	D6S60 D6S	serine/tl protein-coding
chr1-149C:6.136159	0.608401	0.957267	0.635561	0.525063	0.981636	chr1	1492423	1492622	+	0	NA	intron (NALuXs1 SI	14673 NM_001317	83858	Hs. 729021NM_031921	ENSG00000ATAD3B	AAA-T0B3 ATPase	ε protein-coding
chr15-59C:4.668585	-0.71232	1.120815	-0.63554	0.525079	0.981636	chr15	59654859	59655058	+	0	NA	intron (NTigger4a	2347 NM_00132C	2958	Hs. 512934NM_004492	ENSG00000GTF2A2	HAT18745 general	tprotein-coding
chr14-67C:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr14	67374536	67375263	+	0	NA	intron (NFLAM_C4a	14571 NM_004094	1965	Hs. 151777NM_004094	ENSG00000EIF2S1	EIF-2 EIF	ekaryotiprotein-coding
chr16-717:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr16	71761149	71761957	+	0	NA	exon (NM_exon (NM_	-3066 NR_00305E	692111	NR_00305E	ENSG00000SNORD71	HBII-239 small	nucsnRNA
chr16-84C:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr16	84609627	84610962	+	0	NA	intron (NMLTIK LTF	7784 NM_02114E	23406	Hs. 289092NM_02114E	ENSG00000COTL1	CLP	coactosin protein-coding
chr19-534:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr19	53433928	53436861	+	0	NA	intron (NALuSp SIN	3410 NM_00100E	38856	Hs. 433293NM_00100E	ENSG00000ZNF761	ZNF468	zinc finfprotein-coding
chr2-202C:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr2	20293838	20294532	+	0	NA	intron (Nintron (N	33201 NM_00128E	23369	Hs. 467824NM_015317	ENSG00000PUM2	PUMH2 PUM	pumilio fprotein-coding
chr3-154C:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr3	1.54E+08	1.54E+08	+	0	NA	intron (Nintron (N	41855 NM_02086E	170506	Hs. 446277NM_02086E	ENSG00000DXH36	DDX36 G4F	DEAH-box protein-coding
chr6-3747:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr6	37472233	37472884	+	0	NA	intron (Nintron (N	27335 NM_13849E	154467	Hs. 284207NM_13849E	ENSG00000CCDC167	C6orf129 coiled-c	protein-coding
chr9-115C:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr9	1.15E+08	1.15E+08	+	0	NA	intron (NMLRb SINE	77917 NM_00216C	3371	Hs. 143255NM_00216C	ENSG00000TNC	150-225 T	tenascin protein-coding
chr9-1347:7.38373	-0.54319	0.854732	-0.63551	0.525098	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	-78843 NR_13804E	414316	Hs. 571561NR_13804E	ENSG00000COL5A1-AS	C9orf104 COL5A1	arncRNA
chr1-2227:10.44258	0.462462	0.727722	0.635493	0.525107	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (Nintron (N	-11913 NM_20746E	400823	Hs. 697606NM_20746E	ENSG00000FAM177B	-	family wiprotein-coding
chr1-228:10.44258	0.462462	0.727722	0.635493	0.525107	0.981636	chr1	2.28E+08	2.28E+08	+	0	NA	TTS (NR_CTS (NR_C	1068 NR_03741E	1.01E+08	NR_03741E	ENSG00000MIR3620	mir-3620	microRNA ncRNA
chr16-66C:10.44258	0.462462	0.727722	0.635493	0.525107	0.981636	chr16	66940469	66942489	+	0	NA	intron (Nintron (N	5963 NM_00136E	8824	Hs. 282975NM_00386E	ENSG00000CES2	CE-2 CES2	chromoxyle protein-coding
chr19-127:11.85367	-0.43567	0.68597	-0.63511	0.525354	0.981636	chr19	1271063	1272525	+	0	NA	TTS (NM_CTS (NM_C	-2371 NM_017914	55009	Hs. 591383NM_017914	ENSG00000C19orf24	-	chromosomprotein-coding
chr4-1194:11.85367	-0.43567	0.68597	-0.63511	0.525354	0.981636	chr4	1.19E+08	1.2E+08	+	0	NA	intron (Nintron (N	51890 NR_03763C	645513	Hs. 677546NR_03763C	ENSG00000CLOC645513	-	septin 7 pseudo
chr6-318:11.85367	-0.43567	0.68597	-0.63511	0.525354	0.981636	chr6	31836360	31841148	+	0	NA	intron (NALuXs1 SI	1678 NR_00274E	26797	NR_00274E	ENSG00000SNORD52	RNU52 U52	small nucsnRNA
chr1-111:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr1	11132765	11133308	+	0	NA	intron (Nintron (N	-10862 NR_04660C	1.01E+08	Hs. 679133NR_04660C	ENSG00000MTOR-AS1	-	MTOR antncRNA
chr10-13:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr10	1.33E+08	1.33E+08	+	0	NA	intron (NLMIMA4 LIN	13094 NM_00101E	503542	Hs. 64968 NM_00101E	ENSG00000CSPRN	SHAD00 Sf	shadow of protein-coding
chr13-11:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (N (ACC)n Si	22382 NM_00100E	8451	Hs. 339782NM_00358E	ENSG00000CUL4A	-	culin 4#protein-coding
chr17-29C:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr17	29266064	29267596	+	0	NA	intron (Nintron (N	19973 NM_00520E	1411	Hs. 46275 NM_00520E	ENSG00000CRYBA1	CRYB1 CTF	crystallin protein-coding
chr4-266C:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr4	26689519	26692235	+	0	NA	intron (NTigger1 I	106793 NM_018317	55296	Hs. 479403NM_018317	ENSG00000TBC1D19	-	TBC1 domε protein-coding
chr5-1294:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr5	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	-18159 NR_125744E	1.04E+08	Hs. 628633NR_12574E	ENSG00000ADAMTS19-	-	ADAMTS19 ncRNA
chr6-856C:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr6	85628110	85630635	+	0	NA	intron (Nintron (N	12079 NM_00115E	10492	Hs. 571177NM_00637E	ENSG00000SYNCRIP	GRY-RBP C	synaptotil protein-coding
chr9-128C:9.605986	-0.4795	0.755183	-0.63494	0.525467	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	9830 NM_00136E	6709	Hs. 372331NM_003127	ENSG00000SPTAN1	EIEE5 NE#	spectrin protein-coding
chr12-69C:7.350448	-0.54845	0.864262	-0.63458	0.525749	0.981636	chr12	69564918	69565374	+	0	NA	intron (NTigger3b	-19577 NR_03747E	1.01E+08	NR_03747E	ENSG00000MIR3913-2	mir-3913	microRNA ncRNA
chr1-151E:7.350448	-0.54667	0.861561	-0.63451	0.525749	0.981636	chr1	1.62E+08	1.52E+08	+	0	NA	intron (Nintron (N	16491 NR_03028C	693139	NR_03028C	ENSG00000MIR554	-	microRNA ncRNA
chr15-944:7.399446	-0.54667	0.861561	-0.63451	0.525749	0.981636	chr15	94444984	94445789	+	0	NA	intron (Nintron (N	89456 NM_00115E	55784	Hs. 33368 NM_01834E	ENSG00000MCTP2	-	multiple protein-coding
chr11-34C:9.572704	-0.48347	0.762094	-0.63439	0.525825	0.981636	chr11	34881609	34881870	+	0	NA	TTS (NM_CTS (NM_C	-34391 NM_00116E	8050	Hs. 502315NM_003477	ENSG00000PDHX	DLDB E3E	pyruvate protein-coding
chr19-10C:9.605986	-0.49416	0.779056	-0.6343	0.525885	0.981636	chr19	10671019	10672317	+	0	NA	intron (Nintron (N	17322 NM_00111E	3609	Hs. 465888NM_00451E	ENSG00000ILF3	CBTF DRBF	interleuk protein-coding
chr4-397E:9.605986	-0.49416	0.779056	-0.6343	0.525885	0.981636	chr4	39765374	39765613	+	0	NA	intron (NALuJb SIN	67357 NM_001111	3093	Hs. 50308 NM_00533E	ENSG00000UBE2K	E2-25K HU	ubiquitin protein-coding
chr1-202E:5.1379	-0.656	1.034368	-0.6342	0.52595	0.981636	chr1	2.03E+08	2.03E+08	+	0	NA	3' UTR (N3' UTR (N	9608 NM_002871	5877	Hs. 90875 NM_002871	ENSG00000RAB1F	MSS4 RASC	RAB interprotein-coding
chr11-10E:5.1379	-0.656	1.034368	-0.6342	0.52595	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	37655 NM_00347E	8065	Hs.			

chr10-295 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr10	29508338	29508905	+	0 NA	intron (Nintron (N	36476 NR_030335	693189	NR_030335	ENSG000002MIR604	MIRN604 tmicroRNA ncRNA	
chr11-354 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr11	35428228	35429749	+	0 NA	Intergeni MLT2F LTF	-8930 NM_0011195	6506 Hs. 502338	NR_004171	ENSG000002SLC1A2	EAAT2 E1E solute c protein-coding	
chr11-472 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr11	47221616	47223285	+	0 NA	intron (NAluJr SIN	7508 NM_001300	1643 Hs. 700338	ENSG000002DDB2	DBB UV-I damage s protein-coding		
chr11-117 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr11	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	65875 NM_014956	22897 Hs. 504009	NR_014956	ENSG000002CEP164	NPHP15 centrosome protein-coding	
chr12-481 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr12	48129290	48135554	+	0 NA	promoter-promoter-	-375 NR_106766	1.02E+08	NR_106766	ENSG000002MIR6505	hsa-mir-61 microRNA ncRNA	
chr12-101 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr12	1.01E+08	1.01E+08	+	0 NA	intron (NAluJr SIN	-20976 NR_049838	1.01E+08	NR_049838	ENSG000002MIR548A	microRNA ncRNA	
chr12-112 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr12	1.12E+08	1.12E+08	+	0 NA	exon (NM exon (NM	-83672 NR_106921	1.02E+08	NR_106921	ENSG000002MIR6861	hsa-mir-61 microRNA ncRNA	
chr12-125 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr12	1.22E+08	1.22E+08	+	0 NA	3' UTR (N3' UTR (N	-25287 NM_152755	254050	Hs. 374856	NR_152755	ENSG000002LRR343	leucine r protein-coding
chr12-125 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr12	1.23E+08	1.23E+08	+	0 NA	intron (NAluSc5 SI	-21669 NR_036187	1E+08	NR_036187	ENSG000002MIR4304	microRNA ncRNA	
chr14-742 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr14	74268886	74292411	+	0 NA	intron (Nintron (N	13286 NR_148467	5826 Hs. 94395	NR_005056	ENSG000002ABCD4	ABC4 EST1ATP bindi protein-coding	
chr14-102 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr14	1.02E+08	1.02E+08	+	0 NA	TTS (NM_C TTS (NM_C	43596 NM_001348	122416	Hs. 432946	NR_152326	ENSG000002ANKRD9	ankyrin r protein-coding
chr15-407 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr15	40771945	40779476	+	0 NA	intron (Nintron (N	5730 NM_001130	643338	Hs. 631715	NR_001130	ENSG000002C15orf62	chromosome protein-coding
chr15-725 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr15	72344989	72350374	+	0 NA	intron (Nintron (N	-27524 NM_005284	60677 Hs. 348342	NR_005284	ENSG000002CELP6	BRUNOL6 CUGBP E protein-coding	
chr17-692 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr17	6998738	6999401	+	0 NA	intron (Nintron (N	3020 NM_000697	239 Hs. 654431	NR_000697	ENSG000002ALOX12	L2-LOX L2arachid protein-coding	
chr17-291 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr17	29103488	29107392	+	0 NA	intron (N L2c LINE	-29831 NM_004740	9220 Hs. 462599	NR_004740	ENSG000002TIAF1	MAJN SPR2 TGFBI-inc protein-coding	
chr18-747 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr18	74503643	74504231	+	0 NA	intron (Nintron (N	4349 NM_001168	55748 Hs. 149188	NR_018236	ENSG000002CNDP2	CN2 CPGL carnosine protein-coding	
chr18-797 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr18	79753957	79755156	+	0 NA	TTS (NM_C TTS (NM_C	73127 NM_001205	9150 Hs. 465499	NR_004715	ENSG000002CTDP1	CCFDN PCFCTD phosph protein-coding	
chr18-797 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr18	79940111	79943344	+	0 NA	intron (Nintron (N	9926 NM_001146	80148 Hs. 288284	NR_025078	ENSG000002SLC66A2	PQLC1 solute c protein-coding	
chr19-125 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr19	12542945	12546360	+	0 NA	intron (NMERS4A LI	6830 NM_144976	163050	Hs. 655615	NR_144976	ENSG000002ZNF564	zinc finger protein-coding
chr19-164 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr19	16400729	16405558	+	0 NA	intron (Nintron (N	68827 NM_001258	58513 Hs. 654635	NR_021235	ENSG000002EPL5L1	EPL5L1 epidermal protein-coding	
chr19-187 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr19	18531897	18533296	+	0 NA	intron (Nintron (N	-10526 NM_006532	8178 Hs. 515266	NR_006532	ENSG000002ELL	C19orf17 elongatic protein-coding	
chr19-195 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr19	19349051	19357516	+	0 NA	intron (Nintron (N	32454 NM_015325	23383 Hs. 654935	NR_015325	ENSG000002MAU2	KIAA0892 MAU2 sist protein-coding	
chr19-552 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr19	55289061	55296588	+	0 NA	intron (NAluSx SIN	8827 NM_032430	84446 Hs. 182081	NR_032430	ENSG000002BRSK1	hSAD1 BR serine protein-coding	
chr2-2334 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	2.33E+08	2.33E+08	+	0 NA	intron (Nintron (N	81931 NM_018218	55230 Hs. 96513	NR_018218	ENSG000002USP40	ubiquitin protein-coding	
chr2-176 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	17621313	17622961	+	0 NA	intron (Nintron (N	6612 NM_001696	529 Hs. 517338	NR_001696	ENSG000002ATP6V1E1	ARCL2C ATATPase H protein-coding	
chr2-205 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	20999589	21000267	+	0 NA	TTS (NM_C TTS (NM_C	-1399 NR_027055	439931	Hs. 517433	NR_027055	ENSG000002THAP7-AS1	THAP7 antncRNA
chr2-214 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	21479992	21481966	+	0 NA	intron (NAluSx1 SI	10479992	645426	Hs. 376511	NR_001207	ENSG000002TMEM191C	transmembrane protein-coding
chr2-305 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	30575979	30581817	+	0 NA	exon (NM exon (NM	-4233 NM_001318	9514 Hs. 17958	NR_004861	ENSG000002GAL3ST1	CST galactose protein-coding	
chr2-434 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	43980644	43986317	+	0 NA	intron (Nintron (N	-15731 NM_001003	29780 Hs. 475074	NR_013327	ENSG000002PARVB	CGI-56 parvin b protein-coding	
chr2-505 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr2	50436629	50442437	+	0 NA	intron (Nintron (N	32091 NR_162128	1.13E+08	NR_162128	MIR12114	microRNA ncRNA	
chr3-1571 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr3	1.57E+08	1.57E+08	+	0 NA	Intergeni L2a LINE	-25038 NM_020307	57018 Hs. 4859	NR_020307	ENSG000002CCNL1	ANI6A B cyclin L1 protein-coding	
chr4-8607 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr4	860744	864994	+	0 NA	intron (N Tigger1 I	-36740 NM_006651	10815 Hs. 478933	NR_006651	ENSG000002CPLX1	CPX-1 CPX complex protein-coding	
chr5-1387 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr5	13875128	13876848	+	0 NA	intron (Nintron (N	68492 NM_001366	1767 Hs. 212366	NR_001366	ENSG000002DNAH5	CILD3 DNA dynein a protein-coding	
chr6-152 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr6	1.52E+08	1.52E+08	+	0 NA	intron (N L2b LINE	-57657 NR_120501	1.01E+08	Hs. 571205	NR_120501	SYNE1-AS1	SYNE1 antncRNA
chr7-670 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr7	67009767	67012093	+	0 NA	intron (Nintron (N	14097 NR_018264	55253 Hs. 520917	NR_018264	ENSG000002TYW1	RSADF1 TY tRNA-yW s protein-coding	
chr7-9895 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr7	98993545	98995218	+	0 NA	intron (Nintron (N	-18784 NR_110102	1.02E+08	Hs. 636663	NR_110102	LOC101927	uncharacterized ncRNA
chr9-9271 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr9	92712895	92714129	+	0 NA	3' UTR (N3' UTR (N	-43381 NM_022755	64768 Hs. 459898	NR_022755	ENSG000002IPPK	C9orf12 inositol- protein-coding	
chr9-1365 7.203756	0.546451	0.865756	0.631184	0.52792	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	3381 NM_003088	6621 Hs. 113265	NR_003088	ENSG000002SNAPC4	P17Alfa small nuc protein-coding	
chr12-511 6.707168	0.577379	0.915	0.631015	0.528031	0.981636	chr12	51107638	51108495	+	0 NA	intron (NAluSx3 SI	-24470 NM_030805	81566 Hs. 524422	NR_030805	ENSG000002CSRNP2	C2orf2 cysteine protein-coding	
chr15-768 6.707168	0.577379	0.915	0.631015	0.528031	0.981636	chr15	76850480	76852454	+	0 NA	intron (N LIPREC2 I	10477 NM_001145	49855 Hs. 458988	NR_020843	ENSG000002SCAPER	IDDRP MS1S-phase c protein-coding	
chr16-156 6.707168	0.577379	0.915	0.631015	0.528031	0.981636	chr16	1582199	1582815	+	0 NA	intron (N MLT1D LTF	1980 NR_135176	1.05E+08	Hs. 663322	NR_135176	ENSG000002LOC105371	uncharacterized ncRNA
chr16-256 6.707168	0.577379	0.915	0.631015	0.528031	0.981636	chr16	2596026	2597169	+	0 NA	intron (Nintron (N	-6787 NR_015441	652276 Hs. 720448	NR_015441	ENSG000002LOC652276	potassium pseudo	
chr3-9677 6.707168	0.577379	0.915	0.631015	0.528031	0.981636	chr3	9677682	9678832	+	0 NA	intron (Nintron (N	-25576 NM_153635	151835 Hs. 121333	NR_153635	ENSG000002CPNE9	copine f protein-coding	
chr5-173 6.707168	0.577379	0.915	0.631015	0.528031	0.981636	chr5	1.73E+08	1.73E+08	+	0 NA	intron (Nintron (N	13961 NM_013988	662 Hs. 145722	NR_001205	ENSG000002BNIP1	NIP1 SEC2BCL2 inte protein-coding	
chr19-231 3.453371	-0.78681	1.247571	-0.63067	0.528253	0.981636	chr19	23219527	23220423	+	0 NA	Intergeni Intergeni	30419 NM_001355	440519 Hs. 675814	NR_001355	ENSG000002ZNF724	ZNF724F zinc finger protein-coding	
chr2-2375 3.453371	-0.78681	1.247571	-0.63067	0.528253	0.981636	chr2	2.38E+08	2.38E+08	+	0 NA	intron (NAluJb SIN	17381 NM_001278	140739 Hs. 471788	NR_080678	ENSG000002UBE2F	NCE2 ubiquitin protein-coding	
chr1-2075 9.639267	-0.47561	0.754169	-0.63064	0.528273	0.981636	chr1	2.07E+08	2.07E+08	+	0 NA	intron (N LIMEg LIN	11925 NR_125345	1604 Hs. 126517	NR_000574	ENSG000002CD55	CHAPLE CFCD55 mole protein-coding	
chr14-525 9.639267	-0.47561	0.754169	-0.63064	0.528273	0.981636	chr14	52946587	52948189	+	0 NA	intron (NAluY SINE	3662 NM_006832	10979 Hs. 509342	NR_006832	ENSG000002FERMT2	KIND2 MIC fermitin protein-coding	
chr19-1119 9.639267	-0.47561	0.754169	-0.63064	0.528273	0.981636	chr19	11169428	11171303	+	0 NA	intron (Nintron (N	-14553 NM_001317	14784 Hs. 381225	NR_182515	ENSG000002SPC24	SPC24 con protein-coding	
chr2-1698 9.639267	-0.47561	0.754169	-0.63064	0.528273	0.981636	chr2	1.7E+08	1.7E+08	+	0 NA</							



chr3-1944	9.63141	-0.47428	0.753977	-0.62904	0.529323	0.981636	chr3	1.94E+08	1.94E+08	+	0	NA	intron (N(TGTAATA)	8651	NM_024524	79572	Hs.529609	ENSG000004ATP13A3	AFURS1	ATPase 1;protein-coding
chr5-6911	9.63141	-0.47428	0.753977	-0.62904	0.529323	0.981636	chr5	69115545	69117582	+	0	NA	exon (NM_exon (NM_022902	22549	NM_022902	64924	Hs.63197	ENSG000004SLC30A5	ZNT5 ZNT1	solute c;protein-coding
chr5-179f	9.63141	-0.47428	0.753977	-0.62904	0.529323	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (N(intron (N	9264	NR_11056f	1.02E+08	Hs.66325	ENSG000004LOC10192f	-	uncharactercncRNA
chr6-158f	9.63141	-0.47428	0.753977	-0.62904	0.529323	0.981636	chr6	1.59E+08	1.59E+08	+	0	NA	intron (N(LIPA5 LIN	4893	NR_106981	1.02E+08	NR_106981	ENSG000004MIR7161	hsa-mir-7	miRNA ncRNA
chr7-107f	9.63141	-0.47428	0.753977	-0.62904	0.529323	0.981636	chr7	1.08E+08	1.08E+08	+	0	NA	intron (N(intron (N	38815	NM_00010f	1738	HS.13171	ENSG000004DLD	DLDD DLDF	hydrolylprotein-coding
chr8-381f	9.63141	-0.47428	0.753977	-0.62904	0.529323	0.981636	chr8	38168109	38172497	+	0	NA	intron (N(AluSx3 SI	6190	NM_01446f	27257	Hs.42531	ENSG000004CLSM1	CASM YJL1LSM1	homcprotein-coding
chr20-43f	6.632747	0.572659	0.910553	0.628914	0.529405	0.981636	chr20	43638058	43638430	+	0	NA	intron (N(AluSg2 SI	-28775	NM_00127f	4605	HS.17971	ENSG000004MYBL2	B-MYB BMYB	protcprotein-coding
chr18-74f	7.237038	0.549811	0.874726	0.628552	0.529642	0.981636	chr18	74260786	74263611	+	0	NA	intron (N(AluSx SIN	29765	NM_14892f	1528	HS.46541	ENSG000004CYB5A	CYB5 MCBE	cytochornprotein-coding
chr20-321f	7.237038	0.549811	0.874726	0.628552	0.529642	0.981636	chr20	32139502	32140668	+	0	NA	intron (N(L2c LINE	30357	NM_00136f	9777	HS.65466	ENSG000004TM9SF4	dJ836N17	transmemtprotein-coding
chr2-5564f	7.424869	-0.53979	0.859173	-0.62827	0.529828	0.981636	chr2	55642794	55643600	+	0	NA	exon (NM_exon (NM_02046f	-25575	NM_02046f	57223	HS.51618	ENSG000004PPP4R3B	FLFL2 PP4	protein f;protein-coding
chr7-121f	7.424869	-0.53979	0.859173	-0.62827	0.529828	0.981636	chr7	1.21E+08	1.21E+08	+	0	NA	intron (N(MER103C I	28118	NM_05716f	51384	HS.27237	ENSG000004WNT16	-	Wnt familtprotein-coding
chr1-551f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr1	55151062	55152937	+	0	NA	intron (N(intron (N	63365	NM_01530f	23358	HS.47700	ENSG000004USP24	-	ubiquitirprotein-coding
chr15-75f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr15	75861494	75861915	+	0	NA	intron (N(intron (N	17660	NM_00114f	92912	HS.23033	ENSG000004UBE2Q2	-	ubiquitirprotein-coding
chr17-42f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr17	4222859	4223141	+	0	NA	intron (N(intron (N	40748	NM_00125f	51479	HS.69608	ENSG000004ANKFY1	ANKHZH B1ankyrin	lprotein-coding
chr17-591f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr17	59126351	59127543	+	0	NA	intron (N(LIMB3 LIN	10925	NR_030411	768216	NR_030411	ENSG000004MIR454	MIRN454	microRNA ncRNA
chr2-702f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr2	70209088	70211020	+	0	NA	non-codiron-codir	-19035	NR_14597f	54980	HS.72004	ENSG000004C2orf42	-	chromosonprotein-coding
chr7-137f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr7	1.38E+08	1.38E+08	+	0	NA	intron (N(AluS6 SI	40532	NM_00131f	64764	HS.49027	ENSG000004CREB3L2	BBF2H7	cAMP res;pprotein-coding
chr9-132f	5.163323	-0.64594	1.028808	-0.62786	0.530099	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	non-codiron-codir	20367	NM_012204	9329	HS.22027	ENSG000004GTF3C4	KAT12 TF3	general tprotein-coding
chr10-68f	9.887284	0.472169	0.752176	0.627738	0.530176	0.981636	chr10	68375626	68375845	+	0	NA	exon (N(Alu SINE	31454	NM_017987	55680	HS.65314	ENSG000004RUFY2	RAB1P4R ZRUN	and fprotein-coding
chr11-864f	7.162617	0.545267	0.868686	0.627691	0.530206	0.981636	chr11	8647905	8648927	+	0	NA	exon (NM_exon (NM_01481f	10420	NM_01481f	9866	HS.13083	ENSG000004TRIM66	C1lorf29	tripartitprotein-coding
chr11-942f	7.162617	0.545267	0.868686	0.627691	0.530206	0.981636	chr11	94288980	94289476	+	0	NA	Intergeni(LIMEf LIN	-8470	NM_01834f	55784	HS.33368	ENSG000004MTCP2	-	multiple protein-coding
chr3-1247f	7.162617	0.545267	0.868686	0.627691	0.530206	0.981636	chr3	1.25E+08	1.25E+08	+	0	NA	3' UTR (N3' UTR (N	30833	NR_03608f	1E+08	NR_03608f	ENSG000004MIR544B	-	microRNA ncRNA
chr5-134f	7.162617	0.545267	0.868686	0.627691	0.530206	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (N(intron (N	18656	NM_03215f	84105	HS.71001	ENSG000004PCBD2	DCOH2 DCC	pterin-4 protein-coding
chr9-127f	7.162617	0.545267	0.868686	0.627691	0.530206	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (N(intron (N	20861	NM_02283f	64855	HS.52240	ENSG000004NIBAN2	C9orf88 F	niban apcprotein-coding
chr12-68f	9.594428	-0.49781	0.793169	-0.62762	0.530252	0.981636	chr12	6836305	6836589	+	0	NA	intron (N(intron (N	-4478	NM_00129f	2784	HS.63165	ENSG000004GNB3	CSNB1H	G proteirprotein-coding
chr1-156f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	exon (NM_exon (NM_01465f	6255	NM_01465f	9673	HS.53237	ENSG000004SLC25A44	-	solute c;protein-coding
chr10-13f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr10	13616553	13617117	+	0	NA	intron (N(intron (N	29870	NM_00367f	8559	HS.66064	ENSG000004PRPF18	PRP18 hPr	pre-mRNA protein-coding
chr12-26f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr12	26977266	26978050	+	0	NA	intron (N(AluS SIN	36726	NM_016551	51768	HS.43864	ENSG000004TM7SF3	-	transmemtprotein-coding
chr15-28f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr15	28211824	28213058	+	0	NA	intron (N(intron (N	109711	NM_00466f	8924	HS.43489	ENSG000004HERC2	D15F37S1	HECT and protein-coding
chr15-63f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr15	63161904	63161578	+	0	NA	intron (N(intron (N	-1464	NR_03408f	1E+08	NR_03408f	ENSG000004USP3-AS1	USP3	antincRNA
chr15-91f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr15	91001051	91001991	+	0	NA	intron (N(intron (N	-6986	NM_19941f	9055	HS.36640	ENSG000004PRC1	ASE1	protein rprotein-coding
chr19-14f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr19	14694890	14697243	+	0	NA	intron (N(AluS6 SI	6018	NM_00135f	84449	HS.51521	ENSG000004ZNF333	-	zinc fingernprotein-coding
chr2-273f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr2	27333326	27337653	+	0	NA	promoter-promoter-	-53	NR_03842f	1.01E+08	HS.66650	ENSG000004GTF3C2-AS	GTF3C2	ancRNA
chr3-5274f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr3	52745281	52747083	+	0	NA	exon (NM_exon (NM_00134f	24758	NM_00134f	6787	HS.63192	ENSG000004CNEK4	NRK2 STK2	NIMA rel;pprotein-coding
chr4-3557f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr4	355788	356397	+	0	NA	intron (N(AluSg4 SI	5935	NR_03029f	693156	NR_03029f	ENSG000004MIR571	MIRN571	microRNA ncRNA
chr4-657f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr4	6578626	6580884	+	0	NA	intron (N(CCATCA)R	4566	NM_015274	23324	HS.18846	ENSG000004MAN2B2	-	mannoside protein-coding
chr6-155f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr6	15501024	15501947	+	0	NA	intron (N(intron (N	161543	NR_03644f	84062	HS.57114	ENSG000004DTNBP1	BLOC1S8 I	dystrobre protein-coding
chr6-431f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr6	43194838	43198914	+	0	NA	intron (N(intron (N	14680	NM_01508f	23113	HS.48543	ENSG000004CUL9	H7AP1 PAF	cullin 9 protein-coding
chr8-202f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr8	20224725	20226834	+	0	NA	Intergeni(Intergeni	28398	NM_00169f	526	HS.29591	ENSG000004ATP6V1B2	ATP6B1B2	ATPase H;protein-coding
chr9-136f	7.170475	0.54308	0.866051	0.627076	0.530609	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	exon (NM_exon (NM_03982f	14297	NR_03982f	1.01E+08	NR_03982f	ENSG000004MIR4673	-	microRNA ncRNA
chr11-10f	7.317166	-0.55412	0.883746	-0.62702	0.530648	0.981636	chr11	1.02E+08	1.02E+08	+	0	NA	intron (N(AluS SIN	12525	NM_00119f	10413	HS.50369	ENSG000004YAP1	COB1 YAP	Yes assocprotein-coding
chr10-68f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr10	68378631	68379391	+	0	NA	intron (N(intron (N	28178	NM_017987	55680	HS.65314	ENSG000004RUFY2	RAB1P4R ZRUN	and fprotein-coding
chr10-96f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr10	96550489	96550725	+	0	NA	intron (N(intron (N	36405	NM_02012f	56889	HS.50067	ENSG000004TM9SF3	EP70-P-	is transmemtprotein-coding
chr10-10f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (N(intron (N	7602	NM_01790f	55662	HS.50078	ENSG000004HIF1AN	FIH1	hypoxia iprotein-coding
chr11-12f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr11	1.26E+08	1.26E+08	+	0	NA	intron (N(intron (N	4114	NM_00127f	3703	HS.50423	ENSG000004SIT3A	ITM1 STT3	STT3 oli;pprotein-coding
chr2-177f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr2	17714380	17715033	+	0	NA	intron (N(intron (N	39104	NM_00114f	79677	HS.50272	ENSG000004SMC6	SMC-6 SMC	structure;pprotein-coding
chr2-739f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr2	73941899	73942374	+	0	NA	intron (N(AluSx1 SI	15256	NR_13489f	1716	HS.46902	ENSG000004DGPUK	MTDPS3 N	C deoxyguar protein-coding
chr4-569f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr4	56989665	56989864	+	0	NA	intron (N(intron (N	10868	NM_00093f	5431	HS.60275	ENSG000004POLR2B	POLY2RB RF	RNA polynprotein-coding
chr6-8561f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr6	85619643	85620083	+	0	NA	intron (N(LIMC1 LIN	21588	NM_00115f	10492	HS.57117	ENSG000004SYNCRIP	GRY-8BP	synaptote;pprotein-coding
chr8-419f	7.368014	-0.53982	0.861001	-0.62696	0.530683	0.981636	chr8	41954567	41955314	+	0	NA	intron (N(intron (N	-58199	NM_00114f	286	HS.65443	ENSG000004ANK1	ANK SPH1	ankyrin lprotein-coding
chr1-2410	10.94702	0.446048	0.711622	0.626804	0.530787	0.981636	chr1	2.47E+08	2.47E+08	+	0	NA	3' UTR (N3' UTR (N	15507	NM_00129f	7678	HS.42123	ENSG000004ZNF124	HZF-16 H	zinc fingernprotein-coding

chr1-1627 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (N)LM5a LI	-27070 NM_001304	51478 Hs. 492925NM_016371	ENSG000004HSD17B7	PRAP SDR2 hydroxyst protein-coding
chr1-1835 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr1	1.84E+08	1.84E+08	+	0	NA	intron (N)MIRc SINE	115786 NM_001303	23127 Hs. 387999NM_015101	ENSG000004COLGALT2	C1orf17 collagen protein-coding
chr10-996 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr10	99685732	99686432	+	0	NA	intron (N)intron (N)	26453 NM_001345	57089 Hs. 28326 NM_020354	ENSG000004CENTPD7	LALP1 ectonucle protein-coding
chr10-102 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (N)AluSg7 SI	17008 NM_004311	403 Hs. 182215NM_004311	ENSG000004ARL3	ARL3 JBI ADP ribos protein-coding
chr10-125 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (N)intron (N)	-4554 NR_039704	1.01E+08 NR_039704	ENSG000004MIR4484	mir-4484 microRNA ncRNA
chr11-655 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr11	65551964	65552598	+	0	NA	exon (NM)exon (NM)	5947 NM_021070	4054 Hs. 289015NM_021070	ENSG000004TBP3	DASS GPH latent tr protein-coding
chr15-96 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr15	96337278	96338438	+	0	NA	3' UTR (N)3' UTR (N)	4093 NM_001145	7026 Hs. 347991NM_021000	ENSG000004NR2F2	HAT-1 ARF nuclear l protein-coding
chr17-276 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr17	10367596	10370072	+	0	NA	intron (N)intron (N)	-19198 NM_002308	3965 Hs. 81337 NM_002308	ENSG000004LGALS9	ARUP L GAL galectin protein-coding
chr17-584 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr17	58488323	58488623	+	0	NA	promoter-promoter-intron (N)intron (N)	-65 NM_001080	124535 Hs. 380061NM_001080	ENSG000004HSF5	HSF 5 HS1 heat shoc protein-coding
chr17-76 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr17	76084578	76086714	+	0	NA	intron (N)intron (N)	6464 NM_180999	353174 Hs. 714915NM_180999	ENSG000004ZACN	L2 L GIC2 zinc acti protein-coding
chr19-105 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr19	10367236	10370072	+	0	NA	intron (N)MLT1 J2 LI	1918 NM_003331	7297 Hs. 75516 NM_003331	ENSG000004TYK2	IMD35 JTK tyrosine protein-coding
chr19-205 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr19	20545279	20548280	+	0	NA	intron (N)AluJr4 SI	19002 NM_001155	1E+08 Hs. 515695NM_001155	ENSG000004ZNF737	ZNF102 zinc fing protein-coding
chr19-357 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr19	35753157	35754070	+	0	NA	TTS (NM)TTS (NM)	3416 NM_144617	126393 Hs. 534535NM_144617	ENSG000004HSPB6	HLL55 Hs heat shoc protein-coding
chr19-367 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr19	36024542	36028643	+	0	NA	exon (NM)exon (NM)	6043 NM_001195	25999 Hs. 466535NM_015525	ENSG000004CLIP3	CLIPR-59 CAP-Gly c protein-coding
chr2-1591 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr2	1.59E+08	1.59E+08	+	0	NA	intron (N)intron (N)	7690 NR_106945	1.02E+08 NR_106945	ENSG000004MIR6888	hsa-mir-618 microRNA ncRNA
chr2-2178 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr2	2.18E+08	2.18E+08	+	0	NA	exon (NM)exon (NM)	2752 NR_106867	1.02E+08 NR_106867	ENSG000004MIR6809	hsa-mir-618 microRNA ncRNA
chr3-3305 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr3	33033892	33034397	+	0	NA	intron (N)intron (N)	62688 NM_001075	2720 Hs. 443031NM_000404	ENSG000004GLB1	EBP ELNR1 galactosi protein-coding
chr5-213 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr5	213352	214202	+	0	NA	intron (N)LM1D1 LIN	4376 NM_145265	133957 Hs. 294145NM_145265	ENSG000004CCDC127	- coiled-cc protein-coding
chr5-1195 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr5	1.2E+08	1.2E+08	+	0	NA	intron (N)intron (N)	77540 NM_000414	3295 Hs. 406861NM_000414	ENSG000004HSD17B4	DBP MFE-2 hydroxyst protein-coding
chr6-4301 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr6	43010610	43012192	+	0	NA	TTS (NM)TTS (NM)	2545 NM_014623	4201 Hs. 278362NM_014623	ENSG000004MEA1	HYS MEA male-enhe protein-coding
chr7-5708 7.178332	0.540846	0.868907	0.622444	0.53365	0.981636	chr7	5709201	5709201	+	0	NA	intron (N)intron (N)	3160 NR_106934	1.02E+08 NR_106934	ENSG000004MIR6874	hsa-mir-618 microRNA ncRNA
chr1-2735 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr1	27334143	27335484	+	0	NA	intron (N)intron (N)	-7209 NM_001193	84958 Hs. 469175NM_032872	ENSG000004SYTL1	JFC1 SLP1 synaptot protein-coding
chr1-4665 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr1	46657753	46658642	+	0	NA	intron (N)intron (N)	7681 NM_001255	64756 Hs. 100874NM_022745	ENSG000004ATPAF1	ATP11 ATF ATP syntl protein-coding
chr1-2265 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (N)intron (N)	39067 NM_001618	142 Hs. 177769NM_001618	ENSG000004PARP1	ADPRT ADP poly (ADP- protein-coding
chr14-776 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr14	77672555	77674141	+	0	NA	3' UTR (N)3' UTR (N)	34675 NM_006020	8846 Hs. 94542 NM_006020	ENSG000004ALKBH1	ABH ABH1 alkB homc protein-coding
chr14-814 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr14	81480680	81481145	+	0	NA	intron (N)Charlie2a	-30755 NR_109995	1.01E+08 Hs. 116304NR_109995	ENSG000004LINC02308	- long intncRNA
chr17-487 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr17	4892253	4893697	+	0	NA	intron (N)intron (N)	-6561 NM_001145	1E+08 Hs. 579245NM_001145	ENSG000004C17orf107	- chromoson protein-coding
chr2-1275 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr2	12727463	12729589	+	0	NA	intron (N)intron (N)	-8841 NR_036072	1E+08 NR_036072	ENSG000004MIR3125	mir-3125 microRNA ncRNA
chr20-516 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr20	51673310	51676674	+	0	NA	intron (N)AluSx1 SI	93398 NR_006045	10079 Hs. 649234NM_006045	ENSG000004ATP9A	ATPIIA ATPase pI protein-coding
chr22-295 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr22	29328241	29329218	+	0	NA	3' UTR (N)3' UTR (N)	4529 NR_003688	1E+08 NR_003688	ENSG000004SNORD125	- small nucsnoRNA
chr22-376 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr22	37650245	37653327	+	0	NA	intron (N)intron (N)	6591 NR_109952	1.02E+08 NR_109952	ENSG000004LOC101927	- uncharactncRNA
chr6-1571 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr6	1.57E+08	1.57E+08	+	0	NA	intron (N)intron (N)	127311 NM_018452	729515 Hs. 157212NM_018452	ENSG000004TMEM242	BMO33 C6c transmant protein-coding
chr9-1047 7.211614	0.544183	0.874328	0.622402	0.533678	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (N)MIR SINE	36183 NR_130760	55335 Hs. 579245NM_018375	ENSG000004NIPSNAP3E	FP944 NIPSNAP3E protein-coding
chr11-351 12.34055	-0.4185	0.672637	-0.62218	0.533824	0.981636	chr11	35139548	35143564	+	0	NA	intron (N)intron (N)	2385 NM_001001	960 Hs. 502325NM_000610	ENSG000004CD44	CDW44 CSF CD44  mole protein-coding
chr12-911 12.34055	-0.4185	0.672637	-0.62218	0.533824	0.981636	chr12	91160045	91176029	+	0	NA	intron (N)AluSx8 SI	10609 NM_133505	1634 Hs. 156315NM_001920	ENSG000004CCN	CCD1 DSPC decorin protein-coding
chr15-633 12.34055	-0.4185	0.672637	-0.62218	0.533824	0.981636	chr15	63056408	63069593	+	0	NA	intron (N)intron (N)	-13613 NR_147233	1.11E+08 Hs. 602995NR_147233	TPM1-AS	TPM1-AS1 TPM1  antncRNA
chr5-955 12.34055	-0.4185	0.672637	-0.62218	0.533824	0.981636	chr5	95539343	95541849	+	0	NA	intron (N)LM5 LINE	14409 NM_014635	9652 Hs. 482868NM_014635	ENSG000004TTC37	KIAA0372 tetratric protein-coding
chr1-1517 10.95488	0.444612	0.714635	0.622153	0.533842	0.981636	chr1	1.52E+08	1.52E+08	+	0	NA	intron (N)intron (N)	-1526 NM_001134	51686 Hs. 713785NM_016175	ENSG000004OAZ3	AZ3 OAZ-3 tornithine protein-coding
chr19-521 10.95488	0.444612	0.714635	0.622153	0.533842	0.981636	chr19	5213910	5214603	+	0	NA	intron (N)intron (N)	126556 NM_130854	5802 Hs. 744925NM_002855	ENSG000004PTPRS	PTPS GMA  protein tr protein-coding
chr6-2836 10.95488	0.444612	0.714635	0.622153	0.533842	0.981636	chr6	28364466	28366939	+	0	NA	exon (NM)exon (NM)	-9431 NM_001135	64288 Hs. 656415NM_030895	ENSG000004ZSCAN31	ZNF20-Lp zinc fing protein-coding
chr20-25 32.87025	0.310905	0.499734	0.622141	0.533849	0.981636	chr20	27957889	27958096	+	0	NA	IntergeniALR Alpha	646473 NR_132315	1E+08 Hs. 529357NR_132315	ENSG000004FRG1CP	- FSHD regipseudo
chr1-1508 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (N)AluSx SI	-6389 NM_000396	1513 Hs. 632465NM_000396	ENSG000004CTSK	CTS02 CTS cathepsi protein-coding
chr1-1567 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (N)intron (N)	-15523 NM_001007	4914 Hs. 406295NM_002525	ENSG000004NTRK1	MTC TRK lneurotro protein-coding
chr1-1735 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr1	1.74E+08	1.74E+08	+	0	NA	intron (N)intron (N)	13340 NM_001300	149041 Hs. 30258 NM_172071	ENSG000004RC3H1	RNF198 RC3 ring fing protein-coding
chr1-2066 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr1	2.07E+08	2.07E+08	+	0	NA	intron (N)intron (N)	4376 NM_001004	8444 Hs. 164267NM_003582	ENSG000004DYRK3	DYRK5 REC dual spc protein-coding
chr1-2236 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (N)intron (N)	42362 NM_001031	7159 Hs. 523968NM_005425	ENSG000004TP53BP2	53BP2 ASF  tumor prc protein-coding
chr1-2295 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr1	2.3E+08	2.3E+08	+	0	NA	exon (NM)exon (NM)	31390 NM_014405	27097 Hs. 270621NM_014405	ENSG000004TAF5L	PAF65B TATA-box protein-coding
chr12-133 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	intron (N)intron (N)	23749 NM_001255	7574 Hs. 489605NM_019591	ENSG000004ZNF26	HEL-179 zinc fing protein-coding
chr17-186 10.9216	0.442243	0.710982	0.622017	0.533931	0.981636	chr17	18667212	18674896	+	0	NA	3' UTR (N)3' UTR (N)	11260 NM_001368	2310 Hs. 592125NM_001368	134 FOXO3B	FKHRLP1 forkhead protein-coding
chr2-2																



chr1-2256 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr1	2.26E+08	2.26E+08	0	NA	intron (Nintron (N	13657	NM_01469E	9725	Hs. 119387NM_01469E	ENSG00000CTMEM63A	KIAA0792	transmembrane protein-coding	
chr11-703 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr11	70348459	70349778	0	NA	intron (Nintron (N	-49388	NM_13856E	2017	Hs. 596164NM_005231	ENSG00000CTTN	EMS1	cortactin protein-coding	
chr12-194 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr12	19493881	19495843	0	NA	intron (Nintron (N	54263	NM_001267	121536	Hs. 126497NM_153207	ENSG00000CAEBP2	-	AE binding protein-coding	
chr12-266 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr12	26994076	26995806	0	NA	intron (Nintron (N	19443	NM_016551	51768	Hs. 438864NM_016551	ENSG00000TM7SF3	-	transmembrane protein-coding	
chr12-965 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr12	96007907	96013224	0	NA	intron (N2b LINE	-14200	NM_00125E	3034	Hs. 190783NM_00210E	ENSG00000CAL	HIS1 HSTD	histidine protein-coding	
chr12-122 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr12	1.22E+08	1.22E+08	0	NA	intron (NAluSq SI	-32911	NM_15275E	254050	Hs. 374856NM_15275E	ENSG00000LRR4C3	-	leucine protein-coding	
chr15-456 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr15	49304043	49305049	0	NA	intron (NMLTII LITR	-118696	NM_00200E	2252	Hs. 56726E NM_00200E	ENSG00000PGF7	HBGF-7 KC	fibroblast protein-coding	
chr15-75E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr15	75604659	75611208	0	NA	intron (N2c LINE	17792	NM_005701	10073	Hs. 215777NM_005701	ENSG00000SNUPN	KPNBL RN	snurportin protein-coding	
chr16-16E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr16	1632491	1635392	0	NA	intron (NAluSc SIN	19301	NM_02082E	57585	Hs. 603676NM_02082E	ENSG00000CRAMP1	CRAMP1L C	cramped protein-coding	
chr16-75E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr16	75567932	75571577	0	NA	intron (Nintron (N	3375	NM_00728E	11345	Hs. 461379NM_00728E	ENSG00000GABARAPL2	ATG8 ATG8	GABA type protein-coding	
chr16-75E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr16	75577177	75579922	0	NA	TTS (NM_C TTS (NM_C	12170	NM_00728E	11345	Hs. 461379NM_00728E	ENSG00000GABARAPL2	ATG8 ATG8	GABA type protein-coding	
chr17-297 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr17	29756735	29757119	0	NA	intron (NAluSx3 SI	4505	NM_00128E	85464	Hs. 654754NM_03338E	ENSG00000SSH2	SSH-2 SSI	slingshot protein-coding	
chr17-50E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr17	50550412	50550914	0	NA	intron (Nintron (N	3489	NM_022827	64847	Hs. 103147NM_022827	ENSG00000SPATA20	HEL-S-98	spermatogonium protein-coding	
chr19-93E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr19	9326329	9334282	0	NA	intron (NLM3c LIN	5610	NM_00120E	1.01E+08	Hs. 728944NM_00117E	ENSG00000ZNF559-5Z	-	ZNF559-Z protein-coding	
chr19-477 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr19	47781130	47785571	0	NA	intron (NAluY SINE	4647	NM_00300E	6415	Hs. 63154E NM_00300E	ENSG00000SELENOV	SEPW1 sel	selenoprotein-coding	
chr20-351 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr20	35140281	35143277	0	NA	intron (NMR8B DNA	5557	NM_00114E	55741	Hs. 720177NM_01821E	ENSG00000EDEM2	C20orf31 ER	degrac protein-coding	
chr20-351 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr20	35493921	35500391	0	NA	intron (Nintron (N	32496	NR_02693E	140873	Hs. 158688NM_08082E	ENSG00000C20orf17E	dJ4770.4	chromosome protein-coding	
chr22-21E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr22	21683169	21683603	0	NA	intron (Nintron (N	17374	NM_14817E	23759	Hs. 438858NM_014337	ENSG00000PPL12	CYC4 CYP	peptidyl protein-coding	
chr3-497E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr3	49727016	49728415	0	NA	intron (Nintron (N	-3741	NM_013334	29925	Hs. 56748E NM_013334	ENSG00000GMPBP	LGMDR19 GDP	mannan protein-coding	
chr3-134E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr3	1.34E+08	1.34E+08	0	NA	intron (Nintron (N	39922	NM_00295E	6259	Hs. 65456E NM_00295E	ENSG00000CRK	D3S3195 J	receptor protein-coding	
chr3-197E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr3	1.98E+08	1.98E+08	0	NA	intron (Nintron (N	-8610	NR_030627	1E+08	NR_030627	ENSG00000MIR922	MIRN922	microRNA ncRNA	
chr4-785E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr4	7852899	7855337	0	NA	intron (Nintron (N	18190	NM_001371090	22902	Hs. 740904NM_014961	ENSG00000CRUFY3	RIPX SINCRN	and I protein-coding	
chr4-707E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr4	70782706	70785706	0	NA	intron (NAluSx SIN	49796	NM_00134E	373	Hs. 792	NM_00165E	ENSG00000TRIM23	ARD1 ARF1	tripartite protein-coding
chr5-656E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr5	65606159	65612785	0	NA	intron (Nintron (N	14867	NM_00165E	7726	Hs. 485041NM_00344E	ENSG00000TRIM26	APP RNF9E	tripartite protein-coding	
chr6-301E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr6	30188646	30190477	0	NA	intron (Nintron (N	23845	NM_00124E	-954	NR_03978E	ENSG00000MIR4640	-	microRNA ncRNA	
chr6-308E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr6	30889164	30890964	0	NA	promoter-promoter-	-38231	NM_003131	6722	Hs. 52014C NM_003131	ENSG00000MIR640	MCM1	serum response protein-coding	
chr6-431E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr6	43130930	43135146	0	NA	intron (NMR3c SINE	-11234	NR_14903E	1E+08	Hs. 105944NR_14903E	ENSG00000LOC10012E	-	uncharacterized ncRNA	
chr7-1301 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr7	1.3E+08	1.3E+08	0	NA	intron (Nintron (N	-11618	NR_12121E	1.02E+08	Hs. 57163C NR_12121E	LINC01507	XLOC_000E	intcncRNA	
chr9-137E 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr9	79705357	79711467	0	NA	intron (N2a LINE	-119	NR_024514	11093	Hs. 13143E NM_13902E	ENSG00000ADAMT53	ADAM-TS1E	ADAM meta protein-coding	
chr9-1334 7. 708202	0.517387	0.836363	0.618615	0.53617	0.981636	chr9	1.33E+08	1.33E+08	0	NA	promoter-promoter-	-11733	NM_00103E	1E+08	Hs. 714127NM_00103E	ENSG00000NBPF10	AB6 AG1 NBPF	membrane protein-coding	
chr1-1461 13. 65412	0.408664	0.660639	0.618589	0.536187	0.981636	chr1	1.46E+08	1.46E+08	0	NA	exon (NM_exon (NM	190879	NR_135021	1.05E+08	Hs. 15689E NR_135021	ENSG00000LINC02424E	-	long intcncRNA	
chr12-181 10. 10072	-0.4576	0.740301	-0.61812	0.536493	0.981636	chr12	78168630	78169105	0	NA	intron (Nintron (N	-14587	NR_001304	51478	Hs. 42929E NM_016371	ENSG00000HSD17B7	PRAP SDR5	hydroxysteroid protein-coding	
chr1-627 10. 88832	0.439875	0.712105	0.617711	0.536766	0.981636	chr1	61.63E+08	61.63E+08	0	NA	intron (Nintron (N	-5583	NM_00132E	90338	Hs. 655967NM_03328E	ENSG00000ZNF160	F11 HKR1E	zinc finger protein-coding	
chr19-531 10. 88832	0.439875	0.712105	0.617711	0.536766	0.981636	chr19	53108234	53109801	0	NA	exon (NM_exon (NM	9002	NM_014321	23594	Hs. 49760	NM_014321	ENSG00000ORC6	ORC6L	origin recognition protein-coding
chr16-46E 6. 694009	-0.70004	1.133565	-0.61755	0.536871	0.981636	chr16	46698541	46698781	0	NA	TTS (NM_C TTS (NM_C	11855	NM_001277	400818	Hs. 44508C NM_001037	ENSG00000NBPF9	AEO1	NBPF membrane protein-coding	
chr1-149 10. 92946	0.440791	0.713995	0.617359	0.536998	0.981636	chr1	1.49E+08	1.49E+08	0	NA	intron (Nintron (N	28062	NM_03094E	81693	Hs. 534494NM_03094E	ENSG00000CAMN	PRO1028E	ammonium aspartate protein-coding	
chr14-10E 7. 741484	0.520617	0.843487	0.61722	0.53709	0.981636	chr14	1.03E+08	1.03E+08	0	NA	intron (NAluSx SIN	-9807	NM_014634	9647	Hs. 11272E NM_014634	ENSG00000PPM1F	CAMKP1 Ca	protein-coding	
chr22-21E 7. 741484	0.520617	0.843487	0.61722	0.53709	0.981636	chr22	21962341	21962969	0	NA	intron (Nintron (N	1734	NM_001317	7264	Hs. 40411E NM_00331E	ENSG00000TSTA3	FX P35B1	tissue specific protein-coding	
chr6-570E 12. 37383	-0.41549	0.673538	-0.61687	0.537319	0.981636	chr6	57098364	57103021	0	NA	exon (NM_exon (NM	10504	NM_001031	26036	Hs. 48562E NM_01555E	ENSG00000ZNF451	COASTER c	zinc finger protein-coding	
chr10-17E 6. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr10	17699209	17700307	0	NA	intron (Nintron (N	-52443	NM_00109E	653657	Hs. 56413E NM_00101E	ENSG00000TMEM236	HSA-23A F	transmembrane protein-coding	
chr11-68E 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr11	68064693	68065158	0	NA	intron (Nintron (N	20131	NR_106811	1.02E+08	NR_106811	ENSG00000MIR6753	hsa-mir-6753	microRNA ncRNA	
chr12-297 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr12	29719947	29720740	0	NA	intron (Nintron (N	63599	NM_001367	83857	Hs. 401954NM_03192E	ENSG00000TMTC1	ARG99 OLF	transmembrane protein-coding	
chr13-11E 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr13	1.14E+08	1.14E+08	0	NA	intron (Nintron (N	9185	NM_00082E	2621	Hs. 64634E NM_00082E	ENSG00000GAS6	AXLL4 ACS	mediator protein-coding	
chr2-320E 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr2	32025082	32025458	0	NA	intron (NAluSg SIN	-14262	NR_126034	51072	Hs. 44496E NM_01595E	ENSG00000MEMO1	C2orf4 C	growth factor protein-coding	
chr22-461 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr22	46104355	46105497	0	NA	intron (Nintron (N	-7823	NR_02947E	406883	NR_02947E	ENSG00000MIRLET7A5	LET7A3 MI	microRNA ncRNA	
chr4-1381 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr4	1.38E+08	1.38E+08	0	NA	3' UTR (3' UTR (N	-36821	NR_03786E	641365	Hs. 43563C NR_03786E	ENSG00000LINC0061E	-	long intcncRNA	
chr7-564 5. 640496	-0.60231	0.976685	-0.61669	0.537438	0.981636	chr7	5607946	5608369	0	NA	Intergenic CpG	15341	NM_00308E	6624	Hs. 11840C NM_00308E	ENSG00000FSCN1	FANI HSN	fast acroprotein-coding	
chr7-105E 5. 640496	-0.60231	0.976685	-0.61669</																

chr11-684	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chr11	68438706	68439238	+	0	NA	intron (Nintron (N	-21780	NM_001352	55291	Hs.503022NM_018312	ENSG000003PPP6R3	C11orf23 protein f	protein-coding				
chr11-115	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (NAluJb SIN	-6732	NM_001243	25988	Hs.504091NM_015517	ENSG000003HINFP	Hinf-P MIhistone f	protein-coding				
chr14-911	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chr14	91188944	91190849	+	0	NA	intron (Nintron (N	54808	NM_001177	8111	Hs.8882	NM_003483	ENSG000003GPR68	A12A6 GPFg	protein-coding			
chr16-716	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chr16	71668940	71669568	+	0	NA	intron (Nintron (N	29447	NR_033337	11E+08	Hs.725111	NR_033337	ENSG000003SNORA70D	U70D	small	lncsnoRNA		
chr19-376	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chr19	37649560	37650054	+	0	NA	intron (NAluJb SIN	5658	NM_00132C	22835	Hs.668737	NM_014898	ENSG000003ZFP30	ZFP30	zinc	finger protein-coding		
chr19-488	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chr19	48831007	48832835	+	0	NA	intron (NAluSx1 SI	4570	NM_01624E	51171	Hs.18788	NM_01624E	ENSG000003HSD17B14	DHRS10 SE	hydroxyst	protein-coding		
chrX-6573	7.18619	0.538504	0.877516	0.613669	0.539434	0.981636	chrX	65735507	65736117	+	0	NA	intron (NLa2 LINE	68158	NM_002244	4478	Hs.87752	NM_002244	ENSG000003MSN	HEL70 IM	moesin	protein-coding		
chr1-5655	10.12615	-0.45262	0.737625	-0.61362	0.53947	0.981636	chr1	56502994	56521594	+	0	NA	intron (Nintron (N	67269	NM_00371E	8613	Hs.40515E	NM_00371E	ENSG000003PLP3	Dri42 LPF	phospholip	protein-coding		
chr11-125	10.12615	-0.45262	0.737625	-0.61362	0.53947	0.981636	chr11	12528243	12528873	+	0	NA	3' UTR (N3' UTR (N	-145863	NM_021961	7003	Hs.655331	NM_021961	ENSG000003TEAD1	AA NTEF-1	TEA domain	protein-coding		
chr11-32	10.12615	-0.45262	0.737625	-0.61362	0.53947	0.981636	chr11	32096809	32100823	+	0	NA	intron (NMLTJ2 LI	7742	NM_002901	5954	Hs.97887	NM_002901	ENSG000003RCN1	HE-S-84 reticuloc	protein-coding			
chr13-115	10.12615	-0.45262	0.737625	-0.61362	0.53947	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (NMER102b I	7374	NR_04499E	650669	Hs.369201	NM_01039799	ENSG000003GAS6-AS1	GAS6	antincRNA			
chr10-793	7.845186	-0.51584	0.841304	-0.61315	0.539778	0.981636	chr10	79394008	79394219	+	0	NA	intron (Nintron (N	46644	NM_00572E	10105	Hs.381072	NM_00572E	ENSG000003PPIF	CYP3 CyP-	peptidyl f	protein-coding		
chr8-3047	7.845186	-0.51584	0.841304	-0.61315	0.539778	0.981636	chr8	30477216	30477415	+	0	NA	intron (NAluV SINE	-91914	NR_04620E	1E+08	Hs.12681E	NR_04620E	ENSG000003RBPMS-AS1	RBPMS	antncRNA			
chr19-262	7.270929	0.332076	0.541655	0.613076	0.539826	0.981636	chr19	26918117	26918364	+	0	NA	IntergeniALR Alphe	-875191	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENSG000003LOC101927		uncharacter	ncRNA		
chr20-323	6.715026	0.574561	0.937187	0.613069	0.539883	0.981636	chr20	32318204	32318642	+	0	NA	intron (NLMB8 LIN	-39921	NM_01533E	171023	Hs.37404E	NM_01533E	ENSG000003ASXL1	BOPS MDS	ASXL trar	protein-coding		
chr1-842	5.632638	-0.60016	0.979043	-0.61301	0.539873	0.981636	chr1	84207979	84208758	+	0	NA	intron (Nintron (N	26736	NM_001242	5567	Hs.48732E	NM_002731	ENSG000003PRKACB	PKA C-beta	protein-coding			
chr20-373	5.632638	-0.60016	0.979043	-0.61301	0.539873	0.981636	chr20	37055040	37055661	+	0	NA	intron (Nintron (N	40647	NM_00132E	5933	Hs.20774E	NM_00289E	ENSG000003CRL1	CP107 PRE	R trans	protein-coding		
chr20-254	5.632638	-0.60016	0.979043	-0.61301	0.539873	0.981636	chr22	25459101	25459581	+	0	NA	intron (N(CT)n Sin	3695	NR_10687E	1.02E+08	NR_10687E	ENSG000003MR6817	hsa-mir-6	microRNA	ncRNA			
chr3-1235	5.632638	-0.60016	0.979043	-0.61301	0.539873	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	22745	NM_05302E	4638	Hs.47737E	NM_00596E	ENSG000003MYLK	AAT7 KRP myosin	l	protein-coding		
chr9-778	5.632638	-0.60016	0.979043	-0.61301	0.539873	0.981636	chr9	77808929	77809296	+	0	NA	intron (Nintron (N	-160790	NM_00429E	9630	Hs.65779E	NM_00429E	ENSG000003GNA14		G	protein-coding		
chr1-2625	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr1	26257559	26258427	+	0	NA	intron (Nintron (N	-11286	NM_001281	64793	Hs.63795	NM_02277E	ENSG000003CEP85	CCDC21	centrosom	protein-coding		
chr10-285	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr10	28596925	28598198	+	0	NA	intron (Nintron (N	64443	NM_01662E	51322	Hs.743224	NM_01662E	ENSG000003WAC	BM-016 DFW	domain	protein-coding		
chr10-685	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr10	68500813	68501493	+	0	NA	intron (NAluSx SIN	17065	NM_00132A	8034	Hs.18040E	NM_152707	ENSG000003SLC25A16	D10S105E solute	c	protein-coding		
chr10-871	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr10	87189776	87190743	+	0	NA	intron (NAluSz SIN	-35189	NM_00109E	728118	Hs.71056E	NM_00109E	ENSG000003NUTM2A	FAM22A NUT	cell	protein-coding		
chr14-34	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr14	34820320	34821159	+	0	NA	intron (NLMC1 LIN	-53452	NR_16077E	1.12E+08	Hs.50914C	NR_16077E	LOC11226E		uncharacter	ncRNA		
chr14-884	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr14	88466993	88468045	+	0	NA	3' UTR (N3' UTR (N	81862	NM_01841E	55812	Hs.52551E	NM_01841E	ENSG000003SPATA7	HEL-S-29E	spermatog	protein-coding		
chr15-654	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr14	65446727	65449752	+	0	NA	intron (NAluJo SIN	-25292	NM_02096E	57722	Hs.458607	NM_02096E	ENSG000003IGDCCA7	DDM36 NOF	immunog	protein-coding		
chr17-376	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr17	37615679	37616343	+	0	NA	promoter-promoter-	-972	NR_106744	1.02E+08	NR_106744	ENSG000003MIR378J	hsa-mir-2	microRNA	ncRNA			
chr19-84	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr19	8461911	8462732	+	0	NA	intron (Nintron (N	17346	NM_03120E	4670	Hs.46580E	NM_00596E	ENSG000003HNRNPM	CEAR HNR	heterog	protein-coding		
chr2-157	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr2	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	71115	NM_001347	90	Hs.47031E	NM_00110E	ENSG000003ACVR1	ACTRI AC	activin f	protein-coding		
chr22-42	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr22	42619355	42623839	+	0	NA	intron (Nintron (N	6352	NR_02942E	267010	Hs.574857	NR_02942E	ENSG000003CRNU12	RNU12-1 F	RNA, U12	snRNA		
chr3-158	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr3	1.59E+08	1.59E+08	+	0	NA	intron (NLMC3 LIN	12144	NM_00130E	85476	Hs.51835E	NM_02499E	ENSG000003GFM1	COXPDI EFG	elongat	protein-coding		
chr4-5764	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr4	5764612	5765208	+	0	NA	intron (NLMC3 LIN	53709	NM_00130E	2121	Hs.64869E	NM_01455E	ENSG000003MIR378J	DWF-1 EVC	EvC cilic	protein-coding		
chr5-7874	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr5	7874617	7876324	+	0	NA	intron (Nintron (N	6322	NR_13448E	4552	Hs.481551	NM_00245E	ENSG000003MTRR	MSR cbE	5-methyl	protein-coding		
chr7-477	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr7	4770916	4771928	+	0	NA	TTS (NM_CTS (NM_C	-4201	NM_001364	9907	Hs.55844E	NM_01485E	ENSG000003AP521	KIAA0415 adaptor	l	protein-coding		
chr8-1705	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr8	17037088	17038328	+	0	NA	intron (NTHE1B-int	10470	NR_14623E	286097	Hs.403594	NM_18172E	ENSG000003M1CUC3	EFHA2	mitochon	protein-coding		
chr9-1047	5.665919	-0.59333	0.967933	-0.61298	0.539887	0.981636	chr9	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	4766	NM_01546E	25934	Hs.53027E	NM_01546E	ENSG000003NIPSNAP3	HSPC299 nipsnap	l	protein-coding		
chr16-29	10.11829	-0.45134	0.736379	-0.61292	0.539931	0.981636	chr16	29517052	29519969	+	0	NA	IntergeniLIPA5 LI	-12636	NM_00135E	440353	NM_001355401	NPIP1B2		nuclear	l	protein-coding		
chr19-362	10.11829	-0.45134	0.736379	-0.61292	0.539931	0.981636	chr19	36220793	36221117	+	0	NA	intron (NAluSx1 SI	-5871	NM_00104E	147929	Hs.59633E	NM_152477	ENSG000003ZNF565		zinc	finger	protein-coding	
chr2-1331	10.11829	-0.45134	0.736379	-0.61292	0.539931	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-138114	NR_110294	1.02E+08	Hs.661917	NR_110294	ENSG000003NCKAP5-AS		NCKAP5	arcncRNA		
chr5-1747	10.11829	-0.45134	0.736379	-0.61292	0.539931	0.981636	chr5	1.75E+08	1.75E+08	+	0	NA	3' UTR (N3' UTR (N	5863	NM_00136E	4488	Hs.89404	NM_00244E	ENSG000003MSX2	CRS2 FPP ms	home	protein-coding		
chr8-125	10.11829	-0.45134	0.736379	-0.61292	0.539931	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	intron (NMER104 DN	33554	NM_01484E	9897	Hs.27004E	NM_01484E	ENSG000003WASHC5	KIAA0196 WASH	com	protein-coding		
chr13-198	9.607836	-0.47015	0.767117	-0.61288	0.539953	0.981636	chr13	19844549	19844853	+	0	NA	intron (NAluSq SIN	18935	NM_00103E	9205	Hs.53098E	NM_01424E	ENSG000003ZMYM5	HSPC050 zinc	finger	protein-coding		
chr19-46	9.607836	-0.47015	0.767117	-0.61288	0.539953	0.981636	chr19	4695092	4696072	+	0	NA	intron (Nintron (N	16300	NM_001242	1E+08	Hs.67813E	NM_001242901	DPP9-AS1	DPP9	anti	protein-coding		
chr7-261	9.607836	-0.47015	0.767117	-0.61288	0.539953	0.981636	chr7	26198633	26199720	+	0	NA	intron (Nintron (N	1570	NM_002137	3181	Hs.487774	NM_002137	ENSG000003HNRNPA2B1	HNRNPA2B1	heterog	protein-coding		
chrX-5338	7.129335	-0.441757	0.884008	0.612841	0.539981	0.981636	chrX	53382029	53382519	+	0	NA	exon (NM exon (NM	23491	NR_10691E	1.02E+08	NR_10691E	ENSG000003MIR6857	hsa-mir-6	microRNA	ncRNA			
chr14-705	7.38558	-0.53118	0.866883	-0.61275	0.540043	0.981636	chr14	70581014	70581314	+	0	NA	IntergeniLIME3B LI	19526	NM_001284	10001	Hs.49735E	NM_00546E	ENSG000003MED6	ARC33 NY-	mediator	protein-coding		
chr17-19	7.38558	-0.53118	0.866883	-0.61275	0.540043	0.981636	chr17	19927275	19927490	+	0	NA												



chr14-321	11.4339	0.426072	0.697774	0.610615	0.541454	0.981636	chr14	32153786	32156233	+	0 NA	3' UTR (N3' UTR (N	-47036 NR_104084	1.02E+08	NR_104084	ENSG0000CRNU6-7	U6-7	RNA, U6 ssnRNA	
chr13-102	7.862752	-0.50763	0.83142	-0.61056	0.541493	0.981636	chr13	1.03E+08	1.03E+08	+	0 NA	exon (NM exon (NM	45470 NM_001010	196541	Hs. 508623	NR_001010	ENSG00000METTL21C	C13orf39 methyltransferase protein-coding	
chr15-731	7.862752	-0.50763	0.83142	-0.61056	0.541493	0.981636	chr15	73179044	73179461	+	0 NA	intron (NLTR4 LTF	-120658 NR_162148	1.13E+08	NR_162148	MIR12135	-	microRNA ncRNA	
chr16-65	7.862752	-0.50763	0.83142	-0.61056	0.541493	0.981636	chr16	65052748	65053478	+	0 NA	intron (Nintron (N	68951 NM_001797	1009	Hs. 116471	NR_001797	ENSG00000CDH11	CAD11 CDF cadherin protein-coding	
chr2-8802	7.862752	-0.50763	0.83142	-0.61056	0.541493	0.981636	chr2	88028735	88029477	+	0 NA	intron (Nintron (N	26522 NM_001304	5103	Hs. 469254	NR_001304	ENSG00000KRC1	CHBP2 lysine ribonucleoprotein-coding	
chr21-25	7.862752	-0.50763	0.83142	-0.61056	0.541493	0.981636	chr21	25945437	25946769	+	0 NA	intron (NLIM4 LINE	194287 NM_001136	351	Hs. 43498	NR_000484	ENSG00000CAPP	AAA ABET amyloid L protein-coding	
chr9-1377	7.862752	-0.50763	0.83142	-0.61056	0.541493	0.981636	chr9	1.38E+08	1.38E+08	+	0 NA	intron (Nintron (N	25770 NR_147508	651337	Hs. 60319	NR_147508	ENSG00000LOC651337	uncharacterized ncRNA	
chr14-73	7.418861	-0.52606	0.861685	-0.6105	0.541528	0.981636	chr14	73296678	73297051	+	0 NA	intron (NALuSx SIN	-50863 NR_135248	1.02E+08	Hs. 66059	NR_135248	LOC101928	uncharacterized ncRNA	
chr15-342	7.418861	-0.52606	0.861685	-0.6105	0.541528	0.981636	chr15	34226601	34226856	+	0 NA	intron (NALuS2 SI	1712 NM_001286	51234	Hs. 25090	NR_016454	ENSG00000CEMC4	PIG17 TMERF2 membrane protein-coding	
chr20-394	7.418861	-0.52606	0.861685	-0.6105	0.541528	0.981636	chr20	394277	394966	+	0 NA	intron (NALuJo SIN	13278 NM_001301	57761	Hs. 51682	NR_021158	ENSG00000TRIB3	C20orf97 tribbles protein-coding	
chr20-38	7.418861	-0.52606	0.861685	-0.6105	0.541528	0.981636	chr20	38035214	38035545	+	0 NA	intron (Nintron (N	1633 NM_021211	58490	Hs. 27883	NR_021211	ENSG00000RPRD1B	C2orf27 regulatory protein-coding	
chr3-1944	7.418861	-0.52606	0.861685	-0.6105	0.541528	0.981636	chr3	1.94E+08	1.94E+08	+	0 NA	intron (NALuJb SIN	3681 NM_001367	79572	Hs. 52960	NR_024524	ENSG00000ATP13A3	AFURS1 ATPase 1 protein-coding	
chr9-193	7.418861	-0.52606	0.861685	-0.6105	0.541528	0.981636	chr9	19335991	19336997	+	0 NA	intron (Nintron (N	43742 NM_00101C	6194	Hs. 40807	NR_00101C	ENSG00000RPS6	S6 ribosomal protein-coding	
chr12-156	10.11043	-0.45006	0.737228	-0.61048	0.541544	0.981636	chr12	15894293	15897043	+	0 NA	intron (NALuJr SIN	13281 NM_001718	1171	Hs. 74397	NR_001718	ENSG00000STRAP	MAWD PT-1 serine/threonine protein-coding	
chr13-41	10.11043	-0.45006	0.737228	-0.61048	0.541544	0.981636	chr13	41370780	41371127	+	0 NA	intron (NTiger2 I	-58915 NM_001354	9617	Hs. 38217	NR_004294	ENSG00000MTRF1	MRF1 MTTF mitochondrion protein-coding	
chr2-2374	10.11043	-0.45006	0.737228	-0.61048	0.541544	0.981636	chr2	2.37E+08	2.37E+08	+	0 NA	intron (Nintron (N	2124 NM_057166	1293	Hs. 23324	NR_004366	ENSG00000COL6A3	BTHLM1 DY collagen protein-coding	
chr5-1347	10.11043	-0.45006	0.737228	-0.61048	0.541544	0.981636	chr5	1.35E+08	1.35E+08	+	0 NA	intron (NALuSg SIN	28011 NM_014825	9879	Hs. 40654	NR_014825	ENSG00000CDDX46	PRPF5 PRF DEAD-box protein-coding	
chr7-305	10.11043	-0.45006	0.737228	-0.61048	0.541544	0.981636	chr7	30598530	30613234	+	0 NA	intron (NLIM5 LIN	11004 NM_002047	2617	Hs. 40432	NR_002047	ENSG00000GARS	CMT2D DSM glycolytic protein-coding	
chr8-3901	10.11043	-0.45006	0.737228	-0.61048	0.541544	0.981636	chr8	39017148	39030672	+	0 NA	intron (NALuSx1 SI	-5225 NR_145988	1.1E+08	NR_145738	ENSG00000SNORD38D	-	small nucleolar RNA	
chr21-428	8.230214	0.498928	0.817467	0.610334	0.541641	0.981636	chr21	42871938	42872589	+	0 NA	intron (NALuS2 SI	7012 NM_001266	10785	Hs. 24881	NR_018665	ENSG00000WDR4	GAMOS6 MIWD repeat protein-coding	
chr6-116	9.690115	-0.465	0.762528	-0.60982	0.541981	0.981636	chr6	1.17E+08	1.17E+08	+	0 NA	intron (NLIP44 LIN	11768 NM_001366	3841	Hs. 18297	NR_002266	ENSG00000KPN5A	IPOA6 SRF karyopherin protein-coding	
chr2-2027	4.981685	0.630691	1.034364	0.609738	0.542036	0.981636	chr2	2.03E+08	2.03E+08	+	0 NA	intron (NALuV SINE	69434 NM_001288	130026	Hs. 51662	NR_138468	ENSG00000ICAIL	ALS2CR14 islet cell protein-coding	
chr16-887	9.365272	0.485021	0.795532	0.609682	0.542072	0.981636	chr16	88734209	88734675	+	0 NA	exon (NM exon (NM	3262 NR_103774	1E+08	Hs. 43771	NR_1027451	LOC100288	uncharacterized ncRNA	
chr6-714	9.365272	0.485021	0.795532	0.609682	0.542072	0.981636	chr6	71416978	71417289	+	0 NA	intron (Nintron (N	3612 NR_121614	79940	Hs. 36833	NR_026807	ENSG00000LINC00472	G6orf155 long intcncRNA	
chr1-192	8.238072	0.496974	0.81543	0.609462	0.542218	0.981636	chr1	1.93E+08	1.93E+08	+	0 NA	Intergeni Intergeni	-46388 NR_126003	1.03E+08	Hs. 24348	NR_126003	LINC01032	-	long intcncRNA
chr10-428	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr10	42811797	42814465	+	0 NA	intron (NLIMDa LIN	30336 NM_014755	9790	Hs. 10848	NR_014755	ENSG00000BMS1	ACC BMS1 BMS1 ribc protein-coding	
chr10-67	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr10	67948243	67949608	+	0 NA	intron (NLIM4 LINE	57523 NM_001314	23411	Hs. 36977	NR_012238	ENSG00000SIRT1	SIRT2 SIRT2 sirtuin protein-coding	
chr10-68	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr10	68061451	68065702	+	0 NA	intron (Nintron (N	11707 NM_001278	26091	Hs. 51891	NR_015601	ENSG00000HERC4	-	HECT and protein-coding
chr10-11	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr10	1.11E+08	1.11E+08	+	0 NA	intron (NALuSg SIN	31469 NM_005444	9126	Hs. 24485	NR_005444	ENSG00000SMC3	BAM BMH C structure protein-coding	
chr10-115	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr10	1.2E+08	1.2E+08	+	0 NA	intron (NALuJb SIN	20352 NM_024834	79892	Hs. 12424	NR_024834	ENSG00000MCMBP	C10orf115 minichromosome protein-coding	
chr11-34	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr11	34932946	34934791	+	0 NA	intron (NLIMC5a LI	-7969 NR_039831	1.01E+08	NR_039831	ENSG00000MIR1343	-	microRNA ncRNA	
chr11-46	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr11	46307043	46307608	+	0 NA	intron (NALuJo SIN	-25601 NM_201532	8525	Hs. 20426	NR_003646	ENSG00000DGK7	DAGK5 DAC diacylglycerol protein-coding	
chr11-11	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr11	1.11E+08	1.11E+08	+	0 NA	intron (NLIM8 LIN	120831 NM_001258	57569	Hs. 61306	NR_020808	ENSG00000ARHGAP20	RARHGAP18 GTPase protein-coding	
chr12-104	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr12	1.04E+08	1.04E+08	+	0 NA	intron (NMER58 DN	9446 NM_01332C	29915	Hs. 50655	NR_01332C	ENSG00000HCFC2	HCF-2 HCF host cell protein-coding	
chr13-114	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	Intergeni LIM4 LINE	1795 NR_039724	1.01E+08	NR_039724	ENSG00000MIR4502	-	microRNA ncRNA	
chr14-582	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr14	58234325	58235100	+	0 NA	3' UTR (N3' UTR (N	-10093 NR_038122	5684	Hs. 55879	NR_038122	ENSG00000PSMA3	HCS PSC3 proteasome protein-coding	
chr14-73	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr14	73062351	73067194	+	0 NA	intron (Nintron (N	6238 NM_021235	58517	Hs. 53110	NR_021235	ENSG00000CRBM25	NET52 REI RNA binding protein-coding	
chr14-10	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr14	1.02E+08	1.02E+08	+	0 NA	intron (NALuSc SIN	36818 NM_014844	9895	Hs. 19566	NR_014844	ENSG00000TECPR2	KIAA0329 tectonin protein-coding	
chr15-64	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr15	64684903	64686312	+	0 NA	3' UTR (N3' UTR (N	17674 NM_001301	4947	Hs. 74492	NR_002537	ENSG00000CAZ2	AZ2 ornithine protein-coding	
chr15-654	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr15	65461083	65462006	+	0 NA	intron (Nintron (N	-38597 NR_020962	57722	Hs. 45860	NR_020962	ENSG00000IGDCC4	DDM36 NOF immunoglobulin protein-coding	
chr15-71	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr15	71163674	71165088	+	0 NA	intron (Nintron (N	22932 NM_024817	79875	Hs. 38705	NR_024817	ENSG00000THSD4	ADAMTSL-5 thrombospondin protein-coding	
chr16-295	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr16	29992928	29993945	+	0 NA	intron (Nintron (N	2181 NM_003605	8479	Hs. 56737	NR_003605	ENSG00000CHIRP3	-	HIRA intcncRNA
chr16-821	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr16	82138313	82140911	+	0 NA	Intergeni LIP2 LIN	30612 NM_005792	10200	Hs. 34440	NR_005792	ENSG00000MPHOSPH6	MPP MPP-1M-phase protein-coding	
chr17-74	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr17	742956	748949	+	0 NA	exon (NM exon (NM	6312 NM_015721	50628	Hs. 49962	NR_015721	ENSG00000GEM14	HC56 HCAF gene nucleic protein-coding	
chr17-38	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr17	3833544	3834715	+	0 NA	intron (Nintron (N	12117 NM_001114	55421	Hs. 12096	NR_018553	ENSG00000CNCBP3	C17orf85 nuclear cap protein-coding	
chr17-15	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr17	15553267	15554461	+	0 NA	intron (Nintron (N	9619 NM_001204	51E+08	Hs. 16459	NR_001204	ENSG00000TVP23C-CI	FAM18B2 TVP23C-CI protein-coding	
chr2-2304	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr2	2.3E+08	2.3E+08	+	0 NA	intron (Nintron (N	62477 NM_001206	6672	Hs. 36905	NR_003111	ENSG00000SP100	lysp100b SP100 nucleic protein-coding	
chr22-45	5.658062	-0.59116	0.970259	-0.60928	0.542336	0.981636	chr22	45525729	45526212	+	0 NA	intron (Nintron (N	23087 NM_001996	2192	Hs. 24601	NR_001996	ENSG00000FBLN1	FBLN FIBL fibulin 1 protein-coding	
chr3-1207	5.65806																		

chr10-68c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr10	68009697	68014464	+	0 NA	intron (N)Tigger1 I	-1197 NR_131184	1E+08	NR_131184	POU5F1P5	Oct4-pg5	POU class:pseudo	
chr10-73c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr10	73045972	73057421	+	0 NA	intron (N)AluSq2 SI	45278 NM_000917	5033	Hs. 500047NM_000917	ENSG000004P4HA1	P4HA	prolyl 4-protein-coding	
chr10-93c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr10	93385486	93389138	+	0 NA	intron (N)intron (N)	95022 NM_013451	26509	Hs. 60208cNM_013451	ENSG00000CMYOF	FER1L3	myoferlin protein-coding	
chr10-93c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr10	93393835	93400664	+	0 NA	exon (NM)exon (NM)	85085 NM_013451	26509	Hs. 60208cNM_013451	ENSG00000CMYOF	FER1L3	myoferlin protein-coding	
chr10-12c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr10	1.26E+08	1.26E+08	+	0 NA	intron (N)Alu SINE	-7828 NR_120633	1.02E+08	Hs. 63426cNR_120633	ENSG00000EDRF1-AS1	EDRF1	antncRNA	
chr11-474 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr11	47410226	47418729	+	0 NA	intron (N)intron (N)	5887 NM_001128	91252	Hs. 523664NM_152264	ENSG00000CLC39A13	EDSSPD3 I	solute c protein-coding	
chr11-831 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr11	83176299	83185075	+	0 NA	intron (N)intron (N)	6797 NR_133914	1.07E+08	Hs. 59534cNR_133914	PCF11-AS1	PCF11	antncRNA	
chr13-11c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr13	1.1E+08	1.1E+08	+	0 NA	intron (N)intron (N)	12241 NM_001267	1E+08	Hs. 64003cNM_001267044	COL4A2-AS1	COL4A2	aprotein-coding	
chr15-558 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr15	55858922	55863291	+	0 NA	intron (N)intron (N)	56025 NM_001284	4734	Hs. 1565 NM_006154	ENSG00000CNEDD4	NEDD4-1 FNEDD4	E3 protein-coding	
chr15-58c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr15	58640060	58643624	+	0 NA	intron (N)intron (N)	51765 NR_07341c	664618	Hs. 670224NR_002927	HSP90AB4F	HSP90Bd	heat shockpseud	
chr15-717 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr15	71758184	71760643	+	0 NA	intron (N)MIRB SINE	-51141 NM_01634c	10002	Hs. 187354NM_01424c	ENSG00000CNR2E3	ESCS PNR	nuclear i protein-coding	
chr15-101 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr15	1.01E+08	1.01E+08	+	0 NA	exon (NM)exon (NM)	74134 NM_01491c	22856	Hs. 11048cNM_01491c	ENSG00000CHSY1	CHSY CSS1	chondroitin protein-coding	
chr16-84c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr16	84588048	84591503	+	0 NA	intron (N)intron (N)	28303 NM_02114c	23406	Hs. 28909cNM_02114c	ENSG00000COTL1	CLP	coactosin protein-coding	
chr17-61c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr17	61924146	61924829	+	0 NA	intron (N)intron (N)	3495 NM_02074c	57508	Hs. 27964cNM_02074c	ENSG00000INTS2	INT2 KIAI	integrat protein-coding	
chr2-5561 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr2	55614505	55615197	+	0 NA	intron (N)intron (N)	2771 NM_001122	57223	Hs. 51618cNM_02046c	ENSG00000PPP4R3B	FLFL2 PP4	intron f protein-coding	
chr2-6507 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr2	65071426	65072358	+	0 NA	exon (NM)exon (NM)	15476 NM_00131c	23177	Hs. 70925cNM_015147	ENSG00000CEP68	KIAA0582	centrosome protein-coding	
chr2-218 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr2	1.22E+08	1.22E+08	+	0 NA	intron (N)intron (N)	5986 NM_03239c	84365	Hs. 36784cNM_03239c	ENSG00000CNIFK	MKI671P N	nucleolar protein-coding	
chr2-1217 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr2	2.19E+08	2.19E+08	+	0 NA	intron (N)AluSx3 SI	15445 NM_02093c	57695	Hs. 16606cNM_02093c	ENSG00000UCSP37	-	ubiquitin protein-coding	
chr2-218c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr2	2.19E+08	2.19E+08	+	0 NA	intron (N)intron (N)	15686 NM_00127c	9125	Hs. 14876cNM_005444	ENSG00000CNOT9	CAF40 CT1	CCR4-NOT protein-coding	
chr20-601 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr20	6011087	6012932	+	0 NA	intron (N)intron (N)	4760 NM_00132c	54675	Hs. 74395cNM_01909c	ENSG00000CRLS1	C20orf15c	cardiolin protein-coding	
chr3-160c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr3	1.61E+08	1.61E+08	+	0 NA	intron (N)AluJb SIN	-13969 NR_003001	67767	Hs. 67595cNM_003001	ENSG00000SCARNA7	U90	small Ca ncRNA	
chr3-187c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr3	1.87E+08	1.87E+08	+	0 NA	intron (N)MER49 LTF	-32659 NR_135551	1.02E+08	NR_135551	ENSG00000CLOC10192c	-	uncharacterncRNA	
chr4-767 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr4	76775010	76777141	+	0 NA	intron (N)LP1B LIN	122069 NR_00102c	345079	Hs. 25729cNM_00102c	ENSG00000SOWAHB	ANKRD56	sonowd protein-coding	
chr5-691c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr5	69127352	69129049	+	0 NA	intron (N)intron (N)	-32608 NR_14573c	1.1E+08	NR_14573c	ENSG00000SNORA50	-	small nucsnRNA	
chr5-129c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr5	1.3E+08	1.3E+08	+	0 NA	intron (N)intron (N)	-68994 NR_12574c	1.04E+08	Hs. 62863cNR_12574c	ENSG00000ADAMTS19	-	ADAMTS19 ncRNA	
chr7-474 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr7	4747071	4749369	+	0 NA	intron (N)intron (N)	-27403 NM_001364	9907	Hs. 55844cNM_01485c	ENSG00000CAP521	KIAA0415	adaptor i protein-coding	
chr7-662c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr7	66286902	66287203	+	0 NA	intron (N)LH5 LINE	81718 NM_00359c	8460	Hs. 421194NM_00359c	ENSG00000TPST1	TANG013A	tyrosin protein-coding	
chr8-937c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr8	93722497	93725527	+	0 NA	intron (N)AluJr SIN	-16099 NR_02725c	55472	Hs. 19278cNM_01860c	ENSG00000RBM12B-AS	8orf39 FRBM12B	ancRNA	
chr8-107c 7.888176	-0.50126	0.826958	-0.60615	0.544415	0.981636	chr8	1.08E+08	1.08E+08	+	0 NA	intron (N)AluSz6 SI	36013 NM_00156c	3646	Hs. 40559cNM_00156c	ENSG00000EIF3E	EIF3P4E	eukaryot i protein-coding	
chr1-168c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr1	1675869	1676960	+	0 NA	exon (NM)exon (NM)	16818 NM_00111c	728661	Hs. 65525cNM_00111c	ENSG00000SLC35E2B	SLC35E2B	solute c protein-coding	
chr1-151c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	exon (NM)exon (NM)	4169 NM_02083c	57592	Hs. 18675cNM_02083c	ENSG00000ZNF687	PDB6	zinc fing protein-coding	
chr1-176c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr1	1.76E+08	1.76E+08	+	0 NA	intron (N)Tigger1 I	36460 NM_001001	64326	Hs. 523744NM_02245c	ENSG00000COP1	RFWD2 RNF	COP1 E3 protein-coding	
chr1-180c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (N)Tigger1 I	26771 NR_03060c	1E+08	NR_03060c	ENSG00000MIR3121	mir-3121	microRNA ncRNA	
chr1-209c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr1	2.1E+08	2.1E+08	+	0 NA	3' UTR (N)3' UTR (N)	24352 NM_01438c	27042	Hs. 194754NM_01438c	ENSG00000CUTP25	C1orf107 UTP25	sm protein-coding	
chr11-74c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr11	74918543	74920097	+	0 NA	intron (N)LM5C LIN	29771 NM_00127c	143570	Hs. 37014cNM_18296c	ENSG00000XRR1A	-	X-ray rac protein-coding	
chr12-10c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr12	1.02E+08	1.02E+08	+	0 NA	intron (N)MER5A DN	18850 NM_01605c	51019	Hs. 40569cNM_01605c	ENSG00000WASHC3	CCDC53 C	WASH comp protein-coding	
chr14-36c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr14	36310291	36312027	+	0 NA	intron (N)intron (N)	9478 NM_00130c	51562	Hs. 36864cNM_01658c	ENSG00000CMBIP	-	MAP3K12 t protein-coding	
chr18-127 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr18	12713854	12715813	+	0 NA	intron (N)AluSx SIN	11791 NM_02023c	56984	Hs. 46465cNM_02023c	ENSG00000PSMG2	CLAST3 HC	proteasom protein-coding	
chr2-878c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr2	8785321	8786400	+	0 NA	exon (NM)exon (NM)	51752 NM_00134c	57498	Hs. 9873	NR_02073c	ENSG00000KIDINS22C	ARMS SIN	kinase D protein-coding
chr2-222c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr2	2.23E+08	2.23E+08	+	0 NA	intron (N)intron (N)	72683 NM_001354	2181	Hs. 65577cNM_00445c	ENSG00000ACSL3	ACS3 FACL	acyl-CoA protein-coding	
chr2-22c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr2	24544738	24548749	+	0 NA	non-codirnon-codir	7075 NM_001284	83606	Hs. 9850	NR_031444	ENSG00000GUCD1	C22orf13	guanyil protein-coding
chr5-180c 8.212648	-0.491971	0.811952	-0.605911	0.544574	0.981636	chr5	1.8E+08	1.8E+08	+	0 NA	intron (N)intron (N)	-31478 NR_17506c	255246	Hs. 19055cNM_17506c	ENSG00000RASGEF1C	-	RasGEF dc protein-coding	
chr2-134c 10.14371	-0.4464	0.736979	-0.60571	0.544708	0.981636	chr2	1.35E+08	1.35E+08	+	0 NA	intron (N)AluJb SIN	29305 NM_001241	905	Hs. 74411cNM_001241	ENSG00000CCNT2	CYCT2	cyclin T2 protein-coding	
chr5-662c 10.14371	-0.4464	0.736979	-0.60571	0.544708	0.981636	chr5	6620705	6626970	+	0 NA	intron (N)intron (N)	9207 NR_03794c	54888	Hs. 48152cNM_01775c	ENSG00000NSUN2	MISU MRTE	NOP2/Sun protein-coding	
chr1-157c 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr1	15727940	15731488	+	0 NA	intron (N)intron (N)	109524 NM_02019c	56950	Hs. 66170	NR_02019c	ENSG00000CSDYD2	HSKM-B K	SET and p protein-coding
chr11-94c 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr11	94864567	94867738	+	0 NA	exon (NM)exon (NM)	97796 NM_001301	154810	Hs. 503594NM_130847	ENSG00000AMOTL1	JEAP	angiomot i protein-coding	
chr11-117 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr11	1.17E+08	1.17E+08	+	0 NA	exon (NM)exon (NM)	2604 NM_00471c	9159	Hs. 64861cNM_00471c	ENSG00000CPCSK7	LPC PC7 F	prote i protein-coding	
chr14-35c 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr14	35644668	35645730	+	0 NA	intron (N)MLT1A0 LI	111035 NM_032594	84684	Hs. 62813	NR_032594	ENSG00000INSM2	IA-6 IA6 INS	trapezoid protein-coding
chr16-10c 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr16	108916	110627	+	0 NA	intron (N)LM4E4b LI	28902 NM_00107c	8131	Hs. 19699	NR_01207c	ENSG00000NPRL3	C16orf35 NPR3	like protein-coding
chr19-11c 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr19	11002950	11005652	+	0 NA	intron (N)AluSx1 SI	20149 NM_001128	6597	Hs. 32752cNM_00307c	ENSG00000CMARCA4	BAF190 B	SWI1/SNF i protein-coding	
chr19-184 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr19	18443637	18447500	+	0 NA	intron (N)(G) Simp	-7435 NR_045574	51477	Hs. 40587cNM_01636c	ENSG00000ISYNA1	INO1 INOS	inositol- protein-coding	
chr19-184 7.690636	-0.510052	0.842578	-0.605347	0.544949	0.981636	chr19	18455346	18459741	+	0 NA	intron (N)intron (N)	-19410 NR_045574	51477	Hs. 40587cNM_01636c	ENSG00000ISYNA1	INO1 INOS	inositol- protein-coding	
chr2-131 7.690636	-0.510052	0.842578																



chr12-122.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr12	1.23E+08	1.23E+08	0	NA	intron (AluSz SIN	21920 NM_014708	9735 Hs. 300555NM_014708	ENSG00000KNTC1	ROD	kinetochprotein-coding		
chr16-474.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr16	47456709	47456908	0	NA	intron (intron (N	4255 NM_03079C	81533 Hs. 42217 NM_03079C	ENSG00000ITFG1	2310047C2	integrin protein-coding		
chr17-486.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr17	4861473	4861955	0	NA	intron (AluSx SIN	28374 NM_170663	50488 Hs. 443417NM_01571C	ENSG00000MINK1	B55 MAP4#	missshaper protein-coding		
chr17-644.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr17	64483092	64484186	0	NA	intron (intron (N	13415 NM_00721E	11232 Hs. 437009NM_00721E	ENSG00000POLG2	HP55	MTPC DNA	polynprotein-coding	
chr19-341.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr19	3419890	3420310	0	NA	intron (AluJo SIN	53527 NM_00124E	4782 Hs. 170131NM_005597	ENSG00000NFIC	CTF CTF5	nuclear fprotein-coding		
chr2-6817.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr2	68170192	68172000	0	NA	intron (HALI LINE	13208 NM_020143	56902 Hs. 262855NM_020143	ENSG00000CPN01	KHRBP1 RF	partner cprotein-coding		
chr2-1117.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr2	1.12E+08	1.12E+08	0	NA	intron (Tigger4a	-28419 NR_03992E	1.01E+08	NR_03992E	ENSG00000MIR4771	2-AAA ABET7	amyloid tprotein-coding	
chr21-261.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr21	26109505	26111557	0	NA	intron (intron (N	29859 NM_00113E	351 Hs. 434988NM_000484	ENSG00000APP	MIRN944 f	microRNA ncRNA		
chr3-1895.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr3	1.9E+08	1.9E+08	0	NA	intron (intron (N	135542 NR_03064Z	1E+08	NR_03064Z	ENSG00000MIR944	MIRN944 f	microRNA ncRNA	
chr5-8105.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr5	81053464	81054374	0	NA	intron (NLIP45 LIN	-93012 NR_10501E	1.03E+08	Hs. 737159NR_10501E	ENSG00000RASGRF2	-f	RASGRF2	ncRNA
chr6-4225.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr6	42231117	42232263	0	NA	intron (intron (N	-13829 NR_018141	55173 Hs. 380887NM_018141	ENSG00000MRP510	MRP-510	Fam120hcnr	protein-coding	
chr7-1347.5.650204	-0.58898	0.977503	-0.60254	0.546817	0.981636	chr7	1.35E+08	1.35E+08	0	NA	intron (intron (N	14562 NM_03313E	800 Hs. 490203NM_00434Z	ENSG00000CALD1	CDM H-CAI	caldesmon protein-coding		
chr13-467.7.723918	0.513221	0.851781	0.602527	0.546823	0.981636	chr13	46728315	46729905	0	NA	intron (intron (N	68051 NM_001984	2098 Hs. 432491NM_001984	ENSG00000ESD	FGH	esterase protein-coding		
chr15-722.7.723918	0.513221	0.851781	0.602527	0.546823	0.981636	chr15	72250100	72251163	0	NA	non-codinn-codir	-19277 NM_00120E	5315 Hs. 534777NM_002654	ENSG00000PKM	CTHBP HEL	pyruvate protein-coding		
chr20-495.7.723918	0.513221	0.851781	0.602527	0.546823	0.981636	chr20	49904274	49905933	0	NA	3' UTR (3' UTR (N	8636 NM_00113E	9825 Hs. 48513 NM_00603E	ENSG00000SPATA2	PD1 PPP1F	spermatogprotein-coding		
chr4-8465.7.723918	0.513221	0.851781	0.602527	0.546823	0.981636	chr4	84694276	84694637	0	NA	intron (intron (N	111329 NM_00126E	1040 Hs. 654899NM_00126E	ENSG00000CDS1	CDS 1	CDP-diacylprotein-coding		
chr9-124.7.723918	0.513221	0.851781	0.602527	0.546823	0.981636	chr9	1.25E+08	1.25E+08	0	NA	intron (intron (N	29628 NM_00207E	2800 Hs. 59504 NM_00207E	ENSG00000COLGA1	golgin-97	golgin Alprotein-coding		
chr1-1807.7.411003	-0.52418	0.869982	-0.60251	0.546832	0.981636	chr1	1.8E+08	1.8E+08	0	NA	intron (intron (N	-279796 NM_001004	5768 Hs. 719177NM_00282E	ENSG00000QSOX1	Q6 QSCN6	quiescin protein-coding		
chr10-572.7.411003	-0.52418	0.869982	-0.60251	0.546832	0.981636	chr10	5723184	5724015	0	NA	intron (intron (N	38761 NM_001321	54906 Hs. 610717NM_01778E	ENSG00000TASOR2	C10orf18	transcrip protein-coding		
chr2-4309.7.411003	-0.52418	0.869982	-0.60251	0.546832	0.981636	chr2	43932928	43932572	0	NA	intron (intron (N	62739 NM_13325E	10128 Hs. 368084NM_13325E	ENSG00000LRPPRC	CLONE-23E	leucine rprotein-coding		
chr2-2004.7.411003	-0.52418	0.869982	-0.60251	0.546832	0.981636	chr2	2E+08	2E+08	0	NA	intron (intron (N	61494 NM_001321	130535 Hs. 605777NM_152387	ENSG00000KCTD18	6530404F	potassium protein-coding		
chr4-6728.7.411003	-0.52418	0.869982	-0.60251	0.546832	0.981636	chr4	672814	673098	0	NA	intron (AluSq SIN	1320 NR_03374Z	521 Hs. 85539 NM_00710C	ENSG00000ATP5ME	ATP5I ATF	ATP synt protein-coding		
chr17-356.6.689602	0.568204	0.94319	0.602428	0.54689	0.981636	chr17	35020803	35021508	0	NA	intron (A)n Simp	40643 NM_01397E	3980 Hs. 100299NM_002311	ENSG00000CLIG3	LIG2 LIG3	DNA ligas protein-coding		
chr13-111.7.160767	0.532695	0.884454	0.602287	0.546983	0.981636	chr13	1.14E+08	1.14E+08	0	NA	intron (intron (N	40053 NM_00134E	55002 Hs. 317593NM_01790E	ENSG00000TMC03	C13orf11	transmem protein-coding		
chr18-634.7.160767	0.532695	0.884454	0.602287	0.546983	0.981636	chr18	63417358	63417642	0	NA	intron (L2a LINE	4976 NM_00486E	9525 Hs. 126555NM_00486E	ENSG00000VPS4B	MIG1 SKD1	vacuolar protein-coding		
chr20-467.7.160767	0.532695	0.884454	0.602287	0.546983	0.981636	chr20	46374358	46374998	0	NA	intron (intron (N	-10220 NM_001281	51006 Hs. 593344NM_01594E	ENSG00000SLC35C2	BA39402	Isolute c protein-coding		
chr5-1391.7.160767	0.532695	0.884454	0.602287	0.546983	0.981636	chr5	1.39E+08	1.39E+08	0	NA	intron (MIR SINE	78224 NM_001037	643074 Hs. 483521NM_022464	ENSG00000SILL1	BAP MSS1	L SILL1	nuclprotein-coding	
chr6-2048.7.160767	0.532695	0.884454	0.602287	0.546983	0.981636	chr6	20488668	20488981	0	NA	intron (AluSc5 SI	-45633 NM_017774	54901 Hs. 657604NM_017774	ENSG00000CDKAL1	-	CDK5 reg protein-coding		
chr11-745.7.377722	-0.52932	0.879026	-0.60216	0.547066	0.981636	chr11	74952591	74953343	0	NA	intron (intron (N	3701 NM_01475E	9789 Hs. 282702NM_01475E	ENSG00000SPCS2	-	signal pprotein-coding		
chr3-1341.7.377722	-0.52932	0.879026	-0.60216	0.547066	0.981636	chr3	1.34E+08	1.34E+08	0	NA	TTS (NM_C TTS (NM_C	93899 NM_00295E	6259 Hs. 654562NM_00295E	ENSG00000RYK	D3S3195	receptor protein-coding		
chr6-822.7.377722	-0.52932	0.879026	-0.60216	0.547066	0.981636	chr6	82204132	82204589	0	NA	intron (intron (N	43384 NM_00130C	25998 Hs. 306422NM_01552E	ENSG00000IBTK	BTBD26 B1	inhibitor protein-coding		
chr1-1947.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr1	19471351	19471686	0	NA	intron (intron (N	12777 NM_00128E	832 Hs. 43276C NM_00493C	ENSG00000CAPZB	CAPB CAPF	capping e protein-coding		
chr10-121.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr10	12163815	12164889	0	NA	TTS (NM_C TTS (NM_C	31539 NM_01414Z	11164 Hs. 555956NM_01414Z	ENSG00000NUD15	YSAL YSAL	nudix hycprotein-coding		
chr11-891.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr11	8914812	8915862	0	NA	intron (intron (N	4148 NM_00120E	56672 Hs. 13118C NM_02064Z	ENSG00000CAKIP1	BCA3 C11c	A-kinase protein-coding		
chr12-111.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr12	1.12E+08	1.12E+08	0	NA	intron (AluJb SIN	17428 NM_02495E	80018 Hs. 530941NM_02495E	ENSG00000NAA25	C12orf30 N	(alpha)-protein-coding		
chr15-1011.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr15	1.01E+08	1.01E+08	0	NA	intron (intron (N	18728 NM_01491E	22856 Hs. 110488NM_01491E	ENSG00000CHS1Y	CHS1Y CSS1	chondroit protein-coding		
chr17-295.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr17	29505407	29505606	0	NA	intron (AluSq2 SI	61531 NM_198147	116236 Hs. 106511NM_198147	ENSG00000ABHD15	-	abhydrol e protein-coding		
chr19-211.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr19	21052675	21053824	0	NA	intron (intron (N	-28898 NR_117087	148206 Hs. 72918E NM_18251E	ENSG00000ZNF714	-	zinc fingprotein-coding		
chr19-554.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr19	55405890	55406800	0	NA	intron (intron (N	1443 NM_014501	27338 Hs. 39639E NM_014501	ENSG00000UBE2S	E2-EFP E2	ubiquitin protein-coding		
chr2-1681.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr2	1681461	1683006	0	NA	intron (intron (N	62282 NM_01229E	7837 Hs. 332197NM_01229E	ENSG00000PXDN	ASG7 COF	peroxidase protein-coding		
chr2-1018.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr2	1.02E+08	1.02E+08	0	NA	intron (NL3 LINE	-98385 NR_103791	1.01E+08	Hs. 51624E NR_103791	LINC01127-	long intncRNA		
chr4-1417.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr4	1.19E+08	1.19E+08	0	NA	intron (MIRb SINE	59007 NM_020961	57721 Hs. 596872NM_020961	ENSG00000METTL14	hMETTL14	methyltr protein-coding		
chr5-143C.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr5	14304025	14307627	0	NA	intron (Tigger3a	-158157 NR_14581E	1.1E+08	NR_14581E	SNORD170-	small nucsnRNA		
chr5-1093.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr5	1.09E+08	1.09E+08	0	NA	intron (AluJr SIN	-28515 NR_14904C	285638 Hs. 532104NR_14904C	ENSG00000LOC28563E	-	uncharactncRNA		
chr8-2814.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr8	28149071	28149669	0	NA	intron (intron (N	2448 NM_00449E	3182 Hs. 591731NM_00449E	ENSG00000HNRNPAB	ABBP1 HNf	heteroger protein-coding		
chr8-1167.7.880318	-0.49965	0.829793	-0.60214	0.547078	0.981636	chr8	1.17E+08	1.17E+08	0	NA	intron (NLIMCa LIN	56231 NM_001284	55140 Hs. 49133E NM_018091	ENSG00000ELP3	KAT9	elongator protein-coding		
chr12-111.7.111769	0.533742	0.886499	0.602079	0.547122	0.981636	chr12	1.12E+08	1.12E+08	0	NA	3' UTR (3' UTR (N	5707 NM_032334	84294 Hs. 86970 NM_032334	ENSG00000UTP23	C8orf53	UTP23 sm protein-coding		
chr12-112.7.623039	0.561086	0.931994	0.602028	0.547156	0.981636	chr12	1.12E+08	1.12E+08	0	NA	intron (AluJr SIN	93856 NM_00110E	283450 Hs. 53094E NM_17381E	ENSG00000HECTD4	C12orf51 HECT	dom protein-coding		
chr10-101.7.657355	0.506838	0.841971	0.601966	0.547197	0.981636	chr10	1.02E+08	1.02E+08	0	NA	intron (NLIMB7 LIN	22302 NM_00203E	6311 Hs. 76253 NM_00297E	ENSG00000ATXN2	ATX2 SCA2	ataxin 2 protein-coding		
chr14-954.7.657355	0.506838	0.841971	0.601966	0.547197	0.981636	chr14	95449583	95450116	0	NA	intron (intron (N	25986						

chr16-274.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr16	27479634	27489832	+	0	NA	intron (Nintron (N	-31340 NR_037158	283888	Hs.66093ENR_037158	ENSG000002IL21R-AS1-	IL21R	antncRNA
chr17-43c.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr17	43015244	43018627	+	0	NA	intron (NAluSp SIN	5450 NM_006373	10493	Hs.514199NM_006373	ENSG000002VAT1	VAT1	vesicle protein-coding
chr18-23f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr18	23536317	23544351	+	0	NA	intron (Nintron (N	36823 NM_01332f	29919	Hs.46477ENM_01332f	ENSG000002CRM1	C18orf8 E	regulator protein-coding
chr19-11f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr19	11940268	11942752	+	0	NA	intron (NLTR12C LI	16403 NM_14456e	90592	Hs.52848ENM_14456e	ENSG000002ZNF700	-	zinc finger protein-coding
chr19-15x.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr19	15634387	15637054	+	0	NA	intron (Nintron (N	11067 NM_00585f	10270	Hs.59449ENM_00585f	ENSG000002AKAF8	AKAP 95 A	kinase protein-coding
chr19-35e.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr19	35651026	35659491	+	0	NA	intron (NAluSc8 SI	6935 NM_00186g	1340	Hs.43166ENM_00186g	ENSG000002COX6B1	COX6B COX	cytochrome protein-coding
chr2-240f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr2	24066596	24068952	+	0	NA	exon (NM exon (NM	8552 NM_01604f	51639	Hs.17786ENM_01604f	ENSG000002SF3B6	CAF-110 F	splicing protein-coding
chr20-46f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr20	46064134	46065061	+	0	NA	intron (Nintron (N	25365 NM_02096f	57727	Hs.45499ENM_02096f	ENSG000002NCOA5	CIA ba46E	nuclear protein-coding
chr20-51f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr20	51668688	51670465	+	0	NA	intron (Nintron (N	98814 NM_00604f	10079	Hs.649234NM_00604f	ENSG000002ATP9A	ATP11A	ATPase protein-coding
chr21-43f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr21	43685124	43687148	+	0	NA	intron (Nintron (N	26376 NM_01505e	23076	Hs.56572ENM_01505e	ENSG000002RRP1B	KIAA0179 R	ribosomal protein-coding
chr21-46f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr21	46580479	46583001	+	0	NA	Intergeni LIP10 LI	23342 NM_00627f	6285	Hs.422181NM_00627f	ENSG000002S100B	NEF S100 S	100 cal protein-coding
chr3-165f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr3	16500774	16501113	+	0	NA	intron (Nintron (N	12756 NM_01515c	23180	Hs.98910 NM_01515c	ENSG000002CFTN1	MIG2 PIB1	raftlin, protein-coding
chr4-707f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr4	70763128	70767030	+	0	NA	intron (NAluS26 SI	30669 NM_00134f	22902	Hs.740904NM_01496f	ENSG000002RUFY3	RIPX SIN	RUN and F protein-coding
chr5-553f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr5	31267187	31267035	+	0	NA	intron (Nintron (N	74775 NM_00493f	1004	Hs.12477ENM_00493f	ENSG000002CDH6	CAD6 KCAI	cadherin protein-coding
chr5-796f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr5	79661643	79662809	+	0	NA	intron (NMER11C LI	66992 NM_01536c	23517	Hs.274531NM_01536c	ENSG000002MTREX	Dob1 KIA	Mtr4 exos protein-coding
chr7-127f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	intron (NTigger1 E	-27610 NM_15361c	202333	Hs.48262ENM_15361c	ENSG000002CMYA5	C5orf10 S	cardiomyocyte protein-coding
chr7-128f.8.187224	0.487013	0.811451	0.600175	0.54839	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	2350 NM_00166f	381	Hs.65320ENM_00166f	ENSG000002CARF5	-	ADP ribos protein-coding
chr1-896f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr1	89687733	89688913	+	0	NA	Intergeni MER6A DNA	-47982 NR_02436e	402483	Hs.72235ENM_001039682	LINC0100c	-	long intncRNA
chr1-169f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr1	1.7E+08	1.7E+08	+	0	NA	intron (NLa2 LINE	55203 NM_03227f	84230	Hs.41283ENM_03227f	ENSG000002LRRC8C	AD158 FAL	leucine protein-coding
chr11-74f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr11	74881654	74883166	+	0	NA	intron (NLIPIA16 LI	43767 NM_00136f	55732	Hs.443551NM_01818f	ENSG000002C1orf112	-	chromosome protein-coding
chr11-96f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr11	96372287	96373930	+	0	NA	intron (NLIPIA2 LIN	66681 NM_00127c	143570	Hs.37014ENM_18296f	ENSG000002XRRA1	-	X-ray rac protein-coding
chr12-56f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr12	56303142	56304046	+	0	NA	intron (Nintron (N	16708 NM_00136f	79780	Hs.52508ENM_01414f	ENSG000002CCDC82	HSPC048	coiled-co protein-coding
chr14-10f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	Intergeni AluJo SIN	-3264 NM_00407f	1431	Hs.74325ENM_00407f	ENSG000002CCS	-	citrate protein-coding
chr15-34f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr15	34361115	34362236	+	0	NA	intron (Nintron (N	36279 NM_00182f	1152	Hs.173724NM_00182f	ENSG000002CKB	B-CK BCK	creatine protein-coding
chr17-75f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr17	784452	784857	+	0	NA	intron (Nintron (N	5521 NM_15361f	254531	Hs.352614NM_15361f	ENSG000002LPCAT4	AGPAT7 AN	lysochospholipid protein-coding
chr17-511f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr17	51182519	51183690	+	0	NA	intron (Nintron (N	2301 NM_01814f	55178	Hs.18272ENM_01814f	ENSG000002MRM3	RM1L1 RN	mitochondrial protein-coding
chr18-68f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr18	68690229	68691331	+	0	NA	intron (Nintron (N	16382 NM_00101f	4831	Hs.46345ENM_00251f	ENSG000002NME2	NDBK NDP	NME2 protein-coding
chr2-202f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr2	20261349	20263342	+	0	NA	TTS (NM_C	24328 NM_00135c	5495	Hs.440534NM_01902f	ENSG000002TMX3	PDIA13 T	thioredoxin protein-coding
chr2-327f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr2	32780492	32781247	+	0	NA	intron (NTigger3b	-36912 NM_00100f	6382	Hs.224607NM_00299f	ENSG000002SDC1	CD138 SDC	syndecan protein-coding
chr2-371f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr2	37127641	37129258	+	0	NA	intron (NLIPIA2 LIN	-44564 NR_02709f	285045	Hs.43466ENM_02709f	ENSG000002LINC0048e	-	long intncRNA
chr2-206f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr2	2.06E+08	2.06E+08	+	0	NA	intron (Nintron (N	19373 NM_00113f	5610	Hs.131431NM_00275f	ENSG000002EIF2AK2	EIF2AK1 E	karyotic protein-coding
chr2-207f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr2	2.08E+08	2.08E+08	+	0	NA	intron (NLIPIA4 LI	80090 NM_01775f	54891	Hs.44503ENM_01775f	ENSG000002IN08D	-	IN08D con protein-coding
chr20-13f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr20	1306212	1306583	+	0	NA	3' UTR (N3' UTR (N	7276 NM_01568f	27111	Hs.65701ENM_01568f	ENSG000002SDCBP2	SITAC SIT	syndecan protein-coding
chr3-330f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr3	33090279	33091323	+	0	NA	3' UTR (N3' UTR (N	6031 NM_00107f	2720	Hs.443031NM_00040f	ENSG000002GLB1	EBP ELN1	galactosyl protein-coding
chr3-457f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr3	45713397	45713267	+	0	NA	intron (Nintron (N	24986 NM_00131f	22908	Hs.15650ENM_01401f	ENSG000002SACM1L	SACT1	SAC1 like protein-coding
chr3-136f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr3	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	90090 NM_00053f	5096	Hs.63788 NM_00053f	ENSG000002PCCB	-	propionyl protein-coding
chr3-179f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr3	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	18779 NM_00430f	86	Hs.43523ENM_00430f	ENSG000002ACTL6A	ACTL6 ARF	actin like protein-coding
chr4-8911f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr4	89113771	89115516	+	0	NA	3' UTR (N3' UTR (N	1826 NM_14571f	166815	Hs.58924 NM_14571f	ENSG000002TIGD2	HEL106	tigger protein-coding
chr5-384f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr5	38490724	38491391	+	0	NA	intron (Nintron (N	45511 NM_18280f	133584	Hs.20103 NM_15240f	ENSG000002EGFLAM	AGRINL ACE	EGF like, protein-coding
chr5-796f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr5	79668947	79670312	+	0	NA	intron (Nintron (N	-20207 NM_15361c	202333	Hs.48262ENM_15361c	ENSG000002CMYA5	C5orf10 S	cardiomyocyte protein-coding
chr6-897f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr6	89701188	89701710	+	0	NA	intron (Nintron (N	-62702 NM_02046f	57226	Hs.17727ENM_02046f	ENSG000002LYRM2	DJ1 2208.	LYR motif protein-coding
chr6-155f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr6	1.55E+08	1.55E+08	+	0	NA	intron (NLIPIA1 LI	9866 NM_01602c	51106	Hs.27990ENM_01602c	ENSG000002TFB1M	CGI-75 C	transcript protein-coding
chr7-139f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N	12273 NM_00111f	28996	Hs.731417NM_02274f	ENSG000002HIPK2	PRO0593	homeodomain protein-coding
chr8-175f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr8	17564427	17565186	+	0	NA	intron (NMER1B DNA	-11627 NM_00620f	5157	Hs.45857ENM_00620f	ENSG000002PDGFRL	PDGRL PR	platelet protein-coding
chr9-121f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (NMI13 SINE	-3029 NM_00135f	2934	Hs.552237ENM_00017f	ENSG000002GSN	ADF AGE	gelatin protein-coding
chr9-130f.5.683485	-0.58229	0.970196	-0.60017	0.54839	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	3' UTR (N3' UTR (N	11259 NR_10691f	1.02E+08	NR_10691f	ENSG000002MIR6856	hsa-mir-6	microRNA ncRNA
chr1-666f.7.921457	-0.49654	0.82753	-0.60002	0.54849	0.981636	chr1	66620385	66622766	+	0	NA	intron (NLIPIA5 LI	-6865 NR_03606f	1E+08	NR_03606f	ENSG000002MIR3117	mir-3117	microRNA ncRNA
chr14-617f.7.921457	-0.49654	0.82753	-0.60002	0.54849	0.981636	chr14	61793010	61794934	+	0	NA	intron (Nintron (N	81821 NR_					



chr5-7115	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr5	71196754	71197681	+	0	NA	intron (Nintron (N	10914 NR_02702E	728411 Hs. 88181	NM_207331	ENSG00000GUSBP1	-	USB pset pseudo
chr6-3187	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr6	31879457	31885454	+	0	NA	intron (N-G-rich Lc	-3409 NM_001117E	80736 Hs. 33535E	NM_025257	ENSG00000SLC44A4	-	G6orf29 Csolute cεprotein-coding
chr7-4304	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr6	43048208	43050287	+	0	NA	intron (Nintron (N	4698 NM_00116E	9820 Hs. 52013E	NM_01478C	ENSG00000CUL7	3M1 CUL-7	cullin 7 protein-coding
chr7-1665	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr7	16695101	16697496	+	0	NA	intron (Nintron (N	35084 NM_00136E	28969 Hs. 48763E	NM_01403E	ENSG00000BZW2	HSPC028 Mbasic letprotein-coding	
chr7-6663	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr7	66638408	66641178	+	0	NA	3' UTR (N3' UTR (N	10912 NM_001167E	154881 Hs. 546627	NM_15303E	ENSG00000KCTD7	CLN14 EPW	potassium protein-coding
chr7-745E	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr7	74594551	74596241	+	0	NA	promoter-promoter-	-572 NR_16211E	1.13E+08	NR_16211E	MIR10525	-	microRNA ncRNA
chr9-127E	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	26753 NR_03747E	1.01E+08	NR_03747E	ENSG00000MIR3911	mir-3911	microRNA ncRNA
chr9-131E	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	12951 NM_00135E	10585 Hs. 52244E	NM_00717E	ENSG00000POMT1	LGM2K L	protein-coding
chr9-1364	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	exon (NM_exon (NM_	-7057 NM_01989E	56623 Hs. 12099E	NM_01989E	ENSG00000INPP5E	CORS1 CPI	inositol protein-coding
chr9-136E	8.195082	0.485096	0.81379	0.596095	0.551112	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	-15639 NM_01989E	56623 Hs. 12099E	NM_01989E	ENSG00000INPP5E	CORS1 CPI	inositol protein-coding
chr11-11C	7.87246	-0.49803	0.835728	-0.59592	0.551229	0.981636	chr11	1.1E+08	1.1E+08	+	0	NA	intron (NAluSx S S	33506 NM_00126C	5962 Hs. 263671	NM_00290E	ENSG00000CRDX	DFNB24	radixin protein-coding
chr12-77E	7.87246	-0.49803	0.835728	-0.59592	0.551229	0.981636	chr12	77989439	77991267	+	0	NA	intron (N LOR1a LTF	159459 NM_01490E	89795 Hs. 655301	NM_01490E	ENSG00000CNAV3	POMF1L1 S	neuron nεprotein-coding
chr17-424	7.87246	-0.49803	0.835728	-0.59592	0.551229	0.981636	chr17	42417939	42419090	+	0	NA	intron (NAluSp S N	4742 NM_01223E	284119 Hs. 437191	NM_01223E	ENSG00000CAVIN1	CAVIN CGL	caecolae protein-coding
chr18-30C	7.87246	-0.49803	0.835728	-0.59592	0.551229	0.981636	chr18	30021667	3002235	+	0	NA	intron (NLMC4 LIN	10496 NM_01464E	9663 Hs. 13234E	NM_01464E	ENSG00000LPIN2	-	lipin 2 protein-coding
chr2-323E	7.87246	-0.49803	0.835728	-0.59592	0.551229	0.981636	chr2	32380958	32381441	+	0	NA	intron (Nintron (N	24171 NM_01625E	57448 Hs. 150107	NM_01625E	ENSG00000BTRC6	APOLLON E	baculovir protein-coding
chr5-151E	7.87246	-0.49803	0.835728	-0.59592	0.551229	0.981636	chr5	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	883 NM_00130E	6678 Hs. 11177E	NM_00311E	ENSG00000SPARC	BM-40 O1	secreted protein-coding
chr1-274	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr1	2744281	27746696	+	0	NA	intron (N L2c LINE	19527 NM_00114E	199870 Hs. 46935E	NM_15266E	ENSG00000CFAM76A	-	family wiprotein-coding
chr10-694	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr10	69401010	69402148	+	0	NA	3' UTR (N3' UTR (N	15339 NM_001057E	6865 Hs. 8837E	NM_001057E	ENSG00000TACR2	NK2R NKN	tachykinin protein-coding
chr13-41E	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr13	41816410	41816609	+	0	NA	intron (Nintron (N	144576 NM_00100E	23078 Hs. 36828E	NM_01505E	ENSG00000VWA8	KIAA0564 v	von Wille protein-coding
chr13-451	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr13	45138449	45139067	+	0	NA	intron (NAluSz S N	18248 NM_00412E	2963 Hs. 65458E	NM_00412E	ENSG00000GTF2F2	BTF4 RAP	general tprotein-coding
chr2-118E	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr2	11803323	11806328	+	0	NA	intron (Nintron (N	32161 NR_03622E	1E+08	NR_03622E	ENSG00000MIR4262	-	microRNA ncRNA
chr2-3904	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr2	39049019	39049218	+	0	NA	intron (NAluSx S N	71345 NM_00563E	6654 Hs. 70989E	NM_00563E	ENSG00000SOS1	GF1 GGF1 S	Ras/Fprotein-coding
chr5-138E	7.665213	0.504695	0.847057	0.595821	0.551295	0.981636	chr5	13837273	13837509	+	0	NA	intron (N L2a LINE	107089 NM_00136E	1767 Hs. 21236E	NM_00136E	ENSG00000DNAH5	CILD3 DN	dynein aεprotein-coding
chr3-158E	8.742518	0.474386	0.796209	0.595806	0.551305	0.981636	chr3	1.59E+08	1.59E+08	+	0	NA	intron (N L3 LINE C	7798 NM_02273E	64747 Hs. 58663E	NM_02273E	ENSG00000MPSD1	SMAP4	major facprotein-coding
chr11-95E	5.214171	-0.62507	1.049746	-0.59545	0.551542	0.981636	chr11	95806602	95806809	+	0	NA	intron (N LIP45 LIN	16207 NM_01467E	9702 Hs. 101014	NM_01467E	ENSG00000CEP57	MVA2 PIG	centrosom protein-coding
chr17-601	7.698494	0.50786	0.852967	0.595404	0.551573	0.981636	chr17	60184206	60185572	+	0	NA	intron (Nintron (N	34916 NM_000717E	762 Hs. 89485	NM_000717E	ENSG00000CCA4	CAIV Car	4carbonic protein-coding
chr16-75E	10.262089	-0.43312	0.726765	-0.59521	0.551706	0.981636	chr16	75231772	75234877	+	0	NA	intron (NAluJb S N	5336 NM_00117E	9564 Hs. 47974	NM_014567E	ENSG00000BCAR1	CAS CASI B	carc protein-coding
chr10-10C	11.87964	0.406873	0.684045	0.594805	0.551974	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (NAluSp S N	6578 NM_001001E	282991 Hs. 34906	NM_17380E	ENSG00000BLOC152	BLOS2 B	biogenesis protein-coding
chr16-19E	9.625401	-0.46322	0.778838	-0.59476	0.552005	0.981636	chr16	19575334	19575614	+	0	NA	intron (NAluSq2 S N	19771 NM_00136E	57020 Hs. 654964	NM_020314E	ENSG00000VPS35L	C16orf62	VPS35 encprotein-coding
chr1-154	11.92078	0.407759	0.685819	0.594557	0.552139	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	exon (NM_exon (NM_	15692 NM_001367E	57198 Hs. 43570C	NM_02045E	ENSG00000ATPB82	ATP1D	ATPase fεprotein-coding
chr1-1737	11.92078	0.407759	0.685819	0.594557	0.552139	0.981636	chr1	1.74E+08	1.74E+08	+	0	NA	intron (NAluJb S N	43139 NM_01445E	27252 Hs. 49503E	NM_01445E	ENSG00000KLHL20	KHLHX KLF	kelch lik protein-coding
chr12-71E	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr12	7136131	7137448	+	0	NA	intron (Nintron (N	6418 NM_01471E	9746 Hs. 53537E	NM_01471E	ENSG00000CLSTN3	CDHR14 C	csaltryn protein-coding
chr17-28E	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr17	28523073	28532106	+	0	NA	intron (Nintron (N	40320 NM_001267E	90410 Hs. 53431	NM_174887E	ENSG00000IFT20	-	intraflag protein-coding
chr19-10E	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr19	10365005	10366347	+	0	NA	exon (NM_exon (NM_	14896 NM_003331E	7297 Hs. 75516	NM_003331E	ENSG00000CTYK2	IMD35 JTK	tyrosine protein-coding
chr3-121E	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-7301 NM_00533E	3059 Hs. 14601	NM_00533E	ENSG00000HCL51	CTTNL HS1	hematopoiprotein-coding
chr3-129E	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (NAluSx S N	28680 NM_001204E	339122 Hs. 38113E	NM_19849E	ENSG00000RAB43	RAB11B RA	RAB43, mεprotein-coding
chr6-419E	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr6	41904386	41904831	+	0	NA	TTS (NM_C	-9233 NM_018561E	25862 Hs. 59357E	NM_018561E	ENSG00000CUSP49	-	ubiquitin protein-coding
chr7-6654	8.228364	0.488151	0.821154	0.594469	0.552198	0.981636	chr7	66544521	66545778	+	0	NA	intron (Nintron (N	47258 NR_111974E	493754 Hs. 73240E	NR_00293E	ENSG00000GS1-124E	-	RAB guanipseudo
chr1-6667	5.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr1	66676073	66677403	+	0	NA	intron (Nintron (N	48798 NR_03606E	1E+08	NR_03606E	ENSG00000MIR3117	mir-3117	microRNA ncRNA
chr1-220C	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (NAluSg S N	18949 NM_00444E	2058 Hs. 49778E	NM_00444E	ENSG00000EPRS	EARS GLUF	glutamyl- protein-coding
chr10-68E	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr10	68004039	68006615	+	0	NA	intron (N LIMA3 LIN	5556 NR_131184E	1E+08	NR_131184E	POU5F1P5	OL4-α	POU classpseud
chr11-11E	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	9074 NM_001144E	23187 Hs. 54062E	NM_015157E	ENSG00000PHLDB1	L5L5A	pleckstrin protein-coding
chr12-10E	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	3' UTR (N3' UTR (N	59359 NM_001251E	55198 Hs. 50660E	NM_018171E	ENSG00000APPL2	DIP13B	adaptor fεprotein-coding
chr13-21C	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr13	21053620	21054113	+	0	NA	intron (N LIMB4 LIN	7720 NM_01457E	26524 Hs. 78960	NM_01457E	ENSG00000LATS2	KPM	large tunprotein-coding
chr13-97E	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr13	97356943	97358740	+	0	NA	intron (Nintron (N	-76328 NM_02103E	5911 Hs. 50848E	NM_02103E	ENSG00000RAP2A	K-REV KRE	RAP2A, mεprotein-coding
chr14-884	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr14	88406349	88407806	+	0	NA	intron (N LIP47 LIN	21420 NM_01841E	55812 Hs. 52551E	NM_01841E	ENSG00000SPATA7	HEL-5-29ε	spermatog protein-coding
chr20-137	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr20	13781063	13783118	+	0	NA	intron (NAluSz S N	2796 NM_01664E	51575 Hs. 369284	NM_01664E	ENSG00000ESF1	ABTAP ZC	ESF1 nuclprotein-coding
chr20-23E	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr20	23389441	23390174	+	0	NA	intron (N LIMB7 LIN	25444 NM_001317E	64412 Hs. 70946E	NM_02248E	ENSG00000GZF1	JLSM ZBTE	EDNF indt protein-coding
chr3-4371	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr3	43711923	43713636	+	0	NA	intron (Nintron (N	-21185 NM_00134E	55129 Hs. 65665E	NM_01807E	ENSG00000ANO10	SCAR10 TV	anoctamir protein-coding
chr4-119E	7.905741	-0.4933	0.830207	-0.59419	0.552387	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (N LIP42 LIN	26377 NM_001001E	401152 Hs. 17370E	NM_001001E	ENSG00000C4orf3	ALN HCVF1	chromoson protein-coding
chr7-149E	7.905741	-0.4933	0.830207	-0.59419	0.552387</														

chr2-112c	8.35749	-0.47949	0.812118	-0.59043	0.554906	0.981636	chr2	11207335	11207993	+	0	NA	intron (Nintron (N	52197	NM_001282	130814	Hs.27441ENM_152391	ENSG00000SLC66A3	C2orf22	Fsolute c protein-coding	
chr5-151c	8.35749	-0.47949	0.812118	-0.59043	0.554906	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	13383	NM_001325	2878	Hs.386793ENM_002084	ENSG00000GPX3	GPx-P	GSF glutathione protein-coding	
chr8-526f	12.48394	0.401223	0.68004	0.589999	0.555191	0.981636	chr8	52657258	52657908	+	0	NA	exon (NM_exon (NM	56852	NM_014781	9821	Hs.196102ENM_014781	ENSG00000CRB1CC1	ATG17	CC1RBI induc protein-coding	
chr1-119f	7.631931	0.501396	0.849921	0.589933	0.555236	0.981636	chr1	11956421	11957111	+	0	NA	intron (NMIRb SINE	22049	NM_001316	5351	Hs.75093	NM_000302	ENSG00000PLOD1	ED56	ED56 procollagen protein-coding
chr19-49f	7.631931	0.501396	0.849921	0.589933	0.555236	0.981636	chr19	49161523	49161965	+	0	NA	intron (NAluSx1 SI	3952	NM_01763f	54795	Hs.467101ENM_01763f	ENSG00000TRPM4	LTrpCA4	PF transient protein-coding	
chr3-188c	3.90697	-0.69548	1.178947	-0.58992	0.555247	0.981636	chr3	1.88E+08	1.88E+08	+	0	NA	intron (NCharlieL	102663	NM_001167	4026	Hs.72022CNM_00557f	ENSG00000CLPP	LIM	domain protein-coding	
chr6-756c	3.90697	-0.69548	1.178947	-0.58992	0.555247	0.981636	chr6	75693918	75694117	+	0	NA	intron (NAluSp SIN	-55222	NM_00136E	4646	Hs.149387NM_004499	ENSG00000MY06	DFNA22	DF myosin I V protein-coding	
chr8-672f	7.625923	0.515088	0.873236	0.589861	0.555284	0.981636	chr8	67257335	67257534	+	0	NA	intron (Nintron (N	86347	NM_006421	10565	Hs.656902ENM_006421	ENSG00000ARFGF1F	ARFGF1	EADP ribosome protein-coding	
chr11-321d	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr11	32101753	32106430	+	0	NA	intron (Nintron (N	13017	NM_002901	5954	Hs.97887	NM_002901	ENSG00000RCN1	HEL-S-84	reticuloc protein-coding
chr14-52f	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr14	52857737	52857271	+	0	NA	intron (NAluV SINE	-68397	NM_19806E	64841	Hs.174802ENM_19806E	ENSG00000GNPNAT1	GNA1	GNP nucleoside protein-coding	
chr22-20f	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr22	20571241	20572931	+	0	NA	intron (Nintron (N	64039	NM_00129f	51586	Hs.517421ENM_01588f	ENSG00000MED15	ARC105	CM mediator protein-coding	
chr3-105f	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr3	1.06E+08	1.06E+08	+	0	NA	intron (NLIIPA7 LIN	205312	NM_001627	214	Hs.59129fENM_001627	ENSG00000ALCAM	CD166	MEM activator protein-coding	
chr3-194d	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr3	1.94E+08	1.94E+08	+	0	NA	intron (Nintron (N	-32371	NM_00448E	2814	Hs.73734	NM_00448E	ENSG00000GP5	CD42d	GPV glycoprotein protein-coding
chr5-572f	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr5	57230890	57235503	+	0	NA	intron (Nintron (N	19122	NM_001127	65056	Hs.44427fENM_02291f	ENSG00000GPBP1	GPBP	SDSH GC-rich protein-coding	
chr7-107f	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr7	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	53363	NM_00010E	1738	Hs.131711NM_00010f	ENSG00000CLD	DLDD	DLDD dihydrolip protein-coding	
chr9-110f	10.62274	-0.42467	0.720216	-0.58965	0.555426	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (NAluSx SIN	71791	NM_00135f	1902	Hs.126667NM_001401	ENSG00000LPAR1	EDG2	GP2E lysophosph protein-coding	
chr11-72f	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr11	72031679	72032015	+	0	NA	intron (Nintron (N	17556	NR_10417f	1E+08	Hs.713607NR_10417f	ENSG00000LOC10012e-		uncharactericnRNA	
chr11-117c	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (NLMC4 LIN	9007	NR_11026E	5049	Hs.72848fENM_00257f	ENSG00000PAFAH1B2	HEL-S-30c	platelet protein-coding	
chr19-43f	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr19	43898942	43899594	+	0	NA	intron (NAluSc SIN	2535	NR_038334	1.01E+08	Hs.76561	NR_038334	ENSG00000LOC10050f-		uncharactericnRNA
chr2-613f	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr2	61341469	61342168	+	0	NA	intron (NAluSx1 SI	75559	NR_003707	1E+08	Hs.67582fNR_003707	ENSG00000SNORA70B		small nucsnRNA	
chr3-456f	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr3	45677727	45680759	+	0	NA	non-codir-non-codir	9639	NR_033947	64474	Hs.71288fNR_033947	LIMD1-AS1	LIMD1	antncRNA	
chr3-179f	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (Nintron (N	49567	NM_014407	27094	Hs.59128fENM_014407	ENSG00000KCNMB3	BKBETA3	f potassium protein-coding	
chr3-186f	8.349632	-0.47793	0.810558	-0.58963	0.555439	0.981636	chr3	1.87E+08	1.87E+08	+	0	NA	intron (Nintron (N	14109	NM_01630E	51726	Hs.31719fENM_01630f	ENSG00000DNAJB11	ABBP-2	fAeDNAJ heat protein-coding	
chr1-321f	5.716767	-0.57543	0.976502	-0.58927	0.555679	0.981636	chr1	32154862	32155254	+	0	NA	intron (NAluS2 SI	-24617	NM_17585E	200081	Hs.47887	NM_17585E	ENSG00000TXLNA	IL14	TXLIL taxilin protein-coding
chr10-11f	5.716767	-0.57543	0.976502	-0.58927	0.555679	0.981636	chr10	1109354	1109674	+	0	NA	intron (NAluSp SIN	-50254	NR_01537f	399706	Hs.721191NM_00101C	ENSG00000LINC0020C	C10orf13f	lnc intncRNA	
chr14-68f	5.716767	-0.57543	0.976502	-0.58927	0.555679	0.981636	chr14	68930484	68931156	+	0	NA	intron (NMIR SINE	48482	NM_00110E	87	Hs.23575fENM_00110f	ENSG00000ACTN1	BDPLT15	actinin protein-coding	
chr18-26f	5.716767	-0.57543	0.976502	-0.58927	0.555679	0.981636	chr18	26059380	26060174	+	0	NA	intron (NLM1E1 LIN	30836	NM_001007	6760	Hs.129261NM_005637	ENSG00000SS18	SSXT	SYT SS18 sub protein-coding	
chr9-122f	5.716767	-0.57543	0.976502	-0.58927	0.555679	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (NLM1E2 LIN	29896	NM_012197	23637	Hs.271341NM_012197	ENSG00000CRABGAP1	GAPCENAI	TRAB GTPase protein-coding	
chr16-70f	10.15342	-0.43873	0.744697	-0.58914	0.555766	0.981636	chr16	70371792	70371991	+	0	NA	intron (Nintron (N	24988	NM_01833E	55308	Hs.656037NM_01833f	ENSG00000CDX19A	DDX19-DD	DEAD-box protein-coding	
chr11-704f	7.168625	0.530055	0.899756	0.589109	0.555788	0.981636	chr11	70484835	70485366	+	0	NA	intron (Nintron (N	86573	NM_001184	2017	Hs.595164NM_005231	ENSG00000CTTN	EMS1	coractin protein-coding	
chr15-801f	7.168625	0.530055	0.899756	0.589109	0.555788	0.981636	chr15	80183700	80183899	+	0	NA	intron (NMIR SINE	30800	NM_000137	2184	Hs.73875	NM_000137	ENSG00000CAFAH		fumarylac protein-coding
chr16-287f	7.168625	0.530055	0.899756	0.589109	0.555788	0.981636	chr16	28722576	28722906	+	0	NA	intron (NAluSx SIN	-1511	NR_10705E	1.02E+08	NR_10705f	ENSG00000MIR6862-2	hsa-mir-6	microRNA ncRNA	
chr17-78f	7.168625	0.530055	0.899756	0.589109	0.555788	0.981636	chr17	78098880	78099666	+	0	NA	intron (NAluJo SIN	12526	NR_040071	1E+08	Hs.635442NR_040071	ENSG00000TNRC6C-AS	TM6C	lnc TNRC6C antncRNA	
chr2-702f	7.369864	-0.52735	0.895729	-0.58874	0.556038	0.981636	chr2	70291149	70291382	+	0	NA	intron (Nintron (N	1959	NM_001317	6637	Hs.465167NM_00309f	ENSG00000CSNRPG	SMG	Sm-G small nuc protein-coding	
chr1-204f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr1	20499750	20502734	+	0	NA	exon (NM_exon (NM	6909	NM_024544	79594	Hs.10101	NM_024544	ENSG00000MUL1	Clorf166	mi tochoanc protein-coding
chr1-156f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (NAluJr SIN	-5376	NM_00119E	11243	Hs.53047fENM_00722f	ENSG00000PMF1		polymyanc protein-coding	
chr12-53f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr12	53513261	53515443	+	0	NA	3' UTR (N3' UTR (N	368	NR_046221	1.01E+08	Hs.63360fNR_046221	ENSG00000LOC10065f-		uncharactericnRNA	
chr12-11f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	15104	NM_01623E	51434	Hs.71993fENM_01623f	ENSG00000ANAPC7	APC7	anaphase protein-coding	
chr16-174f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr16	1748018	1749913	+	0	NA	intron (NMER2 DNA	13980	NR_03613E	1E+08	NR_03613f	ENSG00000MIR3177	mir-3177	microRNA ncRNA	
chr16-31f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr16	31038877	31040105	+	0	NA	intron (Nintron (N	5933	NM_004604	6810	Hs.83734	NM_004604	ENSG00000STX4	STX4A	p3f syntaxin protein-coding
chr16-69f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr16	69355576	69355964	+	0	NA	intron (NTiger 3b	-7236	NM_14467f	146456	Hs.72911fENM_14467f	ENSG00000TMED6	PR034237	transmem protein-coding	
chr19-114f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr19	11445345	11445568	+	0	NA	exon (NM_exon (NM	-9672	NM_00130E	115948	Hs.12401fENM_144504f	ENSG00000CCDC151	CILD30	coiled-cp protein-coding	
chr19-19f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr19	19335844	19341030	+	0	NA	intron (Nintron (N	17608	NM_01532E	23383	Hs.65493fENM_01532f	ENSG00000MAU2	KIAA0892	MAU2 sist protein-coding	
chr19-45f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr19	45277270	45280659	+	0	NA	intron (NAluJo SIN	27179	NM_00119E	55787	Hs.34314	NM_031417	ENSG00000MARK4	MARK4L	M marker tubul protein-coding
chr20-47f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr20	47648540	47649239	+	0	NA	intron (Nintron (N	13715	NM_018837	55959	Hs.16201fENM_018837	ENSG00000SULF2	HSLUF-2	sulfatase protein-coding	
chr5-507f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr5	50774057	50774534	+	0	NA	intron (NSVA_B Ret	106881	NM_001331	79668	Hs.369581NM_02461f	ENSG00000PARP8	ARTD16	pApo (ADP- protein-coding	
chr5-177f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	17262	NM_00681f	10960	Hs.75864	NM_00681f	ENSG00000LMAN2	C5orf8	GF lectin, n protein-coding
chr5-179f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (NAluSc SIN	-20948	NM_14586f	4056	Hs.706741NM_14586f	ENSG00000CLTC4S		leukotric protein-coding	
chr6-736f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr6	73640998	73641879	+	0	NA	intron (Nintron (N	12554	NM_012434	26503	Hs.597422NM_012434	ENSG00000SLC17A5	AST	ISSD	solute c protein-coding
chr7-989f	8.20294	0.483132	0.820653	0.588717	0.556051	0.981636	chr7	98967821	98968810	+	0	NA									



chr11-655.8.341774	-0.47641	0.811779	-0.58687	0.557289	0.981636	chr11	65976547	65976756	+	0	NA	intron (NCpG)	14917	NM_00514E	9092	Hs.	50288E	NM_00514E	ENSG000003SART1	Aral HAF spliceos	protein-coding			
chr20-365.8.341774	-0.47641	0.811779	-0.58687	0.557289	0.981636	chr20	36927299	36929110	+	0	NA	intron (NAIuY SINE)	23504	NM_00136E	25939	Hs.	580681	NM_01547E	ENSG000003SAMH1	CHBL2 DCI	SAM and I	protein-coding		
chr1-551(8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr1	55104981	55106805	+	0	NA	intron (Nintron (N	65671	NR_110451	255738	Hs.	18844	NM_17493E	ENSG000003PCSK9	FH3 HCHOI	proprotein	protein-coding		
chr1-228(8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr1	2.28E+08	2.28E+08	+	0	NA	intron (Nintron (N	669	NM_001024	375	Hs.	286221	NM_00165E	ENSG000003ARF1	PVNH8	ADP ribos	protein-coding		
chr10-145.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr10	14565946	14569002	+	0	NA	intron (NL2 LINE L	4525	NM_00128E	83641	Hs.	44631E	NM_03145E	ENSG000003FAM107B	C10orf45	family wiprotein	protein-coding		
chr12-781.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr12	78129977	78130911	+	0	NA	intron (Nintron (N	229302	NR_135021	1.05E+08	Hs.	15689E	NR_135021	ENSG000003LINC02424-		long intencRNA			
chr14-103.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (NLIMS LINE	27400	NM_00112E	4140	Hs.	35828	NM_00237E	ENSG000003MARK3	CTAK1 KP7	microtub	protein-coding		
chr17-307.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr17	30766220	30769125	+	0	NA	intron (NAIuY SINE	57020	NM_01598E	51379	Hs.	64937E	NM_01598E	ENSG000003CRLF3	CREME-9	Cytokine	protein-coding		
chr18-587.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr18	58737841	58738231	+	0	NA	intron (Nintron (N	-66163	NM_00128E	1.02E+08	Hs.	64487E	NM_001289967	LOC101927-		uncharact	protein-coding		
chr2-290(8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (Nintron (N	50051	NM_01490E	2744	Hs.	11644E	NM_01490E	ENSG000003GLS	AAD20 CAS	glutamine	protein-coding		
chr2-231(8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (NL2c LINE	11405	NM_002807	5707	Hs.	3887	NM_002807	ENSG000003PSMD1	P112 Rpn2	proteasom	protein-coding		
chr21-348.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr21	34806405	34807863	+	0	NA	intron (NLIMCa LIN	61309	NR_03888E	1.01E+08	Hs.	12017E	NR_03888E	ENSG000003LINC0142E	lincRNA-u	long intencRNA			
chr5-528.8.375056	-0.4719	0.804379	-0.58666	0.557433	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (NL1PABA LI	183262	NM_00104E	6558	Hs.	16258E	NM_00104E	ENSG000003SLC12A2	BSC BSC2	solute c	protein-coding		
chr2-1905.7.939023	-0.4885	0.832674	-0.58666	0.557433	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	3' UTR (N3' UTR (N	51250	NM_01326E	6772	Hs.	64299E	NM_00731E	ENSG000003STAT1	CANDF 7	invalign t	protein-coding		
chr2-241(7.939023	-0.4885	0.832674	-0.58666	0.557433	0.981636	chr2	2.42E+08	2.42E+08	+	0	NA	5' UTR (N5' UTR (N	3583	NM_00133E	84289	Hs.	52917E	NM_03232E	ENSG000003ING5	p28 ING5	inhibitor	protein-coding		
chr13-20(8.316351	-0.48269	0.822943	-0.58654	0.557514	0.981636	chr13	20010067	20010352	+	0	NA	intron (NAIuSz SIN	50395	NR_14836E	7750	Hs.	50743E	NM_00345E	ENSG000003ZMY2	FIM MYM	fzinc fing	protein-coding		
chr17-68(10.61488	-0.42344	0.721988	-0.58649	0.557547	0.981636	chr17	68037239	68047066	+	0	NA	exon (NM exon (NM	6162	NM_00132E	3838	Hs.	59423E	NM_00226E	ENSG000003KPNA2	IPOA1 QIF	karyopher	protein-coding		
chr14-771.5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr14	77109803	77111033	+	0	NA	intron (Nintron (N	12160	NM_003342E	85457	Hs.	70906E	NM_03342E	ENSG000003C1PC	K1AA1737	CLOCK	inprotein-coding		
chr15-657.5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr15	65705273	65706849	+	0	NA	intron (Nintron (N	-9125	NR_14575E	1.1E+08	NR_14575E	ENSG000003SNORD13E		small nucs	ncRNA				
chr16-23(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr16	23067521	23068255	+	0	NA	3' UTR (N3' UTR (N	81382	NM_02071E	57478	Hs.	18381E	NM_02071E	ENSG000003CUSP3		ubiquitin	protein-coding		
chr17-31(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr17	31699919	31970750	+	0	NA	intron (Nintron (N	33327	NM_01535E	23512	Hs.	46273E	NM_01535E	ENSG000003SUZ12	CHET9 JJA	SUZ12	polprotein-coding		
chr18-46(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr18	46037368	46040055	+	0	NA	intron (NLTR83 LTF	33549	NM_02443E	9050	Hs.	56738E	NM_02443E	ENSG000003PSTPIP2	MAYP	proline-s	protein-coding		
chr2-947(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr2	9470401	9472561	+	0	NA	intron (Nintron (N	-3070	NM_00132E	285148	Hs.	66722E	NM_00103E	ENSG000003IAH1		isoamyl	protein-coding		
chr2-235(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr2	2.35E+08	2.35E+08	+	0	NA	intron (Nintron (N	-20740	NM_001371306	62084	NR_04633E	8603	Hs.	65236E	NR_00370E	ENSG000003FAM193A	C4orf8 RE	family wiprotein	protein-coding
chr4-2687(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr4	2687215	2687817	+	0	NA	intron (Nintron (N	-2578	NR_03032E	593178	NR_03032E	ENSG000003MIR593	MIRN593	lmiRNA	ncRNA				
chr7-128(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr7	28109909	28110712	+	0	NA	intron (Nintron (N	17171	NM_001284	55140	Hs.	49133E	NM_01809E	ENSG000003ELP3	KAT9	elongator	protein-coding		
chr8-281(5.452849	-0.57726	0.984273	-0.586483	0.557551	0.981636	chr8	37872098	37875949	+	0	NA	non-codiron-codir	-14431	NM_00595E	4520	Hs.	47199E	NM_00595E	ENSG000003MTF1	MTF-1 ZRF	mat reg	protein-coding		
chr1-3787(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	intron (NMER3 DNA	23566	NM_02301E	65123	Hs.	43872E	NM_02301E	ENSG000003INTS3	Clorf193	integrat	protein-coding		
chr1-157(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	3' UTR (N3' UTR (N	-3599	NR_00156E	360155	Hs.	49180E	NR_00156E	ENSG000003CYCSP52	H6C HPC2	CYCS	psseudo		
chr1-205(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr1	2.05E+08	2.05E+08	+	0	NA	intron (Nintron (N	-15917	NM_20337E	388730	Hs.	14692E	NM_20337E	ENSG000003TMEM81	HC3107 K	V transmem	protein-coding		
chr1-212(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	exon (NM exon (NM	30888	NM_01405E	28982	Hs.	7055	NM_01405E	ENSG000003FLVCR1	AXPC1 FLV	feline l	protein-coding		
chr12-52(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr12	52056822	52058076	+	0	NA	exon (NM exon (NM	6007	NM_173157	3164	Hs.	52443E	NM_00213E	ENSG000003NR4A1	GFRP1 HMF	nuclear	protein-coding		
chr13-45(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr13	45533920	45534830	+	0	NA	intron (Nintron (N	69436	NM_031431	83548	Hs.	50794E	NM_031431	ENSG000003COG3	SEC34	component	protein-coding		
chr15-421(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr15	42161592	42169868	+	0	NA	exon (NM exon (NM	-9094	NM_21360E	255189	Hs.	23187E	NM_21360E	ENSG000003PLA2G4F	PLA2G4F Z	phospholip	protein-coding		
chr16-574(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr16	57428553	57436688	+	0	NA	intron (Nintron (N	14765	NM_02031E	57019	Hs.	4900	NM_02031E	ENSG000003CIAPIN1	Anamorsz	cytokine	protein-coding		
chr17-42(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr17	42313733	42320560	+	0	NA	intron (Nintron (N	29090	NM_00128E	6776	Hs.	43705E	NM_00315E	ENSG000003STAT5A	MGF STAT	signal t	protein-coding		
chr18-35(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr18	35259999	35264821	+	0	NA	intron (Nintron (N	21361	NM_032347E	84307	Hs.	59106E	NM_032347E	ENSG000003ZNF397	ZNF47 ZS	zinc fing	protein-coding		
chr19-374(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr19	37458391	37455776	+	0	NA	5' UTR (N5' UTR (N	12561	NM_00133E	148266	Hs.	53114E	NM_15248E	ENSG000003ZNF569	ZNF47 ZNF	zinc fing	protein-coding		
chr2-156(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr2	15605303	15608972	+	0	NA	intron (Nintron (N	15269	NM_00493E	1653	Hs.	44059E	NM_00493E	ENSG000003DDX1	DBP-RB UK	DEAD-box	protein-coding		
chr2-4431(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr2	44316607	44324734	+	0	NA	3' UTR (N3' UTR (N	39079	NM_00104E	9581	Hs.	44434E	NM_00603E	ENSG000003PREPL	CMS22	prolyl	protein-coding		
chr2-4554(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr2	45541324	45542212	+	0	NA	intron (NMER52A LI	69499	NM_01807E	55133	Hs.	14229	NM_01807E	ENSG000003SRBD1		S1 RNA	biprotein-coding		
chr2-709(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr2	70988927	70989560	+	0	NA	intron (Nintron (N	5630	NM_14458E	113419	Hs.	51608E	NM_14458E	ENSG000003TEX261	TEG-261	testis	protein-coding		
chr4-122(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr4	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	44970	NM_00708E	11162	Hs.	55845E	NM_00708E	ENSG000003NUDT6	ASFGF2 F	ncudigen	protein-coding		
chr6-361(8.699528	-0.463057	0.789772	-0.586317	0.557662	0.981636	chr6	36108641	36110840	+	0	NA	3' UTR (N3' UTR (N	-20773	NR_07299E	5603									

chr2-1332	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-55504 NR_110294	1.02E+08	Hs.661917NR_110294	ENSG00000CNCAP5-AS-	NCKAP5	arncRNA
chr2-1897	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	non-codiron-codir	-3746 NR_148888	64172	Hs.60772	NM_022355	ENSG00000OSGEP11	OSGEP1 Qr0-sialog protein-coding
chr3-5006	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr3	50063142	50063632	+	0	NA	intron (NAluJb SIN	-25532 NM_005778	10181	Hs.43948	CNM_005778	ENSG00000CRBM5	G15 H37 IRNA bindi protein-coding
chr4-684	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr4	6843575	6845283	+	0	NA	intron (NAluSx SI	61697 NM_00110C	9778	Hs.79276	NM_014744	ENSG00000KIAA0232	- KIAA0232 protein-coding
chr4-4836	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr4	48382344	48382578	+	0	NA	intron (Nintron (N	40932 NM_002084C	57606	Hs.479677	NM_020844	ENSG00000SLAIN2	KIAA1458 SLAIN motif protein-coding
chr5-738	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr5	73833416	73835525	+	0	NA	intron (NLIAMA9 LIN	20924 NM_001244	64283	Hs.482521	NM_00108C	ENSG00000CARHGEP28	RGNFEP RIFRho guaniprotein-coding
chr6-1546	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr6	1.55E+08	1.55E+08	+	0	NA	intron (NMTRe SINE	-50005 NR_03610C	1E+08	NR_03610C	ENSG00000MIR1273C	- microRNA ncRNA	
chr7-4756	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr7	47562121	47564217	+	0	NA	intron (Nintron (N	18942 NM_022748	64759	Hs.520814	NR_022748	ENSG00000TNS3	TEM6 TENS tensin 3 protein-coding
chr9-123C	6.144942	-0.54349	0.932217	-0.58301	0.559887	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (N(ATTATAT)	34774 NR_030331	693185	NR_030331	ENSG00000MIR600	MIRN600 tmicroRNA ncRNA	
chr17-434	10.19456	-0.43621	0.748203	-0.58301	0.559888	0.981636	chr17	43401919	43402126	+	0	NA	TTS (NM_C TTS (NM_C	3029 NM_001661	379	Hs.183155	NM_001661	ENSG00000ARL4D	ARF4L ARLADP ribosprotein-coding
chr1-2402	8.39863	-0.47664	0.817562	-0.58301	0.559894	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (NMLTIJ LTF	192144 NM_020066	56776	Hs.24889	NM_020066	ENSG00000FMN2	- formin 2 protein-coding
chr12-622	8.39863	-0.47664	0.817562	-0.58301	0.559894	0.981636	chr12	6227734	6228026	+	0	NA	intron (Nintron (N	27480 NM_00176E	928	Hs.11428	CNM_00176E	ENSG00000CD9	BTCC-1 DFCD9 molecprotein-coding
chr18-505	6.60964	-0.59385	1.018667	-0.58297	0.559913	0.981636	chr18	50906372	50906767	+	0	NA	intron (NAluSx SIN	27451 NM_00239E	4200	Hs.233115	NM_00239E	ENSG00000CME2	ODS1 malic enzprotein-coding
chr4-1908	6.60964	-0.59385	1.018667	-0.58297	0.559913	0.981636	chr4	19818010	19804009	+	0	NA	3' UTR (N3' UTR (N	5658 NR_00300A	67770	Hs.676951	NR_00300A	ENSG00000SCARNA22	ACA11 small Ca_ncRNA
chr7-1587	6.60964	-0.59385	1.018667	-0.58297	0.559913	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	3' UTR (N3' UTR (N	-28040 NR_104054	54892	Hs.18616	NM_01776C	ENSG00000CNCAP2	3KS CAP-Non-SMC cprotein-coding
chr13-19F	8.128519	0.478892	0.82156	0.582905	0.559957	0.981636	chr13	19817890	19818299	+	0	NA	Intergeni Intergeni	-35058 NR_14905E	55269	Hs.21319E	NM_00104E	ENSG00000PSPC1	PSP1 paraspeck protein-coding
chr7-131C	10.128519	0.478892	0.82156	0.582905	0.559957	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (NFLAM_C SI	7775 NR_02415E	378805	Hs.15055E	NM_00108E	ENSG00000CLINC-PIN1	LINCncRNA-F long intncRNA
chr1-151E	6.60388	-0.42238	0.724735	-0.58281	0.560022	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	6935 NM_00133C	5298	Hs.63246E	NM_002651	ENSG00000P14KB	NPK1 P14 phosphatiprotein-coding
chr10-11F	5.493989	0.578726	0.993115	0.582738	0.560069	0.981636	chr10	1.14E+08	1.14E+08	+	0	NA	intron (NTiger1 E	-7073 NM_001267	840	Hs.9216	NM_001227	ENSG00000CASP7	CASP-7 Cn caspase 7 protein-coding
chr1-952	7.931165	-0.48682	0.835526	-0.58265	0.560132	0.981636	chr1	95246713	95246934	+	0	NA	exon (NM exon (NM	12613 NM_01548E	25950	Hs.48351E	NM_01548E	ENSG00000CRWD3	RSUME RWD motif protein-coding
chr14-554	7.931165	-0.48682	0.835526	-0.58265	0.560132	0.981636	chr14	55053983	55054437	+	0	NA	intron (NAluSx SI	2563 NM_14457E	93487	Hs.59433E	NM_14457E	ENSG00000MAPK11P11	C14orf32 mitogen-e protein-coding
chr14-584	7.931165	-0.48682	0.835526	-0.58265	0.560132	0.981636	chr14	58409875	58410723	+	0	NA	intron (NAluJb SIN	14369 NM_207377	387990	Hs.592307	NM_207377	ENSG00000TOMM20L	UNQ9438 transloc protein-coding
chr2-204	7.931165	-0.48682	0.835526	-0.58265	0.560132	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (NAluY SINE	40767 NM_21358E	65059	Hs.47116E	NM_02525E	ENSG00000CRAPH1	ALS2CR18 Bas assoc protein-coding
chr7-1004	7.931165	-0.48682	0.835526	-0.58265	0.560132	0.981636	chr7	1E+08	1E+08	+	0	NA	TTS (NM_C TTS (NM_C	2411 NM_14503C	221908	Hs.41335E	NM_14503C	ENSG00000PPP1R35	C7orf47 protein iprotein-coding
chr12-417	3.973533	-0.67555	1.159506	-0.58262	0.560149	0.981636	chr12	417726	418602	+	0	NA	intron (NAluS26 SI	16520 NM_00113C	84318	Hs.63165E	NM_03235E	ENSG00000CCDC77	- coiled-c protein-coding
chr9-1364	3.973533	-0.67555	1.159506	-0.58262	0.560149	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	TTS (NM_C TTS (NM_C	11232 NM_00131E	56623	Hs.12099E	NM_01989E	ENSG00000INPP5E	CORS1 CPI inositol protein-coding
chr10-104	8.69352	0.475473	0.816195	0.582548	0.560197	0.981636	chr10	1041379	1042037	+	0	NA	intron (Nintron (N	7178 NM_001317	3422	Hs.28365E	NM_00450E	ENSG00000ID11	IPPI1 IPPI isopenter protein-coding
chr15-34F	7.805897	-0.50809	0.872524	-0.58233	0.560347	0.981636	chr15	34900599	34900810	+	0	NA	exon (NM exon (NM	69038 NM_014691	9716	Hs.51095E	NM_014691	ENSG00000AQR	IBP160 f aquarius protein-coding
chr13-727	5.206313	-0.62195	1.068093	-0.5823	0.560364	0.981636	chr13	72798900	72799099	+	0	NA	intron (N L2a LINE	16866 NR_14620E	10464	Hs.44192E	NM_00634E	ENSG00000PIBF1	C13orf24 progester protein-coding
chr12-641	8.333916	-0.47492	0.815824	-0.58214	0.560472	0.981636	chr12	64111149	64111989	+	0	NA	intron (Nintron (N	110227 NM_00130C	144577	Hs.444671	NM_15244C	ENSG00000C12orf66	- chromoson protein-coding
chr8-118E	8.333916	-0.47492	0.815824	-0.58214	0.560472	0.981636	chr8	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	2881 NM_00254E	4982	Hs.81791	NM_00254E	ENSG00000TNFRSF11E	OCIF OPG TNF rece protein-coding
chr11-337	9.192727	-0.47706	0.819509	-0.58213	0.560476	0.981636	chr11	33711209	33711536	+	0	NA	intron (N LMB7 LIN	-10632 NM_00116E	1E+08	Hs.70946E	NM_00116E	ENSG00000C11orf91	- chromoson protein-coding
chr12-11F	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr12	1.16E+08	1.16E+08	+	0	NA	3' UTR (N3' UTR (N	187565 NR_030351	693205	NR_030351	ENSG00000MIR620	MIRN620 tmicroRNA ncRNA	
chr13-75E	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr13	75584400	75585242	+	0	NA	intron (N LIMEf LIN	35071 NM_00600E	7347	Hs.162241	NM_00600E	ENSG00000UCHL3	UCH-L3 ubiquitir protein-coding
chr16-67E	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr16	67549091	67542213	+	0	NA	intron (Nintron (N	4140 NM_00119E	79567	Hs.152717	NM_02451E	ENSG00000RIPOR1	FAM65A RHO fam protein-coding
chr19-17E	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr19	17269903	17270917	+	0	NA	intron (NAluY SINE	2530 NM_01417E	29086	Hs.19072E	NM_01417E	ENSG00000BABAM1	C19orf62 BRISC anc protein-coding
chr2-127E	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	3' UTR (N3' UTR (N	11089 NM_00480E	5433	Hs.71534E	NM_00480E	ENSG00000POLR2D	HSRBP4 HSRNA polyn protein-coding
chr3-119E	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr3	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	19497 NM_01658E	51300	Hs.477287	NM_01658E	ENSG00000TIMMDC1	C3orf1 MC transloc protein-coding
chr7-1521	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	exon (NM exon (NM	75938 NM_001371474	157769	Hs.459174	NM_14496E	ENSG00000CFAM91A1	- family wiprotein-coding
chr8-1237	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr8	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	6901 NM_14496E	157769	Hs.459174	NM_14496E	ENSG00000CFAM91A1	- family wiprotein-coding
chr9-207E	8.666247	0.46014	0.790438	0.582133	0.560477	0.981636	chr9	20767282	20767592	+	0	NA	intron (N LIP2 LIN	-19490 NR_14576E	1.1E+08	NR_14576E	ENSG00000SNORA30B	- small nucsnoRNA	
chr18-48E	5.740341	-0.58165	0.999234	-0.5821	0.560501	0.981636	chr18	48577112	48577626	+	0	NA	intron (Nintron (N	38338 NM_00114E	9811	Hs.14523C	NM_01477E	ENSG00000CTIF	Gm672 K1 cap bindi protein-coding
chr1-3104	8.136377	0.476981	0.819506	0.582035	0.560543	0.981636	chr1	31044228	31044729	+	0	NA	intron (N LIMB8 LIN	21239 NM_00102C	9698	Hs.281707	NM_01467E	ENSG00000PUM1	HSPUM PUM pumilio f protein-coding
chr13-32E	8.136377	0.476981	0.819506	0.582035	0.560543	0.981636	chr13	32521010	32522194	+	0	NA	intron (Nintron (N	-12207 NR_02692E	116828	Hs.658751	NR_02692E	ENSG00000N4BP2L2-1	CG030 N4BP2L2 irncRNA
chr18-57E	8.136377	0.476981	0.819506	0.582035	0.560543	0.981636	chr18	57690100	57697299	+	0	NA	intron (Nintron (N	66323 NM_001242	1.01E+08	Hs.66064E	NM_001242804	LOC100505E-	uncharact protein-coding
chr19-43E	8.136377	0.476981	0.819506	0.582035	0.560543	0.981636	chr19	43631092	43630333	+	0	NA	intron (Nintron (N	18535 NM_03288E	84954	Hs.32168E	NM_03288E	ENSG00000MPND	- MPN doma protein-coding
chr1-148E	12.96296	0.386507	0.664106	0.581996	0.56057	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	10745 NM_01538E	25832	Hs.53467E	NM_01538E	ENSG00000NBPF14	DJ328E19.NBPF mem protein-coding
chr9-9410	10.60702	-0.42218	0.725775	-0.58169	0.560773	0.981636	chr9	94175905	94177076	+	0	NA	TTS (NR_C TTS (NR_C	143 NR_02948E	406888	NR_02948E	ENSG00000MIRLET7F1	LET7F1 MI microRNA ncRNA	
chr2-460E	8.658389	0.461941	0.794255	0.581603	0.560834	0.981636	chr2	46093005	46095365	+	0	NA	intron (N HAL1 LINE	-203222 NM_00143C	2034	Hs.46841	NR_00143C	ENSG00000EPAS1	ECTY4 HIF endotheliprotein-coding
chr4-1077	8.658389	0.461941	0.794255	0.581603	0.560834	0.981636	chr4	1.08E+08	1.08E+08	+	0	NA	intron (N LIM48 LIN	14331 NM_00544C	9061	Hs.36861	CNM_00544C	ENSG00000PAPSS1	ATPSK1 PA3'-phos protein-coding
chr1-421E	5.58364	-0.60371	1.038089	-0.58156	0.560863	0.981636	chr1	42190090	42190289	+	0	NA	intron (Nintron (N	-25444 NM_03355E	2980	Hs.778	NM_03355E	ENSG00000	



chrX-1421	8.674105	0.458342	0.790607	0.579735	0.562094	0.981636	chrX	1421320	1423823	+	0	NA	intron (Nintron (N	22040 NR_02671C	80161 Hs. 521855	ENM_025091	ASMTL-AS1	ASMTL-AS	ASMTL antncRNA
chr10-885	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr10	88935132	88935817	+	0	NA	non-codiron-codir	2790 NR_125377	1E+08	NR_125377	ENSG000002	ACTA2-AS1	UC001kfo ACTA2 antncRNA
chr17-28C	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr17	28070097	28070624	+	0	NA	intron (NAluSc SIN	27683 NM_016231	51701 Hs. 208755	ENM_016231	ENSG000002	CNKLK	nemo like protein-coding
chr2-2061	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr2	2.06E+08	2.06E+08	+	0	NA	3' UTR (N3' UTR (N	-7496 NR_033248	1E+08	Hs. 356055	ENR_033248	GCSHP3	glycine cpsudo
chr20-344	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr20	34428611	34429415	+	0	NA	intron (NAluSz SIN	-37312 NR_030374	693228	NR_030374	ENSG000002	MIR644A	MIR644 miRNA ncRNA
chr3-124F	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr3	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	46212 NM_002213	3693 Hs. 13155	NM_002213	ENSG000002	ITGB5	integrin protein-coding
chr6-565F	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr6	56557371	56557680	+	0	NA	intron (Nintron (N	85364 NM_015548	667 Hs. 60491	ENM_001723	ENSG000002	DST	BP240 BP240 dystonin protein-coding
chr9-271F	8.35934	-0.46886	0.809602	-0.57913	0.562503	0.981636	chr9	27184831	27186169	+	0	NA	exon (NM exon (NM	76359 NM_000456	7010 Hs. 89409	ENM_000456	ENSG000002	TEK	CD202B GLTEK receptor protein-coding
chr1-5207	5.634488	-0.58441	1.009552	-0.57888	0.562672	0.981636	chr1	52078219	52079183	+	0	NA	intron (N L2c LINE	22406 NM_152265	91408 Hs. 42983	ENM_152265	ENSG000002	BTF3L4	basic trypsin protein-coding
chr9-8161	5.634488	-0.58441	1.009552	-0.57888	0.562672	0.981636	chr9	81615786	81616002	+	0	NA	intron (Nintron (N	73641 NM_001303	7088 Hs. 11702	NM_005077	ENSG000002	TLE1	ESG ESG1 TLE1 family protein-coding
chr1-9231	5.701051	-0.57078	0.986175	-0.57878	0.562774	0.981636	chr1	92312474	92313213	+	0	NA	intron (NAluSz6 SI	13784 NM_024813	79871 Hs. 444421	NM_024813	ENSG000002	CRPAP2	C1orf82 FRNA polyn protein-coding
chr16-464	5.701051	-0.57078	0.986175	-0.57878	0.562774	0.981636	chr16	46471	47437	+	0	NA	3' UTR (N3' UTR (N	6654 NM_01631C	51728 Hs. 63222	ENM_01631C	ENSG000002	POLR3K	C11 C11-FRNA polyn protein-coding
chr1-183	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr1	1830872	1831714	+	0	NA	intron (NAluJr SIN	-51262 NM_001353	65220 Hs. 65479	ENM_023018	ENSG000002	NADK	dJ283E3. INAD kinase protein-coding
chr1-192C	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr1	21928183	21929397	+	0	NA	intron (NAluSp SIN	8520 NM_001291	3339 Hs. 562227	ENM_005525	ENSG000002	HSPG2	HSPG PLC heparan s protein-coding
chr1-9336	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr1	93360626	93361173	+	0	NA	3' UTR (N3' UTR (N	14992 NM_001938	1810 Hs. 34841	ENM_001938	ENSG000002	CDR1	NC2 NC2-F down-reg protein-coding
chr13-24F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr13	24505343	24506761	+	0	NA	intron (N LTR12C LI	6726 NM_006437	143 Hs. 74485	ENM_006437	ENSG000002	PARP4	ADPRTL1 poly (ADP- protein-coding
chr13-11C	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	2908 NM_00184E	1284 Hs. 50871	ENM_00184E	ENSG000002	COL4A2	BSVD2 ICF collagen protein-coding
chr14-67C	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr14	67371747	67372315	+	0	NA	intron (NAluJo SIN	11703 NM_004094	1965 Hs. 15177	ENM_004094	ENSG000002	E1F2S1	E1F-2 EIF eukaryot protein-coding
chr14-104	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	exon (NM exon (NM	16417 NM_022489	64423 Hs. 24956	NM_022489	ENSG000002	INF2	C14orf151 inverted protein-coding
chr15-75F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr15	75704427	75705828	+	0	NA	intron (Nintron (N	7721 NM_001897	1464 Hs. 51304	ENM_001897	ENSG000002	CSPG4	HMW-MAA chondroitin protein-coding
chr16-191	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr16	19120169	19120945	+	0	NA	non-codiron-codir	6593 NR_028028	162073 Hs. 53089	ENM_001034	ENSG000002	ITPR1PL2	ITPRIP1 IPR protein-coding
chr16-64F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr16	64989600	64990690	+	0	NA	intron (Nintron (N	131918 NM_001797	1009 Hs. 116471	NM_001797	ENSG000002	CDH11	CAD11 CD1 cadherin protein-coding
chr17-61	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr17	61741534	61742821	+	0	NA	intron (N Tigger1 I	121382 NM_032043	83990 Hs. 12890	ENM_032043	ENSG000002	CBR1P1	BACHI FANBRCA1 int protein-coding
chr18-232	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr18	23203966	23204580	+	0	NA	intron (Nintron (N	48448 NM_138375	91768 Hs. 11108	NM_138375	ENSG000002	CABLE1	CABL1 CAF Cdk5 and protein-coding
chr19-27F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr19	2790894	2791798	+	0	NA	intron (Nintron (N	5843 NM_003245	7064 Hs. 78769	NM_003245	ENSG000002	THOP1	EP24.15 thimet ol protein-coding
chr19-211	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr19	21150918	21153232	+	0	NA	intron (N PABL_A-ir	10035 NM_133473	170959 Hs. 15625	ENM_133473	ENSG000002	ZNF431	zinc fing protein-coding
chr2-856C	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr2	85609197	85610001	+	0	NA	intron (Nintron (N	2467 NM_001013	388969 Hs. 51615	ENM_001013	ENSG000002	C2orf68	HRCN81 chromosom protein-coding
chr2-134F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (N LIME3B LI	5527 NM_001241	905 Hs. 74411	ENM_001241	ENSG000002	CCNT2	CYCT2 cyclin T2 protein-coding
chr3-370C	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr3	37028068	37028954	+	0	NA	intron (Nintron (N	35161 NM_001258	4292 Hs. 19536	ENM_00024E	ENSG000002	MLH1	COCA2 FCC mutL homc protein-coding
chr5-746F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr5	74693708	74694408	+	0	NA	intron (Nintron (N	8510 NM_000521	3074 Hs. 69293	NM_000521	ENSG000002	HEXB	ENC-1AS F hexosamin protein-coding
chr5-157F	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr5	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	53259 NM_173491	134353 Hs. 23648	NM_173491	ENSG000002	LSM11	LMS11, U7 protein-coding
chr6-175C	6.178223	-0.53742	0.928663	-0.57871	0.562787	0.981636	chr6	17507530	17508974	+	0	NA	intron (Nintron (N	3013 NR_110855	1.02E+08	Hs. 62287	ENR_110855	LOC101928	uncharacterncRNA
chr17-205	12.90425	0.381106	0.658798	0.578486	0.562936	0.981636	chr17	20305940	20307993	+	0	NA	intron (N LIME1 LI	-14208 NR_02338C	348254 Hs. 46247	ENR_02338C	CCDC144C	CCDC144C coiled-cp pseudo	
chr1-3601	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr1	36014536	36015061	+	0	NA	intron (Nintron (N	-69296 NM_014466	27285 Hs. 12711	NM_014466	ENSG000002	TEKT2	TEKTB1 Tf tektin 2 protein-coding
chr1-113F	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr1	1.14E+08	1.14E+08	+	0	NA	intron (N (A)n Simp	-4897 NM_001319	64858 Hs. 59141	ENM_02283E	ENSG000002	DCLRE1B	APOLLO SN DNA cross protein-coding
chr10-876	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr10	875874	876209	+	0	NA	intron (N ASTC-int	55664 NM_001351	23185 Hs. 15906	ENM_001351	ENSG000002	LARP4B	KIAA0217 La ribon protein-coding
chr10-877	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr10	87718358	87719332	+	0	NA	intron (Nintron (N	58967 NM_00101E	9060 Hs. 52449	ENM_00467C	ENSG000002	PAPSS2	ATPSK2 BC3'-phosp protein-coding
chr11-47C	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr11	47618443	47620182	+	0	NA	intron (NAluSz SIN	23227 NM_014342	23788 Hs. 26994	ENM_014342	ENSG000002	MTCH2	HSPC032 mitochohc protein-coding
chr19-101	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr19	10124741	10125946	+	0	NA	IntergeniAluXs LI	-5444 NM_00375E	8666 Hs. 52905	ENM_00375E	ENSG000002	EIF3G	EIF3-P42 eukaryot protein-coding
chr2-393C	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr2	39361928	39363452	+	0	NA	intron (N LIMB1 LI	74595 NM_00361E	8491 Hs. 65575	ENM_00361E	ENSG000002	MAP4K3	GLK MAPK mitom-ε protein-coding
chr2-2267	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr2	2.27E+08	2.27E+08	+	0	NA	intron (Nintron (N	7889 NM_005544	3667 Hs. 47150	ENM_005544	ENSG000002	IRS1	HIRS-1 insulin l protein-coding
chr2-2377	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	exon (NM exon (NM	43070 NM_00473E	9208 Hs. 47177	ENM_00473E	ENSG000002	LRRFIP1	FLAP-1 FL LRR bindi protein-coding
chr20-347	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr20	34740935	34742140	+	0	NA	exon (NM exon (NM	36818 NM_00132E	58476 Hs. 51699	ENM_02120E	ENSG000002	TP53INP2	C20orf11C tumor prc protein-coding
chr21-391	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr21	39193198	39194064	+	0	NA	3' UTR (N3' UTR (N	-10117 NM_020343	8624 Hs. 47383	ENM_00372C	ENSG000002	PSMG1	C21LRP DS proteasom protein-coding
chr3-5254	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr3	52540185	52542401	+	0	NA	3' UTR (N3' UTR (N	4688 NM_001124	440957 Hs. 60577	ENM_001124	ENSG000002	CSM1M4	C3orf78 small int protein-coding
chr3-112F	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	3' UTR (N3' UTR (N	17530 NR_10977E	1.01E+08	Hs. 86538	NR_10977E	LINC0127E	long intncRNA
chr5-1511	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	2051 NM_001363	309 Hs. 41211	NM_00115E	ENSG000002	ANXA6	ANX6 CBP annexin f protein-coding
chr5-177F	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	35440 NM_001031	53917 Hs. 16258	NM_130781	ENSG000002	CAB2	ARB24, me protein-coding
chr7-3064	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr7	30645206	30645526	+	0	NA	IntergeniL2a LINE	37090 NM_00188E	1395 Hs. 54624	ENM_00188E	ENSG000002	CRHR2	CRF-RB CF corticot protein-coding
chr9-702F	6.137084	-0.54149	0.936302	-0.57833	0.563042	0.981636	chr9	70286902	70287546	+	0	NA	intron (N HAL LINE	28246 NM_01511C	23137 Hs. 53418	ENM_01511C	ENSG000002	SMC5	SMC5L1 structure protein-coding
chr14-504	11.10777	-0.41426	0.716313	-0.57832	0.563045	0.981636	chr14	50420281	50420861										

chr3-1465.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr3	1.47E+08	1.47E+08	+	0	NA	intron (Nintron (N	13874 NM_001363	5359 Hs. 130755NM_02110f	ENSG00000PLSCR1	MMTRA1B	phospholipin-protein-coding
chr3-197.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (Nintron (N	-35196 NM_03331f	4241 Hs. 184727NM_00592f	ENSG00000MELTF	CD228 [MAF melanotransferin protein-coding	
chr4-757.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr4	757515	758218	+	0	NA	intron (NLMed LIN	23982 NR_036511	1E+08 Hs. 731755NR_036511	ENSG00000CLOC10012f	uncharacterized ncRNA	
chr4-171.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr4	1710441	1710853	+	0	NA	intron (NMER4C LTF	1672 NM_001130	7884 Hs. 29834fNM_00652f	ENSG00000SLBP	HBP stem-loop-protein-coding	
chr4-399.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr4	3990219	39902770	+	0	NA	intron (Nintron (N	75427 NM_001100	23244 Hs. 331431NM_01520f	ENSG00000PDS5A	PIG54 [SCC PDS5 core-protein-coding	
chr4-554.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr4	55486242	55486909	+	0	NA	intron (NHAL1 LINE	59357 NM_001267	9575 Hs. 43697fNM_00489f	ENSG00000CLOCK	KAT13D [bClock circ-protein-coding	
chr4-147.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr4	1.48E+08	1.48E+08	+	0	NA	intron (Nintron (N	94091 NR_039962	1.01E+08 NR_039962	ENSG00000MIR4799	microRNA ncRNA	
chr6-373.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr6	37362557	37362557	+	0	NA	intron (NMIR3 SINE	7948 NR_046395	9025 Hs. 48527fNM_00395f	ENSG00000RNFB	hRNFB ring finger-protein-coding	
chr6-110.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr6	1.1E+08	1.1E+08	+	0	NA	intron (NLM3 LIN	38417 NM_015891	51362 Hs. 428147NM_015891	ENSG00000CDDC40	EBH3 [PRP1 cell divi-protein-coding	
chr7-248.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr7	24871241	24871836	+	0	NA	intron (Nintron (N	21083 NR_104111	26031 Hs. 52025fNM_01555f	ENSG00000OSBPL3	ORP-3 [ORF oxysterol-protein-coding	
chr7-102.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (NAluSq2 SI	3054 NM_001371100				
chr8-233.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr8	23394552	23395217	+	0	NA	intron (NLM8 LIN	9236 NM_00231f	4017 Hs. 626637NM_00231f	ENSG00000CLOXL2	LOR [LOR2] lysyl oxiprotein-coding	
chr8-421.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chr8	42166533	42169523	+	0	NA	intron (Nintron (N	14965 NM_00680f	10947 Hs. 65452fNM_00680f	ENSG00000AP3M2	AP47B [CLA adaptor r-protein-coding	
chrX-273.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chrX	2739454	2743514	+	0	NA	TTS (NM_C TTS (NM_C	-10568 NM_001141	7499 Hs. 17967fNM_17556f	ENSG00000CXG	PBDX Xg glycoprotein-coding	
chrX-154.6.170365	-0.53541	0.928577	-0.57659	0.564218	0.981636	chrX	1.55E+08	1.55E+08	+	0	NA	non-codirnon-codir	-1599 NR_00296f	677817 Hs. 689704NR_00296f	ENSG00000SNORA36A	ACA36 small nucsnRNA	
chr15-77.4.856744	-0.49462	0.857964	-0.57651	0.564273	0.981636	chr15	77459459	77459658	+	0	NA	intron (NLa2 LINE	38670 NM_001304	10363 Hs. 69594 NM_01820f	ENSG00000HMG20A	HMGX1 [HMC high mobiprotein-coding	
chr16-59.10.54046	-0.4293	0.74469	-0.57648	0.564291	0.981636	chr16	53185668	53185872	+	0	NA	intron (NTHEIC-int	-22195 NM_001352	80205 Hs. 59159 NM_01528f	ENSG00000CHD9	AD013 [CHE chrodon protein-coding	
chr15-59.7.923307	-0.48505	0.841494	-0.57642	0.564335	0.981636	chr15	59207784	59208032	+	0	NA	exon (NM exon (NM	1065 NM_03319f	92483 Hs. 307052NM_03319f	ENSG00000LDHAL6B	LDH6B [LDF lactate c-protein-coding	
chr5-336.4.923307	-0.48505	0.841494	-0.57642	0.564335	0.981636	chr5	33645248	33645447	+	0	NA	intron (NLMed LIN	204571 NR_04767f	6897 Hs. 48186fNM_15229f	ENSG00000TARS	ThRS thronyl-protein-coding	
chr1-155.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (Nintron (N	-7431 NR_03028f	693140 NR_03028f	ENSG00000MIR555	MIRN555 [microRNA ncRNA	
chr1-173.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr1	1.74E+08	1.74E+08	+	0	NA	intron (Nintron (N	41000 NM_001171	91687 Hs. 53185fNM_03331f	ENSG00000CENPL	Clorf155 [centromer-protein-coding	
chr1-231.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr1	2.32E+08	2.32E+08	+	0	NA	intron (NChar1e1f	14002 NM_00599f	7257 Hs. 13318 NM_00599f	ENSG00000TSNAX	C3PO [TRAX translin protein-coding	
chr10-10.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (NAluSz LIN	94621 NM_001351	22978 Hs. 97439 NM_01222f	ENSG00000CNT5C2	GMP [NT5B] 5'-nuclec-protein-coding	
chr13-11.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (NLMC4a SI	5536 NM_001352	79587 Hs. 50872fNM_02453f	ENSG00000CAR52	COXP27 [cysteinyln-protein-coding	
chr2-227.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr2	2.28E+08	2.28E+08	+	0	NA	intron (NLP1A5 LIN	72741 NR_14901f	729968 Hs. 68955fNR_14901f	LOC72996f	spore coacncRNA	
chr2-30.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr2	30931390	30937385	+	0	NA	intron (Nintron (N	12079 NR_02692f	150291 Hs. 59220fNM_15304f	ENSG00000MORC2-AS1	C22orf27 [MORC2 antncRNA	
chr4-56.9.203974	0.443477	0.769568	0.576268	0.564434	0.981636	chr4	5661250	5662008	+	0	NA	intron (Nintron (N	46930 NR_147127	132884 Hs. 87306 NM_147127	ENSG00000EVC2	LBN [WAD Evc antic-protein-coding	
chr14-95.9.237256	0.446319	0.774681	0.576132	0.564526	0.981636	chr14	95095531	95096369	+	0	NA	exon (NM exon (NM	37553 NM_00119f	23405 Hs. 87889 NM_03062f	ENSG00000D1CER1	DDC1 [Dicedicer 1, protein-coding	
chr17-40.9.237256	0.446319	0.774681	0.576132	0.564526	0.981636	chr17	4095202	4097148	+	0	NA	intron (Nintron (N	46855 NM_01511f	23140 Hs. 277624NM_01511f	ENSG00000ZZEF1	ZZF4 zinc fing-protein-coding	
chr2-241.2.427426	0.570004	0.989579	0.576007	0.564611	0.981636	chr2	2.41E+08	2.41E+08	+	0	NA	intron (Nintron (N	-18081 NM_00110f	4735 Hs. 71234NM_00440f	ENSG00000SEPTIN2	DDZ4 [NEI septin 2 protein-coding	
chr11-10.11.10962	-0.40609	0.705059	-0.57597	0.564635	0.981636	chr11	1.09E+08	1.09E+08	+	0	NA	intron (NLMCa LIN	43005 NM_00439f	1662 Hs. 59193fNM_00439f	ENSG00000CDDX10	Ddp4 [HRH-DEAD-box protein-coding	
chr3-194.11.10962	-0.40609	0.705059	-0.57597	0.564635	0.981636	chr3	1.95E+08	1.95E+08	+	0	NA	intron (NCpG	2916 NM_13839f	93109 Hs. 47872fNM_13839f	ENSG00000TMEM44	transment-protein-coding	
chr2-471.2.4897556	0.609716	1.058841	0.575833	0.564728	0.981636	chr2	47127637	47127836	+	0	NA	TTS (NM_C TTS (NM_C	27572 NM_17364f	285051 Hs. 53157fNM_17364f	ENSG00000STPG4	C2orf61 [cspemr-taiprotein-coding	
chr1-233.17.588	0.330646	0.574287	0.575752	0.564783	0.981636	chr1	23359518	23367155	+	0	NA	intron (NAluSx4 SI	5050 NM_03063f	80818 Hs. 29379fNM_03063f	ENSG00000ZNF436	ZNF [Zfp4 zinc fing-protein-coding	
chr1-120.22.28746	0.300044	0.521247	0.576228	0.564866	0.981636	chr1	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	19704 NR_10408f	1.02E+08 NR_10408f	ENSG00000RNVU1-19	RNU1-126 [RNA, varisnRNA	
chr17-28.9.188259	0.446952	0.776498	0.575599	0.564886	0.981636	chr17	28328797	28330149	+	0	NA	TTS (NM_C TTS (NM_C	5999 NM_001267	90410 Hs. 70543fNM_17488f	ENSG00000IFT20	IFT20 - intraflag-protein-coding	
chr1-915.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr1	9158793	9159764	+	0	NA	intron (Nintron (N	-7501 NR_02961f	407040 NR_02961f	ENSG00000MIR34A	MIRN34A [microRNA ncRNA	
chr1-170.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr1	1.71E+08	1.71E+08	+	0	NA	IntergeniMLTIH LTF	-26287 NR_12595f	1.02E+08 Hs. 67666fNR_12595f	GORAB-AS1	GORAB antncRNA	
chr1-201.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr1	2.02E+08	2.02E+08	+	0	NA	intron (Nintron (N	-4432 NM_001167	89796 Hs. 58537fNM_02044f	ENSG00000NAV1	POMF1L3 [sneuron r-protein-coding	
chr14-49.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr14	49719423	49721092	+	0	NA	intron (NAluSx SIN	27137 NM_17219f	122773 Hs. 50925fNM_17219f	ENSG00000KLHDC1	MSTO25 kelch don-protein-coding	
chr15-48.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr15	48573794	48575259	+	0	NA	intron (Nintron (N	71262 NM_00013f	2200 Hs. 59113fNM_00013f	ENSG00000FBN1	ACM1C [EC fibryllin-protein-coding	
chr2-30.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr2	30533974	30534502	+	0	NA	intron (N(TC)n SIN	86992 NM_001304	253558 Hs. 46804fNM_18255f	ENSG00000LCLAT1	IAGPAT8 [lysocardiprotein-coding	
chr2-46.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr2	46548654	46549668	+	0	NA	intron (Nintron (N	-6584 NM_00131f	90423 Hs. 43769fNM_08065f	ENSG00000ATP6V1E2	ATP6E1 [A1ATPase H+protein-coding	
chr2-29.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr2	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	164780 NM_00527f	2736 Hs. 11186fNM_00527f	ENSG00000GLI2	CJS [HP9] GLI fami1-protein-coding	
chr2-22.9.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr2	29738831	29743102	+	0	NA	intron (Nintron (N	20963 NM_18252f	164633 Hs. 64360fNM_18252f	ENSG00000CABP7	CALN2 calcium t-protein-coding	
chr6-44.5.468565	0.571442	0.993051	0.575441	0.564993	0.981636	chr6	44299992	44301264	+	0	NA	exon (NM exon (NM	-2930 NM_18253f	202500 Hs. 18918fNM_18253f	ENSG00000TCTE1	D6S46 [DRC t-complex-protein-coding	
chr5-49.23.38834	0.296368	0.515144	0.575311	0.565081	0.981636	chr5	49419249	49419511	+	0	NA	IntergeniALR Alpha	1021908 NM_19844f	133418 Hs. 56141fNM_19844f	ENSG00000EMB	GP70 embgin protein-coding	
chr12-27.7.606507	0.495743	0.861751	0.575274	0.565106	0.981636	chr12	2797716	2798010	+	0	NA	exon (NM exon (NM	2893 NM_002014	2288 Hs. 52418fNM_002014	ENSG00000FKBP4	FKBP51 [FKBP prol-protein-coding	
chr16-28.12.2652	-0.39933	0.694638	-0.57487	0.56538	0.981636	chr16	28209699	28209033	+	0	NA	intron (Nintron (N	3099 NM_015171	23214 Hs. 46046fNM_015171	ENSG00000XPO6	EXP6 [RAN exportin protein-coding	
chr17-13.11.106848	-0.40824	0.710529	-0.57456	0.565587	0.981636	chr17	13495978	13496965	+	0	NA	exon (NM exon (NM	47175 NR_03167f	1E+08 NR_03167f	ENSG00000MIR548H3	MIR548H-3 [microRNA ncRNA	



chr13-951.9.170693	0.440688	0.770616	0.571864	0.567414	0.981636	chr13	95192724	95194733	+	0 NA	intron (NLTR45B LI	-16616 NR_145733	1.E+08	NR_145733	SNORD13G	-	small ncRNA
chr2-607.9.170693	0.440688	0.770616	0.571864	0.567414	0.981636	chr2	60767999	60768551	+	0 NA	intron (NAluSq2 SI	12007 NM_022894	64895 Hs.	387471 NM_022894	ENSG000002PAPOLG	-	poly (A) protein-coding
chr5-176.9.170693	0.440688	0.770616	0.571864	0.567414	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	non-codir non-codir	37801 NM_01629C	51720 Hs.	232721 NM_01629C	ENSG000002UIMC1	RAP80 X2f	ubiquitin protein-coding
chr7-128.9.170693	0.440688	0.770616	0.571864	0.567414	0.981636	chr7	1.29E+08	1.29E+08	+	0 NA	intron (Nintron (N	28586 NM_001364	3663 Hs.	521181 NM_03264C	ENSG000002IRF5	SLEB10	interferon protein-coding
chr9-1281.9.170693	0.440688	0.770616	0.571864	0.567414	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	10597 NM_001131	25792 Hs.	21239E NM_012127	ENSG000002C1Z1	LSFR1 NPECDKNA1	ir protein-coding
chr3-370.7.680929	0.499944	0.874342	0.571794	0.567462	0.981636	chr3	37051263	37051540	+	0 NA	TTS (NM_C TTS (NM_C	58051 NM_00125E	4292 Hs.	195364 NM_00024E	ENSG000002MLH1	COCA2 FCCmutL	homc protein-coding
chr1-120.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr1	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	7057 NM_001351	1.01E+08	Hs. 53467E NM_001351	ENSG000002NBPF26	-	NBPF memt protein-coding
chr11-79.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr11	7999527	8000107	+	0 NA	3' UTR (N3' UTR (N	12480 NM_003754	8665 Hs.	51602E NM_003754	ENSG000002EIF3F	EIF355 MF	eukaryoti protein-coding
chr12-26.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr12	26921664	26925138	+	0 NA	intron (Nintron (N	14580 NM_018164	55726 Hs.	505077 NM_018164	ENSG000002INTS13	ASUN C12c	integratc protein-coding
chr12-96.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr12	96319653	96320521	+	0 NA	intron (NLP2A LIN	64589 NM_001303	2004 Hs.	46523 NM_00523C	ENSG000002ELK3	ERP NET SETS	transprotein-coding
chr12-107.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr12	1.08E+08	1.08E+08	+	0 NA	IntergeniLIMEg LIN	-21212 NR_120474	1.02E+08	Hs. 66702E NR_120474	ENSG000002LOC101929	-	uncharactncRNA
chr12-11.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr12	1.16E+08	1.16E+08	+	0 NA	intron (Nintron (N	142923 NR_030351	693205	NR_030351	ENSG000002MIR620	MIRN620 f	microRNA ncRNA
chr13-7.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr13	72717550	72718833	+	0 NA	intron (NMLT1B LTF	9438 NM_001071	440145 Hs.	28465 NM_001071	ENSG000002MZT1	C13orf37 mitotic	sprotein-coding
chr13-92.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr13	95788914	95792124	+	0 NA	intron (Nintron (N	11380 NM_00626C	5611 Hs.	59214 NM_00626C	ENSG000002DNAJC3	ACPHD ERcDnaJ	heat protein-coding
chr13-11.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr13	1.E+08	1.E+08	+	0 NA	intron (Nintron (N	34531 NM_00184E	1282 Hs.	17441 NM_00184E	ENSG000002COL4A1	BSVD BSVI	collagen protein-coding
chr14-92.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr14	92165309	92165700	+	0 NA	3' UTR (N3' UTR (N	43535 NM_00132E	53981 Hs.	65763E NM_017437	ENSG000002CPSF2	CPSF100	cleavage protein-coding
chr15-59.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr15	59201021	59202087	+	0 NA	intron (NAluSp SIN	-5289 NM_03319E	92483 Hs.	30705E NM_03319E	ENSG000002LDHAL6B	LDH6B LDF	lactate cprotein-coding
chr16-6.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr16	69808059	6981368	+	0 NA	intron (NLMIEg LIN	29933 NM_00137C	348174 Hs.	59206E NM_18261E	ENSG000002CHL18A	MRC1 MRC1	C-type I protein-coding
chr17-45.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr17	45480928	45481478	+	0 NA	intron (NLMIB7 LIN	-5768 NR_03619E	1E+08	NR_03619E	ENSG000002MIR4315-1	-	microRNA ncRNA
chr19-3.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr19	32364402	32365545	+	0 NA	intron (NLP1B LIN	19363 NM_01491C	22847 Hs.	20539E NM_01491C	ENSG000002ZNF507	-	zinc fing protein-coding
chr19-32.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr19	33126351	33128108	+	0 NA	intron (NLMIE3G LI	-4885 NM_17347E	126248 Hs.	21104E NM_17347E	ENSG000002WDR88	PQWD	WD repeat protein-coding
chr2-176.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	17694939	17696676	+	0 NA	intron (Nintron (N	58003 NM_00114E	79677 Hs.	52672E NM_024624	ENSG000002SMC6	SMC-6 SMC	structure protein-coding
chr2-69.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	69543222	69544244	+	0 NA	intron (Nintron (N	-23762 NR_00370E	1E+08	Hs. 693447 NR_00370E	ENSG000002SNORA36C	-	small ncRNA
chr2-75.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	75242428	75242767	+	0 NA	IntergeniLIP2a LIN	43077 NM_01527E	6869 Hs.	63301 NM_00105E	ENSG000002TACR1	NK1R NK1F	tachykinin protein-coding
chr2-135.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	1.36E+08	1.36E+08	+	0 NA	intron (NAluJo SIN	-12953 NR_02967E	406915	NR_02967E	ENSG000002MIR128-1	MIR128A f	microRNA ncRNA
chr2-15.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	1.51E+08	1.51E+08	+	0 NA	intron (NTrigger3b	9082 NM_001177	55183 Hs.	536537 NM_018151	ENSG000002RIF1	-	replicatiprotein-coding
chr2-15.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	46609 NM_001177	55183 Hs.	536537 NM_018151	ENSG000002RIF1	-	replicatiprotein-coding
chr2-2011.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	2.01E+08	2.01E+08	+	0 NA	non-codir non-codir	-9699 NR_04003C	65072 Hs.	66461E NR_04003C	ENSG000002CFLAR-AS1	ALS2 SCR10	CFLAR antncRNA
chr2-23.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr2	2.37E+08	2.37E+08	+	0 NA	intron (Nintron (N	3552 NM_00671C	10920 Hs.	53171E NM_00671C	ENSG000002COP58	COP9 COP9	sigr protein-coding
chr20-29.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr20	2924072	2925308	+	0 NA	intron (NAluSc5 SI	1483 NM_08084I	5786 Hs.	269577 NM_00283E	ENSG000002PTPRA	HEPTP HLF	protein protein-coding
chr20-137.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr20	13775060	13776591	+	0 NA	intron (Nintron (N	9061 NM_01664E	51575 Hs.	369284 NM_01664E	ENSG000002ESF1	ABTAP C2C	ESF1 nucl protein-coding
chr3-112.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr3	11253412	11254963	+	0 NA	intron (NHERV1P OF	1488 NM_000861	3269 Hs.	1570 NM_000861	ENSG000002HRH1	HI-1 HR1	histamine protein-coding
chr3-17.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr3	1.72E+08	1.72E+08	+	0 NA	intron (Nintron (N	83212 NM_00113E	64778 Hs.	74488E NM_02276E	ENSG000002FND3B	FAD104 PF	fibronect protein-coding
chr4-10.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr4	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	-105146 NR_136202	1.05E+08	Hs. 15833 NR_136202	LOC105377-	-	uncharactncRNA
chr4-12.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (NMRB SINE	10929 NM_001237	890 Hs.	58974 NM_001237	ENSG000002CCNA2	CCN1 CCNA	cyclin A2 protein-coding
chr5-5.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr5	31504473	31506139	+	0 NA	intron (Nintron (N	26787 NR_01323E	29102 Hs.	97997 NR_01323E	ENSG000002DROSHA	ETOH12 HS	droscha r protein-coding
chr5-140.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr5	1.41E+08	1.41E+08	+	0 NA	intron (Nintron (N	-17043 NM_00373E	8637 Hs.	594084 NM_00373E	ENSG000002EIF4EBP3	4E-BP3 4E	eukaryoti protein-coding
chr6-130.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr6	1.31E+08	1.31E+08	+	0 NA	intron (NAluSc5 SI	17833 NM_00113E	2037 Hs.	48647C NM_001431	ENSG000002EPB41L2	1-4-G4	Ierythrocy protein-coding
chr7-139.6.162508	-0.53336	0.932787	-0.57179	0.567463	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (NLa2a LINE1	125414 NM_00113E	28996 Hs.	731417 NM_02274C	ENSG000002CHP2C	PROO593	homoeomd protein-coding
chr3-64.2.642673	0.465702	0.815132	0.571321	0.567782	0.981636	chr3	64236915	64237330	+	0 NA	intron (NLTRE1 LTF	-11656 NM_19885E	166336 Hs.	14810E NM_19885E	ENSG000002PRICKLE2	EPM5	prickle f protein-coding
chr17-19.7.964447	-0.48178	0.843279	-0.57132	0.567784	0.981636	chr17	19309642	19310171	+	0 NA	exon (NM exon (NM	-3645 NR_04857E	1.01E+08	Hs. 62167E NR_04857E	ENSG000002EPN2-AS1	-	EPN2 antncRNA
chr1-91.7.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr1	9175049	9175518	+	0 NA	intron (NAluS6 SI	-6921 NR_13273E	1.03E+08	Hs. 59929E NR_13273E	ENSG000002LNTAM344	GUARDIN1 f	long non ncRNA
chr12-53.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr12	53384352	53385582	+	0 NA	intron (NAluS6 SI	4323 NM_00310E	6667 Hs.	620754 NM_00310E	ENSG000002SPI	-	Spl trans protein-coding
chr14-2.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr14	22573018	22575163	+	0 NA	intron (Nintron (N	15134 NM_001344	1603 Hs.	82890 NM_001344	ENSG000002DAD1	OST2	defender protein-coding
chr16-11.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr16	11875387	11877368	+	0 NA	intron (NAluSx1 SI	-25020 NM_01565E	26156 Hs.	40184E NM_01565E	ENSG000002RSL1D1	CSD1 L12	ribosomal protein-coding
chr16-58.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr16	58003306	58003543	+	0 NA	intron (NAluJb SIN	2017 NM_001204	79650 Hs.	40870E NM_02459E	ENSG000002USB1	C16orf57 U6	snRNA protein-coding
chr18-27.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr18	2738530	2738828	+	0 NA	intron (Nintron (N	82792 NM_01529E	23347 Hs.	8118 NM_01529E	ENSG000002SMCHD1	BAMS FSH	structure protein-coding
chr21-33.8.425903	-0.46002	0.805328	-0.57122	0.567852	0.981636	chr21	33343660	33344163	+	0 NA	intron (NAluS6 SI	18913 NM_00062E	3454 Hs.	52940C NM_00062E	ENSG000002IFNAR1	AVP IFN-ε	interferc protein-coding
chr11-64.8.648681	0.45358	0.794235	0.57109	0.567938	0.981636	chr11	64859742	64860021	+	0 NA	intron (Nintron (N	-12228 NM_01752E	55561 Hs.	29359C NM_01752E	ENSG000002CDC42BPG	DMPK2 HSM	CDC42 bir protein-coding





chr4-7614	8.410187	-0.45687	0.810553	-0.56366	0.572988	0.981636	chr4	76143236	76144009	+	0	NA	intron (AluSx4 SI	4775	NM_017426	53371	Hs.43043E	NM_017426	ENSG000005NUP54	-	nucleoporin protein-coding		
chr5-1503	8.410187	-0.45687	0.810553	-0.56366	0.572988	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	exon (NM exon (NM	16124	NR_157074	972	Hs.43656E	NM_00435E	ENSG00000CD74	-	DHLGAL H ACD74 mole protein-coding		
chr15-649	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr15	64971161	64974690	+	0	NA	intron (Nintron (N	16545	NM_001127	51324	Hs.24245E	NM_01663E	ENSG00000SPG21	-	ABHD21 ACSPG21 abl protein-coding		
chr16-756	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr16	75601202	75603634	+	0	NA	intron (NMER21C LI	20863	NM_012091	23536	Hs.72931E	NM_012091	ENSG00000ADAT1	-	HADAT1 adenosin protein-coding		
chr16-84	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr16	84656790	84660599	+	0	NA	intron (Nintron (N	10183	NM_024731	79786	Hs.222731	NM_024731	ENSG00000KHLH36	-	16orf44 kelch lik protein-coding		
chr19-509	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr19	5097350	5100246	+	0	NA	intron (MLT1A0 LI	129685	NM_00137C	23030	Hs.65481E	NM_01501E	ENSG00000KDM4B	-	JMJD2B T lysine deprotein-coding		
chr20-117	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr20	1125067	1129123	+	0	NA	intron (Nintron (N	8493	NM_001322	9491	Hs.471917	NM_006814	ENSG00000PSMF1	-	PI31 proteasom protein-coding		
chr3-1072	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr3	1.08E+08	1.08E+08	+	0	NA	exon (NM exon (NM	161260	NR_02427E	151568	Hs.15904E	NR_015414	ENSG00000LINC0063E	-	long intncRNA		
chr5-177	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	14964	NM_00681E	10960	Hs.75864	NM_00681E	ENSG00000CLMAN2	-	C5orf8 GF lectin, n protein-coding		
chr6-1334	9.153127	0.434493	0.770988	0.563553	0.573058	0.981636	chr6	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	221076	NM_001301	2070	Hs.59668E	NM_00410C	ENSG00000EYAA	-	CDMD1 DFEYEA transprotein-coding		
chr13-11	8.343624	-0.46577	0.826698	-0.56341	0.573156	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (NLIMEc LI	10955	NM_00125E	8858	Hs.1011	NM_003891	ENSG00000PROZ	-	PZ protein z protein-coding		
chr5-9554	8.795373	-0.45482	0.807567	-0.56319	0.573303	0.981636	chr5	95542797	95543058	+	0	NA	intron (Nintron (N	12078	NM_01463E	9652	Hs.48286E	NM_01463E	ENSG00000TTC37	-	KIAA0372 tetraatric protein-coding		
chr19-46	8.218656	0.478881	0.850324	0.563175	0.573316	0.981636	chr19	46997572	46997890	+	0	NA	intron (Nintron (N	22106	NM_002517	4861	Hs.79564	NM_002517	ENSG00000NPAS1	-	MOP5 PASE neuronal protein-coding		
chr12-121	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr12	12146459	12147756	+	0	NA	intron (NAluY SINE	35155	NR_036052	1E+08	NR_036052	ENSG00000MIR1244	-	LMIR1244 microRNA ncRNA			
chr12-282	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr12	28270704	28271211	+	0	NA	intron (NL2a LINE	-80219	NR_14893E	729291	Hs.12927E	NR_14893E	LOC729291	-	uncharactncRNA		
chr14-685	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr14	68971020	68975425	+	0	NA	intron (Nintron (N	6080	NM_001102	87	Hs.23575E	NM_001102	ENSG00000ACTN1	-	BDPLT15 actinin e protein-coding		
chr19-111	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr19	11164931	11168314	+	0	NA	intron (Nintron (N	-10810	NM_001317	147841	Hs.38122E	NM_18251E	ENSG00000SPC24	-	SPBC24 zinc cp protein-coding		
chr19-522	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr19	52287949	52291123	+	0	NA	intron (Nintron (N	-7633	NM_001297	147657	Hs.72931E	NM_144684	ENSG00000ZNF480	-	SNC2 zinc finger protein-coding		
chr2-215	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr2	2.15E+08	2.15E+08	+	0	NA	intron (NTiger4a	8091	NM_004044	471	Hs.90280	NM_004044	ENSG00000AT1C	-	AICAR AIC5-aminoin protein-coding		
chr20-176	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr20	17676017	17679217	+	0	NA	intron (NAluSq2 SI	4625	NM_00136E	6238	Hs.47221E	NM_004587	ENSG00000CRBP1	-	ES/130 ES ribosome protein-coding		
chr3-1414	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr3	14145874	14146617	+	0	NA	intron (Nintron (N	21305	NM_024334	79188	Hs.517817	NM_024334	ENSG00000TMEM43	-	ARVC5 ARV transmem protein-coding		
chr3-4567	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr3	45671170	45675416	+	0	NA	intron (Nintron (N	15589	NR_033947	644714	Hs.71288E	NR_033947	L1MD1-AS1	-	L1MD1 antncRNA		
chr6-1767	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr6	17672730	17675737	+	0	NA	intron (NLIME1 LI	-31897	NR_13461E	1.05E+08	Hs.71870E	NR_13461E	ENSG00000LOC105374	-	uncharactncRNA		
chr8-3061	8.88736	-0.44031	0.781856	-0.56317	0.573322	0.981636	chr8	30611129	30614001	+	0	NA	intron (NAluSx SIN	30611129	30614001	-260176	NM_00120E	1.01E+08	Hs.65949E	NM_00120E	ENSG00000SMIM18	-	small int protein-coding
chr10-691	7.848886	-0.49281	0.875183	-0.56309	0.573375	0.981636	chr10	69192162	69192407	+	0	NA	intron (NLIME3Cz L	12050	NM_00132E	6832	Hs.10646E	NM_003171	ENSG00000SUPV3L1	-	SUV3 Suv3 like protein-coding		
chr15-654	8.895218	-0.44178	0.784603	-0.56306	0.573397	0.981636	chr15	65456367	65460369	+	0	NA	intron (Nintron (N	61532623	61539793	-37041	NM_02096E	57722	Hs.458607	NM_02096E	ENSG00000IGDCC4	-	DDM36 NOF immunogl protein-coding
chr16-511	8.895218	-0.44178	0.784603	-0.56306	0.573397	0.981636	chr16	51139793	51139793	+	0	NA	intron (Nintron (N	12589	NM_001127	6299	Hs.135781	NM_02096E	ENSG00000TMEM43	-	HEL-S-89 spalt lik protein-coding		
chr8-222E	8.895218	-0.44178	0.784603	-0.56306	0.573397	0.981636	chr8	22253385	22254874	+	0	NA	TTS (NR_1TTS (NR_1	8996	NM_001722	661	Hs.14834E	NM_001722	ENSG00000POLR3D	-	BN51T RPCRNA polyn protein-coding		
chr9-1347	8.895218	-0.44178	0.784603	-0.56306	0.573397	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	62972	NR_039691	1.01E+08	NR_039691	ENSG00000MIR3689C	-	microRNA ncRNA			
chr1-1097	8.615399	0.450544	0.800628	0.562739	0.573613	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	exon (NM exon (NM	-16364	NR_02958E	406974	NR_02958E	ENSG00000MIR197	-	MIRN197 microRNA ncRNA			
chr10-93E	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr10	93668637	93670862	+	0	NA	non-codir non-codir	32823	NM_001347	118924	Hs.58665E	NM_14524E	ENSG00000CFRA10AC1	-	C10orf4 FFRA10A as protein-coding		
chr11-63E	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr11	63634617	63635682	+	0	NA	intron (NAluSzb SI	-20680	NM_00112E	11145	Hs.50277E	NM_00706E	ENSG00000PLAAT3	-	AdPLA H-F phospholip protein-coding		
chr11-10E	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr11	10E+08	1.06E+08	+	0	NA	3' UTR (N3' UTR (N	-19435	NM_00133C	143879	Hs.10194E	NM_15243E	ENSG00000KBTBD3	-	BKLBHD3 kelch rep protein-coding		
chr14-504	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr14	50449687	50452720	+	0	NA	intron (NLIM4a LI	-53905	NM_001367	8814	Hs.280881	NM_00419E	ENSG00000CDKL1	-	KKIALRE F cyclin deprotein-coding		
chr15-297	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr15	29762669	29763624	+	0	NA	intron (Nintron (N	57528	NM_00135E	7082	Hs.74399E	NM_003257	ENSG00000TJPI1	-	ZO-1 tight jur protein-coding		
chr15-38E	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr15	38324807	38325838	+	0	NA	intron (NTiger4b	72486	NM_152594	161742	Hs.525781	NM_152594	ENSG00000SPRED1	-	LGSS NFLS sprouty protein-coding		
chr17-35E	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr17	35648052	35648340	+	0	NA	intron (Nintron (N	60874	NM_00103C	163	Hs.51481E	NM_00128E	ENSG00000CAP2B1	-	ADTB2 AP1 adaptor r protein-coding		
chr4-1011	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr4	10112593	10115958	+	0	NA	intron (Nintron (N	2524	NM_00511E	9948	Hs.12854E	NM_00511E	ENSG00000WDR1	-	AIP1 HEL-WD repeat protein-coding		
chr6-566E	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr6	56622445	56626320	+	0	NA	intron (N(ATTTA)r	18507	NM_01554E	667	Hs.60491E	NM_00172E	ENSG00000DST	-	BP240 BP4 dystonin protein-coding		
chr6-8561	8.84622	-0.44303	0.78751	-0.56258	0.573724	0.981636	chr6	85616530	85618748	+	0	NA	intron (NMIRc SINE	-23483	NM_00135C	57231	Hs.485871	NM_02046E	ENSG00000SNX14	-	RGS-PX2 S sorting r protein-coding		
chr1-1801	11.5965	-0.38914	0.691983	-0.56235	0.573875	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	3' UTR (N3' UTR (N	-43623	NM_001004	5768	Hs.71917E	NM_00282E	ENSG00000QXQ1	-	Q6 QSCN6 quiescin protein-coding		
chr2-171E	11.5965	-0.38914	0.691983	-0.56235	0.573875	0.981636	chr2	1.72E+08	1.72E+08	+	0	NA	intron (NHERV4_I-i	61962	NM_00370E	8604	Hs.47060E	NM_00370E	ENSG00000SLC25A12	-	AGC1 ARAL solute e protein-coding		
chr1-236E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (Nintron (N	32357	NM_001291	4548	Hs.498187	NM_000254	ENSG00000CMT8	-	HMG MS c5-methylt protein-coding		
chr12-76E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr12	76392508	76393434	+	0	NA	intron (Nintron (N	30314	NM_00131E	114882	Hs.43084E	NM_020841	ENSG00000OSBPL8	-	MST120 MS oxysterol protein-coding		
chr12-105E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	39695	NM_10346E	88910	Hs.374067	NM_13046E	ENSG00000UBE3B	-	BPST13 KOS ubiquit protein-coding		
chr15-58E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr15	58679187	58680240	+	0	NA	intron (NAluSzb SI	13894	NR_107341E	664618	Hs.70224E	NR_020297	HSP90AB4 HSP90B heat shock pseudo				
chr15-801E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr15	80125167	80126063	+	0	NA	intron (Nintron (N	27199	NM_001242	54649	Hs.59667E	NM_01900E	ENSG00000ZFAND6	-	AWP1 ZAC2 zinc finger protein-coding		
chr16-81E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr16	81660873	81661843	+	0	NA	intron (Nintron (N	-3996	NR_04511E	1E+08	Hs.657151	NR_04511E	LOC10012E	-	uncharactncRNA		
chr20-43E	5.973011	0.531716	0.945896	0.562129	0.574028	0.981636	chr20	43547242	43547635	+	0	NA	IntergeniLIMC5a LI	-11589	NR_17069E	10110	Hs.30086E	NM_01627E					



chr20-394	9.160985	0.432774	0.772975	0.559881	0.575561	0.981636	chr20	3949156	3950215	+	0	NA	intron (NAIuJb SIN	-32122 NR_031722	1E+08	NR_031722 ENSG00000MIR103B2	MIR103-2-microRNA	ncRNA
chr20-518	9.160985	0.432774	0.772975	0.559881	0.575561	0.981636	chr20	5185621	5187346	+	0	NA	intron (NAIuJn (N	59475 NM_003818	8760	Hs.126857NM_003818 ENSG00000CDS2	-	CDP-diacyprotein-coding
chr21-336	9.160985	0.432774	0.772975	0.559881	0.575561	0.981636	chr21	33620658	33621577	+	0	NA	intron (NAIuYe5 SI	20624 NM_145858	9946	Hs.352671NM_145311 ENSG00000CRYZL1	4P11 QOH-crystallin	protein-coding
chr22-314	9.160985	0.432774	0.772975	0.559881	0.575561	0.981636	chr22	31440873	31443244	+	0	NA	exon (NM exon (NM	42454 NM_004147	4733	Hs.115242NM_004147 ENSG00000DRG1	NEDD3	development protein-coding
chr6-7137	9.160985	0.432774	0.772975	0.559881	0.575561	0.981636	chr6	71372761	71373096	+	0	NA	IntergeniAluSq2 SI	4103 NR_029598	407032	NR_029598 ENSG00000MIR30C2	MIRN30C2 microRNA	ncRNA
chr7-6626	9.160985	0.432774	0.772975	0.559881	0.575561	0.981636	chr7	66264038	66265646	+	0	NA	intron (NLIM4 LINE	59508 NM_003596	8460	Hs.421194NM_003596 ENSG00000TPST1	TANGO13A	tyrosylpr protein-coding
chr19-112	8.159951	0.470686	0.840787	0.559815	0.575605	0.981636	chr19	11232388	11233309	+	0	NA	intron (Nintron (N	-6771 NM_018687	55908	Hs.534462NM_018687 ENSG00000ANGPTL8	C19orf80 angiopoic	protein-coding
chr1-4562	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr1	45627999	45635234	+	0	NA	intron (NLIMC LINE	-7562 NM_001114	149483	Hs.18912 NM_152500 ENSG00000CCDC17	-	coiled-cp protein-coding
chr1-1571	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	3216 NR_001566	360155	Hs.49180ENR_001566 ENSG00000CYCSP52	HC6 HCP2	CYCS pset pseudo
chr1-1804	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (NLIMB8 LIN	-13044 NR_030607	1E+08	NR_030607 ENSG00000MIR3121	mir-3121	microRNA
chr1-2305	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	intron (Nintron (N	19485 NM_001346	64801	Hs.27573ENR_002278 ENSG00000ARV1	EIEE38	ARV1 homc protein-coding
chr1-2354	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	TTS (NM_TTS (NM_C	57305 NM_15249C	148789	Hs.49814ENR_15249C ENSG00000B3GALNT2	B3GAlNAc-beta-1,3-	protein-coding
chr10-718	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr10	71823831	71832176	+	0	NA	intron (Nintron (N	16120 NM_001171	64072	Hs.656032NM_022124 ENSG00000CDH23	CDHR23 PIcadherin	protein-coding
chr10-102	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	-24440 NM_001288	4791	Hs.73090 NM_002502 ENSG00000NFKB2	CVI10 H2nuclear	fprotein-coding
chr17-286	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr17	28615187	28622273	+	0	NA	intron (Nintron (N	-4545 NM_001174	124923	Hs.729077NM_14461C ENSG00000CRSKR	SGK494	ribosomal protein-coding
chr19-485	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr19	48906653	48919374	+	0	NA	exon (NM exon (NM	5878 NR_046633	1.01E+08	Hs.569933NR_046633 ENSG00000NUCB1-AS1	NUCB1	antncRNA
chr2-1591	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr2	1.59E+08	1.59E+08	+	0	NA	intron (NMLTID LTF	11479 NR_10694E	1.02E+08	NR_10694E ENSG00000MIR6888	hsa-mir-6miRNA	ncRNA
chr20-359	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr20	35547402	35550899	+	0	NA	intron (NMIR SINE	7072 NM_015966	51614	Hs.47255ENR_015966 ENSG00000ERGLIC3	C20orf47 ERGLI	anc protein-coding
chr2-181	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr22	18079999	18081786	+	0	NA	intron (NLIMA6 LIN	2902 NM_01792E	55670	Hs.517400NM_01792E ENSG00000PEX26	PBD7A PBE peroxisom	protein-coding
chr4-118	9.690855	0.420082	0.750889	0.559446	0.575857	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (NAIuJo SIN	-19038 NR_10382E	729218	Hs.44851ENR_10382E	LOC72921E	uncharacterpseude
chr10-132	8.459185	-0.45541	0.814042	-0.55944	0.575862	0.981636	chr10	13331354	13332548	+	0	NA	intron (NLIMB7 LIN	16342 NM_012247	22929	Hs.124027NM_012247 ENSG00000SEPHS1	SELD SPS selenophc	protein-coding
chr12-962	8.459185	-0.45541	0.814042	-0.55944	0.575862	0.981636	chr12	96225157	96225738	+	0	NA	intron (Nintron (N	-30051 NM_00130C	2004	Hs.46523 NM_00523C ENSG00000ELK3	ERP NET SETS	transprotein-coding
chr1-1105	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	TTS (NM_TTS (NM_C	8071 NM_02276E	64783	Hs.435947NM_02276E ENSG00000CRBM15	OTT OTT1 RNA	bindi protein-coding
chr10-864	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr10	86444982	86446358	+	0	NA	intron (NAIuJr4 SI	76114 NM_00131E	23063	Hs.20309ENR_01504E ENSG00000WAPL	WAPL KIAACWAPL	cohe protein-coding
chr10-915	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr10	91951701	91952920	+	0	NA	intron (Nintron (N	28540 NM_00397E	9044	Hs.50052ENR_00397E ENSG00000BTAF1	MOT1 TAF B-TFIID	lprotein-coding
chr11-74	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr11	74704018	74873471	+	0	NA	intron (NHUERS-P3-	77147 NM_00127C	143570	Hs.37014ENR_18296E ENSG00000XRR1	-	X-ray ras protein-coding
chr12-77	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr12	77048381	77049470	+	0	NA	intron (Nintron (N	16894 NM_20339A	144455	Hs.61637ENR_20339A ENSG00000E2F7	-	E2F trans protein-coding
chr2-2335	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr2	2.34E+08	2.34E+08	+	0	NA	intron (Nintron (N	11936 NM_01821E	55230	Hs.96513 NM_01821E ENSG00000CUSP40	-	ubiquitin protein-coding
chr22-176	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr22	17606846	17608033	+	0	NA	intron (NL2 LINE I	-18247 NM_00128E	1.02E+08	Hs.62992ENR_00128E707	LOC10192E	uncharacter protein-coding
chr22-178	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr22	17868418	17869640	+	0	NA	intron (Nintron (N	37857 NM_001122	57553	Hs.528024NM_015241 ENSG00000MICAL3	MICAL-3	microtub protein-coding
chr4-874	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr4	87438030	87440008	+	0	NA	intron (NAIuSx1 SI	16422 NM_19803E	53343	Hs.14950ENR_02404E ENSG00000NUDT9	NUDT10	nudix hyc protein-coding
chr6-111	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (NAIuSx SIN	102057 NM_15336E	91749	Hs.40057ENR_15336E ENSG00000MFSDB4	KIAA1919 major	fag protein-coding
chr9-1015	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chr9	1.02E+08	1.02E+08	+	0	NA	TTS (NM_TTS (NM_C	30487 NM_01959E	56254	Hs.01959ENR_01959E ENSG00000RNF20	BRE1 BRE1ring	fing protein-coding
chrX-406	5.931872	0.530258	0.947868	0.559422	0.575874	0.981636	chrX	40601207	40601664	+	0	NA	intron (Nintron (N	20465 NM_00576E	10159	Hs.49596ENR_00576E ENSG00000ATP6AP2	APT6M8-9 ATPase	H+ protein-coding
chr1-1175	6.63968	-0.50514	0.902977	-0.55942	0.575878	0.981636	chr1	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	7522 NM_00678A	10885	Hs.31080ENR_00678A ENSG00000WDR3	DIP2 UTP1WD	repeat protein-coding
chr11-666	6.63968	-0.50514	0.902977	-0.55942	0.575878	0.981636	chr11	66630992	66631482	+	0	NA	intron (NAIuSx2 SI	-7380 NM_00289E	5936	Hs.52382ENR_00289E ENSG00000RBM4	LARK RBM4RNA	bindi protein-coding
chr4-7077	5.40986	0.559614	1.000685	0.559231	0.576004	0.981636	chr4	70779798	70780491	+	0	NA	intron (Nintron (N	45734 NM_00134E	22902	Hs.740904NM_014961 ENSG00000RUFY3	RIPX SINCRUN	and fprotein-coding
chr20-492	14.31534	-0.35216	0.62977	-0.5592	0.576028	0.981636	chr20	49279142	49291215	+	0	NA	intron (NHERV1P OE	4495 NR_00303C	692057	NR_00303C ENSG00000SNORD12	HBII-99 small	nucsnRNA
chr1-2516	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr1	2516830	2519082	+	0	NA	intron (Nintron (N	8640 NM_01821E	55229	Hs.26156 NM_01821E ENSG00000PANK4	-	panthoer protein-coding
chr1-1111	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr1	11119289	11121455	+	0	NA	intron (NAIuSx SIN	20353 NR_13506E	1.05E+08	Hs.63496ENR_13506E ENSG00000EXOSC10-#	EXOSC10	ncRNA
chr1-3556	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr1	35565283	35566592	+	0	NA	3' UTR (N3' UTR (N	-7377 NM_17854E	339488	Hs.567844NM_17854E ENSG00000TFAP2E	AP2E	transcrip protein-coding
chr1-1865	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr1	1.86E+08	1.86E+08	+	0	NA	intron (NAIuY SINE	-5279 NR_02237E	10896	Hs.67923ENR_02237E ENSG00000OCLM	TISR	oculomed protein-coding
chr11-622	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr11	6221462	6222676	+	0	NA	intron (Nintron (N	12567 NM_032127	84067	Hs.50179ENR_032127 ENSG00000FAM160A2	C11orf56 family	wiprotein-coding
chr12-118	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	intron (NAIuSx SIN	-52237 NM_00134E	51347	Hs.64442ENR_016281 ENSG00000TAOK3	DPK JIK TAO	kinas protein-coding
chr14-716	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr14	71627202	71627278	+	0	NA	exon (NM exon (NM	86217 NM_00128A	26037	Hs.654657NM_01555E ENSG00000SIPAL11	E6TP1 SPA signal	ir protein-coding
chr14-745	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr14	74520908	74522256	+	0	NA	intron (Nintron (N	27817 NM_19427E	122961	Hs.29107ENR_19427E ENSG00000ISCA2	HBLD1 ISA iron-sulf	protein-coding
chr16-311	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr16	3117157	3118236	+	0	NA	intron (NAIuJb SIN	-2098 NR_024167	81854	Hs.66949ENR_024166	ZNF205-AS-	ZNF205
chr17-808	5.93973	0.527647	0.944256	0.558797	0.5763	0.981636	chr17	80884813	80886181	+	0	NA	intron (Nintron (N	-79865 NR				



chr3-1365	8.912784	-0.43474	0.782378	-0.55566	0.578441	0.981636	chr3	1.37E+08	1.37E+08	+	0	NA	exon (NM exon (NM	-11905	NM_144717	53833	Hs.61232	NM_144717	ENSG000002IL20RB	DIRS1	FNI	interleukin protein-coding
chr5-1282	8.912784	-0.43474	0.782378	-0.55566	0.578441	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (N intron (N	189250	NM_001046	6558	Hs.16258	NM_001046	ENSG000002SLC12A2	BSC1 BSC2	solute carrier protein-coding	
chr7-3291	8.912784	-0.43474	0.782378	-0.55566	0.578441	0.981636	chr7	32916306	32917643	+	0	NA	non-coding non-coding	-25214	NM_015483	25948	Hs.372541	NM_015483	ENSG000002KBTBD2	BKLHD1	kelch repeat protein-coding	
chr7-923	9.657573	0.417402	0.751291	0.55579	0.578498	0.981636	chr7	92397833	92399234	+	0	NA	exon (NM exon (NM	38781	NR_145992	1.05E+08		NM_001317	ENSG000002TMB1MP			transmembrane pseudo
chr3-5261	6.495023	0.506979	0.912565	0.555554	0.578516	0.981636	chr3	52618120	52618840	+	0	NA	intron (N intron (N	67119	NM_00135C	55193	Hs.189922	NM_01816E	ENSG000002PBRM1	BAF180	PF polybrominated protein-coding	
chr13-955	8.920641	-0.43617	0.785126	-0.55555	0.578521	0.981636	chr13	95578705	95579709	+	0	NA	3' UTR (N 3' UTR (N	26487	NM_006984	9071	Hs.534377	NM_006984	ENSG000002CLDN10	CPETRL3	Claudin 1 protein-coding	
chr7-743	5.924014	0.532915	0.959383	0.555477	0.578568	0.981636	chr7	74366917	74367309	+	0	NA	intron (N MLT1C LTF	77638	NM_003388	7461	Hs.64701	NM_003388	ENSG000002CLIP2	CLIP1 CLIFCAP	Glycophorin protein-coding	
chr13-494	4.39385	-0.61665	1.110148	-0.55547	0.578573	0.981636	chr13	49473355	49474120	+	0	NA	intron (N intron (N	-22216	NM_00104C	51131	Hs.36903	NM_00104C	ENSG000002PHF11	APY BCAP	PHD finger protein-coding	
chr1-192	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr1	19293987	19294246	+	0	NA	non-coding non-coding	1620	NR_037847	1.01E+08		NR_037847	LOC100506			uncharacterized ncRNA
chr12-766	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr12	76809816	76810421	+	0	NA	intron (N intron (N	45860	NM_00135E	23390	Hs.4014	NM_01533E	ENSG000002ZDHC17	DHHC-17	zinc finger protein-coding	
chr15-65	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr15	65509823	65510866	+	0	NA	intron (N intron (N	6930	NM_19796E	54878	Hs.45860	NM_01774E	ENSG000002DPP8	DP8 DRP	dipeptidyl protein-coding	
chr2-556	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr2	55683169	55683902	+	0	NA	intron (N AluSg SIN	10309	NM_03310E	87178	Hs.38873	NM_03310E	ENSG000002PNPT1	COXPDI3	polyribin protein-coding	
chr3-155	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr3	1.56E+08	1.56E+08	+	0	NA	intron (N intron (N	35943	NM_00387E	8833	Hs.591314	NM_00387E	ENSG000002GMPS	GATD7	guanine protein-coding	
chr4-58	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr4	51880896	51881473	+	0	NA	intron (N Tigger15e	37605	NM_001287	23142	Hs.60538	NM_01511E	ENSG000002DCUN1D4			defective protein-coding
chr4-526	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr4	52628066	52628551	+	0	NA	intron (N intron (N	28231	NM_001134	64854	Hs.7966	NM_02283E	ENSG000002USP46			ubiquitin protein-coding
chr5-134	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr5	1.34E+08	1.34E+08	+	0	NA	intron (N AluS8 SI	4328	NR_149151	5515	Hs.10581	NM_00271E	ENSG000002PPP2CA	NEDLBA	PF protein-coding	
chr6-87	6.623964	-0.50132	0.902756	-0.55532	0.578674	0.981636	chr6	87218904	87219315	+	0	NA	intron (N intron (N	63544	NM_015021	23036	Hs.44480	NM_015021	ENSG000002ZNF292	Nbla00365	zinc finger protein-coding	
chr11-652	11.61406	-0.38372	0.691143	-0.5552	0.578759	0.981636	chr11	65851391	65856857	+	0	NA	TTS (NM  TTS (NM	4056	NM_005507	1072	Hs.17062	NM_005507	ENSG000002CFL2	CFL HEL	Scofilin 1 protein-coding	
chr9-1937	11.61406	-0.38372	0.691143	-0.5552	0.578759	0.981636	chr9	19374474	19379719	+	0	NA	intron (N intron (N	3140	NM_00101C	6194	Hs.40807	NM_00101C	ENSG000002RPS6	S6	ribosomal protein-coding	
chr11-91	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr11	9152061	9152681	+	0	NA	exon (NM exon (NM	58008	NR_02771E	283102	Hs.68947	NR_02771E	ENSG000002KRT8P41			keratin epsilon pseudo
chr12-105	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (N AluSx SIN	30784	NR_13389E	83892	Hs.524731	NM_031954	ENSG000002KCTD10	BTBD28	MS potassium protein-coding	
chr15-55	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr15	55854907	55856606	+	0	NA	intron (N intron (N	61375	NM_001284	4734	Hs.1565	NM_006154	ENSG000002NEDD4	NEDD4-1	FNEDD4 E3 protein-coding	
chr16-24	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr16	23411873	23412550	+	0	NA	intron (N intron (N	40978	NM_15360E	91949	Hs.185807	NM_15360E	ENSG000002COG7	CDG2E	component protein-coding	
chr18-43	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr18	46095621	46096571	+	0	NA	intron (N AluSx1 SI	2200	NM_001001	498	Hs.29828	NM_00404E	ENSG000002ATP5F1A	ATP5A	ATF ATP synthetase protein-coding	
chr2-2387	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr2	23872478	23873597	+	0	NA	intron (N intron (N	54086	NM_01755E	54454	Hs.46786	NM_01755E	ENSG000002ATAD2B			ATPase F protein-coding
chr2-231	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (N LIPA16 LI	47940	NM_00135E	80210	Hs.162411	NM_02513E	ENSG000002ARMC9	ARM JBT5	armadillo protein-coding	
chr3-1184	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr3	11840230	11842155	+	0	NA	intron (N AluJb SIN	5693	NM_001321	132001	Hs.47547	NM_138807	ENSG000002TAMM41	C3orf31	PF TAMM41 mit protein-coding	
chr5-142	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr5	1.42E+08	1.42E+08	+	0	NA	intron (N LIMed LIN	13858	NR_120664	1.02E+08	Hs.65894	NR_120664	ENSG000002SPRY4-AS1	THCAT68	SPRY4 ant ncRNA	
chr5-172	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr5	1.72E+08	1.72E+08	+	0	NA	intron (N intron (N	37570	NM_001171	285588	Hs.716824	NM_001171	ENSG000002EFCAB9			EF-hand c protein-coding
chr7-151	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	intron (N intron (N	3548	NM_00119E	6522	Hs.64706	NM_00304C	ENSG000002SLC4A2	AE2 BND3	solute carrier protein-coding	
chr8-143	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	intron (N intron (N	8707	NM_00113C	1936	Hs.33338	NM_00196C	ENSG000002EEF1D	EF-1D	EF1 eukaryotic protein-coding	
chr9-1347	6.665104	-0.4976	0.896727	-0.55491	0.578958	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (N intron (N	69608	NR_039691	1.01E+08		NR_039691	ENSG000002MIR3689C			microRNA ncRNA
chr10-852	10.22072	0.408738	0.736668	0.554847	0.578999	0.981636	chr10	8022079	802622	+	0	NA	intron (N intron (N	111255	NM_001351	23185	Hs.15906	NM_01515E	ENSG000002LARP4B	KIAA0217	La ribon protein-coding	
chr1-156	9.698713	0.418473	0.754399	0.554711	0.579092	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (N intron (N	9617	NM_015327	23381	Hs.516837	NM_015327	ENSG000002CMG5	EST1B	LPM5G5 non protein-coding	
chr1-1507	9.698713	0.418473	0.754399	0.554711	0.579092	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (N intron (N	23623	NM_00597E	5546	Hs.51694	NM_00597E	ENSG000002PRCC	RCCP1	TPF proline protein-coding	
chr1-2308	9.698713	0.418473	0.754399	0.554711	0.579092	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	intron (N LIMB3 LIN	14544	NM_00113E	84886	Hs.520494	NM_03280C	ENSG000002Clorf198			chromosome protein-coding
chr12-277	9.698713	0.418473	0.754399	0.554711	0.579092	0.981636	chr12	27755801	27756229	+	0	NA	3' UTR (N 3' UTR (N	15567	NM_00114E	1E+08		NM_00114E	ENSG000002MANSC4			MANSC domain protein-coding
chr3-733	9.698713	0.418473	0.754399	0.554711	0.579092	0.981636	chr3	73383863	73385031	+	0	NA	exon (NM exon (NM	49548	NM_00130C	23024	Hs.660347	NM_01500E	ENSG000002PDZRN3	LNx3	SEM PDZ domain protein-coding	
chr6-135	9.698713	0.418473	0.754399	0.554711	0.579092	0.981636	chr6	1.35E+08	1.35E+08	+	0	NA	intron (N intron (N	4911	NM_00114E	10767	Hs.37852	NM_00662C	ENSG000002HBSL1	EF-1a	ERF HBS1 like protein-coding	
chr6-1438	9.697679	0.452585	0.816349	0.554401	0.579304	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (N AluS6 SI	-29108	NM_00132E	84946	Hs.18567	NM_03286C	ENSG000002LTV1	C6orf93	cLTV1 rib protein-coding	
chr18-76	9.127703	0.429931	0.775615	0.554309	0.579367	0.981636	chr18	76361337	76362487	+	0	NA	3' UTR (N 3' UTR (N	-129740	NR_136504	1.02E+08	Hs.66518	NR_136504	ENSG000002LOC101927			uncharacterized ncRNA
chr1-203	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr1	2.04E+08	2.04E+08	+	0	NA	intron (N intron (N	-40600	NR_00301E	677843	Hs.67613	NR_00301E	ENSG000002SNORA77	ACA63	SN small nucleolar RNA	
chr1-227	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr1	2.27E+08	2.27E+08	+	0	NA	intron (N intron (N	78269	NM_020247	56997	Hs.118241	NM_020247	ENSG000002COQ8A	ADCK3	ARC coenzyme protein-coding	
chr1-241	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr1	2.42E+08	2.42E+08	+	0	NA	3' UTR (N 3' UTR (N	3728	NM_001821	1122	Hs.65454	NM_001821	ENSG000002CHML	REP2	CHM like protein-coding	
chr13-77	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr13	77241373	77243102	+	0	NA	intron (N AluSc SIN	84857	NM_015057	23077	Hs.591221	NM_015057	ENSG000002MYCBP2	Myc-bp2	FMYC binding protein-coding	
chr13-102	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr13	1.03E+08	1.03E+08	+	0	NA	intron (N intron (N	48148	NM_003291	7174	Hs.432424	NM_003291	ENSG000002TPP2	TPP-2	TPF tripeptide protein-coding	
chr14-101	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	promoter-promoter-	-288	NR_02987E	494329		NR_02987E	ENSG000002MIR380			MIR380-3g microRNA ncRNA
chr14-103	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	intron (N intron (N	8385	NM_00113C	3831	Hs.20107	NM_00555E	ENSG000002KCLC1	KLC KNS2	kinesin 1 protein-coding	
chr15-282	6.657246	-0.4957	0.894825	-0.55397	0.579602	0.981636	chr15	28243808	28245148	+	0	NA	intron (N intron (N	77674	NM_004667	8924	Hs.43489	NM_004667	ENSG000002HERC2	D15F37S1	HECT and protein-coding	



chr10-10c.6.672962	-0.49954	0.902876	-0.55328	0.580073	0.981636	chr10	1E+08	1E+08	0	NA	intron (Nintron (N	-5624 NR_002954	677800	Hs.662165NR_002954	ENSG000003SNORA12	U108	small nucsnoRNA	
chr12-12c.6.672962	-0.49954	0.902876	-0.55328	0.580073	0.981636	chr12	1.22E+08	1.22E+08	0	NA	intron (Nintron (N	-10306 NM_001351	65082	Hs.487883NM_022916	ENSG000003VPS33A	MPSPS	VPS33A ccprotein-coding	
chr12-79f.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr12	79815419	79815738	+	0	NA	intron (Nintron (N	98333 NM_001143	4659	Hs.49582 NM_00248C	ENSG000003PPP1R12A	M130 MBS	protein fprotein-coding
chr13-32f.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr13	32759919	32760118	+	0	NA	intron (NAluY SINE	151634 NR_04702C	1.01E+08	Hs.40629NR_047020	LINC00422	-	long intencRNA
chr17-34f.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr17	34992115	34992548	+	0	NA	intron (Nintron (N	11817 NM_013975	3980	Hs.100299NM_002311	ENSG000003LIG3	LIG2 LIG3	long ligasprotein-coding
chr2-483c.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr2	48368007	48368423	+	0	NA	intron (Nintron (N	53533 NM_002158	3344	Hs.468478NM_002158	ENSG000003FOXN2	HTLF	forkhead protein-coding
chr2-149f.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr2	1.5E+08	1.5E+08	0	NA	intron (Nintron (N	-3572 NR_11024C	1.02E+08	Hs.5324 NR_11024C	ENSG000003LOC10192c	-	uncharactncRNA	
chr3-157f.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr3	15787181	15788361	+	0	NA	intron (Nintron (N	10208 NM_001345	23243	Hs.335233NM_015199	ENSG000003ANKRD28	PITK PPP1	ankyrin protein-coding
chr5-140f.6.180073	-0.52294	0.945453	-0.55311	0.580188	0.981636	chr5	1.41E+08	1.41E+08	0	NA	intron (Nintron (N	-8335 NM_003732	8637	Hs.594084NM_003732	ENSG000003EIF4EBP3	4E-BP3 4E	eukaryotiiprotein-coding	
chr5-51f.6.641857	0.420651	0.761024	0.552743	0.580444	0.981636	chr5	51527235	51527434	+	0	NA	intron (Nintron (N	95437 NR_015263	23312	Hs.511386NM_015263	ENSG000003DMXL2	DFNA71 PF	Dmx like protein-coding
chr8-388f.9.641857	0.420651	0.761024	0.552743	0.580444	0.981636	chr8	38835930	38836810	+	0	NA	intron (Nintron (N	30920 NM_001352	6867	Hs.279245NM_006283	ENSG000003TACC1	Ga55	transformprotein-coding
chr2-4657.7.940873	-0.47622	0.861691	-0.55266	0.580498	0.981636	chr2	46577950	46578374	+	0	NA	intron (Nintron (N	2076 NR_104182	1.01E+08	Hs.658541NR_104182	ENSG000003LOC10050c	-	uncharactncRNA
chr12-117.5.980869	0.529029	0.957286	0.552635	0.580513	0.981636	chr12	1.17E+08	1.17E+08	0	NA	intron (Nintron (N	6252 NM_010002	23014	Hs.740376NM_015002	ENSG000003FBX021	FBX21	F-box prprotein-coding	
chr15-88f.5.980869	0.529029	0.957286	0.552635	0.580513	0.981636	chr15	88885074	88885760	+	0	NA	intron (NAluS6 SI	10227 NM_0178232	145864	Hs.447533NM_178232	ENSG000003CHAPLN3	EXLD1 Hs1	hyaluron protein-coding
chr22-46f.5.980869	0.529029	0.957286	0.552635	0.580513	0.981636	chr22	46663147	46664404	+	0	NA	intron (Nintron (N	43389 NM_015124	23151	Hs.475155NM_015124	ENSG000003GRAMD4	DIP	GRAM domprotein-coding
chr7-745f.5.980869	0.529029	0.957286	0.552635	0.580513	0.981636	chr7	74528396	74531834	+	0	NA	intron (NAluS6 SI	-65853 NR_162116	1.13E+08	NR_162116	MIR10525	-	microRNA ncRNA
chr8-253f.5.980869	0.529029	0.957286	0.552635	0.580513	0.981636	chr8	25393515	25394928	+	0	NA	intron (NAluJr4 SI	30040 NM_001083	2796	Hs.82963 NM_000823	ENSG000003GNRH1	GNRH1 GRH1	gonadotrcprotein-coding
chr9-576f.10.18744	0.40614	0.735141	0.552466	0.580629	0.981636	chr9	5762266	5763755	+	0	NA	intron (Nintron (N	70105 NM_024896	79956	Hs.591078NM_024896	ENSG000003ERMP1	FXNA KIA1	endoplasmprotein-coding
chr3-170f.8.863786	-0.43594	0.789091	-0.55246	0.580631	0.981636	chr3	1.71E+08	1.71E+08	0	NA	intron (N2c LINE	2942 NR_135255	200916	Hs.380933NM_001099	ENSG000003RPL22L1	-	ribosomalprotein-coding	
chr5-334f.8.863786	-0.43594	0.789091	-0.55246	0.580631	0.981636	chr5	33464143	33447570	+	0	NA	intron (Nintron (N	6080 NR_047676	6897	Hs.481866NM_152295	ENSG000003TARS	ThrRS	threonyl-protein-coding
chr10-51f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr10	51697013	51698637	+	0	NA	exon (NM exon (NM	1770 NM_015233	23283	Hs.591355NM_015233	ENSG000003CSTF2T	CstF-64T	cleavage protein-coding
chr12-12c.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr12	1.23E+08	1.23E+08	0	NA	intron (NAluS2 SI	71992 NR_162094	1.13E+08	NR_162094	MIR9902-1	-	microRNA ncRNA	
chr12-13c.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr12	1.33E+08	1.33E+08	0	NA	intron (NAluY SINE	31076 NM_006231	5426	Hs.524871NM_006231	ENSG000003POLE	CRCS12 FIDNA	polynprotein-coding	
chr15-40f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr15	4019266	4020260	+	0	NA	intron (Nintron (N	24769 NM_001164	5888	Hs.631709NM_002875	ENSG000003RAD51	BRCC5 FAM	RAD51 reprotein-coding
chr15-50f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr15	50626520	50627214	+	0	NA	intron (Nintron (N	59930 NR_149154	54822	Hs.512894NM_017672	ENSG000003TRPM7	ALSPDC CF	transientprotein-coding
chr16-31f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr16	3127670	3129102	+	0	NA	intron (NAluJr SIN	6496 NR_11090C	1.01E+08	Hs.522143NR_110900	ZNF213-AS	-	ZNF213 arncRNA
chr16-57f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr16	57776810	57777565	+	0	NA	intron (Nintron (N	-2109 NM_001318	3801	Hs.23131 NM_005555	ENSG000003KIFC3	-	kinesin protein-coding
chr17-24f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr17	2471875	2472853	+	0	NA	intron (Nintron (N	39524 NM_024086	79066	Hs.632237NM_024086	ENSG000003METTL16	METTL10D	methyltrprotein-coding
chr17-50f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr17	50481910	50483050	+	0	NA	intron (Nintron (N	3620 NR_018346	55316	Hs.8033 NM_018346	ENSG000003RSAD1	HemW	radical Sprotein-coding
chr18-67f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr18	67505979	67506263	+	0	NA	TTS (NM_C TTS (NM_C	-10425 NR_033921	643542	Hs.652901NR_033921	ENSG000003LOC643542	-	uncharactncRNA
chr2-222f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr2	2.23E+08	2.23E+08	0	NA	intron (NLA_B_Mam	41070 NR_130154	10056	Hs.471452NM_005687	ENSG000003FARSB	FARSLB FF	phenylalprotein-coding	
chr4-478f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr4	47882163	47883001	+	0	NA	intron (Nintron (N	-31645 NR_125875	1.02E+08	Hs.13419CNR_125879	LOC101927	-	uncharactncRNA
chr6-734f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr6	73435658	73436886	+	0	NA	intron (Nintron (N	16025 NM_138441	115004	Hs.658405NM_138441	ENSG000003CGAS	G6orf150 cyclic	Gn protein-coding
chr7-127f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr7	1.27E+08	1.27E+08	0	NA	3' UTR (N3' UTR (N	22471 NM_176814	168850	Hs.159006NM_176814	ENSG000003ZNF800	-	zinc fingprotein-coding	
chr8-129f.4.419274	-0.60508	1.096301	-0.55193	0.580995	0.981636	chr8	1.3E+08	1.3E+08	0	NA	intron (Nintron (N	-57560 NM_031415	56169	Hs.133244NM_031415	ENSG000003GSDMC	MLZE	gasdermiiprotein-coding	
chr10-79f.8.805081	-0.44602	0.808177	-0.55188	0.581032	0.981636	chr10	79398023	79398282	+	0	NA	intron (Nintron (N	47472 NR_153367	219654	Hs.52308CNR_153367	ENSG000003ZCHC24	C10orf56 zinc	fingprotein-coding
chr4-564f.7.98987	-0.47461	0.860208	-0.55174	0.581126	0.981636	chr4	56496065	56497047	+	0	NA	intron (Nintron (N	-8653 NR_206919	132946	Hs.444445NM_206919	ENSG000003CARL9	-	ADP ribosprotein-coding
chr12-13c.9.202125	0.433756	0.786355	0.551603	0.581222	0.981636	chr12	1.32E+08	1.32E+08	0	NA	intron (Nintron (N	7184 NR_002975	677829	Hs.742405NR_002975	ENSG000003SNORA49	ACA49	small nucsnoRNA	
chr16-16f.12.02467	-0.38099	0.690755	-0.55156	0.581248	0.981636	chr16	16265712	16266231	+	0	NA	intron (NAluSx SIN	33376 Hs.460141NR_173614	ENSG000003NOMO2	Nomo PM5	NODAL nucprotein-coding		
chr11-63f.6.469599	0.500676	0.908003	0.551404	0.581357	0.981636	chr11	63949930	63951342	+	0	NA	intron (NAluSx3 SI	11305 NM_00130C	79829	Hs.523755NM_024771	ENSG000003NAA40	NAT11 NatN	(alpha)-protein-coding
chr13-98f.6.469599	0.500676	0.908003	0.551404	0.581357	0.981636	chr13	9839135	98392088	+	0	NA	intron (Nintron (N	130404 NM_003575	8428	Hs.508514NM_003575	ENSG000003STK24	HEL-H-S-95	serine/thprotein-coding
chr15-34f.6.469599	0.500676	0.908003	0.551404	0.581357	0.981636	chr15	34249941	34250985	+	0	NA	intron (Nintron (N	25447 NM_001288	51234	Hs.250906NM_016454	ENSG000003EMC4	PILG17 TMEER	dembrprotein-coding
chr20-35f.6.469599	0.500676	0.908003	0.551404	0.581357	0.981636	chr20	35944150	35945417	+	0	NA	intron (NAluSx1 SI	9843 NM_03363C	51282	Hs.584905NM_016555	ENSG000003SCAND1	RAZ1 SDP1	SCAN dembrprotein-coding
chr9-644f.6.469599	0.500676	0.908003	0.551404	0.581357	0.981636	chr9	6445428	6446711	+	0	NA	intron (NAluJb SIN	32870 NM_152896	115426	Hs.493401NM_152896	ENSG000003UHRF2	NIRF RNFI	ubiquitiiprotein-coding
chr1-392f.10.1953	0.404603	0.733823	0.551363	0.581385	0.981636	chr1	39297720	39303852	+	0	NA	intron (NAluSx SIN	-108287 NR_015038	643314	Hs.658766NM_015038	ENSG000003KIAA0754	-	KIAA0754 protein-coding
chr17-81f.10.1953	0.404603	0.733823	0.551363	0.581385	0.981636	chr17	81921923	81922775	+	0	NA	3' UTR (N3' UTR (N	1117 NM_032711	4097	Hs.252225NM_002355	ENSG000003MAFG	hMAF	MAF bZIP protein-coding
chr2-580f.10.1953	0.404603	0.733823	0.551363	0.581385	0.981636	chr2	58091963	58093607	+	0	NA	intron (Nintron (N	46073 NM_00113C	7444	Hs.715296NM_006299	ENSG000003VRK2	-	VRK seriprotein-coding
chr7-925f.10.1953	0.404603	0.733823	0.551363	0.581385	0.981636	chr7	92532582	92534171	+	0	NA	intron (Nintron (N	4587 NM_03212C	84060	Hs.21590 NM_03212C	ENSG000003CRBM48	C7orf64 FRNA	bindiprotein-coding
chr16-30f.5.4177																		



chr20-175.8.897068	-0.43182	0.784584	-0.55037	0.582062	0.981636	chr20	17941139	1.7242713	+0	NA	3' UTR (N3' UTR (N	21020 NR_00304E	692086 Hs. 680747NR_00304E	ENSG00000SNORD17	HBI-43	small nucsnoRNA
chr3-1504.8.897068	-0.43182	0.784584	-0.55037	0.582062	0.981636	chr3	1.5E+08	1.5E+08	+0	NA	intron (Nintron (N	50029 NM_001303	9819 Hs. 722477NM_01477E	ENSG00000TSC22D2	TILZ4a TITSC22	donor protein-coding
chr5-1392.8.897068	-0.43182	0.784584	-0.55037	0.582062	0.981636	chr5	1.39E+08	1.39E+08	+0	NA	promoter-promoter-	-602 NR_00291E	26821 Hs. 68489ENR_00291E	ENSG00000SNORA74A	RNU19 U19	small nucsnoRNA
chr1-155.6.590682	-0.50732	0.921836	-0.55033	0.58209	0.981636	chr1	45592356	45592932	+0	NA	intron (NAluX1 S1	8603 NM_15229E	4678 Hs. 319334NM_00248E	ENSG00000NASP	FLB7527 F	coiled- $\alpha$ protein-coding
chr2-177.6.045097	-0.56505	1.026896	-0.55025	0.582147	0.981636	chr2	1.08E+08	1.08E+08	+0	NA	intron (Nintron (N	23781 NM_019044	54520 Hs. 10784ENM_019044	ENSG00000CCDC93	-	coiled- $\alpha$ protein-coding
chr12-48.6.461741	0.503157	0.914458	0.550225	0.582165	0.981636	chr12	48070717	48071572	+0	NA	intron (Nintron (N	-34109 NM_001354	5213 Hs. 75160 NM_00028E	ENSG00000PFKM	ATP-PFK1 C	phosphofructokinase protein-coding
chr18-24.6.461741	0.503157	0.914458	0.550225	0.582165	0.981636	chr18	24066721	24067615	+0	NA	intron (Nintron (N	-46159 NM_001292	125488 Hs. 12857ENM_15321E	ENSG00000TTC39C	C18orf17 T	tetratric protein-coding
chr6-152.6.461741	0.503157	0.914458	0.550225	0.582165	0.981636	chr6	1.52E+08	1.52E+08	+0	NA	intron (Nintron (N	-30172 NR_120501	1.01E+08 Hs. 57120ENR_120501	SYNE1-AS1	SYNE1	antncRNA
chr7-736.6.461741	0.503157	0.914458	0.550225	0.582165	0.981636	chr7	73697169	73697615	+0	NA	intron (Nintron (N	13795 NR_045512	114049 Hs. 64706ENM_01752E	ENSG00000CUBD23	HASJ4442 BUD23	rRNA protein-coding
chr4-2677.9.315535	-0.42692	0.776582	-0.54975	0.582494	0.981636	chr4	26770520	26771458	+0	NA	Intergeni LIME LIN	89255 NR_13467E	1.05E+08 Hs. 54885ENR_134673	STIM2-AS1	STIM2	antncRNA
chr12-108.6.221213	-0.51882	0.943763	-0.54974	0.5825	0.981636	chr12	1.09E+08	1.09E+08	+0	NA	intron (NAluSz SIN	3836 NM_001161	54434 Hs. 19976ENM_018984	ENSG00000SSH1	SSH1L	slingshot protein-coding
chr16-367.6.221213	-0.51882	0.943763	-0.54974	0.5825	0.981636	chr16	3670594	3670793	+0	NA	intron (NAluJo SIN	15989 NM_001351	1773 Hs. 62963ENM_00522E	ENSG00000DNASE1	DNL1 DRN1	deoxyribonuclease protein-coding
chr8-6056.6.221213	-0.51882	0.943763	-0.54974	0.5825	0.981636	chr8	60589596	60590082	+0	NA	intron (NMER112 DN	72852 NM_00286E	5862 Hs. 369017NM_00286E	ENSG00000RAB2A	LHX1 RAB2	RAB2A, $\alpha$ protein-coding
chr11-12.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr11	1.2E+08	1.2E+08	+0	NA	intron (NLIME LIN	-7445 NM_001301	23365 Hs. 24598 NM_01531E	ENSG00000ARHGF12	LARG PRO2	Rho guanine protein-coding
chr13-95.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr13	95099461	95099712	+0	NA	intron (Nintron (N	-110758 NR_145733	1.1E+08 NR_145733	SNORD13G	-	small nucsnoRNA
chr17-19.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr17	19939252	19939580	+0	NA	intron (NL2b LINE	38412 NM_007202	11216 Hs. 64267ENM_007202E	ENSG00000AKAP10	AKAP-10 A	kinase protein-coding
chr19-56.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr19	56093390	56093741	+0	NA	intron (Nintron (N	-26881 NR_110741	1.02E+08 Hs. 43465ENR_110741E	ENSG00000LINC01864	-	long intncRNA
chr20-19.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr20	19823968	19824241	+0	NA	Intergeni Intergeni	-62417 NM_001242	54453 Hs. 47227ENM_01899E	ENSG00000RIN2	MACS RASS	Ras and F protein-coding
chr4-7697.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr4	76974260	76976222	+0	NA	intron (Nintron (N	25489 NM_00130E	55752 Hs. 12819ENM_01824E	ENSG00000SEPTIN11	11-Sep	septin 11 protein-coding
chr5-15.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr5	1.52E+08	1.52E+08	+0	NA	intron (Nintron (N	5181 NM_00404E	475 Hs. 12521ENM_00404E	ENSG00000CATOX1	ATX1 HAH1	antioxidant protein-coding
chr6-173.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr6	17397174	17397474	+0	NA	intron (NAluSx SIN	3729 NM_00636E	10486 Hs. 13290ENM_00636E	ENSG00000CAP2	-	cyclase $\epsilon$ protein-coding
chr6-144.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr6	1.45E+08	1.45E+08	+0	NA	intron (NAluSz SIN	149973 NR_13277E	1.07E+08 NR_13277E	SNORA98	-	small nucsnoRNA
chr8-140.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr8	1.41E+08	1.41E+08	+0	NA	intron (NLIMD LINE	-76003 NR_02989E	442893 NR_02989E	ENSG00000MIR151A	MIR151 MI	microRNA ncRNA
chr9-12.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chr9	1.29E+08	1.29E+08	+0	NA	intron (Nintron (N	38235 NR_16319E	56904 Hs. 46023ENM_02014E	ENSG00000SH3GLB2	PP6569 PF	SH3 domain protein-coding
chrX-535.6.616106	-0.49947	0.908589	-0.54972	0.58251	0.981636	chrX	53599611	53600587	+0	NA	intron (Nintron (N	-42825 NR_029484	406889 NR_029484	ENSG00000MIRLET7F2	LET7F2 MI	microRNA ncRNA
chr6-342.9.356674	-0.42428	0.772917	-0.54894	0.583048	0.981636	chr6	34263321	34263604	+0	NA	Intergeni Intergeni	-14454 NM_001287	221491 Hs. 38130ENM_17850E	ENSG00000SMIM29	C6orf11 L	small int protein-coding
chr7-995.6.115552	-0.38167	0.695293	-0.54894	0.583049	0.981636	chr7	99560731	99562605	+0	NA	intron (Nintron (N	2834 NM_00136E	79027 Hs. 59979ENM_02406E	ENSG00000ZNF655	VIK VIK	zinc finger protein-coding
chr2-190.9.340958	-0.4214	0.767708	-0.5489	0.583071	0.981636	chr2	1.91E+08	1.91E+08	+0	NA	intron (NL2 LINE	42253 NM_01490E	2744 Hs. 11644ENM_01490E	ENSG00000GLS	AAD20 CAS	glutamine protein-coding
chr12-70.6.128338	-0.37362	0.680693	-0.54888	0.583084	0.981636	chr12	7080128	7083591	+0	NA	intron (Nintron (N	10034 NM_001354	715 Hs. 524224NM_00173E	ENSG00000C1R	EDSPD1	complement protein-coding
chr1-466.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr1	46635132	46635502	+0	NA	3' UTR (N3' UTR (N	-18426 NM_021404	148932 Hs. 632401NM_14527E	ENSG00000MOB3C	MOB1E MOB	MOB kinase protein-coding
chr1-230.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr1	2.3E+08	2.3E+08	+0	NA	intron (Nintron (N	136145 NM_004481	2590 Hs. 743964NM_004481E	ENSG00000GALNT2	GalNAc-T2	polypeptide protein-coding
chr10-27.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr10	27214151	27215011	+0	NA	intron (Nintron (N	25905 NM_001301	143570 Hs. 530597NM_14569E	ENSG00000ACDB5	acyl-CoA	protein-coding
chr11-74.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr11	74867984	74869379	+0	NA	intron (NLIPA14 LI	80410 NM_00127C	143570 Hs. 37014ENM_18296E	ENSG00000XRR1A	-	X-ray rac protein-coding
chr12-13.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr12	1.32E+08	1.32E+08	+0	NA	intron (Nintron (N	24291 NR_00297E	677829 Hs. 74240ENR_00297E	ENSG00000SNORA49	ACA49	small nucsnoRNA
chr19-56.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr19	56398212	56399655	+0	NA	non-codiron-codir	-5081 NM_00115E	147949 Hs. 146854NM_15247E	ENSG00000ZNF583	-	zinc finger protein-coding
chr20-33.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr20	33670969	33671769	+0	NA	intron (NL3 LINE C	3059 NM_03123E	63941 Hs. 51698ENM_03123E	ENSG00000NECAB3	APBA2BP E	zinc finger protein-coding
chr4-714.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr4	71450603	71451564	+0	NA	intron (Nintron (N	112030 NM_00375E	8671 Hs. 5462 NM_00375E	ENSG00000SLC44A	HNBC1 KNE	solute $\alpha$ protein-coding
chr7-554.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chr7	55491687	55492613	+0	NA	intron (Nintron (N	34730 NM_001321	81552 Hs. 488307NM_03079E	ENSG00000VOPP1	ECOP GASF	VOPP1 WW protein-coding
chrX-4791.6.477457	0.498275	0.908075	0.548716	0.5832	0.981636	chrX	47915231	47916300	+0	NA	exon (NM exon (NM	78863 NM_001737	347344 Hs. 11442ENM_007137E	ENSG00000ZNF81	HFZ20 MR	zinc finger protein-coding
chr17-75.9.673289	0.414161	0.754996	0.548561	0.583307	0.981636	chr17	7508202	7510150	+0	NA	exon (NM exon (NM	24810 NM_000937	5430 Hs. 270017NM_000937	POLR2A	POLR2 POL	RNA polyn protein-coding
chr19-55.9.673289	0.414161	0.754996	0.548561	0.583307	0.981636	chr19	55302774	55304290	+0	NA	intron (NMIR3 SINE	19535 NM_03243C	84446 Hs. 182081NM_03243E	ENSG00000BRSK1	hSAD1	BR serine protein-coding
chr2-22.9.673289	0.414161	0.754996	0.548561	0.583307	0.981636	chr2	49363214	49365390	+0	NA	intron (Nintron (N	8860 NM_01538C	25813 Hs. 505824NM_01538E	ENSG00000SAMM50	CGI-51 O	SAMM50 sc protein-coding
chr4-884.9.673289	0.414161	0.754996	0.548561	0.583307	0.981636	chr4	88433460	88434046	+0	NA	intron (NMSTC LTR	-23366 NM_01632E	51191 Hs. 26663 NM_01632E	ENSG00000CHERC5	CEB1 CEB	HCT and protein-coding
chr13-10.5.718617	-0.55815	1.017837	-0.54836	0.583441	0.981636	chr13	1.03E+08	1.03E+08	+0	NA	intron (NAluJr SIN	40906 NM_00101C	196541 Hs. 50862ENM_00101E	ENSG00000METTL21C	C13orf39	methyltransferase protein-coding
chr5-698.12.09123	-0.37475	0.683424	-0.54835	0.583455	0.981636	chr5	69895568	69895981	+0	NA	intron (NMER3 DNA	5796 NR_16065E	1.03E+08 Hs. 71115ENR_16065E	LOC102724	-	POM121 trpseud
chr11-77.4.452555	-0.59658	1.088532	-0.54806	0.583652	0.981636	chr11	77926999	77927773	+0	NA	intron (Nintron (N	67282 NM_033547	92105 Hs. 53372ENM_033547E	ENSG00000INTS4	INT4 MSTC	integrator protein-coding
chr15-55.4.452555	-0.59658	1.088532	-0.54806	0.583652	0.981636	chr15	55987875	55988824	+0	NA	intron (NLH5 LINE	5263 NM_00132E	4734 Hs. 1565 NM_00615E	ENSG00000NEDD4	NEDD4-1 N	NEDD4 E3 protein-coding
chr16-88.4.452555	-0.59658	1.088532	-0.54806	0.583652	0.981636	chr16	88407862	88408415	+0	NA	Intergeni Intergeni	-19333 NM_00136E	84627 Hs. 54925 NM_001127E	ENSG00000ZNF469	BCS BCS1	zinc finger protein-coding
chr19-79.4.452555	-0.59658	1.088532	-0.54806	0.583652	0.981636	chr19	7984287	7985162	+0	NA	intron (NAGGC n S	20917 NM_00141E	1994 Hs. 18449ENM_00141E	ENSG00000ELAVL1	ELAV1 HUF	ELAV like protein-coding
chr2-2374.4.452555	-0.59658	1.088532	-0.54806	0.583652	0.981636	chr2	2.37E+08	2.37E+08	+0	NA	intron (Nintron (N	3641 NR_10401E	79083 Hs. 10240ENM_02410E	ENSG00000MLPH	SLAC2	

chr5-1317	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr5	38483882	38486213	+	0	NA	intron (Nintron (N	39501	NM_182801	133584	Hs.20103	NM_152405	ENSG00000CEGLM	AGRINL ACEGF like, protein-coding	
chr5-1317	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr5	1.32E+08	1.32E+08	+	0	NA	intron (NAluSz SIN	79072	NM_001008	96459	Hs.591275	NM_133375	ENSG00000FN1P1	- folliculiprotein-coding	
chr5-1793	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr5	1.79E+08	1.79E+08	+	0	NA	intron (Nintron (N	28917	NM_014244	9509	Hs.23871	NM_014244	ENSG00000CADAMTS2	ADAM-TS2 ADAM metz protein-coding	
chr6-3195	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr6	31951289	31952800	+	0	NA	TTS (NM_C	4886	NR_031601	1E+08	NR_031601	ENSG00000MIR1236	MIRN1236 microRNA ncRNA		
chr6-1135	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr6	1.14E+08	1.14E+08	+	0	NA	non-codiron-codir	-24337	NR_125845	1.02E+08	Hs.12928CN	R_125845	ENSG00000HDAC2-AS2	HDAC2 ancncRNA	
chr7-1385	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	96750	NM_001331	136306	Hs.99414	NM_174955	ENSG00000CSVOP1	- SVOP like protein-coding	
chr9-3245	6.682669	-0.48828	0.895047	-0.54554	0.585382	0.981636	chr9	32496191	32497698	+	0	NA	intron (NLM2 LIN	29252	NM_014314	23586	Hs.190622	NM_014314	ENSG00000DDX58	RIG-I RIC DEX H-bc protein-coding	
chr1-7741	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr1	77417962	77419000	+	0	NA	intron (Nintron (N	135394	NM_012093	26289	Hs.559715	NM_012093	ENSG00000AK5	AK6 adenylate protein-coding	
chr11-625	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr11	62643342	62644363	+	0	NA	intron (NAluJo SIN	2761	NM_001325	23193	Hs.595071	NM_014611	ENSG00000GANAB	G2AN GII glucosidase protein-coding	
chr15-784	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr15	78439963	78442843	+	0	NA	intron (Nintron (N	2982	NM_001324	3658	Hs.436031	NM_004133	ENSG00000IREB2	AC03 IRE-iron resp protein-coding	
chr16-692	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr16	69284472	69285104	+	0	NA	intron (NAluSx3 SI	-26562	NM_013245	27183	Hs.12842CN	NM_013245	ENSG00000VPS4A	SKD1 SKD1 vacuolar protein-coding	
chr2-3728	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr2	37281137	37282160	+	0	NA	intron (NMLT1A LI	35436	NM_005813	23683	Hs.660757	NM_005813	ENSG00000PRKD3	EPK2 PKC-protein k protein-coding	
chr2-6122	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr2	61222624	61223444	+	0	NA	intron (Nintron (N	45616	NR_152211	130872	Hs.655602	NM_152392	ENSG00000AHSAP2	AHA1 AHS activator pseudo	
chr3-3	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr3	12834073	12840697	+	0	NA	intron (NLM2E4 LI	3065	NM_001007	6161	Hs.265174	NM_000994	ENSG00000RPL32	L32 PP993 ribosomal protein-coding	
chr4-1195	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr4	1.2E+08	1.2E+08	+	0	NA	intron (NMER5A DNA	75238	NR_037630	645513	Hs.677545	NR_037630	ENSG00000LOC645513	- septin 7 pseudo	
chr5-3891	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr5	38917359	38919089	+	0	NA	intron (NMER115 DN	72212	NM_001322	9180	Hs.120655	NM_003995	ENSG00000OSMR	IL-31R-beoncotat protein-coding	
chr6-154	9.366382	-0.41606	0.762807	-0.54543	0.585457	0.981636	chr6	1.55E+08	1.55E+08	+	0	NA	intron (Nintron (N	-42963	NR_036100	1E+08	NR_036100	ENSG00000MIR1273C	- microRNA ncRNA		
chr10-62	9.640007	-0.41171	0.754487	-0.545365	0.585502	0.981636	chr10	6233310	6234521	+	0	NA	non-codiron-codir	30983	NM_004566	5209	Hs.195471	NM_004566	ENSG00000PFKFB3	IPPK2 PFK6-phospho protein-coding	
chr10-615	9.640007	-0.41171	0.754487	-0.545365	0.585502	0.981636	chr10	61902352	61903132	+	0	NA	intron (Nintron (N	1043	NM_032195	84159	Hs.535297	NM_032195	ENSG00000ARID5B	DESKT MR AT-rich iprotein-coding	
chr12-577	9.640007	-0.41171	0.754487	-0.545365	0.585502	0.981636	chr12	57784994	57787850	+	0	NA	intron (Nintron (N	3635	NM_001172	10102	Hs.632704	NM_005725	ENSG00000TSPM	EFTS EFTS Ts transl protein-coding	
chr2-227	9.640007	-0.41171	0.754487	-0.545365	0.585502	0.981636	chr2	2.28E+08	2.28E+08	+	0	NA	exon (NM exon (NM	52612	NM_001133	3267	Hs.352962	NM_004504	ENSG00000AGFG1	HRB SAR Far GAP wiprotein-coding	
chr3-4937	9.640007	-0.41171	0.754487	-0.545365	0.585502	0.981636	chr3	49371575	49373527	+	0	NA	intron (NAluV SINE	-13951	NM_001325	2876	Hs.76686	NM_000581	ENSG00000GPIX1	GPXD GSH glutathic protein-coding	
chr2-6647	9.838207	-0.42908	0.786869	-0.5453	0.585545	0.981636	chr2	66475545	66476204	+	0	NA	intron (Nintron (N	-35544	NR_046625	1.01E+08	Hs.734695	NR_046625	ENSG00000MEIS1-AS2	MEIS1-AS1 MEIS1 antncRNA	
chr5-1408	9.838207	-0.42908	0.786869	-0.5453	0.585545	0.981636	chr5	1.41E+08	1.41E+08	+	0	NA	intron (NAluSc8 SI	5182	NM_002109	3035	Hs.528035	NM_002109	ENSG00000HARS	CM2W HRS histidyl- protein-coding	
chr1-1991	9.282253	-0.43134	0.791045	-0.54528	0.58556	0.981636	chr1	19912380	19912579	+	0	NA	3' UTR (N3' UTR (N	11138	NM_014585	30814	Hs.272372	NM_014585	ENSG00000PLAZG2E	G1IE sPLA phospholiprotein-coding	
chr14-731	8.167809	-0.468247	0.85874	-0.545272	0.585566	0.981636	chr14	73161265	73161561	+	0	NA	intron (Nintron (N	24906	NM_007318	5663	Hs.3260	NM_000021	ENSG00000PSENI	ACNIN34B p preniliprotein-coding	
chr22-387	8.946065	-0.4305	0.789629	-0.54519	0.585621	0.981636	chr22	38738711	38739408	+	0	NA	intron (Nintron (N	16407	NM_001195	25777	Hs.517622	NM_015374	ENSG00000SUN2	UNCN8V3 Sadl and protein-coding	
chr10-792	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr10	79222378	79222738	+	0	NA	intron (Nintron (N	-124911	NM_005725	10105	Hs.381072	NM_005725	ENSG00000PPIF	CYP3 Cyp-peptidyl protein-coding	
chr14-311	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr14	31172816	31173392	+	0	NA	intron (Nintron (N	34689	NM_015382	25831	Hs.708017	NM_015382	ENSG00000HECTD1	EULIR HECT dome protein-coding	
chr15-658	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr15	65880991	65882644	+	0	NA	intron (Nintron (N	12326	NM_001206	8766	Hs.321541	NM_004663	ENSG00000RAB11A	YL8 RAB11A, n protein-coding	
chr15-825	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr15	82989703	82990465	+	0	NA	TTS (NM_C	3874	NM_031452	83640	Hs.80624	NM_031452	ENSG00000CRAMAC	C15orf18 RNA guaniprotein-coding	
chr2-3945	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr2	39458485	39459480	+	0	NA	intron (NLM2E1 LIN	21566	NR_037875	728730	Hs.655344	NR_037875	ENSG00000MAP4K3-D1	MAP4K3 dincRNA	
chr2-2066	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr2	2.06E+08	2.06E+08	+	0	NA	intron (NAluV SINE	42439	NM_001177	54891	Hs.443915	NM_017755	ENSG00000INOS8D	- INOS8 conprotein-coding	
chr20-938	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr20	9385453	9386328	+	0	NA	intron (NSVA_A Ret	78090	NM_000933	5332	Hs.472101	NM_000933	ENSG00000PLCB4	ARCND2 P phospholiprotein-coding	
chr20-595	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr20	59942541	59943180	+	0	NA	intron (Nintron (N	2471	NM_001190	63939	Hs.54973	NM_022105	ENSG00000FAM217B	C20orf177 family wiprotein-coding	
chr3-1005	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr3	1E+08	1E+08	+	0	NA	3' UTR (N3' UTR (N	-10677	NR_020202	55161	Hs.439152	NM_020202	ENSG00000CNIT2	HEL-5-8a nitrilase protein-coding	
chr4-4194	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr4	41944108	41946296	+	0	NA	intron (Nintron (N	9773	NM_018125	55161	Hs.31082	NM_018125	ENSG00000TMEM33	1600019D1 transmemt protein-coding	
chr4-8296	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr4	82968895	82969876	+	0	NA	intron (NLM2C LINE	41438	NR_110255	132660	Hs.96952	NM_194282	ENSG00000LINS5A	CCDC1 J Lin-15 Df protein-coding	
chr5-6938	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr5	69386660	69388115	+	0	NA	intron (Nintron (N	15933	NM_133335	5884	Hs.16184	NM_002875	ENSG00000RAD17	CCXC HRAI RAD17 pf protein-coding	
chr7-4441	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr7	44419345	44419564	+	0	NA	intron (NLM2A LIN	71204	NM_015332	23386	Hs.488171	NM_015332	ENSG00000NUDCD3	NudCL NudC dome protein-coding	
chr7-8174	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr7	81747074	81748753	+	0	NA	intron (NAluSx SIN	22134	NM_001010	3082	Hs.396530	NM_000601	ENSG00000HGF	DFNB39 F-hepatocyt protein-coding	
chr7-1575	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr7	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	40596	NM_058245	10049	Hs.490745	NM_005494	ENSG00000DNABJ6	DJ4 DnaJ DnaJ heat protein-coding	
chr8-2816	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr8	28160506	28161412	+	0	NA	intron (NAluSx SIN	67820	NM_001284	55140	Hs.491335	NM_018091	ENSG00000CELP3	KAT9 heator protein-coding	
chr8-1406	6.64153	-0.49191	0.902434	-0.54509	0.58569	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (NLM2B LINE	20530	NM_001352	5747	Hs.395482	NM_005607	ENSG00000PTK2	FADK FAK protein t protein-coding	
chr1-1982	8.88921	-0.43029	0.789614	-0.54494	0.585794	0.981636	chr1	1.98E+08	1.98E+08	+	0	NA	intron (NLM2A LIN	55243	NM_133494	140609	Hs.24119	NM_133494	ENSG00000CNEK7	- NIMA rel protein-coding	
chr12-925	8.88921	-0.43029	0.789614	-0.54494	0.585794	0.981636	chr12	92856382	92857471	+	0	NA	intron (NAluJr SIN	72369	NM_003566	8411	Hs.567367	NM_003566	ENSG00000EEA1	MST105 M early enc protein-coding	
chr17-44C	8.88921	-0.43029	0.789614	-0.54494	0.585794	0.981636	chr17	44054497	44054833	+	0	NA	intron (Nintron (N	12006	NM_001371445	12843	NM_001371428				
chr2-2075	8.88921	-0.43029	0.789614	-0.54494	0.585794	0.981636	chr2	2.08E+08	2.08E+08	+	0	NA	intron (NAluSx1 SI	12368	NM_018247	55754	Hs.108533	NM_018247	ENSG00000TMEM30A	C6orf67 C transmemt protein-coding	
chr6-7527	8.88921	-0.43029	0.789614	-0.54494	0.585794	0.981636	chr6	75271786	75273062	+	0	NA	intron (NLM2E1 LI	-9061	NR_036214	1E+08	NR_036214	ENSG00000MIR4253	- microRNA ncRNA		
chr1-2287	6.444176	-0.494447	0.907715	-0.544716	0.585949	0.981636	chr1	22870824	22873750	+	0	NA	intron (NMLT1E2 LI	62519897	62520940	77102	Hs.209155	NM_014495	ENSG00000ANGPTL3	ANG-5 ANG angiopoie protein-coding	
chr10-4951	6.4																				



chr17-395	10.17773	0.398975	0.734925	0.542878	0.587214	0.981636	chr17	39983754	39996546	+	0	NA	exon (NM_exon (NM_9343 NM_002806	5709 Hs.12970 NM_002806	ENSG000003PSMD3	P58 RPN3	proteasome protein-coding	
chr19-256	10.17773	0.398975	0.734925	0.542878	0.587214	0.981636	chr19	25995177	25995652	+	0	NA	Intergeni ALR Alpha -1798017 NR_146733	1.02E+08 Hs.567934NR_110687	ENSG000001LOC101927-		uncharactericRNA	
chr19-477	10.17773	0.398975	0.734925	0.542878	0.587214	0.981636	chr19	47701282	47702714	+	0	NA	exon (NM_exon (NM_11424 NM_014601	30846 Hs.744962NM_014601	ENSG000004EHD2	PAST2	EH domain protein-coding	
chr2-105	10.17773	0.398975	0.734925	0.542878	0.587214	0.981636	chr2	1.05E+08	1.05E+08	+	0	NA	3' UTR (N3' UTR (N_9436 NM_001286	79074 Hs.549577NM_024093	ENSG000002C2orf49	asw	chromosome protein-coding	
chr1-6674	9.389956	-0.42034	0.7743	-0.54287	0.58722	0.981636	chr1	66742960	66743269	+	0	NA	3' UTR (N3' UTR (N_9345 NM_152666	200132 Hs.479222NM_152666	ENSG000001CTCX1D1		telomeric protein-coding	
chr20-215	5.922164	0.51814	0.955188	0.542449	0.587509	0.981636	chr20	21365546	21366689	+	0	NA	intron (N(TA)n Sin 31409 NM_033176	644524	NM_033176	ENSG000002CNKX2-4	NKX2.4 NKX2 homec	protein-coding
chr3-815	5.922164	0.51814	0.955188	0.542449	0.587509	0.981636	chr3	81532035	81534365	+	0	NA	intron (Nintron (N_228445 NM_000158	2632 Hs.436062NM_000158	ENSG000001GBE1	APBD GBE1	1,4-alpha protein-coding	
chr3-1136	5.922164	0.51814	0.955188	0.542449	0.587509	0.981636	chr3	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N_22592 NM_001005	205717 Hs.632572NM_001005	ENSG000001USF3	KIAA2018	upstream protein-coding	
chr5-1791	5.922164	0.51814	0.955188	0.542449	0.587509	0.981636	chr5	1.79E+08	1.79E+08	+	0	NA	intron (Nintron (N_67260 NM_014594	30832 Hs.272322NM_014594	ENSG000002ZNF354C	KID3	zinc fing protein-coding	
chr7-5485	5.922164	0.51814	0.955188	0.542449	0.587509	0.981636	chr7	5489097	5491121	+	0	NA	exon (NM_exon (NM_5808 NR_03031E	693174	NR_03031E	ENSG000001MIR589	MIRN589	lmiRNA ncRNA
chr19-404	10.21102	0.401559	0.740366	0.542379	0.587557	0.981636	chr19	4047126	4048424	+	0	NA	exon (NM_exon (NM_17754 NM_001317	51341 Hs.591384NM_015898	ENSG000002ZBTB7A	FBI-1 FBI zinc fing	protein-coding	
chr11-356	6.582825	-0.50556	0.932118	-0.54237	0.587561	0.981636	chr11	35665123	35665701	+	0	NA	intron (N(LIME3B LI 2637 NM_017583	54765 Hs.192103NM_017583	ENSG000001TRIM44	AN3 DIPB	tripartit protein-coding	
chr1-285	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr1	28536319	28537056	+	0	NA	intron (Nintron (N_16330 NR_003105	54952 Hs.533622NM_017844	ENSG000001TRNAUIAP	PRO1902 S	tRNA sele protein-coding	
chr1-2917	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr1	29178254	29179345	+	0	NA	intron (Nintron (N_3056 NM_005622E	6429 Hs.469972NM_005622	ENSG000001SRSF4	SFRS4 SRF	serine ar protein-coding	
chr1-5181	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr1	51811324	51813302	+	0	NA	intron (NAluJb SIN 24089 NR_03158C	1E+08	NR_03158C	ENSG000001MIR761	hsa-mir-7	miRNA ncRNA
chr1-2254	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr1	2.25E+08	2.25E+08	+	0	NA	3' UTR (N3' UTR (N_25615 NM_002299E	3930 Hs.435166NM_002299	ENSG000001LBR	C14SR DHC	lamin B 1 protein-coding	
chr10-124	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	intron (N(Tiger3a  14039 NM_212554	399818 Hs.720819NM_212554	ENSG000001EEFIAMKT2	C10orf13 EEEF1A	lys protein-coding	
chr11-351	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr11	35168795	35169734	+	0	NA	intron (N(L2b LINE  6314 NR_145794	1.1E+08	NR_145794	SNORD164	small nucsnRNA	
chr12-327	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr12	32725719	32727287	+	0	NA	intron (N(TTC)n Si 29394 NM_00104C	51067 Hs.505231NM_015933	ENSG000001YARS2	CGI-04 ML	tyrosyl-t protein-coding	
chr12-64	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr12	64071176	64071725	+	0	NA	intron (N(L2b LINE  150846 NM_00130C	144577 Hs.444671NM_152444	ENSG000001C12orf66		chromoson protein-coding	
chr12-105	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N_45440 NM_15231E	121053 Hs.225562NM_15231E	ENSG000001C12orf45		chromoson protein-coding	
chr12-107	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr12	1.08E+08	1.08E+08	+	0	NA	intron (N(LIM4 LINE 16079 NM_001317	11137 Hs.506652NM_007062	ENSG000001PWP1	TEF-SSP-5 PWP1	homc protein-coding	
chr13-454	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr13	4509629	45410025	+	0	NA	intron (NAluSx1 SI -8335 NR_047031	1.01E+08 Hs.658033NR_047031	ENSG000001SLC25A30-	SLC25A30	ncRNA	
chr14-106	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	promoter-promoter- 287 NR_00320E	767590	NR_00320E	ENSG000001SNORD114-	14q	(II-12 small nucsnRNA
chr18-256	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr18	256462	259677	+	0	NA	intron (N(LIMEg LIN 9978 NM_005131	9984 Hs.712542NM_005131	ENSG000001THOC1	HPRI P84 THO	compl protein-coding	
chr2-6121	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr2	61218280	61220111	+	0	NA	intron (N(LIMC3 LIN 41777 NR_152211	130872 Hs.655602NM_152392	ENSG000001AHS2P	AHA1 AHS2	activator pseudo	
chr2-6652	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr2	66520424	66521505	+	0	NA	intron (Nintron (N_-53066 NR_110151E	1.01E+08 Hs.667942NR_110151	ENSG000001LINC0179E		long intencRNA	
chr2-2017	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (NAluSx1 SI -4478 NM_033066E	58538 Hs.63085 NM_033066	ENSG000001MPP4	ALS2CR5 E	membrane protein-coding	
chr2-227	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr2	27890773	27893179	+	0	NA	intron (N(MIR SINE  27238 NM_001284	23760 Hs.705322NM_012393	ENSG000001PITPNB	PI-TP-beta	phosphatid protein-coding	
chr3-115	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr3	11554721	11557553	+	0	NA	TTS (NM_C(TTS (NM_C_12661 NM_00112E	9686 Hs.740389NM_014667	ENSG000001VGLL4	VGL-4	vestigial protein-coding	
chr3-273	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr3	27304311	27305168	+	0	NA	intron (Nintron (N_64644 NM_199347	152110 Hs.506119NM_152534	ENSG000001CNK10		NIMA rele protein-coding	
chr3-1361	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr3	1.36E+08	1.36E+08	+	0	NA	exon (NM_exon (NM_49397 NR_001144E	55167 Hs.18631 NM_018133	ENSG000001MSL2	MSL-2 MSL	masl protein-coding	
chr3-1971	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	exon (NM_exon (NM_47281 NR_00136E	1739 Hs.292545NM_004087	ENSG000001DLG1	DLGH1 SAF	discs lar protein-coding	
chr5-164	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr5	16461712	16462923	+	0	NA	intron (Nintron (N_3483 NM_033414	90441 Hs.60300 NM_033414	ENSG000001ZNF622	ZNF622	zinc fing protein-coding	
chr5-6911	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr5	69118625	69120734	+	0	NA	intron (N(LIME3G LI 25665 NM_002290E	64924 Hs.631977NM_022902	ENSG000001SLC30A5	ZNT5 ZNTL	solute c protein-coding	
chr5-1314	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr5	1.31E+08	1.31E+08	+	0	NA	intron (NAluJr SIN 164352 NM_00103E	56990 Hs.508825NM_020244	ENSG000001CDC42SE2	SPEC2	CD42 nuc protein-coding	
chr5-1464	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (Nintron (N_31662 NM_194251	134391 Hs.483732NM_194251	ENSG000001GPR151	GALR4 GAI	G protein-coding	
chr7-229	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr7	22969838	22979753	+	0	NA	intron (N(L2a LINE  43725 NM_032581	84668 Hs.85603 NM_032581	ENSG000001FAM126A	DRCTNNB1 f	family wiprotein-coding	
chr7-2332	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr7	23323930	23329564	+	0	NA	intron (N(LIP3 LIN 27408 NM_138444E	115416 Hs.87385 NM_138444	ENSG000001MALSU1	MALSU1	miRNA tohcn protein-coding	
chr7-3001	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr7	30016586	30019151	+	0	NA	intron (NAluSx4 SI 8834 NR_04647E	55033 Hs.390833NM_017944	ENSG000001FKBP14	EDSKMH EK	FKBP pro protein-coding	
chr8-479	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr8	47925222	47927867	+	0	NA	intron (Nintron (N_33542 NM_001081	5591 Hs.491682NM_006904	ENSG000001PRKDC	DNA-PKC T	protein k protein-coding	
chr8-6708	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr8	67088962	67088962	+	0	NA	intron (Nintron (N_3793 NM_001291	79848 Hs.370147NM_024793	ENSG000001CSP1	CSP1 JBT	centroson protein-coding	
chr8-1002	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr8	1E+08	1E+08	+	0	NA	intron (Nintron (N_13805 NM_001352	25897 Hs.292882NM_015433	ENSG000001RNFP19A	RNFP19	ring fing protein-coding	
chr8-140	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (NAluSx1 SI 51860 NM_001164	27161 Hs.660189NM_012154	ENSG000001AGO2	CASC7 EIF	argonaute protein-coding	
chr9-154	6.674811	-0.48637	0.896868	-0.5423	0.58761	0.981636	chr9	15437258	15440643	+	0	NA	intron (N(LIMB4 LIN 16074 NR_161444E	6619 Hs.546295NM_003084	ENSG000001SNAPC3	PTFbeta s	small nuc protein-coding	
chr8-6717	7.5968	0.484871	0.894157	0.542266	0.587635	0.981636	chr8	67174620	67174990	+	0	NA	intron (Nintron (N_90957 NM_001291	79848 Hs.370147NM_024793	ENSG000001CSP1	CSP1 JBT	centroson protein-coding	
chr11-618	6.485315	0.49588	0.914677	0.542137	0.587724	0.981636	chr11	61875737	61877593	+	0	NA	intron (Nintron (N_1613 NR_106804	1.02E+08	NR_106804	ENSG000001MIR6746	hsa-mir-6	miRNA ncRNA
chr11-12	6.485315	0.49588	0.914677	0.542137	0.587724	0.981636	chr11	1.26E+08	1.26E+08	+	0	NA	intron (Nintron (N_3995 NR_037647	55572 Hs.317193NM_017547	ENSG000001FOXRED1	FP634 HI	FAD deper protein-coding	
chr19-556	6.485315	0.49588	0.914677	0.542137	0.587724	0.981636	chr19	55234030	55234852	+	0	NA	intron (N(LIM4 LINE -3489 NR_106862	1.02E+08	NR_106862	ENSG000001MIR6804	hsa-mir-6	miRNA ncRNA
chr2-2305	6.485315	0.49588	0.914677	0.542137	0.587724	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (N(Tiger1 E -42473 NM_00120E	6672 Hs.369056NM_003113	ENSG000001SP100	lysp100b	SP100 nuc protein-coding	
chr4-165	6.485315	0.49588	0.914677	0.542137	0.587724	0.981636	chr4	16507718	16508193	+	0	NA	intron (Nintron (N_28192 NR_027697	202020 Hs.445319NM_152684	ENSG000001TAPT1-AS1-	TAPT1	antncRNA	
chr6-108	6.485315	0.49588	0.914677	0.542137	0.587724	0.981636	chr6	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N_41763 NM_00130C	8724 Hs.12102 NM_003793	ENSG000001SNX3	Grd19 MC	sorting r protein-coding	
chr1-1677	9.739852	0.419542	0.774015	0.542033	0.587795	0.981636	chr1	1.68E+08	1.68E+08	+	0	NA	intron (N					



chr1-9152	10.68403	0.393666	0.727443	0.541164	0.588395	0.981636	chr1	9152068	9152267	+	0	NA	promoter-promoter-	-390 NR_02961C	407040	NR_02961C	ENSG000002MIR34A	MIRN34A nmicroRNA	ncRNA				
chr8-1245	10.68403	0.393666	0.727443	0.541164	0.588395	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	exon (NM exon (NM	14174 NM_00500F	4715	Hs.15977	NR_00500F	ENSG000002NDUFB9	B22 C1-BE	NADH:ubiquitin-protein-coding			
chr1-1247	14.89476	0.335417	0.619864	0.541114	0.588429	0.981636	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alpha	3210979 NR_00395E	647121	Hs.697682	NR_00395E	ENSG000002CEMBP1	-	emarginin f pseudo			
chr11-515	14.89476	0.335417	0.619864	0.541114	0.588429	0.981636	chr11	51965636	51966224	+	0	NA	IntergeniALR/Alpha	1556783 NR_02450A	646813	Hs.684175	NR_02450A	LOC646813	-	DEXH-box pseudo			
chr1-2361	3.735224	0.643333	1.189587	0.540804	0.588643	0.981636	chr1	2.36E+08	2.36E+08	+	0	NA	intron (N intron (N	42758 NM_00327Z	7107	Hs.49816C	NR_00327Z	ENSG000002GPR137B	TM7SF1	G	protein-coding		
chr12-476	8.822646	-0.4387	0.811342	-0.54071	0.588707	0.981636	chr12	47661914	47662113	+	0	NA	TTS (NM_C TTS (NM_C	44017 NM_02460A	79657	Hs.43785E	NR_02460A	ENSG000002CRPAP3	Tah1 hSpe	RNA	polyn	protein-coding	
chr11-465	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr11	46308733	46314674	+	0	NA	intron (NAluSc SIN	-21223 NM_20153Z	8525	Hs.502461	NR_00364F	ENSG000002DGKZ	DAGK5 DAC	diacylgly	protein-coding		
chr19-585	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr19	58388250	58391922	+	0	NA	intron (NAluSq2 SIN	2817 NM_00100E	6193	Hs.37810E	NR_00100E	ENSG000002RPS5	S5	ribosomal	protein-coding		
chr20-354	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr20	35469829	35470544	+	0	NA	intron (NLa2 LINE	10203 NM_00131E	11190	Hs.44397E	NR_00718E	ENSG000002CEP250	C-NAP1 CF	centrosom	protein-coding		
chr3-1225	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	TTS (NM_C TTS (NM_C	-16666 NM_00226A	3836	Hs.16100E	NR_00226A	ENSG000002KPNA1	IPOA5 NPI	karyopher	protein-coding		
chr4-3865	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr4	38694183	38698006	+	0	NA	intron (NTigger20e	-31466 NR_02680A	79667	Hs.29275	NR_024614	ENSG000002KLF3-AS1	-	KLF3	antncRNA		
chr5-6237	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr5	62373887	62374247	+	0	NA	intron (NAluJr SIN	29838 NM_00134E	27292	Hs.73166E	NR_01447E	ENSG000002D1MT1	D1M1 D1M1	D1M1	rR	protein-coding	
chr5-6925	9.399664	-0.41217	0.762958	-0.54023	0.589037	0.981636	chr5	69259789	69260962	+	0	NA	intron (NAluX3 SIN	25489 NM_00179E	1022	Hs.18429E	NR_00179E	ENSG000002CDK7	CAK CAK1	cyclin	de	protein-coding	
chr7-7475	8.922491	-0.42612	0.789086	-0.54002	0.589187	0.981636	chr7	74721087	74722002	+	0	NA	intron (N(AT)n Sin	7374 NR_110044	1.02E+08	Hs.65477E	NR_110044	ENSG000002LOC10192E	-	uncharactncRNA			
chr4-1027	7.024893	0.484244	0.896939	0.539885	0.589277	0.981636	chr4	1.03E+08	1.03E+08	+	0	NA	exon (NM exon (NM	-76460 NR_136202	1.05E+08	Hs.15833	NR_136202	LOC105377	-	uncharactncRNA			
chr21-157	8.468893	-0.44587	0.825873	-0.53988	0.589279	0.981636	chr21	15781992	15782510	+	0	NA	intron (NLMJ2 LINE	52269 NM_00135E	29761	Hs.743994	NR_01339E	ENSG000002USP25	USP21	ubiquitin	protein-coding		
chr12-53	6.138934	-0.5267	0.975773	-0.53978	0.58935	0.981636	chr12	53008822	53009197	+	0	NA	intron (NAluSg SIN	2553 NM_00133C	1975	Hs.648394	NR_001417	ENSG000002EIF4B	EIF-4B PF	eukaryot	protein-coding		
chr17-75	10.14445	0.396395	0.73482	0.539445	0.58958	0.981636	chr17	75293707	75240285	+	0	NA	exon (NM exon (NM	21595 NM_014001	23163	Hs.87726	NR_014001	ENSG000002GGA3	-	golgi	ass	protein-coding	
chr19-347	10.14445	0.396395	0.73482	0.539445	0.58958	0.981636	chr19	34737987	34742300	+	0	NA	intron (N intron (N	5900 NM_00102E	339318	Hs.72047E	NR_00102E	ENSG000002ZNF181	HHZ181	zinc	fin	protein-coding	
chr7-7647	10.14445	0.396395	0.73482	0.539445	0.58958	0.981636	chr7	76470565	76471901	+	0	NA	non-codirnon-codir	3767 NR_00326E	619190	Hs.60997E	NR_00326E	FDPSP2	FDPSP2 PF	farnesyl	pseudo		
chr1-3233	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr1	32302908	32306068	+	0	NA	intron (NAluJr SIN	12405 NM_00496A	3065	Hs.88556	NR_00496A	ENSG000002HDAC1	GON-10 HH	histone	protein-coding		
chr1-1785	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (NAluJr SIN	47999 NM_00467E	9068	Hs.591474	NR_00467E	ENSG000002ANGPTL1	ANG3 ANG	angiopoie	protein-coding		
chr11-12	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (N intron (N	-44778 NM_01461E	2900	Hs.53873E	NR_01461E	ENSG000002GRIK4	EAA1 GRIK	glutamate	protein-coding		
chr14-582	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr14	58292810	58295644	+	0	NA	intron (NHSMAR1 DN	3910 NR_029434	379025	Hs.53108E	NR_029434	ENSG000002PSMA3-AS1	-	PSMA3	antncRNA		
chr15-635	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr15	63259681	63261955	+	0	NA	intron (N intron (N	-16732 NM_00114E	83464	Hs.51170E	NR_031301	ENSG000002APH1B	APH-1B PF	aph-1	non	protein-coding	
chr16-162	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr16	16272594	16273781	+	0	NA	intron (NLa2 LINE	-26972 NR_12870E	1.04E+08	NR_12870E	ENSG000002MIR3179-4	hsa-mir-5	microRNA	ncRNA			
chr22-385	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr22	58292810	58295644	+	0	NA	exon (NM exon (NM	5871 NM_00130C	23466	Hs.592201	NR_01429E	ENSG000002CBX6	-	chromoxo	protein-coding		
chr3-2744	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr3	27448109	27449200	+	0	NA	non-codirnon-codir	8124 NM_00125E	9497	Hs.25007E	NR_00361E	ENSG000002SLCAA7	NBC2 NBC2	solute	c	protein-coding	
chr3-1237	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (N intron (N	90327 NM_05302E	4638	Hs.47737E	NR_00596E	ENSG000002MYLK	AAT7 KRP	myosin	l	protein-coding	
chr4-1865	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr4	1.87E+08	1.87E+08	+	0	NA	IntergeniMLT1E1A L	-28818 NM_00595E	4543	Hs.243467	NR_00595E	ENSG000002MTNR1A	MEL-1A-IR	melatonin	protein-coding		
chr5-122	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr5	1.22E+08	1.22E+08	+	0	NA	intron (N intron (N	6709 NM_001317	4015	Hs.102267	NR_002317	ENSG000002CLOX	AAT10	lysyl	oxi	protein-coding	
chr5-1285	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	exon (NM exon (NM	22621 NM_00199E	2201	Hs.519294	NR_00199E	ENSG000002PBN2	CCA DA9	E	fibryllir	protein-coding	
chr6-289	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr6	28915229	28921438	+	0	NA	intron (NL2 LINE L	5652 NM_00651C	5987	Hs.519294	NR_00651C	ENSG000002TRIM27	RFNRF7	tripartit	protein-coding		
chr6-3651	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr6	36519940	36521412	+	0	NA	intron (N intron (N	26803 NM_007271	11329	Hs.40957E	NR_007271	ENSG000002STK38	NDR NDR1	serine/tf	protein-coding		
chr8-429	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr8	42988619	42993140	+	0	NA	intron (NLMJA3 LIN	-65420 NR_03369E	2339	Hs.37031E	NR_002027	ENSG000002PNTA	PPTA PGG1	farnesyl	tr	protein-coding	
chr9-275	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr9	27217085	27226473	+	0	NA	intron (NLMJA7 LIN	61014 NR_02667E	158035	Hs.201554	NR_02667E	ENSG000002LINC0003Z	C9orf14 L	long	intencRNA		
chr9-1114	9.391806	-0.4108	0.761577	-0.5394	0.589609	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (NAluJb SIN	-76667 NM_20585E	26248	Hs.38131E	NR_20585E	ENSG000002COR2K2	HSHTPCRHC	o	factory	protein-coding	
chr1-2008	10.12874	0.399446	0.740568	0.539378	0.589626	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (N intron (N	-19183 NM_00529E	2848	Hs.53431E	NR_00529E	ENSG000002GPR25	-	G	protein	protein-coding	
chr16-675	9.407522	-0.41356	0.766753	-0.53937	0.589634	0.981636	chr16	67543110	67543499	+	0	NA	intron (N intron (N	5842 NM_00119E	79567	Hs.152717	NR_02451E	ENSG000002RIPOR1	FAM65A	RHO	family	protein-coding	
chr7-1125	9.407522	-0.41356	0.766753	-0.53937	0.589634	0.981636	chr7	1.13E+08	1.13E+08	+	0	NA	intron (N intron (N	28568 NM_15255E	154743	Hs.489734	NR_15255E	ENSG000002CBMT2	C7orf60 S	base	metf	protein-coding	
chr19-445	8.705536	0.450143	0.835234	0.539265	0.589704	0.981636	chr19	44629025	44629638	+	0	NA	intron (NL2a LINE	90327 NM_00113E	5817	Hs.171844	NR_00650E	ENSG000002PVR	CD155 HVE	PVR	cell	protein-coding	
chr8-8375	11.67277	-0.37616	0.697916	-0.53898	0.589899	0.981636	chr8	8372786	8373184	+	0	NA	intron (N intron (N	14259 NM_00136E	157285	Hs.38386E	NR_00108E	ENSG000002PRAG1	NACK PEAK	PEAK1	rel	protein-coding	
chr1-1235	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alpha	2451193 NR_00395E	647121	Hs.697682	NR_00395E	ENSG000002CEMBP1	-	emarginin	f pseudo		
chr1-1503	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (NAluSp SIN	16406 NM_00469E	9129	Hs.11776	NR_00469E	ENSG000002PRPF3	HPRP3 HPF	pre-mRNA	protein-coding		
chr1-176	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr1	1.76E+08	1.76E+08	+	0	NA	intron (NMER61-int	107822 NM_001001	64326	Hs.523744	NR_022457	ENSG000002COP1	FRPFD2 RFN	COP1	E3	u	protein-coding
chr12-125	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (N MamRep137	12131 NM_00151E	2967	Hs.35534E	NR_00151E	ENSG000002GTF2H3	BTF2 P3	general	tr	protein-coding	
chr4-1134	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr4	1.13E+08	1.13E+08	+	0	NA	TTS (NM_C TTS (NM_C	164203 NM_00135A	287	Hs.620557	NR_00114E	ENSG000002ANK2	ANK-2 LQ1	ankyrin	2	protein-coding	
chr5-495	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr5	49589319	49590088	+	0	NA	IntergeniALR/Alpha	851585 NM_19844E	133418	Hs.561411	NR_19844E	ENSG000002CEMB	GP70	emarginin	protein-coding		
chr9-1274	10.67432	0.386676	0.717602	0.538845	0.589994	0.981636	chr9	1.27E+08	1.27E+08	+	0	NA	intron (NAluJb SIN	5181 NM_00713E	763								



chr11-47: 6.974045	0.472046	0.880223	0.536279	0.591765	0.981636	chr11	47323854	47324776	+	0	NA	exon (NM exon (NM	28387 NM_000256	4607 Hs. 52490ENM_000256	ENSG00000MYBPC3	CMD1MM C myosin bi	protein-coding
chr8-6721 6.974045	0.472046	0.880223	0.536279	0.591765	0.981636	chr8	67214567	67215134	+	0	NA	intron (MLT1C-int	128931 NM_006421	10565 Hs. 656902NM_006421	ENSG00000ARFGF1	ARFGF1 EADP ribo	sprotein-coding
chr8-1275 6.974045	0.472046	0.880223	0.536279	0.591765	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (AluS6 SI	23981 NR_03161C	1E+08 NR_03161C	ENSG00000MIR1205	MIRN1205 microR	ncRNA
chr17-401 10.15231	0.394851	0.736542	0.536088	0.591898	0.981636	chr17	40161591	40165114	+	0	NA	intron (AluS6 SI	1419 NR_106922	1.02E+08 NR_106922	ENSG00000MIR6866	hsa-mir-61 micro	ncRNA
chr2-1612 6.518597	0.499825	0.9329	0.535776	0.592113	0.981636	chr2	1.61E+08	1.61E+08	+	0	NA	intron (AluSp SI	-16325 NR_110162	1.01E+08 Hs. 660925NR_110162	ENSG00000LINC0180C	-	long intencRNA
chr6-8965 7.118702	-0.46873	0.875005	-0.53569	0.592174	0.981636	chr6	89650081	89650779	+	0	NA	intron (intron (	-11683 NM_020466	57226 Hs. 177275NM_020466	ENSG00000CLYRM2	DJ12208.2LYR motif	protein-coding
chr8-1287 7.118702	-0.46873	0.875005	-0.53569	0.592174	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (intron (	-2563 NR_031612	1E+08 NR_031612	ENSG00000MIR1207	MIRN1207 micro	ncRNA
chr20-465 9.614584	0.407064	0.760002	0.535609	0.592229	0.981636	chr20	4698746	4700629	+	0	NA	exon (NM exon (NM	13231 NM_000311	5621 Hs. 472011NM_000311	ENSG00000PRNP	ASCR AlTfprion pr	protein-coding
chr1-2036 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr1	2.04E+08	2.04E+08	+	0	NA	intron (intron (	13106 NM_001365	493 Hs. 343522NM_001684	ENSG00000ATP2B4	ATP2B2 MAPATPase p	protein-coding
chr1-224C 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (NLIPA7 LI	32245 NR_136593	1E+08 Hs. 65839CNR_136590	LOC100287-	septin 7 pseudo	
chr10-10C 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (intron (	33357 NM_001347	10613 Hs. 150087NM_00645	ENSG00000CERLIN1	C10orf69 ER lipid	protein-coding
chr10-12F 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	intron (intron (	27412 NM_001321	1488 Hs. 501345NM_00132	ENSG00000CTBP2	-	C-terminu
chr13-405 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr13	40946649	40947866	+	0	NA	intron (intron (	-25483 NR_003365	283507 Hs. 442781NM_00336	ENSG00000SUGT1P3	SUGT1L1 SUGT1	psuedo
chr14-202 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr14	203561766	203561866	+	0	NA	exon (NM exon (NM	13858 NM_001042	10038 Hs. 409412NM_00548	ENSG00000PARP2	NPM2 AL poly (ADP	protein-coding
chr16-18E 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr16	18553058	18553257	+	0	NA	intron (AluS2 SI	8955 NM_001004	283820 Hs. 460141NM_17361	ENSG00000NOMO2	ADMT PM5 NODAL	mocprotein-coding
chr17-26E 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr17	2697927	2698434	+	0	NA	exon (NM exon (NM	-5261 NR_106834	1.02E+08 NR_106834	ENSG00000MIR6776	hsa-mir-61 micro	ncRNA
chr17-454 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr17	45472309	45472762	+	0	NA	intron (intron (	2900 NR_036271	1E+08 NR_036271	ENSG00000MIR4315-	-	microRNA
chr18-751 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr18	74157583	74159100	+	0	NA	intron (intron (	9818 NM_014177	29090 Hs. 532835NM_01417	ENSG00000TMM21	C18orf55 transloc	protein-coding
chr20-414 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr20	41453500	41456183	+	0	NA	intron (intron (	-88023 NM_05284C	90187 Hs. 726525NM_05284	ENSG00000EMILIN3	C20orf13C elastin	nprotein-coding
chr22-217 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr22	21796488	21797576	+	0	NA	intron (intron (	-61238 NM_01331F	29799 Hs. 517435NM_01331	ENSG00000CYPEL1	FKSG3 yippee lip	protein-coding
chr3-5162 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr3	51627546	51631790	+	0	NA	intron (AluSx SI	-41507 NM_001125	51368 Hs. 517884NM_01592	ENSG00000TEX264	ZS1G11 testis e	protein-coding
chr3-186E 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr3	1.87E+08	1.87E+08	+	0	NA	intron (intron (	10141 NM_01630E	51726 Hs. 317192NM_01630	ENSG00000DNAJB11	ABBP-2 AE DnaJ	heatprotein-coding
chr4-140C 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr4	1.41E+08	1.41E+08	+	0	NA	intron (MLT1A LI	-13780 NR_07721E	644962 Hs. 67650CNR_07721	SNRNP181	-	trinucleu
chr7-153C 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr7	1536081	1536422	+	0	NA	intron (intron (	-1371 NR_14903E	1E+08 Hs. 65698CNR_14903	LOC100287-	uncharactncRNA	
chr8-423C 6.418752	0.488188	0.911712	0.535463	0.592333	0.981636	chr8	42327257	42327626	+	0	NA	intron (AluS8 SI	-11053 NM_00269C	5423 Hs. 654484NM_00269	ENSG00000POLB	-	DNA poly
chr13-521 6.418995	-0.44705	0.834898	-0.53546	0.592333	0.981636	chr13	52185786	52186346	+	0	NA	intron (AluJr SI	8401 NR_00281E	1.01E+08 Hs. 553875NR_00281	ENSG00000MRPS31P5	MRPS31P3 mitoch	ncRNA
chr1-407 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr1	40762195	40764247	+	0	NA	intron (AluSx SI	6297 NR_029833	407031 NR_029833	ENSG00000MIR30C1	MIRN30C1 micro	ncRNA
chr1-1504 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (AluS6 SI	-24979 NM_001271	80222 Hs. 288974NM_02515	ENSG00000TARS5	COXP2D1 Threonyl	-protein-coding
chr10-111 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr10	1118405	1119885	+	0	NA	intron (intron (	-40623 NR_01537F	399706 Hs. 721191NM_00101	ENSG00000LINC0020C	C0orf13F long int	ncRNA
chr10-734 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr10	73427380	73429298	+	0	NA	intron (intron (	5222 NM_001024	118490 Hs. 631825NM_00102	ENSG00000MSS51	ZMYND17 MSS51	mi
chr12-12C 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (L2a LINE	2308 NM_02084E	57605 Hs. 272755NM_02084	ENSG00000PITPM2	NIR-3 NIF phosphat	protein-coding
chr16-88E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr16	88839170	88840878	+	0	NA	intron (intron (	-16196 NR_134671	51693 Hs. 461722NM_01620	ENSG00000TRAPPCC2	HSPC176 F traffick	protein-coding
chr17-767 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr17	76776629	76778193	+	0	NA	intron (AluS6 SI	-21633 NR_110837	1.02E+08 Hs. 61720CNR_11083	ENSG00000LINC0208C	-	long intencRNA
chr17-802 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr17	80272597	80274314	+	0	NA	intron (intron (	12603 NM_020954	57674 Hs. 195642NM_02091	ENSG00000CRNF213	AL017 C17ring fin	protein-coding
chr19-44E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr19	4493017	4500059	+	0	NA	intron (intron (	21948 NM_001367	729359 Hs. 591387NM_00108	ENSG00000PLIN4	K1AA1881 perlipi	protein-coding
chr19-514 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr19	5144818	5147211	+	0	NA	intron (intron (	176901 NM_00137C	23030 Hs. 654815NM_01501	ENSG00000KDM4B	JMJ2B Tl tyrosine	deprotein-coding
chr19-10C 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr19	10360414	10361843	+	0	NA	intron (intron (	19444 NM_003331	7297 Hs. 75516 NM_00333	ENSG00000TYK2	IMD35 JTK tyrosine	protein-coding
chr19-117 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr19	11770240	11771463	+	0	NA	intron (AluJb SI	3851 NM_152355	126068 Hs. 675132NM_15235	ENSG00000ZNF441	-	zinc fin
chr19-36E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr19	36397976	36401910	+	0	NA	intron (intron (	19151 NM_001321	284406 Hs. 558734NM_13346	ENSG00000ZFP82	ZNF545 ZFP82	z
chr19-45E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr19	45825412	45826791	+	0	NA	intron (intron (	-10793 NM_03078E	81492 Hs. 146544NM_03078	ENSG00000RSPH6A	RSHL1 RSF radial	protein-coding
chr21-43C 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr21	43028007	43029049	+	0	NA	intron (intron (	39876 NM_001321	875 Hs. 533015NM_000071	ENSG00000CBS	CBSL HIP4cystathio	protein-coding
chr22-41F 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr22	41879884	41881614	+	0	NA	exon (NM exon (NM	-20195 NR_029507	407039 NR_029507	ENSG00000MIR33A	MIR33 MI fathric	ncRNA
chr3-144E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr3	14480984	14482837	+	0	NA	intron (NMIR SINE	58432 NM_00108C	80852 Hs. 517815NM_00108	ENSG00000GRIP2	-	glutamate
chr3-182E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr3	1.86E+08	1.86E+08	+	0	NA	intron (intron (	23119 NM_021627	59343 Hs. 401385NM_02162	ENSG00000SEN2	AXAM2 SMI SUMO	specprotein-coding
chr5-175C 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr5	1.72E+08	1.72E+08	+	0	NA	intron (NMIRb SINE	56774 NR_130933	1E+08 Hs. 531911NM_00100	7542 LOC10028E-	-	uncharactncRNA
chr6-425E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr6	42596618	42597817	+	0	NA	intron (intron (	33188 NM_001184	23304 Hs. 529925NM_01525	ENSG00000CUBR2	C6orf133 ubiquit	protein-coding
chr6-736E 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr6	73626705	73630188	+	0	NA	intron (AluS6 SI	25546 NM_012434	26503 Hs. 597422NM_01243	ENSG00000SLC17A5	AST ISSD solute	protein-coding
chr8-473C 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr8	47330817	47331574	+	0	NA	intron (NLIMCa LI	70257 NM_00108C	23514 Hs. 381055NM_00108	ENSG00000CPIDR	K1AA0146 scaffo	protein-coding
chr9-114C 6.459891	0.489599	0.914389	0.535439	0.592347	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	intron (AluSx1 SI	45203 NM_001633	259 Hs. 436911NM_00			

chr9-9594	6.42661	0.485771	0.911783	0.532771	0.594192	0.981636	chr9	95942244	95943443	+	0	NA	intron (NALIME LI	66835 NM_00101C	375748 Hs. 432364NM_020207	ENSG000000ERCC6L2	BMFS2 C9c	ERCC exciprotein-coding
chr9-131f	6.42661	0.485771	0.911783	0.532771	0.594192	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	43014 NM_00136E	642515 NM_00136E	ENSG000000PRRT1B	DSPD2 IFI	proline i protein-coding
chr9-134c	6.42661	0.485771	0.911783	0.532771	0.594192	0.981636	chr9	1.34E+08	1.34E+08	+	0	NA	intron (NALuSc8 SI	11555 NM_00135E	266655 Hs. 65486NM_00135E	ENSG000000BRD30S	LINC00094BRD3	oppcprotein-coding
chr9-136f	6.42661	0.485771	0.911783	0.532771	0.594192	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (Nintron (N	-1331 NR_036251	1E+08 NR_036251	ENSG000000MIR4292	-	microRNA ncRNA
chrX-288C	6.42661	0.485771	0.911783	0.532771	0.594192	0.981636	chrX	288078	288955	+	0	NA	intron (MLT1C LTF	5038 NM_00137C	55344 Hs. 52256NM_01839C	ENSG000000PLCXD1	LLOXC01-	phosphatiprotein-coding
chr17-60f	9.37609	-0.408	0.765996	-0.53264	0.594282	0.981636	chr17	60519018	60520382	+	0	NA	intron (Nintron (N	6540 NM_00128E	10513 Hs. 84084 NM_00638C	ENSG000000APPBP2	APP-BP2 F	amylloid t protein-coding
chr2-2374	9.37609	-0.408	0.765996	-0.53264	0.594282	0.981636	chr2	2.37E+08	2.37E+08	+	0	NA	intron (Nintron (N	11652 NM_05716E	1293 Hs. 23324NM_00436E	ENSG000000COL6A3	BTHLM1 D	collagen protein-coding
chr3-273f	9.37609	-0.408	0.765996	-0.53264	0.594282	0.981636	chr3	27393487	27394796	+	0	NA	intron (NALuJb SIN	-24681 NM_152534	152110 Hs. 50611E NM_152534	ENSG000000NEK10	-	NIMA relaprotein-coding
chr11-99f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr11	9967273	9968389	+	0	NA	intron (NALuSp SIN	128689 NR_12053E	1.02E+08 Hs. 585524NR_12053E	ENSG000000LOC10192E	-	uncharactncRNA
chr16-16f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr16	1692296	1696700	+	0	NA	intron (NLIMC5 LIN	-12000 NM_00131E	23162 Hs. 20776E NM_01513E	ENSG000000MAPK81P3	J1P-3 J1F	mitogen-ε protein-coding
chr19-101f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr19	1012830	1014702	+	0	NA	intron (Nintron (N	7357 NM_03342C	91304 Hs. 51500E NM_03342C	ENSG000000TMEM259	ASBABP1 C	transmem protein-coding
chr19-43f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr19	43647321	43649055	+	0	NA	TTS (NM_C	-8338 NM_14529E	199731 Hs. 370984NM_14529E	ENSG000000CADM4	IGSF4C NF	cell adheprotein-coding
chr2-333f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr2	33388401	33390265	+	0	NA	intron (Nintron (N	-29183 NR_03962E	1.01E+08 NR_03962E	ENSG000000MIR4430	-	microRNA ncRNA
chr2-274f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr2	46083840	46084768	+	0	NA	IntergeniMIR SINE	-1693 NR_02703E	400931 Hs. 23583E NM_20747E	ENSG000000MIRLET7B	linc-Ppar	MIRLET7B ncRNA
chr4-181f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr4	1818292	1818905	+	0	NA	intron (NALuSx3 SI	25286 NM_00116E	2261 Hs. 1420 NM_00014E	ENSG000000FGFR3	ACH CD33E	fibroblas protein-coding
chr4-176f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr4	1.77E+08	1.77E+08	+	0	NA	intron (NLIPA3 LIN	101055 NM_00542E	7424 Hs. 43521E NM_00542E	ENSG000000VEGFC	F1t4-L LW	vascular protein-coding
chr7-475f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr7	47515521	47517998	+	0	NA	intron (Nintron (N	-51956 NR_14581E	1.1E+08 NR_14581E	SNORD151	-	small nucsnoRNA
chr8-390f	7.144126	-0.46168	0.866837	-0.5326	0.59431	0.981636	chr8	39098997	39100169	+	0	NA	intron (NLIME4b LI	-7946 NM_00131E	203102 Hs. 52154E NM_145004	ENSG000000ADAM32	-	ADAM metaprotein-coding
chr14-39f	9.405672	-0.42346	0.795159	-0.53255	0.594343	0.981636	chr14	39051636	39053105	+	0	NA	intron (NCharlie6	-50770 NR_14654E	1.05E+08 NR_14654E	ENSG000000SEC23A-AS	-	SEC23A arncRNA
chr5-176f	6.723809	-0.4844	0.907073	-0.53249	0.594389	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (Nintron (N	2969 NM_01398C	662 Hs. 14572E NM_00120E	ENSG000000BNIP1	NIP1 SEC2	BCL2 inte protein-coding
chr1-163f	15.86251	0.320365	0.601639	0.532486	0.594389	0.981636	chr1	16602528	16603152	+	0	NA	intron (NERVL-E-ir	10765 NM_01794C	55672 Hs. 467587NM_01794C	ENSG000000NBPF1	AB13 AB14	NBPF memt protein-coding
chr15-101f	7.151984	-0.4635	0.870518	-0.53244	0.594418	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (NTigger1 E	-15558 NM_00130E	80213 Hs. 28891E NM_025141	ENSG000000TM2D3	BLP2	TM2 domaiprotein-coding
chr17-67f	7.151984	-0.4635	0.870518	-0.53244	0.594418	0.981636	chr17	6757841	6759231	+	0	NA	intron (Nintron (N	2490 NM_00135E	54739 Hs. 44197E NM_01752E	ENSG000000XAF1	BIRC4BP F	XIAP assc protein-coding
chr5-137f	7.151984	-0.4635	0.870518	-0.53244	0.594418	0.981636	chr5	13780654	13781810	+	0	NA	intron (Nintron (N	163248 NM_00136E	1767 Hs. 21236E NM_00136E	ENSG000000DNAH5	CILD3 DNF	dynein α protein-coding
chr1-1514	10.69004	0.383771	0.720839	0.532394	0.594453	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	11668 NM_00279E	5692 Hs. 89545 NM_00279E	ENSG000000PSMB4	HN3 HSN3	proteasoneprotein-coding
chr1-180C	10.69004	0.383771	0.720839	0.532394	0.594453	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (NTigger2 E	60258 NM_01481C	9857 Hs. 41304E NM_01481C	ENSG000000CEP350	CAP350 G	centrosone protein-coding
chr17-601	10.69004	0.383771	0.720839	0.532394	0.594453	0.981636	chr17	60183007	60183334	+	0	NA	exon (NM exon (NM	33197 NM_000717	762 Hs. 89485 NM_000717	ENSG000000CA4	CAIV Car4	carbonic protein-coding
chr9-126f	9.827839	-0.40074	0.752875	-0.53228	0.59453	0.981636	chr9	1.27E+08	1.27E+08	+	0	NA	intron (NL3 LINE C	4870 NM_00109E	403341 Hs. 17763E NM_20348E	ENSG000000ZBTB34	ZNF918	zinc fingprotein-coding
chr20-27f	11.20345	-0.3863	0.725771	-0.53222	0.594547	0.981636	chr20	27533405	27533704	+	0	NA	IntergeniALR/Alphe	1069111 NR_13231E	1E+08 Hs. 529357NR_13231E	ENSG000000FRG1CP	-	FSHD regipseudo
chr2-2574	9.184559	0.427133	0.802698	0.532122	0.594642	0.981636	chr2	25749356	25750325	+	0	NA	exon (NM exon (NM	44851 NM_00136E	55252 Hs. 11981E NM_01826E	ENSG000000ASXL2	ASXL2 SH	ASXL tral protein-coding
chr11-51f	15.87037	0.319372	0.600347	0.531979	0.594741	0.981636	chr11	51374666	51374930	+	0	NA	IntergeniALR/Alphe	965651 NR_024504	646813 Hs. 68417E NR_024504	LOC64681E	-	DEXH-box pseudo
chr7-648f	4.436839	-0.5907	1.110623	-0.53186	0.594821	0.981636	chr7	64805198	64805611	+	0	NA	intron (NALuSg7 SI	10976 NM_001217	7697 Hs. 18408C NM_00652E	ENSG000000ZNF138	pHZ-32	zinc fingprotein-coding
chr7-873f	4.436839	-0.5907	1.110623	-0.53186	0.594821	0.981636	chr7	87334513	87334870	+	0	NA	intron (NLIMB7 LIN	10801 NR_015381	11257 Hs. 27432E NM_00723E	ENSG000000TP53TG1	LINC0009E	TP53 tarncRNA
chr10-77f	6.574967	-0.50382	0.947323	-0.53183	0.59484	0.981636	chr10	77813724	77813944	+	0	NA	intron (Nintron (N	112921 NM_004747	9231 Hs. 65269C NM_004747	ENSG000000CDLG5	LP-DLG P-	discs lar protein-coding
chr1-120f	3.7098	0.632911	1.190394	0.531682	0.594946	0.981636	chr1	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	-88351 NR_00324E	67846 Hs. 65718E NR_00324E	ENSG000000PFN1P2	Clorf152 P	profilin pseudo
chr10-40f	3.7098	0.632911	1.190394	0.531682	0.594946	0.981636	chr10	40919053	40919797	+	0	NA	IntergeniALR/Alphe	441666 NR_02438C	441666 Hs. 25572E NR_02438C	ENSG000000LOC44166E	-	zinc fingpseudo
chr8-253f	3.7098	0.632911	1.190394	0.531682	0.594946	0.981636	chr8	25369775	25370619	+	0	NA	intron (Nintron (N	-8685 NR_15996E	1.05E+08 NR_15996E	LOC10537E	-	uncharactncRNA
chr3-134f	12.58782	-0.35432	0.666424	-0.53167	0.594952	0.981636	chr3	1.34E+08	1.34E+08	+	0	NA	exon (NM exon (NM	8473 NR_10688E	1.02E+08 NR_10688E	ENSG000000MIR6827	hsa-mir-	ε microRNA ncRNA
chr12-58f	9.425087	-0.40688	0.765316	-0.53165	0.59497	0.981636	chr12	58871698	58874318	+	0	NA	intron (Nintron (N	46538 NM_00113E	121227 Hs. 25373E NM_15337E	ENSG000000LRIG3	LIG3	leucine i protein-coding
chr22-45f	9.425087	-0.40688	0.765316	-0.53165	0.59497	0.981636	chr22	45518937	45521110	+	0	NA	intron (NALuSx1 SI	17140 NM_00199E	2192 Hs. 24601 NM_00199E	ENSG000000FBLN1	FBLN1 FIB1	fibulin I protein-coding
chr9-124f	9.425087	-0.40688	0.765316	-0.53165	0.59497	0.981636	chr9	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	18486 NM_00116E	10783 Hs. 197071 NM_01439E	ENSG000000NEK6	SID6-151E	NIMA relaprotein-coding
chr5-142f	6.493173	0.493418	0.928251	0.531566	0.595033	0.981636	chr5	1.42E+08	1.42E+08	+	0	NA	intron (Nintron (N	31087 NM_030571	80762 Hs. 9788 NM_030571	ENSG000000NDF1P1	N4WBP5	Nedd4 fanprotein-coding
chr19-271f	21.67857	0.284716	0.535846	0.53134	0.595183	0.981636	chr19	27144836	27145859	+	0	NA	IntergeniALR/Alphe	-648084 NR_14673E	1.02E+08 Hs. 567934NR_11068E	ENSG000000LOC101927	-	uncharactncRNA
chr10-86f	6.989761	0.467579	0.880432	0.531079	0.595364	0.981636	chr10	86903811	86904772	+	0	NA	intron (NLIMEC LIN	-51468 NM_00133C	6623 Hs. 34947C NM_00308E	ENSG000000SNCG	BCSG1 SR	synucleir protein-coding
chr15-50f	6.989761	0.467579	0.880432	0.531079	0.595364	0.981636	chr15	50963195	50964062	+	0	NA	intron (NLIMA4A LI	19499 NR_02764E	1E+08 Hs. 73049E NR_02764E	DCAF13P3	-	DBD1 and pseudo
chr19-47f	6.989761	0.467579	0.880432	0.531079	0.595364	0.981636	chr19	47224656	47225436	+	0	NA	intron (NALuSp SIN	-1896 NR_03615E	1E+08 NR_03615E	ENSG000000MIR3190	mir-3190	microRNA ncRNA
chr2-370f	6.989761	0.467579	0.880432	0.531079	0.595364	0.981636	chr2	37076357	37078489	+	0	NA	intron (NALuSx SIN	6949 NM_019024	54497 Hs. 744084NM_019024	ENSG000000HEATR5B	-	HEAT repcprotein-coding
chr22-38f	6.989761	0.467579	0.880432	0.531079	0.595364	0.981636	chr22	38227534	38228435	+	0	NA	intron (Nintron (N	-3264 NR_132774	1.07E+08 NR_132774	SNORA92	-	small nucsnoRNA
chr1-123f	14.8772	0.331412	0.604127	0.531	0.595419	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	IntergeniALR/Alphe	2039735 NR_00395E	647121 Hs. 69768E NR_00395E	ENSG000000EMBP1	-	embin g pseudo
chr1-923f	6.948622	0.466167	0.877929	0.530984	0.59543	0.981636	chr1	92328324	92330073	+	0	NA	intron (NLIPBa LIN	30139 NM_02481E	79871 Hs. 444421NM_02481E	ENSG000000RPAP2	Clorf82 REN	polyn protein-coding
chr10-12f	6.948622	0.466167	0.877929	0.530984	0.59543	0.981636	chr10	12002380	12004235	+	0	NA	intron (Nintron (N	39502 NM_01554E	26019 Hs. 37068E NM_01554E	ENSG000000UPF2	HUPF2 REN	UPF2 regt protein-coding
chr10-124f	6.948622	0.466167	0.877929	0.530984	0.59543	0.981636	chr10	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	7507 NM_00132E	4942 Hs. 52332E NM_000274	ENSG000000OAT	GACR HOG	



chr7-7451	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr7	74517914	74523100	+	0 NA	intron (MER5A DNA	66601 NM_01632E	9569 Hs. 647056NM_00568E	ENSG000002GTF2IRD1	BEN CREAM	GTF2I	ref	protein-coding	
chr7-8075	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr7	80757598	80758495	+	0 NA	intron (intron (N	111393 NM_00128E	948 Hs. 120949NM_00007E	ENSG000002CD36	BDPLT10	CCD36	mole	protein-coding	
chr7-1404	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (AluSc SIN	13689 NM_01344E	23608 Hs. 74488E	ENSG000002MKRN1	RNF61	makorin 1	protein-coding		
chr7-155	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr7	1.55E+08	1.55E+08	+	0 NA	3' UTR (N3' UTR (N	11124 NM_00554E	3638 Hs. 52081E	ENSG000002INS1G1	CL6	insulin 1	protein-coding		
chr8-4236	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr8	42361387	42363018	+	0 NA	intron (AluSc SIN	15027 NM_01442E	27121 Hs. 159311NM_01442E	ENSG000002DKK4	DKK-4	dickkopf	protein-coding		
chr9-9265	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr9	92636180	92638135	+	0 NA	intron (AluSz SIN	19107 NR_03650E	1E+08 Hs. 66039E	NR_03650E	LOC10012E	-	uncharactericnRNA		
chr9-1205	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr9	1.21E+08	1.21E+08	+	0 NA	intron (AluJb SIN	54264 NR_07355E	55755 Hs. 26956E	ENSG000002CDK5RAP2	C48 Cep21	CDK5	regu	protein-coding	
chr9-1285	6.95648	0.463933	0.875265	0.530049	0.596078	0.981636	chr9	1.29E+08	1.29E+08	+	0 NA	intron (intron (N	37202 NR_16319E	56904 Hs. 46002E	ENSG000002SH3GLB2	PP6569 PF	SH3	doma	protein-coding	
chr16-148	8.979347	-0.426	0.803806	-0.52998	0.596124	0.981636	chr16	14838672	14838976	+	0 NA	intron (MER20 DNA	5103 NM_01428E	23420 Hs. 74396E	ENSG000002CNOMO1	Nomo PM5	NODAL	mod	protein-coding	
chr1-2431	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr1	2.43E+08	2.43E+08	+	0 NA	intron (intron (N	-58406 NR_02940E	731275 Hs. 72235E	ENSG000002LINC01347	-	long	intencnRNA		
chr13-985	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr13	98368841	98369107	+	0 NA	intron (AluXs1 SI	153151 NM_00357E	8428 Hs. 508514NM_00357E	ENSG000002STK24	HEL-S-95	serine/tf	protein-coding		
chr16-891	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr16	8915949	8917554	+	0 NA	intron (intron (N	19888 NM_00128E	7874 Hs. 38693E	ENSG000002CASP7	HAUSP TEF	ubiquitin	protein-coding		
chr18-91	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr18	9195268	9195655	+	0 NA	intron (L1MC5a LI	23253 NM_00120E	23253 Hs. 46458E	ENSG000002ANKRD12	ANCO-2 A	ankyrin 1	protein-coding		
chr3-1225	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr3	1.23E+08	1.23E+08	+	0 NA	3' UTR (N3' UTR (N	-19606 NM_00226E	3836 Hs. 16100E	ENSG000002KPN1A1	IPOA5 NP1	karyopher	protein-coding		
chr6-111	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr6	1.1E+08	1.1E+08	+	0 NA	intron (intron (N	28837 NM_03219E	84154 Hs. 37226E	ENSG000002RPF2	BXDC1 ba	ribosome	protein-coding		
chr8-1197	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chr8	1.2E+08	1.2E+08	+	0 NA	intron (intron (N	72269 NM_00318E	6873 Hs. 12275E	ENSG000002TAF2	CIF150 MF	TATA-box	protein-coding		
chrX-414	6.700235	-0.47877	0.903431	-0.52995	0.596146	0.981636	chrX	41149758	41150283	+	0 NA	intron (intron (N	64575 NM_00103E	8239 Hs. 77578	ENSG000002CASP9X	DFFRX FAF	ubiquitin	protein-coding		
chr12-466	9.853262	-0.39561	0.746713	-0.52981	0.596246	0.981636	chr12	4654982	4655346	+	0 NA	intron (MER58A DN	6050 NM_00500E	4704 Hs. 75227	ENSG000002NUFA9	CC6 C1-3E	NADH:ubiq	protein-coding		
chr18-456	9.853262	-0.39561	0.746713	-0.52981	0.596246	0.981636	chr18	45952097	45953615	+	0 NA	intron (intron (N	14473 NM_02096E	57724 Hs. 51484E	ENSG000002EPG5	HEEW1 KI	ectopic f	protein-coding		
chr7-1211	9.853262	-0.39561	0.746713	-0.52981	0.596246	0.981636	chr7	1.21E+08	1.21E+08	+	0 NA	intron (L1PA8 LIN	136069 NM_00110E	79974 Hs. 18965E	ENSG000002CPED1	C7orf58	cadherin	protein-coding		
chr12-691	7.102986	-0.46518	0.878326	-0.52962	0.596373	0.981636	chr12	6918139	6918544	+	0 NA	intron (intron (N	3761 NM_00197E	2026 Hs. 51191E	ENSG000002EN02	HEL-S-27E	enolase 2	protein-coding		
chr7-1395	5.963303	0.519178	0.980396	0.529559	0.596418	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (intron (N	11653 NM_00136E	6916 Hs. 52075E	ENSG000002TBXAS1	BDPLT14 C	thromboxa	protein-coding		
chrX-111	5.963303	0.519178	0.980396	0.529559	0.596418	0.981636	chrX	11118575	11119125	+	0 NA	intron (MLT1G LTF	7518 NM_00533E	3052 Hs. 21157E	ENSG000002HCCS	CCHL LSDM	holocyto	protein-coding		
chr19-1317	10.19345	0.395815	0.747881	0.529249	0.596633	0.981636	chr19	13768311	13769893	+	0 NA	intron (intron (N	4580 NM_03228E	84245 Hs. 43937E	ENSG000002MR11	M1P1 MRD1	methylythi	protein-coding		
chr19-265	27.34394	0.257414	0.486755	0.528838	0.596918	0.981636	chr19	26390848	26391677	+	0 NA	Intergeni	ALR Alphe	-1402169 NR_14673E	1.02E+08 Hs. 567934NR_11068E	ENSG000002LOC101927	-	uncharactericnRNA		
chr19-365	7.142276	-0.47472	0.897679	-0.52883	0.596921	0.981636	chr19	36511093	36511685	+	0 NA	3' UTR (N3' UTR (N	16882 NM_00116E	33924 Hs. 18103	ENSG000002ZNF260	OZRF1 PEX	zinc fing	protein-coding		
chr20-507	4.888588	-0.55692	1.053406	-0.52869	0.597021	0.981636	chr20	50924853	50926381	+	0 NA	intron (intron (N	-5367 NR_10001E	1.02E+08 Hs. 30189E	ENSG000002ADNP-AS1	-	ADNP	antncnRNA		
chr3-1386	4.888588	-0.55692	1.053406	-0.52869	0.597021	0.981636	chr3	1.39E+08	1.39E+08	+	0 NA	intron (intron (N	42270 NM_00125E	5291 Hs. 23981E	ENSG000002PIK3CB	P110BETA	phosphati	protein-coding		
chr15-328	9.309527	-0.41596	0.786801	-0.52867	0.597033	0.981636	chr15	32898702	32898965	+	0 NA	intron (intron (N	169341 NM_00110E	342184 Hs. 65764E	ENSG000002FMN1	FMN LD	formin 1	protein-coding		
chr13-521	12.16751	-0.3623	0.685475	-0.52854	0.597121	0.981636	chr13	52168713	52169239	+	0 NA	non-codiron-codir	-9115 NM_00114E	4752 Hs. 40998E	ENSG000002NEK3	HSPK36	NIMA	rel	protein-coding	
chr17-416	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr17	41693862	41694772	+	0 NA	Intergeni	Intergeni	5432 NM_00580E	10209 Hs. 15058E	ENSG000002EIF1	A121 EIF	eukaryoti	protein-coding	
chr2-7137	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr2	71375557	71376394	+	0 NA	intron (intron (N	44193 NM_01449E	27332 Hs. 434401NM_01449E	ENSG000002ZNF638	NP220 ZFN	zinc fing	protein-coding		
chr3-5285	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr3	52851137	52851424	+	0 NA	intron (intron (N	-4728 NR_10703E	1.02E+08 Hs. 10703E	ENSG000002MIR8064	hsa-mir-	miRNA	ncRNA		
chr4-758	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr4	75807080	75807451	+	0 NA	intron (intron (N	82743 NM_00129E	8615 Hs. 74487E	ENSG000002USO1	P115 TAP USO1	vesi	protein-coding		
chr5-1264	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr5	1.26E+08	1.26E+08	+	0 NA	intron (intron (N	13662 NM_00114E	65983 Hs. 36355E	ENSG000002GRAMD2B	GRAMD3 NS	GRAM	dom	protein-coding	
chr5-154	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr5	1.54E+08	1.54E+08	+	0 NA	intron (AluJr SIN	-41783 NR_03162E	1E+08 Hs. NR_03162E	ENSG000002MIR1294	MIR1294	miRNA	ncRNA		
chr6-751	6.659096	-0.48233	0.91272	-0.52846	0.597183	0.981636	chr6	75173294	75173720	+	0 NA	intron (AluSq2 SI	32546 NM_08064E	1303 Hs. 10130E	ENSG000002COL12A1	BA209D8.1	collagen	protein-coding		
chr12-71	8.873494	-0.42705	0.808327	-0.52831	0.597282	0.981636	chr12	7106068	7106590	+	0 NA	intron (HTAL LINE	-1979 NR_02694E	283314 Hs. 74421E	ENSG000002C1RL-AS1	MATL2963	C1RL	antncnRNA		
chr2-241	9.409372	-0.40411	0.764936	-0.52829	0.597298	0.981636	chr2	2.41E+08	2.41E+08	+	0 NA	TTS (NM_C	6309 NM_18250E	130916 Hs. 15955E	ENSG000002MTERF4	MTERF2	mitochon	protein-coding		
chr20-375	9.409372	-0.40411	0.764936	-0.52829	0.597298	0.981636	chr20	37514571	37514830	+	0 NA	Intergeni	Intergeni	5603 NM_00131E	10904 Hs. 47265E	ENSG000002BLCAP	BC10	BLCAP	apc	protein-coding
chr5-568	9.409372	-0.40411	0.764936	-0.52829	0.597298	0.981636	chr5	56868755	56868903	+	0 NA	intron (AluV SINE	-40621 NR_13655E	133383 Hs. 85950	ENSG000002SETD9	C5orf35	SET	doma	protein-coding	
chr6-170	9.409372	-0.40411	0.764936	-0.52829	0.597298	0.981636	chr6	1.71E+08	1.71E+08	+	0 NA	intron (intron (N	14013 NM_00319E	6908 Hs. 59087E	ENSG000002TBP	GTF2D GTF	TATA-box	protein-coding		
chr1-8971	9.440803	-0.40959	0.77543	-0.52821	0.597356	0.981636	chr1	89712777	89713221	+	0 NA	exon (NM exon (NM	79879 NM_03227E	84230 Hs. 41283E	ENSG000002LRRRC8	AD158 FAI	leucine	protein-coding		
chr11-65	6.549543	-0.5124	0.970098	-0.52819	0.597368	0.981636	chr11	65579467	65579666	+	0 NA	intron (L2b LINE	3513 NM_00109E	254102 Hs. 50286E	ENSG000002EHPB1L1	-	EH	doma	protein-coding	
chr1-841	9.845404	-0.39429	0.746517	-0.52817	0.597383	0.981636	chr1	8415869	8416488	+	0 NA	intron (intron (N	7654 NM_01042E	473 Hs. 46304E	ENSG000002CRERE	ARG ARP	arginine	protein-coding		
chr15-825	9.845404	-0.39429	0.746517	-0.52817	0.597383	0.981636	chr15	82534856	82539500	+	0 NA	intron (MER20 DNA	3279 NR_11194E	6218 Hs. 43342E	ENSG000002RPS17	DBA4 RPS1	ribosomal	protein-coding		
chr19-404	9.845404	-0.39429	0.746517	-0.52817	0.597383	0.981636	chr19	40422717	40423595	+	0 NA	exon (NM exon (NM	2836 NM_01337E	29950 Hs. 26989E	ENSG000002SERTAD1	SEI1 TRIF	SERTA	don	protein-coding	
chr4-1187	9.845404	-0.39429	0.746517	-0.52817	0.597383	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (L2a LINE	36277 NM_01482E	9871 Hs. 18964E	ENSG000002SEC24D	CLCRP2	SEC24	hon	protein-coding	
chr5-347	9.845404	-0.39429	0.746517	-0.52817	0.597383	0.981636	chr5</													

chr3-5256	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr3	52561218	52564126	+	0	NA	intron (AluJo SIN	26067	NM_001124	440957	Hs.660577	NM_001124	ENSG000003SMIM4	C3orf78	small	intn	protein-coding		
chr4-1766	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr4	1.77E+08	1.77E+08	+	0	NA	intron (NL2 LINE L	106578	NM_005425	7424	Hs.43521E	NM_005425	ENSG000003VEGFC	Flt4-L	L L	vascular	protein-coding		
chr5-1684	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr5	16845524	16846612	+	0	NA	intron (CharlieE	90220	NM_012334	4651	Hs.48172C	NM_012334	ENSG000003MYO10	-	-	myosin X	protein-coding		
chr5-1575	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr5	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	-53732	NR_13620E	1.03E+08	Hs.57088E	NR_13620A	LOC102724	-	-	uncharactercNA	-		
chr5-1723	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr5	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	67637	NR_136093	1E+08	Hs.531911	NR_001007542	LOC10028E	-	-	uncharactercNA	-		
chr6-3068	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr6	30684337	30685303	+	0	NA	exon (NM_exon (NM	1825	NM_133471	170954	Hs.10115C	NM_133471	ENSG000003PPP1R18	HKMT1098		protein f	protein-coding		
chr8-1303	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (NMLTIK LTF	57827	NM_001362	50807	Hs.65555E	NM_01848E	ENSG000003ASAP1	ADAM1 CEM	ArfGAP	wi	protein-coding		
chr9-1285	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (AluSzl SIN	-28339	NM_01490E	22845	Hs.53156E	NM_01490E	ENSG000003DOLK	CDG1M DK		dolichol	protein-coding		
chrX-1371	7.16955	-0.45479	0.864411	-0.52613	0.598796	0.981636	chrX	13712503	13716724	+	0	NA	intron (Nintron (N	20007	NM_001011	6399	Hs.59223E	NM_01456E	ENSG000003TRAPP2	MIP2A SEI	trafficki	protein-coding	-		
chr17-1007	12.61325	-0.35038	0.665989	-0.52611	0.598812	0.981636	chr17	6764954	6774945	+	0	NA	intron (NLMEd LIN	-6266	NM_15323C	162517	Hs.368364	NM_15323C	ENSG000003FBX039	CT144 Fbx	F-box	prc	protein-coding		
chr7-1006	12.61325	-0.35038	0.665989	-0.52611	0.598812	0.981636	chr7	1E+08	1E+08	+	0	NA	intron (Nintron (N	16715	NM_001287	7586	Hs.61536C	NM_00343E	ENSG000003KSCAN1	KOX18 PHZ	zinc	fin	protein-coding		
chr22-317	6.625814	-0.48793	0.927442	-0.52611	0.598813	0.981636	chr22	31763079	31763302	+	0	NA	intron (AluSg SIN	9167	NM_00136E	9681	Hs.43502E	NM_01466E	ENSG000003DEPDC5	DEP.5 FFED	DEP	doma	protein-coding		
chr7-1204	6.625814	-0.48793	0.927442	-0.52611	0.598813	0.981636	chr7	42048024	42048223	+	0	NA	intron (Nintron (N	189086	NM_00016E	2737	Hs.21509	NM_00016E	ENSG000003GLI3	ACL5 GCP5	GLI	family	protein-coding		
chr1-1805	10.6979	0.382291	0.726803	0.525989	0.598896	0.981636	chr1	1.81E+08	1.81E+08	+	0	NA	3' UTR (N3' UTR (N	8411	NR_145481	1.03E+08	Hs.66531E	NR_145481	ENSG000003KIAA1614	-	-	KIAA1614	ncRNA		
chr11-115	10.6979	0.382291	0.726803	0.525989	0.598896	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	exon (NM_exon (NM	4548	NM_00113C	10525	Hs.277704	NM_00638E	ENSG000003HYOU1	GRP-170		Hypoxia t	protein-coding		
chr1-6255	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr1	62533691	62534531	+	0	NA	intron (AluSzl SIN	-63409	NM_01449E	27329	Hs.20915E	NM_01449E	ENSG000003ANGPTL3	ANG-5 ANC	angiopoie	protein-coding	-		
chr12-111	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr12	1.11E+08	1.11E+08	+	0	NA	intron (NLMCS LIN	39883	NM_001291	10019	Hs.506784	NM_00547E	ENSG000003SH2B3	IDDM20 LASH2B	adap	protein-coding	-		
chr12-688	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr12	68274423	68275420	+	0	NA	exon (NM_exon (NM	10395	NM_00107E	9057	Hs.67958C	NM_00398E	ENSG000003SLC7A6	LAT-2 LAT1	solute	cp	protein-coding		
chr19-403	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr19	4031792	4032557	+	0	NA	intron (Nintron (N	24438	NM_015897	51588	Hs.10577E	NM_015897	ENSG000003PIAS4	PIAS-gamm	protein	protein-coding	-		
chr2-850	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr2	85006424	85008030	+	0	NA	intron (Nintron (N	36066	NM_02012E	56888	Hs.65496E	NM_02012E	ENSG000003KCMF1	DEBT91 F1	potassium	protein-coding	-		
chr6-3218	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr6	32184571	32187867	+	0	NA	3' UTR (N3' UTR (N	-1897	NM_00120E	177	Hs.53434E	NM_00113E	ENSG000003AGER	RAGE SCAF	advanced	protein-coding	-		
chr7-3058	7.177408	-0.45657	0.868081	-0.52595	0.59892	0.981636	chr7	30583694	30584187	+	0	NA	IntergeniMER4-int	-6161	NR_03888E	401320	Hs.56170E	NR_03888E	GARS-DT	-	-	GARS	divnc	ncRNA	
chr1-2105	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr1	21093644	21094612	+	0	NA	intron (Nintron (N	17255	NM_00376E	8672	Hs.467084	NM_00376E	ENSG000003EIF4G3	eIF-4G 3 eukaryot	protein-coding	-	-		
chr1-2687	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr1	26878485	26880518	+	0	NA	3' UTR (N3' UTR (N	10786	NM_01806E	54707	Hs.14333	NM_01806E	ENSG000003GPN2	ATPBD1B GPN	-	loop	protein-coding	-	
chr1-1445	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr1	1.45E+08	1.45E+08	+	0	NA	intron (AluV SINE	166292	NM_00133C	647135	Hs.49757E	NM_001271	ENSG000003SRGAP2B	SRGAP2L2 SLIT	-	ROBc	protein-coding	-	
chr10-113	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr10	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	5632	NM_198514	374354	Hs.369924	NM_198514	ENSG000003NHLRC2	FINCA	NHL	repe	protein-coding	-	
chr11-714	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr11	71494182	71501625	+	0	NA	intron (Nintron (N	24400	NR_10681E	1.02E+08	NR_10681E	ENSG000003MIR6754	hsa-mir-6	mi	microRNA	ncRNA	-		
chr12-644	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr12	64466987	64469566	+	0	NA	intron (AluSg SIN	16156	NM_013254	29110	Hs.505874	NM_013254	ENSG000003TBK1	FTDLS4 ITAK	bin	protein-coding	-		
chr12-101	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (Nintron (N	-39139	NR_04983E	1.01E+08	NR_04983E	ENSG000003MIR5484Q	-	-	microRNA	ncRNA	-		
chr12-125	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	-12480	NR_01246E	23545	Hs.25786	NR_01246E	ENSG000003ATP6VAO2	A2 ARCL		ATPase H+	protein-coding	-	
chr14-203	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr14	20368452	20369254	+	0	NA	exon (NM_exon (NM	25239	NM_01014E	10038	Hs.40941E	NM_00548E	ENSG000003PARP2	ADPRT2 AL	poly	(ADP-	protein-coding	-	
chr14-584	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr14	58408889	58409819	+	0	NA	TTS (NM_2TTS (NM_2	13424	NM_207377	387990	Hs.592307	NM_207377	ENSG000003TOMM20L	UNQ9438	transloc	protein-coding	-		
chr14-102	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr14	64725	64725	+	0	NA	intron (NL2c LINE	64725	NM_00134E	122416	Hs.43294E	NM_15232E	ENSG000003ANKRD9	-	-	ankyrin	protein-coding	-	
chr16-163	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr16	16374356	16376414	+	0	NA	promoter-promoter-	-662	NM_00128E	1.01E+08	Hs.63656E	NM_00128E	ENSG000003NPIP8	LCR16a9 N	nuclear	protein-coding	-		
chr16-234	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr16	23477721	23479453	+	0	NA	intron (Nintron (N	-25443	NM_15360E	91949	Hs.185807	NM_15360E	ENSG000003COG7	CDG2E	component	protein-coding	-		
chr16-317	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr16	31727389	31727926	+	0	NA	intron (NLM9 LIN	14428	NM_00113C	124411	Hs.52882E	NM_001004	ENSG000003ZNF720	-	-	zinc	fin	protein-coding	-
chr17-186	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr17	18054379	18059198	+	0	NA	intron (Nintron (N	17380	NM_02405E	79018	Hs.18742E	NM_02405E	ENSG000003GID4	C17orf39 GID	compl	protein-coding	-		
chr17-215	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr17	21533990	21536590	+	0	NA	non-codiron-codir	16834	NR_160801	339263	Hs.51401E	NR_00111E	ENSG000003LINC0269E	C17orf51	long	intnc	ncRNA	-	
chr17-824	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr17	82464420	82465500	+	0	NA	intron (NMSTA LTR	6219	NM_01233E	26502	Hs.52655E	NM_01233E	ENSG000003NARF	IOP2	nuclear	protein-coding	-		
chr19-83C	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr19	8309379	8316634	+	0	NA	intron (AluSzl SIN	-4648	NM_01657E	51293	Hs.55849E	NM_01657E	ENSG000003CD320	8D6 8D6A	CD320	mol	protein-coding	-	
chr19-104	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr19	10485429	10486713	+	0	NA	TTS (NM_2TTS (NM_2	16700	NM_01228E	9817	Hs.46587C	NM_01228E	ENSG000003KEAP1	InrF2 KLF	kelch	lik	protein-coding	-	
chr19-404	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr19	40236338	40240376	+	0	NA	intron (Nintron (N	-11668	NM_024877	79935	Hs.63290E	NM_024877	ENSG000003CNTD2	CCNP	cyclin	N	protein-coding	-	
chr19-52C	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr19	52061824	52062262	+	0	NA	intron (HERV4_I-i	-13205	NM_01465C	9668	Hs.655934	NM_01465C	ENSG000003ZNF432	-	-	zinc	fin	protein-coding	-
chr2-2591	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr2	55919928	55922323	+	0	NA	intron (Nintron (N	2657	NM_00103E	2202	Hs.76224	NM_00410E	ENSG000003EFEMP1	DHRD DRAI	EGF	cont	protein-coding	-	
chr2-1304	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr2	1.3E+08	1.3E+08	+	0	NA	intron (NLM4 LINE	16839	NR_03323E	55627	Hs.51645E	NM_017751	ENSG000003SMPD4	NET13 NS	sphingom	protein-coding	-		
chr2-2034	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	3' UTR (N3' UTR (N	78154	NM_00128E	10152	Hs.47115E	NM_00575E	ENSG000003ABI2	ABI-2 ABI	abl	inter	protein-coding	-	
chr2-376	6.964337	0.461714	0.878137	0.525788	0.599035	0.981636	chr2	37615977	37619703																



chr19-617 9.21784	0.42981	0.820559	0.523801	0.600417	0.981636	chr19	617265	617464	+	0 NA	TTS (NM_CTTT (NM_C	16173 NM_005035	5442 Hs. 254111:NM_005035:ENSG000003POLRMT	APOLMT MI RNA polynprotein-coding		
chr19-358 7.185266	-0.45837	0.875444	-0.52359	0.600563	0.981636	chr19	35897040	35897860	+	0 NA	intron (NAluSz SIN	2287 NM_001321	84807 Hs. 466531:NM_032721:ENSG000003NFKBID	IKBNS IkeNFKB inhprotein-coding		
chr4-140:9.894402	-0.39329	0.751159	-0.52357	0.600576	0.981636	chr4	1.4E+08	1.4E+08	+	0 NA	3' UTR (N3' UTR (N	7752 NM_001153	60592 Hs. 48081:NM_032547:ENSG000003SCOC	HRHFB207short coiprotein-coding		
chr8-179:10.63133	0.377329	0.720736	0.523533	0.600604	0.981636	chr8	17952886	17954808	+	0 NA	intron (Nintron (N	30859 NM_001352	5108 Hs. 49114:NM_006197:ENSG000003PCM1	PTK4 RET pericentriprotein-coding		
chr1-2281 6.393328	0.481788	0.920407	0.523545	0.600606	0.981636	chr1	2.28E+08	2.28E+08	+	0 NA	intron (Nintron (N	1805 NM_001155	2908 Hs. 376939:NM_000858:ENSG000003GUK1	GMC guanylateprotein-coding		
chr12-102 6.997619	0.465373	0.889118	0.523409	0.600689	0.981636	chr12	1.02E+08	1.02E+08	+	0 NA	intron (Nintron (N	12374 NM_016053	51019 Hs. 405692:NM_016053:ENSG000003WASHC3	CCDC53 CCWASH comp protein-coding		
chr13-111 6.997619	0.465373	0.889118	0.523409	0.600689	0.981636	chr13	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	8543 NM_001267	1E+08 Hs. 640033:NM_001267:COL4A2-AS-	COL4A2 arprotein-coding		
chr11-117 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr11	1.17E+08	1.17E+08	+	0 NA	intron (Nintron (N	63508 NM_014956	22897 Hs. 504005:NM_014956:ENSG000003CEP164	NPHP15 centrosonprotein-coding		
chr12-162 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr12	1637478	1637814	+	0 NA	intron (NAluSg4 SI	8415 NM_032642	81029 Hs. 306051:NM_030777:ENSG000003WNT5B	Wnt familprotein-coding		
chr16-197 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr16	1977759	1979144	+	0 NA	TTS (NM_CTTT (NM_C	3018 NM_172166	124056 Hs. 191762:NM_144603:ENSG000003NOX01	P41NOX P4NADPH oxiprotein-coding		
chr17-285 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr17	28546958	28547480	+	0 NA	3' UTR (N3' UTR (N	5405 NM_001330	9094 Hs. 414045:NM_005144:ENSG000003UNC119	HRG4 IMD1unc-119 lprotein-coding		
chr17-644 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr17	64481403	64481842	+	0 NA	intron (NAluSz SIN	15432 NM_007215	11232 Hs. 437005:NM_007215:ENSG000003POLG2	HP55 MTPCDNA polynprotein-coding		
chr19-164 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr19	16424102	16425202	+	0 NA	intron (Nintron (N	47318 NM_001258	58513 Hs. 654633:NM_021233:ENSG000003EPS15L1	EPS15R epidermalprotein-coding		
chr2-153 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr2	15304795	15305351	+	0 NA	intron (NHEID-int	256621 NM_015905	51594 Hs. 467755:NM_015905:ENSG000003CNBAS	ILF52 NAC neuroblasprotein-coding		
chr2-1214 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr2	1.21E+08	1.21E+08	+	0 NA	intron (NAluY SINE	-35678 NR_023343	1E+08 Hs. 689633:NR_023343:ENSG000003RNU4ATAC	MOPD1 RFWRNA, U4atsnRNA		
chr20-286 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr20	2861396	2862008	+	0 NA	exon (NM exon (NM	-2493 NM_002838	5786 Hs. 269577:NM_002838:ENSG000003PTPRA	HEPTP HLF protein tprotein-coding		
chr4-1685 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr4	1.69E+08	1.69E+08	+	0 NA	IntergeniLIPA15 LI	27827 NM_032783	84869 Hs. 659311:NM_032783:ENSG000003CBRR4	SDR45C1 carbonyl protein-coding		
chr5-738 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr5	73785092	73785675	+	0 NA	intron (Nintron (N	-28163 NM_001244	64283 Hs. 482521:NM_001083:ENSG000003ARHGFE28	RGNFEF RFH Rho guaniprotein-coding		
chr6-1361 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr6	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	62348 NM_138415	113115 Hs. 121533:NM_138415:ENSG000003MTFR2	DUF011 FAM mitochoncprotein-coding		
chr8-1442 6.923198	0.460316	0.879494	0.523387	0.600705	0.981636	chr8	1.44E+08	1.44E+08	+	0 NA	intron (Nintron (N	21345 NR_107057	1.02E+08	83660 Hs. 569433:NM_015055:ENSG000003TLN2	MIR7112-1microRNA ncRNA	
chr15-627 7.095129	-0.46347	0.885523	-0.52339	0.600706	0.981636	chr15	62720181	62720547	+	0 NA	intron (Nintron (N	73053 NM_015055	83660 Hs. 569433:NM_015055:ENSG000003TLN2	ILWEQ talin 2 protein-coding		
chr19-104 7.095129	-0.46347	0.885523	-0.52339	0.600706	0.981636	chr19	10400563	10400762	+	0 NA	intron (NAluJb SIN	2876 NR_031592	1E+08	NR_031592:ENSG000003MIR1181	MIRN1181 microRNA ncRNA	
chr2-681:7.095129	-0.46347	0.885523	-0.52339	0.600706	0.981636	chr2	68134225	68134438	+	0 NA	non-codirnon-codir	23196 NM_001258	116143 Hs. 631877:NM_138458:ENSG000003WDR92	WD repeatprotein-coding		
chr3-8164 7.095129	-0.46347	0.885523	-0.52339	0.600706	0.981636	chr3	81642684	81642883	+	0 NA	exon (NM exon (NM	118862 NM_000158	2632 Hs. 436062:NM_000158:ENSG000003GBE1	APBD GBC 1,4-alpha protein-coding		
chr13-236 9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr13	23659279	23663587	+	0 NA	intron (NLIPECC LI	82073 NM_018647	55504 Hs. 149166:NM_018647:ENSG000003TNFRSF19	TAJ TAJ-2 TNF recep protein-coding		
chr17-287 9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr17	28725048	28725604	+	0 NA	promoter-promoter-	-388 NR_000014	26809	NR_000014:ENSG000003SNORD42A	RNU42A u small ncnoRNA	
chr18-95 9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr18	9557171	9557959	+	0 NA	intron (NLMC4 LIN	59724 NM_052003	9989 Hs. 743233:NM_005134:ENSG000003PPP4R1	MGE1 PP4 protein tprotein-coding		
chr19-175 9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr19	17515843	17521770	+	0 NA	intron (NAluSx1 SI	-4495 NM_001098	199786 Hs. 434133:NM_173544:ENSG000003NIBAN3	BCNP1 FAM niban apcprotein-coding		
chr2-392:9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr2	39256436	39260857	+	0 NA	intron (Nintron (N	-14663 NR_144521	344387 Hs. 403201:NM_001005:ENSG000003CDKL4	cyclin dprotein-coding		
chr22-24:9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr22	24369732	24374251	+	0 NA	intron (NAluSx SIN	29883 NR_001254	23384 Hs. 474384:NM_015333:ENSG000003SPECCIL	CYTSA GBE sperm antprotein-coding		
chr3-514:9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr3	51461100	51462523	+	0 NA	intron (NLIPE4 LIN	38191 NM_001171	9730 Hs. 716623:NM_014703:ENSG000003DCAF1	RIP VPRB DBD1 and protein-coding		
chr7-130 9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr7	1.31E+08	1.31E+08	+	0 NA	non-codirnon-codir	-4479 NR_029517	407024	NR_029517:ENSG000003MIR29B1	MIRN29B1 microRNA ncRNA	
chr8-9109 9.870828	-0.38928	0.743809	-0.52336	0.600724	0.981636	chr8	91014466	91019624	+	0 NA	intron (NHAL LINE	23814 NM_018710	450229 Hs. 202517:NM_018710:ENSG000003PIP42	TMEM55A phosphatiprotein-coding		
chr10-24:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr10	240979	241414	+	0 NA	intron (NAluJb SIN	61202 NM_001202	10771 Hs. 292265:NM_006624:ENSG000003ZMYND11	BRAM1 BSZ zinc fing protein-coding		
chr10-35:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr10	35041674	35043170	+	0 NA	intron (NMER21A LI	31861 NM_001198	8453 Hs. 82919	NR_003591:ENSG000003CUL2	cullin 2 protein-coding	
chr11-201 4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr11	20107796	20108873	+	0 NA	intron (Nintron (N	52142 NM_001025	120237	NR_001025:ENSG000003DBX1	developiprotein-coding	
chr13-11:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr13	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	25801 NM_001008	8451 Hs. 339733:NM_003585:ENSG000003CUL4A	cullin 4 protein-coding		
chr15-28:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr15	28642611	28643623	+	0 NA	IntergeniLMB5 LIN	-11325 NR_036443	440248 Hs. 531505:NM_199045:ENSG000003HERC2P9	hect dompseudoe		
chr19-21:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr19	21040416	21040850	+	0 NA	intron (NMTB LTR	19976 NM_001172	80264 Hs. 729020:NM_025185:ENSG000003ZNF430	zinc fing protein-coding		
chr4-175:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr4	17592138	17592820	+	0 NA	intron (NLMEM2 LIN	15175 NM_015907	51056 Hs. 570791:NM_015907:ENSG000003CLAP3	HEL-S-10c leucine epsilon protein-coding		
chr5-430:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr5	43054432	43055796	+	0 NA	intron (NLIPE6 LIN	11857 NR_034127	1E+08	LOC100132	uncharactncRNA	
chr5-1504 4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr5	1.54E+08	1.54E+08	+	0 NA	exon (NM exon (NM	14517 NM_001242	4238 Hs. 432818:NM_005927:ENSG000003MFAP3	microfractprotein-coding		
chr6-734:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr6	73428109	73429260	+	0 NA	intron (Nintron (N	23613 NM_138441	115004 Hs. 658405:NM_138441:ENSG000003CGAP3	C6orf150 cyclic GW protein-coding		
chr7-109:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr7	10993961	10994902	+	0 NA	intron (NAluSz SIN	20559 NR_033433	9678 Hs. 655688:NM_014663:ENSG000003PHF14	PHD fingeprotein-coding		
chr8-377:4.906154	-0.54397	1.039627	-0.52324	0.600809	0.981636	chr8	37773274	37752208	+	0 NA	intron (Nintron (N	11606 NM_001345	11212 Hs. 304792:NM_007195:ENSG000003PLPBP	EPVB6D PF finger protein-coding		
chr11-662 9.159135	0.422324	0.807527	0.522984	0.600985	0.981636	chr11	66275972	66276204	+	0 NA	exon (NM exon (NM	-2087 NR_073078	254263 Hs. 437072:NM_182555:ENSG000003CNH2	CNH2-2 Cr cornichon protein-coding		
chr19-451 9.159135	0.422324	0.807527	0.522984	0.600985	0.981636	chr19	45145392	45145717	+	0 NA	exon (NM exon (NM	14596 NM_198478	284353 Hs. 299255:NM_198478	NKPD1	NTPase K protein-coding	
chr5-112:7.069710	-0.47091	0.900459	-0.52296	0.601	0.981636	chr5	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	19543 NM_003135	6728 Hs. 637001:NM_003135:ENSG000003SRP19	signal rprotein-coding		
chr8-477:16.88712	0.305977	0.585339	0.522735	0.601159	0.981636	chr8	47735922	47737655	+	0 NA	TTS (NM_CTTT (NM_C	1376 NM_005195	1052 Hs. 440231:NM_005195:ENSG000003CEBPD	C/EBP-de CCAAT enr protein-coding		
chr17-501 11.68248	-0.36928	0.706654	-0.52257	0.601273	0.981636	chr17	50186655	50186938	+	0 NA	exon (NM exon (NM	-14320 NR_024192	373861 Hs. 25934	NR_194072	HLS1	H1.9 histone lpsudo
chr1-246:6.931056	0.458097	0.876822	0.522452	0.601356	0.981636	chr1	2.47E+08	2.47E+08	+	0 NA	intron (Nintron (N	14864 NM_022366	64216 Hs. 7395	NR_022366:ENSG000003TFB2M	Hkp1 mtTF transcrip protein-coding	
chr1-245:6.931056	0.458097	0.876822	0.522452	0.601356	0.981636	chr1	2.47E+08	2.47E+08	+	0 NA	intron (NLMB2					

chr3-1362	4.939436	-0.53643	1.03114	-0.52023	0.602901	0.981636	chr3	1.36E+08	1.36E+08	+	0	NA	intron (AluX3 S1	67851	NM_000532	5096	Hs.63788	NM_000532	ENSG000000CCB	-	propionylprotein-coding
chr4-1064	4.939436	-0.53643	1.03114	-0.52023	0.602901	0.981636	chr4	1.06E+08	1.06E+08	+	0	NA	intron (intron (N	-15290	NM_001142	9255	Hs.59168	NM_004757	ENSG000000AIMP1	-	EMAP2 EM2 aminoacylprotein-coding
chr7-1557	4.939436	-0.53643	1.03114	-0.52023	0.602901	0.981636	chr7	1.56E+08	1.56E+08	+	0	NA	3' UTR (N3' UTR (N	28425	NR_132318	6469	Hs.164537	NM_000193	ENSG000000CSHM	-	HHG1 HLP2 sonic hecprotein-coding
chr8-1054	4.939436	-0.53643	1.03114	-0.52023	0.602901	0.981636	chr8	1.05E+08	1.05E+08	+	0	NA	intron (NLTR12C LI	67517	NM_001362	23414	Hs.431009	NM_012082	ENSG000000ZFPM2	-	DIH3 FOG2 zinc fingprotein-coding
chr9-3744	4.939436	-0.53643	1.03114	-0.52023	0.602901	0.981636	chr9	37449444	37449932	+	0	NA	intron (AluSx SIN	15762	NM_014872	9925	Hs.16127	NM_014872	ENSG000000ZBTB5	-	zinc fingprotein-coding
chr9-1377	4.939436	-0.53643	1.03114	-0.52023	0.602901	0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	intron (LIMEf LIN	20173	NR_147508	651337	Hs.60319	NR_147508	ENSG000000LOC651337	-	uncharactncRNA
chr13-277	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr13	27094133	27094332	+	0	NA	intron (AluJr4 S1	-13101	NR_046547	1.01E+08	Hs.524922	NR_046547	USP12-AS1	-	USP12 antncRNA
chr13-422	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr13	42286391	42288009	+	0	NA	intron (intron (N	15048	NM_016248	11215	Hs.10510	NM_016248	ENSG000000AKAP11	-	AKAP-11 A-kinase protein-coding
chr14-507	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr14	50759469	50760205	+	0	NA	intron (intron (N	-61960	NR_135258	1.05E+08	Hs.569387	NR_135258	ENSG000000LOC10537	-	uncharactncRNA
chr14-576	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr14	57235883	57236802	+	0	NA	intron (intron (N	32923	NM_006544	10640	Hs.743987	NM_006544	ENSG000000EXOC5	-	HSEC10 PFexocyst (protein-coding
chr2-365	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr2	36590382	36591065	+	0	NA	intron (intron (N	7445	NM_001042	9637	Hs.25856	NM_005102	ENSG000000FEZ2	-	HUM3CL fasciculprotein-coding
chr5-324	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr5	32428101	32428300	+	0	NA	intron (AluSx SIN	16540	NR_144318	51663	Hs.435231	NM_016107	ENSG000000ZFR	-	SPG71 ZFF zinc fingprotein-coding
chr5-113	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (NLIMB4 LIN	28693	NM_152624	167227	Hs.44387	NM_152624	ENSG000000DCP2	-	NUDT20 decappingprotein-coding
chr6-756	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr6	75624170	75625117	+	0	NA	intron (MER104 DN	22913	NM_015571	26054	Hs.458784	NM_015571	ENSG000000SEN6	-	SSP1 SUSF SUMO specprotein-coding
chr7-9261	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr7	92613856	92614112	+	0	NA	3' UTR (N3' UTR (N	-23594	NM_001040	257415	Hs.18564	NM_152788	ENSG000000FAM133B	-	family wiprotein-coding
chr7-1039	7.120552	-0.45636	0.877249	-0.52022	0.602913	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (intron (N	30285	NM_016015	51631	Hs.731488	NM_016015	ENSG000000LUCTL2	-	CGI-59 CUCUC7 likeprotein-coding
chr8-1019	8.296889	-0.39166	0.752909	-0.5202	0.602923	0.981636	chr8	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	5838	NM_016096	51123	Hs.374488	NM_016096	ENSG000000ZNF706	-	HSPC038 Fzinc fingprotein-coding
chr1-2647	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr1	26473958	26476335	+	0	NA	exon (NM exon (NM	2706	NM_005517	3151	Hs.18116	NM_005517	ENSG000000HMG2	-	HMG17 high mobiprotein-coding
chr10-314	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr10	31461172	31470131	+	0	NA	intron (AluJr4 S1	-65896	NM_001368	1.01E+08	Hs.730227	NM_001368	LOC100505	-	putative protein-coding
chr18-274	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr18	2747291	2749252	+	0	NA	intron (LTR105 Mc	92389	NM_015298	23347	Hs.8118	NM_015298	ENSG000000SMCHD1	-	BAMS FSH structureprotein-coding
chr18-325	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr18	3253359	3259252	+	0	NA	TTS (NM_CTS (NM_C	4092	NM_001303	10627	Hs.19008	NM_006471	ENSG000000MYL12A	-	HEL-5-24 myosin I protein-coding
chr2-1514	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr2	1.51E+08	1.51E+08	+	0	NA	intron (Charlie4z	60441	NM_001177	55183	Hs.536537	NM_018151	ENSG000000CRIF1	-	replicatiprotein-coding
chr20-198	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr20	19895491	1989967	+	0	NA	intron (AluJr SIN	8163	NM_018993	54453	Hs.47227	NM_018993	ENSG000000CRIN2	-	MACS RASS Ras and Fprotein-coding
chr4-559	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr4	55902241	55902804	+	0	NA	exon (NM exon (NM	-46423	NM_025009	9662	Hs.518767	NM_01464	ENSG000000CEP135	-	CEP14 KIAF centrosomeprotein-coding
chr5-3892	9.86297	-0.38795	0.745849	-0.52015	0.602958	0.981636	chr5	38926570	38928739	+	0	NA	intron (THE1C-int	81642	NM_001323	9180	Hs.12065	NM_003999	ENSG000000OSMR	-	IL-31R-beoncostatiprotein-coding
chr1-110	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	18548	NM_001201	9122	Hs.35130	NM_004699	ENSG000000SLC16A4	-	MCT4 MCT5olute cprotein-coding
chr10-68	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr10	68000068	68001481	+	0	NA	intron (MLT1C LTF	10109	NR_131184	1E+08	NR_131184	POU5F1P5	-	Oct4-pg5 POU classpseudo	
chr10-12	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr10	1.23E+08	1.23E+08	+	0	NA	intron (intron (N	16946	NM_024942	80007	Hs.50128	NM_024942	ENSG000000C10orf88	-	chromosonprotein-coding
chr12-934	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr12	9340905	93411140	+	0	NA	intron (intron (N	31594	NM_001301	11163	Hs.50632	NM_019094	ENSG000000NUD4	-	DIPP-2B Iundix hycprotein-coding
chr12-107	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (intron (N	18326	NR_039717	1.01E+08	NR_039717	ENSG000000MIR4496	-	microRNA ncRNA	
chr12-11	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (LIME3G LI	2724	NR_037430	1.01E+08	NR_037430	ENSG000000MIR3657	-	microRNA ncRNA	
chr14-617	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr14	61786434	61789134	+	0	NA	intron (MERS7A1 LI	-24378	NM_001367	83851	Hs.40413	NM_031914	ENSG000000SYT16	-	CHR14SYT synaptotprotein-coding
chr15-58	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr15	58845164	58846315	+	0	NA	intron (L1MA2 LIN	74437	NM_001040	54629	Hs.59112	NM_019092	ENSG000000MINDY2	-	FAM63B MINDY lysprotein-coding
chr15-67	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr15	67233673	67235428	+	0	NA	intron (L3 LINE C	20111	NM_024666	79719	Hs.25464	NM_024666	ENSG000000AAGAB	-	KPPP1 PPPalpha ancprotein-coding
chr17-17	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr17	1781261	1782359	+	0	NA	intron (AluSq2 S1	10139	NM_001328	5176	Hs.53276	NM_00261	ENSG000000SERPINF1	-	EPC-1 O1serpin fprotein-coding
chr17-46	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr17	46215738	46216210	+	0	NA	intron (AluSx SIN	9400	NM_001193	284058	Hs.64874	NM_01544	ENSG000000KANSL1	-	CENP-36 KAT8 regprotein-coding
chr18-25	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr18	25090571	25091351	+	0	NA	intron (intron (N	-102982	NR_146903	1.05E+08	NR_146903	LINCO1894	-	long intncRNA	
chr19-13	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr19	43659601	43661519	+	0	NA	intron (7SLRNA sr	9609	NM_002656	5329	Hs.46687	NM_002656	ENSG000000PLAUR	-	CD87 U-Pp plasminogenprotein-coding
chr2-43	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr2	1.36E+08	1.36E+08	+	0	NA	intron (intron (N	-6104	NR_110200	1.02E+08	Hs.60217	NR_110196	ENSG000000DARS-AS1	-	DARS antncRNA
chr2-179	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr2	1.8E+08	1.8E+08	+	0	NA	intron (intron (N	42074	NM_020943	57703	Hs.31136	NM_020943	ENSG000000CWC22	-	EIF4GL NCWC22 splprotein-coding
chr2-206	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr2	2.07E+08	2.07E+08	+	0	NA	exon (NM exon (NM	-4661	NR_036077	1E+08	NR_036077	ENSG000000MIR3130	-	MIR3130-2 microRNA ncRNA	
chr2-364	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr2	36473689	36474323	+	0	NA	intron (intron (N	7634	NM_012473	25828	Hs.21192	NM_012473	ENSG000000TXN2	-	COXP29 thiaredoxin protein-coding
chr4-478	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr4	47890340	47890549	+	0	NA	intron (MIRc SINE	-23783	NR_125878	1.02E+08	Hs.13419	NR_125879	LOC101927	-	uncharactncRNA
chr5-143	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr5	1.43E+08	1.43E+08	+	0	NA	intron (LIME3G LI	16766	NM_001364	2908	Hs.12292	NM_00017	ENSG000000NR3C1	-	GCCR GCCR nuclear rprotein-coding
chr6-317	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr6	31789567	31793904	+	0	NA	exon (NM exon (NM	4017	NM_006295	7407	Hs.52002	NM_006295	ENSG000000CVARS	-	G7A NDMSC valyl-tR protein-coding
chr6-41	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr6	41788634	41791063	+	0	NA	TTS (NM_CTS (NM_C	2405	NM_001134	1E+08	Hs.73163	NM_001134	ENSG000000TOMM6	-	OTAP TOM6 translocprotein-coding
chr6-83	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr6	83184360	83185385	+	0	NA	intron (L2 LINE L	8393	NM_001195	5238	Hs.66166	NM_015599	ENSG000000PGM3	-	AGM1 IMD2 phosphog protein-coding
chr6-96	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr6	96544729	96544731	+	0	NA	intron (Tigger6b	-18445	NM_020482	9457	Hs.63260	NM_020482	ENSG000000FHL5	-	17000276Cfour and protein-coding
chr6-152	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr6	152324	152E+08	+	0	NA	intron (intron (N	-49227	NM_001347	23345	Hs.12967	NM_015299	ENSG000000SYNE1	-	8B ARCA1 spectrin protein-coding
chr7-35	7.153834	-0.45122	0.867682	-0.52003	0.603041	0.981636	chr7	35902378	35												





chr1-2111 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr1	21100184	21100784	+ 0 NA	intron (Nintron (N	10899 NM_00376C	8672 Hs. 467084NM_00376C	ENSG00000CEIF4G3	eIF-4G 3	eukaryotiiprotein-coding
chr10-69 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr10	69011208	69011932	+ 0 NA	intron (NAluJb SIN	22767 NM_015634	26128 Hs. 27958C NM_015634	ENSG00000KIF1BP	KBP KIAA1K1F1	bincprotein-coding
chr12-98 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr12	98670912	98673094	+ 0 NA	intron (NMIR SINE	26703 NM_18186E	317 Hs. 552567NM_00116C	ENSG00000CAPAF1	APAF-1	Cfapoptoticprotein-coding
chr12-13 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr12	1.32E+08	1.32E+08	+ 0 NA	intron (Nintron (N	-21858 NR_00329E	347918 Hs. 12211E NM_18261C	ENSG00000EP400P1	EPA400NL	EP400 pseudo
chr14-39 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr14	39133864	39134500	+ 0 NA	intron (Nintron (N	19898 NM_00361E	8487 Hs. 652307NM_00361E	ENSG00000GEMIN2	SIP1 SIP1ip	nucleprotein-coding
chr15-80 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr15	80131585	80132086	+ 0 NA	intron (Nl2c LINE	-21164 NM_000137	2184 Hs. 73875 NM_000137	ENSG00000CFAH	-	fumarylacprotein-coding
chr2-263 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr2	26367093	26368941	+ 0 NA	intron (Nl2a LINE	-21228 NM_001321	165082 Hs. 63187E NM_15383E	ENSG00000ADGRF3	GPR113	PCadhesion protein-coding
chr2-105 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr2	1.05E+08	1.05E+08	+ 0 NA	intron (Nintron (N	18990 NM_00131E	2274 Hs. 443687NM_00145C	ENSG00000FHL2	AAG11 DRF4	and protein-coding
chr2-175 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr2	1.75E+08	1.75E+08	+ 0 NA	TTS (NM_C TTS (NM_C	53814 NR_03063C	NR_03063C	ENSG00000MIR933	MIRN933	microRNA ncRNA
chr2-196 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr2	1.97E+08	1.97E+08	+ 0 NA	exon (NM exon (NM	23242 NM_00120E	9330 Hs. 47099E NM_01208E	ENSG00000GTF3C3	TFIIIC102	general tprotein-coding
chr21-29 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr21	29320752	29323620	+ 0 NA	intron (THE1B LTF	16982 NR_02765E	571 Hs. 15427E NM_00118E	ENSG00000BACH1	BACH-1 BTBT	domaiprotein-coding
chr21-37 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr21	37509162	37509638	+ 0 NA	intron (NlIME4b LI	89101 NM_13043E	1859 Hs. 36824C NM_00139E	ENSG00000DYRK1A	DYRK DYRK	dual specprotein-coding
chr9-100 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr9	1E+08	1E+08	+ 0 NA	intron (Nintron (N	79164 NM_001161	5488 Hs. 49464E NM_01774E	ENSG00000TEXT10	Ipil hA2C	testis eprotein-coding
chr9-134 7.187115	-0.44611	0.867345	-0.51433	0.607018	0.981636	chr9	1.35E+08	1.35E+08	+ 0 NA	intron (Nintron (N	57679 NR_039691	NR_039691	ENSG00000MIR3689C	-	microRNA ncRNA
chr11-70 7.605583	-0.43893	0.853394	-0.51433	0.607019	0.981636	chr11	70798368	70798567	+ 0 NA	exon (NM exon (NM	-64323 NR_07353E	220070 Hs. 32676E NM_14530E	ENSG00000SHANK2-AS	Cl1orf76	SHANK2 arncRNA
chr12-10 6.409044	0.476744	0.927035	0.514267	0.607065	0.981636	chr12	1.09E+08	1.09E+08	+ 0 NA	intron (NAluSp SIN	-4621 NR_03899E	1E+08 Hs. 66099E NR_03899E	USP30-AS1-	USP30	antncRNA
chr17-8 6.409044	0.476744	0.927035	0.514267	0.607065	0.981636	chr17	82062507	82063362	+ 0 NA	exon (NM exon (NM	2870 NM_02215E	64118 Hs. 51459E NM_02215E	ENSG00000CDUS1L	DUS1	PP31dihydruprotein-coding
chr2-99 6.409044	0.476744	0.927035	0.514267	0.607065	0.981636	chr2	99553484	99554735	+ 0 NA	intron (NlIME4a LI	-64092 NR_13565E	51455 Hs. 443077NM_01631E	ENSG00000REV1	AIBP80 RE	REV1 DNA protein-coding
chr3-47 6.409044	0.476744	0.927035	0.514267	0.607065	0.981636	chr3	47411273	47411964	+ 0 NA	exon (NM exon (NM	30597 NM_001304	25930 Hs. 25524 NM_01546E	ENSG00000PTPN23	HD-PTP	HE protein tprotein-coding
chr5-43 10.1426	0.387325	0.753482	0.514047	0.607219	0.981636	chr5	43127437	43127961	+ 0 NA	intron (Nintron (N	6134 NM_00133C	7690 Hs. 535804NM_00343E	ENSG00000ZNF131	ZBTB35	pf zinc fingprotein-coding
chr5-13 9.638157	0.401642	0.78149	0.513944	0.607291	0.981636	chr5	1.35E+08	1.35E+08	+ 0 NA	3' UTR (N3' UTR (N	-6923 NM_00130C	9879 Hs. 40654E NM_01482E	ENSG00000DDX46	PRPF5 Pr	DEAD-box protein-coding
chr19-48 17.44057	0.300202	0.584177	0.51389	0.607329	0.981636	chr19	48965697	48967343	+ 0 NA	intron (Nintron (N	1211 NM_00014E	2512 Hs. 43367C NM_00014E	ENSG00000FTL	LFTD NBL1	ferritin protein-coding
chr10-68 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr10	68057929	68059360	+ 0 NA	intron (NAluSc SIN	16639 NM_00127E	26091 Hs. 51891 NM_015601	ENSG00000CHERC4	-	HECT and protein-coding
chr11-70 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr11	70377013	70377337	+ 0 NA	intron (Nintron (N	-21331 NM_13856E	2017 Hs. 596164NM_005231	ENSG00000CTTN	EMS1	contactiiprotein-coding
chr11-83 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr11	83201044	83201641	+ 0 NA	intron (NlIP8 LIN	7630 NM_00130C	338699 Hs. 50343E NM_18260E	ENSG00000ANKRD42	PPP1R79	Sankyrin iiprotein-coding
chr12-30 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr12	80070268	80671383	+ 0 NA	intron (Nintron (N	6419 NM_00119C	10526 Hs. 50513E NM_00639E	ENSG00000IP08	RANBP8	importin protein-coding
chr13-11 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr13	1.11E+08	1.11E+08	+ 0 NA	intron (Nintron (N	7212 NM_01821E	55739 Hs. 408327NM_01821E	ENSG00000NAXD	CARND	LPENAD PHX protein-coding
chr17-41 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr17	41974535	41974870	+ 0 NA	3' UTR (N3' UTR (N	6905 NM_00133C	1267 Hs. 273621NM_03313E	ENSG00000CNP	CNP1	2', 3'-cycprotein-coding
chr19-34 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr19	34472281	34473163	+ 0 NA	Intergeni LIM5a LI	-9036 NM_00108C	126374 Hs. 58501C NM_00108C	ENSG00000WTIP	-	WT1 interprotein-coding
chr19-53 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr19	53154928	53155208	+ 0 NA	intron (NAluSj SIN	3985 NM_032584	84671 Hs. 46723E NM_032584	ENSG00000ZNF347	ZNF1111	zinc fingprotein-coding
chr2-12 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr2	1.28E+08	1.28E+08	+ 0 NA	intron (NlIMEg LI	25632 NM_01796E	55677 Hs. 46987E NM_01796E	ENSG00000IWS1	-	interactsprotein-coding
chr2-128 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr2	1.28E+08	1.28E+08	+ 0 NA	intron (Nintron (N	2180 NM_004807	9394 Hs. 512841NM_004807	ENSG00000HS6ST1	HH15	HS6heparan sprotein-coding
chr2-218 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr2	2.19E+08	2.19E+08	+ 0 NA	intron (NAluSj SIN	5272 NM_001271	9125 Hs. 448767NM_005444	ENSG00000CNOT9	CAF40	CTICCR4-NOT protein-coding
chr2-219 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr2	2.19E+08	2.19E+08	+ 0 NA	intron (NlIME3 SINE	3658 NM_00131E	23549 Hs. 258551NM_01210C	ENSG00000DNPEP	ASPEP	DAFaspartyl protein-coding
chr4-13 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr4	13569585	13569992	+ 0 NA	3' UTR (N3' UTR (N	-21964 NR_01545C	285548 Hs. 529284NR_015450	LINC0109E-	-	long intncRNA
chr4-12 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr4	1.23E+08	1.23E+08	+ 0 NA	intron (Nintron (N	26719 NM_00134E	166378 Hs. 70964E NM_145207	ENSG00000SPATA5	AFG2	EHLML spermatogprotein-coding
chr5-17 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr5	1.78E+08	1.78E+08	+ 0 NA	intron (Nintron (N	3511 NM_00136E	54540 Hs. 48428E NM_019057	ENSG00000FAM193B	IRIZIO	family wiprotein-coding
chr6-12 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr6	1.28E+08	1.28E+08	+ 0 NA	intron (Nintron (N	-52421 NR_125849	1.02E+08 Hs. 65677E NR_125849	LOC10192E-	-	uncharactncRNA
chr9-10 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chr9	1.1E+08	1.1E+08	+ 0 NA	intron (Nintron (N	12949 NM_00119E	445815 Hs. 59190E NM_00720E	ENSG00000PALM2-AK1	AKAP-2 AK	PALM2-AK1 protein-coding
chrX-27 7.145976	-0.44938	0.874787	-0.5137	0.607464	0.981636	chrX	2734835	2735734	+ 0 NA	3' UTR (N3' UTR (N	-16768 NM_001141	7499 Hs. 17967E NM_17556E	ENSG00000CXG	PBDX	Xg glycofprotein-coding
chr1-150 11.64023	0.354608	0.689274	0.513682	0.607474	0.981636	chr1	1.5E+08	1.5E+08	+ 0 NA	non-codirnon-codir	2491 NM_001077	51107 Hs. 10840E NM_01602E	ENSG00000APH1A	6530402NC	aph-1 honprotein-coding
chr1-178 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr1	1.79E+08	1.79E+08	+ 0 NA	non-codirnon-codir	5479 NR_00318E	400798 Hs. 66808E NM_207467	ENSG00000C1orf220	-	chromosomncRNA
chr10-42 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr10	42592469	42594048	+ 0 NA	exon (NM exon (NM	-40388 NR_026777	1E+08 Hs. 278064NR_026777	ENSG00000ZNF37BP	KOX21	ZNF zinc fingpseudo
chr16-4 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr16	47152948	47153948	+ 0 NA	TTS (NM_C TTS (NM_C	9380 NR_110904	1.02E+08 Hs. 63465E NR_110903	ITFG1-AS1-	ITFG1	antncRNA
chr17-63 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr17	63711979	63712343	+ 0 NA	intron (Nintron (N	11823 NR_04627E	729683 Hs. 534931NR_04627E	LOC72968E-	-	uncharactncRNA
chr2-38 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr2	38342674	38343634	+ 0 NA	intron (NAluJb SIN	33376 NM_00133C	64225 Hs. 59495E NM_02237E	ENSG00000ATL2	ARL3IP2	atlastin protein-coding
chr4-13 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr4	13592747	13593454	+ 0 NA	intron (NlTiger4a	36425 NM_148894	259282 Hs. 74493E NM_148894	ENSG00000BOD1L1	BOD1L	PFMBiorientprotein-coding
chr9-12 6.897774	0.454401	0.885021	0.513435	0.607647	0.981636	chr9	1.29E+08	1.29E+08	+ 0 NA	exon (NM exon (NM	22240 NR_16319E	56904 Hs. 46023E NM_02014E	ENSG00000SH3GLB2	PP6569	PF SH3 domaiprotein-coding
chr1-19 6.897774	-0.50889	0.991459	-0.51328	0.607757	0.981636	chr1	19626159	19626374	+ 0 NA	intron (Nintron (N	-16963 NM_182744	4681 Hs. 65450E NM_00538C	ENSG00000CNBL1	D1S1733E	NBL1, DA protein-coding
chr11-6 5.888394	-0.38294	0.746442	-0.51303	0.607932	0.981636	chr11	65119196	65121436	+ 0 NA	TTS (NM_C TTS (NM_C	1818 NM_001997	2197 Hs. 38720E NM_001997	ENSG00000FAU	FAU1	Fub1FAU ubiq protein-coding
chr15-4 9.888394	-0.38294	0.746442	-0.51303	0.607932	0.981636	chr15	42217657	42220354	+ 0 NA	intron (NlIMA8 LIN	-10701 NM_01528E	23339 Hs. 88025 NM_01528E	ENSG00000CVPS39	TLP	VAMV6 VPS39 subprotein-coding
chr19-12 9.888394															



chr1-1261	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr1	1.76E+08	1.76E+08	+	0	NA	intron (Nintron (N	44536 NM_001001	64326 Hs. 523744NM_022457	ENSG00000COP1	RFWD2	RNF COP1 E3 tprotein-coding
chr11-685	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr11	68936223	68938162	+	0	NA	intron (Nintron (N	33341 NM_00218C	3508 Hs. 503044NM_00218C	ENSG00000IGHMBP2	CATF1	CM1 immunogl protein-coding
chr15-43C	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr15	43008022	43008908	+	0	NA	intron (NMER52A LI	-87687 NM_17350C	146057 Hs. 646511NM_17350C	ENSG00000CTBK2	SCA11	TTE tau tubulprotein-coding
chr15-74E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr15	74800784	74802630	+	0	NA	exon (NM exon (NM	-11128 NM_002181E	79748 Hs. 620644NM_02181E	ENSG00000LMAN1L	ARGC1-53L	lectin, nprotein-coding
chr16-68E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr16	68249205	68250936	+	0	NA	intron (Nintron (N	4697 NM_00136E	23659 Hs. 632199NM_01232C	ENSG00000PLA2G15	AGC	GXVPL phospholiprotein-coding
chr17-647	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr17	64785167	64786739	+	0	NA	intron (Nintron (N	-3954 NR_02689E	1.09E+08 Hs. 117855NR_02689E	ENSG00000CARHGP27F	-	ARHGP27F pseudo
chr19-104	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr19	10450355	10450794	+	0	NA	intron (Nintron (N	-2358 NM_00620E	5141 Hs. 89901 NM_00620E	ENSG00000PDE4A	DPD2E	PDF phosphodi protein-coding
chr19-214	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr19	21400251	21400619	+	0	NA	intron (Nintron (N	3302 NM_14532E	284443 Hs. 656555NM_14532E	ENSG00000ZNF493	-	zinc fingprotein-coding
chr19-45E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr19	45296834	45298102	+	0	NA	intron (Nintron (N	25407 NM_00182A	1158 Hs. 334347NM_00182A	ENSG00000CKM	CKMM	CPK- creatine protein-coding
chr2-117E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr2	11781742	11784585	+	0	NA	intron (Nintron (N	15719 NR_03607I	1E+08 NR_03607I	ENSG00000MIR548S	-	microRNA ncRNA
chr2-554C	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr2	55402922	55403253	+	0	NA	intron (NCharlele	16769 NM_00136E	55704 Hs. 292922NM_01808A	ENSG00000CCDC88A	APE	GIRDI coiled-cprotein-coding
chr3-185E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr3	1.85E+08	1.85E+08	+	0	NA	non-codiron-codir	9269 NM_00124E	9175 Hs. 591306NM_00472I	ENSG00000MAP3K13	LZK	MEKK1 mitogen-ε protein-coding
chr4-896E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr4	896601	897071	+	0	NA	intron (Nintron (N	35480 NM_00525E	2580 Hs. 369607NM_00525E	ENSG00000GAK	DNAJ26	DN cyclin G protein-coding
chr9-126E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr9	1.27E+08	1.27E+08	+	0	NA	intron (NLIM4 LINE	13751 NM_014007	23099 Hs. 555581NM_014007	ENSG00000ZBTB43	ZBTB22B	zinc fing protein-coding
chr9-129C	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	exon (NM exon (NM	14352 NR_07298E	57171 Hs. 21701 NM_02043E	ENSG00000ZLPPP1	LSFR2	dolichylc protein-coding
chrX-130C	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chrX	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	46988 NM_00118A	63035 Hs. 49674E NM_02194E	ENSG00000BCORL1	BCOR-L1	CBCL6 core protein-coding
chrX-130E	6.946772	0.453513	0.888391	0.510488	0.60971	0.981636	chrX	1.3E+08	1.3E+08	+	0	NA	non-codiron-codir	3825 NM_00136E	1654 Hs. 728565NM_00135E	ENSG00000DDX3X	Cap-Rf	DEAD-box protein-coding
chr1-2131	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr1	21327827	2133E+08	+	0	NA	intron (NLIP46 LIN	109506 NM_01224A	26750 Hs. 59141E NM_01242A	ENSG00000RPS6KC1	RPK118	RS ribosomal protein-coding
chr12-124	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (NMIRb SINE	-8941 NR_10694C	1.02E+08 NR_10694C	ENSG00000MIR6880	hsa-mir-ε	microRNA ncRNA
chr15-41E	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr15	41274863	41275385	+	0	NA	intron (Nintron (N	-8866 NR_15282E	729082 Hs. 380164NR_02675E	ENSG00000OIP5-AS1	cyano	lOIP5 anticrncRNA
chr16-74E	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr16	74907174	74908820	+	0	NA	TTS (NM_C TTS (NM_C	77126 NM_03058I	79726 Hs. 280951NM_03058I	ENSG00000WDR59	CDW12	FPF WD repeat protein-coding
chr17-647	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr17	64755673	64758624	+	0	NA	intron (NAluJr SIN	-23611 NR_10672E	1.02E+08 NR_10672E	ENSG00000MIR6080	hsa-mir-ε	microRNA ncRNA
chr2-744	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr2	67409751	67410387	+	0	NA	3' UTR (N3' UTR (N	12736 NM_01900E	54465 Hs. 353022NM_01900E	ENSG00000ETAA1	ETAA16	ETAA1 actprotein-coding
chr2-747	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr2	74474373	74475613	+	0	NA	exon (NM exon (NM	-2313 NM_05305C	116540 Hs. 534527NM_05305C	ENSG00000MRPL53	L53MT	mitochondr protein-coding
chr20-62E	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr20	62279260	62283762	+	0	NA	intron (Nintron (N	-21385 NM_17557E	11047 Hs. 90107 NM_00700E	ENSG00000ADRM1	ARM-1	ARM adhesion protein-coding
chr4-271E	7.476641	0.435574	0.853565	0.5103	0.609841	0.981636	chr4	2719504	2722014	+	0	NA	intron (NLIME3B LI	35577 NM_02430E	79155 Hs. 368551NM_02430E	ENSG00000TNIP2	ABIN2	FLNINFAIP3 iprotein-coding
chr1-1114	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	intron (NHV1 scrNA	2418 NM_02410E	79084 Hs. 20477E NM_02410E	ENSG00000WDR77	HKMT1069	WD repeat protein-coding
chr10-31E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr10	3128399	3129028	+	0	NA	intron (Nintron (N	-5391 NR_13275E	1.07E+08 NR_13275E	SNORD142	SNORA85	s small nucsnoRNA
chr14-31E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr14	31370448	31371647	+	0	NA	intron (NMER58A DN	49503 NM_01547E	25938 Hs. 74497E NM_01547E	ENSG00000HEATR5A	C14orf12E	HEAT repeat protein-coding
chr15-101	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (NMER72 LTR	23735 NM_15233A	123283 Hs. 65716E NM_15233A	ENSG00000TARSL2	-	thronyl- protein-coding
chr2-864E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr2	86492121	86493222	+	0	NA	TTS (NM_C TTS (NM_C	51210 NM_00114E	55818 Hs. 55742E NM_01843E	ENSG00000KDM3A	JHDM2A	JF lysine deprotein-coding
chr2-1957	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr2	1.96E+08	1.96E+08	+	0	NA	intron (Nintron (N	51783 NM_02034E	57181 Hs. 65015E NM_02034E	ENSG00000SLC39A10	LZT-Hs2	solute c protein-coding
chr2-210E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (NLIMed LIN	34074 NM_00126I	65061 Hs. 348711NM_13915E	ENSG00000CDK15	ALS2CR7	F cyclin deprotein-coding
chr3-580E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr3	58096131	58096906	+	0	NA	intron (NAluSx1 SI	74117 NR_13553A	1.05E+08 Hs. 613914NR_13553A	ENSG00000FLNB-AS1	-	FLNB anticrncRNA
chr4-150E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr4	1.51E+08	1.51E+08	+	0	NA	intron (NTiger2 E	187200 NM_00119E	987 Hs. 48093E NM_00672E	ENSG00000LRBA	BGL	CDCA1 LPS resp protein-coding
chr5-371E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr5	37190204	37190602	+	0	NA	intron (NAluJo SIN	-58643 NR_13426E	1.05E+08 Hs. 17099E NR_13426E	ENSG00000LOC105374	-	uncharacterncRNA
chr5-693E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr5	69355257	69355988	+	0	NA	intron (Nintron (N	-13675 NM_13334E	5884 Hs. 16184 NM_00287E	ENSG00000CRAD17	CCYC	HRAI RAD17 cheprotein-coding
chr5-115E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr5	1.16E+08	1.16E+08	+	0	NA	intron (Nintron (N	5841 NM_02017E	56929 Hs. 47367E NM_02017E	ENSG00000FEMIC	EURO2	IMAGE fem-1 hon protein-coding
chr8-5621	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr8	56216637	56217421	+	0	NA	intron (Nintron (N	5240 NM_00101I	79145 Hs. 43691E NM_02430C	ENSG00000CHHD7	CXO23	coiled-c protein-coding
chr9-324E	7.179257	-0.44426	0.870762	-0.5102	0.609912	0.981636	chr9	32431604	32431952	+	0	NA	exon (NM exon (NM	47135 NM_00136E	48 Hs. 56722E NM_00219E	ENSG00000AC01	ACONS	HEI acitase protein-coding
chr11-99E	10.35771	-0.37111	0.727727	-0.50996	0.610079	0.981636	chr11	9989110	9989520	+	0	NA	intron (NLIPA17 LI	150173 NR_12053E	1.02E+08 Hs. 585524NR_12053E	ENSG00000LOC10192E	-	uncharacterncRNA
chr17-64E	10.35771	-0.37111	0.727727	-0.50996	0.610079	0.981636	chr17	64535734	64566089	+	0	NA	intron (Nintron (N	43934 NR_13364A	90799 Hs. 56973E NM_13836E	ENSG00000CEP95	CCDC45	centrosom protein-coding
chr19-404	10.35771	-0.37111	0.727727	-0.50996	0.610079	0.981636	chr19	40440308	40442030	+	0	NA	3' UTR (N3' UTR (N	1429 NM_01336E	29946 Hs. 51541E NM_01336E	ENSG00000SERTAD3	RBT1	SERTA don protein-coding
chr19-58E	10.35771	-0.37111	0.727727	-0.50996	0.610079	0.981636	chr19	58297827	58298286	+	0	NA	3' UTR (N3' UTR (N	-7318 NR_14444E	1.05E+08 Hs. 435404NR_14444E	ENSG00000ERVK3-1	-	endogeno ncRNA
chr9-836E	10.35771	-0.37111	0.727727	-0.50996	0.610079	0.981636	chr9	83651702	83652307	+	0	NA	Intergeni LIMB8 LIN	28860 NM_00100I	414328 Hs. 530261NM_00100I	ENSG00000IDNK	C9orf103	IDNK glucr protein-coding
chr19-26E	37.97564	0.216625	0.424906	0.509818	0.610179	0.981636	chr19	26549334	26550130	+	0	NA	Intergeni ALR Alpha	-1243699 NR_14673E	1.02E+08 Hs. 567934NR_110687	ENSG00000LOC101927	-	uncharacterncRNA
chr1-274C	7.44336	0.432141	0.848033	0.50958	0.610345	0.981636	chr1	27406937	27409650	+	0	NA	exon (NM exon (NM	15671 NM_00528I	8227 Hs. 66542 NM_00528I	ENSG00000GPR3	ACCA	G protein-coding
chr1-388E	7.44336	0.432141	0.848033	0.50958	0.610345	0.981636	chr1	38853176	38857047	+	0	NA	intron (Nintron (N	4661 NM_00127I	6421 Hs. 532461NM_02215E	ENSG00000CRRAGC	GTR2	RAGC Ras relat protein-coding
chr1-1204	7.44336	0.432141	0.848033	0.50958	0.610345	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (NMIRc SINE	-62651 NR_00324E	767846 Hs. 65718E NM_00324E	ENSG00000PFN1P2	Clorf152	profilin pseudo
chr1-213C	7.44336	0.432141	0.848033	0.50958	0.610345	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	exon (NM exon (NM	7129 NM_00130C	90806 Hs. 15707E NM_14456E	ENSG00000ANGEL2	Cer4d	KI angel hon protein-coding
chr1-2191	7.44336	0.432141	0.848033	0.50958	0.610345	0.981636	chr1	2.19E+08	2.19E+08	+	0	NA	intron (NLIPA10 LI	22195 NM_00130C	127018 Hs. 657617NM_13879A	ENSG00000LYPLAL1	Q96A0	lyosphos protein-coding
chr10-13E	7.44336	0.432141	0.848033	0.50958	0.610345	0.981636	chr10	13321757	13322764	+	0	NA	intron (NAluSx SIN	21230 NM_00132E	5264 Hs. 49873E NM_00621A			

chr13-98c	7.61529	-0.42885	0.843217	-0.50858	0.611045	0.981636	chr13	98377938	98378309	+	0	NA	intron (Nintron (N	144002 NM_003576	8428 Hs. 508514NM_003576	ENSG000003STK24	HEL-S-95 serine/tf protein-coding		
chr15-57c	7.61529	-0.42885	0.843217	-0.50858	0.611045	0.981636	chr15	57285320	57288469	+	0	NA	3' UTR (N3' UTR (N	-8237 NR_145748	1.1E+08	NR_145748	ENSG000003SNORD13D	- small nucsnoRNA	
chr16-69c	7.61529	-0.42885	0.843217	-0.50858	0.611045	0.981636	chr16	69372856	69373214	+	0	NA	intron (Nintron (N	12972 NM_005652	7014 Hs. 63335	NM_005652	ENSG000003TERF2	TRBF2 TRF telomeric protein-coding	
chr20-38c	7.61529	-0.42885	0.843217	-0.50858	0.611045	0.981636	chr20	38542824	38543490	+	0	NA	intron (Nintron (N	26394 NR_039606	1.01E+08	NR_039606	ENSG000003MIR54802	- microRNA ncRNA	
chr5-6607	7.61529	-0.42885	0.843217	-0.50858	0.611045	0.981636	chr5	66075728	66077321	+	0	NA	intron (Nintron (N	-67716 NM_001322	140890 Hs. 49367	NM_001322	ENSG000003SREK1	SFRS12 SF splicing protein-coding	
chr2-5814	4.222104	0.565297	1.111567	0.508558	0.611062	0.981636	chr2	58142720	58143641	+	0	NA	intron (Nintron (N	96468 NM_00113C	7444 Hs. 71529	ENM_00629E	ENSG000003CVRK2	- VRK serir protein-coding	
chr15-847	7.982397	0.426055	0.837963	0.508441	0.611144	0.981636	chr15	84767956	84768490	+	0	NA	intron (NAluSz SIN	19631 NM_01463C	9640 Hs. 79347	NM_01463C	ENSG000003ZNF592	CAMOS SC2 zinc fing protein-coding	
chr7-1124	10.38128	-0.37502	0.73789	-0.50824	0.611286	0.981636	chr7	1124E+08	1.12E+08	+	0	NA	intron (Nintron (N	11210 NM_001197	3475 Hs. 7879	NM_001155C	ENSG000003IFRD1	PC4 TIS7 interfecc protein-coding	
chr1-123c	6.91349	0.449895	0.885227	0.508226	0.611295	0.981636	chr1	12321909	12322999	+	0	NA	intron (Nintron (N	92424 NM_01537E	55187 Hs. 439381	NM_01537E	ENSG000003VPS13D	SCAR4 vacuolar protein-coding	
chr15-42c	6.91349	0.449895	0.885227	0.508226	0.611295	0.981636	chr15	42981273	42981926	+	0	NA	intron (NAluS SINE	-60821 NM_17350C	146057 Hs. 646511	NM_17350C	ENSG000003TTBK2	SCA11 TTE tau tubul protein-coding	
chr16-24c	6.91349	0.449895	0.885227	0.508226	0.611295	0.981636	chr16	24971143	24975500	+	0	NA	intron (Nintron (N	-16380 NM_00119E	527 Hs. 899107	NM_00169A	ENSG000003ATP6VOC	ATP6C ATF ATPase H+ protein-coding	
chr19-344	6.91349	0.449895	0.885227	0.508226	0.611295	0.981636	chr19	34490992	34492535	+	0	NA	intron (NAluSc8 SI	10005 NM_00108C	126374 Hs. 58501	CNM_00108C	ENSG000003WTIP	- WT1 inter protein-coding	
chr20-29c	6.91349	0.449895	0.885227	0.508226	0.611295	0.981636	chr20	2951237	2951813	+	0	NA	intron (NMER74A LI	28318 NM_080841	5786 Hs. 269577	NM_00283E	ENSG000003PTPRA	HEPT1 HLF protein t protein-coding	
chr1-857f	9.880536	-0.38156	0.750774	-0.50823	0.611295	0.981636	chr1	85703160	85706299	+	0	NA	intron (Nintron (N	3704 NM_00117C	54680 Hs. 5111	NM_01795E	ENSG000003ZNHT6	BKD1 Clorzinc fing protein-coding	
chr1-109c	9.880536	-0.38156	0.750774	-0.50823	0.611295	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (NAluJb SIN	7376 NM_00564E	6884 Hs. 63242E	NM_00564E	ENSG000003TAF13	MRT60 TAF TATA-box protein-coding	
chr17-75c	9.880536	-0.38156	0.750774	-0.50823	0.611295	0.981636	chr17	75210495	75210963	+	0	NA	intron (NAluY SINE	5050 NM_024844	79902 Hs. 362817	NM_024844	ENSG000003NUP85	FROUNT NF nucleopor protein-coding	
chr5-1037f	9.880536	-0.38156	0.750774	-0.50823	0.611295	0.981636	chr5	10379460	10379849	+	0	NA	intron (NAluY SINE	-22710 NR_162106	1.13E+08	MIR10397	- microRNA ncRNA		
chr19-1371f	12.14467	0.343897	0.676729	0.508175	0.611331	0.981636	chr19	37126636	37128521	+	0	NA	exon (NM exon (NM	44858 NM_19912E	199704 Hs. 65923E	NM_15265E	ENSG000003ZNF585A	- zinc fing protein-coding	
chr14-30c	4.964859	-0.52637	1.035896	-0.50813	0.611362	0.981636	chr14	30637218	30638012	+	0	NA	intron (Nintron (N	15296 NM_01610E	23256 Hs. 36916E	NM_01610E	ENSG000003SCFD1	C14orf16 secl fam protein-coding	
chr5-1294	4.964859	-0.52637	1.035896	-0.50813	0.611362	0.981636	chr5	1.72E+08	1.72E+08	+	0	NA	intron (Nricksha_C	62378 NM_00599C	6793 Hs. 74400E	ENM_00599C	ENSG000003STK10	LOK PRO27serine/tf protein-coding	
chr7-1274	4.964859	-0.52637	1.035896	-0.50813	0.611362	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (NHERVL-int	14579 NM_001134	57464 Hs. 48998E	NM_02070A	ENSG000003STRIP2	FAM40B F3 striatin protein-coding	
chr15-63c	7.419786	0.438448	0.862967	0.50807	0.611404	0.981636	chr15	63649008	63649879	+	0	NA	intron (Nintron (N	-48616 NR_03408C	1E+08	Hs. 63116E	NR_03408C	ENSG000003USP3-AS1	- USP3 anticncRNA
chr19-40c	7.419786	0.438448	0.862967	0.50807	0.611404	0.981636	chr19	4021897	4022126	+	0	NA	intron (NAluJo SIN	14275 NM_015897	51588 Hs. 10577E	NM_015897	ENSG000003PIAS4	PIAS-gamm protein i protein-coding	
chr9-100c	7.419786	0.438448	0.862967	0.50807	0.611404	0.981636	chr9	1E+08	1E+08	+	0	NA	intron (NAluSx SIN	125996 NM_001161	54881 Hs. 49464E	NM_01774E	ENSG000003TEX10	Ipil ba2C testis e protein-coding	
chr1-121c	11.11821	0.359931	0.708679	0.50789	0.611531	0.981636	chr1	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	10460 NR_10418E	1.01E+08	Hs. 56852E	NR_10418E	ENSG000003SRGAP2-AS-	SRGAP2 arncRNA
chr11-87c	6.717801	-0.46863	0.922977	-0.50774	0.611637	0.981636	chr11	8751378	8751630	+	0	NA	intron (NLTR12C LI	-12724 NR_12059E	1.03E+08	Hs. 61327E	NR_120590	LOC102724-	uncharactncRNA
chr19-19c	13.61567	-0.37339	0.735526	-0.50765	0.611695	0.981636	chr19	1993177	1993394	+	0	NA	intron (Nintron (N	22429 NM_017797	55643 Hs. 46554E	NM_017797	ENSG000003BTBD2	- BTB domain protein-coding	
chr1-2074	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr1	20743417	20750252	+	0	NA	intron (NAluJb SIN	-14131 NM_00110E	400745 Hs. 59152E	NM_00110E	ENSG000003SH2D5	- SH2 domain protein-coding	
chr1-402c	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr1	40235610	40237341	+	0	NA	exon (NM exon (NM	-11462 NM_00100E	127391 Hs. 40626E	NM_00100E	ENSG000003TMC02	dJ39G22.2 transmem protein-coding	
chr19-21c	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr19	21326062	21327646	+	0	NA	intron (NAluSp SIN	2556 NM_02126E	7562 Hs. 46629E	NM_02126E	ENSG000003ZNF708	KOXS ZNF zinc fing protein-coding	
chr2-2267	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr2	2.27E+08	2.27E+08	+	0	NA	intron (NAluSz SIN	13254 NM_005544	3667 Hs. 47150E	NM_005544	ENSG000003IRS1	HIRS-1 insulin r protein-coding	
chr4-119c	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr4	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	70209 NR_03763C	645513 Hs. 67754E	NR_03763C	ENSG000003LOC64551E	septin 7 pseudo	
chr5-349c	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr5	34921631	34923663	+	0	NA	intron (Nintron (N	-6912 NM_00101E	134218 Hs. 131887	NM_19428E	ENSG000003DNJC21	BMF53 DNADnaJ heat protein-coding	
chr5-128c	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	195240 NM_00104E	6558 Hs. 16258E	NM_00104E	ENSG000003SLC12A2	BSC BSC2 solute c protein-coding	
chr5-1764	10.34985	-0.36985	0.728571	-0.50763	0.61171	0.981636	chr5	1.76E+08	1.76E+08	+	0	NA	intron (Nintron (N	43704 NM_014901	22838 Hs. 43488E	NM_014901	ENSG000003RNF44	- ring fing protein-coding	
chr10-77c	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr10	8771525	8772457	+	0	NA	intron (NAluSq SIN	6002 NM_012311	22944 Hs. 39791E	NM_012311	ENSG000003KIN	BTCD KIN17 DN protein-coding	
chr10-87c	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr10	87711684	87717489	+	0	NA	intron (Nintron (N	54708 NM_00101E	9060 Hs. 524491	NM_00467C	ENSG000003PAPSS2	ATPSK2 BC3'-phospf protein-coding	
chr12-57c	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr12	57957559	57958270	+	0	NA	3' UTR (N3' UTR (N	16347 NM_03327E	91419 Hs. 61188	NM_03327E	ENSG000003ATP23	KUB3 XRCC ATP23 met protein-coding	
chr2-1961	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr2	1.96E+08	1.96E+08	+	0	NA	intron (Nintron (N	25961 NM_00422E	9262 Hs. 88297	NM_00422E	ENSG000003STK17B	DRAK2 serine/tf protein-coding	
chr3-533c	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr3	53333759	53334977	+	0	NA	intron (NLMEd LIN	-1241 NR_14571E	1.1E+08	NR_14571E	ENSG000003SNORD38C	- small nucsnoRNA	
chr4-757c	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr4	75799332	75802019	+	0	NA	exon (NM exon (NM	67052 NM_00129C	8615 Hs. 744877	NM_00371E	ENSG000003USP1	P115 TAP USO1 vesiprotein-coding	
chr5-1317	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr5	1.32E+08	1.32E+08	+	0	NA	intron (NAluSp SIN	76173 NM_00100E	96459 Hs. 59127E	NM_13337E	ENSG000003FNIP1	- follicul protein-coding	
chr7-7344	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr7	73449421	73451360	+	0	NA	intron (Nintron (N	16612 NM_00350E	8326 Hs. 64702E	NM_00350E	ENSG000003FZD9	CD349 FZI frizzled protein-coding	
chr8-266c	7.65643	-0.42575	0.838975	-0.50747	0.611827	0.981636	chr8	26655307	26657343	+	0	NA	3' UTR (N3' UTR (N	77920 NM_001244	1808 Hs. 593187	NM_00138E	ENSG000003DPYSL2	CRMP-2 CF dihydrase protein-coding	
chr1-1541	11.68922	0.353701	0.69707	0.50741	0.611867	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	exon (NM exon (NM	4214 NM_00118E	4817 Hs. 14640E	NM_00560C	ENSG000003CNIT1	- nitrilase protein-coding	
chr1-161c	12.15253	0.342623	0.675815	0.506977	0.612171	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (NTiger3b	10882 NM_00119E	103 Hs. 12341	NM_001111	ENSG000003ADAR	ADAR1 AGS adenosine protein-coding	
chr1-160c	12.15253	0.342623	0.675815	0.506977	0.612171	0.981636	chr1	1.6E+08	1.6E+08	+	0	NA	intron (NAluSp SIN	-13015 NR_00219C	474338 Hs. 62117E	NR_002190	SUMO1P3	- SUMO1 pseudo	
chr1-105f	7.965372	0.418626	0.825935	0.50685	0.61226	0.981636	chr1	1.85E+08	1.85E+08	+	0	NA	intron (Nintron (N	28720 NM_030934	81627 Hs. 10714E	NM_030934	ENSG000003TRMT1L	C1orf25 t rRNA metf protein-coding	
chr10-181c	7.965372	0.418626	0.825935	0.50685	0.61226	0.981636	chr10	1.1E+08	1.1E+08	+	0	NA	intron (NLC2 LINE	16348 NM_001324	7511 Hs. 39062E	NM_02038E	ENSG000003XPNPEP1	APP1 SAMF X-prolyl protein-coding	
chr12-31c	7.965372	0.418626	0.825935	0.50685	0.61226	0.981636	chr12	31972263	31972559	+	0	NA	intron (NAluY SINE	12996 NM_01816E	55196 Hs. 44512E	NM_01816E	ENSG000003RESF1	C12orf35 retroel protein-coding	
chr3-100c	7.965372	0.418626	0.825935	0.50685	0.61226	0.981636	chr3	1E+08	1E+08	+	0	NA	intron (NAluSx SIN	19033 NM_00119E	55773 Hs. 47700E	NM_01830E	ENSG000003TBC1D23	NS4ATP1 FBC1 dom protein-coding	
chr7-591c	7.965372	0.418626	0.825935	0.50685	0.61226	0.981636	chr7	5912628	5913071	+	0	NA	exon (NM exon (NM	14116 NM_0					



chr10-734	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr10	73422948	73426310	+	0	NA	exon (NM exon (NM	8932	NR_001024	118490	Hs.631822	NR_001024	ENSG000000MSS51	ZMYND17	MSS51	mitprotein-coding
chr11-947	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr11	9473475	9474887	+	0	NA	intron (Nintron (N	13169	NR_003442	7702	Hs.523471	NR_003442	ENSG000000ZNF143	SBF1 STAR	zinc fingprotein-coding	
chr11-727	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr11	72707012	72709822	+	0	NA	intron (Nintron (N	7943	NR_146788	1.01E+08	Hs.50316E	NR_146788	ENSG000000ARAF1-AS2	ARAF1	antncRNA	
chr11-12	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	54536	NR_001301	23365	Hs.24598	NR_001301	ENSG000000ARHGFP12	LARG PRO2	Rho guanoprotein-coding	
chr12-496	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr12	49800262	49804644	+	0	NA	intron (NAluScl SIN	25960	NR_001366	57701	Hs.143067	NR_001366	ENSG000000CNKAP5L	Cep169 FFNCK	ascoprotein-coding	
chr15-228	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr15	22880569	22883729	+	0	NA	intron (Nintron (N	35164	NR_001033	23191	Hs.26704	NR_001033	ENSG000000CYFIP1	P140SRA-1	cytoplasm protein-coding	
chr16-16	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr16	1637374	1638922	+	0	NA	intron (Nintron (N	23508	NR_002082	57585	Hs.60367	NR_002082	ENSG000000CRAMP1	CRAMP1L	cramped protein-coding	
chr17-18	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr17	18065139	18065835	+	0	NA	3' UTR (N3' UTR (N	-22461	NR_001388	1819	Hs.178582	NR_001388	ENSG000000DRG2	-	developm protein-coding	
chr17-38	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr17	38366118	38369943	+	0	NA	exon (NM exon (NM	16186	NR_014598	30837	Hs.514132	NR_014598	ENSG000000SOC7S	NAP4 NCKA	suppress protein-coding	
chr18-361	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr18	36171183	36173231	+	0	NA	intron (NAluJr SIN	15228	NR_13460E	1.02E+08	Hs.60067	NR_13460E	ENSG000000LOC101927	-	uncharactncRNA	
chr19-311	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr19	311270	312255	+	0	NA	intron (Nintron (N	-20359	NR_00371E	8612	Hs.46550E	NR_00371E	ENSG000000PLP2	LPP2 PAP	phospholiprotein-coding	
chr19-40	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr19	4032575	4034424	+	0	NA	exon (NM exon (NM	25763	NR_015897	51588	Hs.10577E	NR_015897	ENSG000000PIA5A	PIA5-gamm	protein iprotein-coding	
chr19-11	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr19	11213982	11216261	+	0	NA	intron (NAluV SINE	11493	NR_13490E	1.05E+08	Hs.579864	NR_13490E	ENSG000000LOC105372	-	uncharactncRNA	
chr19-162	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr19	16228066	16233263	+	0	NA	intron (NAluSg SIN	32753	NR_03249E	8907	Hs.71040	NR_03249E	ENSG000000AP1M1	AP47 CLAF	adaptor rprotein-coding	
chr2-262	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr2	26286667	26288294	+	0	NA	intron (Nintron (N	31569	NR_00114E	165082	Hs.63187E	NR_00114E	ENSG000000ADGRF3	GPR113 PC	adhesion protein-coding	
chr2-950	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr2	95092777	95093524	+	0	NA	intron (NLIAP6 LIN	28407	NR_001321	64969	Hs.65525E	NR_001321	ENSG000000MRP5S	MRP-5S	SEmitochonprotein-coding	
chr2-117	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr2	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	18414	NR_019044	54520	Hs.10784E	NR_019044	ENSG000000CCDC93	-	coiled-c protein-coding	
chr2-242	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr2	2.42E+08	2.42E+08	+	0	NA	intron (Nintron (N	14758	NR_17832E	23192	Hs.28361E	NR_17832E	ENSG000000ATG4B	APG4B AU1	autophagy protein-coding	
chr20-25	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr20	25683342	25686638	+	0	NA	intron (NLIAP7 LIN	1949	NR_00129C	26152	Hs.61881	NR_00129C	ENSG000000ZNF337	-	zinc fingprotein-coding	
chr20-49	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr20	49241640	49243202	+	0	NA	intron (NMIRb SINE	23126	NR_01789E	55661	Hs.65234	NR_01789E	ENSG000000DDX27	DRS1 Drs1	DEAD-box protein-coding	
chr22-46	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr22	46219618	46221366	+	0	NA	intron (NAluJo SIN	29801	NR_207327	150383	Hs.10311E	NR_207327	ENSG000000CDPF1	C22orf40	cysteine protein-coding	
chr3-162	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr3	16221976	16223013	+	0	NA	intron (Nintron (N	5718	NR_00131E	117248	Hs.41130E	NR_00131E	ENSG000000GALNT15	GALNACT15	polypeptiprotein-coding	
chr4-181	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr4	1813782	1817005	+	0	NA	intron (Nintron (N	22081	NR_00116E	2261	Hs.1420	NR_00116E	ENSG000000FGFR3	ACH CD33	fibroblas protein-coding	
chr4-174	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr4	17488621	17497119	+	0	NA	intron (NMIR SINE	22420	NR_00032C	5860	Hs.75438	NR_00032C	ENSG000000QDPR	DHPR HDHf	quinoid protein-coding	
chr5-374	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr5	37479491	37482765	+	0	NA	intron (NTHE1B-int	101810	NR_00134E	55100	Hs.21369E	NR_00134E	ENSG000000WDR70	-	WD repeatprotein-coding	
chr8-186	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr8	18629667	18631829	+	0	NA	intron (NMER2 DNA	178119	NR_20690E	178119	Hs.43425E	NR_20690E	ENSG000000PSD3	EFA6D EFAP	pleckstriprotein-coding	
chr8-377	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr8	3775325	37754309	+	0	NA	intron (Nintron (N	-5771	NR_003671	728024	Hs.64713E	NR_003671	ENSG000000LOC728024	-	chromosom pseudo	
chr8-378	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr8	37829851	37831978	+	0	NA	exon (NM exon (NM	18947	NR_01831C	55290	Hs.709301	NR_01831C	ENSG000000BRF2	BRFU TF11	BRF2 RNA protein-coding	
chr9-32	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr9	34250067	34251509	+	0	NA	intron (Nintron (N	71745	NR_001171	51271	Hs.26896E	NR_001171	ENSG000000UBAP1	NAG20 SPC	ubiquitin protein-coding	
chr9-129	7.451218	0.430045	0.853135	0.504075	0.614208	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (NLI2b LINE	13050	NR_00400C	1384	Hs.12068	NR_00400C	ENSG000000CRAT	CAT CAT1	carnitine protein-coding	
chr2-171	10.38313	-0.36637	0.726835	-0.50407	0.614214	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	intron (NLI2b LIN	-2573	NR_02477C	79828	Hs.13514E	NR_02477C	ENSG000000METHL8	TIP	methyltr protein-coding	
chr4-118	10.38313	-0.36637	0.726835	-0.50407	0.614214	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	42694	NR_00209E	57721	Hs.59687E	NR_00209E	ENSG000000METHL14	hMETHL14	methyltr protein-coding	
chr7-728	10.38313	-0.36637	0.726835	-0.50407	0.614214	0.981636	chr7	72881548	72886713	+	0	NA	intron (NAluJr SIN	4773	NR_001367	9883	Hs.65521E	NR_001367	ENSG000000POMI21	P145 POM1	POM121 rprotein-coding	
chr8-377	7.079413	-0.46005	0.91271	-0.50405	0.61423	0.981636	chr8	37768586	37768833	+	0	NA	TTS (NM_TTS (NM_C	6064	NR_00134E	11212	Hs.30479E	NR_00134E	ENSG000000PLPBP	EPVB6D PF	pyridoxalprotein-coding	
chr1-244	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr1	2.45E+08	2.45E+08	+	0	NA	Intergeni Intergeni	5170	NR_13278E	1.07E+08	NR_13278E	SNORA100	-	small nucsnRNA		
chr13-306	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr13	30624027	30624776	+	0	NA	intron (NAluJo SIN	6481	NR_001321	10208	Hs.533831	NR_001321	ENSG000000USPL1	C13orf22	ubiquitin protein-coding	
chr17-371	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr17	37187848	37188232	+	0	NA	intron (Nintron (N	-56761	NR_13277E	1.07E+08	NR_13277E	SNORA90	-	small nucsnRNA		
chr18-797	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr18	79704169	79704399	+	0	NA	intron (Nintron (N	22854	NR_00120E	9150	Hs.46549E	NR_00120E	ENSG000000CTDP1	CCFDN FCF	CTD phosphprotein-coding	
chr2-134	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (NTrigger2 I	22709	NR_001241	905	Hs.74411E	NR_001241	ENSG000000CCNT2	CYCT2	cyclin T2 protein-coding	
chr22-31	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr22	31618037	31618706	+	0	NA	TTS (NM_TTS (NM_C	3160	NR_10695E	1.02E+08	NR_10695E	ENSG000000MIR7109	hsa-mir-7	microRNA ncRNA		
chr8-233	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr8	23306151	23306814	+	0	NA	intron (Nintron (N	18377	NR_00113E	203069	Hs.45864E	NR_00113E	ENSG000000R3HCC1	-	R3H domaiprotein-coding	
chr8-585	7.1714	-0.44233	0.877889	-0.50386	0.614362	0.981636	chr8	58565506	58566337	+	0	NA	intron (Nintron (N	12660	NR_00562E	6386	Hs.200804	NR_00562E	ENSG000000SDCBP	MDA-9 MD	SDCyanecan protein-coding	
chr12-71	10.34199	-0.36858	0.731532	-0.50385	0.614368	0.981636	chr12	71650902	71660298	+	0	NA	intron (NLIIME1 LIN	8248	NR_14498E	196441	Hs.24579E	NR_14498E	ENSG000000ZFC3H1	CCDC131 Czinc	fingprotein-coding	
chr7-416	10.34199	-0.36858	0.731532	-0.50385	0.614368	0.981636	chr7	41689036	41690903	+	0	NA	exon (NM exon (NM	-3950	NR_02711E	285954	Hs.65686E	NR_02711E	ENSG000000INHBA-AS1	-	INHBA antncRNA	
chr11-12	7.607432	-0.4272	0.847997	-0.50377	0.614423	0.981636	chr11	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	553	NR_13718E	399959	Hs.44098	NR_13718E	ENSG000000MIR100HG	AGD1 linc	mir-100-ncRNA	
chr15-417	7.607432	-0.4272	0.847997	-0.50377	0.614423	0.981636	chr15	41767019	41767572	+	0	NA	3' UTR (N3' UTR (N	-7189	NR_00126E	23005	Hs.513661	NR_00126E	ENSG000000MAPKBP1	JNKBP-1 Jmi	togen-ε protein-coding	
chr7-129	7.607432	-0.4272	0.847997	-0.50377	0.614423	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	74207	NR_003344	7328	Hs.64354E	NR_003344	ENSG000000UBE2H	E2-20K G	ubiquitin protein-coding	
chr8-128	7.607432	-0.4272	0.847997	-0.50377	0.614423	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (NLIIME4a LI	-50465	NR_03161E	1E+08	NR_03161E	ENSG000000MIR1208	MIRN1208	microRNA ncRNA		
chr9-110	7.607432	-0.4272	0.847997	-0.50377	0.614423	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (NLIIP44 LIN	-56665	NR_00128E	255220	Hs.147064	NR_00128E	ENSG000000TXND8	SP		

chr5-1135 7.939948	0.413404	0.823847	0.501797	0.61581	0.981636	chr5	1.14E+08	1.14E+08	+	0 NA	intron (NLIPA11 LI	57447 NM_00134E	64848 Hs. 231942NM_022828	ENSG000004YTHDC2	CAHL hYTF YTH domain protein-coding	
chr7-5745 7.939948	0.413404	0.823847	0.501797	0.61581	0.981636	chr7	5745938	5746981	+	0 NA	intron (Nintron (N	-34549 NR_106934	1.02E+08	NR_106934	ENSG000004MIR6874	hsa-mir-ε microRNA ncRNA
chr9-3246 7.939948	0.413404	0.823847	0.501797	0.61581	0.981636	chr9	32467279	32467478	+	0 NA	intron (NL2 LINE I	58818 NM_014314	23586 Hs. 190622NM_014314	ENSG000004DDX58	RIG-I RICDEd/H-bc protein-coding	
chr1-1791 10.37527	-0.3651	0.727678	-0.50174	0.615852	0.981636	chr1	77954351	77971977	+	0 NA	intron (Nintron (N	15908 NR_130152	8880 Hs. 56738CN_003902	ENSG000004FUBP1	FBP FUBP far upst protein-coding	
chr1-1791 10.37527	-0.3651	0.727678	-0.50174	0.615852	0.981636	chr1	1.79E+08	1.79E+08	+	0 NA	intron (Nintron (N	16757 NM_00515E	27 Hs. 159472NM_00515E	ENSG000004ABL2	ABLL ARG ABL prot protein-coding	
chr15-40C 10.37527	-0.3651	0.727678	-0.50174	0.615852	0.981636	chr15	40025597	40027394	+	0 NA	intron (Nintron (N	12686 NM_003134	6727 Hs. 533732NM_003134	ENSG000004SRP14	ALURBP signal re protein-coding	
chr17-43C 10.37527	-0.3651	0.727678	-0.50174	0.615852	0.981636	chr17	43002140	43005024	+	0 NA	TTS (NR TTS (NR_1	-3202 NM_00133C	3430 Hs. 63225E	ENSG000004IF135	IFP35 interfe protein-coding	
chr5-1432 10.37527	-0.3651	0.727678	-0.50174	0.615852	0.981636	chr5	14327189	14329157	+	0 NA	intron (Nintron (N	-135810 NR_14581E	1.1E+08	NR_14581E	SNORD170	small nucsnoRNA
chr19-46C 7.484499	0.433471	0.864049	0.501674	0.615897	0.981636	chr19	46383303	46384399	+	0 NA	exon (NM exon (NM	29713 NM_03204C	83987 Hs. 9787E	ENSG000004CCDC8	3M3 PPP1F coiled-c protein-coding	
chr6-1697 7.484499	0.433471	0.864049	0.501674	0.615897	0.981636	chr6	1.7E+08	1.7E+08	+	0 NA	intron (NL2 LINE I	-17637 NM_02678C	80069 Hs. 677182NM_025002	ENSG000004LINC00574	G6orf208 long intencRNA	
chr1-4361 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr1	43619254	43619938	+	0 NA	intron (Nintron (N	-30553 NM_01466E	9682 Hs. 155983NM_01466E	ENSG000004KDM4A	JHDM3A JM lysine de protein-coding	
chr1-176C 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr1	1.76E+08	1.76E+08	+	0 NA	intron (NLIPA16 LI	-108600 NR_00299E	677679	NR_00299E	ENSG000004SCARNA3	HBI-100 small Ca <sub>v</sub> ncRNA
chr1-201E 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr1	2.02E+08	2.02E+08	+	0 NA	intron (Nintron (N	2299 NR_106797	1.02E+08	NR_106797	ENSG000004MIR6739	hsa-mir-ε microRNA ncRNA
chr1-236E 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr1	2.37E+08	2.37E+08	+	0 NA	intron (NMERGB DNA	16482 NM_001291	4548 Hs. 498187NM_000254	ENSG000004MTR	HMG MS c5-methylp protein-coding	
chr10-72Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr10	72208648	72211231	+	0 NA	intron (NMSTB LTR	6017 NM_00136E	51008 Hs. 500007NM_015947	ENSG000004ASCC1	ASC1P50 cactivatir protein-coding	
chr10-13Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr10	1.33E+08	1.33E+08	+	0 NA	exon (NM exon (NM	5060 NM_138384	92170 Hs. 50157E	ENSG000004MTG1	GTP GTPBF mitochondon protein-coding	
chr11-66Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr11	666232	666634	+	0 NA	intron (Nintron (N	27664 NM_000797	1815 Hs. 99922 NM_000797	ENSG000004DRD4	D4DR dopamine protein-coding	
chr12-121 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr12	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	24544 NM_00127C	10645 Hs. 29734E	ENSG000004CAMK2C	CAMK2C CAM calcium/c protein-coding	
chr12-13Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr12	1.32E+08	1.32E+08	+	0 NA	intron (Nintron (N	21896 NR_00297E	677829 Hs. 74240E	ENSG000004SNORA49	ACA49 small nucsnoRNA	
chr12-13Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr12	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	2677 NM_015394	7556 Hs. 57398E	ENSG000004ZNF10	KOX1 zinc fing protein-coding	
chr14-57Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr14	57208431	57208713	+	0 NA	3' UTR (N3' UTR (N	60333 NM_006544	10640 Hs. 743987NM_006544	ENSG000004EXOC5	HES10 PF exocyst c protein-coding	
chr14-911 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr14	91160596	91165850	+	0 NA	intron (NALuSx SIN	36797 NR_00370E	1E+08	NR_00370E	ENSG000004SNORA11B	small nucsnoRNA
chr16-19E 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr16	1985710	1987018	+	0 NA	3' UTR (N3' UTR (N	2171 NM_00526E	2671 Hs. 27184 NM_00526E	ENSG000004CFER	ALR ERV1 growth f protein-coding	
chr16-24E 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr16	24802003	24802450	+	0 NA	intron (Nintron (N	-43637 NM_00125E	115584 Hs. 16411E	ENSG000004SLC5A11	KST1 RKST1 solute c protein-coding	
chr19-10Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr19	10374801	10375644	+	0 NA	intron (Nintron (N	5350 NM_003331	7297 Hs. 7551E	ENSG000004TYK2	IMD35 JTB tyrosine protein-coding	
chr2-552 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr2	55203977	55205704	+	0 NA	intron (NLIMA3 LIN	-27045 NM_00113E	6233 Hs. 31164E	ENSG000004RPS27A	CEP80 HEL ribosomal protein-coding	
chr2-1591 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr2	1.31E+08	1.31E+08	+	0 NA	intron (Nintron (N	1131 NR_10694E	1.02E+08	NR_10694E	ENSG000004MIR6888	hsa-mir-ε microRNA ncRNA
chr22-37E 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr22	37925868	37929494	+	0 NA	exon (NM exon (NM	21384 NM_03338E	85377 Hs. 51761E	ENSG000004MICAL1	MICAL-L1 MICAL Ii protein-coding	
chr22-41Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr22	41224303	41228184	+	0 NA	intron (NALuSx1 SI	-8616 NR_14820C	1.01E+08	NR_14820C	ENSG000004LOC10050E	uncharactncRNA
chr3-473Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr3	47334877	47337692	+	0 NA	intron (Nintron (N	44737 NR_01546E	25930 Hs. 25524 NM_01546E	ENSG000004PTP23	HD-PTP HP protein-coding	
chr3-484Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr3	48453044	48453610	+	0 NA	intron (Nintron (N	6201 NM_001271	84126 Hs. 69484E	ENSG000004ATRIP	ATR inter protein-coding	
chr5-110Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr5	71060520	71061842	+	0 NA	intron (Nintron (N	6471 NM_00109E	728340 Hs. 19135E	ENSG000004GTF2H2C	GTF2H2C_2 GTF2H2 F protein-coding	
chr5-1414 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr5	1.41E+08	1.41E+08	+	0 NA	exon (NM exon (NM	2421 NM_03209E	56107 Hs. 36816E	ENSG000004PCDHGA9	PCDH-GAMM prot protein-coding	
chr6-154Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr6	15487258	15489520	+	0 NA	intron (Nintron (N	174639 NR_03644E	84062 Hs. 57114E	ENSG000004DTNBP1	BLOC158 D dystrobre protein-coding	
chr7-199Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr7	91993115	91994297	+	0 NA	intron (Nintron (N	52831 NM_005751	10142 Hs. 651221NM_005751	ENSG000004AKAP9	AKAP-9 AK-A-kinase protein-coding	
chr7-129E 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (NALuSx1 SI	15808 NM_003344	7328 Hs. 64354E	ENSG000004UBE2H	E2-20K Gluhiquitir protein-coding	
chr7-143Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr7	1.43E+08	1.43E+08	+	0 NA	TTS (NM TTS (NM_C	-8161 NR_04645E	1180 Hs. 12148E	ENSG000004CLCN1	CLC1 chloride protein-coding	
chr8-304Z 7.417936	0.426618	0.851132	0.501236	0.616205	0.981636	chr8	30401755	30402237	+	0 NA	intron (Nintron (N	-16596 NR_04620E	1E+08	NR_04620E	ENSG000004RBPMS-AS1	RBPM5 antncRNA
chr11-864 3.20406	-0.64115	1.279173	-0.50123	0.616212	0.981636	chr11	86409563	86410377	+	0 NA	intron (Nintron (N	35083 NM_00115E	60494 Hs. 14491E	ENSG000004CCDC81	coiled-cnc protein-coding	
chr2-325Z 9.839396	-0.38382	0.766229	-0.50092	0.616426	0.981636	chr2	32531326	32532076	+	0 NA	promoter-promoter-	-452 NR_03028E	693143	NR_03028E	ENSG000004MIR558	MIRN558 microRNA ncRNA
chr1-2861 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	28611385	28613566	+	0 NA	intron (Nintron (N	19980 NM_00119E	115273 Hs. 652321NM_152304	ENSG000004RAB42	RAB42, m protein-coding	
chr1-379E 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	37967303	37970131	+	0 NA	intron (NMER117 DN	21305 NM_00680E	10946 Hs. 77897 NM_00680E	ENSG000004SF3A3	PRP9 PRPF splicing protein-coding	
chr1-532Z 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	53208135	53214662	+	0 NA	intron (Nintron (N	9236 NM_017887	54987 Hs. 525391NM_017887	ENSG000004CZIB	Clorf123 CXXC motif protein-coding	
chr1-121Z 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	21657 NR_10418E	1.01E+08	NR_10418E	ENSG000004SRGAP2-AS	SRGAP2 antncRNA
chr1-180Z 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	1.81E+08	1.81E+08	+	0 NA	intron (NLIMEg LIN	-38524 NM_02095C	57710 Hs. 73481E	ENSG000004KIAA1614	KIAA1614 protein-coding	
chr1-180Z 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	1.84E+08	1.84E+08	+	0 NA	intron (Nintron (N	50694 NM_00043E	4688 Hs. 58755E	ENSG000004NCF2	NCF-2 NO <sub>2</sub> nitrophil protein-coding	
chr1-1851 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	1.85E+08	1.85E+08	+	0 NA	intron (NALuJb SIN	32439 NM_030934	81627 Hs. 10714E	ENSG000004TRMT1L	Clorf25 l tRNA metl protein-coding	
chr1-225E 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	2.26E+08	2.26E+08	+	0 NA	intron (Nintron (N	7724 NM_01469E	9725 Hs. 119387NM_01469E	ENSG000004TMEM63A	KIAA0792 transmem protein-coding	
chr1-230E 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr1	2.31E+08	2.31E+08	+	0 NA	intron (Nintron (N	2870 NM_03280C	84886 Hs. 520494NM_03280C	ENSG000004Clorf198	chromoson protein-coding	
chr10-73Z 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr10	73377711	73385127	+	0 NA	intron (Nintron (N	-22555 NM_001367	118491 Hs. 591367NM_14517E	ENSG000004CFAP70	TTTC18 cilia anc protein-coding	
chr10-101 7.947806	0.411462	0.821789	0.500691	0.616589	0.981636	chr10	1.02E+08	1.02E+08	+	0 NA	intron (Nintron (N	65636 NM_024541	79591 Hs. 16004 NM_024541	ENSG000004ARMH3	C10orf76 armadill protein-coding	
chr11-354 7.947806	0.411462	0.821789	0.5													



chr10-798 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr10	79801877	79803122	+ 0 NA	intron (Nintron (N	-23403 NR_029407	642361 Hs. 164299NR_029407	ENSG00000CLOC642361-	uncharactercncRNA	
chr10-115 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr10	1.2E+08	1.2E+08	+ 0 NA	intron (N2b LINE	10570 NR_136663	7073 Hs. 501203NR_003252	ENSG00000TIAL1	TCBP TIAF1TIAI	cytc protein-coding
chr11-94C 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr11	9408965	9412708	+ 0 NA	intron (Nintron (N	-17930 NR_002962	677808 Hs. 689722NR_002962	ENSG00000SNORA23	ACA23	small nucsnoRNA
chr11-181 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr11	18102842	18103085	+ 0 NA	intron (Nintron (N	3119 NM_138421	113174 Hs. 591998NM_138421	ENSG00000SAAL1	SPAC1A1	serum amyprotein-coding
chr12-511 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr12	51115363	51115951	+ 0 NA	intron (N1MB3 LIN	-32061 NM_030805	81566 Hs. 524425NR_030805	ENSG00000CSRNP2	C12orf2 C	cysteine protein-coding
chr12-105 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr12	1.05E+08	1.05E+08	+ 0 NA	TTS (NM_C TTS (NM_C	61902 NM_001293	23325 Hs. 12144 NM_015272	ENSG00000WASHC4	KIAA1033 WASH	comp protein-coding
chr14-55 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr14	55056748	55065355	+ 0 NA	intron (NAluSx SIN	6994 NM_144578	93487 Hs. 594338NM_144578	ENSG00000MAPK11P11	C14orf32 mitogen- $\epsilon$	protein-coding
chr15-605 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr15	60368064	60370689	+ 0 NA	intron (Nintron (N	28610 NM_001002	302 Hs. 511605NM_004033	ENSG00000ANXA2	ANX2 ANX2	anexin f protein-coding
chr15-902 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr15	90272219	90272808	+ 0 NA	TTS (NR_C TTS (NR_C	-6754 NR_102428	10519 Hs. 715555NM_006384	ENSG00000CIB1	CIB CIBP calcium $\epsilon$	protein-coding
chr19-55 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr19	55515069	55515268	+ 0 NA	intron (NAluSq SIN	21965 NM_001377	646643 Hs. 532677NM_001101	ENSG00000SBK2	SGK069	SH3 domainprotein-coding
chr2-652E 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr2	65265722	65267165	+ 0 NA	intron (N2a LINE	38748 NM_001005	10097 Hs. 643727NM_005722	ENSG00000ACTR2	ARP2	actin relprotein-coding
chr2-173C 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr2	1.74E+08	1.74E+08	+ 0 NA	3' UTR (N3' UTR (N	54176 NM_001017	6670 Hs. 531587NM_003111	ENSG00000SP3	SPR2	Sp3 relprotein-coding
chr2-216 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr2	2.16E+08	2.16E+08	+ 0 NA	intron (NMLT1F1 LI	4588 NM_022144	7520 Hs. 388733NM_021141	ENSG00000XRCC5	KARP-1 KAP- $\lambda$	ray refprotein-coding
chr2-321 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr21	32361388	32361885	+ 0 NA	intron (Nintron (N	15686 NR_002996	677846 Hs. 712292NR_002996	ENSG00000SNORA80A	ACA67 SNC	small nucsnoRNA
chr3-579 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr3	57908704	57909308	+ 0 NA	intron (Nintron (N	19004 NM_001304	7871 Hs. 476432NM_007155	ENSG00000SLMAP	SLAP	sarcolemin protein-coding
chr3-709 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr3	70958902	70959386	+ 0 NA	non-codirnon-codir	105780 NM_001345	27086 Hs. 59368 NM_032682	ENSG00000POXP1	L2CC4 HSF	forkhead protein-coding
chr4-554 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr4	55448589	55450794	+ 0 NA	intron (Nintron (N	53734 NM_018472	55858 Hs. 479766NM_018472	ENSG00000TMEM165	CDGK2 FT2	transmemt protein-coding
chr7-990 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr7	99047936	99048135	+ 0 NA	intron (Nintron (N	34870 NR_110102	1.02E+08 Hs. 636662NR_110102	ENSG00000LOC101927-	uncharactercncRNA	
chr7-140 7.632856	-0.4207	0.843426	-0.4988	0.617918	0.981636	chr7	1.4E+08	1.4E+08	+ 0 NA	non-codirnon-codir	25720 NM_013446	23608 Hs. 744883NM_013446	ENSG00000MKRN1	RNF61	makorin r protein-coding
chr1-379 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr1	37934070	37934712	+ 0 NA	intron (NMIRb SINE	-2600 NR_158631	3633 Hs. 449942NM_005544	ENSG00000INPP5B	5PTase	inositol protein-coding
chr10-11 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr10	1.11E+08	1.11E+08	+ 0 NA	intron (NAluSg7 SI	17672 NM_005445	9126 Hs. 24485 NM_005445	ENSG00000SMC3	BAM BMH C	structur $\epsilon$ protein-coding
chr11-47 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr11	47172681	47173504	+ 0 NA	intron (Nintron (N	3787 NM_032385	84364 Hs. 436204NM_032385	ENSG00000ARFGAP2	TRZ NBLA1	ADP ribos protein-coding
chr11-74 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr11	74246030	74247234	+ 0 NA	intron (Nintron (N	-64730 NR_120555	1.02E+08 Hs. 569022NR_120555	ENSG00000P4HA3-AS1-	P4HA3	antncRNA
chr12-10 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr12	1.05E+08	1.05E+08	+ 0 NA	3' UTR (N3' UTR (N	21865 NM_152317	121053 Hs. 295562NM_152317	ENSG00000C12orf45	-	chromosonprotein-coding
chr12-12 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr12	1.21E+08	1.21E+08	+ 0 NA	intron (Nintron (N	-19440 NM_153495	10645 Hs. 297342NM_006545	ENSG00000CAMKK2	CAMKK CAM	calcium/c protein-coding
chr13-97 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr13	97382177	97382922	+ 0 NA	intron (Nintron (N	-51620 NM_021033	5911 Hs. 508488NM_021033	ENSG00000RAP2A	K-BOV KRF	RAP2A, m $\epsilon$ protein-coding
chr16-71 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr16	71848421	71848991	+ 0 NA	intron (Nintron (N	2730 NM_001137	342371 Hs. 743223NM_001137	ENSG00000ATXN1L	KEAT BOA1	ataxin 1 protein-coding
chr17-53 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr17	5380326	5382669	+ 0 NA	exon (NM exon (NM	-38144 NM_00116C	84268 Hs. 462085NM_032308	ENSG00000RPAIN	HRIP RIP	RPA interprotein-coding
chr2-218 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr2	2.18E+08	2.18E+08	+ 0 NA	TTS (NR_C TTS (NR_C	292 NR_02950C	407017 NR_02950C	ENSG00000MIR26B	MIRN26B f	microRNA ncRNA
chr20-34 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr20	34416498	34419223	+ 0 NA	intron (Nintron (N	-48465 NR_030374	693229 NR_030374	ENSG00000MIR644A	MIR644 mi	microRNA ncRNA
chr22-45 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr22	45183611	45187043	+ 0 NA	3' UTR (N3' UTR (N	6285 NR_146602	1.05E+08 NR_146602	LOC1053737-	uncharactercncRNA	
chr3-47 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr3	47708915	47710465	+ 0 NA	intron (NAluSx SIN	-47996 NR_145791	1.1E+08 NR_145791	SNORD146	-	small nucsnoRNA
chr3-170 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr3	1.7E+08	1.7E+08	+ 0 NA	intron (Nintron (N	53403 NM_024947	80012 Hs. 529592NM_024947	ENSG00000PHC3	EDR3 HPHE	polymucron protein-coding
chr3-18 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr3	1.87E+08	1.87E+08	+ 0 NA	intron (Nintron (N	-40323 NR_135551	1.02E+08 NR_135551	ENSG00000LOC101925-	uncharactercncRNA	
chr4-800 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr4	80024189	80025352	+ 0 NA	intron (NAluJb SIN	48459 NM_00128E	118429 Hs. 162962NM_005817	ENSG00000ANTXR2	CMG-2 CMC	ANTXR celprotein-coding
chr5-568 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr5	56887426	56888853	+ 0 NA	intron (Nintron (N	-21121 NR_136555	133383 Hs. 89590 NM_153705	ENSG00000SETD9	C5orf35	SET domainprotein-coding
chr5-692 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr5	69272432	69273976	+ 0 NA	intron (Nintron (N	38318 NM_001795	1022 Hs. 184295NM_001795	ENSG00000CDK7	CAK CAK1 cyclin	d $\epsilon$ protein-coding
chr5-13 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr5	1.32E+08	1.32E+08	+ 0 NA	exon (NM exon (NM	-16642 NM_001164	51735 Hs. 483325NM_016344	ENSG00000RAPGEF6	KIAA0011B Rap	guani protein-coding
chr5-180 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr5	1.81E+08	1.81E+08	+ 0 NA	TTS (NM_C TTS (NM_C	27016 NM_006133	830 Hs. 446122NM_006133	ENSG00000CAPZA2	CAPPA2 C $\beta$	capping $\epsilon$ protein-coding
chr7-116 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr7	1.04E+08	1.04E+08	+ 0 NA	intron (Nintron (N	-13686 NR_03033C	693127 NR_03033C	ENSG00000MIR548A3	MIRN548A3 mi	microRNA ncRNA
chr8-104 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr8	1.2E+08	1.2E+08	+ 0 NA	intron (NMLT1A1 LI	40123 NM_003184	6873 Hs. 122752NM_003184	ENSG00000TAF2	CIF150 MF	TATA-box protein-coding
chr9-374 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr9	37488741	37491056	+ 0 NA	intron (N2a LINE	3950 NM_02249C	64425 Hs. 591087NM_02249C	ENSG00000POLR1E	PAF53 PR	RNA polyn protein-coding
chr9-108 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr9	1.09E+08	1.09E+08	+ 0 NA	exon (NM exon (NM	7550 NM_00131E	8518 Hs. 494733NM_003644	ENSG00000ELP1	DYS FD F $\beta$	elongator protein-coding
chr9-124 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr9	1.24E+08	1.24E+08	+ 0 NA	intron (Nintron (N	-8597 NR_02740E	1E+08 Hs. 654983NR_02740E	LOC100125-	uncharactercncRNA	
chr9-134 7.673996	-0.41767	0.837608	-0.49865	0.618026	0.981636	chr9	1.35E+08	1.35E+08	+ 0 NA	intron (NMLT1C LTF	-93231 NR_138045	414316 Hs. 571561NR_138045	ENSG00000COL5A1-AS	C9orf104 COL5A1	ar ncRNA
chr12-68 7.689712	-0.421	0.844424	-0.49856	0.618088	0.981636	chr12	68692190	68693777	+ 0 NA	intron (NAluSx1 SI	6005 NM_020401	57122 Hs. 524574NM_020401	ENSG00000NUP107	NPHS1 NL	nucleopor protein-coding
chr9-100 7.689712	-0.421	0.844424	-0.49856	0.618088	0.981636	chr9	1E+08	1E+08	+ 0 NA	intron (Nintron (N	1084 NM_00119E	1.01E+08 Hs. 598103NM_001198812	MSANTD3-1	C9orf2 C9	MSANTD3-1 protein-coding
chr1-932 7.915862	-0.52861	1.060317	-0.49854	0.618105	0.981636	chr1	93237036	93237681	+ 0 NA	intron (N2a LINE	56642 NM_00130C	343099 Hs. 482872NM_026888	ENSG00000CCDC18	NY-SAR-4 coiled-c $\epsilon$	protein-coding
chr10-49 7.915862	-0.52861	1.060317	-0.49854	0.618105	0.981636	chr10	49913987	49914441	+ 0 NA	intron (Nintron (N	27813 NR_136755	8505 Hs. 535295NM_003631	ENSG00000PARG	PARG99	poly (ADP- $\epsilon$ protein-coding
chrX-270 7.915862	-0.52861	1.060317	-0.49854	0.618105	0.981636	chrX	2700319	2700616	+ 0 NA	intron (N(ATCC)n S	9172 NM_002414	4267 Hs. 653345NM_002414	ENSG00000CCD99	HBA71 MIC	CD99 mole protein-coding
chr6-83 7.915862	-0.52861	1.060317	-0.49854	0.618105	0.981636	chr6	8316307	83181958	+ 0 NA	intron (N(AT)n Si	6192 NM_001195	5238 Hs. 661665NM_015595	ENSG00000PGM3	AGM1 TMD2	phosphog protein-coding

chr11-738	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr11	73871068	73872942	+	0	NA	TTS (NM_CTTT)	(NM_C	-4694	NM_001267	80227	Hs.525017NM_025155	ENSG0000CPA1F1	PAAF1	RpnI	protease	protein-coding		
chr11-13C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr11	1.31E+08	1.31E+08	+	0	NA	intron (Nintron)	(N	3044	NM_001301	399979	Hs.444024NM_014758	ENSG0000SNX19	CHE78	sorting	rprotein-coding			
chr13-48C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr13	48373701	48375808	+	0	NA	intron (Nintron)	(N	38359	NM_001162	10161	Hs.123464NM_005767	ENSG0000CLPAR6	ARWH1	HYF	lyso	phospho	protein-coding	
chr14-301	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr14	30955207	30954685	+	0	NA	intron (NLM3E3A)	(LI	60796	NR_030354	693209	NR_030354	ENSG0000MIR624	MIRN624	[hmicroRNA	ncRNA			
chr14-105	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	intron (Nintron)	(N	-69692	NM_001376	1778	Hs.61408CNR_001376	ENSG0000DYNC1H1	CMT20	DHC	cyto	intron	protein-coding	
chr15-62F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr15	62810523	62810723	+	0	NA	intron (Nintron)	(N	-13334	NR_029709	406965	NR_029709	ENSG0000MIR190A	MIR190	[MmicroRNA	ncRNA			
chr15-651	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr15	65106110	65106352	+	0	NA	5' UTR (N5' UTR)	(N	128	NM_001162	390595	Hs.659255NM_001162	ENSG0000UBAP1L	UBAP-1L	ubiquitin	protein-coding			
chr15-71F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr15	71887546	71888077	+	0	NA	intron (NMER34A)	(LI	77257	NM_014245	10002	Hs.187354NM_014245	ENSG0000CNR2E3	ESCS	[Pnr]	nuclear	rprotein-coding		
chr16-29C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr16	29918029	29920286	+	0	NA	intron (NLMC5a)	(LI	7069	NR_110933	253980	Hs.53459CNR_178863	ENSG0000KCTD13	BACURD1	[Fpotassium	protein-coding			
chr16-58F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr16	58565713	58568109	+	0	NA	intron (NALuSp)	(SIN	-6980	NR_002298	523635	Hs.67751ENR_002298	ENSG0000SNORA50A	ACA50	[Snc	small	nucsnRNA		
chr17-82F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr17	82594895	82595768	+	0	NA	intron (NALuJo)	(SIN	53113	NM_019613	56270	Hs.132161NM_019613	ENSG0000WDR45B	NEDSBAS	[WWD	repeat	protein-coding		
chr18-21F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr18	21581114	21581328	+	0	NA	intron (NALuY)	(SINE	19483	NM_052911	114799	Hs.464733NM_052911	ENSG0000ESCO1	A930014	[I]establis	protein-coding			
chr2-371C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	37101030	37103438	+	0	NA	3' UTR (N3' UTR)	(N	17783	NM_001278	253635	Hs.59525CNR_174931	ENSG0000GPATCH11	CDC75	[CEG	patch	rprotein-coding		
chr2-695F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	69502485	69504084	+	0	NA	intron (Nintron)	(N	16707	NR_00370E	1E+08	Hs.693447NR_00370E	ENSG0000SNORA36C	-	small	nucsnRNA			
chr2-860F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	86069424	86071490	+	0	NA	intron (Nintron)	(N	35429	NM_01542E	25885	Hs.53181ENM_01542E	ENSG0000POLR1A	A190	[AFDCRA	polyn	protein-coding		
chr2-1087	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	1.09E+08	1.09E+08	+	0	NA	intron (NALuJo)	(SIN	10357	NM_006267	5903	Hs.199561NM_006267	ENSG0000CRANBP2	ADANE	[ANF	RAN	bindi	protein-coding	
chr2-216C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	2.1E+08	2.1E+08	+	0	NA	3' UTR (N3' UTR)	(N	-9678	NR_110291	1.02E+08	Hs.63555ENR_110291	LOC10192E-	-	uncharact	ncRNA			
chr2-210C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (NMIR3)	(SINE	2484	NM_021141	7520	Hs.388733NM_021141	ENSG0000XRC5C	KARP-1	[KX	X-ray	re	protein-coding	
chr2-216C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (Nintron)	(N	20075	NM_021141	7520	Hs.388733NM_021141	ENSG0000XRC5C	KARP-1	[KX	X-ray	re	protein-coding	
chr20-35F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr20	35543426	35543807	+	0	NA	intron (Nintron)	(N	1538	NM_01596E	51614	Hs.47255ENM_01596E	ENSG0000CERC3	C2orf47	[E	RGIC	anc	protein-coding	
chr22-197	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr22	19389387	19390049	+	0	NA	intron (Nintron)	(N	42015	NM_00332E	7290	Hs.47420ENM_00332E	ENSG0000HIRA	DGCR1	[TUF	histone	rprotein-coding		
chr4-2454	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr4	24548219	24549932	+	0	NA	intron (Nintron)	(N	-28785	NR_03029E	693158	NR_03029E	ENSG0000MIR573	MIRN573	[hmicroRNA	ncRNA			
chr4-243C	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr4	26392492	26394495	+	0	NA	intron (NALuS)	(SIN	72265	NM_00136E	3516	Hs.47939ENM_00534E	ENSG0000CRBPJ	AOS3	[CBF1	recomb	protein-coding		
chr4-562F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr4	54238843	54244119	+	0	NA	intron (NALuSq2)	(SI	7671	NM_001347	5156	Hs.74615	NM_00620E	ENSG0000PDGFR	CD140A	[PT	platelet	protein-coding	
chr4-108F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr4	1.09E+08	1.09E+08	+	0	NA	TTS (NM_CTTT)	(NM_C	10039	NM_00131E	6164	Hs.438227NM_00099E	ENSG0000RPL34	L34	ribosomal	protein-coding			
chr5-3237	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr5	32375485	32373458	+	0	NA	intron (NALuSx4)	(SI	18004	NR_03030E	693164	NR_03030E	ENSG0000MIR579	MIRN579	[hmicroRNA	ncRNA			
chr7-436F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr7	43632447	43633116	+	0	NA	non-cod	non-cod	49733	NR_00476E	9263	Hs.70948ENM_00476E	ENSG0000STK17A	DRAK1	serine/t	protein-coding			
chr8-179F	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr8	17969827	17970532	+	0	NA	intron (Nintron)	(N	47191	NM_00135E	5108	Hs.49114ENM_00619E	ENSG0000PCMI	PTCA	[RET]	pericent	protein-coding		
chr8-9914	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr8	99148104	99149540	+	0	NA	intron (NLTR75)	(LTF	135556	NM_01789E	157680	Hs.19154CNR_01524E	ENSG0000VPS13B	CHS1	[COH1	vacuolar	protein-coding		
chr9-9801	7.666138	-0.41598	0.83907	-0.49576	0.620061	0.981636	chr9	98011090	98017402	+	0	NA	intron (NALuY)	(SINE	39095	NM_006401	10541	Hs.730654NM_006401	ENSG0000ANP32B	APRIL	[PH	acidic	rprotein-coding		
chr16-70F	8.477675	0.398264	0.803334	0.495764	0.620061	0.981636	chr16	70370440	70371078	+	0	NA	intron (NALuSp)	(SIN	23856	NM_01833E	55308	Hs.656037NM_01833E	ENSG0000DDX19A	DDX19	[DDX	DEAD	box	protein-coding	
chr2-231C	8.477675	0.398264	0.803334	0.495764	0.620061	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (Nintron)	(N	81472	NM_00135E	80210	Hs.162411NM_02513E	ENSG0000ARMC9	ARM	[JBT52	armadil	l1c	protein-coding	
chr5-134F	8.477675	0.398264	0.803334	0.495764	0.620061	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (Nintron)	(N	36143	NM_02198E	10802	Hs.59554CNR_02198E	ENSG0000SEC24A	-	SEC24	hom	protein-coding		
chr9-9821	7.924232	0.417499	0.842151	0.495754	0.620068	0.981636	chr9	98217139	98218123	+	0	NA	intron (Nintron)	(N	-4080	NM_001267	55357	Hs.37101ENM_01842E	ENSG0000TBC1D2	PARIS-1	[TBC1	dom	protein-coding		
chr6-436F	8.469818	0.40016	0.807201	0.495738	0.620079	0.981636	chr6	43604711	43606014	+	0	NA	intron (Nintron)	(N	21991	NM_00128E	54676	Hs.48544ENM_01909E	ENSG0000GTPBP2	JABELS	[GTP	bidi	protein-coding		
chr1-164F	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr1	16485133	16487264	+	0	NA	intron (NALuSx)	(SIN	6503	NR_02338E	114819	Hs.597881NR_02338E	ENSG0000CROCCP3	CROCC2	[L	CROCC	pseudo		
chr1-2251	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr1	22519390	22520503	+	0	NA	intron (Nintron)	(N	-43543	NM_00100E	2046	Hs.28361ENM_02052E	ENSG0000CEPHA8	EEL	[EK3	[E	EPH	re	protein-coding
chr1-1807	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr1	1.81E+08	1.81E+08	+	0	NA	Intergeni	THEIA-int	-	-5316	NR_145481	1.03E+08	Hs.66531ENR_145481	ENSG0000KIAA1614-	-	KIAA1614	ncRNA		
chr1-2117	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr1	2.12E+08	2.12E+08	+	0	NA	3' UTR (N3' UTR)	(N	72815	NR_148994	91548	Hs.36783ENR_148994	LOC91548	-	uncharact	ncRNA			
chr1-228F	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr1	2.28E+08	2.28E+08	+	0	NA	TTS (NR_TTS)	(NR_T	949	NR_10680C	1.02E+08	NR_10680C	ENSG0000MIR6742	hsa-mir-6	microRNA	ncRNA			
chr10-977	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr10	97753289	97755899	+	0	NA	intron (NALuJb)	(SIN	15962	NM_00100E	118813	Hs.74407ENM_14458E	ENSG0000ZFVY27	PROTRUD1	zinc	finger	protein-coding		
chr11-63F	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr11	63952952	63956662	+	0	NA	3' UTR (N3' UTR)	(N	15476	NM_00130C	79829	Hs.52375ENM_02477E	ENSG0000NAA40	NAT11	[Nat	(alpha)	protein-coding		
chr11-12C	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr11	1.22E+08	1.22E+08	+	0	NA	intron (NLIMA2)	(LIN	47472	NR_029671	406911	NR_029671	ENSG0000MIR125B1	MIRN125B1	[hmicroRNA	ncRNA			
chr12-55F	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr12	5580704	55809555	+	0	NA	intron (NALuJb)	(SIN	8595	NM_03308E	84324	Hs.50567ENM_03308E	ENSG0000SARNP	CIP29	[HCC	SAP	doma	protein-coding	
chr12-10F	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (N(TATG)n)	(S	8160	NM_00114E	121642	Hs.37445ENM_00100E	ENSG0000ALKBH2	ABH2	alkB	hom	protein-coding		
chr16-22C	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr16	2231391	2234400	+	0	NA	exon (NM exon)	(NM	-3549	NM_001374	1775	Hs.10350ENM_001374	ENSG0000DNASE1L2	DNAS1L2	deoxyrib	protein-coding			
chr16-16C	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr16	16236777	16239603	+	0	NA	intron (NLM3E3G)	(LI	5595	NM_173614	283820	Hs.460141NM_173614	ENSG0000NOMO2	Nomo	[PM5	NODAL	mo	protein-coding	
chr16-19F	7.425794	0.424472	0.856255	0.495731	0.620084	0.981636	chr16	19651935																	



chr13-106 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr13	1.06E+08	1.06E+08	+	0 NA	3' UTR (N3' UTR (N	42210 NM_004093	1948 Hs. 149232NM_004093	ENSG000002EFNB2	EPLG5 HTF ephrin Bz protein-coding	
chr14-67 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr14	67340764	67341850	+	0 NA	intron (N SVA_A Ret	18497 NM_015994	51382 Hs. 272632NM_015994	ENSG000002ATP6V1D	ATP6M VAT ATPase H+ protein-coding	
chr15-427 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr15	42733368	42735095	+	0 NA	exon (NM_exon (NM	2897 NM_138477	146059 Hs. 599232NM_138477	ENSG000002CDAN1	CDAN1 CDAN1 codanin I protein-coding	
chr15-567 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr15	56703201	56704879	+	0 NA	intron (N intron (N	30046 NM_001288	54816 Hs. 511477NM_001288	ENSG000002ZNF280D	SUHW4 ZNF zinc finger protein-coding	
chr15-84 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr15	84484950	84486464	+	0 NA	intron (N MamGypl TF	-16868 NM_003378	440299 Hs. 454641NR_003378	DNM1P41	DNM1DN1-dynamin I pseudo	
chr16-146 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr16	14603803	14610306	+	0 NA	intron (N AluY SINE	23206 NM_002582	5073 Hs. 253197NM_002582	ENSG000002PARN	DAN DKCB poly (A)-s protein-coding	
chr17-22 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr17	2286569	2286971	+	0 NA	intron (N AluSx SIN	15665 NM_017575	23293 Hs. 448342NM_017575	ENSG000002SMG6	C17orf31 SMG6 nons protein-coding	
chr17-79 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr17	7901628	7904922	+	0 NA	exon (NM_exon (NM	-2848 NR_003000	677763	NR_003000	ENSG000002SCARNA21	ACA68 SCA small Ca <sup>2+</sup> ncRNA
chr17-312 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr17	31260704	31261836	+	0 NA	intron (N intron (N	35969 NM_002544	4974 Hs. 113874NM_002544	ENSG000002CMG	OMGP oligodendrocyte protein-coding	
chr17-146 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr17	46047652	46048138	+	0 NA	intron (N intron (N	48645 NM_001007	246744 Hs. 661831NM_001007	ENSG000002STH	MAPTIT saitohin protein-coding	
chr19-12 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr19	12660822	12665151	+	0 NA	intron (N AluSz SIN	3756 NM_000528	4125 Hs. 356765NM_000528	ENSG000002MAN2B1	LANMAN MAN mannose protein-coding	
chr19-38 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr19	38099808	38102283	+	0 NA	intron (N intron (N	-62051 NR_145800	1.1E+08	NR_145800	SNORD152	small nucleolar RNA
chr19-53 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr19	53080419	53087582	+	0 NA	intron (N LTR36 LTF	3037 NM_001322	90338 Hs. 655967NM_001322	ENSG000002ZNF160	F11 Hkr1 zinc finger protein-coding	
chr2-159 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr2	1.59E+08	1.59E+08	+	0 NA	intron (N LIMB2 LIN	35501 NR_106949	1.02E+08	NR_106949	ENSG000002MIR6888	hsa-mir-6888 microRNA ncRNA
chr2-2304 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr2	2.3E+08	2.3E+08	+	0 NA	intron (N intron (N	50156 NM_001200	6672 Hs. 369055NM_001200	ENSG000002SP100	lysp100b SP100 nucleotide protein-coding	
chr3-486 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr3	48624801	48628579	+	0 NA	intron (N intron (N	-4921 NM_001008	440955 Hs. 631922NM_001008	ENSG000002TMEM89	transmembrane protein-coding	
chr3-489 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr3	48983062	48983348	+	0 NA	non-coding non-coding	-6503 NM_177932	54681 Hs. 654944NM_177932	ENSG000002P4HTM	EGLN4 HIF prolyl 4-protein-coding	
chr3-197 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr3	1.98E+08	1.98E+08	+	0 NA	intron (N intron (N	-18461 NR_030627	1E+08	NR_030627	ENSG000002GN1922	MIRN922 microRNA ncRNA
chr5-4074 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr5	40740691	40742903	+	0 NA	intron (N LIME1 LIN	14615 NM_012382	23548 Hs. 348915NM_012382	ENSG000002TTC33	OSRF tetrahydropteridine protein-coding	
chr6-995 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr6	99554686	99555973	+	0 NA	intron (N intron (N	13331 NM_005190	892 Hs. 430645NM_005190	ENSG000002CCNC	CycC SRB1 cyclin C protein-coding	
chr7-801 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr7	80199279	80206887	+	0 NA	intron (N intron (N	67299 NM_001256	2770 Hs. 134587NM_001256	ENSG000002GN11	Gi G protein-coding	
chr7-1314 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chr7	1.31E+08	1.31E+08	+	0 NA	exon (NM_exon (NM	109941 NM_001321	4289 Hs. 44693 NM_013255	ENSG000002MKLN1	TWA2 muskelin protein-coding	
chrX-154 7.922382	0.406278	0.822914	0.493706	0.621514	0.981636	chrX	1.54E+08	1.54E+08	+	0 NA	intron (N intron (N	24403 NM_001118	2316 Hs. 195464NM_001118	ENSG000002FLNA	ABP-280 filamin A protein-coding	
chr2-9517 12.14282	0.336516	0.681929	0.493477	0.621675	0.981636	chr2	95179071	95182778	+	0 NA	intron (N intron (N	15115 NM_001291	7549 Hs. 590910NM_001291	ENSG000002ZNF2	A1-5 ZNF zinc finger protein-coding	
chr4-988 8.110029	-0.40484	0.820792	-0.49323	0.621847	0.981636	chr4	98898181	98898380	+	0 NA	intron (N Charliel	30853 NM_001133	1977 Hs. 13211 NM_001968	ENSG000002EIF4E	AUTS19 CE eukaryotic protein-coding	
chr10-27 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr10	27206428	27207237	+	0 NA	intron (N intron (N	33654 NM_001301	91452 Hs. 530597NM_145698	ENSG000002ACBD5	acyl-CoA protein-coding	
chr19-45 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr19	4511621	45127133	+	0 NA	exon (NM_exon (NM	3101 NM_001322	23403 Hs. 128702NM_001088	ENSG000002FBX046	20D7-FC4 F-box protein-coding	
chr20-35 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr20	35503473	35504182	+	0 NA	exon (NM_exon (NM	25825 NR_026933	140873 Hs. 158688NM_080828	ENSG000002C20orf17	dJ47704.4 chromosome protein-coding	
chr3-197 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr3	1.98E+08	1.98E+08	+	0 NA	intron (N intron (N	31540 NR_026788	89782 Hs. 518542NM_033025	ENSG000002LMLN	GP63 INV leishmanin protein-coding	
chr5-728 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr5	72825516	72826115	+	0 NA	intron (N MLT1A0 LI	9154 NM_001364	3842 Hs. 482497NM_002270	ENSG000002TNP01	IP02 KPN transport protein-coding	
chr5-112 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr5	1.13E+08	1.13E+08	+	0 NA	intron (N intron (N	-32747 NM_001204	6728 Hs. 637001NM_003135	ENSG000002SRP19	signal receptor protein-coding	
chr7-770 7.384654	0.423082	0.857797	0.493219	0.621858	0.981636	chr7	77002586	77003103	+	0 NA	intron (N intron (N	22022 NR_023388	441263 Hs. 675888NR_023388	ENSG000002DTX2P1	UFPM2S11 DTX2P1-UF pseudo	
chr1-8671 7.906666	0.41016	0.831612	0.493211	0.621863	0.981636	chr1	86719571	86721149	+	0 NA	intron (N intron (N	15784 NR_016005	51100 Hs. 136305NM_016005	ENSG000002SH3GLB1	Bif-1 CGI SH3 domain protein-coding	
chr15-63 7.906666	0.41016	0.831612	0.493211	0.621863	0.981636	chr15	63591434	63591809	+	0 NA	non-coding non-coding	-5766 NM_001367	283807 Hs. 631165NM_203375	ENSG000002FBXL22	Fb122 F-box anc protein-coding	
chr18-45 7.906666	0.41016	0.831612	0.493211	0.621863	0.981636	chr18	45932997	45934096	+	0 NA	intron (N AluSz SIN	33783 NM_020964	57724 Hs. 514845NM_020964	ENSG000002EPG5	HEWE1 KIF ectopic F protein-coding	
chr1-214 9.968823	-0.387	0.784917	-0.49304	0.621985	0.981636	chr1	2.14E+08	2.14E+08	+	0 NA	intron (N intron (N	78878 NM_020197	56950 Hs. 66170 NM_020197	ENSG000002SMYD2	HSKM-B KMS ET and B protein-coding	
chr12-49 7.386504	0.435021	0.882699	0.492831	0.622132	0.981636	chr12	49654192	49654416	+	0 NA	intron (N intron (N	23760 NM_001363	25766 Hs. 706827NM_012272	ENSG000002PRPF40B	HYPIC pre-mRNA protein-coding	
chr2-107 7.376797	0.425127	0.862703	0.492785	0.622165	0.981636	chr2	10794970	10795206	+	0 NA	intron (N intron (N	17697 NM_005742	10130 Hs. 212102NM_005742	ENSG000002PDIA6	PERP5 P5 protein c protein-coding	
chr6-169 7.376797	0.425127	0.862703	0.492785	0.622165	0.981636	chr6	1.7E+08	1.7E+08	+	0 NA	intron (N intron (N	17427 NM_001278	55780 Hs. 47546 NM_018341	ENSG000002ERMARD	ER6770 FER membrane protein-coding	
chr6-3667 13.17714	0.322405	0.654253	0.492783	0.622166	0.981636	chr6	36678787	36687689	+	0 NA	intron (N MIR SINE	4524 NM_000388	1026 Hs. 370771NM_000388	ENSG000002CDKN1A	CAP20 CDK cyclin d protein-coding	
chr19-44 10.82887	-0.35222	0.715475	-0.49229	0.622515	0.981636	chr19	48614913	48618205	+	0 NA	intron (N intron (N	2619 NM_001270	6141 Hs. 515517NM_000975	ENSG000002RPL18	DBA18 L18 ribosomal protein-coding	
chr2-1121 10.82887	-0.35222	0.715475	-0.49229	0.622515	0.981636	chr2	11213738	11216066	+	0 NA	exon (NM_exon (NM	59435 NM_001282	130814 Hs. 274415NM_152391	ENSG000002SLC66A3	C2orf22 Fsolute c protein-coding	
chr1-3284 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr1	32843491	32844318	+	0 NA	intron (N intron (N	18591 NR_135100	64766 Hs. 440888NM_022755	ENSG000002S100BPB	S100BPBR S100P bir protein-coding	
chr10-12 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr10	1.27E+08	1.27E+08	+	0 NA	intron (N intron (N	88816 NM_001291	1793 Hs. 159195NM_001388	ENSG000002DOCK1	DOCK180 dedicator protein-coding	
chr10-131 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr10	1.32E+08	1.32E+08	+	0 NA	intron (N intron (N	40088 NM_001291	55844 Hs. 380372NM_018461	ENSG000002PPP2R2D	B55D B55c protein c protein-coding	
chr11-34 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr11	34959388	34960642	+	0 NA	intron (N LIMB3 LIN	18178 NR_039830	1E+08	NR_039830	ENSG000002MIR1343	microRNA ncRNA
chr11-481 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr11	48155752	48158469	+	0 NA	intron (N AluS5 SI	-59700 NM_001005	119765 Hs. 553566NM_001005	ENSG000002COR4B1	OR11-106 olfactory protein-coding	
chr12-52 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr12	52950556	52951482	+	0 NA	intron (N intron (N	-1159 NM_001256	3856 Hs. 533782NM_002275	ENSG000002KRT8	CARD2 CK-keratin 8 protein-coding	
chr12-12 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr12	1.21E+08	1.21E+08	+	0 NA	TTS (NR_C TTS (NR_C	755 NR_039849	1.01E+08	NR_039849	ENSG000002MIR4700	miR-4700 microRNA ncRNA
chr13-114 5.418458	-0.4853	0.985853	-0.49227	0.622532	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	intron (N intron (N	1436 NM_001322	22821 Hs. 593075NM_007368	ENSG000002RAS3A	GAP1IP4 BFRAS p21 f protein-coding	
chr15-73 5.418458	-0.4853	0.985853	-0.49227	0.												

chr19-131.7.392512.0.420981.0.857924.0.490697.0.623641.0.981636	chr19	13135320	13135909	+	0	NA	exon (NM exon (NM	14761	NM_001271	8677	Hs.43812	NM_003765	ENSG000003STX10	SYN10 hsysyntaxin protein-coding
chr2-1277.7.392512.0.420981.0.857924.0.490697.0.623641.0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	exon (NM exon (NM	8071	NM_03274C	84826	Hs.345844	NM_03274C	ENSG000003SFT2D3	- SFT2 dom protein-coding
chr5-1764.7.392512.0.420981.0.857924.0.490697.0.623641.0.981636	chr5	1.76E+08	1.76E+08	+	0	NA	intron (N intron (N	37544	NM_014613	23197	Hs.484242	NM_014613	ENSG000003CAF2	ETEA UBX1 Fas assoc protein-coding
chr1-3265.7.196823.0.43504.0.886814.0.49057.0.623734.0.981636	chr1	32652700	32653014	+	0	NA	intron (N intron (N	1499	NM_001133	529	Hs.16003	NM_00561C	ENSG000003RBBP4	NURF55 RE RB bindir protein-coding
chr1-2146.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr1	21480590	21482892	+	0	NA	non-codir-non-codir	-2743	NM_00136E	249	Hs.75431	NM_00047E	ENSG000003ALPL	AP-TNAP alkaline protein-coding
chr1-1165.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr1	1.16E+08	1.16E+08	+	0	NA	intron (N intron (N	1989	NM_00116C	476	Hs.37188E	NM_000701	ENSG000003ATP1A1	CMT2DD HCATPase N protein-coding
chr10-625.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr10	6230133	6230260	+	0	NA	intron (N intron (N	28165	NM_00456E	5209	Hs.195471	NM_00456E	ENSG000003PFKFB3	IPPK2 PFK6 phospho protein-coding
chr12-715.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr12	7199345	7203442	+	0	NA	intron (N (AT)n Sin	11030	NM_00031E	5830	Hs.567327	NM_00031E	ENSG000003PEX5	PBD2A PBE peroxisome protein-coding
chr12-928.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr12	92836931	92837443	+	0	NA	intron (N MIR SINE	92108	NM_00356E	8411	Hs.567367	NM_00356E	ENSG000003CEEA1	MST105 MS early enc protein-coding
chr19-326.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr19	32613569	32617628	+	0	NA	intron (N Alu Jo SIN	-7129	NR_14571E	1.1E+08	NR_14571E	ENSG000003SNORA68B	- small nc snoRNA	
chr2-1135.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	intron (N intron (N	-12072	NR_14850T	440900	Hs.66220E	NR_03412E	ENSG000003LINC01191VIN lnc-# long intncRNA	
chr20-455.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr20	45961150	45961841	+	0	NA	intron (N MER103C I	10708	NM_02209E	63925	Hs.17419E	NM_02209E	ENSG000003ZNF335	MCPH10 Nizinc fing protein-coding
chr22-335.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr22	43996517	43997477	+	0	NA	TTS (NM_CTS (NM_C	-2214	NM_00100Q	29780	Hs.475074	NM_013327	ENSG000003PARV	CGI-56 parvin beta protein-coding
chr6-303.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr6	30335356	30335975	+	0	NA	intron (N intron (N	6354	NM_00119E	202658	Hs.41349E	NM_00119E	ENSG000003TRIM39-IF	TRIM39R TRIM39-IF protein-coding
chr7-2992.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr7	29922169	29923748	+	0	NA	3' UTR (N 3' UTR (N	66843	NM_01476E	9805	Hs.52074C	NM_01476E	ENSG000003SCRN1	SES1 secernin protein-coding
chr9-1271.7.963522.0.407571.0.83107.0.490418.0.623838.0.981636	chr9	1.27E+08	1.27E+08	+	0	NA	intron (N intron (N	18481	NM_01209E	23452	Hs.65326E	NM_01209E	ENSG000003ANGPTL2	ARP2 HARF angiopoietin protein-coding
chr17-604.10.86215.0.4389.0.711537.0.49035.0.623888.0.981636	chr17	60471642	60472764	+	0	NA	intron (N LIMB4 LIN	49714	NM_18170T	124773	Hs.129312	NM_18170T	ENSG000003CC10orf64	- chromosom protein-coding
chr2-9725.10.86215.0.4389.0.711537.0.49035.0.623888.0.981636	chr2	97230028	97231431	+	0	NA	intron (N LIPA3 LIN	-47988	NR_10373Z	1.01E+08	Hs.73261E	NR_10373Z	LOC100500E	- uncharactncRNA
chr7-1005.7.40407.0.44321.0.90426.0.490136.0.624038.0.981636	chr7	1.01E+08	1.01E+08	+	0	NA	intron (N FLAM_C SI	-1276	NM_00129E	1.02E+08	Hs.125742	NM_001289933	ZASP	- Z0-2 assc protein-coding
chr1-1764.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr1	1764485	1765601	+	0	NA	intron (N intron (N	-6401	NM_00119E	65220	Hs.65479E	NM_02301E	ENSG000003CNADK	dJ283E3.1NAD kinase protein-coding
chr1-3832.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr1	3832413	3833184	+	0	NA	intron (N Alu Jb SIN	24413	NM_01470A	9731	Hs.13308E	NM_01470A	ENSG000003CEP104	CFAP256 centrosom protein-coding
chr1-1106.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr1	11065026	11071702	+	0	NA	intron (N intron (N	-8346	NM_00313Z	6723	Hs.76244	NM_00313Z	ENSG000003SRM	PAPT SPDS spermidir protein-coding
chr1-3591.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr1	35915206	35918066	+	0	NA	intron (N AluSz SIN	-14469	NM_17742Z	192669	Hs.65765E	NM_02485E	ENSG000003CAGO3	EIF2C3 argonaute protein-coding
chr1-1515.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr1	1.52E+08	1.52E+08	+	0	NA	intron (N AluSc SIN	24707	NR_03028C	693139	NR_03028C	ENSG000003MIR554	MIRN554 microRNA ncRNA	
chr1-2057.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	3' UTR (N 3' UTR (N	-15105	NM_00113E	8934	Hs.11532E	NM_00392E	ENSG000003RAB29	RABTL1 RAF RAB29, mc protein-coding
chr11-455.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr11	45969686	45971602	+	0	NA	intron (N intron (N	47988	NM_00130C	120071	Hs.86543	NM_15231Z	ENSG000003LARGE2	GYLT1B FLARGE xyl protein-coding
chr11-675.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr11	67310200	67310620	+	0	NA	intron (N intron (N	6880	NM_01785T	54961	Hs.29173	NM_01785T	ENSG000003SSH3	SSH3 slingshot protein-coding
chr11-685.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr11	68908779	68911776	+	0	NA	intron (N intron (N	6426	NM_00218C	3508	Hs.50304E	NM_00218C	ENSG000003IGHMBP2	CATF1 CMT immunogl protein-coding
chr12-477.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr12	47792012	47795576	+	0	NA	intron (N intron (N	20556	NM_01784Z	55652	Hs.438867	NM_01784Z	ENSG000003SLC48A1	HRG-1 HRG solute c protein-coding
chr12-507.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr12	50724808	50725385	+	0	NA	intron (N intron (N	-39005	NM_00517I	466	Hs.64856E	NM_00517I	ENSG000003ATF1	EWS-ATF1 activator protein-coding
chr12-100.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr12	1E+08	1E+08	+	0	NA	intron (N Alu Jb SIN	7178	NR_04856E	64431	Hs.11508E	NM_02249E	ENSG000003ACTR6	ARP6 CDA1 actin rel protein-coding
chr12-105.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	3' UTR (N 3' UTR (N	26994	NM_15231E	121053	Hs.29556E	NM_15231E	ENSG000003C12orf45	- chromosom protein-coding
chr12-132.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (N intron (N	-17389	NM_00117Z	2802	Hs.50733E	NM_00589E	ENSG000003GOLGA3	GCP170 ME golgin A protein-coding
chr14-912.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr14	91215565	91217194	+	0	NA	intron (N Alu Jr SIN	28325	NM_00117Z	8111	Hs.8882	NM_00348E	ENSG000003GPR68	AT2A6 GPF6 proteir protein-coding
chr15-428.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr15	42802147	42802542	+	0	NA	intron (N intron (N	-65216	NM_13847T	146059	Hs.59923E	NM_13847T	ENSG000003CDAN1	CDAN1 CDA1 codanin I protein-coding
chr15-900.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr15	90087471	90088811	+	0	NA	intron (N Alu Jr SIN	-5934	NR_146321	1.1E+08	Hs.65524E	NR_146321	ENSG000003ZNF710-AS-	ZNF710 arncRNA
chr15-945.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr15	94399429	94400582	+	0	NA	intron (N intron (N	44075	NM_00115E	55784	Hs.33368	NM_01834E	ENSG000003MCTP2	- multiple protein-coding
chr16-311.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr16	31119606	31121807	+	0	NA	intron (N MIR3 SINE	3042	NM_03218E	84148	Hs.53380E	NM_03218E	ENSG000003KAT8	MOF MYST1 lysine ac protein-coding
chr17-488.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr17	4885797	4888435	+	0	NA	exon (NM exon (NM	-12420	NM_00114E	1E+08	Hs.57924E	NM_00114E	ENSG000003C17orf107-	chromosom protein-coding
chr17-648.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr17	64819715	64824907	+	0	NA	promoter-promoter-	-209	NR_03627I	1E+08	NR_03627I	ENSG000003MIR4315-2-	microRNA ncRNA	
chr17-788.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr17	78802756	78807164	+	0	NA	intron (N intron (N	-22618	NM_00476E	9267	Hs.19121E	NM_00476E	ENSG000003CYTH1	B2-1 CYTC cytohesin protein-coding
chr18-232.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr18	23255915	23257558	+	0	NA	intron (N Alu Sx1 SI	100911	NM_13837E	91768	Hs.11108	NM_13837E	ENSG000003CABLES1	CABL1 CAF Cdk5 and protein-coding
chr18-420.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr18	42003277	42005195	+	0	NA	intron (N MamRep40E	49002	NM_00264T	5289	Hs.464971	NM_00264T	ENSG000003PIK3C3	VPS34 Vps phosphatid protein-coding
chr18-796.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr18	79699880	79701054	+	0	NA	intron (N Tigger1 I	19037	NM_00120Z	9150	Hs.46549E	NM_00471E	ENSG000003CTDP1	CCFDN1 FCFCTD phospho protein-coding
chr19-146.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	14697790	14704333	+	0	NA	intron (N HALL1 LINE	11008	NM_00135Z	84449	Hs.51521E	NM_03243E	ENSG000003ZNF333	- zinc fing protein-coding
chr19-215.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	21518234	21523985	+	0	NA	TTS (NR_ITTS (NR_I	15507	NM_00134E	353088	Hs.572567	NM_001001	ENSG000003ZNF429	- zinc fing protein-coding
chr19-350.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	35019283	35022382	+	0	NA	intron (N L2a LINE	-9638	NM_00103T	6324	Hs.43664E	NM_00103T	ENSG000003SCN1B	ATFB13 BF sodium v protein-coding
chr19-355.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	35630565	35636791	+	0	NA	intron (N intron (N	4642	NM_02432I	79171	Hs.5086	NM_02432I	ENSG000003CRBM42	- RNA bind protein-coding
chr19-365.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	36936769	36943099	+	0	NA	intron (N intron (N	23602	NM_00120A	374900	Hs.40422C	NM_19853E	ENSG000003ZNF568	ZFP568 zinc fing protein-coding
chr19-415.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	41901090	41905266	+	0	NA	intron (N Alu Jr SIN	18735	NM_19900Z	9138	Hs.63155E	NM_00470E	ENSG000003ARHGFP1	GEF1 IMD2 Rho guaniprotein-coding
chr19-445.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	44974452	44980505	+	0	NA	intron (N intron (N	22098	NM_00129A	1209	Hs.444441	NM_00129A	ENSG000003CLPTM1	- CLPTM1 re protein-coding
chr19-500.7.93024.0.404326.0.825274.0.48993.0.624183.0.981636	chr19	50013205	50019027											



chr2-1084	13.15171	0.319128	0.653563	0.48829	0.625345	0.981636	chr2	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	34560 NR_028063	9648 Hs. 436505NM_181455	ENSG000002GCC2	GCC185 R	GRIP and protein-coding
chr9-7025	7.591717	-0.42387	0.868451	-0.48807	0.625497	0.981636	chr9	70298405	70298704	+	0	NA	intron (Nintron (N	39576 NM_01511C	23137 Hs. 534189NM_01511C	ENSG000002SMC5	SMC5L1	structure protein-coding
chr7-1396	8.094313	-0.40167	0.823474	-0.48778	0.625708	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (Ntigger1 I	92059 NM_001113	28996 Hs. 731417NM_02274C	ENSG000002CHIPK2	PRO0593	homeodomain protein-coding
chr1-5146	7.699419	-0.41117	0.842946	-0.48778	0.625709	0.981636	chr1	51461935	51462266	+	0	NA	intron (NAluSp SIN	-40005 NM_001155	2060 Hs. 83722 NM_001981	ENSG000002EPS15	AF-1P AF1	epidermal protein-coding
chr2-1275	7.699419	-0.41117	0.842946	-0.48778	0.625709	0.981636	chr2	1.27E+08	1.27E+08	+	0	NA	intron (NAluSq2 SI	-22097 NM_000122	2071 Hs. 469872NM_000122	ENSG000002ERCC3	BTf2 GTf2	ERCC exciprotein-coding
chr16-888	7.715135	-0.41445	0.849798	-0.48777	0.625761	0.981636	chr16	88394586	88394879	+	0	NA	IntergeniIntergeni	-32739 NM_001367	84627 Hs. 54925 NM_001127	ENSG000002ZNF469	BCS BCS1	zinc finger protein-coding
chr19-496	7.715135	-0.41445	0.849798	-0.48777	0.625761	0.981636	chr19	49649284	49650137	+	0	NA	intron (NAluSp SIN	7501 NM_021228	58506 Hs. 103521NM_021228	ENSG000002SCAF1	SRA1	SR-related protein-coding
chr1-1976	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr1	1.98E+08	1.98E+08	+	0	NA	intron (Nintron (N	86671 NM_001195	163486 Hs. 125056NM_019045	ENSG000002DENND1B	CRF18 L1	CENND domain protein-coding
chr10-118	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr10	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	16722 NM_022063	63877 Hs. 105577NM_022063	ENSG000002FAM204A	C10orf84	family wiprotein-coding
chr11-781	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr11	78196460	78196850	+	0	NA	exon (NM exon (NM	7736 NM_020798	57558 Hs. 531245NM_020798	ENSG000002USP35	-	ubiquitin protein-coding
chr11-866	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr11	86004691	86013652	+	0	NA	intron (NAluXs1 SI	59913 NM_001766	8301 Hs. 163892NM_001766	ENSG000002PICALM	CALM CLTf	phosphatidyl protein-coding
chr13-253	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr13	25312341	25316690	+	0	NA	intron (NAluSq2 SI	12890 NM_014088	9818 Hs. 507537NM_014088	ENSG000002CNP58	NUP45 NUP	nucleoporin protein-coding
chr16-135	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr16	13926513	13927191	+	0	NA	intron (Nintron (N	6695 NM_005233	2072 Hs. 567265NM_005233	ENSG000002ERCC4	ERCC11 F	ERCC exciprotein-coding
chr2-1274	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr2	1.27E+08	1.27E+08	+	0	NA	intron (Nintron (N	43894 NM_017965	55677 Hs. 469872NM_017965	ENSG000002IWS1	-	interact protein-coding
chr3-5815	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr3	58153798	58156696	+	0	NA	intron (Nintron (N	15388 NR_135534	1.05E+08 Hs. 613914NR_135534	ENSG000002FLNB-AS1	-	FLNB anticrRNA
chr6-1135	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr6	1.14E+08	1.14E+08	+	0	NA	non-codirnon-codir	-27944 NR_125845	1.02E+08 Hs. 129282NR_125845	ENSG000002HDAC2-AS2	-	HDAC2 anticrRNA
chr8-4778	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr8	47781969	47783098	+	0	NA	exon (NM exon (NM	-44369 NM_005195	1052 Hs. 440825NM_005195	ENSG000002CEBPD	C/EBP-d CCAAT	encl protein-coding
chr9-272	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr9	27204933	27206757	+	0	NA	intron (Nintron (N	76948 NR_026675	158035 Hs. 201554NR_026675	ENSG000002LINC00032	C9orf14 L	long intencrRNA
chr9-1244	8.127594	-0.39174	0.814361	-0.48767	0.625781	0.981636	chr9	1.24E+08	1.24E+08	+	0	NA	intron (NAlu SINE	5353 NM_002795	5695 Hs. 213477NM_002795	ENSG000002PSMB7	Z	proteasome protein-coding
chr4-824	10.8543	-0.34768	0.713302	-0.48742	0.625958	0.981636	chr4	82423380	82428713	+	0	NA	non-codirnon-codir	4179 NM_001207	9987 Hs. 527105NM_005463	ENSG000002HNRNPDL	HNRNP HNF	heterog protein-coding
chr1-1565	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr1	1569331	1570668	+	0	NA	intron (Nintron (N	4864 NM_014188	29101 Hs. 30026 NM_014188	ENSG000002SSU72	HSPC182 F	SSU72 honprotein-coding
chr10-246	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr10	24630440	24632183	+	0	NA	intron (NAluSq2 SI	-8468 NR_160025	57584 Hs. 524195NM_020824	ENSG000002ARHGAP21	ARHGAP10 Rho	GTPase protein-coding
chr10-681	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr10	68194422	68196034	+	0	NA	intron (Nintron (N	36885 NM_145178	220202 Hs. 175396NM_145178	ENSG000002ATO7H	Math5 NCF	atona1 bl protein-coding
chr11-855	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr11	85984813	85985901	+	0	NA	intron (Nintron (N	83727 NM_007166	8301 Hs. 163892NM_007166	ENSG000002PICALM	CALM CLTf	phosphatidyl protein-coding
chr12-955	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr12	95519949	95522319	+	0	NA	exon (NM exon (NM	27104 NM_001275	84101 Hs. 646421NM_032147	ENSG000002USP44	-	ubiquitin protein-coding
chr14-605	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr14	60977564	60978224	+	0	NA	intron (Nintron (N	3185 NM_001355	57570 Hs. 380155NM_02081C	ENSG000002TRMT5	COXP26 K	tRNA methyl protein-coding
chr14-885	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr14	88595923	88596323	+	0	NA	intron (Nintron (N	1723 NM_020766	79882 Hs. 684046NM_024824	ENSG000002ZC3H14	MRT56 MSU	zinc finger protein-coding
chr15-526	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr15	52603382	52603752	+	0	NA	intron (NLM3A3 LI	-34121 NM_001306	10776 Hs. 512905NM_006628	ENSG000002ARPP19	ARPP-16 a	cAMP regu protein-coding
chr15-663	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr15	66351785	66352264	+	0	NA	intron (Nintron (N	4661 NM_017855	54962 Hs. 744305NM_017855	ENSG000002TIPIN	-	TIMELESS protein-coding
chr17-435	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr17	43513317	43516810	+	0	NA	intron (NLM44a LI	14372 NM_001261	2118 Hs. 434055NM_001988	ENSG000002ETV4	E1A-F E1A	variet protein-coding
chr18-130	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr18	13092630	13093924	+	0	NA	intron (NLMC4 LI	101915 NM_032142	55125 Hs. 100914NM_018065	ENSG000002CEP192	PPP1R62	centrosome protein-coding
chr19-966	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr19	9667158	9668615	+	0	NA	intron (NAluJo SIN	7214 NM_017655	54811 Hs. 371107NM_017655	ENSG000002ZNF562	-	zinc finger protein-coding
chr2-1057	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	10574007	10578520	+	0	NA	intron (Nintron (N	115062 NM_024894	79954 Hs. 222494NM_024894	ENSG000002NOL10	PQB5	nucleolar protein-coding
chr2-3046	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	30466840	30468169	+	0	NA	intron (NLM5A5 LI	20258 NM_001304	253558 Hs. 468045NM_182551	ENSG000002CLAT1	IAGPAT8 A	lysocardiprotein-coding
chr2-3264	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	32649363	32651414	+	0	NA	intron (Nintron (N	15133 NR_039922	1.01E+08 Hs. NR_039922	ENSG000002MIR4765	-	microRNA ncRNA
chr2-1277	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	5452 NM_032744	84826 Hs. 345845NM_032744	ENSG000002SFT2D3	-	SFT2 domain protein-coding
chr2-1350	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (NMER2 DNA	30865 NM_012233	22930 Hs. 306327NM_012233	ENSG000002CRAB3GAP1	P130 RAB3	GTPase protein-coding
chr2-1726	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	1.73E+08	1.73E+08	+	0	NA	3' UTR (N3' UTR (N	45551 NM_00261C	5163 Hs. 470633NM_00261C	ENSG000002PDK1	-	pyruvate protein-coding
chr2-1891	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr2	1.89E+08	1.89E+08	+	0	NA	intron (NLM2 LINE L	7668 NM_000393	1290 Hs. 445827NM_000393	ENSG000002COL5A2	EDSC EDSC	collagen protein-coding
chr20-315	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr20	31516151	31517264	+	0	NA	intron (NLM2c LINE L	2265 NM_178582	81502 Hs. 373741NM_030788	ENSG000002CHM13	H13 IMP1	histocomp protein-coding
chr3-1231	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	intron (NLM2a LINE L	-45780 NR_106966	1.02E+08 Hs. NR_106966	ENSG000002MIR7110	hsa-mir-7	microRNA ncRNA
chr3-1291	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	6664 NM_001127	7555 Hs. 518245NM_003418	ENSG000002CNBP	CNBP1 DM2	CCHC-type protein-coding
chr3-1884	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr3	1.88E+08	1.88E+08	+	0	NA	intron (Nintron (N	159814 NR_046623	1.01E+08 Hs. 674993NR_046623	ENSG000002LPP-AS1	-	LPP anticrRNA
chr3-1953	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr3	1.95E+08	1.95E+08	+	0	NA	intron (NLM1 LINE L	78776 NM_012287	23527 Hs. 593373NM_012287	ENSG000002ACAP2	CENTB2 CN	ARFGAP wiprotein-coding
chr4-7317	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr4	73174560	73177696	+	0	NA	intron (NLM2A2 LI	46929 NM_001286	26057 Hs. 601206NM_015574	ENSG000002ANKRD17	GTAR MASK	ankyrin 1 protein-coding
chr4-8466	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr4	84667103	84667893	+	0	NA	IntergeniIntergeni	48371 NM_001263	1040 Hs. 654899NM_001263	ENSG000002CDS1	CDS1	CDP-diacy protein-coding
chr4-1682	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (Nintron (N	35979 NM_017631	55601 Hs. 591711NM_017631	ENSG000002DDX60	-	DEX/H-hc protein-coding
chr5-7475	5.4106	-0.48299	0.991192	-0.48728	0.626057	0.981636	chr5	74734108	74736101	+	0	NA	intron (Nintron (N</					



chr15-74c.467968	0.389674	0.804195	0.484552	0.627994	0.981636	chr15	74022959	74024316	+	0	NA	intron (NMER91A DN	28921	NM_033244	5371	Hs.526464NM_002675	ENSG000000PML	MYL1P867	promyelocytic protein-coding	
chr19-19c.467968	0.389674	0.804195	0.484552	0.627994	0.981636	chr19	19307478	19311037	+	0	NA	intron (NALuJo SIN	11252	NM_172231	57794	Hs.515274NM_021164	ENSG000000SUGP1	F23858 RE	SURP and protein-coding	
chr6-157c.467968	0.389674	0.804195	0.484552	0.627994	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	intron (NMER21C LI	74250	NM_016224	51429	Hs.19121cNM_016224	ENSG000000SNX9	SDP1 SH3F	sorting rprotein-coding	
chr9-136a.467968	0.389674	0.804195	0.484552	0.627994	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (NFLAM_C SI	10218	NM_015166	23203	Hs.495471NM_015166	ENSG000000PMPCA	Alpha-MPF	peptidase protein-coding	
chr13-111c.377318	-0.48995	1.011515	-0.48437	0.628123	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (NINtron (N	-6447	NM_001354	8874	Hs.50873cNM_003895	ENSG000000ARHGFE7	BETA-PIX HO	guanine protein-coding	
chr14-10c.377318	-0.48995	1.011515	-0.48437	0.628123	0.981636	chr14	1E+08	1E+08	+	0	NA	exon (NM_exon (NM	13119	NM_001352	123096	Hs.57810cNM_152333	ENSG000000SLC25A29	C14orf69 solu	te c protein-coding	
chr13-771c.781243	0.404884	0.836067	0.484272	0.628193	0.981636	chr13	77150094	77150525	+	0	NA	intron (NALuJr SIN	74795	NR_046716	1.01E+08	Hs.56928cNR_046716	ENSG000000MYCBP2-AS	-	MYCBP2	arcncRNA
chr1-123c.14.21931	0.309354	0.639011	-0.484113	0.628306	0.981636	chr1	2.73E+08	1.23E+08	+	0	NA	IntergeniALR/Alpha	1878538	NR_003956	647121	Hs.69768cNR_003956	ENSG000000EMBP1	-	embylin	psudo
chr11-27c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr11	27697578	27698795	+	0	NA	TTS (NR_C TTS (NR_C	1481	NM_170734	627	Hs.50218cNM_001707	ENSG000000BDNF	ANON2 BUL	brain derprotein-coding	
chr14-71c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr14	71057734	71058718	+	0	NA	intron (NLIMB5 LIN	150767	NM_001308	22990	Hs.44655cNM_014982	ENSG000000PCNX1	PCNX PCN	pecanex Iprotein-coding	
chr18-26c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr18	26083248	26087401	+	0	NA	intron (NALuJr SIN	5289	NM_001007	6760	Hs.129261NM_005637	ENSG000000SS18	SSXT SYT	SS18 subprotein-coding	
chr2-3247c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr2	32477208	32478743	+	0	NA	intron (NINtron (N	-54178	NR_030285	693143	NR_030285	ENSG000000MIR558	MIRN558 mi	croRNA ncRNA	
chr3-690c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr3	69032858	69033561	+	0	NA	intron (NALuSx SIN	14626	NR_036087	1E+08	NR_036087	ENSG000000MIR3136	mir-3136	microRNA ncRNA	
chr6-176c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr6	17636629	17637370	+	0	NA	intron (NINtron (N	36697	NM_016255	51439	Hs.95260	ENSG000000FAM8A1	ahp	family wiprotein-coding	
chr9-122c.119736	-0.39556	0.817184	-0.48406	0.628347	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (NALuJb SIN	45969	NM_012197	23637	Hs.271341NM_012197	ENSG000000RABGAP1	GAPCENA TRAB	GTPase protein-coding	
chr1-154c.13.15957	0.317938	0.656828	0.48405	0.62835	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	exon (NM_exon (NM	17223	NM_000748	1141	Hs.2306	ENSG000000CHRN2B	EFNL3 nAc	cholinerg protein-coding	
chr1-100c.7.650422	-0.41242	0.852067	-0.48403	0.628366	0.981636	chr1	1.01E+08	1.01E+08	+	0	NA	intron (NINtron (N	3004	NM_001144	14867	Hs.53390cNM_13349c	ENSG000000SLC30A7	ZNT7 ZnT	solute c protein-coding	
chr1-229c.7.650422	-0.41242	0.852067	-0.48403	0.628366	0.981636	chr1	2.29E+08	2.29E+08	+	0	NA	intron (NINtron (N	-14994	NM_006542	10638	Hs.29616cNM_006542	ENSG000000SPHAR	S-phase	protein-coding	
chr12-121c.7.650422	-0.41242	0.852067	-0.48403	0.628366	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NINtron (N	17296	NM_001178	144406	Hs.709837NM_14466c	ENSG000000WDR66	CFAP251 CWD	repeat protein-coding	
chr1-206c.8.428678	0.399159	0.824752	0.483975	0.628404	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (NINtron (N	-65104	NM_014002	9641	Hs.32104cNM_014002	ENSG000000IKBKE	IKK-E IKK	inhibitor protein-coding	
chr15-224c.7.11257	0.546462	1.129113	0.483975	0.628404	0.981636	chr15	22945676	22946422	+	0	NA	intron (NALuJb SIN	-28736	NM_001033	23191	Hs.26704	ENSG000000CYFIP1	P140SR4	-lyctoplasm protein-coding	
chr19-13c.4.171257	0.546462	1.129113	0.483975	0.628404	0.981636	chr19	13307785	13308439	+	0	NA	intron (NINtron (N	157701	NM_004907	9592	Hs.50162cNM_004907	ENSG000000IER2	ETR101	immediate protein-coding	
chr10-35c.7.237963	-0.4314	0.8916	-0.48385	0.628489	0.981636	chr10	35051259	35051670	+	0	NA	intron (NALuYe5 SI	22819	NM_001198	8453	Hs.812919	ENSG000000CUL2	-	cullin 2	protein-coding
chr16-48c.7.237963	-0.4314	0.8916	-0.48385	0.628489	0.981636	chr16	48551909	48552575	+	0	NA	intron (NINtron (N	57938	NM_153025	9683	Hs.51183cNM_153025	ENSG000000N4BP1	-	NEDD4	bir protein-coding
chr6-111c.7.237963	-0.4314	0.8916	-0.48385	0.628489	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	exon (NM_exon (NM	-109387	NR_034105	643749	Hs.48622cNR_034105	ENSG000000TRAF3IP2	C6UAS C6c	TRAF3IP2	ncRNA
chr4-8297c.2.213767	-0.61802	1.277995	-0.48359	0.628679	0.981636	chr4	82971361	82972166	+	0	NA	intron (NL3 LINE C	39060	NR_110255	132660	Hs.96952	ENSG000000CLIN5A	CXDCD1 JCl	in-54 Df	protein-coding
chr1-653c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr1	6530834	6533415	+	0	NA	intron (NINtron (N	-12063	NM_198681	57449	Hs.28423cNM_020631	ENSG000000PLEKHG5	CMTRIC DS	pleckstrin protein-coding	
chr1-431c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr1	43165790	43169621	+	0	NA	intron (NINtron (N	4007	NR_106791	1.02E+08	NR_106791	ENSG000000MIR6733	hsa-mir-62	microRNA ncRNA	
chr1-681c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr1	68147807	68149414	+	0	NA	exon (NM_exon (NM	35000	NR_031664	1E+08	NR_031664	ENSG000000MIR1262	MIRN1262 mi	croRNA ncRNA	
chr1-1114c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr1	1.11E+08	1.11E+08	+	0	NA	non-codiron-codir	8328	NM_024102	79084	Hs.20477cNM_024102	ENSG000000WDR77	HKMT1069 WD	repeat protein-coding	
chr1-2027c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr1	2.03E+08	2.03E+08	+	0	NA	intron (NINtron (N	10428	NM_001347	10765	Hs.18891	ENSG000000KDM5B	CT31 JAR1	lysine deprotein-coding	
chr1-2302c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr1	2.3E+08	2.3E+08	+	0	NA	intron (NINtron (N	150115	NM_001258	79605	Hs.52046cNM_024554	ENSG000000PGDB5	-	pyggyBac	protein-coding
chr11-47c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr11	47280731	47286876	+	0	NA	intron (NALuSzl SIN	-11693	NR_120566	1.02E+08	Hs.66495cNR_120566	ENSG000000LOC101925	-	uncharactercna	ncRNA
chr11-687c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr11	68755938	68763547	+	0	NA	intron (NINtron (N	-8222	NM_001035	9633	Hs.14593cNM_004923	ENSG000000TESMIN	CXDCD2 MI	testis e protein-coding	
chr11-71c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr11	71091025	71092266	+	0	NA	intron (NINtron (N	133151	NM_012305	22941	Hs.26872cNM_012305	ENSG000000SHANK2	AUTS17 CS	SH3 and nprotein-coding	
chr12-53c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr12	53210411	53213313	+	0	NA	intron (NMER3 DNA	-5611	NM_000088	3695	Hs.65447cNM_000088	ENSG000000ITGB7	-	integrin	protein-coding
chr13-244c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr13	24489273	24498289	+	0	NA	intron (NINtron (N	18997	NM_006437	143	Hs.74485cNM_006437	ENSG000000PARP4	ADPRTL1 A	poly (ADP- protein-coding	
chr13-95c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr13	95582506	95588153	+	0	NA	intron (NINtron (N	32609	NM_006984	9071	Hs.534377NM_006984	ENSG000000CLDN10	CEPML3 F	claudin Iprotein-coding	
chr14-34c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr14	9132	NM_018453	55837	Hs.43326cNM_018453	ENSG000000EAPP	EMO36 C14E2F	assoc protein-coding							
chr14-497c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr14	49775428	49777978	+	0	NA	intron (NALuSzl SI	8550	NM_014315	23588	Hs.509264NM_014315	ENSG000000KLHDC2	HCLP-1 HC	kelch dom protein-coding	
chr15-56c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr15	56231085	56234058	+	0	NA	intron (THEIB-int	11303	NM_001367	64864	Hs.74508cNM_022841	ENSG000000RFXY7	RFXDC2	regulator protein-coding	
chr15-90c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr15	90938715	90952565	+	0	NA	intron (NALuSzl SIN	-9403	NM_001101	91433	Hs.65589cNM_033544	ENSG000000CCDC1	-	RCC1	dom protein-coding
chr16-487c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr16	4879941	4882338	+	0	NA	3' UTR (N3' UTR (N	32759	NM_001288	29855	Hs.44021cNM_01693c	ENSG000000UBN1	VT VT4	ubinucler protein-coding	
chr16-15c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr16	15600884	15604269	+	0	NA	intron (NGA-rich L	8519	NR_106761	1.02E+08	NR_106761	ENSG000000MIR6506	hsa-mir-62	microRNA ncRNA	
chr16-274c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr16	27496915	27507397	+	0	NA	intron (NMIR3 SINE	47757	NM_00152C	2975	Hs.37171cNM_00152C	ENSG000000GTF3C1	TFI11C TF	general t protein-coding	
chr16-564c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr16	56496172	56499143	+	0	NA	intron (NINtron (N	22367	NM_031885	583	Hs.33373cNM_031885	ENSG000000CBS2	BBS RP74	Bardet-Bi protein-coding	
chr16-717c.8.434686	0.386566	0.799485	0.483519	0.628727	0.981636	chr16	71757739	71760137	+	0	NA									



chr1-2847 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr1	28476671	28479250	+	0	NA	intron (AluJb SIN	-27983 NM_001048	1104 Hs. 469722NM_001266	ENSG000000CC1	CHC1 RC1 boxator protein-coding
chr12-118 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	intron (AluSq2 SI	24098 NM_001346	51347 Hs. 644422NM_016281	ENSG000000TAOK3	DPK JJK TAO kinase protein-coding
chr13-49C 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr13	49005899	49006772	+	0	NA	intron (intron (N	29673 NR_103528	22862 Hs. 50801CNM_014923	ENSG000000FNDC3A	FNDC3 HUC fibronectin protein-coding
chr13-77I 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr13	77044330	77045584	+	0	NA	3' UTR (N3' UTR (N	-17798 NM_012158	26224 Hs. 508284NM_012158	ENSG000000FBXL3	FBXL3 FBLX2 F-box ancr protein-coding
chr13-77I 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr13	77183889	77185269	+	0	NA	intron (LIM5 LINE	109665 NR_046716	1.01E+08 Hs. 569288NR_046716	ENSG000000MYCBP2-AS-	MYCBP2 arncRNA
chr14-21C 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr14	21074427	21075173	+	0	NA	exon (NM_exon (NM	-3928 NM_001282	57447 Hs. 52520ENM_01625C	ENSG000000NDRG2	SYLD NDRG famiprotein-coding
chr14-10I 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	intron (intron (N	11878 NM_001100	7517 Hs. 592232NM_005432	ENSG000000XRCC3	CMW6 X-ray rep protein-coding
chr15-61S 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr15	61989245	61991646	+	0	NA	intron (intron (N	70002 NM_017684	54832 Hs. 511668NM_017684	ENSG000000VPS13C	PRMK23 vacuolar protein-coding
chr15-77I 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr15	77178598	77179529	+	0	NA	exon (NM_exon (NM	46341 NR_026813	81698 Hs. 65693ENM_030944	LINCO0597C15orf5	long intencRNA
chr17-11F 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr17	17810626	17811666	+	0	NA	TTS (NM_CTS (NM_C	2399 NR_106833	1.02E+08 NR_106833	ENSG000000MIR6777	hsa-mir-6777 miRNA ncRNA
chr19-11E 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr19	11654476	11655278	+	0	NA	IntergeniIntergeni	12212 NR_002944	664709 Hs. 534822NR_002944	HNRNP1P1 HNRPA1L-2 heterog pseudo	
chr19-16C 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr19	16392702	16393496	+	0	NA	intron (N(ATA)n SI	68273 NM_01627C	10365 Hs. 68513CNM_01627C	ENSG000000KLF2	LKLF Kruppel protein-coding
chr2-5394 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr2	53941845	53942633	+	0	NA	intron (intron (N	28754 NM_014614	23198 Hs. 413801NM_014614	ENSG000000PSME4	PAZ00 proteasone protein-coding
chr2-1087 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr2	1.09E+08	1.09E+08	+	0	NA	intron (intron (N	8761 NM_144978	165055 Hs. 362702NM_144978	ENSG000000CCDC138	coiled-co protein-coding
chr3-274E 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr3	27463082	27463820	+	0	NA	intron (AluY SINE	-6673 NM_00361E	9497 Hs. 250072NM_00361E	ENSG000000SLC4A7	NBC2 NBC2 solute c protein-coding
chr3-709S 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr3	70997176	70997515	+	0	NA	intron (intron (N	67579 NM_001345	27086 Hs. 59368 NM_032682	ENSG000000FOX1P	12CC4 HSF forkhead protein-coding
chr5-169 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr5	16908000	16909770	+	0	NA	intron (LIMB5 LIN	27403 NM_012334	4651 Hs. 48172CNM_012334	ENSG000000MYO10	myosin X protein-coding
chr5-146 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (intron (N	31444 NM_194251	134391 Hs. 483732NM_194251	ENSG000000GPR151	GALR4 GAI G protein-coding
chr6-756S 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr6	75686004	75686847	+	0	NA	intron (LIP46 LIN	-62814 NM_001368	4646 Hs. 149387NM_004999	ENSG000000MYO6	DFNA22 DF myosin I protein-coding
chr6-1114 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (intron (N	-16140 NR_034108	643749 Hs. 486222NR_034108	ENSG000000TRAF3IP2	C6UAS C6c TRAF3IP2 ncRNA
chr7-102E 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (LIP45 SI	-11545 NM_024652	79706 Hs. 722104NM_024652	ENSG000000PRKRIP1	C114 KRBC PRKR inte protein-coding
chr8-192T 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr8	1927584	1928110	+	0	NA	intron (AluSg SIN	-43550 NR_12634E	1.04E+08 Hs. 734498NR_12634E	ENSG000000KBTBD11-C	KBTBD11 cnrRNA
chr8-291I 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chr8	29114750	29115683	+	0	NA	intron (intron (N	147854 NM_015254	23303 Hs. 444767NM_015254	ENSG000000KIF13B	GAKIN kinesin I protein-coding
chrX-154E 5.443882	-0.47629	0.985743	-0.48318	0.628967	0.981636	chrX	1.55E+08	1.55E+08	+	0	NA	intron (AluSc5 SI	2238 NM_001321	43505 Hs. 43505 NM_003639	ENSG000000IKBK9	AMCBX1 IE inhibitor protein-coding
chr4-560Z 7.61714	-0.41719	0.863778	-0.48298	0.62911	0.981636	chr4	56025012	56025236	+	0	NA	intron (AluJb SIN	76224 NM_025005	9662 Hs. 518767NM_01464E	ENSG000000CEP135	CEP4 KIAA centrosome protein-coding
chr7-6434 7.61714	-0.41719	0.863778	-0.48298	0.62911	0.981636	chr7	64346541	64346807	+	0	NA	intron (LIMB2 LIN	32713 NM_00117C	728927 Hs. 386162NM_00117C	ENSG000000ZNF736	zinc fing protein-coding
chr8-306Z 7.61714	-0.41719	0.863778	-0.48298	0.62911	0.981636	chr8	30623690	30624620	+	0	NA	intron (LIP45 LIN	-14425 NM_00120E	1.01E+08 Hs. 659499NM_00120E	ENSG000000SMIM18	small int protein-coding
chr17-41E 11.32361	-0.33849	0.700893	-0.48294	0.629137	0.981636	chr17	41904370	41906862	+	0	NA	exon (NM_exon (NM	13335 NM_00109E	47 Hs. 387567NM_00109E	ENSG000000ACLY	ACL ATPCI ATP citr protein-coding
chr5-138E 8.956698	0.37724	0.781385	0.482784	0.629249	0.981636	chr5	13857937	13858530	+	0	NA	intron (LIP47 LIN	86337 NM_00136E	1767 Hs. 212362NM_00136E	ENSG000000DNAH5	CILD3 DNA dynein a protein-coding
chr5-390I 8.956698	0.37724	0.781385	0.482784	0.629249	0.981636	chr5	39011019	39012561	+	0	NA	intron (THE1C-int	62609 NM_00128E	253260 Hs. 40792CNM_15275E	ENSG000000RICTOR	ACTO3 PIA RPTOR inte protein-coding
chr6-309I 8.956698	0.37724	0.781385	0.482784	0.629249	0.981636	chr6	30912070	30912398	+	0	NA	intron (intron (N	-1974 NM_02044E	57176 Hs. 59752CNM_02044E	ENSG000000CVARS2	COXP20 v valyl-tRNA protein-coding
chr16-47E 11.07522	0.350419	0.726008	0.482655	0.629334	0.981636	chr16	47654152	47654643	+	0	NA	intron (LIP45 LIN	193066 NM_001031	5257 Hs. 78060 NM_00029E	ENSG000000PHKB	phosphory protein-coding
chr2-975E 8.086455	-0.40013	0.829437	-0.48241	0.629515	0.981636	chr2	97580016	97580215	+	0	NA	intron (intron (N	9762 NM_00135E	57730 Hs. 532921NM_02097C	ENSG000000ANKRD36B	KIAA1641 ankyrin I protein-coding
chr12-307 8.94884	0.379044	0.786755	0.481782	0.629961	0.981636	chr12	30746388	30747442	+	0	NA	intron (Tigger1 I	7599 NM_00131E	65981 Hs. 234355NM_02392E	ENSG000000CAPRIN2	C1QDC1 EF caprin f protein-coding
chr3-432E 8.94884	0.379044	0.786755	0.481782	0.629961	0.981636	chr3	43282743	43291557	+	0	NA	intron (AluJb SIN	92977 NM_00134E	55129 Hs. 656657NM_01807E	ENSG000000ANO10	SCAR10 TV anactamir protein-coding
chr1-122E 8.964556	0.375503	0.779746	0.481572	0.63011	0.981636	chr1	12249785	12250736	+	0	NA	intron (MER21C LIN	20230 NM_001537E	55187 Hs. 439381NM_01537E	ENSG000000VPS13D	SCAR4 vacuolar protein-coding
chr3-149C 8.964556	0.375503	0.779746	0.481572	0.63011	0.981636	chr3	1.49E+08	1.49E+08	+	0	NA	intron (AluSq2 SI	-24745 NR_04664E	1.01E+08 Hs. 742422NR_04664E	ENSG000000HLTF-AS1	HLTF antincRNA
chr6-169E 8.964556	0.375503	0.779746	0.481572	0.63011	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (LIM2c LIN	15356 NM_00135E	253769 Hs. 131902NM_18255E	ENSG000000WDR27	WD repeat protein-coding
chr7-115E 8.964556	0.375503	0.779746	0.481572	0.63011	0.981636	chr7	1153320	1155870	+	0	NA	intron (intron (N	5601 NM_00136E	90637 Hs. 648111NM_182491	ENSG000000ZFAND2A	AIRAP zinc fing protein-coding
chr7-101I 8.176592	-0.39593	0.822167	-0.48157	0.630112	0.981636	chr7	1.01E+08	1.01E+08	+	0	NA	intron (AluYm SI	2127 NM_00060Z	5054 Hs. 414799NM_00060Z	ENSG000000SERPINE1	PAI1 PAI-1 serpin f protein-coding
chr3-52I 8.997837	0.378558	0.786451	0.481349	0.630268	0.981636	chr3	5256177	5216206	+	0	NA	exon (NM_exon (NM	28204 NM_014674	9695 Hs. 22461CNM_014674	ENSG000000EDEMI	EDEM ER degrac protein-coding
chr10-57E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr10	5756790	5770826	+	0	NA	TTS (NM_CTS (NM_C	49266 NM_001494	2665 Hs. 229055NM_001494	ENSG000000GDI2	HEL-S-46C di sc protein-coding
chr12-95E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr12	95512797	95515624	+	0	NA	non-codirnon-codir	34028 NM_00127E	84101 Hs. 646421NM_032147	ENSG000000CASP4	ubiquitin protein-coding
chr15-44E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr15	44656090	44660124	+	0	NA	intron (Charlie5	5555 NM_00116E	80208 Hs. 656271NM_025137	ENSG000000SPG11	ALS5 CMT2 SPG11 ves protein-coding
chr15-55I 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr15	55192053	55192880	+	0	NA	intron (intron (N	4475 NM_016304	51187 Hs. 274772NM_016304	ENSG000000RSL24D1	C15orf15 ribosomal protein-coding
chr15-55E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr15	55836260	55844411	+	0	NA	intron (intron (N	76796 NM_001284	4734 Hs. 1565 NM_006154	ENSG000000NEDD4	NEDD4-1 NEDD4 E3 protein-coding
chr15-55E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr15	55849905	55852518	+	0	NA	intron (MLTIN2 LI	65920 NM_001284	4734 Hs. 1565 NM_006154	ENSG000000NEDD4	NEDD4-1 NEDD4 E3 protein-coding
chr18-10E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr18	10552377	10555442	+	0	NA	IntergeniMamRep1E	27882 NM_00382E	8774 Hs. 464622NM_00382E	ENSG000000CNAPG	GAMMASNAF NSF attac protein-coding
chr19-43E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr19	43663732	43667992	+	0	NA	intron (LIP47 SIN	4307 NM_00265E	5329 Hs. 466871NM_00265E	ENSG000000PLAUR	CD87 MU plasminog protein-coding
chr2-702I 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr2	70215548	70218769	+	0	NA	intron (intron (N	-26139 NR_14597C	54980 Hs. 720049NM_01788C	ENSG000000C2orf42	chromosome protein-coding
chr2-216I 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (intron (N	52850 NM_021141	7520 Hs. 388735NM_021141	ENSG000000XRCC5	KARP-1 KX-ray rep protein-coding
chr2-229E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	exon (NM_exon (NM	-84427 NM_001284	92737 Hs. 234074NM_13907E	ENSG000000DNER	WDB4 betdelta not protein-coding
chr20-19E 8.153018	-0.39115	0.812626	-0.48134	0.630274	0.981636	chr20	19995988	20001836	+	0	NA	intron (intron (N	-18378 NM_18152E	51126 Hs. 368783NM_01610C	ENSG000000NAA20	NAT3 NAT3N(alpha)- protein-coding
chr20-50E 8.153018	-0.39115	0.812626	-0.481													



chr5-3494	8.442544	0.38473	0.803672	0.478715	0.632141	0.981636	chr5	34943822	34946299	+	0	NA	intron (Nintron (N	15467	NM_00134E	134218	Hs.131887NM_194283	ENSG000002DNAJC21	BMFS3 DN^DnaJ	heatprotein-coding	
chr8-1406	8.442544	0.38473	0.803672	0.478715	0.632141	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (NAluV SINE	28366	NM_001352	5747	Hs.395482NM_005607	ENSG000002PTK2	FADK FAK	protein-coding	
chr9-9355	8.442544	0.38473	0.803672	0.478715	0.632141	0.981636	chr9	93557704	93559087	+	0	NA	intron (Nintron (N	-18189	NM_005392	5253	Hs.211441NM_005392	ENSG000002PHF2	CENP-35 CPHD	fingerprotein-coding	
chr10-844	8.111878	-0.39397	0.823104	-0.47864	0.632192	0.981636	chr10	84438320	84438747	+	0	NA	exon (NM exon (NM	13364	NM_001284	54462	Hs.461988NM_018999	ENSG000002CCSER2	FAM190B coiled-cc	protein-coding	
chr14-214	8.111878	-0.39397	0.823104	-0.47864	0.632192	0.981636	chr14	21497500	21499447	+	0	NA	3' UTR (N 3' UTR (N	12867	NM_019852	56339	Hs.168798NM_019852	ENSG000002METTL3	IME4 ME6A	methyltransferase	
chr16-882	8.111878	-0.39397	0.823104	-0.47864	0.632192	0.981636	chr16	8828246	8828892	+	0	NA	intron (NHERV35 I	-20900	NR_147908	1E+08	Hs.73551ENR_147908	LOC100130C-		uncharacterncRNA	
chr16-247	8.111878	-0.39397	0.823104	-0.47864	0.632192	0.981636	chr16	24786747	24787146	+	0	NA	intron (NAluSx3 S1	57295	NM_014494	27327	Hs.655057NM_014494	ENSG000002TNRC6A	CAGH26 F7	trinculecprotein-coding	
chr3-9887	8.111878	-0.39397	0.823104	-0.47864	0.632192	0.981636	chr3	98879903	98880950	+	0	NA	intron (Nintron (N	21269	NM_080927	131566	Hs.203691NM_080927	ENSG000002DCBLD2	L1E5 ESI	dicoidinprotein-coding	
chr7-4498	8.111878	-0.39397	0.823104	-0.47864	0.632192	0.981636	chr7	44982323	44985581	+	0	NA	non-codiron-codir	1558	NR_002952	677798	Hs.74474ENR_002952	ENSG000002SNORA9	ACA9 SNOF	small nuc snoRNA	
chr3-9406	8.940982	0.38095	0.796161	0.478483	0.632306	0.981636	chr3	9460349	9461388	+	0	NA	intron (Nintron (N	63168	NM_01028C	55209	Hs.288164NM_018187	ENSG000002SETD5		SET domainprotein-coding	
chr1-1204	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	-16308	NR_003242	767846	Hs.65718ENR_003242	ENSG000002PFN1P2		Clorf152 profilin pseudo	
chr1-2444	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	IntergeniLIMB7 LIN	49002	NM_00112E	159	Hs.49831ENM_00112E	ENSG000002ADSS	ADEH ADS	adenylost protein-coding	
chr11-354	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr11	35492745	35494900	+	0	NA	intron (Nintron (N	32244	NM_001001	25891	Hs.55044	NM_01543C	ENSG000002PAMR1	DKFZP586F	peptidaseprotein-coding
chr11-831	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr11	83198675	83198942	+	0	NA	intron (NMLT1G3 LI	5096	NM_00130C	338699	Hs.50343ENM_18260E	ENSG000002ANKRD42	PPP1R79 Sankyrin	1 protein-coding	
chr11-118	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr11	1.18E+08	1.18E+08	+	0	NA	intron (NLTR1B2 LI	40825	NM_00593C	4297	Hs.25885ENM_00593C	ENSG000002KMT2A	ALL-1 CX	lysine meprotein-coding	
chr17-414	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr17	814239	815201	+	0	NA	intron (Nintron (N	32367	NM_01814E	55178	Hs.18272ENM_01814E	ENSG000002MRM3	RMLT1 RN	michoncprotein-coding	
chr17-448	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr17	44858266	44860319	+	0	NA	intron (Nintron (N	11409	NR_073504	51751	Hs.151787NM_01643E	ENSG000002CHIGD1B	CLST1124 CHIG1	hypcprotein-coding	
chr2-306	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr2	30600072	30600271	+	0	NA	intron (NLIPI3 LINE	152925	NM_001304	253558	Hs.46804ENM_18255I	ENSG000002CLLAT1	1AGPAT8 A	lysocacidprotein-coding	
chr4-254	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr4	25409944	25410885	+	0	NA	intron (Nintron (N	33151	NM_013367	29945	Hs.15217ENM_013367	ENSG000002ANAPCA	APCA	anaphase protein-coding	
chr4-122	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	77050	NM_015312	84162	Hs.40814ENM_015312	ENSG000002KIAA1109	ALKKUCS FKIAA1109		protein-coding
chr4-183	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr4	1.84E+08	1.84E+08	+	0	NA	intron (NAluSz SIN	17560	NM_021942	60684	Hs.44324ENM_021942	ENSG000002TRAPP11	C4orf41 F	traffickiprotein-coding	
chr4-184	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr4	1.85E+08	1.85E+08	+	0	NA	intron (NAluSz SIN	-5853	NR_131967	1.05E+08	Hs.338354NR_13196E	ENSG000002LINC0236E	LVCAT8	long intencRNA	
chr5-1604	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr5	1.6E+08	1.6E+08	+	0	NA	exon (NM exon (NM	6598	NM_00136E	10569	Hs.43534ENM_00642E	ENSG000002CSLU7	9G8 hsLu7 SLU7	homcprotein-coding	
chr9-106	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr9	1.07E+08	1.07E+08	+	0	NA	intron (Nintron (N	73011	NM_021224	58499	Hs.37037ENM_021224	ENSG000002ZNF462	ZFP1P Zf	zinc fingprotein-coding	
chr9-110	8.401404	0.383453	0.801772	0.478257	0.632467	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (NMan SINE1	30054	NM_15336E	79987	Hs.522334NM_15336E	ENSG000002SVPEP1	C9orf13 Cushi,	vcprotein-coding	
chr10-158	8.393546	0.385262	0.805641	0.478206	0.632503	0.981636	chr10	15800697	15801953	+	0	NA	intron (NTigger2 I	59182	NM_02494E	80013	Hs.15887ENM_02494E	ENSG000002MINDY3	C10orf97 MINDY	lysprotein-coding	
chr16-581	8.393546	0.385262	0.805641	0.478206	0.632503	0.981636	chr16	58191018	58191300	+	0	NA	intron (NLMIB3 LIN	6947	NM_00189E	1459	Hs.82201	NM_00189E	ENSG000002CSNK2A2	CK2A2 CK2	casein kiprotein-coding
chr4-5344	8.393546	0.385262	0.805641	0.478206	0.632503	0.981636	chr4	53443904	53445153	+	0	NA	intron (Nintron (N	-55549	NR_046622	1.01E+08	Hs.66237ENR_046622	ENSG000002LNX1-AS1		LNX1 anticncRNA	
chr1-124	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr1	12497640	12498334	+	0	NA	intron (NCharlie2	-9259	NR_00302E	677885	Hs.65845ENR_00302E	ENSG000002SNORA59A	ACA59	small nuc snoRNA	
chr10-86	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr10	86509159	86510601	+	0	NA	intron (NAluSx3 S1	11724	NM_00131E	23063	Hs.20309ENM_01504E	ENSG000002WAPL	F0E KIAAC	WAPL coheprotein-coding	
chr12-557	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr12	55774195	55775062	+	0	NA	intron (NAluS2 S1	31506	NM_00581I	10220	Hs.60088ENM_00581I	ENSG000002GDF11	BMP-11 B	growth diprotein-coding	
chr12-89	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr12	89598836	89600179	+	0	NA	intron (Nintron (N	-73244	NM_00119E	1.01E+08	Hs.25130	NM_00119E	ENSG000002POC1B-GAI	IMP4 GAI	POC1B-GAI protein-coding
chr14-24	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr14	24186091	24187096	+	0	NA	intron (Nintron (N	2221	NM_02465E	79711	Hs.41186ENM_02465E	ENSG000002IPO4	Imp4	importin protein-coding	
chr14-914	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr14	91455463	91457256	+	0	NA	TTS (NM_C TTS (NM_C	-38539	NM_00108C	440193	Hs.52553ENM_00108C	ENSG000002CCDC88C	DAPLE HKF	coiled-ccprotein-coding	
chr15-84	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr15	74800276	74800674	+	0	NA	exon (NM exon (NM	-11718	NR_03973E	1.01E+08	NR_03973E	ENSG000002MIR4513		microRNA ncRNA	
chr15-84	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr15	84604922	84605189	+	0	NA	intron (Nintron (N	4046	NM_001007	54993	Hs.59402ENM_017894	ENSG000002ZSCAN2	ZFP29 ZNF	zinc fingprotein-coding	
chr17-364	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr17	36494645	36496523	+	0	NA	TTS (NM_C TTS (NM_C	8903	NM_00128I	9326	Hs.2210	NM_00477E	ENSG000002ZNHIT3	PEHO TRIF	zinc fingprotein-coding
chr17-56	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr17	56935615	56936133	+	0	NA	IntergeniCharlie1e	-21825	NM_00508E	7706	Hs.52895ENM_00508E	ENSG000002TRIM25	IFP RNFI4	tripartitprotein-coding	
chr2-936	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr2	9368666	9369270	+	0	NA	intron (Nintron (N	53623	NM_00131E	9270	Hs.46766ENM_00476E	ENSG000002ITGB1BP1	ICAP-1A I	integrin protein-coding	
chr2-133	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	166255	NR_13557E	1.02E+08	Hs.680114NR_13557E	ENSG000002CNKAP5-AS-		NCKAP5 arncRNA	
chr2-169	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr2	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	78376	NM_17207C	130507	Hs.37954ENM_17207C	ENSG000002UBR3	ZNF650	ubiquitin protein-coding	
chr3-522	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr3	52253470	52254701	+	0	NA	TTS (NM_C TTS (NM_C	7918	NM_001122	132160	Hs.37356ENM_14464I	ENSG000002PPM1M	PP2C-eta	protein-coding	
chr5-786	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr5	7864100	7865888	+	0	NA	intron (NLMIME3G LI	4037	NM_02409I	79072	Hs.65316ENM_02409I	ENSG000002FASTKD3		FAST kinaseprotein-coding	
chr5-170	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr5	1.71E+08	1.71E+08	+	0	NA	intron (NLIPI2 LINE	37395	NM_002289	64901	Hs.41081ENM_02289E	ENSG000002RANBP17		RAN bindiprotein-coding	
chr6-713	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr6	1.11857	NM_02457E	79627	Hs.648434NM_02457E	ENSG000002OGFRL1		79627	Hs.648434NM_02457E	ENSG000002OGFRL1	dJ331H24.	opioid gprotein-coding			
chr6-140	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr6	1.41E+08	1.41E+08	+	0	NA	IntergeniLIMA1 LIN	-147827	NR_03967E	1.01E+08	NR_03967E	ENSG000002MIR4465		microRNA ncRNA	
chr6-167	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr6	1.67E+08	1.67E+08	+	0	NA	intron (Nintron (N	6087	NM_19442E	11116	Hs.48717ENM_00704E	ENSG000002FGFR10P	FOP	FGFR11	oncprotein-coding
chr7-14	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N	50325	NM_00136E	84255	Hs.446021NM_03229E	ENSG000002SLC37A3		solute cprotein-coding	
chr8-47	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr8	47784646	47786562	+	0	NA	intron (NAluJo SIN	-47440	NM_00519E	1052	Hs.44082ENM_00519E	ENSG000002CEBPD	C/EBP-de CCAAT	enprotein-coding	
chr9-278	5.436024	-0.47391	0.99108	-0.47818	0.632524	0.981636	chr9	2782471	2783427	+	0	NA	IntergeniMERS7								



chr3-1967.7.408228	0.416414	0.873691	0.476614	0.633637	0.981636	chr3	1.96E+08	1.96E+08	0	NA	intron (NLIPA6 LIN	-42117 NR_037950	1.01E+08	Hs. 73318CRN_037950	TM4SF19-1-	TM4SF19-1ncRNA
chr5-177.7.408228	0.416414	0.873691	0.476614	0.633637	0.981636	chr5	1.77E+08	1.77E+08	0	NA	intron (Nintron (N	21892 NM_001308	23567	Hs. 484256NM_012275	ENSG000003ZNF346	JAZ Zfp34zinc finger protein-coding
chr7-1287.7.408228	0.416414	0.873691	0.476614	0.633637	0.981636	chr7	1.29E+08	1.29E+08	0	NA	promoter-promoter-	-709 NM_001195	1E+08	Hs. 641532NM_001195	ENSG000003ATP6V1FN6-	ATP6V1F rprotein-coding
chr1-1175.8.596909	-0.38224	0.803123	-0.47595	0.634112	0.981636	chr1	1.1795686	11793985	0	NA	intron (Nintron (N	9842 NM_00133C	4524	Hs. 211442NM_005957	ENSG000003MTHFR	methyleneprotein-coding
chr12-125.8.596909	-0.38224	0.803123	-0.47595	0.634112	0.981636	chr12	1.24E+08	1.24E+08	0	NA	intron (NLTRIOCL LI	30335 NM_001304	80212	Hs. 114111NM_02514C	ENSG000003CCDC92	coiled-ccprotein-coding
chr1-4668.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr1	46688201	46690181	0	NA	intron (Nintron (N	15155 NR_03882E	1E+08	Hs. 56864ENR_038827	ENSG000003EFCB41A-#KIAA0494-EFCB41A	ncRNA
chr1-2201.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr1	2.2E+08	2.2E+08	0	NA	intron (NAluSz SIN	-10868 NR_029711	406969	NR_029711	ENSG000003MIR194-1	MIRN194-1microRNA ncRNA
chr1-2315.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr1	2.31E+08	2.31E+08	0	NA	3' UTR (N3' UTR (N	13705 NM_001010C	83932	Hs. 554892NM_03201F	ENSG000003SPR1N	Clorf124 SprT-like protein-coding
chr12-928.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr12	92858004	92859716	0	NA	intron (Nintron (N	70435 NM_00356E	8411	Hs. 567367NM_00356E	ENSG000003CEEA1	MST105 MSearly encprotein-coding
chr13-973.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr13	973755078	97375900	0	NA	intron (Nintron (N	-58680 NR_021033	5911	Hs. 50848CM_021033	ENSG000003RAP2A	K-REV KRE RAP2A, meprotein-coding
chr14-738.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr14	73211567	73214440	0	NA	intron (Nintron (N	-24503 NR_158677	89932	Hs. 509905NM_17346E	ENSG000003PAPLN	PPN papilin, protein-coding
chr15-658.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr15	65884201	65886080	0	NA	intron (NAluSc8 SI	15649 NM_00120E	8766	Hs. 321541NM_00466E	ENSG000003CRAB11A	YL8 RAB11A, nprotein-coding
chr17-572.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr17	57262057	57265284	0	NA	intron (Nintron (N	6651 NM_140721	124540	Hs. 658922NM_13896E	ENSG000003MSI2	MSI2H musashi fprotein-coding
chr18-468.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr18	46888418	46890885	0	NA	intron (NLIMB3 LIN	27856 NR_148702	9063	Hs. 57769 NM_004671	ENSG000003PIA52	ARIP3 DIF protein-coding
chr21-425.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr21	42908766	42911703	0	NA	3' UTR (N3' UTR (N	15364 NM_00130E	90625	NR_001308491	ERVH48-1	C2orf105 endogeno protein-coding
chr4-3172.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr4	3172600	3175389	0	NA	intron (Nintron (N	-70375 NM_00133C	345222	Hs. 442291NM_00101E	ENSG000003MSANTD1	C4orf44 Myb/SANT protein-coding
chr4-1278.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr4	1.29E+08	1.29E+08	0	NA	intron (NLIMC5 LIN	132718 NM_001287	79960	Hs. 12420 NM_02490C	ENSG000003JADE1	PHF17 jade fasp protein-coding
chr5-1074.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr5	10747146	10748822	0	NA	intron (Nintron (N	13250 NM_004394	1611	Hs. 75189 NM_004394	ENSG000003DAP	death assprotein-coding
chr5-4865.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr5	48650730	48651968	0	NA	IntergeniALR Alpha	1789939 NM_198445	133418	Hs. 561411NM_19844E	ENSG000003EMB	GR70 embigin protein-coding
chr5-9581.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr5	95814318	95817522	0	NA	intron (NL2a LINE	6806 NM_002064	2745	Hs. 28988 NM_002064	ENSG000003CLRX	GRX GRX1 glutaredc protein-coding
chr6-3185.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr6	31891385	31893229	0	NA	intron (Nintron (N	4682 NM_00131E	10919	Hs. 70921ENM_00670E	ENSG000003EHMT2	BAT8 C6or euchromat protein-coding
chr7-3822.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr7	38229337	38230419	0	NA	intron (Nintron (N	43769 NM_00100C	445347	Hs. 534032NM_001003799	TARP	CD3G TCRC TCR gammeprotein-coding
chr7-1074.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr7	1.07E+08	1.07E+08	0	NA	intron (Nintron (N	31563 NM_012257	26959	Hs. 162032NM_012257	ENSG000003HBP1	HMG-box tprotein-coding
chr7-1498.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr7	1.49E+08	1.49E+08	0	NA	intron (NHAL1 LINE	15394 NM_015694	27153	Hs. 38512 NM_015694	ENSG000003ZNF777	zinc finger protein-coding
chr9-3504.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr9	35047768	35048014	0	NA	IntergeniAluSz6 SI	5651 NM_20329E	138724	Hs. 148255NM_20329E	ENSG000003C9orf131	chromosonprotein-coding
chr9-1287.8.409262	0.381629	0.801936	0.475885	0.634156	0.981636	chr9	1.29E+08	1.29E+08	0	NA	intron (Nintron (N	11871 NM_018201	54662	Hs. 3376 NM_018201	ENSG000003TBC1D13	TBC1 domeprotein-coding
chr9-4355.19.28824	0.263595	0.554055	0.475755	0.634249	0.981636	chr9	43588022	43588348	0	NA	IntergeniALR Alpha	462019 NR_16066E	1.03E+08	NR_160669	LOC102724-	methylenepseudo
chr13-114.8.604767	-0.38388	0.807512	-0.47539	0.634508	0.981636	chr13	1.14E+08	1.14E+08	0	NA	intron (NCPG	37112 NM_00132C	22821	Hs. 593075NM_00736E	ENSG000003CRAS3	GAP1 IP4 BFB RAS p21 fprotein-coding
chr7-1162.8.078597	-0.39859	0.838742	-0.47522	0.634629	0.981636	chr7	1.16E+08	1.16E+08	0	NA	intron (NTHE1C-int	21733 NM_15282E	26136	Hs. 59228E NM_015641	ENSG000003TES	TEST TES testin L protein-coding
chr17-246.7.642564	-0.41051	0.864173	-0.47504	0.634762	0.981636	chr17	2466340	2469937	0	NA	intron (Nintron (N	48100 NM_02408E	79066	Hs. 632237NM_02408E	ENSG000003METTL16	METT MET methyltr lprotein-coding
chr9-1311.7.642564	-0.41051	0.864173	-0.47504	0.634762	0.981636	chr9	1.31E+08	1.31E+08	0	NA	intron (Nintron (N	24914 NM_00131E	8021	Hs. 654533NM_00508E	ENSG000003NUP214	CAIN CAN nucleopor protein-coding
chrX-1295.7.642564	-0.41051	0.864173	-0.47504	0.634762	0.981636	chrX	1.3E+08	1.3E+08	0	NA	intron (Nintron (N	11308 NM_00128E	6594	Hs. 152292NM_00306E	ENSG000003SMARCA1	ISWI NURF SWI SNF rprotein-coding
chr14-771.7.44151	0.419764	0.883648	0.475035	0.634762	0.981636	chr14	77113752	77114907	0	NA	3' UTR (N3' UTR (N	16071 NM_03342E	85457	Hs. 709066NM_03342E	ENSG000003CIPC	KIAA1737 CLOCK intron-coding
chr19-415.11.27461	-0.3395	0.714855	-0.47493	0.63484	0.981636	chr19	41300307	41301011	0	NA	intron (Nintron (N	-9513 NM_05284E	90324	Hs. 437497NM_05284E	ENSG000003CCDC97	coiled-ccprotein-coding
chr10-115.8.589051	-0.38068	0.801557	-0.47492	0.634841	0.981636	chr10	11920994	11921203	0	NA	3' UTR (N3' UTR (N	-26388 NR_038222	219731	Hs. 576787NR_038222	ENSG000003PROSER2-#	PROSER2 ncRNA
chr11-108.8.589051	-0.38068	0.801557	-0.47492	0.634841	0.981636	chr11	1.08E+08	1.08E+08	0	NA	intron (NAluJb SIN	66363 NM_001351	472	Hs. 367437NM_000051	ENSG000003ATM	AT1 ATA1 ATM serir protein-coding
chr17-388.8.589051	-0.38068	0.801557	-0.47492	0.634841	0.981636	chr17	38319136	38319541	0	NA	intron (NAluSp SIN	22170 NM_032351	84311	Hs. 537275NM_032351	ENSG000003MRPL45	L45mt MRf mitochondonprotein-coding
chr12-131.7.863677	0.397603	0.837303	0.474862	0.634886	0.981636	chr12	1.32E+08	1.32E+08	0	NA	intron (Nintron (N	35020 NM_00459E	6433	Hs. 30817 NM_00459E	ENSG000003SFSWAP	SFRS8 SW splicing protein-coding
chr20-397.7.863677	0.397603	0.837303	0.474862	0.634886	0.981636	chr20	3989702	3990004	0	NA	intron (NMLT11 LTF	25705 NM_001134	11237	Hs. 547575NM_00721E	ENSG000003RNF24	GILF ring finger protein-coding
chr20-355.9.47871	0.36942	0.778283	0.47466	0.635029	0.981636	chr20	35688935	35689395	0	NA	intron (Nintron (N	10187 NM_00119E	9054	Hs. 194692NM_02110C	ENSG000003CNFS1	HUSSY-08 NFS1 cyst protein-coding
chr12-121.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr12	1.21E+08	1.21E+08	0	NA	intron (NAluXs3 SI	-20471 NM_15349E	10645	Hs. 29734E NM_00654E	ENSG000003CAMKK2	CKMK CAM calcium/cprotein-coding
chr16-311.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr16	31112139	31112789	0	NA	3' UTR (N3' UTR (N	4078 NM_001122	10295	Hs. 51352C NM_005881	ENSG000003BCKDK	BCKDK BE branched protein-coding
chr18-215.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr18	21563577	21563832	0	NA	intron (Nintron (N	37000 NM_052911	114799	Hs. 464733NM_052911	ENSG000003ESCO1	A9300141 establist protein-coding
chr21-403.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr21	43741570	43747681	0	NA	intron (Nintron (N	5929 NM_001331	8566	Hs. 284491NM_003681	ENSG000003PDXK	C2orf124 pyridoxal protein-coding
chr3-1307.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr3	1E+08	1E+08	0	NA	intron (Nintron (N	22532 NM_00119E	55773	Hs. 477003NM_01830E	ENSG000003TBC1D23	NS4orf11 TBC1 domeprotein-coding
chr5-3242.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr5	32428879	32429091	0	NA	intron (NAluYml SI	15755 NR_14431E	51663	Hs. 435231NM_016107	ENSG000003ZFR	SPG71 ZFF zinc finger protein-coding
chr5-811.7.912674	0.396975	0.836664	0.474474	0.635162	0.981636	chr5	81137558	81137805	0	NA	intron (NMLT1B LTF	-95639 NM_00182E	1160	Hs. 80691 NM_00182E	ENSG000003CKMT2	SMTCCK creatine protein-coding
chr1-2115.8.194158	-0.38828	0.818601	-0.47432	0.635272	0.981636	chr1	2.11E+08	2.11E+08	0	NA	intron (Nintron (N	-23042 NM_00461E	7188	Hs. 52393CNM_00461E	ENSG000003TRAF5	MGC:3978C TNF receeprotein-coding
chr16-892.8.194158	-0.38828	0.818601	-0.47432	0.635272	0.981636	chr16	89269733	89270920	0	NA	intron (Nintron (N	-25802 NR_13633E	1.05E+08	Hs. 657381NR_13633E	ENSG000003LOC105371	uncharactncRNA
chr7-9945.14.14304	0.300054	0.6326	0.474319	0.635272	0.981636	chr7	99492189	99497512	0	NA	in					

chr12-641.8.173402	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr12	64140598	64140842	+	0 NA	intron (N)LIPA2 LIN	81576 NM_00130C	144577 Hs. 444671NM_15244CENS00000C12orf66	-	chromosomprotein-coding	
chr15-658.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr15	65597848	65598936	+	0 NA	exon (NM) exon (NM)	12739 NM_00136E	81556 Hs. 6686 NM_03080CENS00000INTS14	C15orf44	integratrprotein-coding	
chr16-211.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr16	2113327	2114054	+	0 NA	intron (N)intron (N)	-6937 NR_106777E	1.02E+08 NR_106777EENS00000MIR6511B1MIR6511B-	microRNA ncRNA		
chr19-491.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr19	49861767	49862202	+	0 NA	intron (N)CpG-1495E	-2695 NR_110733C	1.02E+08 Hs. 710299NR_110730	PTOV1-AS2-	PTOV1 antncRNA	
chr2-2918.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr2	29137238	29137652	+	0 NA	intron (N)LIPA17 LI	22030 NM_001287	79745 Hs. 122927NM_02469EENS00000CLIP4	RSNL2	CAP-Gly protein-coding	
chr2-6132.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr2	61328864	61329178	+	0 NA	intron (N)AluSp SIN	88356 NR_003707	1E+08 Hs. 67582ENR_003707ENS00000SNORA70B	-	small nucsnoRNA	
chr2-2016.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr2	2.02E+08	2.02E+08	+	0 NA	intron (N)intron (N)	6171 NM_152388	65062 Hs. 12319 NM_152388ENS00000TMEM237	ALS2CR4 J	transmemprotein-coding	
chr20-1918.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr20	19966247	19968952	+	0 NA	intron (N)intron (N)	-49691 NM_18152E	51126 Hs. 368788NM_01610CENS00000NAA20	NAT3 NAT3(alpha)-	protein-coding	
chr3-9858.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr3	98585602	98586244	+	0 NA	intron (N)AluY SINE	7688 NM_000097	1371 Hs. 476982NM_000097ENS00000CPOX	-	COX CPO C	coproporf protein-coding
chr3-1237.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (N)MERC33 DN	63456 NR_046622E	1.01E+08 Hs. 66731ENR_046622ENS00000MYLK-AS2	-	MYLK antncRNA	
chr6-1005.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr6	1.01E+08	1.01E+08	+	0 NA	intron (N)intron (N)	-125336 NM_00506E	6492 Hs. 52029ENR_00506EENS00000SLM1	bHLHe14	SIM bHLH protein-coding	
chr7-139C.8.178442	-0.38513	0.815281	-0.47239	0.636651	0.981636	chr7	1.39E+08	1.39E+08	+	0 NA	intron (N)AluSp SIN	-8421 NR_16210E	1.13E+08 NR_16210E	MIR10399	-	microRNA ncRNA
chr6-9954.8.581193	-0.37917	0.802772	-0.47233	0.636693	0.981636	chr6	99547906	99548190	+	0 NA	intron (N)L2 LINE L	20612 NM_00519C	892 Hs. 43064ENM_00519CENS00000CCNC	-	CycC SRB cyclin C	protein-coding
chr11-74.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr11	74208138	74208162	+	0 NA	intron (N)intron (N)	38128 NM_001271	51400 Hs. 503251NM_016147ENS00000PPME1	ABDH19 P	protein-coding	
chr14-584.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr14	58411579	58412407	+	0 NA	intron (N)intron (N)	15249 NM_001304	26520 Hs. 44052ENM_01246CENS00000TIMM9	TIM9 TIM9	translocprotein-coding	
chr2-4392.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr2	439252347	43925852	+	0 NA	intron (N)intron (N)	70390 NM_13325E	10128 Hs. 368084NM_13325EENS00000LRPPRC	CLONE-23E	leucine rprotein-coding	
chr3-478.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr3	47832815	47833283	+	0 NA	intron (N)FLAM_C SI	-16506 NR_03159E	1E+08 NR_03159EENS00000MIR1226	MIRN1226	microRNA ncRNA	
chr3-998E.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr3	99866726	99867243	+	0 NA	intron (N)intron (N)	8989 NM_00137C	11259 Hs. 10467ENM_01489CENS00000FILIP1L	D0C-1 DOC	filamin A protein-coding	
chr4-845E.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr4	8458010	8458415	+	0 NA	intron (N)Tiger2 E	17415 NM_00135C	152992 Hs. 566191NM_02495CENS00000TRM744	C4orf23	mRNA metprotein-coding	
chr4-942E.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr4	94282726	94283835	+	0 NA	exon (NM) exon (NM)	29971 NM_001254	56916 Hs. 41040ENM_02015EENS00000SMARCAD1	ADERM BAS	SWI/SNF-1 protein-coding	
chr6-854E.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr6	85466870	85467789	+	0 NA	intron (N)intron (N)	17246 NM_00252E	4907 Hs. 15395ENM_00252EENS00000CTN5E	CALJA CD75	-nuclecprotein-coding	
chr8-616E.8.137302	-0.3879	0.821348	-0.47227	0.636731	0.981636	chr8	61600279	61601187	+	0 NA	intron (N)LIM2 LINE	89078 NM_001164	444 Hs. 33242ENM_00431EENS00000ASPH	AAH BAH	caspartateprotein-coding	
chr1-1931.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr1	1.93E+08	1.93E+08	+	0 NA	exon (NM) exon (NM)	5389 NR_031691	1E+08 NR_031691ENS00000MIR1278	MIRN1278	microRNA ncRNA	
chr11-658.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr11	65538122	65539843	+	0 NA	TTS (NM_C)TTS (NM_C)	13899 NM_00104E	57410 Hs. 23883ENM_02068CENS00000SCYL1	GKLP HTO1	SCY1 like protein-coding	
chr12-214.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr12	21472718	21473513	+	0 NA	intron (N)intron (N)	28520 NM_002907	5965 Hs. 23506ENM_002907ENS00000RECQL	RECQL1 ReCq	like protein-coding	
chr13-111.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr13	1.1E+08	1.1E+08	+	0 NA	intron (N)intron (N)	1824 NM_001267	1E+08 Hs. 64003ENM_001267044	COL4A2-AS-	COL4A2 arprotein-coding	
chr2-1281.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr2	1.28E+08	1.28E+08	+	0 NA	intron (N)LIMB7 LIN	57352 NM_0027671	56886 Hs. 74330ENM_02012CENS00000UGGT1	HUGT1 UCG	UDP-glucprotein-coding	
chr3-8694.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr3	86944631	86944830	+	0 NA	3' UTR (N)3' UTR (N)	46419 NM_00132C	389136 Hs. 606507NM_01620CENS00000VGLL3	VGL-3 VGL	vestigialprotein-coding	
chr9-134E.8.614475	-0.37487	0.793838	-0.47222	0.63677	0.981636	chr9	1.35E+08	1.35E+08	+	0 NA	intron (N)intron (N)	-39677 NR_13804E	414316 Hs. 571561NR_13804EENS00000COL5A1-AS	C9orf104 COL5A1	arncRNA	
chr12-95E.8.90585	-0.367861	0.780273	-0.471452	0.637318	0.981636	chr12	95504162	95505491	+	0 NA	intron (N)intron (N)	30674 NM_001317	10988 Hs. 44498ENM_00683EENS00000METAP2	MMP2 MNPE	methionylprotein-coding	
chr13-79E.8.90585	-0.367861	0.780273	-0.471452	0.637318	0.981636	chr13	79369940	79372377	+	0 NA	exon (NM) exon (NM)	35063 NM_00128E	64062 Hs. 55852ENM_01860EENS00000CRBM26	ARRS2 C1E	RNA bindiprotein-coding	
chr14-921.8.90585	-0.367861	0.780273	-0.471452	0.637318	0.981636	chr14	92133693	92133998	+	0 NA	intron (N)intron (N)	11876 NM_001322	53981 Hs. 65762ENM_017437ENS00000CPSF2	CPSF100	cleavage protein-coding	
chr19-52E.8.90585	-0.367861	0.780273	-0.471452	0.637318	0.981636	chr19	52595943	52596882	+	0 NA	promoter-promoter-intron (N)intron (N)	-272 NR_02313E	7696 Hs. 37364ENM_003438	ZNF137 p	zinc fingpseudo	
chr21-371.8.90585	-0.367861	0.780273	-0.471452	0.637318	0.981636	chr21	37126677	37130092	+	0 NA	intron (N)intron (N)	45437 NM_00331E	7267 Hs. 368214NM_00331EENS00000CTTC3	DCRR1 RN	tetratricprotein-coding	
chrX-248E.8.90585	-0.367861	0.780273	-0.471452	0.637318	0.981636	chrX	2489750	2490422	+	0 NA	exon (NM) exon (NM)	10453 NM_001171	9189 Hs. 13145ENM_00472EENS00000ZBED1	ALTE DREF	zinc fingprotein-coding	
chr1-2202.8.450402	-0.382835	0.812133	-0.471394	0.637359	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (N)intron (N)	13985 NR_001587	6791 Hs. 65484ENR_001587	AURKAP1	AURKAP1 aurora k	pseudo
chr16-66E.8.450402	-0.382835	0.812133	-0.471394	0.637359	0.981636	chr16	66609594	66610767	+	0 NA	intron (N)intron (N)	5449 NR_03761E	123920 Hs. 29819ENM_144601ENS00000CMTM3	BNAS2 CKI	CKLF like protein-coding	
chr2-1201.8.450402	-0.382835	0.812133	-0.471394	0.637359	0.981636	chr2	1.2E+08	1.2E+08	+	0 NA	intron (N)LIMB7 LIN	67824 NM_024121	79134 Hs. 376722NM_024121ENS00000TMEM185B	FAM11B	transmemprotein-coding	
chr20-377.8.450402	-0.382835	0.812133	-0.471394	0.637359	0.981636	chr20	37737697	37738645	+	0 NA	intron (N)intron (N)	44141 NM_030877	56259 Hs. 472667ENM_030877ENS00000CTNBL1	C0orf33	catenin hprotein-coding	
chr3-333E.8.450402	-0.382835	0.812133	-0.471394	0.637359	0.981636	chr3	33388973	33390198	+	0 NA	3' UTR (N)3' UTR (N)	50793 NM_00112E	7342 Hs. 72912CNM_014517ENS00000CUBP1	LBP-1B L	upstream protein-coding	
chr15-40E.8.104021	-0.39236	0.832348	-0.47138	0.637366	0.981636	chr15	40028351	40029036	+	0 NA	intron (N)intron (N)	10488 NM_003134	6727 Hs. 53373ENM_003134ENS00000SRP14	ALURBP	signal rprotein-coding	
chr1-1224.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr1	12242282	12244865	+	0 NA	intron (N)AluJr SIN	13543 NM_01537E	55187 Hs. 43938ENM_01537EENS00000VPS13D	SCAR4	vacuolar protein-coding	
chr1-316E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr1	31630391	31630938	+	0 NA	exon (NM) exon (NM)	12964 NM_00152E	3061 Hs. 38822ENM_00152EENS00000HCRTR1	OX1R	hypocretinprotein-coding	
chr1-450E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr1	45005137	45009276	+	0 NA	intron (N)intron (N)	4118 NM_02460E	79654 Hs. 525084NM_02460EENS00000HECTD3	-	HECT domprotein-coding	
chr1-211E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr1	2.11E+08	2.11E+08	+	0 NA	intron (N)AluJo SIN	24803 NM_018254	55758 Hs. 35639ENM_018254ENS00000RCOR3	-	REST coreprotein-coding	
chr10-28E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr10	28558719	28558950	+	0 NA	intron (N)intron (N)	25716 NM_01662E	51322 Hs. 74322ENM_01662EENS00000WAC	BM-016 DE	WF domain protein-coding	
chr11-12E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr11	1.3E+08	1.3E+08	+	0 NA	intron (N)intron (N)	19907 NM_00616E	4798 Hs. 53053ENM_00616EENS00000NFRKB	IN080G	nuclear fprotein-coding	
chr12-501.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr12	50140639	50142924	+	0 NA	intron (N)AluSx SIN	25588 NM_14719C	91012 Hs. 27052ENM_14719CENS00000CCERS5	LASS5 Trt	ceramide protein-coding	
chr12-50E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr12	50994896	50995609	+	0 NA	intron (N)AluSx1 SI	13963 NM_001174	4891 Hs. 50554ENM_000617ENS00000SLC11A2	AHM101 D	solute cprotein-coding	
chr14-10E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (N)AluSq SIN	54493 NM_00112E	4140 Hs. 35828 NM_00237EENS00000MARK3	CTAK1 KP7	microtub protein-coding	
chr15-74E.8.41712	-0.379756	0.806137	-0.471081	0.637583	0.981636	chr15	74671157	74671633	+	0 NA	intron (N)intron (N)	24629 NM_00114E	80153 Hs. 96852 ENM_02508EENS00000EDC3	LSM16 MR1	enhancer protein-coding	



chr17-597.7.879393	0.39364	0.837599	0.469962	0.638382	0.981636	chr17	59735854	59736872	+	0 NA	intron (AluSx SIN	28709 NM_001325	81671 Hs.444566NM_03093f	ENSG000000VMP1	EPG3 TANC vacuole nprotein-coding
chr5-1396.7.879393	0.39364	0.837599	0.469962	0.638382	0.981636	chr5	1.4E+08	1.4E+08	+	0 NA	intron (MSTA LTR	-27207 NM_001317	51523 Hs.189115NM_01646f	ENSG000000CX5C	CF5 HSPC1CX5C fingprotein-coding
chr10-103.5.872057	-0.45139	0.96084	-0.46979	0.638505	0.981636	chr10	1.04E+08	1.04E+08	+	0 NA	intron (Nintron (N	35248 NM_001365	9644 Hs.678727NM_01463f	ENSG000000SH3PXD2A	FISH SH3W SH3 and fprotein-coding
chr1-193.9.443578	0.356786	0.759514	0.469756	0.638529	0.981636	chr1	1.93E+08	1.93E+08	+	0 NA	intron (Nintron (N	-28866 NM_003783	8707 Hs.518834NM_00378f	ENSG000000B3GALT2	BETA3GAL beta-1,3-protein-coding
chr14-73.9.443578	0.356786	0.759514	0.469756	0.638529	0.981636	chr14	73022308	73022487	+	0 NA	intron (N(TA N Sin	3709 NM_02126C	53349 Hs.33510fNM_02126f	ENSG000000ZFVYE1	DFCP1 PPF zinc fingprotein-coding
chr15-504.9.443578	0.356786	0.759514	0.469756	0.638529	0.981636	chr15	50495982	50497103	+	0 NA	intron (Nintron (N	50124 NM_203494	373509 Hs.677755NM_20349f	ENSG000000CUSP50	- ubiquitin protein-coding
chr16-134.9.443578	0.356786	0.759514	0.469756	0.638529	0.981636	chr16	53470536	53471117	+	0 NA	exon (NM exon (NM	32383 NM_02247f	64400 Hs.380897NM_02247f	ENSG000000AKTIP	FT1 FTS AKT interprotein-coding
chr19-535.5.469305	-0.46706	0.994502	-0.46964	0.63861	0.981636	chr19	13924033	13924565	+	0 NA	intron (Alu SINE	14118 NM_00137C	79883 Hs.44849fNM_02482f	ENSG000000PODNL1	SLRR5  podocan lprotein-coding
chr2-325.5.469305	-0.46706	0.994502	-0.46964	0.63861	0.981636	chr2	32590154	32590959	+	0 NA	intron (Nintron (N	-15738 NR_12579f	1.04E+08 Hs.666092NR_12579f	ENSG000000BIRC6-AS2	linc-birc6 BIRC6 antncRNA
chr2-457.5.469305	-0.46706	0.994502	-0.46964	0.63861	0.981636	chr2	45715348	45715764	+	0 NA	intron (MERA3 DNF	43722 NM_01523f	25814 Hs.47512fNM_01523f	ENSG000000ATXN10	E46L HUM ataxin 1 protein-coding
chr4-983.5.469305	-0.46706	0.994502	-0.46964	0.63861	0.981636	chr4	98330351	98330825	+	0 NA	intron (N(SVA B Ret	69204 NM_02115f	5910 Hs.13285fNM_02115f	ENSG000000RAP1GDS1	GDS1 SmgGrap1 GTPe protein-coding
chr8-1175.5.469305	-0.46706	0.994502	-0.46964	0.63861	0.981636	chr8	1.18E+08	1.18E+08	+	0 NA	intron (Nintron (N	-51487 NR_14579f	1.1E+08 NR_14579f	SNORD168	- small nucsnoRNA
chr14-678.8.606617	-0.37336	0.79504	-0.46962	0.63863	0.981636	chr14	67677588	67678011	+	0 NA	3' UTR (N3' UTR (N	-3167 NM_00637f	10490 Hs.741177NM_00637f	ENSG000000VTI1B	VTI1 VTI1vesicle tprotein-coding
chr2-37.8.606617	-0.37336	0.79504	-0.46962	0.63863	0.981636	chr2	37881597	37883667	+	0 NA	intron (AluSx SIN	-23665 NM_03338f	85377 Hs.51761fNM_03338f	ENSG000000MICAL1	MICAL-L1 MICAL Ii protein-coding
chr3-177.8.606617	-0.37336	0.79504	-0.46962	0.63863	0.981636	chr3	1.77E+08	1.77E+08	+	0 NA	intron (N(LIME3 Cz I	165889 NM_001321	79718 Hs.714201NM_02466f	ENSG000000TBL1XR1	C21 DC42  transducin protein-coding
chr7-7764.8.606617	-0.37336	0.79504	-0.46962	0.63863	0.981636	chr7	77644344	77644493	+	0 NA	Intergeni Intergeni	52347 NR_134254	1.01E+08 Hs.72451 NR_03836f	ENSG000000APTR	RSBN1L-AS Alu-mediated ncRNA
chr15-985.8.375981	0.378447	0.807307	0.468777	0.639229	0.981636	chr15	98933291	98933886	+	0 NA	intron (AluJb SIN	72038 NM_00110f	145814 Hs.592021NM_00110f	ENSG000000PGPEP1L	- pyroglutamate protein-coding
chr10-61.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr10	61955376	61954608	+	0 NA	intron (AluSp SIN	52393 NM_03219f	84159 Hs.535297NM_03219f	ENSG000000ARID5B	DESRT MR AT-rich iprotein-coding
chr11-832.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr11	83270710	83274305	+	0 NA	intron (Nintron (N	13900 NM_00128f	60492 Hs.36886fNM_02182f	ENSG000000CCDC90B	MDSO11 ME coiled-c protein-coding
chr12-194.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr12	50439026	50439660	+	0 NA	intron (Nintron (N	-17228 NR_13275f	1.07E+08 NR_13275f	SNORD133	L124 Z4 small nucsnoRNA
chr13-506.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr13	19854127	19854473	+	0 NA	intron (AluSc SIN	9336 NM_00103f	9205 Hs.53098fNM_01424f	ENSG000000ZMYM5	HSPC050 Zinc fingprotein-coding
chr15-424.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr15	42465144	42465447	+	0 NA	intron (AluJo SIN	-7728 NM_001284	64397 Hs.51114fNM_02247f	ENSG000000ZNF106	SH3BP3 Zf zinc fingprotein-coding
chr17-296.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr17	29688426	29688673	+	0 NA	intron (AluSx3 SI	-87126 NM_032854	84940 Hs.14304fNM_03285f	ENSG000000COR06	- coronin fprotein-coding
chr4-122.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (Nintron (N	18265 NM_01531f	84162 Hs.452597NM_01531f	ENSG000000KIAA1109	ALKKUCS FK IAA1109 protein-coding
chr7-6736.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr7	6739838	6740790	+	0 NA	intron (Nintron (N	5009 NR_00221f	441194 Hs.71559fNR_00221f	ENSG000000PMS2CL	PMS2P13 PMS2 C-t pseudo
chr9-1212.8.170584	-0.38349	0.818105	-0.46875	0.639247	0.981636	chr9	1.21E+08	1.21E+08	+	0 NA	non-codiron-codir	836 NR_10356f	57700 Hs.52237fNM_02025f	ENSG000000GSN-AS1	C9orf31 G SN antiscRNA
chr5-173.8.368123	0.380246	0.811203	0.468744	0.639253	0.981636	chr5	1.73E+08	1.73E+08	+	0 NA	TTS (NR_CTS (NR_C	895 NR_00298f	67744 Hs.69272fNR_00298f	ENSG000000SNOR47B	U19-27 small nucsnoRNA
chr5-8227.11.32546	-0.33061	0.705439	-0.46866	0.63931	0.981636	chr5	82274435	82277071	+	0 NA	3' UTR (N3' UTR (N	2601 NM_00102f	6228 Hs.52719fNM_00102f	ENSG000000RPS23	BTDD MAB ribosomal protein-coding
chr2-272.5.394884	-0.47819	1.020494	-0.46858	0.639367	0.981636	chr2	27216362	27216657	+	0 NA	promoter-promoter-	-860 NM_004341	790 Hs.37701fNM_004341	ENSG000000CAD	CDG1Z EIF carbamoyl protein-coding
chr20-496.7.979238	0.40378	0.861001	0.468499	0.639428	0.981636	chr20	49842750	49842976	+	0 NA	intron (MLTIC1 LTR	-20996 NR_16213f	1.13E+08 NR_16213f	MIR12122	- microRNA ncRNA
chr1-149.8.547911	-0.38379	0.81938	-0.46839	0.639504	0.981636	chr1	1.49E+08	1.49E+08	+	0 NA	intron (Nintron (N	4494 NM_001364	1.01E+08 NM_001364	ENSG000000NOTCH2NL2	CN2N NOTCH notch 2 lprotein-coding
chr12-29.9.427862	0.360159	0.769323	0.468151	0.639677	0.981636	chr12	29356223	29356422	+	0 NA	intron (Nintron (N	24850 NM_01657f	51290 Hs.33945fNM_01657f	ENSG000000ERGC12	CDNA14 ERV ERC ancprotein-coding
chr20-336.9.427862	0.360159	0.769323	0.468151	0.639677	0.981636	chr20	33636706	33637404	+	0 NA	intron (Nintron (N	-25452 NM_08082f	128864 Hs.32410fNM_08082f	ENSG000000C20orf144	dJ63M2.6 chromoson protein-coding
chr6-1508.8.573335	-0.3777	0.806813	-0.46814	0.639683	0.981636	chr6	1.51E+08	1.51E+08	+	0 NA	intron (AluSx SIN	24653 NM_00135f	25902 Hs.59134fNM_01544f	ENSG000000MTHFD1L	FTFHS SDC1  methylene protein-coding
chr10-177.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr10	17721616	17723602	+	0 NA	Intergeni LIP3 LIN	-29592 NM_00109f	653567 Hs.56413fNM_00101f	ENSG000000TMEM236	FAM23A PF transmem protein-coding
chr13-946.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr13	94619444	94619850	+	0 NA	intron (Nintron (N	17790 NR_18098f	160897 Hs.43936fNM_18098f	ENSG000000GPR180	ITR G protein protein-coding
chr14-501.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr14	50198188	50199564	+	0 NA	intron (Nintron (N	32702 NM_00693f	6655 Hs.29153fNM_00693f	ENSG000000SOS2	NS9 SOS-2 SOS Ras/fprotein-coding
chr14-693.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr14	69083817	69082511	+	0 NA	intron (Nintron (N	68094 NR_001284	8816 Hs.50978fNM_00386f	ENSG000000DCAF5	BCRG2 BCF DDB1 and protein-coding
chr14-73.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr14	73726383	73727513	+	0 NA	exon (NM exon (NM	-12563 NM_00602f	9240 Hs.19470fNM_00602f	ENSG000000PNMA1	MA1 PNMA famprotein-coding
chr17-307.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr17	30770422	30772740	+	0 NA	intron (AluSx1 SI	53111 NM_01598f	51379 Hs.64937fNM_01598f	ENSG000000CRLF3	CREME-9 cytokine protein-coding
chr17-568.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr17	56897660	56899521	+	0 NA	intron (NMER106A I	-7235 NR_03740f	1.01E+08 NR_03740f	ENSG000000MIR3614	mir-3614 microRNA ncRNA
chr2-6104.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr2	61047802	61049883	+	0 NA	3' UTR (N3' UTR (N	-17028 NM_00133f	84542 Hs.46865fNM_03250f	ENSG000000KIAA1841	- KIAA1841 protein-coding
chr2-2307.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr2	2.31E+08	2.31E+08	+	0 NA	intron (Nintron (N	-71868 NM_001287	81618 Hs.111577NM_03092f	ENSG000000ITM2C	BRI3 BRIC integral protein-coding
chr5-1284.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr5	1.28E+08	1.28E+08	+	0 NA	intron (NMER11B LI	90601 NM_00119f	2201 Hs.519294NM_00119f	ENSG000000FBN2	CCA DA9 E fibriillin protein-coding
chr6-872.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr6	87254967	87258255	+	0 NA	exon (NM exon (NM	-65977 NM_001287	57150 Hs.70769 NM_02042f	ENSG000000SMIM8	C6orf162 small intprotein-coding
chr7-665.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr7	6650842	6655810	+	0 NA	exon (NM exon (NM	16008 NM_00127f	1E+08 Hs.11266fNM_00127f	ENSG000000ZNF316	MZF-3 zinc fingprotein-coding
chr9-1348.8.647756	-0.37072	0.791903	-0.46814	0.639688	0.981636	chr9	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	23875 NR_039691	1.01E+08 NR_039691	ENSG000000MIR3689C	- microRNA ncRNA
chr10-615.4.683561	0.495611	1.059526	0.467766	0.639952	0.981636	chr10	61981134	61981869	+	0 NA	intron (AluSx6 SI	-67856 NM_001244	84159 Hs.535297NM_03219f	ENSG000000CARID5B	DESRT MR AT-rich iprotein-coding
chr7-7737.4.683561	0.495611	1.059526	0.467766	0.639952	0.981636	chr7	77375433	77376466	+	0 NA	intron (Nintron (N	-7375433 NR_11007f	1.02E+08 Hs.54775fNR_11007f	LOC101927-	uncharacterncRNA
chr9-9600.4.683561	0.495611	1.059526	0.467766	0.639952	0.981636	chr9	96004503	96005168	+	0 NA	intron (Nintron (N	16976 NR_02412f	1E+08 Hs.43431fNR_02412f	ENSG000000LINC00092	NCRNA0009 long intncRNA
chr6-304.8.11.83591	-0.32064	0.685586	-0.46769	0.640007	0.981636	chr6	30490388	30493890	+	0 NA	intron (Nintron (N	2629 NM_00551f	3133 Hs.650174NM_00551f	ENSG00000	

chr20-355	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr20	35913275	35915977	+	0	NA	intron (NLM2 LINE	40000	NM_03363C	51282	Hs.58490	ENSG00000SCAND1	RAZ1 SDP1SCAN	dom protein-coding		
chr3-3801	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr3	38014899	38016837	+	0	NA	intron (Nintron (N	8652	NM_00113C	5333	Hs.80776	NM_00622F	ENSG00000PLCD1	NDNC3 PLC	phospholipase protein-coding	
chr5-967f	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr5	96762326	96762909	+	0	NA	3' UTR (N3' UTR (N	19015	NR_10428E	831	Hs.43618	ENSG00000CAST	BS-17 PLA	calpastat protein-coding		
chr6-136f	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr6	1.37E+08	1.37E+08	+	0	NA	intron (NTHE1D-int	9630	NM_00028E	5191	Hs.28093	ENSG00000PEX7	PBB9 PTS	peroxisome protein-coding		
chr7-4401	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr7	44011238	44013779	+	0	NA	intron (Nintron (N	6686	NR_00365E	84820	Hs.65702	ENSG00000POLR2J4	RB11-phiRNA	polynpseudo		
chr7-647f	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr7	64706147	64707135	+	0	NA	exon (NM_exon (NM	27577	NR_10689E	1.02E+08	NR_10689E	ENSG00000MIR6839	hsa-mir-ε	microRNA ncRNA		
chr7-741f	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr7	74105007	74113336	+	0	NA	intron (NMIR3 SINE	15954	NM_001204	3984	Hs.64703	ENSG00000LIMK1	LIMK1 LIMLIM	doma protein-coding		
chr7-1314	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	90054	NM_00101E	5420	Hs.74421	ENSG00000PODXL	Gp200 PC	podocaly protein-coding		
chr7-139c	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	exon (NM_exon (NM	-32244	NR_16210E	1.13E+08	NR_16210E	MIR10399	-	microRNA ncRNA		
chr7-143f	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr7	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	9587	NM_00120E	9747	Hs.73514	ENSG00000TCAP1	FAM115A	TRPM8	chem protein-coding	
chr9-151f	8.921566	0.364425	0.780629	0.466834	0.640618	0.981636	chr9	15195661	15196662	+	0	NA	intron (NTrigger1 E	54057	NM_00116E	158219	Hs.56363	ENSG00000TTC39B	C9orf52	tetratric protein-coding		
chr19-12f	14.62206	0.290537	0.62237	0.466824	0.640626	0.981636	chr19	12523553	12532858	+	0	NA	intron (Nintron (N	23277	NM_14497E	163050	Hs.65561	ENSG00000ZNF564	-	zinc fing protein-coding		
chr1-210f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr1	21086881	21087896	+	0	NA	intron (NALuJb SIN	23995	NM_00376E	8672	Hs.46708	ENSG00000EIF4G3	eIF-4G 3 eukaryot	protein-coding		
chr12-10f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	31292	NM_05716E	9815	Hs.43499	ENSG00000GIT2	CAT-2 CAIGIT	Arfg protein-coding		
chr14-92f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr14	92144715	92146901	+	0	NA	intron (Nintron (N	23839	NM_00132E	53981	Hs.65763	ENSG00000CPSF2	CPSF100	cleavage protein-coding		
chr15-24f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr15	24997900	24998771	+	0	NA	intron (Nintron (N	11405	NR_00129E	33827	NR_00129E	ENSG00000SNORD108	HBI1-437	small nucsnRNA		
chr15-76f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr15	76933686	76934255	+	0	NA	intron (NMIRb SINE	2221	NM_00290E	5955	Hs.79088	ENSG00000RCRN2	E6BP ERC	reticuloc protein-coding		
chr16-67f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr16	67071612	67074532	+	0	NA	intron (NBLACKJACK	-36869	NM_00132C	80262	Hs.51366	ENSG00000C16orf70	C16orf67	l chromosom protein-coding		
chr16-71f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr16	71933648	71934614	+	0	NA	intron (Nintron (N	38600	NM_00127C	9798	Hs.23219	ENSG00000ISTI	CHMP8 OLC	ISTI fact protein-coding		
chr16-75f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr16	75643265	75644101	+	0	NA	intron (Nintron (N	4004	NM_00113C	3735	Hs.3100	ENSG00000CKARS	CMTR1B DF	lysyl-tRNA protein-coding		
chr17-15f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr17	15969880	15971239	+	0	NA	intron (Nintron (N	25642	NM_00067E	136	Hs.16704	ENSG00000ADORA2B	ADORA2	adenosine protein-coding		
chr17-64f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr17	64634343	64636411	+	0	NA	intron (NLMIB7 LIN	26930	NM_02273E	64750	Hs.51501	ENSG00000SMURF2	-	SMAD spec protein-coding		
chr19-46f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr19	46379224	46380526	+	0	NA	intron (NMER105 DN	32788	NM_006247	5536	Hs.65460	ENSG00000PPP5C	PP5 PPP5	protein f protein-coding		
chr2-324f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr2	32475347	32476372	+	0	NA	intron (Nintron (N	-56294	NR_03028E	693143	NR_03028E	ENSG00000MIR558	MIRN558	tmicroRNA ncRNA		
chr2-610f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr2	61077442	61078491	+	0	NA	intron (NCharlie	11757	NM_00133C	84542	Hs.46865	ENSG00000KIAA1841	-	KIAA1841	protein-coding	
chr2-108f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr2	1.09E+08	1.09E+08	+	0	NA	intron (NLMIP2 LIN	15212	NM_14497E	165055	Hs.36270	ENSG00000CCDC138	-	coiled-c protein-coding		
chr2-182f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr2	1.83E+08	1.83E+08	+	0	NA	intron (Nintron (N	25724	NR_073367	54431	Hs.51663	ENSG00000DNACJ10	ErdJ5 JPE	DnaJ	heat protein-coding	
chr20-35f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr20	35053985	35054760	+	0	NA	intron (NMIRc SINE	38435	NM_01563E	26133	Hs.16807	ENSG00000TRPC4AP	C20orf18	transient protein-coding		
chr21-33f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr21	33512628	33514075	+	0	NA	intron (NALuSg SIN	-21628	NM_00132C	54943	Hs.45830	ENSG00000DNACJ28	C2orf155	DnaJ	heat protein-coding	
chr22-40f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr22	40958713	40959964	+	0	NA	intron (Nintron (N	7960	NM_01424E	9978	Hs.47494	ENSG00000RBI1	BA554C2	ring-box	protein-coding	
chr22-42f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr22	42605559	42607231	+	0	NA	intron (NALuJo SIN	8488	NR_10382C	84271	Hs.50580	ENSG00000POLDIP3	PDIP3 PD1	DNA polyn	protein-coding	
chr3-283f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr3	28335753	28337730	+	0	NA	exon (NM_exon (NM	-11980	NM_00104C	152098	Hs.51063	ENSG00000ZCWPW2	ZCW2	zinc fing	protein-coding	
chr3-489f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr3	48961733	48963225	+	0	NA	intron (Nintron (N	-27429	NM_00103E	54681	Hs.65494	ENSG00000P4HTM	EGLN4 HIF	prolyl 4-	protein-coding	
chr3-142f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr3	1.42E+08	1.42E+08	+	0	NA	intron (NALuSx SIN	11576	NM_00103E	256356	Hs.13590	ENSG00000CGK5	-	glycerol	protein-coding	
chr3-172f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	32131	NM_00113E	64778	Hs.74488	ENSG00000FNDC3B	FAD104 PF	fibronect	protein-coding	
chr4-731f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr4	73161274	73163066	+	0	NA	intron (NALuJo SIN	60887	NM_00128E	26057	Hs.60120	ENSG00000ANKRD17	GTAR MAS	ankryn r	protein-coding	
chr5-372f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr5	37217972	37219012	+	0	NA	intron (NMER68 LTF	-30554	NR_13426E	1.05E+08	Hs.17099	ENSG00000LOC105374	-	uncharact	ncRNA	
chr5-112f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (NALuSp SIN	16724	NM_152624	167227	Hs.44387	ENSG00000DCP2	NUDT20	decapping	protein-coding	
chr5-176f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr5	1.76E+08	1.76E+08	+	0	NA	intron (Nintron (N	-8801	NM_00125E	51491	Hs.69628	ENSG00000NOP16	HSPC111 FNOP16	nucprotein-coding	R-PTP-ka	protein t protein-coding
chr6-128f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr6	1.28E+08	1.28E+08	+	0	NA	intron (N(T)n Simp	123291	NM_001291	5796	Hs.15591	ENSG00000PTPRK	-	uncharact	ncRNA	
chr6-136f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr6	1.37E+08	1.37E+08	+	0	NA	intron (NALuSx SIN	66255	NR_12585E	1.02E+08	Hs.66651	ENSG00000LOC10192E	-	uncharact	ncRNA	
chr8-477f	5.89748	-0.44293	0.949299	-0.46658	0.640797	0.981636	chr8	47796745	47800872	+	0	NA	intron (Nintron (N	-60644	NM_00519E	1052	Hs.44082	ENSG00000CEBPD	C/EBP-de	CCAAT	enh protein-coding	
chr11-11f	8.383839	0.376606	0.807471	0.466402	0.640928	0.981636	chr11	1.1E+08	1.1E+08	+	0	NA	exon (NM_exon (NM	72036	NM_03339C	85463	Hs.37628	ENSG00000ZC3H12C	MCPIP3	zinc fing	protein-coding	
chr17-21f	8.383839	0.376606	0.807471	0.466402	0.640928	0.981636	chr17	21313333	21313675	+	0	NA	exon (NM_exon (NM	25468	NM_00275E	5606	Hs.51401	ENSG00000MAP2K3	MAPK3 ME	mitogen-ε	protein-coding	
chr17-42f	8.383839	0.376606	0.807471	0.466402	0.640928	0.981636	chr17	42685059	42686115	+	0	NA	intron (NMIRc SINE	3056	NM_00363E	8506	Hs.40873	ENSG00000CNTNAP1	CASPR KCH	contacti	protein-coding	
chr20-16f	8.383839	0.376606	0.807471	0.466402	0.640928	0.981636	chr20	16740364	16740987	+	0	NA	intron (Nintron (N	-7678	NM_020157	56914	Hs.41119	ENSG00000OTOR	FDP MI	lotorapli	protein-coding	
chr4-701f	8.383839	0.376606	0.807471	0.466402	0.640928	0.981636	chr4	7011197	7011277	+	0	NA	intron (NMIRb SINE	23954	NM_00128E	57533	Hs.51861	ENSG00000TBC1D14	-	TBC1	dom protein-coding	
chr17-41f	8.23951	-0.26581	0.570118	-0.46624	0.641041	0.981636	chr17	41689500	41692900	+	0	NA	3' UTR (N3' UTR (N	2360	NM_005801	10209	Hs.15058	ENSG00000EIF1	A121 EIF	eukaryot	protein-coding	
chr16-58f	8.070739	-0.39703	0.851731	-0.46615	0.641111	0.981636	chr16	58194555	58194754	+	0	NA	intron (Nintron (N	3452	NM_00189E	1459	Hs.82201	ENSG00000CSNK2A2	CK2A2 CK2	casein	protein-coding	
chr17-20f	13.11658	0.310021	0.665613	0.465767	0.641382	0.981636	chr17	20257566	20258664	+	0	NA	intron (Nintron (N	-63059	NR_02338C	348254	Hs.46247	ENSG00000CCDC144C	CCDC144C	coiled-c	pseudo	
chr19-57f	11.39988	-0.32549	0.698936	-0.46659	0.641435	0.981636	chr19	57841061	57841512	+	0	NA	exon (NM_exon (NM	-8573	NM_00328E	84914	Hs.64259	ENSG00000ZNF587	ZF6	zinc fing	protein-coding	
chr6-328f</																						



chr16-31 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr16	31037390	31037714	+	0	NA	intron (NAuSc SIN	3994 NM_004604	6810 Hs. 83734 NM_004604	ENSG000003STX4	STX4A p3ε syntaxin protein-coding
chr17-195 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr17	19950900	19952191	+	0	NA	intron (NSVA_B Ret	26283 NM_007202	11216 Hs. 642676 NM_007202	ENSG000003AKAP10	AKAP-10 A-kinase protein-coding
chr18-265 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr18	2691394	2691837	+	0	NA	intron (NLTR67B LI	35728 NM_015295	23347 Hs. 8118 NM_015295	ENSG000003SMCHD1	BAMS FSH structure protein-coding
chr2-1577 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	70088 NM_001347	90 Hs. 470316 NM_001110	ENSG000003ACVR1	ACTR1 ACV activin β protein-coding
chr20-135 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr20	1351653	1352527	+	0	NA	intron (NLIM3 LIN	-22951 NM_080498	27111 Hs. 657015 NM_015685	ENSG000003SDCBP2	SITAC1 S1 syndecan protein-coding
chr6-2825 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr6	28283860	28284632	+	0	NA	intron (Nintron (N	2709 NM_032507	84547 Hs. 144527 NM_032507	ENSG000003PGBD1	HUCEP-4 SpiggyBac protein-coding
chr7-1405 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (NAuJ SINE	52416 NM_001362	84255 Hs. 446021 NM_032295	ENSG000003SLC37A3	- solute cε protein-coding
chr15-735 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr15	73949499	73949711	+	0	NA	intron (Nintron (N	-21357 NR_040066	1E+08 Hs. 599785 NR_040066	ENSG000003LOXL1-AS1	- LOXL1 antcRNA
chr19-240 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr19	24094370	24094933	+	0	NA	intron (NLIPREC2 I	7464 NM_001275	9534 Hs. 434406 NM_004875	ENSG000003ZNF254	BZMF-5 HE zinc fing protein-coding
chr13-111 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	12869 NM_001255	8858 Hs. 1011 NM_003891	ENSG000003PROZ	PZ protein-z protein-coding
chr3-1415 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr3	1.42E+08	1.42E+08	+	0	NA	intron (Nigger18a	35514 NM_001675	483 Hs. 477785 NM_001675	ENSG000003ATP1B3	ATPB-3 CAT protein-z protein-coding
chr9-1141 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	-19335 NR_030255	619556 NR_030255	ENSG000003MIR455	MIRN455 microRNA ncRNA
chr1-2306 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	intron (N(TATT)n S	33134 NM_007357	22796 Hs. 21180C NM_007357	ENSG000003COG2	CDG2Q LDL component protein-coding
chr14-501 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr14	50160658	50161154	+	0	NA	intron (NAuJb SIN	-44334 NR_049738	79609 Hs. 558541 NM_024555	ENSG000003VCPKMT	C14orf138 valosin c protein-coding
chr3-1952 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr3	1.95E+08	1.95E+08	+	0	NA	intron (NMER2 DNA	-17767 NM_152531	152002 Hs. 478741 NM_152531	ENSG000003XXYLT1	C3orf21 xyloside protein-coding
chr7-1314 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (NAuSx SIN	83768 NM_001321	4289 Hs. 44693 NM_013255	ENSG000003MKLN1	TWA2 muskelin protein-coding
chr1-227 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr1	2.27E+08	2.27E+08	+	0	NA	intron (NLIMEg LIN	143702 NM_020247	56997 Hs. 118241 NM_020247	ENSG000003COQ8A	ADCK3 ARC coenzyme protein-coding
chr20-381 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr20	28158312	28161842	+	0	NA	intron (Nintron (N	5193 NM_001322	7052 Hs. 517035 NM_004615	ENSG000003TGM2	TG(C) TG transglut protein-coding
chr22-425 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr22	42840426	42841112	+	0	NA	intron (NAuJo SIN	16504 NM_014577	26286 Hs. 685225 NM_014577	ENSG000003ARFGAP3	ARFGAP1 ADP ribos protein-coding
chr9-471 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr9	4716012	4719834	+	0	NA	intron (Nintron (N	8704 NM_001195	50808 Hs. 732022 NM_016285	ENSG000003CAK3	AK3L1 ADP adenylatε protein-coding
chr1-4595 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr1	45961465	45962246	+	0	NA	intron (NLIPA5 LIN	9307 NM_001324	23139 Hs. 319481 NM_015115	ENSG000003MAST2	MAST205 microtubul protein-coding
chr1-2195 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (Nintron (N	-56608 NR_046437	55532 Hs. 284455 NM_018715	ENSG000003SLC30A10	HMDPC HMD solute cε protein-coding
chr10-745 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr10	74838994	74839725	+	0	NA	intron (NAuS2 SI	12759 NM_001377	23522 Hs. 35758 NM_012335	ENSG000003KAT6B	GTPTS MOF lysine ac protein-coding
chr14-584 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr14	58418615	58421826	+	0	NA	intron (NLIMD1 LI	7022 NM_001304	26520 Hs. 440525 NM_012465	ENSG000003TIMM9	TIM9 TIMε translocε protein-coding
chr17-735 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr17	7382277	7420112	+	0	NA	intron (Nintron (N	7523 NM_024792	79850 Hs. 154395 NM_024792	ENSG000003TLC3DA	CT120 FAM TLC doma protein-coding
chr17-215 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr17	75694859	75695463	+	0	NA	intron (NMER20 DNA	-26298 NM_001321	3691 Hs. 632225 NM_000215	ENSG000003ITGB4	CD104 GPI integrin protein-coding
chr19-257 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr19	21752126	21753708	+	0	NA	non-codir non-codir	2172 NR_024525	641367 Hs. 680125 NR_024525	ENSG000003LOC641367	- cyclin Y pseudo
chr2-2635 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	26389336	26391586	+	0	NA	non-codir non-codir	-11459 NM_145035	92749 Hs. 393714 NM_145035	ENSG000003DRC1	C2orf39 Cdynein rε protein-coding
chr2-305 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	30563097	30563750	+	0	NA	intron (Nintron (N	116177 NM_001304	235558 Hs. 468045 NM_182551	ENSG000003LCLAT1	LAPGAT8 β lysolacardi protein-coding
chr2-1325 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-58770 NR_135572	1.02E+08 Hs. 680114 NR_135572	ENSG000003NCKAP5-AS	- NCKAP5 arncRNA
chr2-1355 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	-53223 NM_005915	4175 Hs. 444115 NM_005915	ENSG000003MCM6	MCG40308 minichron protein-coding
chr20-195 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr20	19945893	19946556	+	0	NA	intron (Nintron (N	56658 NM_018995	54453 Hs. 472272 NM_018995	ENSG000003RIN2	MACS RRSε Ras and F protein-coding
chr3-1283 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr3	12831518	12832451	+	0	NA	intron (Nintron (N	8466 NM_001007	6161 Hs. 265174 NM_000994	ENSG000003RPL32	L32 PPP9ε ribosomal protein-coding
chr3-1415 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr3	1.42E+08	1.42E+08	+	0	NA	intron (NLIMC4a LI	63446 NM_001305	5922 Hs. 98445 NM_006505	ENSG000003RASA2	GAP1M RAS p21 ε protein-coding
chr4-4755 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr4	47569295	47569722	+	0	NA	intron (Nintron (N	-83161 NR_107022	1.02E+08 NR_107022	ENSG000003MIR8053	hsa-mir-ε microRNA ncRNA
chr4-1685 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (Nintron (N	-41702 NR_017631	55601 Hs. 591715 NM_017631	ENSG000003DDX60	- DEX/H-ε protein-coding
chr5-1491 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr5	1.49E+08	1.49E+08	+	0	NA	intron (NAuJb SIN	4137 NM_001377	22885 Hs. 49688 NM_014945	ENSG000003ABLIM3	HMFN1661 actin bir protein-coding
chr7-6705 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	67057583	67058187	+	0	NA	intron (NLIME2 LIN	56512 NR_039794	1.01E+08 NR_039794	ENSG000003MIR4650-2	- microRNA ncRNA
chr7-7424 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	74248253	74249648	+	0	NA	intron (Nintron (N	5449 NM_181471	5982 Hs. 647062 NM_002914	ENSG000003RFC2	RFC40 replicatε protein-coding
chr7-9462 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	94622265	94622774	+	0	NA	intron (NAuS2 SI	33614 NM_001095	8910 Hs. 371195 NM_003915	ENSG000003SGCE	DYT11 ESC sarcoglyc protein-coding
chr7-9825 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	98260354	98261783	+	0	NA	IntergeniAluS2 SIN	-8832 NM_015395	25851 Hs. 592281 NM_015395	ENSG000003TECP1	- tectonin protein-coding
chr7-1355 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	1.36E+08	1.36E+08	+	0	NA	exon (NM exon (NM	-45364 NM_001133	647087 Hs. 200022 NM_001133	ENSG000003STMP1	C7orf73 Fshort trε protein-coding
chr7-1515 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	3829 NR_030407	768213 NR_030407	ENSG000003MIR671	MIRN671 microRNA ncRNA
chr8-6155 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr8	61533300	61534624	+	0	NA	intron (NAuSp SIN	155849 NM_001164	444 Hs. 332422 NM_004315	ENSG000003ASPH	AAH BAH Caspartatε protein-coding
chr8-1422 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr8	1.43E+08	1.43E+08	+	0	NA	exon (NM exon (NM	4887 NM_001275	8629 Hs. 535905 NM_003724	ENSG000003JRK	JH8 jerky Jrk heliε protein-coding
chr2-1325 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (NLIMC3 LIN	-58278 NR_110294	1.02E+08 Hs. 661917 NR_110294	ENSG000003NCKAP5-AS	- NCKAP5 arncRNA
chr2-2061 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr2	2.06E+08	2.06E+08	+	0	NA	promoter-promoter-	71 NR_002585	26798 NR_002585	ENSG000003SNORD51	RNU51 U51 small nuc snoRNA
chr6-573 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr6	57325421	57329898	+	0	NA	intron (Nintron (N	10029 NM_000947	5558 Hs. 654585 NM_000947	ENSG000003PRIM2	PRIM2A pε DNA nucε protein-coding
chr13-244 5.213431	0.465375	1.002892	0.464033	0.642624	0.981636	chr13	24458086	24458786	+	0	NA	intron (NAuJb SIN	54342 NM_006437	143 Hs. 744855 NM_006437	ENSG000003PARP4	ADPRT-3 ε poly (ADP- protein-coding
chr1-5514 5.213431	0.465375	1.002892	0.464033													



chr19-211 8.929424	0.362651	0.786361	0.461177	0.644672	0.981636	chr19	21180522	21180769	+	0 NA	intron (N LIMB2 LIN	38605 NM_133473	170959 Hs. 156255NM_133473	ENSG000002ZNF431	-	zinc fingerprotein-coding
chr19-422 8.929424	0.362651	0.786361	0.461177	0.644672	0.981636	chr19	42287649	42291154	+	0 NA	exon (NM exon (NM	4736 NM_015122	23152 Hs. 388233NM_015122	ENSG000002C1C	-	MRD45 capicua protein-coding
chr4-3208 8.929424	0.362651	0.786361	0.461177	0.644672	0.981636	chr4	3208815	3210758	+	0 NA	intron (N intron (N	-34583 NM_001330	345222 Hs. 442291NM_001012	ENSG000002MSANTD1	-	C4orf44 Myb/SANT protein-coding
chr5-138 8.929424	0.362651	0.786361	0.461177	0.644672	0.981636	chr5	1.39E+08	1.39E+08	+	0 NA	intron (N intron (N	50370 NM_001322	1495 Hs. 445981NM_001903	ENSG000002CTNNA1	-	CAP102 MYC catenin ε protein-coding
chr13-772 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr13	77220849	77221369	+	0 NA	intron (N intron (N	105985 NM_001507	23077 Hs. 591221NM_015057	ENSG000002MYCBP2	-	Myc-bp2 MYC band protein-coding
chr14-102 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr14	1.02E+08	1.02E+08	+	0 NA	intron (N intron (N	54432 NM_001348	122416 Hs. 432945NM_152322	ENSG000002ANKRD9	-	ankyrin 1 protein-coding
chr3-3908 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr3	39085849	39086873	+	0 NA	non-cod non-codir	21266 NM_001278	64689 Hs. 721945NM_031899	ENSG000002GORASP1	-	GOLPH5 GF golgi ree protein-coding
chr5-7045 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr5	70431093	70431999	+	0 NA	intron (N Tigger I	16172 NM_001515	2966 Hs. 191355NM_001515	ENSG000002GTF2H2	-	BTF2 BTF2 general protein-coding
chr6-5308 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr6	53007289	53009675	+	0 NA	intron (N AluS2 SIN	12862 NR_001445	125050 NR_001445	ENSG000002CRN7SK	-	7SK RNA compc snRNA
chr6-1522 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr6	1.52E+08	1.52E+08	+	0 NA	intron (N intron (N	-15763 NM_001347	23345 Hs. 12967 NM_015293	ENSG000002SYNE1	-	8B ARCA1 spectrin protein-coding
chr7-6708 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chr7	67003712	67004563	+	0 NA	intron (N MER65A LI	7304 NM_018264	55253 Hs. 520917NM_018264	ENSG000002TYW1	-	RSAFD1 TY tRNA-yW s protein-coding
chrX-4508 5.221289	0.462452	1.002854	0.461136	0.644701	0.981636	chrX	45084710	45086032	+	0 NA	intron (N Tigger5b	115505 NM_176815	79742 Hs. 98321 NM_024685	ENSG000002DIPK2B	-	4930578C1 divergent protein-coding
chr10-177 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr10	7769332	7769844	+	0 NA	intron (N intron (N	18405 NM_012311	22944 Hs. 397915NM_012311	ENSG000002KIN	-	BTDC KIN1 kin17 DN <sup>β</sup> protein-coding
chr10-766 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr10	16762825	16763512	+	0 NA	intron (N intron (N	54256 NM_012425	6251 Hs. 524161NM_012425	ENSG000002CRSU1	-	RSP-1 Ras suppr protein-coding
chr12-106 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr12	1.06E+08	1.06E+08	+	0 NA	intron (N LIPA3 LIN	13777 NM_001160	55703 Hs. 62696 NM_018082	ENSG000002POLR3B	-	C128 HLD <sup>ε</sup> RNA polyn protein-coding
chr13-771 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr13	77186896	77187954	+	0 NA	intron (N intron (N	111911 NR_046711	1.01E+08 Hs. 569288NR_046711	ENSG000002MYCBP2-AS	-	MYCBP2 arncRNA
chr16-281 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr16	28171719	28173504	+	0 NA	intron (N intron (N	39354 NM_015171	23214 Hs. 460465NM_015171	ENSG000002XPO6	-	EXP6 RANE exportin protein-coding
chr16-691 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr16	69698206	69699945	+	0 NA	3' UTR (N3' UTR (N	9600 NR_145753	1.1E+08 NR_145753	SNORD13H	-	small nucsnRNA
chr2-4228 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr2	42286386	42287401	+	0 NA	intron (N intron (N	73145 NR_134948	9167 Hs. 339635NM_004715	ENSG000002COX7A2L	-	COX7AR CC cytochron protein-coding
chr2-2381 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr2	2.38E+08	2.38E+08	+	0 NA	intron (N AluSq2 SI	12222 NM_001291	151176 Hs. 24951 NM_152521	ENSG000002ERFE	-	C1QTNF15 erythrof protein-coding
chr3-133 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr3	1.34E+08	1.34E+08	+	0 NA	intron (N intron (N	43111 NM_001282	55573 Hs. 518265NM_017545	ENSG000002CDV3	-	H41 CDV3 homc protein-coding
chr3-1841 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr3	1.84E+08	1.84E+08	+	0 NA	intron (N AluS2 SI	3038 NM_003907	8893 Hs. 283551NM_003907	ENSG000002EIF2B5	-	CACH CLE eukaryot protein-coding
chr4-182 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr4	1820692	1820988	+	0 NA	intron (N AluSx1 SI	27528 NM_001163	2261 Hs. 1420 NM_000142	ENSG000002FGFR3	-	ACH CD33 <sup>ε</sup> fibroblas protein-coding
chr6-182 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr6	18253331	18254220	+	0 NA	intron (N AluJo SIN	10755 NM_001134	7913 Hs. 484813NM_003472	ENSG000002DEK	-	D6S231E DEK protc protein-coding
chr6-5656 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr6	56568204	56568741	+	0 NA	exon (NM exon (NM	74417 NM_015548	667 Hs. 604915NM_001723	ENSG000002CST	-	BP240 BP <sup>α</sup> dystonin protein-coding
chr7-143 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr7	1.44E+08	1.44E+08	+	0 NA	intron (N L2a LINE	3865 NM_001363	28596 Hs. 743565NM_173675	ENSG000002TCAP2	-	FAM115C FTRPM8 che protein-coding
chr8-5621 5.889622	-0.44081	0.956519	-0.46085	0.644908	0.981636	chr8	56218238	56219019	+	0 NA	non-cod non-codir	6839 NM_001011	79145 Hs. 436913NM_024300	ENSG000002CHHD7	-	COX23 coiled-cc protein-coding
chr14-526 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr14	52645285	52646363	+	0 NA	intron (N AluSx SIN	49734 NM_014584	30001 Hs. 525335NM_014584	ENSG000002ERO1A	-	ERO1-L EF endoplasm protein-coding
chr15-596 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr15	59637962	59639112	+	0 NA	3' UTR (N3' UTR (N	18768 NM_001322	2958 Hs. 512934NM_004492	ENSG000002GTF2A2	-	HsT18745 nervon t protein-coding
chr15-756 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr15	75679685	75683254	+	0 NA	intron (N intron (N	31379 NM_001897	1464 Hs. 513044NM_001897	ENSG000002CSGP4	-	HMW-MAA χ chondroit protein-coding
chr19-131 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr19	13136542	13137492	+	0 NA	intron (N intron (N	13358 NM_001271	8677 Hs. 43812 NM_003765	ENSG000002STX10	-	SYN10 hsysyntaxin protein-coding
chr2-1213 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr2	1.21E+08	1.21E+08	+	0 NA	3' UTR (N3' UTR (N	-55323 NM_014555	29842 Hs. 156471NM_014555	ENSG000002TFCP2L1	-	CRTR1 LBF transcrip protein-coding
chr2-1330 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr2	1.33E+08	1.33E+08	+	0 NA	intron (N AluY SINE	-17428 NM_110294	1.02E+08 Hs. 661917NR_110294	ENSG000002NCKAP5-AS	-	NCKAP5 arncRNA
chr6-995 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr6	99531651	99532545	+	0 NA	3' UTR (N3' UTR (N	11104 NM_001195	1E+08 Hs. 634505NM_001195	ENSG000002CTSD3	-	thiosulf <sup>ε</sup> protein-coding
chr7-325 8.67318	-0.36507	0.792413	-0.46071	0.645005	0.981636	chr7	32554118	32554953	+	0 NA	intron (N intron (N	59246 NM_015060	23080 Hs. 128055NM_015060	ENSG000002AVL9	-	KIAA0241 AVL9 cell protein-coding
chr9-1124 5.25457	0.467288	1.014813	0.460467	0.645181	0.981636	chr9	1.12E+08	1.12E+08	+	0 NA	intron (N MER75B DN	40726 NM_032303	84263 Hs. 59486 NM_032303	ENSG000002HSDL2	-	C9orf99 SHydroxyst protein-coding
chr1-4497 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr1	44976421	44978350	+	0 NA	intron (N LIME2 LIN	9210 NM_020365	8891 Hs. 533545NM_020365	ENSG000002EIF2B3	-	EIF-2B E eukaryot protein-coding
chr15-57 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr15	57252855	57255069	+	0 NA	intron (N intron (N	24695 NR_145748	1.1E+08 NR_145748	ENSG000002SNORD13D	-	small nucsnRNA
chr17-313 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr17	31326170	31327781	+	0 NA	intron (N AluSx1 SI	-5353 NM_001003	2123 Hs. 591195NM_014212	ENSG000002E1Z2A	-	EVDA EVL <sup>ε</sup> ectropic protein-coding
chr2-664 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr2	66463972	66465363	+	0 NA	intron (N intron (N	-24337 NR_046625	1.01E+08 Hs. 734695NR_046625	ENSG000002MEI51-AS2	-	MEI51-AS1 MEI51 antncRNA
chr20-133 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr20	1.33E+08	1.33E+08	+	0 NA	intron (N intron (N	-54270 NR_110294	1.02E+08 Hs. 661917NR_110294	ENSG000002NCKAP5-AS	-	NCKAP5 arncRNA
chr20-573 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr20	57358674	57358873	+	0 NA	3' UTR (N3' UTR (N	725 NM_001190	1E+08 NM_001190	ENSG000002MTRNR2L3	-	HN3 MT-RNR2 protein-coding
chr5-1441 8.624182	-0.36618	0.795537	-0.46029	0.645308	0.981636	chr5	1.44E+08	1.44E+08	+	0 NA	intron (N MamRTE1 I	2625 NM_001271	81555 Hs. 372055NM_030795	ENSG000002YIPF5	-	FinGER5 C yip1 dome protein-coding
chr16-71 8.681038	-0.36657	0.796753	-0.46008	0.645466	0.981636	chr16	71918131	71919076	+	0 NA	intron (N AluSx3 SI	23072 NM_001272	9798 Hs. 232194NM_014761	ENSG000002ISTI	-	CHMP8 OLC ISTI factc protein-coding
chr14-506 8.665322	-0.36358	0.790862	-0.45972	0.645716	0.981636	chr14	50638915	50642482	+	0 NA	intron (N intron (N	27608 NM_021815	60485 Hs. 642842NM_021815	ENSG000002CAV1	-	SUV45 salvador protein-coding
chr14-607 8.665322	-0.36358	0.790862	-0.45972	0.645716	0.981636	chr14	60716079	60718005	+	0 NA	intron (N intron (N	7309 NM_017422	51804 Hs. 97849 NM_017422	ENSG000002SIX4	-	AREC3 SIX homec protein-coding
chr18-68 8.665322	-0.36358	0.790862	-0.45972	0.645716	0.981636	chr18	68696216	68698239	+	0 NA	exon (NM exon (NM	17881 NM_001350	54495 Hs. 440534NM_019022	ENSG000002TMX3	-	PDIA13 TX thioeredo protein-coding
chr2-2267 8.665322	-0.36358	0.790862	-0.45972	0.645716	0.981636	chr2	2.27E+08	2.27E+08	+	0 NA	intron (N intron (N	17620 NM_005544	3667 Hs. 471505NM_005544	ENSG000002IRS1	-	HIRS-1 insulin 1 protein-coding
chr22-24 8.665322	-0.36358	0.790862	-0.45972	0.645716	0.981636	chr22	24364924	24365382	+	0 NA	intron (N AluS2 SIN	23045 NM_001254	23384 Hs. 474384NM_015330	ENSG000002SPECC1L	-	CYLLA GBE sperm ant protein-coding
chr3-122 8.66532																



chr2-1994	8.896143	0.359689	0.784231	0.458651	0.646485	0.981636	chr2	1.99E+08	1.99E+08	+	0	NA	exon (NM_exon (NM_24513 NR_134967	23314	Hs. 516617NM_015266	ENSG000003SATB2	GLSS	SATB home protein-coding		
chr20-37	8.896143	0.359689	0.784231	0.458651	0.646485	0.981636	chr20	37365585	37366327	+	0	NA	intron (NLIME4b LI	19828	NM_198291	6714	Hs. 195656NM_005417	ENSG000003SRC	ASV SRC1 SRC protc protein-coding	
chr11-12	11.84562	-0.31424	0.685155	-0.45864	0.646493	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	TTS (NR_TTS (NR_C	223	NR_003125	85391	NR_003125	ENSG000003SNORD14E	-	small nucsnoRNA
chr7-2618	11.84562	-0.31424	0.685155	-0.45864	0.646493	0.981636	chr7	26187840	26197691	+	0	NA	intron (Nintron (N	7981	NM_002137	3181	Hs. 487774NM_002137	ENSG000003HNRNP2A2B1	HNRNP2A2B1	F hetero gene protein-coding
chr15-43	9.394581	0.357381	0.792445	0.458625	0.646504	0.981636	chr15	43335925	43336224	+	0	NA	intron (NAluJr SIN	5402	NM_001012	161823	Hs. 533913NM_001012	ENSG000003ADAL	-	adenosine protein-coding
chr12-53	9.96374	0.341135	0.744382	0.458279	0.646752	0.981636	chr12	53516456	53517422	+	0	NA	non-codiron-codir	2955	NR_046221	1.01E+08	Hs. 633602NR_046221	ENSG000003LOC100652	-	uncharactncRNA
chr9-125	9.96374	0.341135	0.744382	0.458279	0.646752	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	93805	NM_00133C	26130	NM_00133C	ENSG000003GAPVD1	GAPX5 GAGTPase ac protein-coding	
chr3-4471	9.9226	0.339944	0.74219	0.458028	0.646932	0.981636	chr3	44719857	44722452	+	0	NA	exon (NM_exon (NM_	8452	NM_145044	115560	Hs. 401045NM_145044	ENSG000003ZNF501	ZNF ZNF52 zinc fing protein-coding	
chr3-1566	9.9226	0.339944	0.74219	0.458028	0.646932	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	20297	NM_001184	25976	Hs. 744055NM_015505	ENSG000003TIPARP	ARTD14 P TCCD indt protein-coding	
chr9-125	9.9226	0.339944	0.74219	0.458028	0.646932	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	82789	NM_153266	79987	Hs. 522334NM_153266	ENSG000003SVEP1	C9orf13 Cushi, v protein-coding	
chr1-1104	9.412146	0.363691	0.794869	0.457824	0.647079	0.981636	chr1	1.84E+08	1.84E+08	+	0	NA	intron (NAluSz SIN	55856	NM_000433	4688	Hs. 587555NM_000433	ENSG000003NCF2	NCF-2 NOA neurotrophin protein-coding	
chr1-778	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr1	7789384	7791577	+	0	NA	intron (NTHE1C LTF	6051	NM_00128E	8863	Hs. 162202NM_016831	ENSG000003PER3	FASPS3 G period ciprotein-coding	
chr1-1554	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr1	15547246	15548086	+	0	NA	intron (NAluSz SIN	5500	NR_135613	1.07E+08	NR_135613	ENSG000003SCARNA21E	-	small Ca;ncRNA
chr1-192	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr1	19236589	19240318	+	0	NA	intron (Nintron (N	13041	NM_001271	23065	Hs. 439202NM_015047	ENSG000003EMC1	CAV1PMR BER membr protein-coding	
chr1-216	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr1	21693100	21693512	+	0	NA	intron (Nintron (N	-23949	NM_00135C	5909	Hs. 148175NM_002885	ENSG000003RAP1GAP	RAP1GAP1 FRAP1 GTPe protein-coding	
chr1-2201	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (Nintron (N	7230	NR_03170E	1E+08	NR_03170E	ENSG000003MIR664A	MIR664 MimicroRNA ncRNA	
chr16-841	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr16	84129183	84129707	+	0	NA	intron (Nintron (N	-12503	NM_003791	8720	Hs. 75890	NR_003791	ENSG000003MBTFS1	PCSK8 SIF membrane protein-coding
chr17-15	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr17	15639427	15641998	+	0	NA	intron (Nintron (N	-121008	NM_001282	374286	Hs. 548021NM_006382	ENSG000003CDRT1	C17ORF1 CMT1A dup protein-coding	
chr19-21C	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr19	2101310	2102500	+	0	NA	3' UTR (N3' UTR (N	4990	NM_00103E	113177	Hs. 424045NM_052875	ENSG000003IZUM04	C19orf36 IZUMO fan protein-coding	
chr19-10	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr19	10627401	10640480	+	0	NA	intron (NAluSj SIN	8387	NR_02002E	57153	Hs. 534566NM_020425	ENSG000003SLC44A2	CTL2 PP12 solute ce protein-coding	
chr2-8617	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr2	86178432	86179763	+	0	NA	intron (N(AAAACA)r	14011	NR_03993E	1.01E+08	NR_03993E	ENSG000003MIR4779	-	microRNA ncRNA
chr20-381	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr20	38135347	38140382	+	0	NA	TTS (NM_TTS (NM_I	27406	NM_00132E	7052	Hs. 517033NM_004613	ENSG000003TGM2	TG(C) TCG transglut protein-coding	
chr3-524	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr3	52403180	52406604	+	0	NA	intron (Nintron (N	5116	NM_00465E	8314	Hs. 106674NM_00465E	ENSG000003BAP1	HUCEP-13 BRCA1 ass protein-coding	
chr8-431	9.43387	0.349077	0.762651	0.457716	0.647156	0.981636	chr8	43160321	43166760	+	0	NA	intron (NAluSg7 SI	23076	NM_15231E	138050	Hs. 600384NM_15231E	ENSG000003HGSNAT	HGNAT MPS heparan-e protein-coding	
chr9-703	9.109213	-0.35659	0.779196	-0.45764	0.647211	0.981636	chr9	70327963	70329158	+	0	NA	intron (NMSTA-int	69582	NM_01511C	23137	Hs. 534185NM_01511C	ENSG000003SMC5	SMC5L1 structure protein-coding	
chr22-317	9.109213	-0.35659	0.779196	-0.45764	0.647211	0.981636	chr22	31700144	31701681	+	0	NA	intron (Nintron (N	-38348	NM_00132E	23761	Hs. 420555NM_014335	ENSG000003PISD	DJ858B16 phosphatiprotein-coding	
chr11-63	8.342699	0.375097	0.820093	0.457383	0.647396	0.981636	chr11	63854052	63854382	+	0	NA	intron (N(TG)n SIN	15107	NM_00116E	2011	Hs. 567261NM_004954	ENSG000003MARK2	EMK-1 EMK microtub protein-coding	
chr15-50	8.342699	0.375097	0.820093	0.457383	0.647396	0.981636	chr15	50944424	50945018	+	0	NA	non-codiron-codir	592	NR_027642	1E+08	Hs. 730493NR_027642	DCAF13P3	-	DBD1 and pseudo
chr8-871	8.350557	0.373297	0.816159	0.457383	0.647396	0.981636	chr8	38119551	38119780	+	0	NA	intron (NAluSz SIN	13872	NM_00110E	9070	Hs. 512533NM_004674	ENSG000003ASH2L	ASH2 ASH2ASH2 like protein-coding	
chr7-7764	9.101355	-0.35509	0.776433	-0.45734	0.647427	0.981636	chr7	77641755	77642179	+	0	NA	IntergeniAluSp SIN	54298	NR_134254	1.01E+08	Hs. 72451	NR_038361	ENSG000003APTR	RSBN1L-ASAlu-medi ncRNA
chr10-114	9.392731	0.347872	0.760896	0.457188	0.647536	0.981636	chr10	1.15E+08	1.15E+08	+	0	NA	intron (NMER6B LI	4969	NM_13916E	142940	Hs. 21187	NR_13916E	ENSG000003TRUB1	PUS4 TruB pset protein-coding
chr12-11	9.392731	0.347872	0.760896	0.457188	0.647536	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	24831	NM_002567	5037	Hs. 433862NM_002567	ENSG000003PEBP1	HCNP HCNF phosphatiprotein-coding	
chr3-256	9.392731	0.347872	0.760896	0.457188	0.647536	0.981636	chr3	25608895	25609098	+	0	NA	intron (Nintron (N	55376	NM_00106E	7155	Hs. 475733NM_00106E	ENSG000003TOP2B	TOP2B TbDNA topoiprotein-coding	
chr11-37	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr11	3792443	3794784	+	0	NA	intron (Nintron (N	3933	NR_157591	4928	Hs. 524755NM_005387	ENSG000003CNP98	ADIR2 NUF nucleopor protein-coding	
chr11-85	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr11	85991797	85995742	+	0	NA	intron (Nintron (N	75315	NM_00716E	8301	Hs. 163893NM_00716E	ENSG000003PICALM	CALM CLTF phosphatiprotein-coding	
chr13-11	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (NTigger3b	35039	NM_00134E	55002	Hs. 317593NM_01790E	ENSG000003MTC03	C13orf11 transmem protein-coding	
chr15-43	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr15	43020256	43023021	+	0	NA	intron (NMER2 DNA	84400	NM_17491E	197131	Hs. 591121NM_17491E	ENSG000003CUBR1	JBS ubiquitin protein-coding	
chr18-54	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr18	54158362	54159778	+	0	NA	intron (Nintron (N	63242	NR_00297C	677819	Hs. 655869NR_00297C	ENSG000003SNORA37	ACA37 small nucsnoRNA	
chr2-546	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr2	54650096	54651174	+	0	NA	intron (Nintron (N	-73967	NM_00103E	400954	Hs. 656692NM_00103E	ENSG000003EML6	-	EMAP like protein-coding
chr3-1327	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	intron (NAluSc SIN	-3910	NR_002811	348808	Hs. 586111NR_002811	ENSG000003PNHP3-AS1	NCRNAA0011NHP3 antncRNA	
chr3-1837	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (NAluSp SIN	49131	NR_046727	1.01E+08	NR_046727	YEATS2-AS-	YEATS2 arncRNA	
chr5-1381	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr5	13819535	13820263	+	0	NA	intron (NAluSp SIN	124581	NM_00136E	1767	Hs. 212366NM_00136E	ENSG000003DNAH5	CILD3 DNA dynein ap protein-coding	
chr5-1764	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr5	1.76E+08	1.77E+08	+	0	NA	intron (NAluJb SIN	39339	NM_014901	22838	Hs. 434885NM_014901	ENSG000003CRNF44	-	ring fing protein-coding
chr6-5662	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr6	56627297	56632281	+	0	NA	intron (Nintron (N	13100	NM_01554E	667	Hs. 604915NM_001725	ENSG000003DST	BP240 BP dystonin protein-coding	
chr6-854	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr6	85486907	85488485	+	0	NA	intron (NAluJr SIN	37613	NM_00252E	4907	Hs. 153952NM_00252E	ENSG000003CNT5E	CALJA CD75-e nuclec protein-coding	
chr7-3821	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr7	38217120	38217624	+	0	NA	intron (Nintron (N	39127	NM_03201E	83930	Hs. 309755NM_03201E	ENSG000003STARD3NL	MENTHO STARD3 N- protein-coding	
chr9-9214	8.657464	-0.36206	0.792059	-0.45711	0.647593	0.981636	chr9	92147675	92149079	+	0	NA	intron (Nintron (N	6910	NR_027341	158314	Hs. 149944NR_027341	LINC00475	C9orf44 long intncRNA	
chr10-61	8.196007	-0.37726	0.825332	-0.45711	0.647603	0.981636	chr10	61958184	61958805	+	0	NA	intron (NAluSg4 SI	56818	NM_03219E	84159	Hs. 535297NM_03219E	ENSG000003ARID5B	DESRT MRFA7 rich protein-coding	
chr11-12	8.196007	-0.37726	0.825332	-0.45711	0.647603	0.981636	chr11	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-7343	NR_13718E	399599	Hs. 44098	NR_02443C	ENSG000003MIR100HG	AGD1 lincmir-100 lncRNA
chr5-154	8.196007	-0.37726	0.825332	-0.45711	0.647603	0.981636	chr5	1.55E+08	1.55E+08	+	0	NA	intron (NLM3 LINE	7356	NM_001301	9337	Hs. 26703	NM_00477E	ENSG000003CNOT8	CAF1 CAL1 CCR4-NOT protein-coding
chr8-128	8.196007	-0.37726	0.825332	-0.45711	0.647603	0.981636	chr													



chr3-585 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr3	58500862	58502489	+	0	NA	3' UTR (N3' UTR (N	3310 NM_153331	200845	Hs.13982	NM_153331	ENSG00000CKTD6	KCASH3	potassium protein-coding
chr3-1556 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr3	1.56E+08	1.56E+08	+	0	NA	intron (Nintron (N	66349 NM_003875	8833	Hs.591314	NM_003875	ENSG00000GMPS	GATD7	guanine protein-coding
chr3-1972 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (NLM3f LIN	44685 NR_039966	1.01E+08	NR_039966	ENSG00000CIR4797	-	microRNA ncRNA	
chr4-534 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr4	53434692	53435842	+	0	NA	intron (Nintron (N	57614 NM_001134	81608	Hs.555109	NM_001134	ENSG00000FIP1L1	FIP1 Rhe factor i protein-coding	
chr4-1228 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr4	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	33548 NM_007088	11162	Hs.558458	NM_007088	ENSG00000NUD76	ASF62 FCnudi hycprotein-coding	
chr5-7861 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr5	78618522	78619257	+	0	NA	intron (Nintron (N	29883 NM_005775	10184	Hs.79299	NM_005775	ENSG00000LHFFL2	LHFFL2 tetprotein-coding	
chr6-3072 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr6	30726251	30727622	+	0	NA	TTS (NM_CTS (NM_C	5433 NM_001293	203068	Hs.63648C	NM_178014	ENSG00000TUBB	CDC6M CS tubulin t protein-coding	
chr8-4796 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr8	47962387	47965146	+	0	NA	intron (Nintron (N	2825 NM_182746	4173	Hs.460184	NM_005914	ENSG00000MCM4	CDC21 CDCminichron protein-coding	
chr8-1023 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (NMIR SINE	73900 NM_001282	51366	Hs.49244E	NM_015902	ENSG00000CUBR5	DD5 EDD Eubiquitin protein-coding	
chr9-9664 5.915046	-0.4325	0.952885	-0.45388	0.649914	0.981636	chr9	96644186	96645540	+	0	NA	intron (Nintron (N	10454 NM_153698	195827	Hs.44640	NM_153698	ENSG00000PRXL2C	AAED1 C9cperoxidase protein-coding	
chr1-1704 8.432836	0.375705	0.827943	-0.453782	0.649986	0.981636	chr1	1704046	1705094	+	0	NA	exon (NM exon (NM	4631 NR_002946	8511	Hs.67176C	NR_002946	ENSG00000MMP23A	MIFR MIFF matrix pseudo	
chr1-2582 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr1	25826048	25834614	+	0	NA	intron (Nintron (N	-6725 NR_024498	646471	Hs.727271	NR_024498	LOC646471	-	uncharactericrNA
chr1-2048 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr1	40487041	40493718	+	0	NA	intron (Nintron (N	13089 NM_00132C	339559	Hs.43438E	NM_198494	ENSG00000ZFP69	ZFP69A ZFP699 zfp protein-coding	
chr1-4045 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr1	2.05E+08	2.05E+08	+	0	NA	intron (Nintron (N	32320 NM_00239C	4194	Hs.49749E	NM_00239C	ENSG00000MMD4	HDMX MDM4MDM4 reg protein-coding	
chr12-102 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr12	1.02E+08	1.02E+08	+	0	NA	intron (NSVA_A Ret	-27281 NM_001301	51019	Hs.40569E	NM_01605C	ENSG00000WASHC3	CCDC53 CCWASH comp protein-coding	
chr16-111 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr16	11551343	11557248	+	0	NA	intron (Nintron (N	-27048 NM_00137C	400499	Hs.459937	NM_00137C	ENSG00000LOC400499	-	putative protein-coding
chr16-572 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr16	57250997	57253336	+	0	NA	exon (NM exon (NM	6907 NM_01210C	23568	Hs.63287E	NM_01210C	ENSG00000MRL2BP	BART BARTADP ribos protein-coding	
chr19-458 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr19	45898260	45900147	+	0	NA	intron (NAluSp SIN	3410 NM_001012	339344	Hs.51547E	NM_001012	ENSG00000CARYLP	P42pop Myb relat protein-coding	
chr19-484 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr19	48472892	48475712	+	0	NA	exon (NM exon (NM	4933 NM_00422E	9266	Hs.144011	NM_00422E	ENSG00000CYTH2	ARNO CTS1 cytohesin protein-coding	
chr2-2019 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (NLM2D LIN	-16610 NM_03306E	58538	Hs.63085	NM_03306E	ENSG00000MPP4	ALS2CR5 Lmembrane protein-coding	
chr2-2164 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (NMSTB LTR	36389 NM_001127	50485	Hs.516674	NM_01414C	ENSG00000SMARCAL1	HARP HHA4 SWI/SNF protein-coding	
chr9-8627 9.938316	0.336864	0.742586	0.453636	0.650091	0.981636	chr9	86270097	86272264	+	0	NA	intron (NTiger3c	11358 NM_03094C	81689	Hs.449291	NM_03094C	ENSG00000TSCA1	HBLD2 ISA iron-sulf protein-coding	
chr1-3512 12.30708	-0.30608	0.67476	-0.45361	0.65011	0.981636	chr1	35175203	35191897	+	0	NA	3' UTR (N3' UTR (N	9685 NR_13670E	6421	Hs.355934	NM_00506E	ENSG00000SFPQ	POMP100 Fsplicing protein-coding	
chr12-129 13.134636	-0.35116	0.774222	-0.45356	0.650145	0.981636	chr12	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	-12448 NR_03971E	1.01E+08	NR_03971E	ENSG00000MIR4498	mir-4498 microRNA ncRNA		
chr19-108 9.134636	-0.35116	0.774222	-0.45356	0.650145	0.981636	chr19	40800665	40801773	+	0	NA	exon (NM exon (NM	1697 NM_05304E	112398	Hs.515417	NM_01755E	ENSG00000EGLN2	EIT-6 EITe1g1-9 fan protein-coding	
chr7-1236 8.855003	0.358343	0.790405	0.453636	0.650285	0.981636	chr7	1.04E+08	1.24E+08	+	0	NA	intron (NAluSg SIN	43428 NM_20716E	442721	Hs.59226C	NM_20716E	ENSG00000LMD02	C-LMOD Cl leiomodir protein-coding	
chr1-187 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr1	1875067	1875772	+	0	NA	intron (NAluS26 SI	15668 NM_002074	2782	Hs.43042E	NM_002074	ENSG00000GNB1	MRD42 G protein protein-coding	
chr1-3625 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr1	36290364	36295074	+	0	NA	intron (Nintron (N	-13649 NM_00116E	79729	Hs.52449E	NM_02467E	ENSG00000SH3D21	Clorf113 SH3 doma protein-coding	
chr10-311 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr10	3111241	3120002	+	0	NA	intron (Nintron (N	11012 NM_00132E	5214	Hs.26010	NM_00262E	ENSG00000PFK	ATP-PFK Fphosphofr protein-coding	
chr10-319 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr10	3168062	3170731	+	0	NA	intron (Nintron (N	3320 NM_001347	10513	Hs.52830C	NM_01488E	ENSG00000PITRM1	MP1 PreP1 ptrilysyl protein-coding	
chr11-235 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr11	2396074	2397457	+	0	NA	intron (Nintron (N	-3985 NM_001297	10078	Hs.523424	NM_00570E	ENSG00000TSSC4	-	tumor sup protein-coding
chr14-68 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr14	68896502	68898746	+	0	NA	intron (Nintron (N	81678 NM_001102	87	Hs.23575C	NM_00110E	ENSG00000ACTN1	BDPLT15 actinin t protein-coding	
chr16-69 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr16	69341167	69344293	+	0	NA	TTS (NM_CTS (NM_C	2958 NM_01610E	51388	Hs.58572E	NM_01610E	ENSG00000NIP7	ACT1-37 HS nucleolar protein-coding	
chr2-372 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr2	37256901	37257322	+	0	NA	TTS (NR_CTS (NR_C	2545 NR_14640E	55471	Hs.43346E	NM_01860E	ENSG00000NDUFA7	C2orf56 NADH:ubiq protein-coding	
chr3-177 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr3	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	150557 NM_001324	79718	Hs.714201	NM_02466E	ENSG00000TBL1XR1	R21 DC42 transducin protein-coding	
chr6-174 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr6	17848235	17849700	+	0	NA	intron (NAluSx SIN	138668 NM_001123	63917	Hs.94499	NM_02211E	ENSG00000K1F13A	CKBIN baEkinasin f protein-coding	
chr7-776 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr7	77632833	77634258	+	0	NA	intron (NAluS8 SI	62720 NR_134254	1.01E+08	NR_03836E	ENSG00000CAPTR	RSBN1L-AS Alu-medie ncRNA		
chr9-656 9.126779	-0.34969	0.771473	-0.45328	0.650346	0.981636	chr9	65693005	65693843	+	0	NA	5' UTR (N5' UTR (N	17496 NM_00136E	220869	Hs.35595C	NM_001024	ENSG00000CBWD5	CBWD3 DC2 COBW dome protein-coding	
chr15-898 9.37282	0.360798	0.796138	0.453185	0.650415	0.981636	chr15	89800671	89805265	+	0	NA	intron (Nintron (N	11884 NM_00115C	290	Hs.1239	NM_00115C	ENSG00000ANPEP	APN CD13 alanyl an protein-coding	
chr1-186 8.904001	0.357866	0.789987	0.453003	0.650547	0.981636	chr1	1.86E+08	1.86E+08	+	0	NA	intron (Nintron (N	35786 NM_00329E	7175	Hs.27964C	NM_00329E	ENSG00000TPR	-	translocat protein-coding
chr2-2317 8.904001	0.357866	0.789987	0.453003	0.650547	0.981636	chr2	2.32E+08	2.32E+08	+	0	NA	intron (Nintron (N	10217 NM_00128E	64708	Hs.335061	NM_02273C	ENSG00000COPS7B	CSN7B SGN COP9 sig protein-coding	
chr2-402 8.904001	0.357866	0.789987	0.453003	0.650547	0.981636	chr2	40317168	40317841	+	0	NA	intron (NAluSc SIN	-28996 NM_00136E	158	Hs.75527	NM_00002E	ENSG00000ADSL	AMPS ASAS adenylos protein-coding	
chr6-176 8.904001	0.357866	0.789987	0.453003	0.650547	0.981636	chr6	17637654	17638163	+	0	NA	intron (Nintron (N	37606 NM_01625E	51439	Hs.95260	NM_01625E	ENSG00000FAM8A1	AHCP family w protein-coding	
chr1-2058 10.46819	0.329942	0.728361	0.452992	0.650554	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (Nintron (N	3297 NM_17385A	254428	Hs.20274	NM_17385A	ENSG00000SLC41A1	MgtE translocat protein-coding	
chr10-882 8.649606	-0.3605	0.796047	-0.45286	0.650651	0.981636	chr10	882870	883240	+	0	NA	intron (Nintron (N	48650 NM_001351	23185	Hs.15906E	NM_01515E	ENSG00000CLARP4B	KIAA0217 La ribon protein-coding	
chr11-122 8.649606	-0.3605	0.796047	-0.45286	0.650651	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (NAluS2 SIN	-51755 NM_01461E	2900	Hs.53873E	NM_01461E	ENSG00000GRK4	EAA1 GRK1 glutamate protein-coding	
chr17-187 8.649606	-0.3605	0.796047	-0.45286	0.650651	0.981636	chr17	18795943	18796566	+	0	NA	intron (NCharlie4e	7219 NM_00131E	51030	Hs.87295	NM_01607E	ENSG00000TVP23B	CGI-148 F trans-gol protein-coding	
chr18-48 8.649606	-0.3605	0.796047	-0.45286	0.650651	0.981636	chr18	48822810	48823150	+	0	NA	intron (NLM1B LIN	119827 NM_00119E						





chr15-422	6.38436	-0.40922	0.915288	-0.4471	0.654804	0.981636	chr15	42212471	42213226	+	0	NA	intron (NAL1 LINE)	-4544	NM_015288	23339	Hs. 88025	NM_015288	ENSG000000VPS39	TLP VAM6 VPS39	sufl protein-coding		
chr15-772	6.38436	-0.40922	0.915288	-0.4471	0.654804	0.981636	chr15	77260747	77261431	+	0	NA	intron (NL1P3 LIN)	-35685	NR_026813	81698	Hs. 656938	NM_030944	LINC00597	C15orf5	long intencRNA		
chr2-132f	6.38436	-0.40922	0.915288	-0.4471	0.654804	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	exon (NM_exon (NM_	24088	NM_001321	116372	Hs. 432398	NM_144586	ENSG000000LYPD1	LYPDC1 PLYL6 PLAUF	protein-coding		
chr20-314	6.38436	-0.40922	0.915288	-0.4471	0.654804	0.981636	chr20	3148554	3148753	+	0	NA	exon (NM_exon (NM_	11212	NM_02182f	60493	Hs. 741168	NM_02182f	ENSG000000FASTKD5	dJ1187M17	FAST	kinase protein-coding	
chr4-139f	6.38436	-0.40922	0.915288	-0.4471	0.654804	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (N intron (N	68995	NR_15996f	1.08E+08	Hs. 605782	NR_159963	LOC107984	-	-	uncharacterRNA	
chr7-659f	6.38436	-0.40922	0.915288	-0.4471	0.654804	0.981636	chr7	65901634	65902082	+	0	NA	intron (NLIMEc LIN	28784	NM_001284	154807	Hs. 427232	NM_173517	ENSG000000VKORC1L1	-	-	vitamin K protein-coding	
chr19-121	6.608467	-0.36302	0.812545	-0.44677	0.655038	0.981636	chr19	21170773	21171053	+	0	NA	intron (NALuSx3 SI	28873	NM_13347f	170959	Hs. 156256	NM_13347f	ENSG000000ZNF431	-	-	zinc finger protein-coding	
chr18-112	10.40162	0.32470	0.727309	0.446441	0.655278	0.981636	chr18	12355773	12356880	+	0	NA	intron (NALuSz SI	20950	NM_00679f	10939	Hs. 726355	NM_00679f	ENSG000000AFG3L2	SCA28 SPA AFG3	like protein-coding		
chr15-49f	12.32465	-0.301	0.674304	-0.44638	0.655321	0.981636	chr15	49624088	49626403	+	0	NA	exon (NM_exon (NM_	4197	NM_001144	56986	Hs. 127432	NM_020234	ENSG000000DTWD1	MDS009	DTW	domain protein-coding	
chr8-224f	5.486871	-0.45465	1.018778	-0.44627	0.655399	0.981636	chr8	22406623	22407173	+	0	NA	intron (NManRep60f	14062	NM_001351	23516	Hs. 491238	NM_01535f	ENSG000000SLC39A14	HCIN HMN	solute c protein-coding		
chr11-32f	9.167918	-0.34726	0.778338	-0.44616	0.655484	0.981636	chr11	32600710	32601734	+	0	NA	TTS (NM_C TTS (NM_C	17391	NM_00636f	10480	Hs. 502244	NM_00636f	ENSG000000EIF3M	B5 GA17 Eukaryot	protein-coding		
chr1-180f	10.40948	0.323227	0.724674	0.44603	0.655575	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (NALuSx1 SI	-73829	NM_001004	5768	Hs. 71917f	NM_00282f	ENSG000000QSOX1	Q6 QSCN6	quiescent protein-coding		
chr1-2007	10.40948	0.323227	0.724674	0.44603	0.655575	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (NALuSz SI	23541	NM_001297	23271	Hs. 23585	NM_20345f	ENSG000000CAMSAP2	CAMSAP1 Lcal	modulin protein-coding		
chr11-118	10.40948	0.323227	0.724674	0.44603	0.655575	0.981636	chr11	1.18E+08	1.19E+08	+	0	NA	intron (NL2a LINE)	-31871	NM_00134f	143941	Hs. 653445	NM_00108f	ENSG000000TTC36	HBP21	tetratric protein-coding		
chr14-49f	10.40948	0.323227	0.724674	0.44603	0.655575	0.981636	chr14	49830430	49838455	+	0	NA	exon (NM_exon (NM_	18346	NM_00471f	9147	Hs. 655964	NM_00471f	ENSG000000CNEMF	NY-CO-1 S	nuclear e protein-coding		
chr6-431f	10.40948	0.323227	0.724674	0.44603	0.655575	0.981636	chr6	43152444	43153404	+	0	NA	intron (NALuSz SI	-18345	NM_003131	6722	Hs. 52014C	NM_003131	ENSG000000SRF	MCMI	serum res protein-coding		
chr1-108f	12.36578	-0.29921	0.670957	-0.44595	0.655633	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	5' UTR (N5' UTR (N	5693	NM_00134f	55119	Hs. 342307	NM_18061f	ENSG000000PRPF38B	NET1	pre-mRNA	protein-coding	
chr22-384	12.36578	-0.29921	0.670957	-0.44595	0.655633	0.981636	chr22	38482351	38491647	+	0	NA	intron (NALuSz SI	18903	NM_00685f	11015	Hs. 74507f	NM_00685f	ENSG000000KDELR3	ERD2L3	KDEL	endc protein-coding	
chr4-788f	5.907188	-0.4302	0.965648	-0.44551	0.655954	0.981636	chr4	78877461	78879009	+	0	NA	intron (N intron (N	61203	NM_00104f	152559	Hs. 657312	NM_17745f	ENSG000000PAQR3	RKTG	progester protein-coding		
chr6-405f	5.907188	-0.4302	0.965648	-0.44551	0.655954	0.981636	chr6	4053978	4054383	+	0	NA	intron (NALuJr4 SI	24957	NM_17356f	222826	Hs. 657342	NM_17356f	ENSG000000FAM217A	G6orf146	family wiprotein-coding		
chr6-154f	5.907188	-0.4302	0.965648	-0.44551	0.655954	0.981636	chr6	1.55E+08	1.55E+08	+	0	NA	intron (N intron (N	-46983	NR_03610f	1E+08	NR_03610f	ENSG000000LOC1273C	-	-	microRNA	ncRNA	
chr1-5511	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr1	55119027	55127410	+	0	NA	intron (NL2c LINE)	82996	NR_110451	255738	Hs. 18844	NM_17493f	ENSG000000PCSK9	FH3 HCHOI	proprate protein-coding		
chr1-109f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	3' UTR (N3' UTR (N	11552	NM_00564f	6884	Hs. 63242f	NM_00564f	ENSG000000TAF13	MRT60 TAF	TATA-box	protein-coding	
chr11-741	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr11	74112726	74114171	+	0	NA	intron (N intron (N	57254	NM_015531	26005	Hs. 55793f	NM_015531	ENSG000000C2CD3	OFD14	C2	domain protein-coding	
chr13-211	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr13	21142360	21144343	+	0	NA	intron (NLIMB4 LIN	2349	NM_00136f	10284	Hs. 52489f	NM_00587f	ENSG000000SAP18	2HOR0202 Sin3A	ass	protein-coding	
chr13-37f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr13	36973918	36976343	+	0	NA	intron (NALuSc LIN	24210	NM_01333f	29880	Hs. 50776f	NM_01333f	ENSG000000ALG5	ba421P11	ALG5	doliprotein-coding	
chr15-761	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr15	77480018	77480246	+	0	NA	intron (NALuJb SI	-45469	NR_13569f	1.02E+08	Hs. 637111	NR_13569f	ENSG000000LOC10192f	-	-	uncharacterRNA	
chr16-91f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr16	9103004	9108100	+	0	NA	intron (N intron (N	13908	NM_014117	29035	Hs. 22149f	NM_014117	ENSG000000C16orf72	PROO149	chromoson	protein-coding	
chr2-7021	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr2	70219442	70224741	+	0	NA	intron (NLIMB7 LIN	26537	NR_147227	7072	Hs. 41312f	NM_022037	ENSG000000TIA1	TIA-1 WDM	TIA1	cyt protein-coding	
chr2-1121	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr2	1.02E+08	1.12E+08	+	0	NA	intron (N intron (N	-30126	NR_153214	129804	Hs. 43769f	NM_153214	ENSG000000FBLN7	TM14	fibulin 7	protein-coding	
chr3-385f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr3	38501927	38502436	+	0	NA	intron (NALuSx1 SI	5841	NR_13493f	9941	Hs. 51789f	NM_005107	ENSG000000EXOG	ENDOGL1 Exo	endor	protein-coding	
chr3-179f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (NALuSp SI	8018	NM_016331	51193	Hs. 63257f	NM_016331	ENSG000000ZNF639	ANC-2H01 zinc	finger	protein-coding	
chr3-191f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr3	1.91E+08	1.91E+08	+	0	NA	intron (N intron (N	-44055	NR_12060f	1.03E+08	NR_12060f	LINC-00f	-	-	uncharacterRNA		
chr5-1107	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr5	1.11E+08	1.11E+08	+	0	NA	intron (NALuY SINE	6424	NM_00130f	91137	Hs. 75639	NM_13877f	ENSG000000SLC25A46	HMSN6B	solute c protein-coding		
chr6-565f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr6	56562753	56567080	+	0	NA	intron (NL1P47 LIN	77973	NM_01554f	667	Hs. 60491f	NM_00172f	ENSG000000DST	BP240 BP	dystonin	protein-coding	
chr7-995f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr7	99563417	99570138	+	0	NA	intron (NALuJb SI	7943	NM_00136f	79027	Hs. 59979f	NM_024061	ENSG000000ZNF655	VIK VIK-1	zinc	finger	protein-coding
chr8-102f	9.144344	-0.34294	0.77003	-0.44536	0.656059	0.981636	chr8	1.03E+08	1.03E+08	+	0	NA	intron (N intron (N	11954	NM_001301	51582	Hs. 45910f	NM_01587f	ENSG000000CAZIN1	AZI AZI1 antizyme	protein-coding		
chr16-11f	10.45062	0.324378	0.728555	0.445234	0.65615	0.981636	chr16	11548228	11550903	+	0	NA	non-codiron-codir	-22318	NM_00137f	400499	Hs. 45993f	NM_00137f	ENSG000000LOC40049f	-	-	putative	protein-coding
chr10-87	3.69279	-0.53141	1.193628	-0.4452	0.656172	0.981636	chr10	87014534	870145927	+	0	NA	IntergeniFLAM_C	25242	NM_00114f	643161	Hs. 72994f	NM_00114f	ENSG000000FAM25A	ba96C23.5	family wiprotein-coding		
chr1-160f	5.203723	0.451674	1.014858	0.445061	0.656276	0.981636	chr1	1.6E+08	1.6E+08	+	0	NA	IntergeniIntergeni	-5950	NM_00559f	4807	Hs. 30956	NM_00559f	ENSG000000CNHLH1	HEN1 NSCI	nescient	protein-coding	
chr11-621	5.203723	0.451674	1.014858	0.445061	0.656276	0.981636	chr11	62121704	62133438	+	0	NA	intron (N intron (N	7469	NM_17352f	160298	Hs. 278221	NM_17352f	ENSG000000C11orf42	-	-	chromoson	protein-coding
chr16-57f	5.203723	0.451674	1.014858	0.445061	0.656276	0.981636	chr16	57055161	57055884	+	0	NA	intron (NAG-rich I	-37061	NM_152727	22184	Hs. 39800f	NM_152727	ENSG000000CPNE2	COPN2 CPN	copine 2	protein-coding	
chr18-46f	5.203723	0.451674	1.014858	0.445061	0.656276	0.981636	chr18	46032489	46033527	+	0	NA	intron (N intron (N	39252	NM_02443f	9050	Hs. 567384	NM_02443f	ENSG000000PSTPIP2	MAYP	proline-s	protein-coding	
chr18-55f	5.203723	0.451674	1.014858	0.445061	0.656276	0.981636	chr18	55259973	55260610	+	0	NA	intron (NMIR3 SINE	42369	NM_00134f	6925	Hs. 60515f	NM_00319f	ENSG000000TCF4	E2-2 FECI	transcri	protein-coding	
chrX-535f	5.203723	0.451674	1.014858	0.445061	0.656276	0.981636	chrX	53563790	53565011	+	0	NA	intron (N intron (N	-7126	NR_02948f	406889	NR_02948f	ENSG000000MIRLET7F2	LET7F2 M	microRNA	ncRNA		
chr17-41f	6.351079	-0.41519	0.932939	-0.44504	0.656294	0.981636	chr17	118677142	11867514	+	0	NA	3' UTR (N3' UTR (N	-1905	NM_01814f	55175	Hs. 13268	NM_01814f	ENSG000000KLHL11	-	-	kelch 11	protein-coding
chr19-581	8.911858	0.355938	0.799801	0.445034	0.656295	0.981636	chr19	58177721	58178645	+	0	NA	IntergeniIntergeni	-4806	NM_016324	10782	Hs. 83761	NM_016324	ENSG000000ZNF274	HFB101 Zf	zinc	finger	protein-coding
chr2-231f	8.911858	0.355938	0.799801	0.445034	0.656295	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	non-codiron-codir	-73736	NR_039937	1.01E+08	NR_039937	ENSG000000MIR4777	-	-	microRNA	ncRNA	



chr3-5262	8.67503	-0.35472	0.800584	-0.44307	0.657715	0.981636	chr3	52625068	52625416	+	0	NA	intron (Nintron (N	60357	NM_00135C	55193	Hs.189922	CNM_01816	ENSG00000	PBRM1	BAF180	PE	polybrom	protein-coding
chr6-1046	5.162583	0.449804	1.015213	0.443063	0.65772	0.981636	chr6	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	53486	NM_001321	57531	Hs.43434C	NM_020771	ENSG00000	HACE1	SPPRS	HECT	dom	protein-coding
chr7-5985	5.162583	0.449804	1.015213	0.443063	0.65772	0.981636	chr7	5985771	5986507	+	0	NA	intron (Nintron (N	-15456	NM_17356E	222967	Hs.44233E	NM_17356E	ENSG00000	CRSPH10B	-	-	radial s	protein-coding
chr7-470	9.588235	-0.33744	0.761634	-0.44305	0.657729	0.981636	chr7	4742050	4743300	+	0	NA	intron (NAluJo SIN	-32933	NM_001364	9907	Hs.55844C	NM_01485E	ENSG00000	AP521	KIAA0415	adaptor	protein-coding	
chr1-4106	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr1	41000561	41003195	+	0	NA	intron (Nintron (N	-12712	NR_03786E	1.01E+08	Hs.66005E	NR_03786E	ENSG00000	SLFN1L-AS-	SLFN1L	arc	ncRNA	
chr15-425	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr15	42566490	42567287	+	0	NA	3' UTR (N3' UTR (N	-8718	NM_02075E	57519	Hs.122061	NM_02075E	ENSG00000	STARD9	KIF16A	STAR	rel	protein-coding
chr2-1301	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr2	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	7625	NR_03232C	55627	Hs.51645C	NM_017751	ENSG00000	SMPP4	NET13	INSM	shingomy	protein-coding
chr21-255	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr21	25980439	25981004	+	0	NA	intron (Nintron (N	159699	NM_00113E	351	Hs.43498C	NM_000484	ENSG00000	APP	AAA ABET	amyloid t	protein-coding	
chr22-395	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr22	39524210	39525384	+	0	NA	IntergeniL2a LINE	4233	NM_18281C	468	Hs.496487	NM_00167E	ENSG00000	ATF4	CREB-2	CF	activatir	protein-coding
chr4-757	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr4	75766653	75767509	+	0	NA	intron (NL2 LINE I	42559	NM_00129C	8615	Hs.744877	NM_00371E	ENSG00000	USO1	P115	TAP USO1	vesiprotein-coding	
chr4-1026	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr4	1.03E+08	1.03E+08	+	0	NA	intron (Nzaphod3 I	78498	NM_00590E	4126	Hs.48041E	NM_00590E	ENSG00000	MAN5A	MAN5B	mannoside	protein-coding	
chr8-8644	6.376503	-0.40726	0.919509	-0.44291	0.657831	0.981636	chr8	86448757	86449159	+	0	NA	intron (NAluJr SIN	59728	NM_01603E	51115	Hs.14538E	NM_01603E	ENSG00000	CRMDN1	CGI-90	F	regulator	protein-coding
chr5-177	9.449586	0.345645	0.780591	0.442798	0.657912	0.981636	chr5	1.78E+08	1.78E+08	+	0	NA	intron (Nintron (N	-6910	NM_01622E	51428	Hs.48428E	NM_01622E	ENSG00000	DDX41	ABS IMPLF	DEAD-box	protein-coding	
chr1-217	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr1	2.18E+08	2.18E+08	+	0	NA	intron (Nintron (N	12386	NM_001297	55105	Hs.36234	NM_01804C	ENSG00000	GPATCH2	CT110	GP	G-patch	protein-coding
chr13-20	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr13	20050922	20051591	+	0	NA	intron (N(T)n Simp	-51445	NR_12638C	1.04E+08	Hs.57801E	NR_12638C	ENSG00000	LINC01072	-	-	long intenc	ncRNA
chr14-954	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr14	95432867	95433605	+	0	NA	intron (Nintron (N	42599	NM_00136E	161176	Hs.41502	NM_02463E	ENSG00000	SYN3E	C14orf13	se	protein-coding	
chr15-43	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr15	43394912	43396295	+	0	NA	exon (NM exon (NM	24502	NM_00128E	27229	Hs.584887	NM_01444E	ENSG00000	TGBCP4	W67	GPC-4	tubulin	protein-coding
chr17-15	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr17	15566614	15561446	+	0	NA	intron (NL2 LINE I	2453	NM_001204	1.01E+08	Hs.65701E	NM_01568E	ENSG00000	TVP23C-CI	FAM18B2	F	TVP23C-CI	protein-coding
chr17-49	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr17	49804156	49805489	+	0	NA	intron (Nintron (N	16141	NM_00119E	11143	Hs.21907	NM_00706E	ENSG00000	KAT7	HBO1	HBO	lysine ac	protein-coding
chr2-112	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	intron (NLM5 LINE	7304	NM_03282A	84910	Hs.65629E	NM_03282A	ENSG00000	TMEM87B	-	-	transmem	protein-coding
chr20-13	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr20	1332927	1333738	+	0	NA	intron (NMR13 SINE	-4193	NM_08049E	27111	Hs.65701E	NM_01568E	ENSG00000	SDCBP2	SITAC	SIT	syndecan	protein-coding
chr22-37	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr22	37665834	37666520	+	0	NA	3' UTR (N3' UTR (N	7454	NM_02031E	57026	Hs.63276E	NM_02031E	ENSG00000	PDXP	CIN PLP	cyridoxal	protein-coding	
chr22-50	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr22	50300310	50301141	+	0	NA	intron (Nintron (N	6921	NM_012401	23654	Hs.3989	NM_012401	ENSG00000	PLXNB2	MM1	Nb	aCplexin B	protein-coding
chr3-735	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr3	73595777	73597525	+	0	NA	intron (NLMC4 LIN	-26917	NR_046681	1.02E+08	Hs.733334	NR_046681	ENSG00000	PDZRN3-AS-	PDZRN3	arc	ncRNA	
chr4-7614	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr4	76140863	76141489	+	0	NA	intron (Nintron (N	7221	NM_01742E	53371	Hs.43043E	NM_01742E	ENSG00000	NUP54	-	-	nucleopor	protein-coding
chr6-570	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr6	57055501	57055974	+	0	NA	TTS (NM_C	8990	NM_00128E	57691	Hs.709521	NM_020931	ENSG00000	KIAA1586	-	-	KIAA1586	protein-coding
chr7-396	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr7	39660809	39661713	+	0	NA	intron (THEIB-int	37899	NM_00540E	5898	Hs.6906	NM_00540E	ENSG00000	RALA	RAL	RAS	like	protein-coding
chr7-5607	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr7	56076149	56076862	+	0	NA	intron (NCharlielC	12219	NM_00136E	25870	Hs.27969E	NM_015411	ENSG00000	SUMF2	pFGE	sulfatas	protein-coding	
chr8-334	5.692453	0.426497	0.963324	0.442735	0.657957	0.981636	chr8	33450144	33450717	+	0	NA	intron (Nintron (N	22715	NM_03266A	84750	Hs.45871E	NM_03266A	ENSG00000	FUT10	FUCTY	fucosyltr	protein-coding	
chr11-91	8.94514	0.35883	0.810534	0.442708	0.657977	0.981636	chr11	9165192	9165421	+	0	NA	intron (Nintron (N	70943	NR_02771E	283100	Hs.68947E	NR_02771E	ENSG00000	KRT8P41	-	-	keratin	psudo
chr22-324	8.94514	0.35883	0.810534	0.442708	0.657977	0.981636	chr22	32485246	32485581	+	0	NA	intron (Nintron (N	10176	NM_00103E	25793	Hs.5912	NM_01217E	ENSG00000	FBX07	FBX	FBX07F-box	prc	protein-coding
chr6-8974	5.237004	0.456386	1.030935	0.442691	0.657989	0.981636	chr6	89743377	89744513	+	0	NA	intron (NAluSp SIN	75669	NM_014611	23195	Hs.52994E	NM_014611	ENSG00000	MDM1	Real	midasin	protein-coding	
chr20-13	8.221431	-0.37071	0.837619	-0.44258	0.658072	0.981636	chr20	13817872	13818071	+	0	NA	non-codirnon-codir	32943	NR_14798E	87130	Hs.47216E	NR_02412C	ENSG00000	NDUFAF5	C2orf7	NADH	ubiq	protein-coding
chr11-671	9.920751	0.331015	0.748021	0.442521	0.658112	0.981636	chr11	671140	675393	+	0	NA	intron (NAluSx1 SI	-22325	NM_00127E	283232	Hs.448664	NM_17494C	ENSG00000	TMEM80	-	-	transmem	protein-coding
chr19-46	9.920751	0.331015	0.748021	0.442521	0.658112	0.981636	chr19	4668200	4668703	+	0	NA	intron (Nintron (N	1952	NM_019107	56005	Hs.46564E	NM_019107	ENSG00000	MYDGF	C19orf10	myeloid	protein-coding	
chr2-69	9.920751	0.331015	0.748021	0.442521	0.658112	0.981636	chr2	69039861	69044172	+	0	NA	intron (NL2a LINE	28872	NM_053034	84168	Hs.47216E	NR_02412C	ENSG00000	ANTXR1	ATR GAPO	ANTXR	cel	protein-coding
chr3-150	9.920751	0.331015	0.748021	0.442521	0.658112	0.981636	chr3	15083999	15085966	+	0	NA	intron (Nintron (N	14166	NM_00130E	64145	Hs.47556E	NM_02234C	ENSG00000	CRBSN	Rabenosyr	rabenosyr	protein-coding	
chr3-179	9.920751	0.331015	0.748021	0.442521	0.658112	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (NLR17 LTF	17166	NM_15224C	64393	Hs.37160E	NM_02247C	ENSG00000	ZMAT3	PAG608	Wizinc	finger	protein-coding
chr16-22	15.60368	0.27051	0.610852	0.442416	0.658188	0.981636	chr16	22533199	22537473	+	0	NA	exon (NM exon (NM	-10302	NR_00367E	653786	Hs.56494E	NR_00367E	ENSG00000	OTOA1	-	-	OTOA	psuedo
chr19-254	16.64585	0.262327	0.5933	0.442149	0.658382	0.981636	chr19	25454775	25456535	+	0	NA	IntergeniALR/Alpha	-1292208	NR_00360E	1E+08	Hs.14931E	NR_00360E	ENSG00000	HAVCR1P1	-	-	hepatitis	psuedo
chr10-314	9.136486	-0.34149	0.772403	-0.44212	0.658406	0.981636	chr10	31407941	31409652	+	0	NA	intron (NLRPA3 LIN	-9041	NM_00136E	1.01E+08	Hs.730227	NM_00136E	ENSG00000	LOC10050E	-	-	putative	protein-coding
chr10-68	9.136486	-0.34149	0.772403	-0.44212	0.658406	0.981636	chr10	68023429	68038720	+	0	NA	intron (Nintron (N	-20191	NR_131184	1E+08	NR_131184	POU5F1P5	Oct4-pg5	POU	class	psuedo		
chr11-18	9.136486	-0.34149	0.772403	-0.44212	0.658406	0.981636	chr11	18365797	18366102	+	0	NA	3' UTR (N3' UTR (											



chr7-129f.5.700311	0.423835	0.959648	0.441657	0.658738	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	57037 NM_003344	7328 Hs. 64354ENM_003344	ENSG000003CUBE2H	E2-20K G ubiquitin protein-coding
chr7-140f.5.700311	0.423835	0.959648	0.441657	0.658738	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (NAluSx1 SI	-30660 NR_130117	64761 Hs. 12646 NM_02275C	ENSG000003PARP12	ARTD12 MS poly (ADP- protein-coding
chr8-480f.5.700311	0.423835	0.959648	0.441657	0.658738	0.981636	chr8	48056727	48058163	+	0	NA	intron (NAluS6 SI	49014 NM_00335C	7336 Hs. 49169ENM_00335C	ENSG000003CUBE2V2	DDVIT1 DE ubiquitin protein-coding
chr8-144f.5.700311	0.423835	0.959648	0.441657	0.658738	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	5342 NM_015201	23246 Hs. 535901ENM_015201	ENSG000003BOP1	- BOP1 ribc protein-coding
chr9-110f.5.700311	0.423835	0.959648	0.441657	0.658738	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (NAluSp SIN	5813 NM_00119E	445815 Hs. 59190ENM_00720C	ENSG000003PALM2-AK1	AKAP-2 AK PALM2-AK1 protein-coding
chr9-114f.5.700311	0.423835	0.959648	0.441657	0.658738	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	3' UTR (N3' UTR (N	7007 NM_00060E	5005 Hs. 719954ENM_00060E	ENSG000003CORM2	AGP-B AGF orosomuc protein-coding
chr5-128f.9.954032	0.333719	0.755621	0.441649	0.658743	0.981636	chr5	1.29E+08	1.29E+08	+	0	NA	intron (NTHE1B-int	34036 NM_00199E	2201 Hs. 519294ENM_00199E	ENSG000003FBN2	CCA DA9 F fibullin protein-coding
chr12-57f.8.332991	0.366028	0.828886	0.441559	0.658786	0.981636	chr12	57615596	57615863	+	0	NA	intron (Nintron (N	-4181 NM_13348E	65012 Hs. 72772ENM_13348E	ENSG000003SLC26A10	- solute c protein-coding
chr9-437f.17.60575	0.253809	0.574813	0.441555	0.658815	0.981636	chr9	43777445	43777877	+	0	NA	IntergeniALR/Alpha	651495 NR_16066E	1.03E+08 NR_160669	LOC102724	- methylene pseudo
chr2-880f.5.873906	-0.43644	0.988463	-0.44154	0.658825	0.981636	chr2	86035480	86035684	+	0	NA	intron (NMLT1J LTF	20201 NM_001304	51315 Hs. 469254ENM_01661E	ENSG000003KRCC1	CHBP2  lysine i protein-coding
chr19-36f.9.069923	-0.34941	0.791537	-0.44144	0.658897	0.981636	chr19	38218795	36219193	+	0	NA	intron (NAluV SINE	-3910 NM_00104C	147929 Hs. 59633ENM_152477	ENSG000003ZNF565	- zinc fin protein-coding
chr1-159f.10.95507	0.314458	0.712446	0.441378	0.65894	0.981636	chr1	1.59E+08	1.59E+08	+	0	NA	intron (NLMeh LIN	25013 NM_00120C	3428 Hs. 38025CENM_005531	ENSG000003IFI16	IFNGI1P1 F interferc protein-coding
chr17-39f.10.95507	0.314458	0.712446	0.441378	0.65894	0.981636	chr17	39470315	39471801	+	0	NA	exon (NM exon (NM	9572 NM_01508E	51755 Hs. 34502ENM_01508E	ENSG000003CDK12	CRK7 CRKf cyclin de protein-coding
chr16-69f.6.869685	0.383351	0.868787	0.441249	0.659033	0.981636	chr16	6867255	6871101	+	0	NA	exon (NM exon (NM	-2584 NM_00132E	339123 Hs. 533771ENM_00100E	ENSG000003JMJD8	C16orf20 jumoni c protein-coding
chr16-69f.6.255604	0.411399	0.932663	0.441101	0.65914	0.981636	chr16	69375430	69375913	+	0	NA	intron (NFLAM_A SI	10336 NM_00565E	7014 Hs. 63335 NM_00565E	ENSG000003TERP2	TRBP2 TRF telomeric protein-coding
chr16-74f.6.247746	0.414028	0.939135	0.440861	0.659313	0.981636	chr16	74955227	74955744	+	0	NA	intron (NFLSINE_Ve	29638 NM_030581	79726 Hs. 280951ENM_030581	ENSG000003WDR59	CDW12 FPFWD repeat protein-coding
chr4-176f.5.684595	0.429235	0.975026	0.440229	0.659771	0.981636	chr4	1.76E+08	1.76E+08	+	0	NA	IntergeniMER52A LI	23388 NM_02192E	60559 Hs. 42194 NM_02192E	ENSG000003SPCS3	PRO3567 Signal p protein-coding
chr5-125f.5.684595	0.429235	0.975026	0.440229	0.659771	0.981636	chr5	13295336	13296167	+	0	NA	intron (NMT1Rb SINE	102065 NM_00493E	1004 Hs. 12477ENM_00493E	ENSG000003CDH6	CAD6 KCAL cadherin protein-coding
chr1-255f.5.170441	0.44683	1.015171	0.440152	0.659827	0.981636	chr1	25555095	25556284	+	0	NA	intron (Nintron (N	12104 NM_015627	26119 Hs. 590911ENM_015627	ENSG000003LDLRAP1	ARH ARH1 low densi protein-coding
chr14-99f.5.170441	0.44683	1.015171	0.440152	0.659827	0.981636	chr14	99397626	99398288	+	0	NA	3' UTR (N3' UTR (N	82902 NM_19912E	84193 Hs. 510407ENM_03223E	ENSG000003SETD3	C14orf154SET domain protein-coding
chr21-32f.5.170441	0.44683	1.015171	0.440152	0.659827	0.981636	chr21	22361 NR_00299E	32351766	+	0	NA	intron (Nintron (N	26361 NR_00299E	677846 Hs. 71229ENM_00299E	ENSG000003SNORA80A	ACA67 SNC small nucsnRNA
chr4-112f.5.170441	0.44683	1.015171	0.440152	0.659827	0.981636	chr4	1.12E+08	1.12E+08	+	0	NA	intron (NLa2 LINE	5718 NM_025144	80216 Hs. 65282ENM_025144	ENSG000003ALPK1	8430410J1 alpha kir protein-coding
chr9-890f.5.170441	0.44683	1.015171	0.440152	0.659827	0.981636	chr9	89075112	89075772	+	0	NA	intron (Nintron (N	83974 NM_00522E	1903 Hs. 58511ENM_00522E	ENSG000003S1PR3	EDG-3 EDC sphingosiprotein-coding
chr1-360f.10.98835	0.317058	0.720447	0.440085	0.659876	0.981636	chr1	36014068	36014420	+	0	NA	intron (NAluSx SIN	-69850 NM_01446E	27285 Hs. 127111ENM_01446E	ENSG000003TEKT2	TEKT1 TE tektin 2 protein-coding
chr2-111f.10.4252	0.320287	0.727926	0.439999	0.659938	0.981636	chr2	11195053	11198367	+	0	NA	intron (Nintron (N	41243 NM_00128E	130814 Hs. 27441ENM_152391	ENSG000003SLC66A3	C2orf22 F solute c protein-coding
chr3-475f.10.4252	0.320287	0.727926	0.439999	0.659938	0.981636	chr3	47509240	47510224	+	0	NA	intron (Nintron (N	3613 NM_00136E	54859 Hs. 31110CENM_01771E	ENSG000003ELP6	C3orf75 Telongator protein-coding
chr13-49f.9.887469	0.328298	0.746148	0.439999	0.659944	0.981636	chr13	49162881	49164937	+	0	NA	intron (NLM2 LINE	53592 NM_01492E	52862 Hs. 50801ENM_01492E	ENSG000003FNDC3A	FNDC3 FN fibronectin protein-coding
chr1-329f.10.3762	0.32061	0.728911	0.439849	0.660047	0.981636	chr1	32943285	32943484	+	0	NA	intron (NAluSc8 SI	21425 NM_001127	127544 Hs. 591504ENM_153341	ENSG000003RNF19B	IBRDC3 N ring fin protein-coding
chr15-50f.10.3762	0.32061	0.728911	0.439849	0.660047	0.981636	chr15	50609315	50609609	+	0	NA	intron (Nintron (N	-62796 NM_203494	373509 Hs. 67775ENM_203494	ENSG000003USP50	- ubiquitin protein-coding
chr13-52f.9.613659	-0.33225	0.755404	-0.43984	0.660055	0.981636	chr13	52473877	52474565	+	0	NA	intron (NAluJb SIN	-14772 NR_00279E	220115 Hs. 52844ENR_00279E	TPTE2P3	TPTEps1 transment pseudo
chr17-49f.9.613659	-0.33225	0.755404	-0.43984	0.660055	0.981636	chr17	49798886	49800619	+	0	NA	intron (NAluJo SIN	11071 NM_00119E	11143 Hs. 21907 NM_00706E	ENSG000003KAT7	HBO1 HBO lysine ac protein-coding
chr6-856f.9.613659	-0.33225	0.755404	-0.43984	0.660055	0.981636	chr6	85626798	85626997	+	0	NA	intron (Nintron (N	14554 NM_00115E	10492 Hs. 571177ENM_00637E	ENSG000003SYNCRIP	GRY7-RBP C synaptot protein-coding
chr1-100f.10.92178	0.31193	0.709235	0.439812	0.660074	0.981636	chr1	90013001	90029117	+	0	NA	intron (Nintron (N	25949 NM_01187E	284965 Hs. 306221ENM_181781	ENSG000003ZNF326	ZNF75 Z fin zinc fin protein-coding
chr10-73f.10.92178	0.31193	0.709235	0.439812	0.660074	0.981636	chr10	73846103	73848716	+	0	NA	non-codnon-codir	27146 NM_001367	818 Hs. 52304ENM_00122E	ENSG000003CAMK2G	CAMK CAM calcium/c protein-coding
chr12-11f.10.92178	0.31193	0.709235	0.439812	0.660074	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (NAluSz SIN	32301 NM_001347	28981 Hs. 52838ENM_01405E	ENSG000003IFT81	CDV-1 CDV intraflag protein-coding
chr5-180f.10.92178	0.31193	0.709235	0.439812	0.660074	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (NLa2 LINE	17581 NM_00130E	5601 Hs. 484371ENM_00275E	ENSG000003MAPK9	JNK-55 J mitogen- protein-coding
chr18-59f.9.621517	-0.33369	0.759206	-0.43952	0.660286	0.981636	chr18	59903058	59903257	+	0	NA	3' UTR (N3' UTR (N	3161 NM_021127	5366 Hs. 96 NM_021127	ENSG000003PMA1P1	APR NOXA phorbol-1 protein-coding
chr7-76f.9.621517	-0.33369	0.759206	-0.43952	0.660286	0.981636	chr7	76304029	76304739	+	0	NA	TTS (NM_C TTS (NM_C	1711 NM_00154C	3315 Hs. 52097ENM_00154C	ENSG000003HSPB1	CM2F7 HEL heat shoc protein-coding
chr10-10f.10.38406	0.319149	0.72627	0.439436	0.660346	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (NLM1E LIN	-3962 NM_001351	22978 Hs. 97439 NM_01222E	ENSG000003CNT5C2	GMP NT5B 5' -nuclec protein-coding
chr2-191f.10.38406	0.319149	0.72627	0.439436	0.660346	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (Nintron (N	127015 NM_001161	4430 Hs. 43962CENM_01222E	ENSG000003MYO1B	MMI-alpha myosin II protein-coding
chr5-115f.8.63389	-0.35718	0.813055	-0.43931	0.660438	0.981636	chr5	1.16E+08	1.16E+08	+	0	NA	intron (Nintron (N	9238 NM_18183E	51014 Hs. 642817ENM_18183E	ENSG000003TMED7	CK1-109 transment protein-coding
chr5-149f.8.63389	-0.35718	0.813055	-0.43931	0.660438	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	8854 NM_001271	1452 Hs. 52986ENM_00189E	ENSG000003CSNK1A1	CK1 CK1a casein kiprotein-coding
chr22-24f.9.183634	-0.35027	0.797691	-0.43911	0.660581	0.981636	chr22	24546024	24546474	+	0	NA	intron (NAluYk3 SI	8889 NM_001284	83606 Hs. 9850 NM_031444	ENSG000003GUCD1	C22orf13 guanyl yl protein-coding
chr19-11f.17.62146	0.252036	0.574013	0.439077	0.660606	0.981636	chr19	11613548	11621395	+	0	NA	exon (NM exon (NM	19988 NM_14529E	199692 Hs. 52666ENM_14529E	ENSG000003ZNF627	- zinc fin protein-coding
chr16-10f.9.177626	-0.33904	0.727577	-0.43884	0.660778	0.981636	chr16	10962644	10963988	+	0	NA	intron (NMLT1B LTF	18752 NM_01522E	23274 Hs. 35490 NM_01522E	ENSG000003CLEC16A	Gop-1 K IAC-type I protein-coding
chr16-53f.9.177626	-0.33904	0.727577	-0.43884	0.660778	0.981636	chr16	53285770	53289257	+	0	NA	intron (NAluSq2 SI	79062 NM_00135E	80205 Hs. 59159 NM_015287	ENSG000003CHD9	AD013 CHI chromodn protein-coding
chr3-381f.9.177626	-0.33904	0.727577	-0.43884	0.660778	0.981636	chr3	38190845	38191348	+	0	NA	intron (NAluJr SIN	25559 NM_00510E	9943 Hs. 47597ENM_00510E	ENSG000003OXS1	OSR1 oxidative protein-coding
chr5-129f.9.177626	-0.33904	0.727577	-0.43884	0.660778	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (NLIPIA10 LI	-38120 NM_001257	1E+08 Hs. 582534ENM_001257	ENSG000003MINAR2	KIAA1024 membrane protein-coding
chr6-142f.6.343221	-0.41331	0.941862	-0.43882	0.660793	0.981636	chr6	1.4E+08	1.4E+08	+	0	NA	3' UTR (N3' UTR (N	71772 NM_01648E	51534 Hs. 431367ENM_01648E	ENSG000003VTA1	C6orf55 vesicle tr protein-coding



chr2-112:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr2	1.12E+08	1.12E+08	0	NA	intron (Nintron (N	60701 NM_005054	84220 Hs.469633NM_005054	ENSG00000CRGPD5	BS-63 BSE RANBP2	liprotein-coding
chr20-37:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr20	37385704	37387763	0	NA	intron (Nintron (N	40605 NM_198291	6714 Hs.195656NM_005417	ENSG00000SRC	ASV SRC1 SRC	protcprotein-coding
chr21-41:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr21	41901111	41902038	0	NA	intron (Nintron (N	-22092 NM_02211E	63977 Hs.47389ENM_02211E	ENSG00000PRDM15	C21orf83 PR SET	dcprotein-coding
chr3-185:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr3	1.85E+08	1.85E+08	0	NA	intron (Nintron (N	4621 NM_080652	90407 Hs.677577NM_080652	ENSG00000TMEM41A	2900010K transment	protein-coding
chr6-105:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr6	1.05E+08	1.05E+08	0	NA	3' UTR (N3' UTR (N	36018 NM_147147	11149 Hs.22166CNC_00707E	ENSG00000BVES	CARICK HE blood	vesprotein-coding
chr8-9714:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr8	97143145	97144980	0	NA	TTS (NM_C TTS (NM_C	133866 NM_033512	85453 Hs.173094NM_033512	ENSG00000TSPYL5	TSPY	likeprotein-coding
chr9-131:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr9	1.3132288	1.3132878	0	NA	intron (Nintron (N	146981 NM_003822	8777 Hs.16937ENM_003822	ENSG00000MPDZ	H9C7 MUPF	multiple protein-coding
chr9-128:5.708169	0.421158	0.963359	0.437176	0.661984	0.981636	chr9	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	7733 NR_04974Z	81605 Hs.49522ENM_030914	ENSG00000URMI	Cyrc74	ubiquitirprotein-coding
chr14-70:11.45951	0.305433	0.698658	0.437171	0.661987	0.981636	chr14	70946959	70948546	0	NA	intron (NMER11B LI	40293 NM_00130E	22990 Hs.44655ENM_01498E	ENSG00000PCNX1	PCNX PCNX	pancanex lprotein-coding
chr12-147:8.667172	-0.35302	0.807528	-0.43717	0.661991	0.981636	chr12	98728027	98728968	0	NA	intron (NAluSz6 SI	83197 NM_18186E	317 Hs.552567NM_00116C	ENSG00000APAF1	APAF-1 C	apoptoticprotein-coding
chr4-147:8.667172	-0.35302	0.807528	-0.43717	0.661991	0.981636	chr4	1.48E+08	1.48E+08	0	NA	intron (NLIPIA11 LI	149829 NR_03996Z	1.01E+08 NR_03996Z	ENSG00000MIR4799	-	microRNA ncRNA
chr5-172:8.667172	-0.35302	0.807528	-0.43717	0.661991	0.981636	chr5	1.73E+08	1.73E+08	0	NA	intron (NAluJb SIN	14145 NM_00394E	8992 Hs.48418ENM_00394E	ENSG00000ATP6VOE1	ATP6H ATF	ATPase H+protein-coding
chr12-49:9.169768	-0.3376	0.77239	-0.43708	0.66205	0.981636	chr12	49564328	49564540	0	NA	intron (Nintron (N	2005 NM_001012	10445 Hs.25313 NM_006337	ENSG00000MCRS1	ICP22BP1 mi	microspherprotein-coding
chr14-59:9.169768	-0.3376	0.77239	-0.43708	0.66205	0.981636	chr14	59494933	59495532	0	NA	intron (Nintron (N	10715 NM_001647E	51528 Hs.44685ENM_01647E	ENSG00000JKAMP	C14orf10C JNK1 MAP3	protein-coding
chr6-723:9.169768	-0.3376	0.77239	-0.43708	0.66205	0.981636	chr6	7230422	7231288	0	NA	exon (NM exon (NM	82344 NM_001292	6745 Hs.11403ENM_003144	ENSG00000SSR1	TRAPA	signal sprotein-coding
chrX-137:9.169768	-0.3376	0.77239	-0.43708	0.66205	0.981636	chrX	13729208	13730092	0	NA	intron (NAluSp SIN	4970 NM_001011	6399 Hs.59223ENM_01456E	ENSG00000TRAPP2C	MIP2A SEE	traffickiprotein-coding
chr5-175:12.00695	0.306156	0.700515	0.437044	0.662079	0.981636	chr5	1.74E+08	1.74E+08	0	NA	exon (NM exon (NM	-39120 NM_001144	133491 Hs.13146ENM_001144	ENSG00000CC5orf47	-	chromosonprotein-coding
chr5-73:8.845295	0.349827	0.80047	0.437027	0.662092	0.981636	chr15	75612113	75612489	0	NA	intron (NAluSx SIN	13424 NM_005701	10073 Hs.21577 NM_005701	ENSG00000SNUPN	KPNBL RNL	snurportirprotein-coding
chr17-18:8.845295	0.349827	0.80047	0.437027	0.662092	0.981636	chr17	18206490	18207474	0	NA	intron (Nintron (N	-18653 NM_00414C	3996 Hs.51398ENM_00414C	ENSG00000LLGL1	DLG4 HUGL	LLGL scriprotein-coding
chr1-154:10.92964	0.310535	0.710758	0.436906	0.662179	0.981636	chr1	1.54E+08	1.54E+08	0	NA	intron (NAluSx SIN	8099 NM_001367	57198 Hs.43570CNC_02045E	ENSG00000ATP8B2	ATP1D	ATPase pfprotein-coding
chr11-75:10.92964	0.310535	0.710758	0.436906	0.662179	0.981636	chr11	75612113	75612489	0	NA	exon (NM exon (NM	11520 NM_00675E	6888 Hs.43867ENM_00675E	ENSG00000TALD01	TAL TAL-	T transaldolprotein-coding
chr12-13:10.92964	0.310535	0.710758	0.436906	0.662179	0.981636	chr12	1.33E+08	1.33E+08	0	NA	intron (Nintron (N	12686 NM_15294Z	10795 Hs.124047NM_00341E	ENSG00000ZNF268	HZF3	zinc fingprotein-coding
chr19-147:10.92964	0.310535	0.710758	0.436906	0.662179	0.981636	chr19	14712977	14723334	0	NA	intron (Nintron (N	28107 NM_00135Z	84449 Hs.51521ENM_03243E	ENSG00000ZNF333	-	zinc fingprotein-coding
chr19-57:10.92964	0.310535	0.710758	0.436906	0.662179	0.981636	chr19	57251800	57256063	0	NA	exon (NM exon (NM	13299 NM_00102Z	390980 Hs.22488 NM_00102Z	ENSG00000ZNF805	-	zinc fingprotein-coding
chr20-50:10.92964	0.310535	0.710758	0.436906	0.662179	0.981636	chr20	50617549	50627237	0	NA	intron (NAluSz SIN	-7608 NR_031634	1E+08 NR_031634	ENSG00000MIR1302	-	MIRN1302-microRNA ncRNA
chr6-896:8.340849	0.363995	0.833193	0.436867	0.662208	0.981636	chr6	89692307	89692973	0	NA	exon (NM exon (NM	-53893 NM_02046E	57226 Hs.17727ENM_02046E	ENSG00000LYRM2	DJ12208.2 LYR	motifprotein-coding
chr16-57:6.368645	-0.40531	0.928302	-0.43661	0.662391	0.981636	chr16	57755663	57779237	0	NA	promoter-promoter-	-672 NM_00131E	3801 Hs.23131 NM_00555C	ENSG00000KIFC3	-	kinesin fprotein-coding
chr3-143:6.368645	-0.40531	0.928302	-0.43661	0.662391	0.981636	chr3	1.43E+08	1.43E+08	0	NA	exon (NM exon (NM	49469 NM_00132C	23350 Hs.59657ENM_00108C	ENSG00000U2SURP	SR140 f5A U2	snRNP protein-coding
chr4-563:5.74145	0.425606	0.975218	0.436422	0.662531	0.981636	chr4	5633089	5633928	0	NA	intron (NMIR SINE	75051 NM_147127	132884 Hs.87306 NM_147127	ENSG00000EVC2	LBN WAD	EVC ciliE protein-coding
chr4-70:5.74145	0.425606	0.975218	0.436422	0.662531	0.981636	chr4	70725978	70726645	0	NA	intron (NL2 LINE L	4347 NM_001037	22902 Hs.740904NM_014961	ENSG00000RUFY3	RIPX SINC	RUN and Fprotein-coding
chr12-88:9.597943	-0.32949	0.755016	-0.43641	0.662541	0.981636	chr12	88116874	88117989	0	NA	intron (Nintron (N	24785 NM_025114	80184 Hs.150444NM_025114	ENSG00000CEP290	3H11Ag BE	centrososnprotein-coding
chr3-17:9.597943	-0.32949	0.755016	-0.43641	0.662541	0.981636	chr3	1.77E+08	1.77E+08	0	NA	intron (Nintron (N	146881 NM_001321	79718 Hs.714201NM_02466E	ENSG00000TBL1XR1	C21 DC42	transduciprotein-coding
chr1-123:9.349741	0.337071	0.773071	0.435994	0.662841	0.981636	chr1	12323810	12325485	0	NA	intron (NMIR SINE	94617 NM_01537E	55187 Hs.439381NM_01537E	ENSG00000VPS13D	SCARA	vacuolar protein-coding
chr2-132:9.564661	-0.33331	0.764686	-0.43588	0.662922	0.981636	chr2	1.33E+08	1.33E+08	0	NA	intron (Nintron (N	-121864 NR_13557Z	1.02E+08 Hs.680114NR_13557Z	ENSG00000CNKAP5-AS-	-	NCKAP5 arncRNA
chr2-21:12.42264	-0.29954	0.687223	-0.43587	0.662934	0.981636	chr2	2.18E+08	2.18E+08	0	NA	intron (Nintron (N	-1318 NR_14579Z	1.1E+08 NR_14579Z	SNORA115	-	small nucsnoRNA
chr15-49:9.424162	0.341021	0.782609	0.435749	0.663019	0.981636	chr15	49105965	49106358	0	NA	IntergeniMLT1C LTF	49438 NM_00114Z	9318 Hs.369614NM_00423E	ENSG00000COPS2	ALIEN CSN	COP9 sigr protein-coding
chr15-63:9.424162	0.341021	0.782609	0.435749	0.663019	0.981636	chr15	63303598	63303925	0	NA	intron (NAluJb SIN	26156 NM_031301	83464 Hs.51170ENM_031301	ENSG00000APHIB	APH-1B PF	aph-1 honprotein-coding
chr10-27:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr10	27231117	27232408	0	NA	exon (NM exon (NM	8724 NM_001301	91452 Hs.530599NM_14569E	ENSG00000ACBD5	-	acyl-CoA protein-coding
chr11-11:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr11	1.17E+08	1.17E+08	0	NA	exon (NM exon (NM	15803 NM_03272E	84811 Hs.437341NM_03272E	ENSG00000BUD13	Cwc26 f6A BUD13	honprotein-coding
chr12-67:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr12	6726003	6726349	0	NA	intron (NAluY SINE	1889 NM_001164	50813 Hs.53082ENM_01631E	ENSG00000COPS7A	CSN7 CSN7	COP9 sigr protein-coding
chr14-77:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr14	77550668	77557037	0	NA	intron (NAluSx SIN	-57237 NM_19929E	145501 Hs.29742 NM_18250E	ENSG00000ISM2	TAIL1 THE	isthmin 2protein-coding
chr15-84:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr15	84688663	84690277	0	NA	intron (Nintron (N	26669 NM_01430C	23478 Hs.9534 NM_01430C	ENSG00000SEC11A	1810012E SEC11	honprotein-coding
chr2-118:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr2	11807163	11808317	0	NA	intron (Nintron (N	29246 NR_03622E	1E+08 NR_03622E	ENSG00000MIR4262	-	microRNA ncRNA
chr2-332:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr2	33297373	33294419	0	NA	intron (NAluSx SIN	-124420 NR_03962E	1.01E+08 NR_03962E	ENSG00000MIR4430	-	microRNA ncRNA
chr20-50:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr20	50595990	5096497	0	NA	intron (Nintron (N	16833 NM_00100E	29058 Hs.472024NM_01414E	ENSG00000TMEM230	C20orf30 transment	protein-coding
chr20-31:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr20	31523990	31525199	0	NA	intron (NLIIME4b LI	10152 NM_17858Z	81502 Hs.373741NM_03078E	ENSG00000HMI3	H13 IMP1	histocomr protein-coding
chr4-75:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr4	75485334	75486459	0	NA	intron (NMERS7A-ir	23400 NR_10372E	25898 Hs.48297 NM_01543E	ENSG00000RCHY1	ARNIP CHI	ring fingprotein-coding
chr5-181:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr5	1810642	1813024	0	NA	intron (NLMCS5-LIN	10426 NM_00455E	4726 Hs.408257NM_00455E	ENSG00000CNDUF56	CI-13K1 C	NADH:ubiprotein-coding
chr6-74:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr6	7416435	7417143	0	NA	intron (NAluJo SIN	26960 NM_00134E	83732 Hs.43747ENM_03148C	ENSG00000RIOK1	AD034 RIC	RIO kinasprotein-coding
chr8-431:6.443066	-0.39608	0.909215	-0.43563	0.663104	0.981636	chr8	43113881	43116599	0	NA	intron (Nintron (N	21725 NM_032237	84197 Hs.49164ENM_032237	ENSG00000POMK	MDDGAI2 W	

chr19-166 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr19	16873022	16874103	+	0 NA	intron (Nintron (N	10288 NM_001297	23309 Hs. 13999 NM_015262	ENSG000003IN3B	-	SIN3	trarprotein-coding			
chr2-9915 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr2	99191494	99193055	+	0 NA	intron (Nintron (N	11090 NR_028356	51263 Hs. 346736	NR_016503	ENSG000003MRPL30	-	L28MT L3C	mitochondncprotein-coding		
chr2-1275 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr2	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	52863 NM_001145	79595 Hs. 32995 NM_024545	ENSG000003CAP130	-	Sin3A	assprotein-coding			
chr2-1591 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr2	1.59E+08	1.59E+08	+	0 NA	intron (NAluSx1 SI	-13312 NR_106949	1.02E+08	NR_106949	ENSG000003MIR6888	-	hsa-mir-6	microRNA ncRNA		
chr20-446 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr20	44512680	44513448	+	0 NA	intron (Nintron (N	9006 NM_006811	10955 Hs. 272166	NR_006811	ENSG000003SERINC3	-	AIGP1 DIF	serine rprotein-coding		
chr3-1448 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr3	14485807	14486698	+	0 NA	non-codinnon-codir	54090 NM_00108C	80852 Hs. 51781	ENM_00108C	ENSG000003GRIP2	-		glutamateprotein-coding		
chr3-2733 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr3	27338770	27338465	+	0 NA	intron (NLIPIA6 LIN	31216 NM_199347	152110 Hs. 50611	ENM_152534	ENSG000003NEK10	-		NIMA relaprotein-coding		
chr3-1496 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr3	1.39E+08	1.49E+08	+	0 NA	intron (Nintron (N	46412 NM_00413C	2992 Hs. 477892	NR_00413C	ENSG000003GYG1	-	GSD15 GV	glycogenprotein-coding		
chr3-1837 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr3	1.84E+08	1.84E+08	+	0 NA	intron (Nintron (N	46785 NR_046727	1.01E+08	NR_046727	YEATS2-AS-		YEATS2	arncRNA		
chr4-1656 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr4	16508869	16510380	+	0 NA	intron (NLMIR SINE	282961 NR_027697	202020 Hs. 44531	ENM_152684	ENSG000003TAPT1-AS1	-		TAPT1	antncRNA	
chr4-2672 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr4	26724612	26725730	+	0 NA	intron (NLM4 LINE	135073 NR_134675	1.05E+08	Hs. 54885	NR_134673	STIM2-AS1-		STIM2	antncRNA	
chr4-7562 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr4	75651460	75651758	+	0 NA	intron (Nintron (N	-21081 NM_00133C	8999 Hs. 59169	ENM_003945	ENSG000003CDKL2	-	KKIAMRE F	cyclin dprotein-coding		
chr6-4256 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr6	42594899	42596524	+	0 NA	intron (NAluJb SIN	31682 NM_001184	23304 Hs. 52992	ENM_015255	ENSG000003UBR2	-	G6orf133	ubiquitinrprotein-coding		
chr6-1114 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr6	1.11E+08	1.11E+08	+	0 NA	intron (NLI2 LINE N	-75882 NR_034105	643749 Hs. 48622	ENR_034105	ENSG000003TRAF3IP2-6	CUAS C6c	TRAF3IP2	ncRNA		
chr6-1366 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr6	1.37E+08	1.37E+08	+	0 NA	intron (NMIIRb SINE	27920 NR_125855	1.02E+08	Hs. 66651	ENR_125858	LOC101925-		uncharactncRNA		
chr6-1496 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr6	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	-3126 NR_077247	645958 Hs. 632614	NR_077247	RPS18P9	RPS18_6_7	ribosomalpseudo			
chr6-158 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr6	1.58E+08	1.58E+08	+	0 NA	intron (Nintron (N	56007 NM_001175	8871 Hs. 43449	494NM_003895	ENSG000003SYN2J	-	INPP5H	synaptoterpprotein-coding		
chr7-112 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr7	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	-97818 NM_001197	3475 Hs. 7879 NM_001155	ENSG000003IFRD1	-	PC4 TIS7	interfercpprotein-coding			
chr7-1406 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr7	1.41E+08	1.41E+08	+	0 NA	intron (Nintron (N	-54912 NR_117084	23608 Hs. 74488	ENM_013445	ENSG000003MKRN1	-	RNF61	makorin rprotein-coding		
chr8-6156 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr8	61502047	61502376	+	0 NA	TTS (NM_TTS (NM_I	187595 NM_001164	444 Hs. 33242	ENM_004315	ENSG000003CASPH	-	AAH BAH C	aspartateprotein-coding		
chr9-9356 6.435208	-0.39409	0.909115	-0.43349	0.664661	0.981636	chr9	93551059	93552899	+	0 NA	intron (Nintron (N	-23915 NM_005392	5253 Hs. 211441	ENM_005392	ENSG000003PHF2	-	CENP-35 C	PHD fingprotein-coding		
chr17-818 5.178299	0.443657	1.024264	0.433147	0.664908	0.981636	chr17	81822514	81823245	+	0 NA	3' UTR (N3' UTR (N	10412 NM_001285	348262 Hs. 51463	ENM_207365	ENSG000003MCRIP1	-	FAM195B C	MAPK regu	protein-coding	
chr3-1885 10.87279	0.312271	0.721086	0.433057	0.664973	0.981636	chr3	1.89E+08	1.89E+08	+	0 NA	intron (NAluSx1 SI	43506 NR_046623	1.01E+08	Hs. 67499	ENR_046623	ENSG000003LPP-AS1	-		LPP	antisncRNA
chr1-2095 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr1	20930266	20930694	+	0 NA	intron (NTigger1 I	57952 NR_031657	1E+08	NR_031657	ENSG000003MIR1256	-	MIRN1256	microRNA ncRNA		
chr12-191 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr12	19127002	19127427	+	0 NA	IntergeniTigger1 E	-2519 NM_019012	54477 Hs. 188614	ENM_019012	ENSG000003PLEKHA5	-	PEPP-2 P	PFleckstriprotein-coding		
chr3-3702 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr3	37025927	37026454	+	0 NA	intron (Nintron (N	32840 NM_001255	4292 Hs. 19536	494NM_000245	ENSG000003MLH1	-	COCA2 FCC	mutL homc	protein-coding	
chr6-8975 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr6	89758299	89759876	+	0 NA	intron (Nintron (N	61157 NM_014611	23195 Hs. 52994	ENM_014611	ENSG000003MDM1	-	Real	midasin fprotein-coding		
chr7-1284 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr7	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	20414 NM_018395	55798 Hs. 43321	ENM_018395	ENSG000003METTL2B	-	METL MET	methyltrp	protein-coding	
chr7-1492 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr7	1.49E+08	1.49E+08	+	0 NA	intron (NLIIMA3 LIN	8282 NR_144367	1E+08	Hs. 49051	ENM_001195	ENSG000003ZNF783	-		zinc fing	protein-coding
chr8-4166 5.667029	0.419331	0.968559	0.432944	0.665056	0.981636	chr8	41609157	41609915	+	0 NA	intron (Nintron (N	31020 NM_001365	137964 Hs. 35575	ENM_178815	ENSG000003GPAT4	-	1-AGPAT	glycogenl-protein-coding		
chr1-1566 9.654798	-0.33	0.762743	-0.43265	0.665269	0.981636	chr1	1.57E+08	1.57E+08	+	0 NA	exon (NM_exon (NM	4419 NM_006617	10763 Hs. 52797	197NM_006617	ENSG000003CNES	-	Nbla0017C	nestin	protein-coding	
chr13-114 7.207456	0.578916	1.338677	0.432454	0.665411	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	-11998 NR_039724	1.01E+08	NR_039724	ENSG000003MIR4502	-		microRNA ncRNA		
chr10-414 10.9375	0.309127	0.714953	0.432374	0.665469	0.981636	chr10	41313961	41314259	+	0 NA	IntergeniALR Alpha	1053935 NR_02438C	441666 Hs. 25572	ENR_02438C	ENSG000003LOC441666	-		zinc fingpseudo		
chr4-9888 10.19142	0.521658	1.207508	0.432012	0.665732	0.981636	chr4	98880947	98881146	+	0 NA	exon (NM_exon (NM	48087 NM_00113C	1977 Hs. 13211	NM_001965	ENSG000003EIF4E	-	AUTS19 C	eukaryoti	protein-coding	
chr11-13 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr11	1.3E+08	1.3E+08	+	0 NA	exon (NM_exon (NM	-18246 NM_002197	6768 Hs. 50433	ENM_021975	ENSG000003ST14	-	ARCT11 H	suppressi	protein-coding	
chr12-461 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr12	4612670	4613968	+	0 NA	intron (NMIIR SINE	8456 NM_001282	8798 Hs. 43953	ENM_003845	ENSG000003DYRK4	-		dual spec	protein-coding	
chr12-885 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr12	88516926	88518821	+	0 NA	intron (Nintron (N	62598 NM_000895	4254 Hs. 1048	NM_000895	ENSG000003KITLG	-	DCUA DFN	KIT ligar	protein-coding	
chr15-891 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr15	89185376	89187107	+	0 NA	intron (Nintron (N	35308 NM_000325	6017 Hs. 1933	NM_000325	ENSG000003RLBP1	-	CRALBP	retinalde	protein-coding	
chr16-372 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr16	-12863 NM_016292	3729767	+	0 NA	intron (Nintron (N	-10131 Hs. 30345	NM_016292	ENSG000003TRAP1	-	HSP 75 H	SNF recep	protein-coding		
chr16-68 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr16	68053602	68056605	+	0 NA	intron (Nintron (N	-30267 NM_173163	4775 Hs. 43658	ENM_004555	ENSG000003NFATC3	-	NF-AT4c N	nuclear f	protein-coding	
chr19-18 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr19	18310800	18313958	+	0 NA	intron (Nintron (N	10697 NM_012321	25804 Hs. 51525	ENM_012321	ENSG000003LSM4	-	GRP YER11	LSM4 homc	protein-coding	
chr21-448 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr21	44809395	44810579	+	0 NA	intron (Nintron (N	7746 NR_109925	1.02E+08	Hs. 11614	ENR_109928	LINC01424-		long intc	ncRNA	
chr3-1503 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr3	15030961	15032701	+	0 NA	intron (NAluSx SIN	33484 NM_022497	64432 Hs. 65776	494NM_022497	ENSG000003MRPS25	-	MRP-S25 F	mitochnc	protein-coding	
chr7-5334 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr7	5334264	5335135	+	0 NA	intron (Nintron (N	51756 NM_00104C	222962 Hs. 4302	ENM_153247	ENSG000003SLC29A4	-	ENT4 PMA1	solute c	protein-coding	
chr7-6684 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr7	6684941	6685596	+	0 NA	IntergeniAluY SINE	21679 NM_006955	7559 Hs. 43147	197NM_006955	ENSG000003ZNF12	-	G10T-3 H	zinc fing	protein-coding	
chr7-1587 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr7	1.59E+08	1.59E+08	+	0 NA	exon (NM_exon (NM	-54687 NR_104054	54892 Hs. 18616	NM_01776C	ENSG000003NCAPG2	-	3KS CAP-	non-SMC	protein-coding	
chr8-4295 5.674887	0.416681	0.964854	0.431859	0.665844	0.981636	chr8	42956758	42957629	+	0 NA	intron (Nintron (N	60215 NM_03241C	84376 Hs. 16285	ENM_03241C	ENSG000003HOOK3	-	HK3	hook micr	protein-coding	



chr11-944	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr11	9445355	9446397	+	0	NA	3' UTR (N3' UTR (N	14822 NR_03653E	644656 Hs. 59784eNR_03653E	ENSG000001C064465E	-	uncharactericrRNA
chr11-137	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr11	13714860	13715855	+	0	NA	intron (Nintron (N	46689 NM_03222E	84188 Hs. 501991NM_03222E	ENSG000001FARI	MLSTD2 PF fatty acyprotein-coding	
chr12-12f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr12	1263335	1264445	+	0	NA	intron (NAluSq10 S	236142 NM_001301	23085 Hs. 60121eNM_17803E	ENSG000001CERC1	Cast2 ELK/ELKS/RABc protein-coding	
chr12-66f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr12	6603877	6604622	+	0	NA	intron (NAluSx1 S1	2202 NM_001297	1108 Hs. 16223eNM_00127E	ENSG000001CHD4	CHD-4 Mi- chromodomain protein-coding	
chr12-101f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr12	1.06E+08	1.02E+08	+	0	NA	3' UTR (N3' UTR (N	45425 NM_01837C	55332 Hs. 525634NM_01837C	ENSG000001DRAM1	DRAM DNA damage protein-coding	
chr12-122f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	3' UTR (N3' UTR (N	28103 NM_00135C	55596 Hs. 37706 NM_01761E	ENSG000001ZCCHC8	- zinc fing protein-coding	
chr14-347f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr14	34789710	34792455	+	0	NA	intron (NAluSp SIN	-76259 NR_02813C	1073 Hs. 180141NM_021914	ENSG000001CF12	NEM7 cofilin 2 protein-coding	
chr14-747f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr14	74787807	74789979	+	0	NA	intron (NAluV SINE	25077 NR_01958E	56252 Hs. 531111NM_01958E	ENSG000001YLP1M1	C14orf17 YLP motif protein-coding	
chr17-394f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr17	39468052	39468926	+	0	NA	intron (NAluSp SIN	7003 NM_01508E	51755 Hs. 34502eNM_01508E	ENSG000001CDK12	CRK7 CRKF cyclin d protein-coding	
chr17-444f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr17	44422665	44423567	+	0	NA	intron (NAluSq4 S1	13735 NM_001304	23131 Hs. 46312eNM_00100E	ENSG000001GPATCH8	GPATCH8 KIG-patch c protein-coding	
chr17-826f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr17	82633882	82634519	+	0	NA	intron (NLM2B2 LIN	14244 NM_01961E	56270 Hs. 132161NM_01961E	ENSG000001WDR45B	NEDSBAS WWD repeat protein-coding	
chr19-126f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr19	12671369	12671935	+	0	NA	TTS (NR_1TTS (NR_1	1899 NM_03233E	84292 Hs. 657204NM_03233E	ENSG000001WDR83	MORGI1 WD repeat protein-coding	
chr2-4357f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr2	4357442	43575663	+	0	NA	intron (Nintron (N	20772 NM_00108E	63892 Hs. 36959eNM_02206E	ENSG000001THADA	ARMC13 GI THADA arn protein-coding	
chr2-237f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	intron (Nintron (N	26065 NM_00127E	140739 Hs. 4718eNM_08067E	ENSG000001UBE2F	NCE2 ubiquitin protein-coding	
chr20-200f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr20	20028047	20029346	+	0	NA	intron (N(ATATAC)r	10901 NM_181527	51126 Hs. 36878eNM_01610E	ENSG000001NAA20	NAT3 NAT3(N(alpha)- protein-coding	
chr20-508f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr20	50897104	50898128	+	0	NA	intron (NTigger-3 I	12175 NM_00128E	23394 Hs. 29373eNM_01533E	ENSG000001ADNP	ADNP1 HWT activator protein-coding	
chr21-437f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr21	43763507	43783269	+	0	NA	IntergeniAluSg SIN	12687 NM_00100E	1476 Hs. 695 NM_00100E	ENSG000001CCSTB	CPI-1 CST1 cystatin protein-coding	
chr3-141f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr3	14181116	14183820	+	0	NA	intron (Nintron (N	3651 NM_01446E	27258 Hs. 11163eNM_01446E	ENSG000001LSM3	SMX4 USS2 LSM3 homc protein-coding	
chr3-3708f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr3	37082414	37082613	+	0	NA	intron (NLMC1 LIN	89163 NM_00125E	4292 Hs. 195364NM_00024E	ENSG000001MLH1	COCA2 FCC mutL homc protein-coding	
chr3-1882f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr3	1.88E+08	1.88E+08	+	0	NA	intron (NMLT1F2 LI	5795 NM_00116E	4026 Hs. 72022eNM_00557E	ENSG000001LPP	- LIM doma protein-coding	
chr4-2541f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr4	25414779	25415661	+	0	NA	intron (Nintron (N	37957 NM_013367	29945 Hs. 15217eNM_013367	ENSG000001ANAPC4	APC4 anaphase protein-coding	
chr6-719Cf	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr6	7190914	7192563	+	0	NA	intron (NLM8B LIN	83777 NM_00100E	6239 Hs. 29824eNM_00295E	ENSG000001RREB1	FINB HNT ras respc protein-coding	
chr6-1751f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr6	17514449	17514831	+	0	NA	intron (NAluSx SIN	-3375 NR_11085E	1.02E+08 Hs. 62287eNR_11085E	LOC10192E	- uncharactericrRNA	
chr6-1091f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr6	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	-11389 NR_15243E	221262 Hs. 373914NM_117367	ENSG000001CCDC162F	G6orf183 coiled-c pseudo	
chr7-1352f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr7	1.35E+08	1.35E+08	+	0	NA	intron (NAluSx SIN	1339 NR_106764	1.02E+08 Hs. NR_106764	ENSG000001MIR6509	hsa-mir-ε microRNA ncRNA	
chr8-3821f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr8	38214128	38215866	+	0	NA	IntergeniAluSx SIN	-16494 NM_00116E	23259 Hs. 43496eNM_015214	ENSG000001DDHD2	SAMWD1 SF DDHD doma protein-coding	
chr9-9348f	6.42735	-0.39204	0.913445	-0.42919	0.667786	0.981636	chr9	93484516	93484769	+	0	NA	intron (NAluSx SIN	350364NM_19884E	ENSG000001FAM120AOC	C9orf100C family wiprotein-coding		
chr16-85f	5.716027	0.418375	0.975097	0.42906	0.667879	0.981636	chr16	85075504	85076139	+	0	NA	intron (Nintron (N	12609 NM_00128E	9764 Hs. 30165eNM_01473E	ENSG000001K1AA0513	- KIAA0513 protein-coding	
chr6-3175f	5.716027	0.418375	0.975097	0.42906	0.667879	0.981636	chr6	31778100	31779130	+	0	NA	intron (NAluJb SIN	-1276 NM_02525E	80737 Hs. 55855eNM_02525E	ENSG000001VWA7	C6orf27 Cvon Willec protein-coding	
chr7-433f	5.716027	0.418375	0.975097	0.42906	0.667879	0.981636	chr7	44391279	44392130	+	0	NA	intron (Nintron (N	-66073 NM_17207E	816 Hs. 351887NM_00122C	ENSG000001CAMK2B	CAM2 CAMM calcium/c protein-coding	
chr7-128f	5.716027	0.418375	0.975097	0.42906	0.667879	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	TTS (NR_1TTS (NR_C	248 NR_030324	693178 Hs. NR_030324	ENSG000001MIR593	MIRN593 ε microRNA ncRNA	
chr16-210f	5.716027	0.418375	0.975097	0.42906	0.667879	0.981636	chr16	2170279	2170864	+	0	NA	intron (Nintron (N	14789 NM_032271	84231 Hs. 71363eNM_032271	ENSG000001TRAF7	CAPDADD TNF recep protein-coding	
chr1-247f	5.965893	-0.41539	0.968394	-0.42894	0.667964	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (NLM2D LIN	22587 NM_02006E	56776 Hs. 24889 NM_02006E	ENSG000001FNM2	- formin 2 protein-coding	
chr12-78f	5.965893	-0.41539	0.968394	-0.42894	0.667964	0.981636	chr12	78029833	78030313	+	0	NA	intron (NTigger4 I	199179 NM_01490E	89795 Hs. 655301NM_01490E	ENSG000001NAV3	POMFILL1 S neuron n protein-coding	
chr17-824f	5.965893	-0.41539	0.968394	-0.42894	0.667964	0.981636	chr17	82471004	82471518	+	0	NA	intron (NAluV SINE	12520 NM_01233E	26502 Hs. 25652eNM_01233E	ENSG000001NARF	TOP2 nuclear f protein-coding	
chr2-7307f	5.965893	-0.41539	0.968394	-0.42894	0.667964	0.981636	chr2	73079277	73079629	+	0	NA	intron (Nintron (N	-7617 NM_14457E	94097 Hs. 368171NM_14457E	ENSG000001SFXN5	BBG-TCC Ssiderofle protein-coding	
chr11-134f	6.871241	-0.38051	0.887091	-0.42894	0.667966	0.981636	chr11	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	-16379 NR_14579C	1.1E+08 Hs. NR_145790	SNORD153	- small nucsnRNA	
chr12-56f	6.871241	-0.38051	0.887091	-0.42894	0.667966	0.981636	chr12	56525255	56525744	+	0	NA	intron (NAluSx6 S1	3664 NM_00289E	5939 Hs. 50572eNM_00289E	ENSG000001RBM52	SXC3 RNA bindi protein-coding	
chr2-1134f	6.871241	-0.38051	0.887091	-0.42894	0.667966	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	intron (NTigger16a	-27807 NM_0012184	200350 Hs. 591554NM_012184	ENSG000001FOXDL1	FOXD5 ba3 forkhead protein-coding	
chr2-2011f	6.871241	-0.38051	0.887091	-0.42894	0.667966	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	intron (Nintron (N	767 NR_04003C	65072 Hs. 66461eNR_04003C	ENSG000001CFLAR-AS1	ALS2CR10 CFLAR antcRNA	
chr1-156f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (Nintron (N	4905 NM_020131	56893 Hs. 28373eNM_020131	ENSG000001UBQLN4	A1U A1U ubiquitin protein-coding	
chr1-241f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	3' UTR (N3' UTR (N	40482 NM_001821	1122 Hs. 65454eNM_001821	ENSG000001CHML	REP2 CHM like protein-coding	
chr10-366f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr10	366073	369135	+	0	NA	intron (NLMC LINE	187610 NM_00120E	10771 Hs. 29226eNM_006624	ENSG000001ZMYND11	BRAM1 BSε zinc fing protein-coding	
chr14-77f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr14	77679013	77679732	+	0	NA	intron (Nintron (N	28651 NM_00602C	8846 Hs. 94542 NM_00602C	ENSG000001ALKBH1	ABH1 ABH1 alkB homc protein-coding	
chr14-101f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr14	50920374	50922300	+	0	NA	intron (Nintron (N	-59725 NM_00137E	1778 Hs. 61408eNM_00137E	ENSG000001DNC1H1	CMT20 DHC dynein c protein-coding	
chr15-505f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr15	50920374	50922300	+	0	NA	intron (Nintron (N	12654 NM_00125E	23431 Hs. 41336eNM_007347	ENSG000001AP4E1	CPSQ4 SPC adaptor i protein-coding	
chr16-727f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr16	72798307	72799048	+	0	NA	exon (NM exon (NM	-133707 NR_12633C	1.02E+08 Hs. 63725eNR_12633C	ENSG000001LINC0157Z	- long intencRNA	
chr17-265f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr17	2699451	2700099	+	0	NA	intron (NAluSx4 SI	-6851 NR_106834	ENSG000001MIR6776	hsa-mir-ε microRNA ncRNA		
chr17-411f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr17	4118428	4119351	+	0	NA	intron (NHERV L	21441 NM_01511E	23140 Hs. 277624NM_01511E	ENSG000001ZPEF1	ZZZ4 zinc fing protein-coding	
chr17-57f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr17	57001812	57002738	+	0	NA	intron (Nintron (N	24168 NM_02162E	59342 Hs. 51495eNM_02162E	ENSG000001SCPEP1	HSCP1 RIS serine c protein-coding	
chr17-64f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr17	64815634	64816633	+	0	NA	intron (Nintron (N	5969 NR_03619E	1E+08 Hs. NR_03619E	ENSG000001MIR4315-1	- microRNA ncRNA	
chr18-62f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr18	62542987	62543808	+	0	NA	intron (Nintron (N	20372 NR_126534	54877 Hs. 114191NM_01774E	ENSG000001ZCHC2	C18orf49 zinc fing protein-coding	
chr19-32f	6.212615	0.395574	0.922535	0.428791	0.668075	0.981636	chr19	32630591	32631									



chr9-325 6.904522	-0.37527	0.880845	-0.42604	0.670079	0.981636	chr19	32595100	32596104	+	0 NA	IntergeniAluSc SIN	12867 NR_14571E	1.1E+08	NR_14571E	ENSG00000SNORA68B	-	small ncRNA	
chr2-1214 6.904522	-0.37527	0.880845	-0.42604	0.670079	0.981636	chr2	1.21E+08	1.21E+08	+	0 NA	intron (N LIP1 LINE	-91800 NR_023344	1E+08	Hs.68963E	NR_023344	ENSG00000RNU4ATAC	MOPD1 RFW RNA, U4atsRNA	
chr5-1093 6.904522	-0.37527	0.880845	-0.42604	0.670079	0.981636	chr5	1.09E+08	1.09E+08	+	0 NA	3' UTR (N3' UTR (N	-10545 NR_14904C	285638	Hs.532104NR_14904C	ENSG00000LOC28563E	-	uncharacterncRNA	
chr7-1521 6.904522	-0.37527	0.880845	-0.42604	0.670079	0.981636	chr7	1.52E+08	1.52E+08	+	0 NA	intron (Nintron (N	66344 NM_001371474						
chr8-7011 6.904522	-0.37527	0.880845	-0.42604	0.670079	0.981636	chr8	70113116	70113938	+	0 NA	3' UTR (N3' UTR (N	-42275 NM_024504	63978	Hs.736037NM_024504	ENSG00000PRDM14	PFM11 PR/SET dcprotein-coding		
chr10-427 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr10	42788511	42788917	+	0 NA	intron (Nintron (N	5919 NM_01475E	9790	Hs.10848 NM_01475E	ENSG00000CBMS1	ACC BMS1 BMS1 ribcprotein-coding		
chr17-803 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr17	80394667	80398133	+	0 NA	3' UTR (N3' UTR (N	-19927 NR_148041	284131	Hs.38967E	NR_173627	ENSG00000ENDOV	-	endonuclcprotein-coding
chr2-4714 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr2	47145069	47146337	+	0 NA	intron (N2a LINE	9605 NM_17364E	285051	Hs.53157E	NR_17364E	ENSG00000STPG64	C2orf61 Csperm-taiprotein-coding	
chr4-5261 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr4	52610176	52610883	+	0 NA	intron (Nintron (N	46010 NM_001134	64854	Hs.7966 NM_02283E	ENSG00000CSP46	-	ubiquitin protein-coding	
chr7-444 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr7	44403121	44403811	+	0 NA	intron (Nintron (N	-77835 NM_17207E	816	Hs.351887NM_00122C	ENSG00000CAMK2B	CAM2 CAM2calcium protein-coding		
chr9-3712 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr9	37126490	37127900	+	0 NA	intron (Nintron (N	6597 NM_00128E	84186	Hs.65470C	NR_03222E	ENSG00000ZCHC7	AIR1 HSPC zinc finprotein-coding	
chr9-1347 6.863383	-0.37865	0.888918	-0.42597	0.670133	0.981636	chr9	1.35E+08	1.35E+08	+	0 NA	intron (NMLT1C LTF	51524 NR_039691	1.01E+08	NR_039691	ENSG00000MIR3689C	-	microRNA ncRNA	
chr1-180E 6.869903	0.322239	0.756539	0.425939	0.670152	0.981636	chr1	1806220	1806818	+	0 NA	exon (NM exon (NM	-26488 NM_00135E	65220	Hs.65479E	NR_02301E	ENSG00000NADK	dJ283E3.1NAD kinaseprotein-coding	
chr19-411 6.91238	-0.37723	0.886851	-0.42536	0.670577	0.981636	chr19	41329672	41332588	+	0 NA	exon (NM exon (NM	20653 NM_00134E	90324	Hs.437497NM_02584E	ENSG00000CCDC97	-	coiled-cpprotein-coding	
chr5-361E 6.91238	-0.37723	0.886851	-0.42536	0.670577	0.981636	chr5	36162363	36162672	+	0 NA	intron (N2a LINE	10406 NM_032637	6502	Hs.23348 NM_00598E	ENSG00000SKP2	FBL1 FBX1 S-phase protein-coding		
chr1-1511 11.91311	0.289907	0.68179	0.425215	0.67068	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	intron (NAluY SINE	4580 NM_02457E	79626	Hs.43236C	NR_02457E	ENSG00000TNFAIP8L	TIPE2 TNF alpheprotein-coding	
chr22-393 13.32383	-0.27584	0.648853	-0.42513	0.670744	0.981636	chr22	39311570	39319065	+	0 NA	promoter-promoter-	-10 NR_000027	116937	NR_000027	ENSG00000SNORD83A	RNU83A U6small ncRNA		
chr2-2312 6.742485	0.380087	0.894133	0.42509	0.670771	0.981636	chr2	2.31E+08	2.31E+08	+	0 NA	intron (NLM4Ea LI	8029 NM_00135E	80210	Hs.162411NM_02513E	ENSG00000ARMC9	ARM JBT5 armadilic protein-coding		
chr13-49E 6.692596	-0.34695	0.816388	-0.42499	0.670848	0.981636	chr13	49687633	49687832	+	0 NA	intron (NLTR40A1 L	3754 NM_03256E	84650	Hs.43327E	NR_03256E	ENSG00000EBPL	EBRP EBP like protein-coding	
chr18-23E 6.692596	-0.34695	0.816388	-0.42499	0.670848	0.981636	chr18	23257665	23258222	+	0 NA	non-codinon-codir	102118 NR_13837E	91768	Hs.11108 NM_13837E	ENSG00000CABLES1	CABL1 CAE Cdk5 and protein-coding		
chr20-28E 7.0.79918	-0.22817	0.536979	-0.42492	0.670895	0.981636	chr20	28387973	28388196	+	0 NA	IntergeniALR Alpha	214581 NR_13231E	1E+08	Hs.52935E	NR_13231E	ENSG00000FRG1CP	-	FSDH regipseudo
chr1-1934 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr1	19340704	19341465	+	0 NA	intron (Nintron (N	28758 NM_00104C	54896	Hs.64762C	NR_01776E	ENSG00000SLC66A1	LAAT-1 LAsolute cpprotein-coding	
chr1-3754 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr1	37543930	37545401	+	0 NA	intron (Nintron (N	9628 NM_02470C	79753	Hs.47232 NM_02470C	ENSG00000SNIP1	PML1 PMRE Smad nuclprotein-coding		
chr10-12E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr10	1.25E+08	1.25E+08	+	0 NA	intron (Nintron (N	3375 NM_00136E	1488	Hs.50134E	NR_00132E	ENSG00000CTBP2	-	C-terminprotein-coding
chr11-47E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr11	47844403	47846103	+	0 NA	intron (NAluSq2 SI	2947 NR_13463E	23279	Hs.64352E	NR_01523E	ENSG00000NUP160	NPH519 nucleoporprotein-coding	
chr11-12E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr11	1.26E+08	1.26E+08	+	0 NA	intron (NAluSz SIN	25239 NR_00313E	6734	Hs.36837E	NR_00313E	ENSG00000SRRA	DP SRPR SRP recepprotein-coding	
chr12-65E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr12	65419170	65420796	+	0 NA	intron (Nintron (N	137328 NR_13503E	1.05E+08	Hs.738044NR_13503E	ENSG00000LOC10536E	-	uncharacterncRNA	
chr12-104 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr12	1.04E+08	1.04E+08	+	0 NA	intron (NAluY SINE	-14495 NM_001261	7296	Hs.65492E	NR_00333E	ENSG00000TXNRD1	GRIM-12 Thioredo protein-coding	
chr14-67E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr14	67316983	67318533	+	0 NA	intron (Nintron (N	42046 NM_015994	51382	Hs.27263C	NR_015994	ENSG00000ATP6V1D	ATP6M VAI ATPase H+protein-coding	
chr19-56E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr19	5699994	5702439	+	0 NA	intron (NAluJo SIN	10921 NM_015414	25873	Hs.40801E	NR_015414	ENSG00000RPL36	L36 ribosomalprotein-coding	
chr19-194 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr19	19493583	19495373	+	0 NA	intron (Nintron (N	21070 NM_032037	83983	Hs.532711NM_032037	ENSG00000TSSK6	CT72 FKSC testis spprotein-coding		
chr2-993E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr2	99385031	99385536	+	0 NA	intron (NAluSp SIN	47894 NM_015904	9669	Hs.15868E	NR_015904	ENSG00000EIF5B	IF2 eukaryotiprotein-coding	
chr2-132E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr2	1.33E+08	1.33E+08	+	0 NA	intron (NAluSc8 SI	72766 NR_13557E	1.02E+08	Hs.680114NR_13557E	ENSG00000NCKAP5-AS-	NCKAP5 arncRNA		
chr2-2031 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr2	2.03E+08	2.03E+08	+	0 NA	intron (NAluSq2 SI	-40611 NM_17753E	57404	Hs.44606E	NR_020674	ENSG00000CYP20A1	CYP-M cytochronprotein-coding	
chr3-125E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr3	1.26E+08	1.26E+08	+	0 NA	intron (NLM87 LIN	17254 NM_02277E	114885	Hs.47744C	NR_02277E	ENSG00000OSBPL11	ORP-11 Ofosoprotein-coding	
chr5-785E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr5	7859466	7860967	+	0 NA	intron (Nintron (N	8815 NM_024091	79072	Hs.65316E	NR_024091	ENSG00000FASTKD3	-	FAST kinaseprotein-coding
chr5-723E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr5	72361496	72361954	+	0 NA	3' UTR (N3' UTR (N	41352 NM_001284	79810	Hs.12690E	NR_024754	ENSG00000PTCD2	-	pentatricprotein-coding
chr6-717E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr6	7178235	7180666	+	0 NA	intron (Nintron (N	71489 NM_00100C	6239	Hs.29824E	NR_00295E	ENSG00000RREB1	FINB HNT ras respprotein-coding	
chr7-2357 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr7	2357319	2359720	+	0 NA	intron (Nintron (N	3692 NM_001037	8662	Hs.371001NM_003751	ENSG00000EIF3B	EIF3-ETA eukaryotiprotein-coding		
chr9-134E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chr9	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	17753 NR_039691	1.01E+08	NR_039691	ENSG00000MIR3689C	-	microRNA ncRNA	
chrX-109E 6.896664	-0.37338	0.878793	-0.42488	0.670923	0.981636	chrX	1.1E+08	1.1E+08	+	0 NA	intron (N2C LINE	-33401 NM_01228E	23630	Hs.52275E	NR_01228E	ENSG00000KCNVE	KCNE1L potassiumprotein-coding	
chr1-1801 11.41652	0.296547	0.698048	0.424823	0.670966	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (NMLRb SINE	31078 NR_00282E	5768	Hs.71917E	NR_00282E	ENSG00000QSOX1	Q6 QSCN6 quiescin protein-coding	
chr15-73E 11.41652	0.296547	0.698048	0.424823	0.670966	0.981636	chr15	73287502	73288459	+	0 NA	intron (Nintron (N	-11930 NR_16214E	1.13E+08	NR_16214E	MIR12135	-	microRNA ncRNA	
chr11-10E 11.36753	0.296806	0.698706	0.424794	0.670987	0.981636	chr11	1.08E+08	1.08E+08	+	0 NA	exon (NM exon (NM	27475 NM_001351	472	Hs.367437NM_000051	ENSG00000ATM	AT1 ATA ATM serirprotein-coding		
chr13-441 11.36753	0.296806	0.698706	0.424794	0.670987	0.981636	chr13	4432851	4434705	+	0 NA	3' UTR (N3' UTR (N	3080 NM_006022	8848	Hs.43638E	NR_006022	ENSG00000TSC22D1	Ptg-2 TGF TSC2 donprotein-coding	
chr1-6231 10.08482	-0.31391	0.739056	-0.42474	0.671025	0.981636	chr1	6231726	6231950	+	0 NA	intron (NLM87 LIN	4126 NM_01240E	23463	Hs.51568E	NR_01240E	ENSG00000ICMT	HSTE14 MIsoprenylprotein-coding	
chr20-32E 10.08482	-0.31391	0.739056	-0.42474	0.671025	0.981636	chr20	32826167	32827449	+	0 NA	intron (NAluSz SIN	6854 NM_01232E	22919	Hs.472437NM_01232E	ENSG00000MAPRE1	EB1 microtub protein-coding		
chr9-154E 10.08482	-0.31391	0.739056	-0.42474	0.671025	0.981636	chr9	15425377	15426627	+	0 NA	intron (NAluSp SIN	3126 NR_16144E	6619	Hs.54629E	NR_003084	ENSG00000SNAPC3	PTFbeta Ssmall ncprotein-coding	
chr14-347 4.154246	-0.48059	1.13171	-0.42466	0.671083	0.981636	chr14	44753470	44753138	+	0 NA	TTS (NM TTS (NM_1	-37981 NR_02813C	1073	Hs.180141NM_021914	ENSG00000CFL2	NEM7 cofilin 2protein-coding		
chr15-22E 4.154246	-0.48059	1.13171	-0.42466	0.671083	0.981636	chr15	22548158											



chr7-7417 6. 419492	-0.38991	0.92217	-0.42281	0.672432	0.981636	chr7	74178956	74180136	+	0 NA	intron (AluSx1 SI	5190 NM_031992	7458 Hs. 520945	ENSG0000EIF4H	WBSR1 W	eukaryoti	protein-coding			
chr9-2036 6. 419492	-0.38991	0.92217	-0.42281	0.672432	0.981636	chr9	20360882	20361195	+	0 NA	intron (MIR SINE	50200 NR_039684	1.01E+08	NR_039684	ENSG0000MIR4473	-	microRNA ncRNA			
chr15-304 10. 12596	-0.31172	0.737673	-0.42258	0.672605	0.981636	chr15	30479693	30482323	+	0 NA	intron (intron (	7025 NR_03665C	1E+08	Hs. 56262	CNR_036650	WHAMMP1	WHDC1P1	WAS	prote	pseudo
chr3-3725 10. 12596	-0.31172	0.737673	-0.42258	0.672605	0.981636	chr3	37298771	37300369	+	0 NA	intron (intron (	55375 NR_14902E	152048	Hs. 59617	ENSG0000LOC15204E	-	uncharact	ncRNA		
chr20-294 13. 36497	-0.27421	0.649006	-0.42251	0.672651	0.981636	chr20	29485095	29485504	+	0 NA	intron (L1ME4b LI	12035 NR_146067	1.03E+08	NR_146067	FRG1EP	-	FSHD	regipseudo		
chr11-672 11. 92097	0.288628	0.683154	0.422494	0.672665	0.981636	chr11	67252925	67255851	+	0 NA	exon (NM_exon (NM	-12085 NM_00161E	156	Hs. 83636	NM_00161E	ENSG0000CGRK2	ADRBK1 B	G	protein	protein-coding
chr11-185 10. 3272	0.320908	0.759621	0.422458	0.672691	0.981636	chr11	18505813	18506604	+	0 NA	intron (AluSx SIN	21004 NM_00629E	7251	Hs. 52351	NM_00629E	ENSG0000TSG101	TSG101 VPS	tumor	protein-coding	
chr19-355 6. 830101	-0.38433	0.909848	-0.42242	0.672721	0.981636	chr19	3535310	3536020	+	0 NA	3' UTR (3' UTR (	-3492 NM_00113E	1E+08	Hs. 66497	NM_00113E	ENSG0000CPL9orf71	-	chromosom	protein-coding	
chr12-198 9. 607651	-0.32165	0.761585	-0.42234	0.672777	0.981636	chr12	1985198	1987906	+	0 NA	intron (intron (	17905 NM_00131E	196513	Hs. 13093	NM_15264C	ENSG0000DCP1B	DCP1	decapping	protein-coding	
chr6-630 9. 607651	-0.32165	0.761585	-0.42234	0.672777	0.981636	chr6	1.31E+08	1.31E+08	+	0 NA	intron (intron (	15487 NM_00135E	2037	Hs. 48647	NM_001431	ENSG0000EPB41L2	4.1-G 4.	lerythrocy	protein-coding	
chr15-1307 11. 38324	0.29413	0.69668	0.422189	0.672887	0.981636	chr15	63744364	63749045	+	0 NA	intron (L2c LINE	87244 NM_03092E	8925	Hs. 21038	NM_00392E	ENSG0000HCERC1	MDFFPMR p	HECT	and	protein-coding
chr14-69C 10. 1181	-0.31039	0.73524	-0.42216	0.672907	0.981636	chr14	69053284	69055009	+	0 NA	exon (NM_exon (NM	74464 NR_07342E	161159	Hs. 60334	NR_07342E	ENSG0000ACTN1-AS1	C14orf84	ACTN1	antncRNA	
chr14-10C 10. 1181	-0.31039	0.73524	-0.42216	0.672907	0.981636	chr14	1E+08	1E+08	+	0 NA	intron (intron (	19485 NM_00418E	7453	Hs. 49759	NM_00418E	ENSG0000WARS	GAMMA-2 F	tryptoph	protein-coding	
chr15-82E 10. 1181	-0.31039	0.73524	-0.42216	0.672907	0.981636	chr15	82833183	82837605	+	0 NA	3' UTR (3' UTR (	25766 NM_00108C	123720	Hs. 37736	NM_00108C	ENSG0000WHAMM	WHAMM1 W	WASP	homc	protein-coding
chr17-35E 10. 1181	-0.31039	0.73524	-0.42216	0.672907	0.981636	chr17	35258299	35259008	+	0 NA	5' UTR (5' UTR (	15581 NM_14497E	162394	Hs. 58579	NM_14497E	ENSG0000SLFN5	-	schlafen	protein-coding	
chr2-302E 10. 1181	-0.31039	0.73524	-0.42216	0.672907	0.981636	chr2	30232742	30252584	+	0 NA	intron (L1ME4a LI	11129 NM_03091E	81606	Hs. 56759	NM_03091E	ENSG0000LBH	-	LBH	regul	protein-coding
chr7-751E 10. 1181	-0.31039	0.73524	-0.42216	0.672907	0.981636	chr7	75188595	75190022	+	0 NA	intron (intron (	-17310 NR_00318E	654817	Hs. 64704	NR_00318E	ENSG0000CNCFC1C	SH3PXD1C	neutrophipseudo		
chr1-110E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr1	11057817	11058258	+	0 NA	intron (AluSx SIN	1981 NM_00313E	6723	Hs. 76244	NM_00313E	ENSG0000SRM	PAPT SPD	spermidir	protein-coding	
chr1-233E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr1	23325317	23325894	+	0 NA	intron (intron (	18679 NM_00110E	10236	Hs. 37376	NM_00582E	ENSG0000HNRNPR	HNRNPR h	heteroger	protein-coding	
chr14-88E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr14	88604473	88604974	+	0 NA	intron (AluSz SIN	10302 NM_20766E	79882	Hs. 68404	NM_02482E	ENSG0000CZC3H14	MRT56 MS	zinc	finger	protein-coding
chr17-39E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr17	39997036	39997621	+	0 NA	exon (NM_exon (NM	16523 NM_00280E	5709	Hs. 12970	NM_00280E	ENSG0000PCSDM3	P58 RPN3	proteasom	protein-coding	
chr22-20E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr22	20562092	20563684	+	0 NA	intron (AluJb SIN	54841 NM_00129E	51586	Hs. 51742	NM_01588E	ENSG0000MED15	ARC105 C	mediator	protein-coding	
chr4-10E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr4	1.05E+08	1.05E+08	+	0 NA	exon (NM_exon (NM	88843 NM_00112E	54790	Hs. 36763	NM_01762E	ENSG0000TET2	KIAA1546	tet	methy	protein-coding
chr4-168E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr4	1.68E+08	1.68E+08	+	0 NA	intron (intron (	63233 NM_0017631	55601	Hs. 59173	NM_0017631	ENSG0000DDX60	-	DEXd/H	b	protein-coding
chr5-146E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr5	14679192	14679391	+	0 NA	intron (intron (	14573 NM_13834E	90268	Hs. 40633	NM_13834E	ENSG0000OTULIN	AIPDS FAM	OTU	deub	protein-coding
chr7-878E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr7	87871169	87871761	+	0 NA	intron (MLT1F2 LI	4895 NM_01884E	55972	Hs. 20841	NM_01884E	ENSG0000SLC25A40	MCFP	solute	c	protein-coding
chr8-767E 6. 460632	-0.38641	0.915872	-0.4219	0.673097	0.981636	chr8	76707798	76708162	+	0 NA	intron (intron (	-24925 NR_02436E	1E+08	Hs. 59642	CNR_02436E	ENSG0000ZFHX4-AS1	-	ZFHX4	antncRNA	
chr10-57E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr10	5771816	5773076	+	0 NA	intron (intron (	40988 NM_00149A	2665	Hs. 29905	NM_00149A	ENSG0000GDI2	HEL-S-46	GDP	disc	protein-coding
chr10-96E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr10	96539644	96540533	+	0 NA	intron (NL3 LINE C	-26162 NM_01246E	7093	Hs. 15429	NM_01246E	ENSG0000TLL2	-	tolloid	l	protein-coding
chr12-62E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr12	62510615	62510814	+	0 NA	intron (L1MB2 LIN	43888 NM_01502E	23041	Hs. 38937	NM_01502E	ENSG0000MON2	-	MON2	homc	protein-coding
chr14-10C 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr14	1.01E+08	1.01E+08	+	0 NA	promoter-promoter-	-310 NR_00321C	767595	NR_00321C	ENSG0000SNORD114-14q	(I1-17	small	nuc	snoRNA	
chr16-11E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr16	11893879	11895483	+	0 NA	intron (AluJr SIN	21275 NM_00209A	2935	Hs. 52878	NM_00209A	ENSG0000GSP17	55169.	2 E	G	protein-coding
chr17-76E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr17	76712960	76714552	+	0 NA	3' UTR (3' UTR (	-2791 NM_00100E	439921	Hs. 52788	NM_00100E	ENSG0000MXR47	-	matrix	re	protein-coding
chr18-51E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr18	51058596	51059372	+	0 NA	intron (intron (	28771 NM_00535E	4089	Hs. 75862	NM_00535E	ENSG0000CMAD4	DPC4 JIP	SMAD	fami	protein-coding
chr2-111E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr2	11188647	11190039	+	0 NA	intron (intron (	33876 NM_00128E	130814	Hs. 27441	NM_152391	ENSG0000SLC66A3	C2orf22 F	solute	c	protein-coding
chr2-876E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr2	87609597	87612152	+	0 NA	Intergeni Intergeni	-18881 NR_039634	1.01E+08	NR_039634	ENSG0000MIR4435-1mir	-	4435-1	microRNA	ncRNA	
chr22-28E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr22	28751896	28753558	+	0 NA	intron (AluY SINE	10046 NM_00131E	150274	Hs. 63278	NM_17200E	ENSG0000CHSCB	DNAJC20 F	HscB	mitc	protein-coding
chr3-256E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr3	25613567	25616161	+	0 NA	intron (intron (	49508 NM_00106E	7155	Hs. 47573	NM_00106E	ENSG0000TOP2B	TOP1IB c	tDNA	topoi	protein-coding
chr3-172E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr3	1.72E+08	1.72E+08	+	0 NA	intron (intron (	90403 NM_00412E	2693	Hs. 13021	NM_00412E	ENSG0000GHSR	GHPD	growth	h	protein-coding
chr3-179A 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr3	1.79E+08	1.79E+08	+	0 NA	intron (AluJo SIN	39169 NM_02162E	59345	Hs. 17303	CNR_02162E	ENSG0000GNB4	CMTD1F	G	protein	protein-coding
chr4-847E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr4	84794326	84795197	+	0 NA	intron (intron (	-170855 NR_15277A	404201	Hs. 46730	NM_20585E	ENSG0000WDFY3-AS2	C4orf12 F	WDYF3	antncRNA	
chr5-323E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr5	32356153	32356879	+	0 NA	intron (AluSx SIN	37059 NR_03030E	693164	NR_03030E	ENSG0000MIR579	MIRN579	microRNA	ncRNA		
chr5-140E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr5	1.4E+08	1.4E+08	+	0 NA	intron (AluSx1 SI	24919 NM_00262E	5201	Hs. 48356	NM_00262E	ENSG0000PFDDN1	PDF PDF1	prefoldir	protein-coding	
chr6-322A 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr6	3224970	32252787	+	0 NA	exon (NM_exon (NM	2275 NM_17801E	347733	Hs. 30070	NM_17801E	ENSG0000TUBB2B	CDCBMT P	tubulin	t	protein-coding
chr6-145E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr6	1.46E+08	1.46E+08	+	0 NA	intron (L1ME3E LI	44133 NM_17308E	257218	Hs. 72329	NM_17308E	ENSG0000SHPRH	Ba54515.	2.SNF2	hist	protein-coding
chr7-448E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr7	44832425	44836671	+	0 NA	exon (NM_exon (NM	13578 NM_20143E	94239	Hs. 48818	NM_01241E	ENSG0000H2APV	H2A.2-1 H2A	histc	protein-coding	
chr7-873E 6. 888806	-0.37152	0.880599	-0.4219	0.673101	0.981636	chr7	87392925	87394892	+	0 NA	intron (Tigger2 E	48244 NM_00114E	54677	Hs. 12503	NM_02115E</					

chr17-296 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr17	29674606	29676479	+	0 NA	intron (NAIuJr SIN	-54119 NM_032854	84940 Hs. 14304cNM_032854	ENSG00000COR06	-	coronin f protein-coding
chr19-374 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr19	37456613	37461023	+	0 NA	intron (NLIMCa LIN	8626 NM_00133C	148266 Hs. 51184fNM_152484	ENSG00000ZNF569	ZAP1 ZNF	zinc finger protein-coding
chr2-737 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr2	73751476	73752871	+	0 NA	IntergeniPABL_B-ir	-14767 NM_00133C	51002 Hs. 157401NM_01605f	ENSG00000TPRKB	CGI-121 CTP53Rk	biprotein-coding
chr2-2304 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr2	2.3E+08	2.3E+08	+	0 NA	intron (NLIMa8 LIN	40486 NM_00120E	6672 Hs. 36905eNM_00311f	ENSG00000SP100	lysp100b	SP100 nucleotide protein-coding
chr21-336 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr21	33616150	33618074	+	0 NA	intron (NALuSz SIN	24629 NM_00133E	9946 Hs. 352671NM_14531f	ENSG00000CRYZL1	4P11 Q0H	crystallin protein-coding
chr22-238 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr22	23820244	23820964	+	0 NA	intron (NLIMB3 LIN	18402 NM_00113E	91319 Hs. 59367eNM_19844f	ENSG00000CERL3	C22orf14 derlin 3	protein-coding
chr22-265 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr22	26524771	26526214	+	0 NA	3' UTR (N3' UTR (N	12960 NR_144522f	1.01E+08 Hs. 405877NR_144529	LOC100507-		uncharacterized
chr22-406 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr22	40551017	40552285	+	0 NA	intron (NALuSx SIN	-17824 NM_00131E	57591 Hs. 65468eNM_02083f	ENSG00000MRFTA	BSAC MAL	myocardin protein-coding
chr3-968 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr3	9680364	9681042	+	0 NA	intron (NALuY SINE	-23130 NM_15363E	151835 Hs. 12133eNM_15363f	ENSG00000CPNE9	-	copine f2 protein-coding
chr4-2257 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr4	2257239	2258174	+	0 NA	intron (Nintron (N	4403 NM_006454	10608 Hs. 65502cNM_006454	ENSG00000MXD4	MAD4 MST1MXA	dimer protein-coding
chr6-3127 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr6	3127845	3130221	+	0 NA	intron (Nintron (N	10322 NM_00433E	670 Hs. 10136 NM_00433f	ENSG00000BPDL	BPH-RP MCBiphenyl	protein-coding
chr6-4293 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr6	42934536	42936173	+	0 NA	intron (Nintron (N	5874 NM_00658E	10695 Hs. 41409eNM_00658f	ENSG00000CNPY3	CAG4A EIF	canopy FC protein-coding
chr7-2207 6.717061	0.373869	0.889409	0.420357	0.674225	0.981636	chr7	2207396	2207861	+	0 NA	intron (NMER2 BL L	25317 NM_001304	8379 Hs. 65483eNM_00355f	ENSG00000MADL1L	MAD1 PIGE	mitotic e protein-coding
chr10-920 6.701345	0.378524	0.900842	0.42019	0.674347	0.981636	chr10	92013870	92014398	+	0 NA	intron (Nintron (N	90364 NM_00397E	9044 Hs. 50052eNM_00397f	ENSG00000BTAF1	MOT1 TAF-B TFIID	l protein-coding
chr17-667 6.701345	0.378524	0.900842	0.42019	0.674347	0.981636	chr17	66741946	66743051	+	0 NA	intron (Nintron (N	-44574 NR_030364	693219 NR_030364	ENSG00000MIR634	MIRN634 l	microRNA ncRNA
chr2-2067 6.701345	0.378524	0.900842	0.42019	0.674347	0.981636	chr2	2.07E+08	2.07E+08	+	0 NA	exon (NM exon (NM	1719 NM_00113E	22868 Hs. 5930 NM_01492f	ENSG00000FASTKD2	KIAA0971	FAST kinase protein-coding
chr5-1506 6.701345	0.378524	0.900842	0.42019	0.674347	0.981636	chr5	1.51E+08	1.51E+08	+	0 NA	intron (NLIME1 LIN	9277 NM_00113E	51164 Hs. 675564NM_01622f	ENSG00000CDCTNA	DYN4 P62	dyactin protein-coding
chr1-1547 6.701345	0.378524	0.900842	0.42019	0.674347	0.981636	chr1	1.55E+08	1.55E+08	+	0 NA	exon (NM exon (NM	4854 NM_00119E	103 Hs. 12341 NM_00111f	ENSG00000ADAR	ADAR1 AGC	adenosine protein-coding
chr19-271 11.42438	0.295174	0.703255	0.419726	0.674686	0.981636	chr19	27134786	27136295	+	0 NA	IntergeniALR/Alph	-657891 NR_14673E	1.02E+08 Hs. 567934NR_11068f	ENSG00000LOC101927-		uncharacterized
chr2-201 6.163617	0.396364	0.944845	0.419501	0.67485	0.981636	chr2	2.01E+08	2.01E+08	+	0 NA	intron (NLIM1 LINE	16424 NR_11062C	130540 Hs. 107944NM_13916f	ENSG00000FLACC1	ALS2CR12	flagellin protein-coding
chr7-1587 6.163617	0.396364	0.944845	0.419501	0.67485	0.981636	chr7	1.59E+08	1.59E+08	+	0 NA	intron (NLIMB3 LIN	37835 NM_02072E	57488 Hs. 49079eNM_02072f	ENSG00000ESY2T	CHR2SYT E	extended protein-coding
chr13-984 5.649464	0.409321	0.975842	0.419454	0.674884	0.981636	chr13	98438378	98439426	+	0 NA	intron (Nintron (N	83223 NM_00357E	8428 Hs. 508514NM_00357f	ENSG00000STK24	HEL-S-95 serine/tl	protein-coding
chr15-443 5.649464	0.409321	0.975842	0.419454	0.674884	0.981636	chr15	44390805	44391143	+	0 NA	intron (NMLTIA1 LI	-36653 NM_01639E	51496 Hs. 497967NM_01639f	ENSG00000CTDSP12	HSPC058 I	CTD small protein-coding
chr19-365 5.649464	0.409321	0.975842	0.419454	0.674884	0.981636	chr19	36808646	36809168	+	0 NA	intron (NMER94B DN	11341 NR_04002E	284408 Hs. 57001cNR_04002f	ENSG00000ZNF790-A	-	ZNF790 arncRNA
chr1-1846 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr1	1846357	1847140	+	0 NA	intron (NALuJr4 SI	44339 NM_002074	2782 Hs. 43042eNM_002074	ENSG00000GNB1	MRD42	G proteir protein-coding
chr17-826 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr17	82609041	82610801	+	0 NA	IntergeniLIM4 LINE	38523 NM_01961f	56270 Hs. 132161NM_01961f	ENSG00000WDR45B	NEDSBAS W	WD repeat protein-coding
chr2-2027 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr2	20277307	20278031	+	0 NA	intron (Nintron (N	49717 NM_00128E	23369 Hs. 46728eNM_01531f	ENSG00000PUM2	PUMH2 PUM	pumilio f protein-coding
chr2-1905 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr2	1.9E+08	1.9E+08	+	0 NA	intron (NLIME3A LI	54611 NM_00104E	84281 Hs. 389311NM_03232f	ENSG00000C2orf88	smAKAP	chromosom protein-coding
chr3-3698 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr3	36988778	36989751	+	0 NA	3' UTR (N3' UTR (N	3867 NM_01480E	9852 Hs. 28020 NM_01480f	ENSG00000EPM2A1P	-	EPM2A intr protein-coding
chr3-4815 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr3	48159405	48160220	+	0 NA	intron (NL2a LINE	28605 NM_00178E	993 Hs. 43770fNM_00178f	ENSG00000CDC25A	-	CDC25A2 cell div protein-coding
chr4-1851 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr4	1.85E+08	1.85E+08	+	0 NA	intron (NALuSc SIN	15810 NM_00129E	57587 Hs. 535734NM_02082f	ENSG00000CFAP97	KIAA1430 cilia anc	protein-coding
chr5-4316 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr5	43169565	43171168	+	0 NA	intron (Nintron (N	-21859 NM_15336E	167359 Hs. 25845 NM_15336f	ENSG00000NIM1K	NIM1	NIM1 seriprotein-coding
chr5-8112 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr5	81129803	81130583	+	0 NA	intron (Nintron (N	-103127 NM_00182E	1160 Hs. 80691 NM_00182f	ENSG00000CKMT2	SMTCCK	creatine protein-coding
chr5-1128 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr5	1.13E+08	1.13E+08	+	0 NA	intron (NALuJb SIN	28505 NM_00313E	6728 Hs. 637001NM_00313f	ENSG00000CRP19	-	signal re protein-coding
chr6-3541 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr6	35410499	35410999	+	0 NA	intron (Nintron (N	-41612 NM_02192E	2178 Hs. 30200eNM_02192f	ENSG00000FANCE	FACE FAE	FA comp protein-coding
chr7-3251 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr7	32510226	32511930	+	0 NA	intron (Nintron (N	15488 NM_01506E	23080 Hs. 12800eNM_01506f	ENSG00000AVL9	KIAA0241 AVL9	cell protein-coding
chr7-5601 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr7	56011918	56013376	+	0 NA	intron (NALuSx SIN	38797 NM_00137C	5723 Hs. 51265eNM_00457f	ENSG00000PSPH	PSP PSPH	phospho e protein-coding
chr8-123C 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr8	1.23E+08	1.23E+08	+	0 NA	intron (NMER2 BL L	9803 NM_00136E	93594 Hs. 49271fNM_14564f	ENSG00000TBC1D31	Gm85 WDRc	TBC1 dom e protein-coding
chr9-9207 4.17967	-0.46881	1.117666	-0.41945	0.674885	0.981636	chr9	92071151	92072356	+	0 NA	intron (NLTR7C LTF	43660 NM_00641E	10558 Hs. 90458 NM_00641f	ENSG00000SPTLC1	HSA1 HSA	serine e protein-coding
chr11-106 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr11	1.06E+08	1.06E+08	+	0 NA	IntergeniMER11B LI	18872 NM_032424	84437 Hs. 26678eNM_032424	ENSG00000MSANTD4	KIAA1826 Myb/SANT	protein-coding
chr12-11 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr12	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	73456 NM_080601	5781 Hs. 50685eNM_002834	ENSG00000PTPN11	BPTP3 CF	protein protein-coding
chr13-77 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr13	77059052	77052190	+	0 NA	intron (Nintron (N	-23943 NR_04671f	1.01E+08 Hs. 56928eNR_04671f	ENSG00000MYCBP2-AS-	MYCBP2	arncRNA
chr14-35 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr14	35093028	35094371	+	0 NA	intron (NALuY SINE	12618 NR_11041E	1.02E+08 Hs. 61713eNR_11041E	ENSG00000LOC101927-		uncharacterized
chr14-911 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr14	91124326	91125666	+	0 NA	intron (NLTR10C LI	-1430 NR_00370E	1E+08 Hs. 693444NR_00370f	ENSG00000SNORA11B	-	small nucsnRNA
chr16-57 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr16	57624952	57767099	+	0 NA	intron (Nintron (N	6327 NR_10683C	NR_10683C	ENSG00000MIR6772	hsa-mir-6	miRNA ncRNA
chr19-406 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr19	40628576	40631458	+	0 NA	TTS (NM_TTS (NM_C	28648 NM_00104E	8425 Hs. 46676eNM_00357f	ENSG00000LTBP4	ARL1C LI	latent t protein-coding
chr4-713 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr4	71356338	71359244	+	0 NA	intron (Nintron (N	18738 NM_00375E	8671 Hs. 5462 NM_00375f	ENSG00000SLC44A	HNBC1 KNE	solute e protein-coding
chr5-1364 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr5	1.38E+08	1.38E+08	+	0 NA	3' UTR (N3' UTR (N	-2617 NR_07344E	51308 Hs. 41609cNM_01660f	ENSG00000CREEP2	C5orf19 S	receptor protein-coding
chr6-1366 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr6	1.37E+08	1.37E+08	+	0 NA	intron (Nintron (N	21708 NR_12585E	1.02E+08 Hs. 66651eNR_12585E	LOC10192E-		uncharacterized
chr9-9426 6.929946	-0.36828	0.878355	-0.41928	0.67501	0.981636	chr9	94280028	94280978	+	0 NA	intron (Nintron (N	-21192 NR_16077E	158257 Hs.			



chr3-4566 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr3	45665845	45666500	+	0 NA	intron (Nintron (N	22710 NR_033947	644714 Hs. 712889NR_033947	LIMD1-AS1	LIMD1 antncRNA
chr4-5271 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr4	52713793	52714228	+	0 NA	TTS (NR_C TTS (NR_C	761 NR_003016	677810 Hs. 635034NR_003016	ENSG000003SNORA26	HBI-6 small nucsnoRNA
chr4-5691 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr4	56917798	56918238	+	0 NA	intron (NAluY SINE	9105 NM_001193	5978 Hs. 307838NM_005612	ENSG00000CREST	DFNA27 GIRE1 silerprotein-coding
chr6-1191 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr6	1.19E+08	1.19E+08	+	0 NA	intron (Nintron (N	-44551 NM_001288	79632 Hs. 443789NM_024581	ENSG00000FAM184A	C6orf60 family wiprotein-coding
chr7-1356 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr7	1.36E+08	1.36E+08	+	0 NA	intron (NAluJr SIN	-29531 NM_00113C	647087 Hs. 200022NM_00113C	ENSG00000STMP1	C7orf73 short trprotein-coding
chr9-5735 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr9	5739916	5740790	+	0 NA	intron (NHERVL-int	92764 NM_02489E	79956 Hs. 591078NM_02489E	ENSG00000CERMP1	FXNA KIAA endoplasm protein-coding
chr9-2187 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr9	21858005	21859592	+	0 NA	intron (Nintron (N	56162 NM_002451	4507 Hs. 193268NM_002451	ENSG00000MTAP	BGDMF DM5F methylthioprotein-coding
chr1-1035 6.880949	-0.36966	0.886364	-0.41706	0.676637	0.981636	chr1	1.04E+08	1.04E+08	+	0 NA	intron (NAluSp SIN	12296 NM_01761E	55599 Hs. 632422NM_01761E	ENSG00000CRNPC3	IGHDF5 RBM RNA bindiprotein-coding
chr1-4338 11.89555	0.285008	0.683406	0.41704	0.676649	0.981636	chr1	43383984	43387962	+	0 NA	intron (Nintron (N	3827 NM_001001	112950 Hs. 301756NM_052877	ENSG00000MED8	ARC32 mediator protein-coding
chr15-824 11.89555	0.285008	0.683406	0.41704	0.676649	0.981636	chr15	82459766	82461377	+	0 NA	IntergeniMamGypLTF	-15702 NR_12037E	1.03E+08 Hs. 694638NR_12037E	LOC102724	uncharactcRNA
chr4-5625 5.723885	0.41539	0.996268	0.416946	0.676718	0.981636	chr4	56259943	5630362	+	0 NA	intron (Nintron (N	78407 NR_147127	132884 Hs. 87306 NM_147127	ENSG00000CEVC2	LBN WAD EvC cilieprotein-coding
chr7-7432 5.723885	0.41539	0.996268	0.416946	0.676718	0.981636	chr7	74323687	74324137	+	0 NA	intron (NTigger3 I	34437 NM_00338E	7461 Hs. 647018NM_00338E	ENSG00000CLIP2	CLIP CLIFCAP-Gly cprotein-coding
chr1-1552 12.39213	0.279101	0.669398	0.416944	0.67672	0.981636	chr1	1.56E+08	1.56E+08	+	0 NA	intron (NAluYa5 SI	2908 NR_00300E	677771 Hs. 678902NR_00300E	ENSG00000SCARNA4	ACA26 small Ca;ncRNA
chr10-105 12.39213	0.279101	0.669398	0.416944	0.67672	0.981636	chr10	1.03E+08	1.03E+08	+	0 NA	TTS (NM_C TTS (NM_C	63298 NM_001351	22978 Hs. 97439 NM_01222E	ENSG00000CNT5C2	GMP NT5B 5' nuclecprotein-coding
chr4-2667 10.15139	-0.30692	0.73676	-0.41658	0.676987	0.981636	chr4	26676829	26680833	+	0 NA	intron (NPRIMA4_L1	94747 NM_018317	55296 Hs. 479403NM_018317	ENSG00000TBC1D19	TBC1 dom;protein-coding
chr9-1346 10.15139	-0.30692	0.73676	-0.41658	0.676987	0.981636	chr9	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	-48562 NR_13804E	414316 Hs. 571561NR_13804E	ENSG00000COL5A1-AS	C9orf104 COL5A1 arncRNA
chr16-900 11.33424	0.29433	0.706818	0.416416	0.677106	0.981636	chr16	90031239	90032244	+	0 NA	intron (NMIRb SINE	-1840 NR_122031	750 Hs. 633032NM_001214	ENSG00000GAS8-AS1	A16orf3 GAS8 antncRNA
chr1-1786 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr1	1.79E+08	1.79E+08	+	0 NA	intron (NTigger3a I	42721 NM_00467E	9068 Hs. 591474NM_00467E	ENSG00000ANGPTL1	C6orf3 ANGF angiopoieprotein-coding
chr1-1966 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr1	1.97E+08	1.97E+08	+	0 NA	intron (NLTR9D LTF	38777 NM_00018E	3075 Hs. 36339E NM_00018E	ENSG00000CFH	AHUS1 AME complemerprotein-coding
chr1-2354 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr1	2.35E+08	2.35E+08	+	0 NA	intron (NAluSq2 SI	64038 NM_15249E	148789 Hs. 498143NM_15249E	ENSG00000B3GALNT2	B3GALNAc-beta-1,3-protein-coding
chr1-2467 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr1	2.47E+08	2.47E+08	+	0 NA	intron (Nintron (N	-25153 NR_015422	149134 Hs. 720494NM_207326	LINC01341	long intncRNA
chr11-108 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr11	1.08E+08	1.08E+08	+	0 NA	intron (NMERSA1 DN	47709 NM_00001E	38 Hs. 23237E NM_00001E	ENSG00000ACAT1	ACAT MAT acetyl-Ccprotein-coding
chr12-71 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr12	7103732	7105150	+	0 NA	intron (NMER6A DNA	-3867 NR_026947	283314 Hs. 744212NR_026947	ENSG00000C1RL-AS1	MATL2963 C1RL antncRNA
chr15-731 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr15	73151108	73151815	+	0 NA	intron (NTHEIC LTF	98977 NM_00117E	4756 Hs. 38861E NM_00249E	ENSG00000NEO1	IGDC22 NC neogenin protein-coding
chr16-433 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr16	4337000	4338001	+	0 NA	exon (NM exon (NM	5276 NM_03257E	84662 Hs. 592087NM_03257E	ENSG00000GLIS2	NKL NPHP7 GLIS famiprotein-coding
chr16-665 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr16	66526656	66531591	+	0 NA	intron (Nintron (N	20999 NM_001271	7084 Hs. 51261E NM_004614	ENSG00000TK2	MTDPS2 MI thymidineprotein-coding
chr16-702 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr16	70329761	70334364	+	0 NA	intron (Nintron (N	14685 NR_003997	1.01E+08 Hs. 63500E NR_003997	ENSG00000LOC10050E	uncharactcRNA
chr16-891 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr16	89101171	89103389	+	0 NA	intron (Nintron (N	8428 NR_10429E	197322 Hs. 461727NM_174917	ENSG00000ACSF3	acyl-CoA protein-coding
chr16-895 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr16	89537674	89538728	+	0 NA	TTS (NM_C TTS (NM_C	-22456 NM_00124E	6137 Hs. 410817NM_000977	ENSG00000RPL13	BBC1 D16S ribosomal protein-coding
chr19-186 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr19	18928452	18929038	+	0 NA	TTS (NR_C TTS (NR_C	9030 NM_01907E	5155 Hs. 143187NM_01907E	ENSG00000DDX49	Dbbp8 R27C DEAD-box protein-coding
chr21-454 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr21	45482858	45483701	+	0 NA	intron (Nintron (N	5013 NR_10687E	1.02E+08 NR_10687E	ENSG00000MIR6815	hsa-mir-6microRNA ncRNA
chr21-463 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr21	46345826	46347100	+	0 NA	intron (Nintron (N	21796 NM_00131E	5116 Hs. 47406E NM_006031	ENSG00000PCNT	KEN MOPD2 peritactprotein-coding
chr3-1005 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr3	1E+08	1E+08	+	0 NA	intron (Nintron (N	19987 NR_02020E	56954 Hs. 43915E NM_02020E	ENSG00000NIT2	HEL-S-8a nitrilaseprotein-coding
chr3-1848 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr3	1.85E+08	1.85E+08	+	0 NA	intron (NLIMEc LIN	51740 NM_00134E	23355 Hs. 26926E NM_01530E	ENSG00000VPS8	KIAA0804 VPS8 subprotein-coding
chr8-2326 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr8	23290166	23290587	+	0 NA	exon (NM exon (NM	2268 NM_00113E	230369 Hs. 458644NM_00113E	ENSG00000R3HCC1	R3H domaiprotein-coding
chr9-8934 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr9	89347988	89349180	+	0 NA	intron (Nintron (N	29733 NM_00128E	79048 Hs. 59904 NM_024077	ENSG00000SECI5BP2	SBP2 SECIS birprotein-coding
chr9-1365 6.724919	0.37163	0.892453	0.416414	0.677107	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	-10385 NM_05281E	64170 Hs. 694071NM_05281E	ENSG00000CARD9	CANDF2 hCaspase irprotein-coding
chr12-126 10.14353	-0.30561	0.734329	-0.41617	0.677283	0.981636	chr12	12671998	12975402	+	0 NA	intron (NL2 LINE I	-6137 NR_03892E	1.01E+08 Hs. 12771E NR_03892E	ENSG00000GPRC5D-AS	GPRC5D arncRNA
chr20-177 10.14353	-0.30561	0.734329	-0.41617	0.677283	0.981636	chr20	17656841	17660381	+	0 NA	exon (NM exon (NM	23628 NM_00136E	6238 Hs. 47221E NM_004587	ENSG00000RRBP1	ES/130 ES ribosome protein-coding
chr3-1886 10.14353	-0.30561	0.734329	-0.41617	0.677283	0.981636	chr3	1.89E+08	1.89E+08	+	0 NA	intron (NLTR16E2 I	-41379 NR_04662E	1.01E+08 Hs. 67499E NR_04662E	ENSG00000LPP-AS1	LPP antisncRNA
chr2-1181 7.239073	0.363407	0.873481	0.416045	0.677377	0.981636	chr2	11815476	11815936	+	0 NA	intron (Nintron (N	21280 NR_03622E	1E+08 NR_03622E	ENSG00000MIR4262	microRNA ncRNA
chr21-171 7.239073	0.363407	0.873481	0.416045	0.677377	0.981636	chr21	39297740	39299132	+	0 NA	exon (NM exon (NM	15196 NR_01896E	54014 Hs. 62713E NM_01896E	ENSG00000BRWD1	C21orf107 bromodome protein-coding
chr17-485 10.34893	0.307746	0.739709	0.416036	0.677383	0.981636	chr17	48940481	48941295	+	0 NA	intron (Nintron (N	3954 NM_001317	11267 Hs. 12724E NM_007241	ENSG00000SNF8	Dot3 EAP2 SNF8 subprotein-coding
chr5-1725 6.945662	-0.37209	0.894577	-0.41594	0.677456	0.981636	chr5	1.72E+08	1.72E+08	+	0 NA	intron (NLIMB7 LIN	60248 NR_13093E	1E+08 Hs. 531911NM_01007542	LOC10028E	uncharactcRNA
chr16-855 5.999175	-0.40584	0.982235	-0.41593	0.677459	0.981636	chr16	85676339	85677083	+	0 NA	TTS (NM_C TTS (NM_C	12243 NM_01609E	51659 Hs. 43318E NM_01609E	ENSG00000GINS2	HSPC037 GINS comp protein-coding
chr1-1800 10.85337	0.298661	0.71834	0.415765	0.677582	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (NLIMEg LIN	-97897 NM_001004	5768 Hs. 71917E NM_00282E	ENSG00000QSOX1	Q6 QSCN6 quiescin protein-coding
chr8-1034 9.633074	-0.31652	0.762171	-0.41529	0.677929	0.981636	chr8	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	12598 NM_01542E	25879 Hs. 53226E NM_01542E	ENSG00000DCAF13	GMB3 HSPCDBD1 and protein-coding
chr1-1614 6.91423	-0.36454	0.878107	-0.41514	0.678037	0.981636	chr1	16142640	16143723	+	0 NA	intron (N (GATG) N S	12888 NM_00132E	1969 Hs. 17159E NM_004431	ENSG00000CEPHA2	ARCC2 CTFEPH receprotein-coding
chr1-2330 6.91423	-0.36454	0.878107	-0.41514	0.678037	0.981636	chr1	23303524	23306391	+	0 NA	3' UTR (N3' UTR (N	-19439 NR_11061E	1.01E+08 Hs. 99836 NR_11061E	LINC0135E	long intncRNA
chr1-2023 6.91423	-0.36454	0.878107	-0.41514	0.678037	0.981636	chr1	2.02E+08	2.02E+08	+	0 NA	exon (NM exon (NM	8624 NM_01417E	29089 Hs. 5199 NM_01417E	ENSG00000UBE2T	FANCT HSF1 ubiquitir protein-coding
chr10-355 6.91423	-0.36454	0.878107	-0.41514	0.678037	0.981636	chr10	35533661	35535998	+	0 NA	intron (NLIMB8 LIN	-70512 NM_15336E	219770 Hs. 63892E NM_15336E	ENSG00000CGJD4	

chr4-1357	5.657322	0.406513	0.979788	0.414899	0.678216	0.981636	chr4	13578389	13578931	+	0	NA	intron (AluJo SIN	-30836	NR_015450	285548	Hs.529284	NR_015450	LINC01096	-	long	intcncRNA		
chr6-1697	5.657322	0.406513	0.979788	0.414899	0.678216	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (intron (	8983	NR_001278	55780	Hs.47546	NR_018341	ENS00000	ERMARD	C6orf70	FER	membr	protein-coding
chr1-2251	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr1	22513030	22514542	+	0	NA	intron (intron (	-49703	NR_001006	2046	Hs.28361	ENS00000	CEPHAS	EEL EK3 EPH	recept	protein-coding		
chr1-3208	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr1	32087017	32087140	+	0	NA	intron (intron (	-5129	NR_049858	1.01E+08	NR_049858	ENS00000	MIR5585	-	microRNA	ncRNA		
chr1-5275	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr1	52750759	52758645	+	0	NA	intron (intron (	37399	NR_024646	79699	Hs.47628	ENS00000	ZYG11B	ZYG11	zinc	finger	protein-coding	
chr1-2294	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr1	2.29E+08	2.29E+08	+	0	NA	intron (MER44 DN	28791	NR_018230	55746	Hs.12457	NR_018230	ENS00000	CNUP133	GAMOS8	NF	nucleopor	protein-coding
chr11-18	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr11	18343147	18344521	+	0	NA	intron (L2b LINE	21267	NR_005316	29655	Hs.57720	NR_005316	ENS00000	GTF2H1	BTF2 P62	general	tRNA	protein-coding
chr11-115	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	3' UTR (3' UTR (	9692	NR_106814	1.02E+08	NR_106814	ENS00000	MIR6756	hsa-mir-6	microRNA	ncRNA		
chr14-77	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr14	77595893	77597058	+	0	NA	intron (AluYh3 SI	20292	NR_004863	9517	Hs.43566	NR_004863	ENS00000	SPTLC2	HSNIC LCE	serine	protein-coding	
chr15-641	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr15	64115240	64115591	+	0	NA	intron (intron (	19434	NR_001242	6642	Hs.18863	NR_003099	ENS00000	SNX1	HST17379	sortin	r	protein-coding
chr16-44	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr16	4431169	4431593	+	0	NA	intron (intron (	5668	NR_001135	9093	Hs.45977	NR_005147	ENS00000	DNAJA3	HCA57 TII	DNAJ	heat	protein-coding
chr16-28	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr16	28395511	28396529	+	0	NA	intron (Tigger4b	-4969	NR_106922	1.02E+08	NR_106922	ENS00000	MIR6862	hsa-mir-6	microRNA	ncRNA		
chr16-574	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr16	57437592	57439147	+	0	NA	intron (intron (	9016	NR_020313	57019	Hs.4900	NR_020313	ENS00000	CIAP1N1	Anamorsircytokine	protein-coding		
chr17-318	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr17	31851783	31853941	+	0	NA	exon (NM exon (NM	6100	NR_001330	55352	Hs.46272	NR_018406	ENS00000	COPRS	C1orf79	coordinat	protein-coding	
chr21-371	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr21	37176374	37177822	+	0	NA	intron (MLTIH LTF	16828	NR_046651	1.01E+08	Hs.57041	NR_046651	ENS00000	TTC3-AS1	-	TTC3	antincRNA	
chr22-42	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr22	42874046	42874499	+	0	NA	intron (AluJr SIN	-16999	NR_001142	26286	Hs.68522	NR_014570	ENS00000	ARFGAP3	ARFGAP1	ADP	ribos	protein-coding
chr3-102	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr3	10269940	10271460	+	0	NA	exon (NM exon (NM	-9651	NR_162141	1.13E+08	MIR12127	-	microRNA	ncRNA				
chr3-393	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr3	39395919	39397381	+	0	NA	3' UTR (3' UTR (	-10070	NR_001304	3921	Hs.44990	NR_002299	ENS00000	RPSA	37LRP 67I	ribosomal	protein-coding	
chr3-525	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr3	52557458	52558415	+	0	NA	intron (intron (	21331	NR_001124	440957	Hs.66057	NR_001124	ENS00000	SMIM4	C3orf78	small	int	protein-coding
chr6-905	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr6	90555457	90556477	+	0	NA	intron (Tigger17	30955	NR_003188	6885	Hs.59483	NR_003188	ENS00000	MAP3K7	CSCF FMD2	mitogen-	protein-coding	
chr8-234	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr8	234090	235420	+	0	NA	intron (intron (	2299	NR_001042	169270	Hs.59138	NR_173530	ENS00000	ZNF596	-	zinc	finger	protein-coding
chr9-111	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (Tigger1 E	-49573	NR_205858	26248	Hs.38131	NR_205858	ENS00000	COR2K2	HSHTPCRH C	factory	protein-coding	
chrX-457	6.683779	0.369976	0.891935	0.414801	0.678288	0.981636	chrX	45754590	45755987	+	0	NA	IntergeniLIPB1 LIN	-8164	NR_029630	407007	NR_029630	ENS00000	MIR222	MIRN222	microRNA	ncRNA		
chr1-200	11.35782	0.290325	0.699989	0.414756	0.67832	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (intron (	65268	NR_021440	4853	Hs.48736	NR_024408	ENS00000	NOTCH2	AGS2 HJC	cytoth	recept	protein-coding
chr7-6664	6.7582	0.375648	0.905858	0.414687	0.678371	0.981636	chr7	66642862	66643504	+	0	NA	TTS (NM_TTS (NM_I	-11336	NR_110037	1.01E+08	Hs.66740	NR_110037	LOC100996	-	uncharact	ncRNA		
chr1-676	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr1	67686052	67690093	+	0	NA	3' UTR (3' UTR (	2871	NR_001924	1647	Hs.80409	NR_001924	ENS00000	GADD45A	DDIT1 GAI	growth	ar	protein-coding
chr10-74	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr10	7473070	74736333	+	0	NA	intron (intron (	76127	NR_001320	26985	Hs.50010	NR_012099	ENS00000	AP3M1	-	adaptor	protein-coding	
chr11-12	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr11	1.28E+08	1.28E+08	+	0	NA	3' UTR (3' UTR (	60657	NR_005238	2113	Hs.36943	NR_005238	ENS00000	EYS1	ETS-1 EWS	ETS	protc	protein-coding
chr12-654	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr12	6544537	6547372	+	0	NA	intron (MER44 DN	10088	NR_080730	25900	Hs.15243	NR_015430	ENS00000	IFFO1	HOM-TRES I	intermedi	protein-coding	
chr14-504	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr14	50421738	50425950	+	0	NA	intron (LTR16C LI	-26546	NR_001367	8814	Hs.28088	NR_004190	ENS00000	CDKL1	KKIALRE F	cyclin	de	protein-coding
chr2-3647	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr2	36479213	36481898	+	0	NA	intron (intron (	117613	NR_001042	9637	Hs.25856	NR_005102	ENS00000	FEZ2	HUM3CL	fascicu	protein-coding	
chr2-1357	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr2	1.36E+08	1.36E+08	+	0	NA	exon (NM exon (NM	-12914	NR_163478	1.08E+08	Hs.59124	NR_001365239	LOC107980	-	uncharact	ncRNA		
chr2-1974	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr2	1.97E+08	1.97E+08	+	0	NA	intron (intron (	6175	NR_002150	3329	Hs.59505	NR_002150	ENS00000	HSPD1	CPN60 GR	heat	shoc	protein-coding
chr3-1224	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (AluSc5 SI	47240	NR_125400	1.03E+08	Hs.67505	NR_125400	ENS00000	LOC102722	-	uncharact	ncRNA	
chr5-9551	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr5	95516274	95517268	+	0	NA	intron (intron (	38234	NR_014630	9652	Hs.48286	NR_014630	ENS00000	TTC37	KIAA0372	tetratric	protein-coding	
chr7-7471	10.13567	-0.3043	0.734128	-0.4145	0.678506	0.981636	chr7	74710849	74718140	+	0	NA	intron (intron (	14424	NR_110044	1.02E+08	Hs.65477	NR_110044	ENS00000	LOC101920	-	uncharact	ncRNA	
chr19-22	6.847667	-0.37504	0.904868	-0.41446	0.678534	0.981636	chr19	2234226	2234459	+	0	NA	promoter-promoter-	-193	NR_031590	1E+08	NR_031590	ENS00000	MIR1227	MIRN1227	microRNA	ncRNA		
chr3-487	6.847667	-0.37504	0.904868	-0.41446	0.678534	0.981636	chr3	48702679	48703027	+	0	NA	intron (L2a LINE	13468	NR_001000	51447	Hs.59598	NR_016291	ENS00000	IP6K2	IHPK2 Ins	inositol	protein-coding	
chr17-187	6.228331	0.390572	0.942975	0.414191	0.678734	0.981636	chr17	18732978	18733840	+	0	NA	intron (L2b LINE	-10645	NR_051988	10517	Hs.59212	NR_031450	ENS00000	FBXW10	Fbw10 HRE	F-box	anc	protein-coding
chr3-1977	6.79682	-0.39072	0.944098	-0.41385	0.678981	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	TTS (NM_TTS (NM_C	-5963	NR_001363	84859	Hs.51841	NR_032770	ENS00000	LRCH3	-	leucine	protein-coding	
chr11-12	4.212952	-0.46028	1.112771	-0.41363	0.679144	0.981636	chr11	12531943	12532984	+	0	NA	3' UTR (3' UTR (	-142003	NR_021961	7003	Hs.65539	NR_021961	ENS00000	TEAD1	AA NTEF-1	TEA	doma	protein-coding
chr12-69	4.212952	-0.46028	1.112771	-0.41363	0.679144	0.981636	chr12	69373805	69375719	+	0	NA	intron (SVA_B Ret	15019	NR_006530	8089	Hs.40229	NR_006530	ENS00000	YEATS4	4930573H YEATS	don	protein-coding	
chr2-6111	4.212952	-0.46028	1.112771	-0.41363	0.679144	0.981636	chr2	61111787	61112715	+	0	NA	intron (LIME1 LIN	32724	NR_036490	339803	Hs.25243	NR_036490	ENS00000	LOC339800	-	uncharact	ncRNA	
chr1-985	6.691637	0.367721	0.889082	0.413597	0.67917	0.981636	chr1	9853344	9854790	+	0	NA	intron (LIMS1 LINE	-29545	NR_014944	22883	Hs.29665	NR_014944	ENS00000	CLSTN1	ALC-ALPHA	calys	ter	protein-coding
chr1-122	6.691637	0.367721	0.889082	0.413597	0.67917	0.981636	chr1	12282831	12285470	+	0	NA	intron (intron (	54120	NR_015370	5587	Hs.43938	NR_015370	ENS00000	VPS13D	SCAR4	vacuol	protein-coding	
chr1-328	6.691637	0.367721	0.889082	0.413597	0.67917	0.981636	chr1	32852528	32853884	+	0	NA	intron (AluSc8 SI	17607	NR_001171	252995	Hs.52423	NR_015370	ENS00000	PND50	PRCP2 iri	fibro	ect	protein-coding
chr1-115	6.691637	0.367721	0.889082	0.413597	0.67917	0.981636	chr1	1.16E+08	1.16E+08	+	0	NA	intron (intron (	22824	NR_001172	81839	Hs.51513	NR_138950	ENS00000	VANGL1	KITENIN I	VANGL	pl	protein-coding
chr1-124	6.691637	0.367721	0.889082	0.413597	0.67917	0.981636	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR Alpha	2956338	NR_003950	647121	Hs.69768	NR_003950	ENS00000					



chr1-1603	12.90444	0.271296	0.65769	0.412498	0.679974	0.981636	chr1	1.6E+08	1.6E+08	+	0	NA	intron (AluSx SIN	12213 NM_001098	1314 Hs. 162121NM_004371	ENSG00000COPA	A1LJK HEF	coatomer protein-coding
chr1-1828	12.90444	0.271296	0.65769	0.412498	0.679974	0.981636	chr1	1.83E+08	1.83E+08	+	0	NA	non-codnon-codir	-27398 NR_148933	647070 Hs. 191518NR_148933	LOC647070	-	uncharactncRNA
chr1-1836	12.90444	0.271296	0.65769	0.412498	0.679974	0.981636	chr1	1.84E+08	1.84E+08	+	0	NA	intron (ALIMB4 LIN	6032 NM_005717	10092 Hs. 518609NM_005717	ENSG00000CARPC5	ARC16 dJ	lactin relprotein-coding
chr19-57	12.90444	0.271296	0.65769	0.412498	0.679974	0.981636	chr19	57327387	57300382	+	0	NA	exon (NM exon (NM	8262 NM_213598	125919 Hs. 202544NM_213598	ENSG00000ZNF543	-	zinc fingprotein-coding
chr7-9952	12.90444	0.271296	0.65769	0.412498	0.679974	0.981636	chr7	99524144	99533980	+	0	NA	intron (intron (N	23052 NM_145111	221786 Hs. 596587NM_145111	ENSG00000FAM200A	C7orf38	family wiprotein-coding
chr2-1012	7.365979	-0.35768	0.867346	-0.41238	0.680062	0.981636	chr2	1.01E+08	1.01E+08	+	0	NA	promoter-promoter-	-33 NR_00307C	692205 Hs. 656509NR_00307C	ENSG00000SNORD89	HB11-289	small nucsnoRNA
chr9-4171	7.365979	-0.35768	0.867346	-0.41238	0.680079	0.981636	chr9	41011142	41014048	+	0	NA	intron (intron (N	20334 NR_034006	1E+08 Hs. 231861NR_034006	FRG1HP	-	FSHD regpseudo
chr1-1101	7.213649	0.357442	0.867219	0.41217	0.680215	0.981636	chr1	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	9276 NM_006784	10885 Hs. 310809NM_006784	ENSG00000WDR3	DIP2 UTP1	WD repeatprotein-coding
chr17-615	7.213649	0.357442	0.867219	0.41217	0.680215	0.981636	chr17	61907507	61908265	+	0	NA	intron (intron (N	20096 NM_020748	57508 Hs. 279646NM_020748	ENSG00000INTS2	INT2 KIAI	integratcprotein-coding
chr17-633	7.213649	0.357442	0.867219	0.41217	0.680215	0.981636	chr17	63393566	63393988	+	0	NA	intron (AluSq2 SI	46490 NM_00133C	1534 Hs. 355264NM_00191E	ENSG00000CYB561	CYB561A1	cytochronprotein-coding
chr2-2245	7.213649	0.357442	0.867219	0.41217	0.680215	0.981636	chr2	2.25E+08	2.25E+08	+	0	NA	intron (Tigger2 I	-2877 NM_001257	8452 Hs. 372286NM_00359C	ENSG00000CUL3	CUL-3 PHA	cullin 3 protein-coding
chr1-3941	4.171812	-0.46581	1.1304	-0.41207	0.680286	0.981636	chr1	39416669	39418379	+	0	NA	intron (intron (N	8451 NM_01503E	643314 Hs. 658766NM_01503E	ENSG00000KIAA0754	-	KIAA0754 protein-coding
chr5-1325	4.171812	-0.46581	1.1304	-0.41207	0.680286	0.981636	chr5	1.33E+08	1.33E+08	+	0	NA	intron (NL2 LINE I	37369 NM_005732	10111 Hs. 633509NM_005732	ENSG00000RAD50	NBSLD RAI	RAD50 dotprotein-coding
chr12-121	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (AluJo SIN	-9152 NM_14466E	144406 Hs. 709837NM_14466E	ENSG00000WDR66	CFAP251 CWD	repatprotein-coding
chr14-313	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr14	31331115	31334290	+	0	NA	intron (NTigger1 I	87848 NM_01547E	25938 Hs. 744979NM_01547E	ENSG00000HEATR5A	C14orf12E	HEAT repeprotein-coding
chr14-914	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr14	91466661	91467435	+	0	NA	intron (intron (N	42656 NM_00136E	55671 Hs. 533887NM_01793E	ENSG00000PPP4R3A	FLFL1 KIAI	protein fprotein-coding
chr14-102	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	32791 NM_03094E	81693 Hs. 534494NM_03094E	ENSG00000CAM	PRO1028	eamion asprotein-coding
chr15-445	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr15	44594190	44595937	+	0	NA	intron (AluS2 SIN	57916 NM_00375E	8669 Hs. 404056NM_00375E	ENSG00000EIF3J	EIF3J2	eukaryotprotein-coding
chr15-636	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr15	63677354	63678006	+	0	NA	intron (intron (N	-76853 NR_03408C	1E+08 Hs. 631163NR_03408C	ENSG00000USP3-AS1	-	USP3 antincRNA
chr15-945	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr15	94336183	94337039	+	0	NA	intron (intron (N	-19319 NM_00115E	55784 Hs. 33368 NM_01834E	ENSG00000CMCTP2	-	multiple protein-coding
chr4-1406	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr4	1.81E+08	1.41E+08	+	0	NA	intron (intron (N	-18731 NR_07721E	644962 Hs. 676509NR_07721E	TNRC18P1	-	trinuclecpseudo
chr5-1802	7.221507	0.355267	0.862305	0.411997	0.680342	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	3' UTR (N3' UTR (N	-26616 NM_17506E	255426 Hs. 190556NM_17506E	ENSG00000CRASGEF1C	-	RasGEF dcprotein-coding
chr1-193	12.40785	0.276634	0.671997	0.411659	0.680589	0.981636	chr1	1.93E+08	1.93E+08	+	0	NA	intron (ALIMB4 LIN	-18387 NM_00135C	51377 Hs. 145469NM_01598A	ENSG00000UCHL5	CGI-70 I	ubiquitir protein-coding
chr10-675	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr10	67969418	67980533	+	0	NA	intron (AluSq2 SI	35908 NR_131184	1E+08 NR_131184	POU5F1P5	Oct4-pg5	POU classpseudo
chr15-412	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr15	41285370	41289048	+	0	NA	intron (AluSx SIN	1867 NR_152821	72908 Hs. 380164NR_026757	ENSG00000OIP5-AS1	cyrano I	OIP5 antincRNA
chr15-928	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr15	92885103	92896004	+	0	NA	intron (intron (N	7257 NR_03760E	1.01E+08 Hs. 622504NR_03760E	LINCO157E	-	long intencRNA
chr16-698	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr16	16283191	16289362	+	0	NA	exon (NM exon (NM	16283 NR_14575E	1.1E+08 NR_145753	SNORD13H	-	small nucsnoRNA
chr2-6524	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr2	65240355	65241911	+	0	NA	intron (intron (N	13438 NM_00100E	10097 Hs. 643727NM_00572E	ENSG00000ACTR2	ARP2	actin relprotein-coding
chr2-189C	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr2	1.89E+08	1.89E+08	+	0	NA	intron (intron (N	68044 NR_03607E	1E+08 NR_03607E	ENSG00000MIR3129	mir-3129	microRNA ncRNA
chr5-1135	10.12781	-0.30297	0.736157	-0.41156	0.680661	0.981636	chr5	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	40240 NM_00134E	64848 Hs. 231942NM_02282E	ENSG00000YTHDC2	CAHL hYTF	YTH domaiprotein-coding
chr8-2335	9.666356	-0.31283	0.760194	-0.41151	0.680695	0.981636	chr8	23333150	23333431	+	0	NA	intron (intron (N	-2918 NR_03832E	1.01E+08 Hs. 66113CNR_03832E	ENSG00000CLOC100507	-	uncharactncRNA
chr13-255	6.444916	-0.38205	0.928871	-0.4113	0.680852	0.981636	chr13	25311474	25311170	+	0	NA	intron (AluSq2 SI	9967 NM_01408E	9818 Hs. 507537NM_01408E	ENSG00000NUP58	NUP45 NUF	nucleopor protein-coding
chr17-376	6.444916	-0.38205	0.928871	-0.4113	0.680852	0.981636	chr17	37898553	37899914	+	0	NA	intron (AluU SINE	19685 NM_08055C	11276 Hs. 594647NM_007247	ENSG00000SYNRG	API6BP1	Synergir protein-coding
chrX-1294	6.444916	-0.38205	0.928871	-0.4113	0.680852	0.981636	chrX	1.29E+08	1.29E+08	+	0	NA	intron (AluSx1 SI	52694 NM_00128E	6594 Hs. 152292NM_00306E	ENSG00000SMARCA1	ISWI NURF	SWI/SNF iprotein-coding
chr1-310	10.86123	0.297158	0.722569	0.411251	0.680888	0.981636	chr1	31003532	31003861	+	0	NA	intron (AluSq2 SI	-35459 NR_00306E	692200 NR_003066	SNORD103C	HB11-251	small nucsnoRNA
chr1-2241	12.366671	0.275615	0.670467	0.411078	0.681015	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (AluSx1 SI	18093 NM_01517E	23219 Hs. 64691 NR_01517E	ENSG00000FBX028	CENP-30 FF	-box prcprotein-coding
chr7-102f	10.61284	-0.29776	0.724861	-0.41078	0.681233	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	10054 NM_00116E	1E+08 Hs. 433879NM_00116E	ENSG00000SPDYE2B	SPDYE2L	speedy/R1 protein-coding
chr20-38	9.212757	-0.32488	0.790993	-0.41072	0.681278	0.981636	chr20	38098954	38099197	+	0	NA	3' UTR (N3' UTR (N	56279 NM_00121E	58490 Hs. 278832NM_00212E	ENSG00000RPRD1B	C0orf77	regulaticprotein-coding
chr12-121	6.161768	0.382246	0.931638	0.410295	0.68159	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	intron (MLT1A0 LI	6704 NM_00128E	64897 Hs. 528671NM_02289E	ENSG00000C12orf43	Custos	chromosonprotein-coding
chr16-718	6.161768	0.382246	0.931638	0.410295	0.68159	0.981636	chr16	71800331	71801677	+	0	NA	intron (AluSp SIN	7830 NM_00103C	164 Hs. 461252NM_00112E	ENSG00000CAGP1G1	ADTG CLAF	adaptor iprotein-coding
chr2-6076	6.161768	0.382246	0.931638	0.410295	0.68159	0.981636	chr2	60797383	60797809	+	0	NA	3' UTR (N3' UTR (N	41328 NM_022894	64895 Hs. 387471NM_022894	ENSG00000PAPOLG	-	poly (A) iprotein-coding
chr10-101	6.873091	-0.36778	0.896399	-0.41029	0.681597	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (LJMEf LIN	106042 NM_024541	79591 Hs. 18004 NM_024541	ENSG00000ARMH3	C10orf76	armadillcprotein-coding
chr11-12C	6.873091	-0.36778	0.896399	-0.41029	0.681597	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (intron (N	39112 NM_001301	23365 Hs. 24598 NM_01531E	ENSG00000ARHGEF12	LARG PROE	Rho guaniprotein-coding
chr20-636	6.873091	-0.36778	0.896399	-0.41029	0.681597	0.981636	chr20	63667208	63667485	+	0	NA	intron (intron (N	9536 NM_032957	51750 Hs. 745057NM_016434	ENSG00000RTEL1	C20orf41	regulatoreprotein-coding
chr1-2797	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr1	27977506	27977299	+	0	NA	intron (AluSx4 SI	18190 NM_01805E	55113 Hs. 55024 NM_01805E	ENSG00000XKR8	XKR8 hXkr	Xkr relateprotein-coding
chr1-8564	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr1	85648485	85651214	+	0	NA	3' UTR (N3' UTR (N	58584 NM_00117C	54680 Hs. 5111 NM_01795E	ENSG00000ZNHIT6	BCD1 Clor	zinc fingprotein-coding
chr10-84C	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr10	84389338	84384722	+	0	NA	intron (NLIPB4 LIN	-40609 NM_001284	54462 Hs. 461988NM_01899E	ENSG00000CCSER2	FAM190B	coiled-cprotein-coding
chr11-671	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr11	67126921	67128363	+	0	NA	intron (intron (N	8379 NR_01230E	22992 Hs. 124147NM_01230E	ENSG00000KDM2A	CXXC8 FBI	lysine dcprotein-coding
chr12-781	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr12	78118088	78119449	+	0	NA	intron (intron (N	240978 NR_135021	1.05E+08 Hs. 156899NR_135021	ENSG00000LINC02424	-	long intencRNA
chr15-43C	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr15	43066580	43067942	+	0	NA	intron (intron (N	38777 NM_17491E	197131 Hs. 591121NM_17491E	ENSG00000UBR1	JBS	ubiquitir protein-coding
chr15-67C	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr15	67077300	67077887	+	0	NA	intron (NL2c LINE	11991 NM_00590E	4088 Hs. 727989NM_00590E	ENSG00000SMAD3	HSPC193 E	SMAD famiprotein-coding
chr15-101	6.906372	-0.36263	0.883853	-0.41028	0.681602	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (AluSp SIN	28846 NM_152334				

chr19-435	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr19	43540445	43544597	+	0	NA	TTS (NM_C TTS (NM_C	9333	NM_17494E	284346	Hs. 213534NM_17494E	ENSG000002ZNF575	-	zinc finger protein-coding	
chr2-3867	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr2	38678862	38681767	+	0	NA	intron (Alu)Jb SIN	14200	NM_138801	130589	Hs. 435012NM_138801	ENSG000002GALM	-	BLOCK25 Galactose protein-coding	
chr2-6075	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr2	60791449	60792713	+	0	NA	intron (intron)	35813	NM_022894	64895	Hs. 387471NM_022894	ENSG000002PAPOLG	-	poly(A) protein-coding	
chr2-2376	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	intron (Alu)Szl SIN	6922	NM_001278	140739	Hs. 47178E	ENSG000002UBEZF	-	ubiquitin protein-coding	
chr20-214	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr20	2144457	2145033	+	0	NA	3' UTR (3' UTR)	42918	NM_08083E	140901	Hs. 100057NM_08083E	ENSG000002STK35	-	CLK1 STK serine/threonine protein-coding	
chr20-351	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr20	35138862	35139463	+	0	NA	intron (Alu)Sc8 SI	8174	NM_00114E	55741	Hs. 720177NM_018217	ENSG000002CEDEM2	-	C20orf31 ER degrad protein-coding	
chr21-437	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr21	43795039	43801896	+	0	NA	intron (intron)	8890	NM_00368E	8568	Hs. 110757NM_00368E	ENSG000002RRP1	-	D21S2056F ribosomal protein-coding	
chr22-492	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr22	49220401	49221631	+	0	NA	intron (Tigger3a)	2382	NM_024324	79174	Hs. 211282NM_024324	ENSG000002CRELD2	-	cysteine protein-coding	
chr22-502	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr22	50222439	50223511	+	0	NA	intron (intron)	21964	NM_031454	83642	Hs. 36540E	ENSG000002SELENOO	-	SELO selenoprotein-coding	
chr3-524E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr3	52463155	52465214	+	0	NA	intron (Alu)S6 SI	8580	NM_001784	11188	Hs. 435292NM_007184	ENSG000002NISCH	-	I-1 IR1 Inischarin protein-coding	
chr3-1362	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr3	1.36E+08	1.36E+08	+	0	NA	intron (LIM4) LINE	29791	NM_00053E	5096	Hs. 63788	NM_00053E	ENSG000002PCCB	-	prionin protein-coding
chr4-131E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr4	1316197	1318828	+	0	NA	intron (intron)	7721	NM_001297	10296	Hs. 13989E	ENSG000002MAEA	-	EMLP EMP macrophage protein-coding	
chr4-271E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr4	2716084	2717594	+	0	NA	intron (Alu)Sx1 SI	39497	NM_02430E	79155	Hs. 368551NM_02430E	ENSG000002TNIP2	-	ABIN2 FLI1 TNFAIP3 protein-coding	
chr4-5801	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr4	5801725	5803142	+	0	NA	intron (MERIA) DNA	85830	NM_00128E	1400	Hs. 13527NM_00131E	ENSG000002CRMP1	-	CRMP-1 DF collapsin protein-coding	
chr4-581E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr4	5818380	5821395	+	0	NA	TTS (NM_C TTS (NM_C	67926	NM_00128E	1400	Hs. 13527NM_00131E	ENSG000002CRMP1	-	CRMP-1 DF collapsin protein-coding	
chr4-156E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr4	1.57E+08	1.57E+08	+	0	NA	intron (THEIC-int)	131466	NR_036641	56034	Hs. 57085E	NM_01620E	ENSG000002PDGFC	-	FALL0TEIN platelet protein-coding
chr5-171E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr5	1719306	37119959	+	0	NA	intron (Alu)Sp SIN	-129414	NR_13426E	1.05E+08	Hs. 17099E	NR_13426E	ENSG000002LOC105374	-	uncharactericnRNA
chr5-176E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (intron)	-31636	NM_00211E	3101	Hs. 41169E	NM_00211E	ENSG000002HK3	-	HKIII HXK hexokinase protein-coding
chr6-386E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr6	38681953	38684266	+	0	NA	intron (AAT)n Si	20036	NM_00670E	2739	Hs. 26884E	NM_00670E	ENSG000002GLO1	-	GLOD1 GLYglyoxalase protein-coding
chr6-875E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr6	87552416	87553192	+	0	NA	intron (intron)	37183	NM_02032E	57038	Hs. 48591NM_02032E	ENSG000002CARS2	-	ArgRS DAL arginyl-t protein-coding	
chr8-2904	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr8	29048309	29049587	+	0	NA	intron (intron)	157634	NM_001324	79618	Hs. 56356E	NM_02456E	ENSG000002HMB0X1	-	HNF1LA Hc homeobox protein-coding
chr9-797E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr9	79727135	79727693	+	0	NA	TTS (NM_C TTS (NM_C	-97116	NR_12121E	1.02E+08	Hs. 57163E	NR_12121E	LINC01507	XLOC_000E	long intencnRNA
chr9-9764	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr9	97641334	97642631	+	0	NA	intron (intron)	8161	NM_00248E	4686	Hs. 59566E	NM_00248E	ENSG000002NCBP1	-	CBP80 NCF nuclear protein-coding
chr9-108E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr9	1.99E+08	1.09E+08	+	0	NA	intron (MIRb) SINE	26519	NM_00131E	8518	Hs. 49473E	NM_00364E	ENSG000002ELP1	-	DYS FD Elongator protein-coding
chr9-135E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (intron)	88208	NM_015447	157922	Hs. 52249E	NM_015447	ENSG000002CAMSAP1	-	calmodulin protein-coding
chr9-137E	6.699495	0.365458	0.892125	0.409649	0.682063	0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	intron (intron)	10085	NR_14750E	651337	Hs. 60319E	NR_14750E	ENSG000002LOC651337	-	uncharactericnRNA
chr1-1112	7.229365	0.353169	0.862427	0.409506	0.682168	0.981636	chr1	11123842	11125111	+	0	NA	intron (intron)	-19422	NR_04660E	1.01E+08	Hs. 67913E	NR_04660E	ENSG000002MOR-AS1	-	MTOR antincRNA
chr10-10E	7.229365	0.353169	0.862427	0.409506	0.682168	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (LTR86B) L	15593	NM_001351	22978	Hs. 97439	NM_01222E	ENSG000002NT5C2	-	GMP NT5B 5'-nuclec protein-coding
chr14-20E	7.229365	0.353169	0.862427	0.409506	0.682168	0.981636	chr14	20369406	20371922	+	0	NA	intron (LIM3E) LIN	27050	NM_00104E	10038	Hs. 40941E	NM_00548E	ENSG000002PARP2	-	ADPRT2 AI poly(ADP- protein-coding
chr19-24E	7.229365	0.353169	0.862427	0.409506	0.682168	0.981636	chr19	24065612	24056825	+	0	NA	intron (BMSR Beta)	23034	NM_00127E	9534	Hs. 43440E	NM_00487E	ENSG000002ZNF254	-	ZFP69A ZK2F699 zinc finger protein-coding
chr20-50E	7.229365	0.353169	0.862427	0.409506	0.682168	0.981636	chr20	50634184	50635152	+	0	NA	intron (intron)	2250	NM_08082E	140876	Hs. 37257E	NM_08082E	ENSG000002RIPOR3	-	C20orf17E RIPOR fan protein-coding
chr21-37E	7.229365	0.353169	0.862427	0.409506	0.682168	0.981636	chr21	37181354	37181763	+	0	NA	intron (intron)	12368	NR_046651	1.01E+08	Hs. 57041E	NR_046651	ENSG000002TTC3-AS1	-	TTC3 antincRNA
chr10-60E	5.916896	-0.41608	1.016301	-0.40941	-0.682242	0.981636	chr10	60878508	60878802	+	0	NA	intron (intron)	65530	NM_00135E	9886	Hs. 73737E	NM_01483E	ENSG000002RHOBTB1	-	RHO relat protein-coding
chr12-62E	4.205094	-0.45725	1.11691	-0.40939	0.682254	0.981636	chr12	62336706	62337650	+	0	NA	TTS (NM_C TTS (NM_C	76774	NR_14708E	9958	Hs. 43495E	NM_00631E	ENSG000002CUSP15	-	UNPH-2 Ubiquitin protein-coding
chr15-40E	4.205094	-0.45725	1.11691	-0.40939	0.682254	0.981636	chr15	40975957	40977293	+	0	NA	Intergeni Intergeni	23154	NM_00114E	79094	Hs. 15556E	NM_02411E	ENSG000002CHAC1	-	ChaC glut protein-coding
chr2-202E	4.205094	-0.45725	1.11691	-0.40939	0.682254	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (intron)	-10988	NM_17351E	150864	Hs. 47113E	NR_17351E	ENSG000002FAM117B	-	ALS2CR13 family wiprotein-coding
chr7-158E	4.205094	-0.45725	1.11691	-0.40939	0.682254	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	intron (Alu)Sp SIN	49978	NM_00135E	55112	Hs. 38994E	NM_01805E	ENSG000002WDR60	-	FAP163 SFWD repeat protein-coding
chr1-404E	7.391403	-0.35086	0.857306	-0.40926	0.68235	0.981636	chr1	40483852	40484695	+	0	NA	intron (Alu)Sx1 SI	6983	NM_00132E	339559	Hs. 4438E	NM_19849E	ENSG000002ZFP69	-	ZFP69A ZK2F699 zinc finger protein-coding
chr9-324E	7.391403	-0.35086	0.857306	-0.40926	0.68235	0.981636	chr9	32498696	32500298	+	0	NA	intron (Alu)Sx2 SI	26699	NM_014314	23586	Hs. 19062E	NM_014314	ENSG000002DDX58	-	RIG-1 RIC DEXD Hc protein-coding
chr16-701	12.37457	0.27438	0.670691	0.409101	0.682466	0.981636	chr16	70121849	70124783	+	0	NA	intron (Alu)Jb SIN	9690	NM_00132E	55066	Hs. 74404E	NM_01799E	ENSG000002PDPR	-	PDP3 pyruvate protein-coding
chr2-9514	12.37457	0.27438	0.670691	0.409101	0.682466	0.981636	chr2	95147656	95157613	+	0	NA	intron (intron)	6951	NM_00131E	84874	Hs. 35566E	NM_03278E	ENSG000002ZNF514	-	zinc finger protein-coding
chr12-10E	7.383545	-0.34903	0.853619	-0.40889	0.682624	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (MIR SINE)	5495	NM_001251	55198	Hs. 50660E	NM_01817E	ENSG000002APL2	-	DIP13B adaptor protein-coding
chr14-574	7.383545	-0.34903	0.853619	-0.40889	0.682624	0.981636	chr14	57409589	57410147	+	0	NA	3' UTR (3' UTR)	19282	NM_001011	122830	Hs. 16546E	NM_001011	ENSG000002NAA30	-	C14orf35 N(alpha)-protein-coding
chr21-14E	7.383545	-0.34903	0.853619	-0.40889	0.682624	0.981636	chr21	14373739	14375601	+	0	NA	intron (intron)	8476	NM_00694E	6782	Hs. 35234E	NM_00694E	ENSG000002HSPA13	-	STCH heat shock protein-coding
chr9-1284	7.383545	-0.34903	0.853619	-0.40889	0.682624	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (MER103) E	-22477	NM_00100E	2733	Hs. 52241E	NM_00149E	ENSG000002CGLE1	-	CAAH CA GLE1 RNA protein-coding
chr3-470E	10.17681	-0.3021	0.738902	-0.40885	0.682649	0.981636	chr3	47037397	47038937	+	0	NA	intron (intron)	26625	NR_02404E	1E+08	Hs. 20152E	NR_02404E	NRADDP	-	neurotroph pseudo
chr10-94E	6.947512	-0.35942	0.879386	-0.40872	0.682747	0.981636	chr10	94336363	94336694	+	0	NA	intron (MER85) DNA	26911	NM_022451	64318	Hs. 74899	NM_022451	ENSG000002NOC3L	-	AD24 C10C NOC3 like protein-coding
chr11-64E	6.947512	-0.35942	0.879386	-0.40872	0.682747	0.981636	chr11	64261973	64263594	+	0	NA	exon (NM exon (NM	11254	NM_00093E	5331	Hs. 52376E	NM_00093E	ENSG000002CLCB3	-	phospholip protein-coding
chr13-197	6.947512	-0.35942	0.879386	-0.40872	0.682747	0.981636	chr13	19758795	19759735	+	0	NA	intron (intron)	23680	NM_001354	55269	Hs. 21319E	NM_00104E	ENSG000002PSPC1	-	PSP1 paraspeck protein-c



chr7-9248 7.196083	0.349472	0.859992	0.406367	0.684473	0.981636	chr7	92487810	92489204	+	0	NA	intron (NCharlie23	-10561	NM_00113C	30816	ENV ENW	endogenot	protein-coding				
chr7-112 7.196083	0.349472	0.859992	0.406367	0.684473	0.981636	chr7	1.12E+08	1.12E+08	+	0	NA	intron (NAluV SINE	-102124	NM_001197	3475	Hs. 7879	ENV ENW	interferc	protein-coding			
chr9-511 7.196083	0.349472	0.859992	0.406367	0.684473	0.981636	chr9	5113828	5114309	+	0	NA	intron (Nintron (N	71571	NM_007175	11172	Hs. 63264	ENV ENW	insulin l	protein-coding			
chr9-3397 7.196083	0.349472	0.859992	0.406367	0.684473	0.981636	chr9	33970922	33972229	+	0	NA	intron (Nintron (N	-18721	NR_00368E	1E+08	ENV ENW	small nuc	snoRNA				
chr9-1017 7.196083	0.349472	0.859992	0.406367	0.684473	0.981636	chr9	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	28023	NM_019592	56254	Hs. 72908	ENV ENW	BRE1 BRE1	ring finger	protein-coding		
chr6-133 9.658498	-0.31131	0.766124	-0.40635	0.684489	0.981636	chr6	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	31771	NM_00486E	9519	Hs. 486507	ENV ENW	MGC:8389 TATA-box	protein-coding			
chr2-7141 7.342405	-0.35227	0.866926	-0.40634	0.684491	0.981636	chr2	71412438	71412996	+	0	NA	intron (N LHS LINE	-40844	NM_00113C	8291	Hs. 25218	ENV ENW	FER1L1 LC	dysferlin	protein-coding		
chr14-675 11.87798	0.280026	0.689221	0.406293	0.684527	0.981636	chr14	67321258	67321470	+	0	NA	intron (Nintron (N	38440	NM_015994	51382	Hs. 27263	ENV ENW	ATP6M VIA	ATPase H	protein-coding		
chr2-921 12.92015	0.268925	0.662202	0.406108	0.684663	0.981636	chr2	92198845	92200155	+	0	NA	IntergeniALR/Alpha	258367	NR_027714	440888	Hs. 73023	ENV ENW	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo
chr11-10 6.658356	0.363781	0.895884	0.406058	0.6847	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	80970	NM_001351	472	Hs. 367437	ENV ENW	ATM	ATM	serin	protein-coding	
chr16-12 6.658356	0.363781	0.895884	0.406058	0.6847	0.981636	chr16	12052331	12052866	+	0	NA	intron (Nintron (N	75864	NM_032167	92017	Hs. 458401	ENV ENW	SNX29	SNX29	l	protein-coding	
chr2-134 6.658356	0.363781	0.895884	0.406058	0.6847	0.981636	chr2	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	88187	NM_00241C	4249	Hs. 4988	ENV ENW	MGAT5	GNT-V GNI	alpha-1, f	protein-coding	
chr2-402 6.658356	0.363781	0.895884	0.406058	0.6847	0.981636	chr2	40278637	40279019	+	0	NA	intron (NAluS SIN	-67672	NM_00136E	158	Hs. 75527	ENV ENW	ADSL	AMP5 ASAS	adenylot	protein-coding	
chr7-748 6.658356	0.363781	0.895884	0.406058	0.6847	0.981636	chr7	7487569	74858663	+	0	NA	IntergeniLIMB4 LIN	-6575	NM_001281	84163	Hs. 647017	ENV ENW	GTF2IRD2	FP630 GTF	GTF2I	rep	protein-coding
chr8-970 6.658356	0.363781	0.895884	0.406058	0.6847	0.981636	chr8	9706432	9707509	+	0	NA	exon (NM exon (NM	-34702	NR_030327	693182	ENV ENW	MIR597	mi	microRNA	ncRNA		
chr12-45 6.202907	0.38378	0.945152	0.406051	0.684705	0.981636	chr12	45874160	45875192	+	0	NA	intron (NTigger1 I	115898	NM_00471E	9169	Hs. 210367	ENV ENW	SCAF11	CASP11 SF	SR-relate	protein-coding	
chr18-54 12.38243	0.273127	0.67307	0.405792	0.684895	0.981636	chr18	54924912	54927104	+	0	NA	intron (NMamRep I	32040	NM_00114E	80323	Hs. 12079	ENV ENW	CCDC68	SE57-1	coiled-c	protein-coding	
chr12-54 10.63041	-0.29187	0.7193	-0.40577	0.684908	0.981636	chr12	54394013	54411130	+	0	NA	intron (NAluSg S	-11273	NM_00113C	25946	Hs. 50565	ENV ENW	ZNF385A	HZF RZF	zinc	finger	protein-coding
chr5-128 10.63041	-0.29187	0.7193	-0.40577	0.684908	0.981636	chr5	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	2594	NM_00199E	2201	Hs. 51929	ENV ENW	PBN2	CCA DA9 E	fibri	protein-coding	
chr6-362 10.63041	-0.29187	0.7193	-0.40577	0.684908	0.981636	chr6	36201054	36201880	+	0	NA	exon (NM exon (NM	4723	NM_01569E	27154	Hs. 52009	ENV ENW	BRPF3	-	bromodome	protein-coding	
chr7-134 10.63041	-0.29187	0.7193	-0.40577	0.684908	0.981636	chr7	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	-24692	NR_10209E	340351	Hs. 64861	ENV ENW	AGBL3	CCP3	ATP GTP	l	protein-coding
chr1-838 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr1	8388365	8390369	+	0	NA	intron (Nintron (N	34465	NM_00104E	473	Hs. 463041	ENV ENW	ERERE	ARG ARP A	arginine-	protein-coding	
chr1-539 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr1	53965173	53966864	+	0	NA	intron (Nintron (N	19668	NM_00125E	115353	Hs. 40094	ENV ENW	LRRRC42	dJ167A19.	leucine	protein-coding	
chr1-1137 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr1	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	-15135	NM_00132E	10745	Hs. 65582	ENV ENW	PHTF1	PHTF1	putative	protein-coding	
chr12-48 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr12	48678565	48679005	+	0	NA	intron (Nintron (N	3453	NM_01782E	54934	Hs. 50541	ENV ENW	KANSL2	C12orf41 KAT8	regu	protein-coding	
chr12-12 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NAluSx SIN	26193	NM_00135E	55596	Hs. 37706	ENV ENW	ZCCHC8	-	zinc	finger	protein-coding
chr15-42 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr15	42229502	42229912	+	0	NA	intron (Nintron (N	-21403	NM_01528E	23339	Hs. 88025	ENV ENW	VP39	TLP VAM6	VPS39	sub	protein-coding
chr16-69 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr16	69787446	69788122	+	0	NA	intron (N L2a LINE	25452	NM_007014	11060	Hs. 40845	ENV ENW	WPP2	AIP2 WPP2	WW	domain	protein-coding
chr2-272 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr2	27219003	27219341	+	0	NA	intron (Nintron (N	1782	NM_00130E	790	Hs. 37701	ENV ENW	CCAD	CDG1Z EIF	carbamoyl	protein-coding	
chr2-32 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr2	32859448	32862143	+	0	NA	3' UTR (N3' UTR (N	59997	NM_00036E	7078	Hs. 64463	ENV ENW	TIMP3	HSMRK222 TIMP	met	protein-coding	
chr4-118 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	exon (NM exon (NM	46108	NM_020961	57721	Hs. 59687	ENV ENW	MTTL14	hMETTL14	methyl	protein-coding	
chr7-233 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr7	23321380	23322118	+	0	NA	intron (N LIPA3 LI	22410	NM_13844E	115416	Hs. 87385	ENV ENW	MALSU1	C7orf30 NMI	tochon	protein-coding	
chr8-230 6.939654	-0.35752	0.881191	-0.40572	0.684948	0.981636	chr8	23011281	23013940	+	0	NA	intron (N LIME3B LI	13800	NM_01517E	23221	Hs. 37268	ENV ENW	RHOBT2	DBC2 EIFE	Rho	relat	protein-coding
chr14-751 10.63827	-0.29315	0.722658	-0.40565	0.684998	0.981636	chr14	75133753	75135735	+	0	NA	3' UTR (N3' UTR (N	-7696	NM_00132E	91754	Hs. 7200	ENV ENW	CNEK9	APUG LCCS	NIMA	rel	protein-coding
chr16-317 10.90237	0.298603	0.735002	0.405527	0.68509	0.981636	chr16	31723534	31723821	+	0	NA	intron (Nintron (N	10448	NM_00113C	124411	Hs. 52882	ENV ENW	ZNF720	-	zinc	finger	protein-coding
chr6-965 5.616182	0.404283	0.997624	0.405246	0.685297	0.981636	chr6	96540436	96540892	+	0	NA	intron (Nintron (N	18858	NM_01532E	23376	Hs. 149367	ENV ENW	UFL1	KIAA0776 UFMI	spec	protein-coding	
chr6-321 10.86909	0.295575	0.729629	0.405103	0.685402	0.981636	chr6	32187876	32188075	+	0	NA	exon (NM exon (NM	2227	NM_00258E	5089	Hs. 50954	ENV ENW	PBX2	G17 HOX12	PBX	home	protein-coding
chr1-111 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr1	11197034	11199714	+	0	NA	intron (Nintron (N	9019	NM_02114E	10218	Hs. 14655	ENV ENW	ANGPTL7	AngX CDT	angiopoie	protein-coding	
chr10-91 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr10	91966806	91968160	+	0	NA	intron (Nintron (N	43713	NM_00397E	9044	Hs. 50052	ENV ENW	BTAF1	MOT1 TAF	B-TFID	l	protein-coding
chr11-78 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr11	78206024	78206251	+	0	NA	intron (Nintron (N	17218	NM_02079E	57558	Hs. 53124	ENV ENW	CUSP35	-	ubiquit	protein-coding	
chr14-40 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr14	30673799	30675751	+	0	NA	intron (Nintron (N	52456	NM_01610E	23256	Hs. 36916	ENV ENW	SCDF1	C14orf16E	secl	fam	protein-coding
chr14-44 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr14	44939957	44941969	+	0	NA	intron (NAluSg SIN	20522	NM_00130E	54813	Hs. 55090	ENV ENW	KLHL28	BTBD5	kelch	lik	protein-coding
chr16-70 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr16	70009488	70013931	+	0	NA	intron (Nintron (N	-18637	NR_03626E	1E+08	ENV ENW	MIR1972-2	-	microRNA	ncRNA		
chr16-87 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr16	87409770	87411845	+	0	NA	intron (NMERSB DNA	18471	NM_02281E	81631	Hs. 356061	ENV ENW	MAP1LC3B	ATG8F LC	microtub	protein-coding	
chr17-56 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr17	54958383	54961581	+	0	NA	intron (Nintron (N	8672	NR_135677	1353	Hs. 59117	ENV ENW	COX11	COX11P	cytochro	protein-coding	
chr17-74 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr17	76768936	76771438	+	0	NA	intron (NAluY SINE	-28857	NR_110837	1.02E+08	Hs. 61720	ENV ENW	LINC0208C	-	long	int	ncRNA
chr18-48 6.666214	0.361536	0.893013	0.40485	0.685588	0.981636	chr18	48816709	48820076	+	0	NA	intron (N L2 LINE L	124415	NM_00119C	4							



chr6-8761 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chr6	87611266	87613862	+	0	NA	intron (Nintron (N	22497 NM_012381	23595 Hs. 41022ENM_012381	ENSG000000C0RC3	LAT1	LATHE origin reprotein-coding	
chr6-1057 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chr6	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	50949 NM_00272f	5550 Hs. 436564NM_00272f	ENSG000000PREP	PE1	PEP prolyl erprotein-coding	
chr7-591f 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chr7	5910169	5912094	+	0	NA	intron (Nintron (N	12398 NM_015622	51622 Hs. 530000NM_015622	ENSG000000CCZ1	C7orf28A	CCZ1 homcprotein-coding	
chr7-101f 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chr7	1.01E+08	1.01E+08	+	0	NA	intron (NAluX1 S1	6481 NM_001084	8985 Hs. 153357NM_001084	ENSG000000PLOD3	LH3	procollagprotein-coding	
chr9-128f 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	-14584 NM_00443f	2021 Hs. 745161NM_00443f	ENSG000000ENDOG	-	endonucleprotein-coding	
chr9-132f 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (NAluX3 S1	17405 NR_13452f	7270 Hs. 54780 NM_007344	ENSG000000TTF1	TTF-1	TTF transcrip protein-coding	
chrX-166f 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chrX	16692955	16693349	+	0	NA	exon (NM exon (NM	19065 NM_001144	56474 Hs. 227049NM_019857	ENSG000000CTPS2	-	CTP syntp protein-coding	
chrX-406f 7.203941	0.347381	0.860114	0.403879	0.686302	0.981636	chrX	40688336	40688673	+	0	NA	exon (NM exon (NM	-40943 NM_00133C	159013 Hs. 495961NM_14497	ENSG000000CXorf38	-	chromosonprotein-coding	
chr6-149f 10.15324	-0.29815	0.738298	-0.40383	0.686337	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	non-codiron-codir	-13058 NM_001204	11104 Hs. 450177NM_007044	ENSG000000KATNA1	-	katanin cprotein-coding	
chr12-114 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr12	1.15E+08	1.15E+08	+	0	NA	intron (Nintron (N	8991 NM_01656f	6926 Hs. 74401fNM_00599f	ENSG000000TBX3	TBX3-ISO1	T-box tr3protein-coding	
chr15-55f 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr15	55830179	55831075	+	0	NA	intron (Nintron (N	86504 NM_001284	4734 Hs. 1565 NM_006154	ENSG000000NEDD4	NEDD4-1	fNEDD4 e3 protein-coding	
chr16-10f 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr16	10927478	10928903	+	0	NA	TTS (NM_TTS (NM_C	14278 NM_01401f	28955 Hs. 592051NM_01401f	ENSG000000DEX1	MYLE	Dexi homcprotein-coding	
chr18-58f 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr18	58500417	58502959	+	0	NA	intron (NMTIR SINE	-50536 NR_03989f	NR_03989f	ENSG000000MIR3591	-	microRNA ncRNA	
chr2-227 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (NAluX1 S1	-20215 NM_00117f	3769 Hs. 46733fNM_00224f	ENSG000000KCNJ13	KIR1.4	KIpotassiumprotein-coding	
chr4-168f 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (Nintron (N	79974 NM_001291	91351 Hs. 535011NM_00101f	ENSG000000DDX60L	-	DEX/H-bcprotein-coding	
chr5-782f 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr5	78259010	78260062	+	0	NA	intron (NLMIA1 LIN	35162 NM_001271	8546 Hs. 532091NM_003664	ENSG000000AP3B1	ADTB3	AD1adaptor rprotein-coding	
chr9-132f 7.416826	-0.34427	0.852675	-0.40376	0.68639	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-6448 NR_024514	11093 Hs. 13143fNM_13902f	ENSG000000ADAMTS13	ADAM-TS1f	ADAM meteprotein-coding	
chr1-126 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	exon (NM exon (NM	10871 NM_001042	389 Hs. 50265fNM_17574f	ENSG000000RHOC	ARH9	ARHc ras homolprotein-coding	
chr10-501 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr10	50112863	50113157	+	0	NA	intron (NLMIB7 LIN	45056 NM_00100f	387680 Hs. 36528fNM_01823f	ENSG000000WASHC2A	FAM21A	fWASH comprotein-coding	
chr14-73f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr14	73913091	73913538	+	0	NA	intron (NLTRE1 LTF	26455 NR_040251	57862 Hs. 27086fNM_02118f	ENSG000000ZNF410	APA-1	APAzinc fingprotein-coding	
chr17-82f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr17	82329129	8229453	+	0	NA	intron (Nintron (N	-5248 NR_026951	284209 Hs. 12169fNM_17362f	ENSG000000C17orf44	C17orf44	long intcncRNA	
chr17-42f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr17	42380741	42380940	+	0	NA	intron (NAluJb SIN	7602 NM_00136f	6774 Hs. 46305fNM_00315f	ENSG000000STAT3	ADM10	ADM signal tprotein-coding	
chr2-179f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr2	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	37251 NM_02094f	57703 Hs. 31136fNM_02094f	ENSG000000CWC22	EIF4GL	NCWC22 splprotein-coding	
chr22-36f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr22	36359450	36359886	+	0	NA	intron (Nintron (N	28399 NM_00247f	4627 Hs. 474751NM_00247f	ENSG000000MYH9	BDPLT6	DFmyosin heprotein-coding	
chr3-132f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	intron (NLMIP7 LIN	14962 NM_17844f	51554 Hs. 31051fNM_01655f	ENSG000000ACKR4	CC-CKR	-11atypical protein-coding	
chr4-474f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr4	47578267	47578913	+	0	NA	intron (Nintron (N	-74709 NR_10702C	1.02E+08	NR_10702C	ENSG000000MIR8053	hsa-mir-5	microRNA ncRNA
chr5-145f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr5	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	51330 NM_001271	1452 Hs. 52986fNM_00189f	ENSG000000CSNK1A1	K11	CK1acasein kiprotein-coding	
chr5-154f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr5	1.54E+08	1.54E+08	+	0	NA	intron (NMTIR SINE	-48536 NR_03162f	fE+08	NR_03162f	ENSG000000MIR1294	MIRN1294	microRNA ncRNA
chr8-119f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr8	1.19E+08	1.19E+08	+	0	NA	TTS (NM_TTS (NM_C	-40569 NR_13429f	1.02E+08	Hs. 67659fNR_13429f	ENSG000000LOC101927	-	uncharactncRNA
chr9-129f 6.898514	-0.36064	0.893856	-0.40346	0.686607	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	3' UTR (N3' UTR (N	20025 NR_106914	1.02E+08	NR_106914	ENSG000000MIR6855	hsa-mir-5	microRNA ncRNA
chr1-246f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr1	24673882	24677432	+	0	NA	Intergenil2 LINE I	32078 NM_00136f	10250 Hs. 1819f	NM_00583f	ENSG000000SSRM1	160-KD	PCserine arprotein-coding
chr1-326f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr1	32691253	32692409	+	0	NA	intron (NMER33 DNA	10939 NM_001161	81943 Hs. 712631NM_03078f	ENSG000000SYNC	SYNC1	SYN syncoilir protein-coding	
chr1-333f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr1	33358961	33359804	+	0	NA	intron (Nintron (N	9030 NR_12597f	1.02E+08	Hs. 56862fNR_12597f	ENSG000000LOC10192f	-	uncharactncRNA
chr1-519f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr1	51939461	51945109	+	0	NA	intron (Nintron (N	48415 NM_00286f	5865 Hs. 12307fNM_00286f	ENSG000000CRAB3B	-	RAB3B, meprotein-coding	
chr10-12f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	50156 NM_001321	1488 Hs. 50134fNM_00132f	ENSG000000CTBP2	-	C-termin protein-coding	
chr11-56f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr11	5668593	5670762	+	0	NA	intron (Nintron (N	15397 NR_03309f	85363 Hs. 12530fNM_03303f	ENSG000000TRIM5	RNF88	TRI tripartitprotein-coding	
chr16-84f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr16	84563710	84569667	+	0	NA	3' UTR (N3' UTR (N	51390 NM_02114f	23406 Hs. 28909fNM_02114f	ENSG000000COTL1	CLP	coactosir protein-coding	
chr17-36f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr17	36571792	36573526	+	0	NA	intron (NAluJb SIN	-19220 NM_02430f	79154 Hs. 46285fNM_02430f	ENSG000000DHR511	ARGH836	Scdehydrogprotein-coding	
chr17-74f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr17	74206149	74207149	+	0	NA	intron (NAluY SINE	3142 NM_00103f	6169 Hs. 38095fNM_00099f	ENSG000000RPL38	L38	ribosomalprotein-coding	
chr17-77f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr17	77214888	77218463	+	0	NA	3' UTR (N3' UTR (N	31462 NM_001144	6397 Hs. 464184NM_00300f	ENSG000000SEC14L1	PRELID4A	SEC14 ilkprotein-coding	
chr19-17f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr19	17204084	17209748	+	0	NA	intron (Nintron (N	-8440 NM_01846f	58550 Hs. 16187	NM_01846f	ENSG000000USE1	D12	MDSOconventprotein-coding
chr19-48f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr19	48188049	48189482	+	0	NA	intron (NAluY SINE	18085 NR_1199341	374920 Hs. 664054NM_199341	ENSG000000ZSWIM9	C19orf68	zinc fingprotein-coding	
chr2-951f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr2	9519165	9522523	+	0	NA	intron (NAluSp SIN	34986 NM_00318f	6868 Hs. 404914NM_00318f	ENSG000000ADAM17	ADAM18	CI ADAM meteprotein-coding	
chr2-156f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr2	15620935	15633854	+	0	NA	intron (Nintron (N	35526 NM_00493f	1653 Hs. 44059fNM_00493f	ENSG000000DDX1	DBP-RE	UBDEAD-box protein-coding	
chr2-1327 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-110282 NR_00107f	116372 Hs. 43239fNM_14458f	ENSG000000LYPD1	LYPD1	PL-LY6/PLAUf protein-coding	
chr20-38f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr20	3800748	38006470	+	0	NA	intron (Nintron (N	3547 NM_001287	994 Hs. 15375fNM_00435f	ENSG000000CDC25B	-	cell diviprotein-coding	
chr21-25f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr21	25596295	25597355	+	0	NA	intron (NTiger19a	10664 NM_01744f	54148 Hs. 42069fNM_01744f	ENSG000000MRPL39	C21orf92	mitochoncprotein-coding	
chr3-472f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr3	47728161	47728966	+	0	NA	intron (NLM5 LINE	53330 NM_003074	6599 Hs. 47617fNM_003074	ENSG000000SMARCC1	BAP155	CFSWI/ SNF rprotein-coding	
chr3-177f 7.408968	-0.3425	0.849006	-0.40341	0.686647	0.981636	chr3	1.72E+08											



chr15-801	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr15	80122732	80123942	+	0 NA	intron (Nintron (N	24921 NM_001242	54469 Hs. 596679	NR_019006	ENSG000002ZFAND6	AWP1 ZA2C zinc finger protein-coding
chr16-676	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr16	67619841	67621710	+	0 NA	exon (NM exon (NM	-24369 NM_001013	146206 Hs. 611432	NR_001013	ENSG000003CARMIL2	CARMIL2 capping protein-coding
chr17-497	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	4970541	4973004	+	0 NA	intron (NAluS6 SI	-1622 NR_106925	1.02E+08	NR_106925	ENSG000003MIR6865	hsa-mir-6microRNA ncRNA
chr17-275	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	27315519	27318348	+	0 NA	IntergeniMER30 DNA	22819 NM_134265	26118 Hs. 446017	NR_015626	ENSG000003WSB1	SWP1 WSEWD repeat protein-coding
chr17-356	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	35684631	356897243	+	0 NA	intron (NAluSq2 SI	-45702 NM_033315	91608 Hs. 744994	NR_033315	ENSG000003RASL10B	RRP17 VTSRAS like protein-coding
chr17-376	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	37617146	37620174	+	0 NA	intron (NAluSp SIN	-3621 NR_106744	1.02E+08	NR_106744	ENSG000003MIR378J	hsa-mir-3microRNA ncRNA
chr17-385	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	38323131	38323603	+	0 NA	TTS (NM_CTS (NM_C	20443 NM_001004	440435 Hs. 462915	NR_001004	ENSG000003GPR179	CSNB1E GFG protein protein-coding
chr17-400	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	40025086	40026686	+	0 NA	TTS (NR_ITTS (NR_I	523 NR_106944	1.02E+08	NR_106944	ENSG000003MIR6884	hsa-mir-6microRNA ncRNA
chr17-470	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr17	47049405	47049799	+	0 NA	IntergeniIntergeni	-70349 NM_20340C	388394 Hs. 367999	NR_20340C	ENSG000003RPRML	- reprimol protein-coding
chr18-96C	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr18	9600638	9601423	+	0 NA	intron (Nintron (N	13529 NR_052003	9989 Hs. 743236	NR_005134	ENSG000003PPP4R1	MEG1 PP4 protein protein-coding
chr2-9355	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr2	9359013	9360424	+	0 NA	intron (Nintron (N	62964 NM_001315	9270 Hs. 467662	NR_004765	ENSG000003ITGB1BP1	ICAP-1A Integrin protein-coding
chr2-261C	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr2	26109738	26113448	+	0 NA	intron (NAluSp SIN	-61495 NM_001168	150946 Hs. 187912	NR_001168	ENSG000003GAREM2	FAM59B GARGB2 asc protein-coding
chr2-8648	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr2	86488498	86491814	+	0 NA	intron (Nintron (N	48660 NM_001146	55818 Hs. 557422	NR_018433	ENSG000003KDM3A	JHDM2A JF lysine deprotein-coding
chr2-1087	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr2	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	-5131 NM_001351	165055 Hs. 362702	NR_106930	ENSG000003CCDC138	- coiled-co protein-coding
chr2-1357	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr2	1.36E+08	1.36E+08	+	0 NA	3' UTR (N3' UTR (N	-35654 NR_04548E	1.01E+08	NR_04548E	ENSG000003LOC100507	- uncharactericncRNA
chr21-648	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr21	6489074	6493711	+	0 NA	intron (Nintron (N	7856 NM_00132C	1.03E+08	NR_00132C	ENSG000003U2AF1L5	- U2 small protein-coding
chr3-4767	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr3	47675379	47679276	+	0 NA	intron (NAluSx1 SI	-15633 NR_145791	1.1E+08	NR_145791	SNORD146	- small nucsnoRNA
chr3-158E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr3	1.59E+08	1.59E+08	+	0 NA	intron (Nintron (N	7642 NM_02016E	56925 Hs. 478067	NR_02016E	ENSG000003LXN	ECI TCI latexin protein-coding
chr4-143E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr4	1.44E+08	1.44E+08	+	0 NA	intron (NMER20 DNA	-16716 NR_104027	1E+08	NR_104027	ENSG000003SMARCA5-A	SMARCA5 encRNA
chr5-149C	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr5	1490338	1493011	+	0 NA	intron (NLooper DN	19182 NR_106722	1.02E+08	NR_106722	ENSG000003MIR6075	hsa-mir-6microRNA ncRNA
chr5-4312	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr5	43123553	43127401	+	0 NA	intron (Nintron (N	3912 NM_00133C	7690 Hs. 535804	NR_003432	ENSG000003ZNF131	ZBTB35 p/zinc finger protein-coding
chr5-4361	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr5	43610258	43610832	+	0 NA	intron (NTiger15e	-7315 NR_073111	1.01E+08	NR_073111	NNT-AS1	- NNT antisncRNA
chr5-1591	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr5	1.59E+08	1.59E+08	+	0 NA	intron (Nintron (N	47386 NM_00119E	153830 Hs. 349306	NR_144722	ENSG000003CRNF145	- ring finger protein-coding
chr5-1772	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (Nintron (N	53406 NM_001031	53917 Hs. 16258	NR_130781	ENSG000003RAB24	- RAB24, m protein-coding
chr6-426E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr6	42657793	42659297	+	0 NA	intron (Nintron (N	64052 NM_000322	5961 Hs. 654488	NR_000322	ENSG000003PRPH2	AOFMD1 AVW peripheral protein-coding
chr6-995E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr6	99556063	99558040	+	0 NA	intron (Nintron (N	11609 NM_00519C	892 Hs. 430642	NR_00519C	ENSG000003CCNC	CycC SRB1 cyclin C protein-coding
chr6-145E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr6	1.45E+08	1.45E+08	+	0 NA	intron (Nintron (N	51108 NM_17308E	257218 Hs. 17308E	NR_17308E	ENSG000003SHPRH	ba54515.2 SNP2 hist protein-coding
chr7-103E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr7	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	18443 NM_004275	9512 Hs. 184211	NR_004275	ENSG000003PMPCB	Beta-MPP peptidase protein-coding
chr8-253E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr8	25323987	25324388	+	0 NA	intron (Nintron (N	-12125 NR_106933	1.02E+08	NR_106933	ENSG000003MIR687E	hsa-mir-6microRNA ncRNA
chr8-305E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr8	30559933	30562498	+	0 NA	intron (Nintron (N	-77365 NM_00120E	1.01E+08	NR_00120E	ENSG000003SMIM18	- small intron protein-coding
chr8-6151	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr8	61511799	61517540	+	0 NA	intron (NAluY SINE	175142 NM_001164	444 Hs. 332422	NR_00431E	ENSG000003ASPH	AAH BAH Caspartate protein-coding
chr8-9371	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr8	93714734	93721976	+	0 NA	intron (Nintron (N	17790 NR_15645E	137392 Hs. 125038	NR_14526E	ENSG000003FAM92A	FAM92A1 F family wiprotein-coding
chr9-280E	7.40111	-0.34074	0.848863	-0.40141	0.68812	0.981636	chr9	28061703	28071941	+	0 NA	intron (NAluY SINE	37118 NM_01487E	9933 Hs. 493306	NR_01487E	ENSG000003PUM3	HA-8 HLA-pumilio F protein-coding
chr14-105	4.163954	-0.46268	1.153944	-0.40096	0.68845	0.981636	chr14	1.05E+08	1.05E+08	+	0 NA	TTS (NM_ITTS (NM_I	12295 NM_01795E	55038 Hs. 34045	NR_01795E	ENSG000003CDCA4	HEPP SEI-cell divi protein-coding
chr1-178E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr1	1.79E+08	1.79E+08	+	0 NA	intron (NLIPIA15 LI	37153 NM_15266E	55103 Hs. 63248E	NR_018037	ENSG000003RALGPS2	dJ5952.1 RAL GF w protein-coding
chr1-183E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr1	1.84E+08	1.84E+08	+	0 NA	intron (Nintron (N	46103 NM_001331	9887 Hs. 59146E	NR_014837	ENSG000003SMG7	Clof16 ESMG7 nons protein-coding
chr1-234E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr1	2.34E+08	2.34E+08	+	0 NA	intron (NLa2 LINE	6288 NM_001301	388753 Hs. 23198	NR_001012	ENSG000003COA6	Clof31 Cytochron protein-coding
chr10-10C	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr10	30312373	30313896	+	0 NA	3' UTR (N3' UTR (N	36204 NM_01810E	55149 Hs. 17394E	NR_01810E	ENSG000003MTPAP	PAPD1 SP mitochoncon protein-coding
chr10-103	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr10	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	46929 NM_001351	22978 Hs. 97439	NR_01222E	ENSG000003NT5C2	GMP NT5B 5' nucloce protein-coding
chr11-12E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr11	1.23E+08	1.23E+08	+	0 NA	intron (NAluJr SIN	40078 NM_02476E	79827 Hs. 59194E	NR_02476E	ENSG000003CLMP	ACAM ASAM CXADR 1i protein-coding
chr11-134	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr11	1.34E+08	1.34E+08	+	0 NA	intron (Nintron (N	9329 NM_014174	29087 Hs. 13645	NR_014174	ENSG000003THYN1	HSPC144 Thymocyte protein-coding
chr13-205	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr13	20994653	20995066	+	0 NA	intron (NAluJo SIN	-45431 NR_10405E	1.02E+08	NR_10405E	ENSG000003LINC00367	- long intncRNA
chr15-70C	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr15	70054575	70056292	+	0 NA	intron (Nintron (N	24035 NR_030714	693214 Hs. 17608	NR_007364	ENSG000003TMED3	MIRN629 f microRNA ncRNA
chr15-79E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr15	79317621	79319284	+	0 NA	intron (Nintron (N	7340 NM_001301	23423 Hs. 71608	NR_007364	ENSG000003TMED3	C15orf22 transmem protein-coding
chr17-294	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr17	29476648	29477020	+	0 NA	intron (NMER2 DNA	85909 NM_02514E	57551 Hs. 597434	NR_020791	ENSG000003TAOK1	KFC-F2 MAF TA0 kinas protein-coding
chr18-35E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr18	35309484	35310057	+	0 NA	non-codirnon-codir	19498 NR_02456E	10778 Hs. 31424E	NR_00662E	ENSG000003ZNF271P	CT-ZFP48 zinc fing pseudo
chr19-84C	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr19	8402142	8402868	+	0 NA	exon (NM exon (NM	-10798 NM_00100E	51257 Hs. 631861	NR_01649E	ENSG000003	2-Mar HSPC240 membrane protein-coding
chr19-45E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr19	45284662	45285292	+	0 NA	intron (NAluSq2 SI	33706 NM_00119E	57787 Hs. 34314	NR_031417	ENSG000003MARK4	MARK4 M microtrub protein-coding
chr2-1547	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr2	15471938	15473723	+	0 NA	intron (NLR1A1B LI	88504 NM_01590E	51594 Hs. 46775E	NR_01590E	ENSG000003NBAS	ILF52 NAC neuroblas protein-coding
chr2-109E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr2	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	-51653 NR_03809E	1E+08	NR_03809E	ENSG000003LIMS4	LIMS3L LIM zinc protein-coding
chr2-113E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr2	1.14E+08	1.14E+08	+	0 NA	intron (NLR79 LTF	2731 NM_001354	11159 Hs. 44642E	NR_00708E	ENSG000003RABL2A	- RAB, memt protein-coding
chr21-46E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr21	46291322	46291956	+	0 NA	3' UTR (N3' UTR (N	5297 NM_001314	54059 Hs. 47406E	NR_058181	ENSG000003YBEY	C21orf57 ybeY meta protein-coding
chr22-17E	6.674071	0.359234	0.896072	0.400899	0.688495	0.981636	chr22	17885007	17885933	+	0 NA	intron (NLM4Ea LI	21416 NM_001122	57553 Hs. 528024	NR_015241	ENSG000003MICAL3	MICAL-3 microtrub protein-coding

chr3-4877	7.211799	0.345279	0.865263	0.399045	0.68986	0.981636	chr3	48770664	48771381	+	0	NA	intron (AluSx SIN	-53744	NM_001146	51447	Hs.595982	NM_016291	ENSG00000	IP6K2	IHPK2 Insinositol protein-coding	
chr4-3764	7.211799	0.345279	0.865263	0.399045	0.68986	0.981636	chr4	37646508	37647152	+	0	NA	intron (AluJr SIN	39546	NM_00108E	768211	Hs.28337E	NM_00108E	ENSG00000	RELL1	- RELT like protein-coding	
chr5-3124	7.211799	0.345279	0.865263	0.399045	0.68986	0.981636	chr5	31249248	31251434	+	0	NA	intron (Nintron (N	56655	NM_004932	1004	Hs.12477E	NM_004932	ENSG00000	CDH6	CAD6 KCAI cadherin protein-coding	
chr8-287	7.211799	0.345279	0.865263	0.399045	0.68986	0.981636	chr8	28739740	28740219	+	0	NA	intron (Nintron (N	38478	NR_07346E	2137	Hs.491354	NM_00144C	ENSG00000	EXTL3	BOTV EXTL exostosin protein-coding	
chr8-1275	7.211799	0.345279	0.865263	0.399045	0.68986	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	5300	NR_10355E	641384	Hs.629674	NM_001037	ENSG00000	TMEM75	- transmembrane ncRNA	
chrX-382	7.211799	0.345279	0.865263	0.399045	0.68986	0.981636	chrX	3825319	3827688	+	0	NA	intron (AluSx3 SI	17391	NR_034031	389906	Hs.63619E	NM_001045547	LOC38990E	-	zinc finger pseudo	
chr1-118	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr1	11832656	11836344	+	0	NA	non-codiron-codir	-5819	NR_03780E	1E+08	Hs.71001E	NR_03780E	NPPA-AS1	NPPA NPPA antincRNA		
chr1-776	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr1	77693301	77695883	+	0	NA	IntergeniIntergeni	-11165	NM_00130E	26009	Hs.48050E	NM_015534	ENSG00000	ZZZ3	ATTA1  zinc finger protein-coding	
chr1-926	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr1	92656718	92659191	+	0	NA	intron (MSTA LTR	127154	NM_00135C	7813	Hs.594434	NM_00566E	ENSG00000	CEV15	EVI-5 NB4 ecotropic protein-coding	
chr1-1471	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr1	1.47E+08	1.47E+08	+	0	NA	intron (AluYm SI	7234	NR_10387C	5565	Hs.50732	NM_00539E	ENSG00000	PRKAB2	- protein lprotein-coding	
chr10-38C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr10	92819925	92810131	+	0	NA	intron (MER11C LI	5836	NM_00132A	7587	Hs.29257E	NM_003421	ENSG00000	ZNF37A	KOX21 ZNF zinc finger protein-coding	
chr11-24C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr11	2402266	2403105	+	0	NA	exon (NM exon (NM	1935	NM_001297	10078	Hs.523424	NM_00570E	ENSG00000	TSSC4	- tumor sup protein-coding	
chr12-63C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr12	6339310	6340721	+	0	NA	intron (Nintron (N	2061	NM_00134E	7132	Hs.279594	NM_00106E	ENSG00000	TNFRSF1A	CD120a FFTN receptor protein-coding	
chr12-92E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr12	92816404	92820144	+	0	NA	intron (NLIME1 LIN	81785	NM_00100A	440107	Hs.59101E	NM_00100A	ENSG00000	PLEKHG7	- pleckstrin protein-coding	
chr12-10C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr12	1E+08	1E+08	+	0	NA	intron (NLIPA15 LI	60558	NM_00100E	23074	Hs.572154	NM_015054	ENSG00000	UHRF1BP1	SHIP164 UHRF1 bir protein-coding	
chr12-121	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	intron (NLTR16C LI	725	NM_00127C	10645	Hs.29734E	NM_00654E	ENSG00000	CAMKK2	CAMKK CAM calcium/c protein-coding	
chr14-55E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr14	55662125	55662832	+	0	NA	intron (Nintron (N	82271	NM_00107E	3895	Hs.509414	NM_00498E	ENSG00000	CKTN1	CG1 KNT kinecin protein-coding	
chr14-60E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr14	60881840	60884556	+	0	NA	intron (NLIM2 LIN	97881	NM_00135C	57570	Hs.38015E	NM_02081C	ENSG00000	TRMT5	COXP26 tRNA methyl protein-coding	
chr14-73E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr14	73574147	73575635	+	0	NA	TTS (NM_C TTS (NM_C	5832	NM_00136A	10965	Hs.44668E	NM_00682E	ENSG00000	ACOT2	CTE-1A CTacyl-CoA protein-coding	
chr15-417	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr15	41760105	41760978	+	0	NA	intron (Nintron (N	-13943	NM_00126E	23005	Hs.513661	NM_01499A	ENSG00000	MAPKBP1	JNKBP-1 Jmiotogen-ε protein-coding	
chr15-43C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr15	43337314	43337801	+	0	NA	intron (Nintron (N	6885	NM_00101E	161823	Hs.53391E	NM_00101E	ENSG00000	ADAL	- adenosine protein-coding	
chr15-65E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr15	65665370	65666024	+	0	NA	intron (Nintron (N	22818	NM_00125A	9187	Hs.17309E	NM_00472E	ENSG00000	SLC24A1	CSNB1D Hsolute cε protein-coding	
chr15-731	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr15	73176889	73178028	+	0	NA	intron (Nintron (N	-122452	NR_162148	1.13E+08	NR_162148	MIR12135	-	microRNA ncRNA		
chr16-29E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr16	29920512	29922182	+	0	NA	intron (NLIME5 LIN	4879	NR_11093C	253980	Hs.53459C	NM_17886E	ENSG00000	CTD13	BACURD1 Fpotassium protein-coding	
chr18-92E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr18	9227452	9228277	+	0	NA	intron (NLIM4A LI	90301	NM_00120A	23253	Hs.46458E	NM_01520E	ENSG00000	ANKRD12	ANCO-2 ANankyrin r protein-coding	
chr19-381	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr19	38152978	38153863	+	0	NA	intron (AluSx SIN	-9676	NR_14580C	1.1E+08	NR_14580C	SNORD152	-	small nucleosRNA		
chr2-581E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr2	58159741	58161614	+	0	NA	TTS (NM_C TTS (NM_C	80703	NM_00117E	55120	Hs.63189C	NM_01806E	ENSG00000	FANCL	FAAP43 PFA nuc protein-coding	
chr2-2307	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (NL3 LINE C	-63582	NM_001287	81618	Hs.111577	NM_03092E	ENSG00000	ITM2C	BRI3 BRIC integral protein-coding	
chr2-238C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	intron (Nintron (N	-29445	NM_01651C	51540	Hs.73190E	NM_01651C	ENSG00000	SCLY	SCL hsSCL senescens protein-coding	
chr3-114C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr3	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	-4563	NM_00116A	26137	Hs.202577	NM_01564E	ENSG00000	ZBTB20	DPZF HOF zinc finger protein-coding	
chr3-184C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	4786	NM_00568E	10057	Hs.36856E	NM_00568E	ENSG00000	ABCC5	ABC33 ESIATP bindi protein-coding	
chr4-175C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr4	17500421	17502268	+	0	NA	intron (Nintron (N	10746	NM_00032C	5860	Hs.75438	NM_00032C	ENSG00000	QDPR	DHPR HDHF quinoid protein-coding	
chr4-1844	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr4	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	-44935	NR_12593C	1.03E+08	Hs.432281	NR_12593E	ENSG00000	LINC0236E	-	long intncRNA
chr5-435E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr5	43536303	43538791	+	0	NA	intron (Nintron (N	19530	NM_006451	10605	Hs.48203E	NM_006451	ENSG00000	PAIP1	-	poly(A) t protein-coding
chr5-957E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr5	95733469	95734270	+	0	NA	intron (NMIRb SINE	-1767	NM_00134E	83890	Hs.50499	NM_03195E	ENSG00000	SPATA9	NYD-SP16 spermatog protein-coding	
chr5-113E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr5	1.14E+08	1.14E+08	+	0	NA	intron (NMSMAR2 DN	46514	NM_00134E	64848	Hs.23194E	NM_00228E	ENSG00000	YTHDC2	CAHL HYTH YTH domain protein-coding	
chr6-7894	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr6	78948792	78950412	+	0	NA	intron (NMER74B LI	82051	NM_00101C	134728	Hs.65621E	NM_00101C	ENSG00000	IRAK1BP1	AIP70 SIV interleuk protein-coding	
chr6-132E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr6	1.32E+08	1.32E+08	+	0	NA	intron (NLIPA8A LI	90935	NM_01552E	26002	Hs.6909	NM_01552E	ENSG00000	MOXD1	MOX PR057 monooxyg protein-coding	
chr7-989E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr7	98980251	98986452	+	0	NA	exon (NM exon (NM	-29814	NR_11010E	1.02E+08	Hs.63666E	NR_11010E	LOC101927	-	uncharacterncRNA	
chr7-129E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-60518	NR_02961E	406959	NR_02961E	ENSG00000	MIR183	MIRN183 microRNA ncRNA		
chr8-102E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	37036	NR_12541E	1.02E+08	Hs.49244E	NR_12541E	ENSG00000	UBR5-AS1	-	UBR5 antincRNA
chr9-134C	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chr9	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	5993	NM_00135E	266655	Hs.65486E	NM_00135E	ENSG00000	BRD30S	LINC00094 BRD3 oppc protein-coding	
chrX-142E	7.17066	0.3437	0.861509	0.398951	0.689929	0.981636	chrX	1425020	1425660	+	0	NA	intron (Nintron (N	24809	NR_02671C	80161	Hs.52185E	NM_025091	ASMTL-AS1	ASMTL-AS ASMTL antncRNA		
chr6-888E	4.674408	-0.42245	1.059262	-0.39882	0.69026	0.981636	chr6	88885272	88886225	+	0	NA	intron (NLIMC4a LI	77870	NM_00128E	8732	Hs.56737E	NM_00380C	ENSG00000	RNGTT	CAP1A HCE RNA guany protein-coding	
chr10-92C	7.692671	0.335712	0.842434	0.398503	0.690259	0.981636	chr10	92026141	92028101	+	0	NA	intron (Nintron (N	103351	NM_00397E	9044	Hs.50052E	NM_00397E	ENSG00000	BTAF1	MOT1 TAF(B-TFIID l protein-coding	
chr17-281	10.64797	-0.28606	0.718686	-0.39803	0.690605	0.981636	chr17	28184842	28187487	+	0	NA	intron (Nintron (N	-40399	NR_00306A	23615	Hs.15719E	NM_02109E	ENSG00000	PYY2	-	peptide l pseudo
chr2-756E	10.64797	-0.28606	0.718686	-0.39803	0.690605	0.981636	chr2	75652649	75653986	+	0	NA	intron (Nintron (N	6534	NM_01476E	9801	Hs.44024	NM_01476E	ENSG00000	MRPL19	L19mt MRF mitochondon protein-coding	
chr9-884E	8.273388	0.338549	0.850759	0.397937	0.690676	0.981636	chr9	88449076	88449515	+	0	NA	intron (Nintron (N	60851	NM_006717	10927	Hs.146804	NM_006717	ENSG00000	CSPIN1	SPIN MDRI spindlin protein-coding	
chr1-246	7.359971	-0.3438	0.863992	-0.39792	0.690692	0.981636	chr1	2.47E+08	2.47E+08	+	0	NA	intron (NPABL_B ir	60225	NM_01544E	25909	Hs.300887	NM_01544E	ENSG00000	AHCTF1	ELYS MDST1AT-hook c protein-coding	
chr10-11E	7.359971	-0.3438	0.863992	-0.39792	0.690692	0.981636	chr10	1.19E+08														



chr12-511.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr12	51100580	51103847	+	0	NA	intron (Nintron (N	-18617	NR_030809	81566	Hs.524422	ENSG000003CSRNP2	C12orf2 Cysteine protein-coding	
chr12-111.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	-7359	NR_106815	1.02E+08	NR_106815	ENSG000003MIR6761	hsa-mir-εmicroRNA ncRNA	
chr13-45.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr13	45397610	45400629	+	0	NA	intron (Nintron (N	-19043	NR_047031	1.01E+08	Hs.65803	ENSG000003SLC25A30-	SLC25A30 ncRNA	
chr13-95.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr13	95120145	95121511	+	0	NA	intron (Nintron (N	-89516	NR_145733	1.1E+08	NR_145733	SNORD13G	small nucleolar RNA	
chr14-351.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr14	35004290	35005569	+	0	NA	intron (Nintron (N	21937	NR_003136	6729	Hs.16753	ENSG000003SRP54	signal protein-coding	
chr15-417.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr15	41709061	41711982	+	0	NA	intron (NAluJr SIN	18936	NR_030356	693211	NR_030356	ENSG000003MIR626	MIRN626 microRNA ncRNA	
chr15-657.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr15	65724954	65729270	+	0	NA	intron (NAluJr4 SI	-7780	NR_039736	1.01E+08	NR_039736	ENSG000003MIR4511	mir-4511 microRNA ncRNA	
chr15-732.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr15	73282977	73283992	+	0	NA	intron (NLTR33 LTF	-16426	NR_162148	1.13E+08	NR_162148	MIR12135	microRNA ncRNA	
chr15-856.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr15	85693440	85695491	+	0	NA	intron (NMER58B DN	64260	NR_120366	1.02E+08	Hs.51311	NR_120366	LOC101925	uncharacterized ncRNA
chr16-37.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr16	3773959	3775169	+	0	NA	intron (Nintron (N	-57040	NR_016292	10131	Hs.30345	ENSG000003TRAP1	HSP 75 HSP TRF receptor protein-coding	
chr16-704.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr16	70494618	70499943	+	0	NA	exon (NM exon (NM	26274	NR_001366	25839	Hs.20868	ENSG000003COG4	CDG2 COE component protein-coding	
chr16-743.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr16	74356305	74360192	+	0	NA	intron (NAluSx SIN	10007	NR_026950	283922	Hs.55872	ENSG000003LOC283922	pyruvate pseudo	
chr16-748.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr16	74891485	74893879	+	0	NA	intron (Nintron (N	92441	NR_030581	79726	Hs.28095	ENSG000003WDR59	CDW12 FPFWD repeat protein-coding	
chr16-778.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr16	78794458	78798146	+	0	NA	intron (Nintron (N	-3428	NR_162122	1.13E+08	NR_162122	MIR11401	microRNA ncRNA	
chr17-225.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	2294945	2300313	+	0	NA	intron (Nintron (N	6156	NR_017575	23293	Hs.44834	ENSG000003SMG6	C17orf31 SMG6 nonprotein-coding	
chr17-417.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	4174796	4181364	+	0	NA	intron (Nintron (N	34383	NR_001254	124936	Hs.51387	ENSG000003CYB5D2	cytochrome protein-coding	
chr17-107.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	10790203	10712310	+	0	NA	TTS (NM_C TTS (NM_C	5826	NR_049723	1.01E+08	Hs.67437	ENSG000003MAGOHP2	MAGOHP2 mago homologue pseudo	
chr17-397.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	39707762	39713141	+	0	NA	exon (NM exon (NM	10473	NR_110533	2064	Hs.44635	ENSG000003ERBB2	CD340 HEF erb-b2 receptor protein-coding	
chr17-481.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	48112710	48114391	+	0	NA	intron (NAluJr SIN	5965	NR_013322	29916	Hs.15827	ENSG000003SNX11	sorting protein-coding	
chr17-634.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	63411500	63416266	+	0	NA	intron (Nintron (N	26384	NR_001330	1534	Hs.35526	ENSG000003CYB561	CYB561A1 cytochrome protein-coding	
chr17-787.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr17	78794458	78798146	+	0	NA	3' UTR (N3' UTR (N	-14259	NR_004762	9267	Hs.19121	ENSG000003CYTH1	B2-1 CYT cytohesin protein-coding	
chr19-591.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr19	5915488	5919316	+	0	NA	3' UTR (N3' UTR (N	3148	NR_004058	828	Hs.58474	ENSG000003CAPS	CAPS1 calyphos protein-coding	
chr19-420.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr19	42078716	42081326	+	0	NA	exon (NM exon (NM	3855	NR_022752	64763	Hs.13323	ENSG000003ZNF574	FPF92 zinc finger protein-coding	
chr2-272.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr2	27236030	27242335	+	0	NA	exon (NM exon (NM	21792	NR_001306	790	Hs.37701	ENSG000003CAD	CDG13 EIF carbamoyl protein-coding	
chr2-3687.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr2	36876471	36876968	+	0	NA	intron (Nintron (N	89817	NR_003162	6801	Hs.12748	ENSG000003STRN	PPP2R6A striatin protein-coding	
chr2-7114.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr2	71142972	71145634	+	0	NA	intron (Nintron (N	13669	NR_005791	10199	Hs.65620	ENSG000003MPSH1	CT90 MPP1M-phase I protein-coding	
chr2-9792.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr2	97923488	97925897	+	0	NA	intron (NAluJb SIN	70806	NR_015348	23505	Hs.46937	ENSG000003TMM131	CC28 PRO1 transmembrane protein-coding	
chr2-2295.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (Nintron (N	13460	NR_001348	9320	Hs.57264	ENSG000003TRIP12	MRD49 TRI thyroid protein-coding	
chr20-325.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr20	3252226	3253620	+	0	NA	intron (Nintron (N	-13733	NR_001174	89359	Hs.10560	ENSG000003SLC4A11	BTR1 CDPL solute carrier protein-coding	
chr20-138.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr20	13808189	13812212	+	0	NA	intron (N L2b LINE	25172	NR_147982	79133	Hs.47216	ENSG000003NDUFAF5	C20orf7 NADH:ubiquinone protein-coding	
chr20-636.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr20	63667671	63669051	+	0	NA	intron (N L2a LINE	10551	NR_032957	51750	Hs.74505	ENSG000003CTEL1	C20orf41 regulator protein-coding	
chr21-39.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr21	39235210	39238512	+	0	NA	intron (Nintron (N	-53347	NR_020343	8624	Hs.47383	ENSG000003PSMG1	C21LRP DIS proteasome protein-coding	
chr3-144.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr3	14146905	14148637	+	0	NA	intron (Nintron (N	22381	NR_024334	79188	Hs.51781	ENSG000003TMM43	ARVC5 ARV transmembrane protein-coding	
chr3-576.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr3	57627353	57630730	+	0	NA	intron (Nintron (N	31252	NR_132366	1.06E+08	Hs.66720	ENSG000003ARF4-AS1	ARF4 antinuclear RNA	
chr3-195.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	intron (Nintron (N	10287	NR_106887	1.02E+08	NR_106887	ENSG000003MIR6829	hsa-mir-εmicroRNA ncRNA	
chr4-137.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr4	13579490	13581880	+	0	NA	intron (Nintron (N	-32861	NR_015450	285548	Hs.52928	ENSG000003LINC01096	long intergenic ncRNA	
chr5-1321.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr5	1.32E+08	1.32E+08	+	0	NA	intron (N HAL1 LINE	9168	NR_047470	1.01E+08	Hs.51956	ENSG000003P4HA2-AS1	P4HA2 antinuclear RNA	
chr5-1797.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	3' UTR (N3' UTR (N	-17363	NR_145867	4056	Hs.70674	ENSG000003LTC4S	leukotriene protein-coding	
chr6-4206.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr6	42067980	42069172	+	0	NA	exon (NM exon (NM	18052	NR_138572	129685	Hs.52012	ENSG000003TAF8	II TAF TATA-box protein-coding	
chr6-905.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr6	90558707	90560324	+	0	NA	intron (Nintron (N	27557	NR_003188	6885	Hs.59483	ENSG000003MAP3K7	CSCF FMD2 mitogen-activated protein-coding	
chr7-764.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr7	764084	766274	+	0	NA	intron (N MR1 SINE	-37503	NR_001164	5575	Hs.52085	ENSG000003PRKAR1B	PRKAR1B protein kinase-coding	
chr7-265.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr7	2656378	2658505	+	0	NA	intron (N GTGATG T	-22801	NR_133463	155185	Hs.42221	ENSG000003AMZ1	archaealysin protein-coding	
chr7-755.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr7	75505331	75508175	+	0	NA	TTS (NR_C TTS (NR_C	13126	NR_001306	442590	Hs.63229	ENSG000003SPDYE5	speedy/RI protein-coding	
chr7-106.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	3' UTR (N3' UTR (N	34286	NR_005746	10135	Hs.48961	ENSG000003NAMPT	111003501 nicotinamide protein-coding	
chr7-158.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	intron (N AluY SINE	-70866	NR_024394	154822	Hs.54478	ENSG000003LINC00685	long intergenic ncRNA	
chr9-114.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	exon (NM exon (NM	29019	NR_001633	259	Hs.43691	ENSG000003AMB	A1M EDC1 alpha-1-n protein-coding	
chr9-130.7.178517.0.341603.0.86163.0.396461.0.691765.0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	18922	NR_003934	8939	Hs.98751	ENSG000003FUBP3	FUBP3 far upstream protein-coding	
chr19-115.13.87034.0.252213.0.636363.0.396335.0.691858.0.981636	chr19	11902175	11906451	+	0	NA	intron (N AluJr SIN	16531	NR_001364	7620	Hs.56528	ENSG000003ZNF69	Cos5 hZNF zinc finger protein-coding	
chr1-747.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr1	74703322	74704096	+	0	NA	Intergeni Intergeni	29341	NR_001888	1429	Hs.83114	ENSG000003CRYZ	crystallin protein-coding	
chr12-132.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	24570	NR_170682	22953	Hs.25858	ENSG000003P2RX2	DFNA41 P2E intergenic protein-coding	
chr13-503.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr13	50380608	50381300	+	0	NA	intron (N LTR85b LI	146495	NR_125753	1.04E+08	Hs.72223	ENSG000003DLEU1-AS1	LINC01308 DLEU1 antinuclear RNA	
chr17-618.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr17	61894073	61894678	+	0	NA	intron (Nintron (N	-38016	NR_032043	83990	Hs.12890	ENSG000003BRIP1	BACH1 FANBRCA1 antinuclear RNA	
chr2-1572.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr2	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	12042	NR_001325	11227	Hs.26902	ENSG000003GALNT5	GALNAC-T6 polypeptide protein-coding	
chr21-348.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr21	34842882	34843677	+	0	NA	intron (N CA)n Sin	45420	NR_001001	861	Hs.14926	ENSG000003RUNX1	AML1 AML1RUNX1 family protein-coding	
chr3-3063.4.66655-0.41975.1.059319-0.39624.0.691926.0.981636	chr3	30630848	306											



chr1-2688 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr1	26888828	268889133	+	0	NA	exon (NM_exon (NM_1303 NM_018066	54707 Hs. 14333 NM_018066	ENSG00000CPN2	ATPBD1B	GPN-loop protein-coding				
chr1-3125 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr1	31258347	31259535	+	0	NA	TTS (NM_TTS (NM_C -19054 NM_024522	79570 Hs. 470256 NM_024522	ENSG00000NKAIN1	FAM77C	sodium/po protein-coding				
chr1-1085 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (NLIM3 LINE 22881 NM_001278	23155 Hs. 658489 NM_015127	ENSG00000CLCC1	MCLC	chloride protein-coding				
chr1-1147 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr1	1.15E+08	1.15E+08	+	0	NA	intron (Nintron (N 18369 NM_001242	7812 Hs. 69855 NM_007158	ENSG00000CSDE1	DIS155E	colloid shock protein-coding				
chr1-2237 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (Nintron (N 5788 NM_001748	824 Hs. 350899 NM_001748	ENSG00000CAPN2	CANP2	Ca/calpain 2 protein-coding				
chr1-2435 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr1	2.43E+08	2.43E+08	+	0	NA	intron (Nintron (N -41240 NR_039824	1.01E+08	NR_039824	ENSG00000MIR4677	mir-4677	microRNA ncRNA			
chr10-104 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	intron (NLIME3Cz L 34101 NM_01472C	9748 Hs. 591922 NM_01472C	ENSG00000SLK	LOSK STRK STE20	lik protein-coding				
chr10-124 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	3' UTR (N3' UTR (N -15961 NM_014661	9679 Hs. 129199 NM_014661	ENSG00000FAM53B	LIAA0140	family wiprotein-coding				
chr12-216 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr12	21635000	21638257	+	0	NA	intron (Nintron (N 21166 NM_001174	3945 Hs. 446149 NM_00230C	ENSG00000LDHB	HEL-S-281	lactate c protein-coding				
chr12-78 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr12	78022063	78023192	+	0	NA	intron (Nintron (N 191733 NM_01490C	8975 Hs. 655301 NM_01490C	ENSG00000NAV3	POMF1L1	Neuron n protein-coding				
chr13-514 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr13	51427863	51430245	+	0	NA	intron (NMIRc SINE 23982 NM_012141	26512 Hs. 43944C NM_012141	ENSG00000INTS6	DBI-1	DD integrat protein-coding				
chr14-356 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr14	35621645	35622360	+	0	NA	intron (NLIPA6 LIN 87838 NM_032594	84684 Hs. 62813 NM_032594	ENSG00000INSM2	IA-6 IA6 INSM	trar protein-coding				
chr15-415 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr15	41394166	41395286	+	0	NA	intron (NAluSx SIN 7770 NR_04562C	51103 Hs. 106525 NM_01601C	ENSG00000NDUFAF1	CGI-65 CCNADH:ubic	protein-coding				
chr15-425 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr15	42560456	42560286	+	0	NA	TTS (NM_TTS (NM_C 12873 NM_00113C	55142 Hs. 14347 NM_018097	ENSG00000HAUS2	C15orf25 HAUS	augn protein-coding				
chr15-505 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr15	50559297	50559775	+	0	NA	non-codiron-codir -12870 NM_203494	373509 Hs. 677758 NM_203494	ENSG00000CUSP50	-	ubiquitir protein-coding				
chr16-89C 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr16	8905693	8908235	+	0	NA	intron (Nintron (N 29675 NM_00128E	7874 Hs. 386939 NM_00347C	ENSG00000CUSP7	HAUSP TEF	ubiquitir protein-coding				
chr16-224 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr16	22496551	22498288	+	0	NA	Intergeni Intergeni -7030 NR_02445E	1E+08	Hs. 648439 NR_02445E	LOC10019C	-	uncharactncRNA			
chr16-311 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr16	31122114	31123003	+	0	NA	intron (NMER3 DNA 4894 NM_03218E	84148 Hs. 53380E NM_03218E	ENSG00000KAT8	MOF MYST1	lysine ac protein-coding				
chr17-171 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr17	17182277	17183874	+	0	NA	intron (Nintron (N 23258 NM_17883E	201164 Hs. 729075 NM_17883E	ENSG00000PLD6	ZUC	phospholip protein-coding				
chr17-315 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr17	31986924	31987634	+	0	NA	intron (NL2 LINE L -20104 NM_00132E	114659 Hs. 514071 NM_05288E	ENSG00000LRRC37B	LRRC37	leucine i protein-coding				
chr17-376 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr17	37637342	37638441	+	0	NA	intron (NHSMAR2 DN 5555 NM_001291	11056 Hs. 590937 NM_00701C	ENSG00000DDX52	HUSSY19	F DExD-box	protein-coding			
chr2-2005 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr2	2E+08	2E+08	+	0	NA	intron (NLIPA4 LIN 24906 NM_00128E	26010 Hs. 12032E NM_01553E	ENSG00000SPATS2L	DNAPT6	Spermatog protein-coding				
chr2-2014 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (Nintron (N 15166 NM_02091E	57679 Hs. 47109E NM_02091E	ENSG00000CALS2	ALS2CR6	Ala sin Rch	protein-coding			
chr2-564 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr2	56406571	56408206	+	0	NA	Intergeni LIMB7 LIN -4648 NM_001164	57091 Hs. 473144 NM_02035E	ENSG00000CASS4	C20orf32	Ca s	protein-coding			
chr3-5275 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr3	52728535	52729965	+	0	NA	intron (NMER1A LI 23144 NM_014041	28972 Hs. 11125 NM_014041	ENSG00000SPCS1	HSPC033	S signal	protein-coding			
chr3-1055 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr3	1.06E+08	1.06E+08	+	0	NA	intron (Nintron (N 179601 NM_001627	214 Hs. 59129E NM_001627	ENSG00000ALCAM	CD166	MEV	activat	protein-coding		
chr4-676E 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr4	67663732	67667432	+	0	NA	intron (NLIM5 LINE 55236 NM_018227	55236 Hs. 212774 NM_018227	ENSG00000UBA6	E1-L2	MOF	ubiquitir protein-coding			
chr4-999 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr4	99902398	99904687	+	0	NA	intron (NMIRb SINE -8996 NR_02417C	8649 Hs. 43333E NM_02197C	ENSG00000LAMTOR3	MAP2K1	IP1 late end	protein-coding			
chr5-7964 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr5	79643174	79647164	+	0	NA	exon (NM_exon (NM 32728 NM_00134E	167153 Hs. 41819E NM_173797	ENSG00000TENT2	APD4 GLD2	terminal	protein-coding			
chr5-8735 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr5	87329989	87338134	+	0	NA	intron (Nintron (N -10023 NR_13092E	644285 Hs. 70925E NR_13092E	LOC64428E	-	uncharactncRNA				
chr5-1435 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr5	1.43E+08	1.43E+08	+	0	NA	TTS (NM_TTS (NM_C 101351 NR_04681E	1.01E+08	Hs. 666717 NR_04681E	ENSG00000ARHGAP26	-	ARHGAP26	ncRNA		
chr6-517 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr6	51789440	51791108	+	0	NA	TTS (NM_TTS (NM_C 17974 NM_00428E	9532 Hs. 74504E NM_00428E	ENSG00000BAG2	BAG-2	dJ4BCL2	asc	protein-coding		
chr6-1697 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (NAluYb SIN -10497 NR_002678C	80069 Hs. 677182E NM_02500E	ENSG00000LINC00574	G6orf208	long	intncRNA			
chr7-1055 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	intron (Nintron (N 3137 NM_00131E	54517 Hs. 52061E NM_01904E	ENSG00000CUSP7	IDDABS	pseudour	protein-coding			
chr7-127 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N 155713 NM_01439C	27044 Hs. 12252E NM_01439C	ENSG00000SND1	TDRD11	Tu s	staphyloc	protein-coding		
chr8-1301 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (NL2b LINE E -19241 NR_04538E	1.01E+08	Hs. 10601E NR_04538E	ENSG00000ASAP1-IT2	-	ASAP1	intncRNA		
chr9-1222 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr9	1.22E+08	1.22E+08	+	0	NA	intron (NLIMEi LIN 12562 NM_00134E	92399 Hs. 368011 NM_13877E	ENSG00000MRRF	MRRF	MTRF	mitochon	protein-coding		
chr9-1305 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N 16239 NM_003934	8939 Hs. 98751 NM_003934	ENSG00000FUBP3	FUBP3	f	fast p	protein-coding		
chrX-6575 7.426534	-0.33426	0.84924	-0.3936	0.693875	0.981636	chrX	65734771	65735414	+	0	NA	intron (NMIR3 SINE 64738 NM_002444	4478 Hs. 87752 NM_002444	ENSG00000MSN	HEL70	IM	moesin	protein-coding		
chr19-797 6.715211	0.360663	0.916433	0.393551	0.693912	0.981636	chr19	7972484	7974345	+	0	NA	intron (NAluY SINE -29748 NM_006351	10469 Hs. 465784 NM_006351	ENSG00000TIMM44	TIM44	transloc	protein-coding			
chr5-1545 7.749527	0.33332	0.847005	0.393528	0.69393	0.981636	chr5	1.54E+08	1.54E+08	+	0	NA	intron (NMIRb SINE 29752 NR_03162E	1E+08	NR_03162E	ENSG00000MIR1294	-	MIRN1294	microRNA	ncRNA	
chr2-8733 6.965078	-0.35027	0.890115	-0.39351	0.693946	0.981636	chr2	8730050	8730390	+	0	NA	3' UTR (N3' UTR (N 48164 NM_00216E	3398 Hs. 18091E NM_00216E	ENSG00000ID2	GIG8	ID2	inhibitor	protein-coding		
chr2-2307 6.965078	-0.35027	0.890115	-0.39351	0.693946	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (Nintron (N 26301 NM_00113C	51719 Hs. 603933 NM_01628E	ENSG00000CAB39	CGI-66	MC	calcium t	protein-coding		
chr4-7612 6.965078	-0.35027	0.890115	-0.39351	0.693946	0.981636	chr4	76129165	76129762	+	0	NA	intron (NLIMD2 LIN 18934 NM_01742E	53371 Hs. 43043E NM_01742E	ENSG00000NUP54	-	nucleopor	protein-coding			
chr5-1284 6.965078	-0.35027	0.890115	-0.39351	0.693946	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (NLIP3 LIN 49584 NM_001199E	2201 Hs. 519294 NM_001199E	ENSG00000FBN2	CCA DA9	E	fibrillin	protein-coding		
chr8-4241 6.965078	-0.35027	0.890115	-0.39351	0.693946	0.981636	chr8	42416807	42417064	+	0	NA	3' UTR (N3' UTR (N 25055 NM_00566E	7419 Hs. 699301 NM_00566E	ENSG00000VDAC3	HD-VDAC3	voltage	protein-coding			
chr12-928 11.10157	-0.27696	0.703997	-0.39342	0.694013	0.981636	chr12	92840359	92843453	+	0	NA	intron (NLIMB2 LIN 87389 NM_00356E	8411 Hs. 567367 NM_00356E	ENSG00000EEA1	MST105	MS	early en	protein-coding		
chr6-1105 11.10157	-0.27696	0.703997	-0.39342	0.694013	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	TTS (NM_TTS (NM_C 31488 NM_001287	262 Hs. 15911E NM_001634	ENSG00000AMD1	ADOMETDC	adenosyl	protein-coding			
chr7-1078 11.10157	-0.27696	0.703997	-0.39342	0.694013	0.981636	chr7	1.08E+08	1.08E+08	+	0	NA	intron (Nigger3a  23279 NM_002291	3912 Hs. 65058E NM_002291	ENSG00000LAMB1	CLM LIS5	laminin	protein-coding			
chr1-1005 7.675106	0.328217	0.835277	0.392943	0.694361	0.981636	chr1	1.01E+08	1.01E+08	+	0	NA	intron (NLIMB3 LIN 41457 NM_001144	148867 Hs. 53390E NM_13349E	ENSG00000SLC30A7	ZNT7	ZnT	solute c	protein-coding		
chr1-1145 7.675106	0.328217	0.835277	0.392943	0.694361	0.981636	chr1	1.15E+08	1.15E+08	+	0	NA	intron (Nintron (N 11179 NM_00587E	10286 Hs. 22960 NM_00587E	ENSG00000BCAS2	CAM1	SPD2	BCAS2	pr	protein-coding	
chr1-1165 7.675106	0.328217	0.835277	0.392943	0.694361	0.981636	chr1	1.16E+08	1.16E+08	+	0	NA	exon (NM_exon (NM 10338 NM_00116C	476 Hs. 37188E NM_00701C	ENSG00000ATP1A1	DMT2	SZF2	HAT	AtPase	n	protein-coding
chr1-1475 7.675106	0.328217	0.835277	0.392943	0.694361	0.981636	chr1	1.48E+08	1.48E+08	+	0	NA	intron (Nintron (N 17222 NM_016334	51463 Hs. 50432C NM_016334	ENSG00000GPR89B	GPHR	GPR8	G			



chr4-5186	7.186375	0.339455	0.866792	0.391622	0.695338	0.981636	chr4	51866891	51868056	+	0	NA	intron (NMER52A L1	23894	NM_001287	23142	Hs.60538ENM_01511E	ENSG00000CDUN1D4	-	defective protein-coding	
chr5-1377	7.186375	0.339455	0.866792	0.391622	0.695338	0.981636	chr5	13774292	13776934	+	0	NA	intron (NMIR3 SINE	168867	NM_001366	1767	Hs.21236CNM_00136E	ENSG00000DNAH5	-	CILD3 DNAdynein a protein-coding	
chr6-4268	7.186375	0.339455	0.866792	0.391622	0.695338	0.981636	chr6	42688151	42689889	+	0	NA	intron (NL2a LINE	33577	NM_000322	5961	Hs.65448ENM_000322E	ENSG00000PRPH2	-	AOFMD AVWperipherin protein-coding	
chr6-160C	7.186375	0.339455	0.866792	0.391622	0.695338	0.981636	chr6	1.6E+08	1.6E+08	+	0	NA	intron (NLTR5A LTF	-9788	NR_003288	729603	Hs.67481CNR_003288E	ENSG00000LOC72960C	-	calciuretic pseudo	
chr7-6505	7.186375	0.339455	0.866792	0.391622	0.695338	0.981636	chr7	65056104	65056823	+	0	NA	intron (NALu5A SINE	-9536	NR_145725	1.1E+08	NR_145725E	ENSG00000SNORA22C	-	small ncnRNA	
chr7-755E	7.186375	0.339455	0.866792	0.391622	0.695338	0.981636	chr7	75591220	75591827	+	0	NA	intron (Nintron (N	-63400	NR_02805E	5387	Hs.659871NM_00539E	ENSG00000PMS2P3	-	PMS2L3 PWPMS1 homopseudo	
chr1-122C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	1220849	1223745	+	0	NA	intron (Nintron (N	-8144	NM_003327	7293	Hs.12978CNM_003327E	ENSG00000TNFRSF4	-	ACT35 CD1TNF receptor protein-coding	
chr1-1241	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	12416692	12418377	+	0	NA	intron (Nintron (N	-89712	NR_00302E	677885	Hs.65845CNR_00302E	ENSG00000SNORA59A	-	ACA59 small ncnRNA	
chr1-868E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	86899274	86900168	+	0	NA	intron (NSVA_D Ret	14405	NM_004261	9403	Hs.36272ENM_004261E	ENSG00000SELENOF	-	15-Seq selenoprotein-coding	
chr1-1111	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	10153	NM_13848E	10390	Hs.363572NM_00609E	ENSG00000CEPT1	-	choline/epsilon protein-coding	
chr1-1508	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (NALuJr SIN	3794	NM_00128E	405	Hs.63244ENM_00166E	ENSG00000ARNT	-	HIF-1-beta-yl hydrolase protein-coding	
chr1-198E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	1.99E+08	1.99E+08	+	0	NA	intron (NL2a LINE	-19607	NR_02962E	406995	NR_02962E	ENSG00000MIR181A1	-	MIR213 MiRNA ncRNA	
chr1-2064	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (Nintron (N	-31320	NM_01400E	9641	Hs.32104ENM_01400E	ENSG00000IKBKE	-	IKK-E IKK inhibitor protein-coding	
chr1-2352	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	intron (NALuJo SIN	-19950	NR_03900E	1.01E+08	NR_03900E	ENSG00000MIR4753	-	mir-4753 microRNA ncRNA	
chr10-131	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr10	13140609	13144884	+	0	NA	Intergeni Intergeni	-18812	NM_01851E	55388	Hs.19836CNM_01851E	ENSG00000MCM10	-	CNA43 DNAmichron protein-coding	
chr10-79C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr10	79207503	79210480	+	0	NA	intron (Nintron (N	-138478	NM_00572E	10105	Hs.381072NM_00572E	ENSG00000PPIF	-	CYP3 CyP-peptidyl protein-coding	
chr11-57C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr11	57312411	57314349	+	0	NA	exon (NM exon (NM	11572	NM_03339E	85456	Hs.53073CNM_03339E	ENSG00000TNKS1BP1	-	TAB182 tankyrase protein-coding	
chr12-67C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr12	6794320	6796664	+	0	NA	intron (Nintron (N	5964	NM_00119E	920	Hs.63165CNM_00061E	ENSG00000CD4	-	CD4mut CD4 molecule protein-coding	
chr12-144	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr12	14473584	14476249	+	0	NA	intron (Nintron (N	89635	NM_18135E	55729	Hs.50485CNM_01817E	ENSG00000ATF71P	-	AM ATF-1 activator protein-coding	
chr12-55E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr12	55979303	55982027	+	0	NA	intron (Nintron (N	6587	NM_00286E	5869	Hs.15765CNM_00286E	ENSG00000RAB5B	-	RAB5B, meprotein-coding	
chr12-57E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr12	54522708	54525417	+	0	NA	intron (NMIRc SINE	-6385	NM_00128E	246329	Hs.41759CNM_14506E	ENSG00000STAC3	-	MYPBB NAM SH3 and cprotein-coding	
chr13-102	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr13	1.03E+08	1.03E+08	+	0	NA	intron (NL2c LINE	9916	NM_00012E	2073	Hs.25842CNM_00012E	ENSG00000ERC5C	-	COF53 ERC ERCC exciprotein-coding	
chr14-52C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr14	52315524	52317247	+	0	NA	intron (Nintron (N	2073	NM_00095E	5732	Hs.2090	NM_00095E	ENSG00000PTGER2	-	EP2 prostaglandin protein-coding
chr14-54E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr14	54522708	54525417	+	0	NA	intron (NL2 LINE L	14156	NM_00658E	10668	Hs.59106	NM_00658E	ENSG00000CGRFR1	-	CGR19 RNFC cell growth protein-coding
chr14-88E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr14	88878259	88882557	+	0	NA	non-codiron-codiron	55757	NM_00136E	123016	Hs.30305CNM_14459E	ENSG00000TTC8	-	BBS8 RP51tetraatric protein-coding	
chr15-34E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr15	34916716	34918944	+	0	NA	intron (NALuJo SIN	51912	NM_014691	9716	Hs.51095CNM_014691E	ENSG00000AQR	-	IBP160 fSquarius protein-coding	
chr15-61E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr15	61915662	61915844	+	0	NA	exon (NM exon (NM	144744	NM_017684	54832	Hs.51166CNM_017684E	ENSG00000VPS13C	-	PARK23 vacuolar protein-coding	
chr15-73E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr15	73297820	73304764	+	0	NA	intron (Nintron (N	1382	NR_16214E	1.13E+08	NR_16214E	MIR12135	-	microRNA ncRNA	
chr16-15E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr16	15882010	15883795	+	0	NA	intron (NALuSx3 SI	5696	NM_00130E	123811	Hs.51417CNM_14460E	ENSG00000FOPNL	-	C16orf63 FGFR10P lprotein-coding	
chr16-28E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr16	28980779	28984500	+	0	NA	intron (NMIR SINE	-2164	NM_00101E	27040	Hs.63217CNM_01438E	ENSG00000LAT	-	LM52 LAT linker fprotein-coding	
chr16-56E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr16	56399586	56405443	+	0	NA	intron (Nintron (N	22475	NM_00132E	267	Hs.295137NM_00114E	ENSG00000AMFR	-	GP78 RNFA4autocrine protein-coding	
chr16-57E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr16	57464147	57468052	+	0	NA	intron (Nintron (N	3420	NM_00329E	5432	Hs.79402	NM_00269E	ENSG00000POLR2C	-	RLP3 RPB2 RNA polymerase protein-coding
chr17-82C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr17	82091511	82095738	+	0	NA	exon (NM exon (NM	-3484	NR_13275E	1.07E+08	NR_13275E	SNORD134	-	ZN22 small ncnRNA	
chr19-107	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr19	10793009	10796995	+	0	NA	intron (NALuJo SIN	14748	NR_03990E	1.01E+08	NR_03990E	ENSG00000MIR4748	-	mir-4748 microRNA ncRNA	
chr19-11C	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr19	11022898	11024578	+	0	NA	intron (Nintron (N	39586	NM_00112E	6597	Hs.327527NM_00307E	ENSG00000SMARCA4	-	BAF190 BAF57 SNF1 protein-coding	
chr19-33E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr19	33088253	33090063	+	0	NA	intron (NMIRc SINE	7977	NM_01802E	55094	Hs.46643CNM_01802E	ENSG00000GPATCH1	-	EGCP GPA1G-patch cprotein-coding	
chr19-41E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr19	41316726	41318595	+	0	NA	intron (NALuJb SIN	7183	NM_00134E	90324	Hs.437497NM_05284E	ENSG00000CCDC97	-	coiled-co protein-coding	
chr19-57E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr19	57325129	57326866	+	0	NA	intron (Nintron (N	5525	NM_21359E	125919	Hs.202544NM_21359E	ENSG00000ZNF543	-	zinc fing protein-coding	
chr2-2011	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	3' UTR (A3' UTR (A	-1176	NM_00120E	8837	Hs.39073CNM_00387E	ENSG00000CFLAR	-	CASH CASFP8 ancon protein-coding	
chr20-33E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr20	33382941	33383742	+	0	NA	intron (NALuSx1 SI	18178	NM_01640E	51654	Hs.43595CNM_01608E	ENSG00000CDK5RAP1	-	C20orf34 CDK5 regt protein-coding	
chr20-49E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr20	49004601	49007459	+	0	NA	intron (NALuSg2 LI	40026	NR_11062E	1.03E+08	NR_11062E	ENSG00000CSEIL-AS1	-	CSEIL antncRNA	
chr21-33E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr21	33611295	33614005	+	0	NA	intron (NLIME3E LI	-23966	NM_01761E	29980	Hs.436341NM_01761E	ENSG00000DONSON	-	B17 C21orf2downstrep protein-coding	
chr22-264	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr22	26493856	26496994	+	0	NA	TTS (NM_C TTS (NM_C	11548	NM_00101E	402055	Hs.709914NM_00101E	ENSG00000SRRD	-	HC/HCC SFSRR1 dome protein-coding	
chr22-29E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr22	29671700	29677134	+	0	NA	intron (Nintron (N	-45586	NM_182527	164633	Hs.64360CNM_182527E	ENSG00000CABP7	-	CALN2 calcium tprotein-coding	
chr3-1014	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr3	10148851	10154690	+	0	NA	3' UTR (A3' UTR (A	9992	NM_19815E	7428	Hs.51779CNM_000551E	ENSG00000CVHL	-	HRCAL RCVn Hippe protein-coding	
chr3-3341	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr3	33418897	33419617	+	0	NA	intron (NALuSg SIN	21121	NM_00112E	7342	Hs.72912CNM_001451E	ENSG00000UBP1	-	LBP-1B LUF upstream protein-coding	
chr3-3701	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr3	37018618	37021121	+	0	NA	intron (NALuS5 SI	26519	NM_00125E	4292	Hs.195364NM_00024E	ENSG00000MLH1	-	COCA2 FCCmutL homoprotein-coding	
chr3-497E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr3	49734596	49736494	+	0	NA	intron (Nintron (N	-11571	NM_01333E	29925	Hs.56748CNM_01333E	ENSG00000GMPBP	-	LGM19 GDP bindp protein-coding	
chr3-5007	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr3	50072930	50077621	+	0	NA	exon (NM exon (NM	-13644	NM_00577E	10181	Hs.43948CNM_00577E	ENSG00000RBM5	-	G15 H37 RNA binding protein-coding	
chr3-125E	7.682963	0.326259	0.833189	0.391579	0.695369	0.981636	chr3	1.26E+08	1.26E+08	+	0	NA	ex								

chr11-914.11.14271	-0.27503	0.705733	-0.38971	0.696751	0.981636	chr11	9149210	9150206	+	0 NA	intron (Nintron (N	55345 NR_027713	283102 Hs. 689472NR_027713	ENSG00000CKRT8P41	-	keratin εpseud
chr1-2522.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr1	25229596	25231083	+	0 NA	intron (Nintron (N	2163 NM_015484	25949 Hs. 20013 NM_015484	ENSG00000SYF2	-	CBP1N NTC SYF2 pre-protein-coding
chr10-69.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr10	69365903	69366370	+	0 NA	intron (NMIR SINE	47289 NM_000188	3098 Hs. 37036ENM_000188	ENSG00000CHK1	-	HK HK1-αhexokinase protein-coding
chr15-424.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr15	42411912	42413575	+	0 NA	TTS (NM_1TTS (NM_1	7964 NM_173088	825 Hs. 143261NM_00007C	ENSG00000CAPN3	-	CANP3 CAN calpain 3 protein-coding
chr17-647.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr17	64792421	64792421	+	0 NA	intron (Nintron (N	-9843 NR_026899	1.09E+08 Hs. 117855NR_026899	ENSG00000ARHGAP27F1	-	ARHGAP27 pseudo
chr18-127.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr18	12709582	12711587	+	0 NA	intron (NLMC5a LI	7542 NM_020232	56984 Hs. 464652NM_020232	ENSG00000PSMG2	-	CLAST3 HC proteasome protein-coding
chr2-235.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr2	2.35E+08	2.35E+08	+	0 NA	intron (Nintron (N	-18892 NR_001371	1306			
chr20-35.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr20	35011666	35012305	+	0 NA	intron (NL2c LINE	-21513 NR_039912	1.01E+08 NR_039912	ENSG00000MIR499B	-	MIR499A l-microRNA ncRNA
chr20-35.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr20	35557393	35558102	+	0 NA	TTS (NM_1TTS (NM_1	15669 NM_015966	51614 Hs. 472555NM_015966	ENSG00000CERGIC3	-	C20orf47 ERGIC anc protein-coding
chr5-180.7.145236	0.337857	0.86696	0.389703	0.696756	0.981636	chr5	1.81E+08	1.81E+08	+	0 NA	intron (Nintron (N	8819 NM_001137	57472 Hs. 60838CM_01545E	ENSG00000CNOT6	-	CCR4 Ccr4 CCR4-NOT protein-coding
chr1-109.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr1	1.09E+08	1.09E+08	+	0 NA	exon (NM exon (NM	30730 NM_001142	22911 Hs. 570055NM_01496E	ENSG00000WDR47	-	WD repeat protein-coding
chr10-778.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr10	77852524	77854854	+	0 NA	intron (Nintron (N	73066 NM_004747	9231 Hs. 652629NM_004747	ENSG00000CDLG5	-	LP-DLG P-discs lar protein-coding
chr13-84.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr13	24284340	24286872	+	0 NA	intron (NAluSq SIN	14856 NM_00128E	221178 Hs. 434298NM_15302E	ENSG00000SPATA13	-	ARHGFE29 spermatog protein-coding
chr14-212.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr14	81486388	81490411	+	0 NA	intron (Nintron (N	-38242 NR_109999	1.01E+08 Hs. 116304NR_109999	ENSG00000LINC02303E	-	long intncRNA
chr17-276.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr17	27622871	27624335	+	0 NA	3' UTR (N3' UTR (N	-7585 NM_00230E	3965 Hs. 81337 NM_00230E	ENSG00000CLGALS9	-	HUAT Lgalactin protein-coding
chr2-134.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr2	1.34E+08	1.34E+08	+	0 NA	intron (Nintron (N	64362 NM_00241C	4249 Hs. 4988 NM_00241C	ENSG00000MGAT5	-	GNT-V GNT alpha-1, f protein-coding
chr2-151.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr2	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	6953 NM_198557	375287 Hs. 302442NM_198557	ENSG00000CRBM43	-	C2orf38 RNA bindi protein-coding
chr2-225.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr2	2.25E+08	2.25E+08	+	0 NA	intron (NAluJr SIN	27261 NM_001257	8452 Hs. 372288NM_00359C	ENSG00000CUL3	-	CUL-3 PHF cullin 3 protein-coding
chr4-5581.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr4	5581521	5581826	+	0 NA	intron (NMSTA-int	56517 NR_126517	10141 Hs. 177972NM_00575C	ENSG00000LINC01587C	-	4orf6 a long intncRNA
chr6-893.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr6	89340541	89342331	+	0 NA	intron (Nintron (N	11286 NM_016021	51465 Hs. 163776NM_016021	ENSG00000CUBE2J1	-	CGI-76 Hs ubiquitin protein-coding
chr7-100.7.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chr7	1E+08	1E+08	+	0 NA	intron (NL2b LINE	3274 NM_17823E	29990 Hs. 632314NM_01344C	ENSG00000PILRB	-	PDFACT1 Pfair in protein-coding
chrX-1674.8.220691	0.316136	0.811724	0.389463	0.696934	0.981636	chrX	16748863	16749407	+	0 NA	intron (NAluJb SIN	29523 NM_03279E	94056 Hs. 744256NM_03279E	ENSG00000SYAP1	-	BSTA PRO2 synapse protein-coding
chr14-10.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr14	1.04E+08	1.04E+08	+	0 NA	IntergeniAluY SINE	14581 NM_00182E	1152 Hs. 173724NM_00182E	ENSG00000CCKB	-	B-C BCK creatine protein-coding
chr15-904.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr15	90409563	90410043	+	0 NA	intron (NLIpA5 LIN	21561 NM_00387C	8826 Hs. 430551NM_00387C	ENSG00000IQGAP1	-	HUMORFA01 IQ motif protein-coding
chr2-665.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr2	66525717	66526535	+	0 NA	intron (Nintron (N	-47904 NR_11015E	1.01E+08 Hs. 667942NR_11015E	ENSG00000LINC0179E	-	long intncRNA
chr2-170.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr2	1.7E+08	1.7E+08	+	0 NA	intron (Nintron (N	-116317 NR_04568E	140469 Hs. 671902NM_13899E	ENSG00000MYO3B	-	myosin II protein-coding
chr2-182.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr2	1.83E+08	1.83E+08	+	0 NA	intron (Nintron (N	81845 NM_01343E	10787 Hs. 603732NM_01343E	ENSG00000CKAP1	-	HEM2 NAP1NCK assoc protein-coding
chr2-241.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr2	2.42E+08	2.42E+08	+	0 NA	3' UTR (N3' UTR (N	-13672 NR_03334E	1E+08 Hs. 621122NR_03334E	BOK-AS1	-	BOK-AS BOK antisncRNA
chr3-313.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr3	3139667	3141369	+	0 NA	exon (NM exon (NM	13578 NR_15994C	51095 Hs. 732722NM_01600C	ENSG00000TRNT1	-	CCA1 CGI- tRNA nucle protein-coding
chr3-3064.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr3	30645074	30647992	+	0 NA	intron (NL3 LINE C	39932 NM_00324E	7048 Hs. 82028 NM_00324E	ENSG00000TGFB7E	-	AAT3 FAA3 transform protein-coding
chr4-769.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr4	76989401	76990314	+	0 NA	intron (NTiger3a	40105 NM_00130E	55752 Hs. 128195NM_01824E	ENSG00000SEPTIN11	-	11-Sep septin 11 protein-coding
chr7-446.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr7	44659916	44661147	+	0 NA	intron (NLMda LIN	53904 NM_00100C	4967 Hs. 488181NM_002541	ENSG00000CGDH	-	AKGHD1 E1h oxoglutarate protein-coding
chr7-475.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr7	47505165	47507195	+	0 NA	intron (Nintron (N	-41377 NR_145811	1.1E+08 NR_145811	SNORD151	-	small nucsnoRNA
chr8-1407.7.895849	-0.32165	0.826176	-0.38933	0.697036	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	intron (NLMb7 LIN	-26605 NR_02989E	442893 NR_02989E	ENSG00000MIR151A	-	MIR151 Ml-microRNA ncRNA
chr15-437.11.13485	-0.27383	0.703555	-0.3892	0.697126	0.981636	chr15	43764345	43769289	+	0 NA	exon (NM exon (NM	10149 NM_02516E	80237 Hs. 70634E NM_02516E	ENSG00000ELL3	-	elongactin protein-coding
chr15-671.11.13485	-0.27383	0.703555	-0.3892	0.697126	0.981636	chr15	6179219	61782799	+	0 NA	intron (Nintron (N	14854 NM_00114E	4088 Hs. 72798CM_00590E	ENSG00000SMAD3	-	HSPC193 E SMAD fam protein-coding
chr2-1717.11.13485	-0.27383	0.703555	-0.3892	0.697126	0.981636	chr2	1.72E+08	1.72E+08	+	0 NA	3' UTR (N3' UTR (N	61345 NM_00132C	1781 Hs. 546255NM_00137E	ENSG00000DYNC1I2	-	DIC74 DNC dynein cy protein-coding
chr3-139.11.13485	-0.27383	0.703555	-0.3892	0.697126	0.981636	chr3	1.39E+08	1.39E+08	+	0 NA	TTS (NM_1TTS (NM_C	12997 NM_00136E	56945 Hs. 745001NM_020191	ENSG00000MRP52	-	C3orf5 CCmitch protein-coding
chr11-86.7.65939	0.332288	0.853795	0.38919	0.697136	0.981636	chr11	86328451	86328995	+	0 NA	intron (NAluSg7 SI	26483 NM_00132E	51501 Hs. 283322NM_016401	ENSG00000HIKESHI	-	Clorf173 heat choc protein-coding
chr1-5427.7.903707	-0.32337	0.831224	-0.38903	0.697252	0.981636	chr1	54279557	54280429	+	0 NA	intron (Nintron (N	43550 NR_103541	619518 Hs. 591433NM_001034	ENSG00000SSBP3-AS1	-	Clorf191 SSBP3 antncRNA
chr17-171.7.903707	-0.32337	0.831224	-0.38903	0.697252	0.981636	chr17	17164438	17164865	+	0 NA	exon (NM exon (NM	41682 NM_17883E	201164 Hs. 729075NM_17883E	ENSG00000PLD6	-	ZUC phospholipid protein-coding
chr20-46.7.903707	-0.32337	0.831224	-0.38903	0.697252	0.981636	chr20	46365900	46367409	+	0 NA	3' UTR (N3' UTR (N	-2196 NM_001281	51006 Hs. 593344NM_01594E	ENSG00000SLC35C2	-	BA39402.1 solute c protein-coding
chr3-120.7.903707	-0.32337	0.831224	-0.38903	0.697252	0.981636	chr3	1.2E+08	1.2E+08	+	0 NA	3' UTR (N3' UTR (N	18917 NM_00109E	116064 Hs. 518084NM_00109E	ENSG00000LRRCS8	-	leucine r protein-coding
chr13-33.8.742703	0.31097	0.799605	0.388904	0.697347	0.981636	chr13	33223932	33224854	+	0 NA	intron (NMLT1 LTF	-18343 NM_00124E	90627 Hs. 156551NM_052851	ENSG00000STARD13	-	ARHGAP37 StAR rel protein-coding
chr1-1514.7.724103	0.327787	0.843011	0.388829	0.697403	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	intron (Nintron (N	14909 NM_00279E	5692 Hs. 89545 NM_00279E	ENSG00000PSMB4	-	HN3 Hsn3 proteasome protein-coding
chr14-75.7.724103	0.327787	0.843011	0.388829	0.697403	0.981636	chr14	75109341	75111048	+	0 NA	intron (Nintron (N	16854 NM_00132E	91754 Hs. 7200 NM_03311E	ENSG00000NEK9	-	APUG LCCS NIMA rel protein-coding
chr3-114.7.724103	0.327787	0.843011	0.388829	0.697403	0.981636	chr3	11407681	11408500	+	0 NA	intron (NTHE1B-int	135693 NM_001144	10533 Hs. 38032 NM_00639E	ENSG00000ATG7	-	APG7-LIKE autophagy protein-coding
chr4-867.7.724103	0.327787	0.843011	0.388829	0.697403	0.981636	chr4	86762086	86762839	+	0 NA	intron (Nintron (N	86922 NM_19796E	345274 Hs. 452996NM_19796E	ENSG00000SLC10A6	-	SOAT solute c protein-coding
chr8-144.7.724103	0.327787	0.843011	0.388829	0.697403	0.981636	chr8	1.44E+08	1.44E+08	+	0 NA	intron (Nintron (N	3206 NM_01620E	51160 Hs. 41817E NM_01620E	ENSG00000VPS28	-	VPS28 solute c protein-coding
chr10-797.4.691974	-0.40951	0.053694	-0.38864	0.697541	0.981636	chr10	79753336	79755583	+	0 NA	intron (NLIpA14 LI	51232 NM_00127E	729262 Hs. 742755NM_0			



chr19-615.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	619685	622126	+	0	NA	intron (NCpG-1289E	12632	NM_005035	5442	Hs.254111	ENSG000003POLRMT	APOLMT	MI	RNA	polyn	protein-coding	
chr19-141.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	1418375	1425695	+	0	NA	intron (Nintron (N	14449	NM_001352	26528	Hs.222511	ENSG000003DAZAP1	-	DAZ	assoc	protein-coding		
chr19-111.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	11026064	11037251	+	0	NA	intron (Nintron (N	47505	NM_001128	6597	Hs.327527	ENSG000003SMARCA4	BAF190	BA	SWI/SNF	r	protein-coding	
chr19-136.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	13840649	13841445	+	0	NA	non-codiron-codir	1871	NR_03651E	284454	Hs.43642E	ENSG000003LOC284454	-	uncharact	ncRNA	-		
chr19-167.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	16517416	16518364	+	0	NA	intron (Nintron (N	14412	NM_006387	10523	Hs.740364	ENSG000003CHERP	DAN16	SCA	calcium	protein-coding		
chr19-172.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	17271423	17275132	+	0	NA	intron (Nintron (N	5834	NM_01417E	29086	Hs.190722	ENSG000003BABAM1	C19orf62	BRISC	anc	protein-coding		
chr19-394.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	39455699	39461179	+	0	NA	intron (Nintron (N	-9784	NR_14580E	1.1E+08	NR_14580E	SNORD175	-	small	nuc	snoRNA		
chr19-575.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	57921316	57922233	+	0	NA	TTS (NM_C	-5262	NM_15247E	147687	Hs.567711	ENSG000003ZNF417	-	zinc	fin	protein-coding		
chr19-584.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr19	58469577	58473110	+	0	NA	exon (NM_exon (NM	4263	NM_014347	25799	Hs.51566C	ENSG000003ZNF324	ZF5128	Z	zinc	fin	protein-coding	
chr2-9625.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr2	96294727	96296273	+	0	NA	intron (Nintron (N	9806	NM_014014	23020	Hs.24611E	ENSG000003SNRNP200	ASCC3L1	E	small	nuc	protein-coding	
chr20-245.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr20	2494423	2494742	+	0	NA	intron (NAluSg SIN	12968	NM_001321	79175	Hs.51684E	ENSG000003ZNF343	dJ734P14	Z	zinc	fin	protein-coding	
chr20-347.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr20	34724848	34727579	+	0	NA	intron (Nl2a LINE	21494	NM_00132E	58476	Hs.516994	ENSG000003TP53INP2	C20orf11C	tumor	prc	protein-coding		
chr20-463.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr20	46379577	46388552	+	0	NA	intron (Nl1ME4a LI	-19606	NM_001281	51006	Hs.593344	ENSG000003SLC35C2	BA39402	I	solute	c	protein-coding	
chr22-264.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr22	26457751	26458152	+	0	NA	exon (NM_exon (NM	21537	NR_07313E	89781	Hs.47443E	ENSG000003HPS4	BLOC352	L	HPS4	b	protein-coding	
chr22-382.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr22	38223977	38226449	+	0	NA	promoter-promoter-	-493	NR_132774	1.07E+08	NR_132774	SNORA92	-	small	nuc	snoRNA		
chr3-5205.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr3	5209960	5214795	+	0	NA	intron (Nintron (N	24670	NM_014674	9695	Hs.22461E	ENSG000003EDEMI	EDEM	ER	degrac	protein-coding		
chr3-1851.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr3	1.85E+08	1.85E+08	+	0	NA	intron (Nintron (N	18630	NR_10671E	1.01E+08	NR_10671E	ENSG000003MIR5588	-	micro	RNA	ncRNA		
chr4-762.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr4	76160322	76164834	+	0	NA	intron (Nintron (N	-14063	NR_103781	53371	Hs.40343E	ENSG000003NUP54	-	nucleop	r	protein-coding		
chr5-313.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr5	31309615	31310920	+	0	NA	intron (NMSTA-int	116581	NM_004932	1004	Hs.12477E	ENSG000003CDH6	CAD6	KCAI	cadherin	protein-coding		
chr5-721.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr5	72184191	72185571	+	0	NA	intron (Nl1MB7 LIN	5094	NM_00132E	4131	Hs.33507E	ENSG000003MAP1B	FUTSCH	M	microtub	protein-coding		
chr5-177E.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr5	1.78E+08	1.78E+08	+	0	NA	intron (Nintron (N	-11592	NM_016222	51428	Hs.48428E	ENSG000003DDX41	ABS MLPF	DEAD	-box	protein-coding		
chr6-111.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	62251	NM_15336E	91749	Hs.40057E	ENSG000003MFS4B	KIAA1919	ma	jo	fac	protein-coding	
chr7-549E.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr7	5498512	5501116	+	0	NA	intron (NAluJo SIN	-3897	NR_03031E	693174	NR_03031E	ENSG000003MIR589	MIRN589	I	micro	RNA	ncRNA	
chr7-3305.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr7	33095116	33102294	+	0	NA	intron (NHALI LINE	10699	NM_20328E	6100	Hs.3268E	ENSG000003RP9	PAP-1	PAF	RP9	pre	-n	protein-coding
chr9-954E.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr9	95453576	95454422	+	0	NA	intron (Nintron (N	-9610	NR_03898E	1.01E+08	Hs.661847	ENSG000003LOC100507	-	uncharact	ncRNA	-		
chr9-136.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	exon (NM_exon (NM	45369	NM_14465E	13815	Hs.11289E	ENSG000003NACC2	BEND9	BTE	NACC	fam	protein-coding	
chr9-269.7.690821	0.324297	0.835563	0.388118	0.697929	0.981636	chr9	26909711	26909910	+	0	NA	intron (NAluSx1 SI	10699	NM_001167	79886	Hs.17835E	ENSG000003CAAP1	C9orf82	C	cas	protein-coding		
chr17-388.11.127	-0.27262	0.703343	-0.3876	0.69831	0.981636	chr17	38846679	38853111	+	0	NA	3' UTR (N3' UTR (N	1763	NR_145761	1.1E+08	NR_145761	ENSG000003SNORA21B	-	small	nuc	snoRNA		
chr5-143.11.127	-0.27262	0.703343	-0.3876	0.69831	0.981636	chr5	14330498	14340114	+	0	NA	intron (Nintron (N	-128677	NR_14581E	1.1E+08	NR_14581E	SNORD170	-	small	nuc	snoRNA		
chr17-501.8.750561	0.309173	0.797933	0.387468	0.69841	0.981636	chr17	5015507	5015968	+	0	NA	intron (NAluSx SIN	4356	NR_12066E	1.03E+08	Hs.666487	ENSG000003LOC102724	-	uncharact	ncRNA	-		
chr22-364.8.750561	0.309173	0.797933	0.387468	0.69841	0.981636	chr22	36477365	36477931	+	0	NA	intron (Nintron (N	3992	NM_01247E	25828	Hs.21192E	ENSG000003TXN2	COXP29	I	thio	protein-coding		
chr1-393.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr1	39305483	39306690	+	0	NA	intron (Nl2a LINE	-102987	NM_01503E	643314	Hs.65876E	ENSG000003KIAA0754	-	KIAA0754	protein-coding			
chr1-156E.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	exon (NM_exon (NM	13131	NM_00108C	375033	Hs.14200E	ENSG000003PEAR1	JEDI	MEGF	lat	protein-coding		
chr10-10.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	3' UTR (N3' UTR (N	76914	NM_00136E	9644	Hs.678727	ENSG000003SH3PXD2A	FISH	SH3	SH3	and	protein-coding	
chr11-44.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr11	4494160	44946408	+	0	NA	intron (Nintron (N	3876	NM_00125E	9537	Hs.554791	ENSG000003TP53I11	PIG11	tumor	prc	protein-coding		
chr12-26E.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr12	26002628	26003411	+	0	NA	intron (Nl1P4 LINE	29264	NM_001164	11228	Hs.69643E	ENSG000003RASSF8	C1orf2	F	ras	protein-coding		
chr13-114.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (NAluSq2 SI	-11677	NM_03243E	283489	Hs.7542	ENSG000003CHAMP1	C13orf8	C	chromos	protein-coding		
chr14-677.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr14	67799697	67800554	+	0	NA	intron (Nintron (N	16465	NM_01534E	23503	Hs.98041	ENSG000003ZFVYE26	FYVE	CEN	zinc	fin	protein-coding	
chr15-73E.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr15	73699271	73699979	+	0	NA	5' UTR (N5' UTR (N	14855	NM_00132E	80381	Hs.74491E	ENSG000003CD276	41G-B7	H	CD276	m	protein-coding	
chr19-127.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr19	12746957	12748220	+	0	NA	exon (NM_exon (NM	-4203	NM_01768E	54831	Hs.435611	ENSG000003BEST2	VMD2L1	best	protein-coding			
chr20-621.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr20	62189166	62189952	+	0	NA	intron (NAluJr SIN	6534	NM_01566E	26164	Hs.34063E	ENSG000003MTG2	GTPBP5	O	mito	chonc	protein-coding	
chr5-784.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr5	78440048	78441323	+	0	NA	intron (Nl1P46 LIN	80287	NM_00486E	9522	Hs.482587	ENSG000003SCAMP1	SCAMP	SCA	secretory	protein-coding		
chr7-778.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr7	77820026	77821619	+	0	NA	intron (Nl1MA5A LI	-19306	NM_02043E	57157	Hs.20396E	ENSG000003PHTF2	-	putative	protein-coding			
chr8-231E.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr8	23158168	23159244	+	0	NA	intron (Nl1MEf LIN	5321	NM_00384C	8793	Hs.213467	ENSG000003TNFRSF10E	CD264	DCF	TNF	rec	protein-coding	
chr9-106E.7.153094	0.335741	0.86708	0.387209	0.698602	0.981636	chr9	1.07E+08	1.07E+08	+	0	NA	intron (Nintron (N	76247	NM_021224	58499	Hs.37037E	ENSG000003ZNF462	ZFP1P	Zf	zinc	fin	protein-coding	
chr1-101E.7.179552	0.314681	0.813358	0.386891	0.698837	0.981636	chr1	10105390	10106482	+</														

chr5-723: 8.228549	0.314321	0.81595	0.385221	0.700074	0.981636	chr5	72335076	72336636	+	0 NA	exon (NM exon (NM_001284	15483	79810	Hs.126906	ENSG000002PTCD2	-	pentatricprotein-coding
chr4-1431	7.77058	-0.34349	0.89169	-0.38521	0.700084	chr4	1.43E+08	1.43E+08	+	0 NA	intron (Nintron (N_00129C	5601	84640	Hs.48084E	ENSG000002USP38	-	HP43.8KD ubiquitin protein-coding
chr11-118	7.649682	0.322755	0.83834	0.384992	0.700243	chr11	1.18E+08	1.18E+08	+	0 NA	TTS (NR_TTS (NR_C_03375E	-20296	10632	Hs.48636C	ENSG000002ATP5MG	-	ATP5JG ATATP syntf protein-coding
chr19-757	7.649682	0.322755	0.83834	0.384992	0.700243	chr19	7550174	7551396	+	0 NA	intron (NCPg-13551	15068	10908	Hs.61386E	ENSG000002PNPLA6	-	BNHS LNMC patatin I protein-coding
chr2-1717	7.649682	0.322755	0.83834	0.384992	0.700243	chr2	1.72E+08	1.72E+08	+	0 NA	exon (NM exon (NM_00132C	60033	1781	Hs.546255C	ENSG000002DYNCL12	-	DC17C4 DNcyein cy protein-coding
chr4-731C	7.649682	0.322755	0.83834	0.384992	0.700243	chr4	73108546	73109710	+	0 NA	intron (NAluSx SIN	-39369	285521	Hs.356697N	ENSG000002COX18	-	COX18HS cytochron protein-coding
chr4-761F	7.649682	0.322755	0.83834	0.384992	0.700243	chr4	76165713	76166652	+	0 NA	intron (Nintron (N_10378F	-17667	53371	Hs.43043E	ENSG000002NUP54	-	nucleopor protein-coding
chr5-528F	7.649682	0.322755	0.83834	0.384992	0.700243	chr5	52888152	52888357	+	0 NA	intron (NAluSx SIN	100338	3672	Hs.44435E	ENSG000002ITGA1	-	CD49A VLA integrin protein-coding
chr4-119F	11.11914	-0.2714	0.705099	-0.38491	0.700305	chr4	1.2E+08	1.2E+08	+	0 NA	intron (Nintron (N_03763C	83150	645513	Hs.67754E	ENSG000002LOC64551E	-	septin 7 pseudo
chr11-337	6.689787	0.354221	0.920494	0.384816	0.700374	chr11	33759899	33760523	+	0 NA	intron (NLM3E3 ALI	14310	FBA FBX3	F-box prc protein-coding			
chr14-344	6.689787	0.354221	0.920494	0.384816	0.700374	chr14	34444076	34444599	+	0 NA	intron (NLM3E3 ALI	17905	171546	Hs.740577N	ENSG000002SPTSSA	-	C14orf147 serine pr protein-coding
chr7-1042	6.689787	0.354221	0.920494	0.384816	0.700374	chr7	1.04E+08	1.04E+08	+	0 NA	intron (NMIR SINE	4381	5001	Hs.43294E	ENSG000002ORC5	-	ORC5L ORC origin re protein-coding
chr12-88C	6.095204	0.327903	0.969646	0.384577	0.700551	chr12	880338	880588	+	0 NA	intron (Nintron (N_001297	52613	5893	Hs.41035E	ENSG000002RAD52	-	RAD52 hom protein-coding
chr12-296	7.410818	-0.3306	0.859694	-0.38455	0.700568	chr12	29652490	29652720	+	0 NA	intron (NLM2C LINE	131337	83857	Hs.401954N	ENSG000002TMTC1	-	ARG99 OLF transmemt protein-coding
chr12-62F	7.410818	-0.3306	0.859694	-0.38455	0.700568	chr12	62509060	62509791	+	0 NA	intron (NLM2B LIN	42599	23041	Hs.38937E	ENSG000002MON2	-	MON2 homc protein-coding
chr13-262	7.410818	-0.3306	0.859694	-0.38455	0.700568	chr13	26219276	26219485	+	0 NA	intron (Nintron (N_18304A	20377	6049	Hs.13688E	ENSG000002RNF6	-	ring fing protein-coding
chr15-637	7.410818	-0.3306	0.859694	-0.38455	0.700568	chr15	63711706	63711940	+	0 NA	intron (NMIRc SINE	-110996	1E+08	Hs.63116E	ENSG000002CASP3-AS1	-	USP3 anticrRNA
chr16-874	7.410818	-0.3306	0.859694	-0.38455	0.700568	chr16	87419091	87419397	+	0 NA	intron (NAluSx SIN	26908	81631	Hs.356661N	ENSG000002MAP1LC3B	-	ATG8F LC microtub protein-coding
chr3-133F	7.410818	-0.3306	0.859694	-0.38455	0.700568	chr3	1.34E+08	1.34E+08	+	0 NA	intron (Nintron (N_16349I	5731	58477	Hs.12152	ENSG000002SRPRB	-	APMCF1 SFRS1 recep protein-coding
chr20-384	11.58845	-0.26565	0.691134	-0.38437	0.700703	chr20	38422837	38426130	+	0 NA	TTS (NR_TTS (NR_C_00291C	847	26776	Hs.40087E	ENSG000002SNORA71B	-	RNU71B U7small nuc snoRNA
chr7-3001	8.725137	0.304146	0.791374	0.384327	0.700736	chr7	30013315	30014184	+	0 NA	non-codir non-codir	12953	55033	Hs.39083E	ENSG000002FKBP14	-	EDSKMH EL FKBP pr protein-coding
chr20-91F	7.194233	0.337203	0.877405	0.384319	0.700742	chr20	9131603	9131924	+	0 NA	intron (NMLT1H2 LI	62709	5332	Hs.472101N	ENSG000002PLCB4	-	ARCND2 PI phospholip protein-coding
chr4-122F	7.194233	0.337203	0.877405	0.384319	0.700742	chr4	1.22E+08	1.22E+08	+	0 NA	intron (NLM3C LIN	-59056	132612	Hs.518957N	ENSG000002CADAD1	-	Tenr adenosine protein-coding
chr5-172C	7.194233	0.337203	0.877405	0.384319	0.700742	chr5	1.72E+08	1.72E+08	+	0 NA	intron (NMLT1E2 LI	-45404	23291	Hs.48413E	ENSG000002FBXW11	-	BTRC2 BTF F-box anc protein-coding
chr7-4997	7.194233	0.337203	0.877405	0.384319	0.700742	chr7	4997331	4997784	+	0 NA	non-codir non-codir	23570	441191	Hs.52063E	ENSG000002RNF216P1	-	RNF216L ring fing pseudo
chr7-755F	7.194233	0.337203	0.877405	0.384319	0.700742	chr7	75559961	75560794	+	0 NA	intron (NAluJo SIN	-32254	5387	Hs.659871N	ENSG000002PMS2P3	-	PMS2L3 PW PMS1 homc pseudo
chr1-246E	7.641824	0.324707	0.845071	0.384237	0.700803	chr1	24640060	24640676	+	0 NA	exon (NM exon (NM_016002	77044	51097	Hs.498397N	ENSG000002PCDH1	-	EDSKMH EL FKBP pr protein-coding
chr20-62F	7.641824	0.324707	0.845071	0.384237	0.700803	chr20	62285834	62286836	+	0 NA	intron (NAluSx SIN	-16561	11047	Hs.90107	ENSG000002ADRM1	-	ARM-1 ARM adhesion protein-coding
chr6-264C	7.641824	0.324707	0.845071	0.384237	0.700803	chr6	26406400	26406676	+	0 NA	intron (Nintron (N_19444I	4263	11119	Hs.19151C	ENSG000002BTN3A1	-	BT3.1 BTF buty protein-coding
chr17-821	10.165768	-0.27885	0.725951	-0.38411	0.700894	chr17	82195064	82195299	+	0 NA	intron (NAluJb SIN	17661	284001	Hs.631724N	ENSG000002CCDC57	-	coiled-c protein-coding
chr1-1737	8.195267	0.310985	0.809622	0.384111	0.700896	chr1	1.74E+08	1.74E+08	+	0 NA	intron (NAluJb SIN	45712	91687	Hs.53185E	ENSG000002CENPL	-	C1orf155 centromer protein-coding
chr1-246F	8.195267	0.310985	0.809622	0.384111	0.700896	chr1	2.47E+08	2.47E+08	+	0 NA	intron (Nintron (N_15144E	25411	25909	Hs.300887N	ENSG000002AHCTF1	-	ELYS MS1AT-hook cr protein-coding
chr10-125	8.195267	0.310985	0.809622	0.384111	0.700896	chr10	1.26E+08	1.26E+08	+	0 NA	intron (Nintron (N_12063E	1.02E+08	5830	Hs.63426E	ENSG000002EDRF1-AS1	-	EDRF1 anticrRNA
chr11-134	8.195267	0.310985	0.809622	0.384111	0.700896	chr11	13412176	13413849	+	0 NA	intron (Nintron (N_001297	27267	84280	Hs.33238E	ENSG000002BTBD10	-	GMRP-1 GWBTB doma protein-coding
chr11-43	8.195267	0.310985	0.809622	0.384111	0.700896	chr11	43447976	43452605	+	0 NA	intron (Nintron (N_18255E	91370	55761	Hs.50118E	ENSG000002TTC17	-	tetratric protein-coding
chr11-115	8.195267	0.310985	0.809622	0.384111	0.700896	chr11	1.19E+08	1.19E+08	+	0 NA	intron (Nintron (N_100135I	12228	25988	Hs.194091N	ENSG000002HINFP	-	HINFP MI histone f protein-coding
chr12-72C	8.195267	0.310985	0.809622	0.384111	0.700896	chr12	7207485	7210956	+	0 NA	intron (Nintron (N_00031E	18858	5830	Hs.567327N	ENSG000002PEX5	-	PBD2A PBE peroxison protein-coding
chr12-804	8.195267	0.310985	0.809622	0.384111	0.700896	chr12	8047161	8050664	+	0 NA	intron (Nintron (N_18141E	16196	55810	Hs.120844N	ENSG000002FOXJ2	-	FHX forkhead protein-coding
chr12-194	8.195267	0.310985	0.809622	0.384111	0.700896	chr12	19473095	19475068	+	0 NA	intron (Nintron (N_1001267	33482	51347	Hs.126497N	ENSG000002AEBP2	-	AE bindir protein-coding
chr12-118	8.195267	0.310985	0.809622	0.384111	0.700896	chr12	1.18E+08	1.18E+08	+	0 NA	intron (NAluJb SIN	10228	51347	Hs.64442C	ENSG000002TAOK3	-	DPK JIK VTAO kinas protein-coding
chr14-212	8.195267	0.310985	0.809622	0.384111	0.700896	chr14	21239780	21240111	+	0 NA	intron (Nintron (N_031314	29534	3183	Hs.50884E	ENSG000002HNRNP	-	C1 C2 HNF heteroger protein-coding
chr16-287	8.195267	0.310985	0.809622	0.384111	0.700896	chr16	28734088	28734894	+	0 NA	intron (Nintron (N_100113C	10239	1.02E+08	Hs.106922E	ENSG000002MIR6862-1	-	hsa-mir-6 microRNA ncRNA
chr16-577	8.195267	0.310985	0.809622	0.384111	0.700896	chr16	57796467	57798045	+	0 NA	intron (Nintron (N_012091	25460	3801	Hs.23131	ENSG000002KIFC3	-	kinesin f protein-coding
chr16-75E	8.195267	0.310985	0.809622	0.384111	0.700896	chr16	75597420	75598292	+	0 NA	3' UTR (N3' UTR (N_10012091	25460	23536	Hs.72931E	ENSG000002ADAT1	-	HADAT1 adenosine protein-coding
chr16-89F	8.195267	0.310985	0.809622	0.384111	0.700896	chr16	89522172	89535723	+	0 NA	intron (NAluSg SIN	20579	6687	Hs.185597N	ENSG000002SPG7	-	CAR CMAR SPG7 mat protein-coding
chr17-72E	8.195267	0.310985	0.809622	0.384111	0.700896	chr17	7212942	7231088	+	0 NA	exon (NM exon (NM_02989E	-3136	442898	Hs.185597N	ENSG000002MIR324	-	MIRN324 mi microRNA ncRNA
chr17-17E	8.195267	0.310985	0.809622	0.384111	0.700896	chr17	17213001	17214955	+	0 NA	intron (Nintron (N_17883E	-7645	201164	Hs.72907E	ENSG000002PLD6	-	ZUC phospholip protein-coding
chr17-494	8.195267	0.310985	0.809622	0.384111	0.700896	chr17	4940403	49412849	+	0 NA	intron (Nintron (N_001281	6412	5245	Hs.51430E	ENSG000002CPHB	-	HEL-215 E prohibit protein-coding
chr17-62F	8.195267	0.310985	0.809622	0.384111	0.700896	chr17	62686855	62688855	+	0 NA	intron (Nintron (N_14788E	-22170	1.05E+08	Hs.44626E	ENSG000002LOC105371	-	uncharactncRNA
chr17-76E	8.195267	0.310985	0.809622	0.384111	0.700896	chr17	76394021	76398504	+	0 NA	exon (NM exon (NM_001142	10984	8877	Hs.68061	ENSG000002SPHK1	-	SPHK sphingosin protein-coding
chr19-114	8.195267	0.310985	0.809622	0.384111	0.700896	chr19	11439318	11442693	+	0 NA	intron (Nintron (N_00130E	-5223	115948	Hs.12401C	ENSG000002CCDC151	-	CILD30 coiled-c protein-coding
chr2-257F	8.195267	0.310985	0.809622	0.384111	0.700896	chr2	25770786	25771431	+	0 NA	intron (NAluSc SIN	25273	55252	Hs.11981E	ENSG000002ASXL2	-	ASXL2 SHH ASXL trar protein-coding
chr2-1087	8.195267	0.310985	0.809622	0.384111	0.700896	chr2	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N_00135I	-8466	165055	Hs.3			



chr19-23c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr19	23389579	23390977	+	0	NA	intron (AluSp SIN	5193 NM_00343C	7644 Hs. 58834 NM_00343C	ENSG000002ZNF91	HPF7 HTF1zinc fingprotein-coding
chr2-241c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr2	2.41E+08	2.41E+08	+	0	NA	TTS (NM_C TTS (NM_C	13986 NM_182501	130916 Hs. 159556 NM_182501	ENSG000002MTERF4	MTERF2D mitochondonprotein-coding
chr4-534c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr4	53401616	53406445	+	0	NA	intron (LIPA3 LIN	26377 NM_001134	81608 Hs. 555105 NM_030917	ENSG000002CIP1L1	FIP1 Rhe factor irprotein-coding
chr4-122c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (N intron (N	39802 NM_015312	84162 Hs. 408142 NM_015312	ENSG000002KIAA1109	ALKKUCS FKIAA1109 protein-coding
chr5-1297c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (N intron (N	-43187 NM_001257	1E+08 Hs. 582534 NM_001257	ENSG000002M1NAR2	KIAA1024I membrane protein-coding
chr5-146c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	exon (NM_exon (NM	58035 NM_01898E	54439 Hs. 61441 NM_01898E	ENSG000002CRBM27	ARRS1 PscRNA bindiprotein-coding
chr6-111c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (AluSj SIN	-111760 NR_03410E	643749 Hs. 486222 NR_03410E	ENSG000002TRAF3IP2	C6UAS C6c TRAF3IP2 ncRNA
chr7-649c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr7	64923209	64928185	+	0	NA	intron (AluSg SIN	22455 NM_02114E	10793 Hs. 520885 NM_02114E	ENSG000002ZNF273	HZF9 zinc fingprotein-coding
chr9-127c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (MIRb SINE	3287 NR_136302	1.03E+08 NR_136302	ENSG000002LOC102722	zinc fingprotein-coding
chr9-137c.7.921272	-0.31557	0.8244	-0.38279	0.701876	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (N intron (N	96183 NR_039691	1.01E+08 NR_039691	ENSG000002MIR3689C	microRNA ncRNA
chr12-447c.3.470382	0.468262	1.223617	0.382687	0.701952	0.981636	chr12	47642679	47643452	+	0	NA	Intergeni(LIMDa LIN	62965 NM_024604	79657 Hs. 437855 NM_024604	ENSG000002CRPAP3	Tah1 hSpaRNA polynprotein-coding
chr1-543c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr1	54391708	54394205	+	0	NA	intron (N intron (N	13438 NM_00100E	23648 Hs. 476706 NM_01807C	ENSG000002SSBP3	CSDP SSDFsingle stprotein-coding
chr1-214c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr1	2.14E+08	2.14E+08	+	0	NA	intron (N intron (N	83673 NM_020197	56950 Hs. 66170 NM_020197	ENSG000002SMYD2	HSKM-B KMS SET and M protein-coding
chr1-214c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr1	2.14E+08	2.14E+08	+	0	NA	intron (L2 LINE L	89218 NM_020197	56950 Hs. 66170 NM_020197	ENSG000002SMYD2	HSKM-B KMS SET and M protein-coding
chr10-69c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr10	69387955	69389848	+	0	NA	intron (N intron (N	28017 NM_001057	6865 Hs. 88372 NM_001057	ENSG000002TACR2	NK2R NKN tachykininprotein-coding
chr10-73c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr10	73859160	73860897	+	0	NA	intron (N intron (N	14527 NM_001367	818 Hs. 52304E NM_00122E	ENSG000002CAMK2G	CAMK CAMM calcium c protein-coding
chr11-64c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr11	64804391	64806549	+	0	NA	intron (N intron (N	-2256 NM_001307	5871 Hs. 534341 NM_00457E	ENSG000002MAP4K2	BL44 GCM mitogen-e protein-coding
chr11-11c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (AluSx1 SI	3216 NM_03272E	84811 Hs. 437341 NM_03272E	ENSG000002BUD13	Cwc26 fS BUD13 honprotein-coding
chr15-42c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr15	42516258	42518705	+	0	NA	intron (N intron (N	21849 NM_00382E	8773 Hs. 511145 NM_00382E	ENSG000002SNAP23	HsT17016 synaptosc protein-coding
chr19-11c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr19	11361557	11364315	+	0	NA	intron (MERR6B DN	7504 NM_00117C	64748 Hs. 6846 NM_022737	ENSG000002PLP2R2	PLP2R2 PRC phospholiprotein-coding
chr19-12c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr19	12602797	12603677	+	0	NA	intron (AluJo SIN	7576 NM_020714	57474 Hs. 65586C NM_020714	ENSG000002ZNF490	zinc fingprotein-coding
chr2-120c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr2	1.21E+08	1.21E+08	+	0	NA	exon (NM_exon (NM	196900 NM_00527C	2736 Hs. 111867 NM_00527C	ENSG000002GLI2	CJS HPe9 GLI famil protein-coding
chr22-46c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr22	46218492	46219189	+	0	NA	intron (N intron (N	31453 NM_207327	150383 Hs. 103111 NM_207327	ENSG000002CDPFI1	C2orf40 cysteine protein-coding
chr22-50c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr22	50282804	50284687	+	0	NA	exon (NM_exon (NM	-13365 NR_110887	5600 Hs. 57732 NM_002751	ENSG000002MAPK11	P38B P38E mitogen-e protein-coding
chr3-144c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr3	14461680	14464375	+	0	NA	intron (MERR4L34	60421 NM_001134	6533 Hs. 52948E NM_00304E	ENSG000002SLC6A6	TAUT solute c protein-coding
chr3-184c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr3	1.85E+08	1.85E+08	+	0	NA	intron (N intron (N	159851 NM_00134E	23355 Hs. 26926E NM_01530E	ENSG000002VP58	KIAA0804 VP58 sub protein-coding
chr7-149c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (AluYe6 SI	8724 NR_163909			
chr8-415c.7.698679	0.322287	0.842555	0.382511	0.702082	0.981636	chr8	41598443	41599505	+	0	NA	5' UTR (N5' UTR (N	20458 NM_00136E	137964 Hs. 35575E NM_17881E	ENSG000002GPAT4	1-AGPAT e glycerol - protein-coding
chr17-38c.7.92913	-0.31724	0.829437	-0.38248	0.702108	0.981636	chr17	38878586	38879383	+	0	NA	intron (N TCCA)n	8926 NM_00614E	3927 Hs. 74115E NM_00614E	ENSG000002CLASP1	Lasp-1 MLIM and S protein-coding
chr19-51c.7.92913	-0.31724	0.829437	-0.38248	0.702108	0.981636	chr19	51694427	51695478	+	0	NA	intron (MIRb SINE	-11896 NR_10810C	1.02E+08 Hs. 64018E NR_10810C	ENSG000002SPACA6P	LINC0112E SPACA6P ncRNA
chr3-123c.7.92913	-0.31724	0.829437	-0.38248	0.702108	0.981636	chr3	12380912	12382560	+	0	NA	intron (N intron (N	30234 NM_01586E	5468 Hs. 16264E NM_005037	ENSG000002PPARG	CIMT1 GLA peroxisom protein-coding
chr4-3971c.7.160952	-0.33273	0.856858	-0.38247	0.702109	0.981636	chr4	39717893	39718120	+	0	NA	intron (N LTR12C LI	19870 NM_001111	3093 Hs. 50308 NM_00533E	ENSG000002UBE2K	E2-25K H ubiquitin protein-coding
chr1-2037c.7.160952	0.333534	0.872275	0.382373	0.702185	0.981636	chr1	2.04E+08	2.04E+08	+	0	NA	intron (N intron (N	5357 NR_04621E	84719 Hs. 66117E NM_032633	LINC0026C Clorf217	long intncRNA
chr17-794c.7.160952	0.333534	0.872275	0.382373	0.702185	0.981636	chr17	7947403	7948543	+	0	NA	exon (NM_exon (NM	15767 NM_00135E	116840 Hs. 34801E NM_053051	ENSG000002CNTROB	LIP8 PPI2 centrobir protein-coding
chr2-121c.7.160952	0.333534	0.872275	0.382373	0.702185	0.981636	chr2	1.21E+08	1.21E+08	+	0	NA	intron (N intron (N	-66702 NR_101455E	29842 Hs. 156471 NM_01455E	ENSG000002TFCP2L1	CRTR1 LFB transcri protein-coding
chr5-694c.7.160952	0.333534	0.872275	0.382373	0.702185	0.981636	chr5	69408660	69409778	+	0	NA	intron (N LIM4b LIN	-5897 NM_001244	153562 Hs. 657687 NM_14472E	ENSG000002MARVELD2	DFNB49 MARVELD2 protein-coding
chr6-373c.7.160952	0.333534	0.872275	0.382373	0.702185	0.981636	chr6	37368471	37369330	+	0	NA	exon (NM_exon (NM	14917 NR_04639E	9025 Hs. 48527E NM_00395E	ENSG000002CRNF8	hRNF8 ring fingprotein-coding
chr7-4007c.7.160952	0.333534	0.872275	0.382373	0.702185	0.981636	chr7	44014981	44016281	+	0	NA	intron (N intron (N	3563 NR_00365E	84820 Hs. 65702E NM_032734	ENSG000002POLR2J4	hsa-mir-7 microRNA ncRNA
chr8-1101c.11.5806	-0.26449	0.691846	-0.3823	0.702241	0.981636	chr8	1.01E+08	1.01E+08	+	0	NA	intron (N intron (N	-7364 NR_10699E	1.02E+08 NR_10699E	ENSG000002MIR7705	hsa-mir-43 replicat protein-coding
chr20-564c.6.607508	0.350882	0.917958	0.382242	0.702282	0.981636	chr20	56447187	56447426	+	0	NA	intron (N LTR78 LTF	-21279 NM_016407	51507 Hs. 517134 NM_016407	ENSG000002CRTF2	C2orf43 replicat protein-coding
chr2-113c.11.16028	-0.26946	0.705519	-0.38193	0.702513	0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	TTS (NR_C TTS (NR_C	3031 NR_02400E	84771 Hs. 71294C NR_024004	DDX11L2	- DEAD/H- bc pseudo
chr8-4784c.11.16028	-0.26946	0.705519	-0.38193	0.702513	0.981636	chr8	47848073	47849157	+	0	NA	intron (N LIPA16 LI	1052 Hs. 44082E NM_00519E	ENSG000002CEBPD	C/EBP-de CCAAT en protein-coding	
chr7-102c.6.949362	-0.34598	0.906039	-0.38186	0.702566	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	Intergeni(AluJo SIN	9025 NM_001114	1E+08 Hs. 61025E NM_001114	ENSG000002UPK3BL1	UPK3BL UFU roplakir protein-coding
chr12-101c.8.163836	0.318648	0.834613	0.381791	0.702616	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (N L2b LINE	7539 NM_001177	400 Hs. 37261E NM_001177	ENSG000002ARL1	ARFL1 ADP ribos protein-coding
chr9-1934c.9.255007	0.298387	0.781847	0.381644	0.702726	0.981636	chr9	19346367	19346898	+	0	NA	exon (NM_exon (NM	33604 NM_00101C	6194 Hs. 40807E NM_00101C	ENSG000002CRPS6	S6 ribosomal protein-coding
chr1-402c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr1	40231547	40232988	+	0	NA	intron (N intron (N	-15670 NM_00100E	127391 Hs. 40626E NM_00100E	ENSG000002TMC02	dJ39G22.2 transmem protein-coding
chr1-2254c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr1	2.25E+08	2.25E+08	+	0	NA	intron (N intron (N	15743 NM_00229E	3930 Hs. 43516E NM_00229E	ENSG000002LBR	C14SR DHC lamin B protein-coding
chr10-924c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr10	92486033	92490238	+	0	NA	intron (N AluSx4 SI	9626 NM_00132E	3416 Hs. 50054E NM_00496E	ENSG000002IDE	INSULYSIN insulin c protein-coding
chr11-32c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr11	32601974	32602352	+	0	NA	TTS (NM_C TTS (NM_C	18332 NM_00636E	10480 Hs. 50224E NM_00636E	ENSG000002EIF3M	B5 GA17 Eukaryot protein-coding
chr12-14c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr12	14379440	14379779	+	0	NA	intron (N HAL LINE	-5672 NM_18135E	55729 Hs. 50485E NM_01817E	ENSG000002ATF7IP	AM ATF- I activat protein-coding
chr12-29c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr12	29659183	29660696	+	0	NA	exon (NM_exon (NM	124003 NM_00136E	83857 Hs. 401954 NM_03192C	ENSG000002TMTC1	ARG99 OLF transmem protein-coding
chr12-79c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr12	79866913	79868166	+	0	NA	intron (N LIM5 LIN	46372 NM_00114E	4659 Hs. 49582 NM_00248C	ENSG000002PPP1R12A	M130 MBS protein protein-coding
chr12-10c.7.913414	-0.31392	0.822635	-0.3816	0.702759	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (N intron (N	37093 NM_001251	55198 Hs. 50660E NM_01817E	ENSG000002APPL2	DIP13B adaptor protein-coding
chr15-																

chr3-1836	7.665398	0.318813	0.838625	0.380162	0.703825	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	-17647	NM_024871	79929	Hs.47846	ENSG0000024871	ENSG0000024871	MAP6D1	MAP6D1 SMAP6	dom protein-coding	
chr5-728	7.665398	0.318813	0.838625	0.380162	0.703825	0.981636	chr5	72852519	72853548	+	0	NA	intron (Nintron (N	4894	NM_001364	3842	Hs.482497	ENSG0000020227	ENSG0000020227	TNP01	IPO2 KPNF	transport protein-coding	
chr6-315	7.665398	0.318813	0.838625	0.380162	0.703825	0.981636	chr6	31506555	31508357	+	0	NA	exon (NM_exon (NM	9311	NM_001285	4277	Hs.73144	ENSG0000000593	ENSG0000000593	MICB	PERB1.2	MHC class protein-coding	
chr8-219	7.665398	0.318813	0.838625	0.380162	0.703825	0.981636	chr8	21988886	21989305	+	0	NA	intron (Nintron (N	-35039	NM_001286	10361	Hs.13105	ENSG0000018279	ENSG0000018279	NPM2	-	nucleoph protein-coding	
chr9-9991	7.665398	0.318813	0.838625	0.380162	0.703825	0.981636	chr9	99915321	99916411	+	0	NA	intron (Nintron (N	9212	NM_017915	55014	Hs.704031	ENSG0000017915	ENSG0000017915	STX17	-	synxin protein-coding	
chr9-134	7.665398	0.318813	0.838625	0.380162	0.703825	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	28888	NR_039691	1.01E+08	NR_039691	ENSG0000039691	ENSG0000039691	MIR3689C	-	microRNA ncRNA	
chr1-220	8.154128	0.309519	0.814463	0.380029	0.703924	0.981636	chr1	22086016	22088234	+	0	NA	intron (Nintron (N	34416	NM_044472	998	Hs.467637	ENSG0000010179	ENSG0000010179	CDC42	CDC42Hs Cell	div protein-coding	
chr14-516	8.154128	0.309519	0.814463	0.380029	0.703924	0.981636	chr14	51642249	51642334	+	0	NA	intron (Nintron (N	9253	NR_037676	145438	Hs.64541	ENSG0000037676	ENSG0000037676	FRMD6-AS1	C14orf82 FRMD6	antncRNA	
chr2-223	8.154128	0.309519	0.814463	0.380029	0.703924	0.981636	chr2	2.24E+08	2.24E+08	+	0	NA	intron (Nintron (N	40111	NM_02083C	57590	Hs.36835	ENSG000002083C	ENSG000002083C	WDFY1	FENS-1 FEW	repeat protein-coding	
chr7-109	8.154128	0.309519	0.814463	0.380029	0.703924	0.981636	chr7	10932648	10933766	+	0	NA	3' UTR (N3' UTR (N	6946	NM_00248E	6946	Hs.50098	ENSG000000248E	ENSG000000248E	NDUFA4	CI-9k CI-NDUFA4	mit protein-coding	
chr7-939	8.154128	0.309519	0.814463	0.380029	0.703924	0.981636	chr7	93993720	93996419	+	0	NA	intron (Nintron (N	9286	NM_001317	10282	Hs.48913	ENSG000000586E	ENSG000000586E	BET1	HEBET1	Bet1 gol protein-coding	
chr8-306	8.154128	0.309519	0.814463	0.380029	0.703924	0.981636	chr8	30686391	30688472	+	0	NA	intron (Nintron (N	-29195	NM_00209E	2961	Hs.77100	ENSG000000209E	ENSG000000209E	GTF2E2	FE TF2E2 general	protein-coding	
chr14-23	5.647614	0.391899	1.031681	0.379864	0.704046	0.981636	chr14	23091844	23092101	+	0	NA	intron (Nintron (N	-3533	NM_017924	55017	Hs.52523	ENSG0000017924	ENSG0000017924	C14orf11C	-	chromoson protein-coding	
chr1-133	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr1	1337621	1339477	+	0	NA	exon (NM_exon (NM	1159	NR_10686E	1.02E+08	NR_10686E	ENSG0000010686	ENSG0000010686	MIR6808	hsa-mir-6	microRNA ncRNA	
chr1-331	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr1	33157901	33159686	+	0	NA	intron (Nintron (N	17757	NM_00133C	55223	Hs.65600	ENSG0000018207	ENSG0000018207	TRIM62	DEAR1	tripartit protein-coding	
chr1-543	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr1	54395106	54395912	+	0	NA	intron (Nintron (N	10885	NM_00100E	23648	Hs.47670	ENSG000001807C	ENSG000001807C	SSBP3	CSDP SSDF	single st protein-coding	
chr1-888	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr1	88862405	88863645	+	0	NA	intron (Nintron (N	2854	NM_001514	2959	Hs.48185	ENSG0000001514	ENSG0000001514	GTF2B	TF2B TFII	general t protein-coding	
chr10-93	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr10	93313295	93314579	+	0	NA	intron (Nintron (N	168397	NM_013451	26509	Hs.60208	ENSG0000013451	ENSG0000013451	MYOF	FERIL3	myoferlin protein-coding	
chr11-77	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr11	77740018	77740948	+	0	NA	intron (Nintron (N	80351	NM_01657E	51773	Hs.42022	ENSG000001657E	ENSG000001657E	RSF1	HBXAP RSF	retomolir protein-coding	
chr16-24	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr16	26140519	2617709	+	0	NA	intron (Nintron (N	12497	NR_015441	65272	Hs.72044	ENSG0000015441	ENSG0000015441	LOC655227E	-	potassiu pseudo	
chr16-14	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr16	14930919	14935694	+	0	NA	intron (Nintron (N	2486	NR_107061	1.02E+08	NR_107061	ENSG0000010761	ENSG0000010761	MIR6770	hsa-mir-6	microRNA ncRNA	
chr17-58	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr17	58345023	58350725	+	0	NA	intron (Nintron (N	4327	NM_00316E	6827	Hs.43948	ENSG000000316E	ENSG000000316E	SUPT4H1	SPT4 SPT4SPT4	homc protein-coding	
chr2-132	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-59083	NM_001077	116372	Hs.43239	ENSG0000014458	ENSG0000014458	LYPD1	LYPD1 PL	PL/PLAUF	protein-coding
chr20-35	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr20	35686691	35688760	+	0	NA	intron (Nintron (N	11627	NM_00119E	9054	Hs.19469	ENSG0000002110	ENSG0000002110	NFS1	HUSSY-08 NFS1	cyst protein-coding	
chr21-28	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr21	28874479	28875775	+	0	NA	TTS (NM_TTS (NM_I	10240	NM_01324C	29104	Hs.16384	ENSG000001324C	ENSG000001324C	N6AMT1	C21orf127N-6	adeni protein-coding	
chr22-42	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr22	42584779	42585928	+	0	NA	non-codiron-codir	-3342	NR_002184	91695	Hs.53404	ENSG0000002184	ENSG0000002184	RRP7B	RRP7B dJ	ribosomal pseudo	
chr3-48	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr3	48782694	48782980	+	0	NA	intron (Nintron (N	65037	NM_001321	5576	Hs.63192	ENSG0000004157	ENSG0000004157	PRKAR2B	PKR2 PRK	ribosom l protein-coding	
chr3-49	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr3	49675967	49679435	+	0	NA	intron (Nintron (N	3350	NM_00164C	327	Hs.51796	ENSG000000164C	ENSG000000164C	APEH	AARE ACPF	acylaminc protein-coding	
chr3-195	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr3	1.95E+08	1.95E+08	+	0	NA	intron (Nintron (N	-48515	NM_152531	152002	Hs.47874	ENSG0000015253	ENSG0000015253	XXYL1	C3orf21	xyloside protein-coding	
chr5-53	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr5	53082687	53084673	+	0	NA	intron (Nintron (N	26077	NM_17680E	4338	Hs.16364	ENSG0000004531	ENSG0000004531	MOC52	MCPBE MOC	myobndent protein-coding	
chr6-37	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr6	37460243	37463876	+	0	NA	exon (NM_exon (NM	28838	NM_01505C	23070	Hs.52010	ENSG000001505C	ENSG000001505C	CMTR1	FTSJD2 K1	cap methy protein-coding	
chr7-15	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	exon (NM_exon (NM	5382	NM_00671E	10922	Hs.64709	ENSG000000671E	ENSG000000671E	PASTK	PAST	Fas acti protein-coding	
chr9-135	8.203125	0.309144	0.81384	0.379859	0.70405	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	15488	NM_01617E	10422	Hs.9194	ENSG0000001617E	ENSG0000001617E	UBAC1	GBDR1 KPC	UBA domain protein-coding	
chr1-45	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr1	45566818	45567470	+	0	NA	intron (Nintron (N	16318	NM_00606E	10327	Hs.47458	ENSG000000606E	ENSG000000606E	AKR1A1	ALDR1 AL	Faldo-ketc protein-coding	
chr16-20	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr16	20859143	20862308	+	0	NA	intron (Nintron (N	-39157	NM_002042	57149	Hs.74501	ENSG0000002042	ENSG0000002042	LYRM1	AL11C6.1	LYR motif protein-coding	
chr19-10	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr19	10552222	10554823	+	0	NA	TTS (NR_TTS (NR_I	1400	NR_03160E	1E+08	NR_03160E	ENSG0000003160	ENSG0000003160	MIR1238	MIRN1238	microRNA ncRNA	
chr19-10	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr19	10775610	10778785	+	0	NA	exon (NM_exon (NM	-3057	NR_03990E	1.01E+08	NR_03990E	ENSG0000003990	ENSG0000003990	MIR4748	mir-4748	microRNA ncRNA	
chr19-36	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr19	36689541	36695579	+	0	NA	intron (Nintron (N	6937	NM_00132E	163081	Hs.41251	ENSG000000132E	ENSG000000132E	ZNF567	-	zinc fing protein-coding	
chr19-52	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr19	52378130	52379141	+	0	NA	intron (Nintron (N	8712	NM_00114E	400713	Hs.50231	ENSG000000114E	ENSG000000114E	ZNF880	-	zinc fing protein-coding	
chr2-32	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr2	32463786	32465750	+	0	NA	exon (NM_exon (NM	-67385	NR_03028E	693143	NR_03028E	ENSG0000003028	ENSG0000003028	MIR558	MIRN558	microRNA ncRNA	
chr2-71	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr2	71363418	71366712	+	0	NA	intron (Nintron (N	33283	NM_014497	27332	Hs.43440	ENSG00000014497	ENSG00000014497	ZNF638	NP220 ZNF	zinc fing protein-coding	
chr5-57	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr5	37172764	37173804	+	0	NA	intron (Nintron (N	-37662	NR_13426E	1.05E+08	NR_13426E	ENSG00000013426	ENSG00000013426	LOC105374	-	uncharactncRNA	
chr6-8	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr6	87581202	87583399	+	0	NA	intron (Nintron (N	7687	NM_02032C	57038	Hs.48591	ENSG0000002032C	ENSG0000002032C	CRARS2	ArgRS DAL	arginyl-t protein-coding	
chr9-13	8.699713	0.29923	0.787876	0.379793	0.704099	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	-25952	NR_00305C	692093	NR_00305C	ENSG000000305C	ENSG000000305C	SNORD62B	U62 U62B	small nucsnRNA	
chr5-6	9.221725	0.295248	0.777443	0.379768	0.704118	0.981636	chr5	635839	636128	+	0	NA	intron (Nintron (N	23643	NM_01814C	55722	Hs.59174	ENSG0000001814C	ENSG0000001814C	CEP72	-	centroson protein-coding	
chr8-9	9.221725	0.295248	0.777443	0.379768	0.704118	0.981636	chr8	94857150	94857626	+	0	NA	intron (Nintron (N	34098	NR_073444	55656	Hs.72766	ENSG0000001786	ENSG0000001786	INTS8	C8orf52 I	integratc protein-coding	
chr1-5	7.4441	-0.32583	0.858017	-0.37974	0.704135	0.981636	chr1	51824884	51825513	+	0	NA	intron (Nintron (N										



chr5-1591 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr5	1.59E+08	1.59E+08	+	0	NA	intron (NLIMB7 LIN	17671 NM_001199	153830 Hs. 349306NM_14472c	ENSG00000CRNF145	-	ring fing	protein-coding
chr5-1687 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr5	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N	15382 NM_002887	5917 Hs. 654907NM_002887	ENSG00000CARS	ArgRS	[DAL arginyl-t	protein-coding
chr7-2281 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr7	22811673	22814571	+	0	NA	3' UTR (N3' UTR (N	9727 NM_01905e	54543 Hs. 11231eNM_01905e	ENSG00000CTOMM7	TOM7	transloc	protein-coding
chr8-2635 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr8	26392666	26393172	+	0	NA	intron (Nintron (N	2778 NM_00133C	665 Hs. 13122eNM_004331	ENSG00000BNIP3L	BNIP3a	[N1ECL2] int	protein-coding
chr8-6151 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr8	61517595	61518129	+	0	NA	intron (Nintron (N	171549 NM_001164	444 Hs. 33242eNM_00431f	ENSG00000ASPH	ANH BAH	Caspasate	protein-coding
chr8-1232 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr8	1.23E+08	1.23E+08	+	0	NA	intron (NAluSz SIN	6492 NM_032847	84933 Hs. 707401NM_032847	ENSG00000C8orf76	-	chromosom	protein-coding
chr9-3333 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr9	33333015	33335677	+	0	NA	intron (NAluJr4 SI	43830 NM_147134	4799 Hs. 413074NM_002504	ENSG00000NFX1	NFX2 TEG-	nuclear t	protein-coding
chr9-1278 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	-3057 NM_001278	2022 Hs. 376753 NM_00011f	ENSG00000CENG	-	endoglin	protein-coding
chrX-4857 7.905556	-0.31225	0.824081	-0.37891	0.704756	0.981636	chrX	48575442	48578544	+	0	NA	intron (Nintron (N	2509 NM_006743	5935 Hs. 301404NM_006743	ENSG00000CRBM3	IS1-RNPL	RNA bindi	protein-coding
chr15-425 9.213867	0.297065	0.784186	0.378819	0.704822	0.981636	chr15	42983743	42984043	+	0	NA	intron (Nintron (N	-63115 NM_17350C	146057 Hs. 646511NM_17350C	ENSG00000CTBK2	SCA11 TTE	tau tubul	protein-coding
chr22-318 7.111954	0.333913	0.881668	0.378729	0.704889	0.981636	chr22	31804133	31804712	+	0	NA	intron (NAluJr SIN	50399 NM_00136e	9681 Hs. 432502NM_014663	ENSG00000DEPDC5	DEP.5 FJF	DEP domain	protein-coding
chr16-368 12.04991	-0.25941	0.685191	-0.3786	0.704988	0.981636	chr16	36858852	36859055	+	0	NA	IntergeniALR Alpha	1112401 NR_03398f	400533 Hs. 499133NR_03398f	ENSG00000CLINCO2167	-	long intenc	ncRNA
chr16-164 7.347597	-0.31931	0.843456	-0.37857	0.705005	0.981636	chr16	74456288	74456528	+	0	NA	intron (NAluJ4 SI	-34938 NM_001011	497190 Hs. 45467cNM_001011	ENSG00000CLEC18B	MRLC2	C-type l	protein-coding
chr19-72 8.119812	0.331466	0.876666	0.378534	0.705034	0.981636	chr19	12698110	12698634	+	0	NA	TTS (NM_C TTS (NM_C	-1741 NM_032301	84261 Hs. 515154NM_032301	ENSG00000CFBXW9	Fbw9 MEC-	F-box anc	protein-coding
chr1-1125 6.495763	-0.36486	0.965862	-0.37776	0.70561	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (NAluS2 SI	19034 NM_138727	54879 Hs. 201921NM_017744	ENSG00000ST7L	FAM4B ST7	suppressi	protein-coding
chr8-1301 11.14456	-0.26701	0.707067	-0.37763	0.705702	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (NL2 LINE L	-74275 NR_04538E	1.01E+08 Hs. 10601fNR_04538E	ENSG00000ASAP1-IT2	-	ASAP1 intnc	ncRNA
chr1-179 10.60996	-0.27542	0.729421	-0.37759	0.705738	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (NLIMC1 LIN	-25929 NM_022371	64222 Hs. 584957NM_022371	ENSG00000CTOR3A	ADIR ADIF	torsin f	protein-coding
chr11-666 7.40296	-0.32864	0.870801	-0.3774	0.705879	0.981636	chr11	66657792	66658134	+	0	NA	intron (NAluJb SIN	19260 NM_001198	5936 Hs. 52382eNM_00289c	ENSG00000RBM4	LARK RBM4	RNA bindi	protein-coding
chr2-1345 7.40296	-0.32864	0.870801	-0.3774	0.705879	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (NAluSg7 SI	31214 NM_001241	905 Hs. 74411eNM_001241	ENSG00000CCNT2	CYCT2	cyclin T2	protein-coding
chr3-1493 7.40296	-0.32864	0.870801	-0.3774	0.705879	0.981636	chr3	1.49E+08	1.49E+08	+	0	NA	3' UTR (N3' UTR (N	8416 NM_01422C	4071 Hs. 35131eNM_01422C	ENSG00000TM4SF1	H-L6 L6	transmem	protein-coding
chr5-394C 7.40296	-0.32864	0.870801	-0.3774	0.705879	0.981636	chr5	39405431	39406414	+	0	NA	intron (NMamGyL TF	19058 NM_001343	1601 Hs. 696631NM_001343	ENSG00000DAB2	DOC-2 DOC	DAB adapt	protein-coding
chr5-1414 7.40296	-0.32864	0.870801	-0.3774	0.705879	0.981636	chr5	1.41E+08	1.41E+08	+	0	NA	promoter-promoter-	90 NM_032091	56105 Hs. 36816cNM_018914	ENSG00000PCDHGA11	PCDH-GAMM	protocad	protein-coding
chr1-212 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr1	21235545	21238201	+	0	NA	intron (Nintron (N	42742 NM_001113	1889 Hs. 19508cNM_001397	ENSG00000ECE1	ECE	endotheli	protein-coding
chr1-214 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr1	21444833	21447137	+	0	NA	intron (Nintron (N	5858 NM_00125e	84224 Hs. 32542eNM_032264	ENSG00000NBPF3	AEE	NBPF mem	protein-coding
chr1-1787 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (NAluJb SIN	11596 NM_152663	55103 Hs. 63248eNM_018037	ENSG00000RALGPS2	dJ595C2.1	RAL GEF w	protein-coding
chr1-244 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (Nintron (N	172689 NM_022463	64388 Hs. 98206 NM_022463	ENSG00000GREM2	CKT5F1B2	gremlin 2	protein-coding
chr10-707 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr10	7775470	7780570	+	0	NA	intron (Nintron (N	8938 NM_012311	22944 Hs. 39791eNM_012311	ENSG00000KIN	BTCD KIN1	kin17 DN	protein-coding
chr10-687 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr10	68784859	68786744	+	0	NA	intron (NLIMB8 LIN	30629 NR_00307e	692211 NR_00307e	ENSG00000SNORD98	-	small nucs	ncRNA
chr10-741 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr10	74130828	74134293	+	0	NA	intron (NAluJb SIN	18268 NM_00132C	26985 Hs. 500104NM_01209f	ENSG00000AP3M1	-	adaptor i	protein-coding
chr10-10 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	12072 NM_001011	84108 Hs. 33580fNM_032154	ENSG00000PCGFB	MBLR RNFI	polycomb	protein-coding
chr11-455 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr11	45912878	45915129	+	0	NA	intron (Nintron (N	3874 NM_004813	9409 Hs. 10091eNM_004813	ENSG00000PEX16	PBD8A PBE	peroxisom	protein-coding
chr11-61 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr11	61327333	61330841	+	0	NA	intron (Nintron (N	-4095 NM_001351	26007 Hs. 6278 NM_015533	ENSG00000TKFC	DAK NET4f	trikiolas	protein-coding
chr11-714 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr11	71454888	71461922	+	0	NA	intron (Nintron (N	5202 NM_018161	55191 Hs. 55698eNM_018161	ENSG00000NADSYN1	-	NAD synt	protein-coding
chr11-116 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	-9189 NM_00003e	335 Hs. 93194 NM_00003e	ENSG00000CAPOA1	apo(a)	apolipop	protein-coding
chr11-125 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr11	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-18988 NM_001143	4798 Hs. 53053eNM_00616e	ENSG00000NFRKB	IN080G	nuclear f	protein-coding
chr11-134 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr11	1.34E+08	1.34E+08	+	0	NA	intron (NMERSA DNA	9894 NM_014384	27034 Hs. 14791 NM_014384	ENSG00000ACAD8	ACAD-8 AFA	yl-CoA	protein-coding
chr12-37 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr12	370028	370694	+	0	NA	intron (NAluSx1 SI	18959 NM_001042	5927 Hs. 76272 NM_00505c	ENSG00000KDM5A	RBBP-2 RE	lysine de	protein-coding
chr12-80 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr12	8051651	8053565	+	0	NA	intron (Nintron (N	13751 NM_00132e	719 Hs. 50465eNM_004054	ENSG00000C3AR1	AZ3B C3A	f complex	protein-coding
chr12-93 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr12	93394891	93398462	+	0	NA	intron (NAluSx4 SI	18098 NM_001301	11163 Hs. 50632eNM_019094	ENSG00000NUDT4	DIPP-2B I	nudix h	protein-coding
chr12-105 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (NMER102c I	11161 NM_00114e	121642 Hs. 37445eNM_001001	ENSG00000ALKBH2	ABH2	alkB hom	protein-coding
chr12-122 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NAluJb SIN	-49739 NM_001351	65082 Hs. 48788eNM_02291f	ENSG00000VPS3A	MPSPS	VPS33A c	protein-coding
chr12-133 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	24405 NM_015114	23141 Hs. 65462eNM_015114	ENSG00000ANKLE2	K1AA0692	ankle1 i	protein-coding
chr13-952 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr13	95260038	95260722	+	0	NA	intron (Nintron (N	41066 NM_00584e	10257 Hs. 50842eNM_00584e	ENSG00000ABCC4	MOAT-B MC	ATP bindi	protein-coding
chr14-34 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr14	34518416	34526279	+	0	NA	intron (NLIM3f LIN	17354 NM_01845e	58937 Hs. 43326eNM_01845e	ENSG00000EAPP	EMO36 C14	E2F assoc	protein-coding
chr14-731 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr14	71319321	713195618	+	0	NA	intron (NAluJr SIN	-43062 NR_15867f	89932 Hs. 50990eNM_173462	ENSG00000PAPLN	PPN	papilin, p	protein-coding
chr14-81 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr14	81201310	81204832	+	0	NA	promoter-promoter-	-237 NR_003021	677845 Hs. 693251NR_003021	ENSG00000SNORA79	ACA65 SNC	small nucs	ncRNA
chr14-99 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636	chr14	99504664	99508504	+	0	NA	3' UTR (N3' UTR (N	25175 NM_00119e	8812 Hs. 51040eNM_00385f	ENSG00000CCNK	CPR4 IDDF	cyclin K	protein-coding
chr15-44 8.169844	0.305844	0.810719	0.377251	0.705987	0.981636</													

chr6-1497	8.382729	-0.30335	0.806966	-0.37591	0.706982	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	44594	NM_00136C	5110	Hs.279257NM_00538	ENSG00000PCMT1	PIMT	protein-lprotein-coding			
chr6-1514	8.382729	-0.30335	0.806966	-0.37591	0.706982	0.981636	chr6	1.51E+08	1.51E+08	+	0	NA	intron (NAluSx SI	7639	NM_024573	79624	Hs.15929	NM_024573	ENSG00000ARMT1	C6orf211	acidic rprotein-coding		
chr3-195	15.3564	0.229507	0.610854	0.375715	0.707129	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	intron (Nintron (N	21507	NR_003264	255812	Hs.566872NR_003264	ENSG00000SDHAP1	SDHAL1 SE	succinate pseudo			
chr13-111	4.214802	-0.43808	1.166189	-0.37565	0.707175	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (NAluJb SIN	11034	NM_001352	79587	Hs.508722NM_024537	ENSG00000CAR52	COXP27 c	cysteiny protein-coding			
chr5-1464	4.676258	-0.40391	1.075531	-0.37554	0.707259	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (NLM6B LIN	36839	NM_0201137	51520	Hs.432674NM_01646C	ENSG00000LARS	HSPC192 l	leucyl-tfprotein-coding			
chr6-312	4.676258	-0.40391	1.075531	-0.37554	0.707259	0.981636	chr6	31200344	31201154	+	0	NA	intron (NLa2 LINE	2989	NR_026791	253018	Hs.659816NR_026791	ENSG00000CHCG27	bcX101P6	HLA complncRNA			
chr6-1496	4.676258	-0.40391	1.075531	-0.37554	0.707259	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	intron (NAluJr SIN	21133	NR_077247	645958	Hs.632614NR_077247	RPS18P9	RPS18_6	7ribosomalpseudo			
chr9-9594	4.676258	-0.40391	1.075531	-0.37554	0.707259	0.981636	chr9	95948433	95949395	+	0	NA	intron (NLM14 LINE	72897	NR_024125	1E+08	Hs.43431CNR_024125	ENSG00000LINC00092	NCRNA0009	long intncRNA			
chr10-731	7.864417	-0.31499	0.838812	-0.37552	0.707277	0.981636	chr10	73132124	73132808	+	0	NA	TTS (NM_C	-6259	NR_145776	1.1E+08	NR_145776	ENSG00000SNORA11F	small	nucsnRNA			
chr14-697	7.864417	-0.31499	0.838812	-0.37552	0.707277	0.981636	chr14	69088936	69091851	+	0	NA	3' UTR (N3' UTR (N	62206	NM_001284	8816	Hs.50978CNM_003861	ENSG00000DCAF5	BCRG2 BCF	DBD1 and protein-coding			
chr5-7377	7.864417	-0.31499	0.838812	-0.37552	0.707277	0.981636	chr5	73779617	73779981	+	0	NA	intron (Nintron (N	-33747	NM_001244	64283	Hs.482521NM_00108C	ENSG00000ARHGF28	RGNF RIF	Rho guaniprotein-coding			
chr10-918	8.374871	-0.30172	0.803811	-0.37537	0.707388	0.981636	chr10	91847433	91849985	+	0	NA	intron (Nintron (N	50283	NM_025235	80351	Hs.329327NM_025235	ENSG00000TNKS2	ARTD6 PAF	tankyrase protein-coding			
chr19-115	8.374871	-0.30172	0.803811	-0.37537	0.707388	0.981636	chr19	1150459	1154399	+	0	NA	intron (Nintron (N	-20207	NM_001100	22904	Hs.408706NM_014963	ENSG00000SBN02	KIAA0963 s	trawberry protein-coding			
chr8-4305	8.374871	-0.30172	0.803811	-0.37537	0.707388	0.981636	chr8	43097669	43098343	+	0	NA	intron (NLMB7 LIN	4691	NM_032237	84197	Hs.491646NM_032237	ENSG00000POMK	MDGA12 N	protein (protein-coding			
chr1-3795	5.153431	-0.38032	1.013219	-0.37536	0.707391	0.981636	chr1	37998341	37998897	+	0	NA	intron (Nintron (N	6895	NM_004466	2275	Hs.57687	NM_004466	ENSG00000PHL3	SLIM2	four and protein-coding		
chr1-2175	5.153431	-0.38032	1.013219	-0.37536	0.707391	0.981636	chr1	2.18E+08	2.18E+08	+	0	NA	intron (Nintron (N	116470	NM_001297	55105	Hs.362343NM_01804C	ENSG00000PATCH2	CT110 GP	A-G-patch cprotein-coding			
chr5-4308	5.153431	-0.38032	1.013219	-0.37536	0.707391	0.981636	chr5	43083281	43084228	+	0	NA	intron (NLTR49-int	-16315	NR_104651	648987	Hs.649466NR_03408E	ENSG00000LOC648987	uncharactncRNA				
chr22-411	5.153431	-0.38032	1.013219	-0.37536	0.707391	0.981636	chr22	41134603	41139152	+	0	NA	intron (NAluS2 SIN	44285	NM_001362	2033	Hs.517517NM_00142E	ENSG00000EP300	KAT3B MKI	E1A bindiprotein-coding			
chr7-9941	9.204159	0.288802	0.769539	0.375292	0.707443	0.981636	chr7	99414732	99419010	+	0	NA	3' UTR (N3' UTR (N	7699	NR_162133	1.13E+08	NR_162133	MIR12119	microRNA	ncRNA			
chr9-1311	9.204159	0.288802	0.769539	0.375292	0.707443	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	19894	NM_001318	8021	Hs.654533NM_00508E	ENSG00000CNP214	CAIN CAN	nucleopor protein-coding			
chr1-2087	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr1	20859967	20860368	+	0	NA	intron (Nintron (N	-73479	NM_016287	5809	Hs.142442NM_016287	ENSG00000HP1BP3	HP1-BP74 h	eterochr protein-coding			
chr1-3531	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr1	35310634	35312070	+	0	NA	intron (NAluS2 SIN	42643	NM_00135C	9202	Hs.269211NM_00509E	ENSG00000ZMYM4	CDIR MYM	zinc fingprotein-coding			
chr1-1502	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr1	1.5E+08	1.5E+08	+	0	NA	intron (NAluS2 SIN	9035	NM_001135	81611	Hs.656466NM_03092C	ENSG00000ANP32E	LANP-L L	acidic nprotein-coding			
chr1-1557	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (Nintron (N	-17725	NR_024117	1E+08	Hs.656361NR_024117	MST02P	misato f	pseudo			
chr10-295	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr10	29549400	29552404	+	0	NA	exon (NM_exon (NM	-5820	NR_03033E	693189	NR_03033E	ENSG00000MIR604	MIRN604 f	microRNA	ncRNA		
chr11-115	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (NAluSx SIN	27172	NM_00518E	867	Hs.504096NM_00518E	ENSG00000CBL	C-CBL CBI	Cbl protcprotein-coding			
chr12-485	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr12	48527489	48530076	+	0	NA	intron (NCharlie17	4575	NM_00165E	377	Hs.119177NM_00165E	ENSG00000ARF3	ADP	ribotcprotein-coding			
chr14-527	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr14	52760964	52761546	+	0	NA	intron (NAluSp SIN	30352	NM_19806E	64841	Hs.478022NM_19806E	ENSG00000GNPNAT1	GNAI1 GNP	glucosami protein-coding			
chr15-618	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr15	61892777	61893707	+	0	NA	intron (NLM1A4 LIN	163324	NR_146444	1.01E+08	Hs.42265	NR_146444	ENSG00000LINC0234E	long	intncRNA		
chr16-85	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr16	85666478	85666906	+	0	NA	intron (Nintron (N	22262	NM_01609E	51659	Hs.43318CNM_01609E	ENSG00000GINS2	HSPC037 E	GINS comrprotein-coding			
chr2-5375	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr2	53794702	53796141	+	0	NA	intron (Nintron (N	8377	NM_015701	27248	Hs.438336NM_015701	ENSG00000CERLEC1	C2orf30 C	endoplasr protein-coding			
chr2-7102	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (NMLT2A1 LI	62483	NM_001042	84281	Hs.389311NM_032321	ENSG00000C2orf88	SKMAP	chromosom	protein-coding		
chr4-714	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr4	714273	714486	+	0	NA	intron (Nintron (N	8547	NM_001317	10336	Hs.144306NM_00631E	ENSG00000PCGF3	DONK1 RN	polycomb	protein-coding		
chr4-541	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr4	5416811	5418877	+	0	NA	intron (NMLT1H2 LI	-106725	NR_12651E	10141	Hs.177972NM_00575C	ENSG00000LINC01587C	4orf6 a	c long intncRNA			
chr5-521	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr5	52141716	52150441	+	0	NA	intron (NAluSp SIN	534	NM_001127	65056	Hs.444279NM_02291E	ENSG00000GPBP1	GPBP SSH	GC-rich f	protein-coding		
chr9-9134	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr9	91341563	91343060	+	0	NA	intron (NMLT1D LTF	19613	NM_00169E	549	Hs.175995NM_00169E	ENSG00000AUH	AU	RNA b	protein-coding		
chr9-125	8.666432	0.296093	0.788992	0.375281	0.707452	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (NAluSg4 SI	71329	NM_00133C	26130	Hs.42376	NM_01563E	ENSG00000GAPVD1	GAPX5 G	ATPase ac	protein-coding	
chr17-54	7.16881	0.331185	0.882952	0.375088	0.707595	0.981636	chr17	5402509	5403157	+	0	NA	intron (NAluJb SIN	-16808	NM_00116E	84268	Hs.462086NM_03230E	ENSG00000RPAIN	HRIP RIP	RPA	inter protein-coding		
chr8-1197	7.16881	0.331185	0.882952	0.375088	0.707595	0.981636	chr8	1.2E+08	1.2E+08	+	0	NA	intron (NLP4 LINE	64209	NM_003184	6873	Hs.125752NM_003184	ENSG00000TAF2	CIF150 MF	TATA-box	protein-coding		
chr9-717	7.16881	0.331185	0.882952	0.375088	0.707595	0.981636	chr9	71708689	71709698	+	0	NA	intron (Nintron (N	59320	NM_00113E	23670	Hs.494146NM_01339C	ENSG00000CEMP2	TMEM2	cell migr	protein-coding		
chr2-1527	4.592129	-0.43475	1.159454	-0.37496	0.707688	0.981636	chr2	1.53E+08	1.53E+08	+	0	NA	intron (NMERS1C LI	34274	NR_146422	151188	Hs.64358CNM_15252E	ENSG00000ARL61P6	AIP-6 AIF	ADP	ribosprotein-coding		
chr1-1971	4.592129	-0.43475	1.159454	-0.37496	0.707688	0.981636	chr1	1.97E+08	1.97E+08	+	0	NA	non-codir non-codir	-12773	NR_00120E	259266	Hs.121026NM_01813E	ENSG00000ASPM	ASP Caln	abnormal	protein-coding		
chr1-151	4.592129	-0.43475	1.159454	-0.37496	0.707688	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	non-codir non-codir	-1880	NM_13827E	149428	Hs.591477NM_13827E	ENSG00000BNIPL	BNIP-S B	NBCL2	intc	protein-coding	
chr4-609	4.592129	-0.43475	1.159454	-0.37496	0.707688	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (NTiger4a	-117701	NM_03278E	84869	Hs.659311NM_03278E	ENSG00000CBR4	SDR45C1	carboxyl	protein-coding		
chr5-7075	4.592129	-0.43475	1.159454	-0.37496	0.707688	0.981636	chr5	70795886	70796502	+	0	NA	intron (Nintron (N	70795886	70796502	1.02E+08	Hs.634012NR_157804	LOC10192E	putative	pseudo			
chr1-586	7.897698	-0.31055	0.828804	-0.3747	0.707883	0.981636	chr1	58663060	58664933	+	0	NA	intron (NLM1E4 LIN	36066	NM_00108E	114803	Hs.744921NM_00108E	ENSG00000MYSM1	2A-DUB 2	Myb like	protein-coding		
chr10-495	7.897698	-0.31055	0.828804	-0.3747	0.707883	0.981636	chr10	49575812	49576658	+	0	NA	intron (NMLT1A0 LI	-12083	NM_00136E	414189	Hs.536156NM_001077	ENSG00000AGAP6	AGAP-6 C	ArFGAP	wiprotein-coding		
chr10-96	7.897698	-0.31055	0.828804	-0.3747	0.707883	0.981636	chr10	96525553	96526819	+	0	NA	intron (NMIRb SINE	-12260	NM_01246E	7093	Hs.154296NM_01246E	ENSG00000TLL2	tolloid	lprotein-coding			
chr10-111	7.897698	-0.31055	0.828804	-0.3747	0.707883	0.981636	chr10	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	36118	NM_00544E	9126	Hs.24485	NM_00544E	ENSG00000SMC3	BAM BMH	C	structure	protein-coding
chr15-644	7.897698	-0.31055	0.828804	-0.3747	0.707883	0.981636	chr15	64409371	64412														



chr19-40c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr19	40010863	40015384	+	0 NA	intron (Nintron (N	16063 NM_178544	339327 Hs. 125008NM_178544	ENSG000002ZNF546	ZNF49	zinc finger protein-coding
chr19-43c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr19	43654639	43656593	+	0 NA	intron (Nintron (N	14553 NM_002656	5329 Hs. 466871NM_002656	ENSG000002PLAUR	CD87 U-P	plasminogen protein-coding
chr19-45c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr19	45618665	45621885	+	0 NA	intron (NAluS SIN	-18063 NM_005282	2828 Hs. 17170 NM_005282	ENSG000002GPR4	-	G protein-coding
chr19-47c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr19	47352191	47363647	+	0 NA	exon (NM exon (NM	8604 NM_014681	9704 Hs. 151706NM_014681	ENSG000002DHC34	DDX34 HRE	DEH-box protein-coding
chr2-272c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr2	27221222	27227300	+	0 NA	intron (Nintron (N	6871 NM_001306	790 Hs. 37701NM_001306	ENSG000002CAD	CDG1Z EIE	carbamoyl protein-coding
chr2-394c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr2	39442515	39444181	+	0 NA	intron (NMamTip3 I	5932 NR_037875	728730 Hs. 655344NR_037875	ENSG000002MAP4K3-D1	-	MAP4K3 dincRNA
chr2-197c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr2	1.97E+08	1.97E+08	+	0 NA	intron (Nintron (N	6859 NM_001132	80219 Hs. 606592NM_001132	ENSG000002COQ10B	-	coenzyme protein-coding
chr2-203c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr2	2.03E+08	2.03E+08	+	0 NA	intron (NAluSq2 SI	94799 NR_001114	65065 Hs. 648844NM_198944	ENSG000002NBEAL1	A530083 C	neurobeac protein-coding
chr20-31c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr20	3199107	3201412	+	0 NA	intron (Nintron (N	4423 NM_023935	65992 Hs. 471977NM_023935	ENSG000002DDRDK1	C20orf11 C	DDRDK domain protein-coding
chr20-35c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr20	35916870	35919923	+	0 NA	intron (Nintron (N	36229 NM_033633	51282 Hs. 584909NM_016558	ENSG000002SCAND1	S1SDP S1N	domain protein-coding
chr20-45c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr20	45964492	45966674	+	0 NA	intron (Nintron (N	6620 NM_022095	63925 Hs. 171493NM_022095	ENSG000002ZNF335	MCPH10 N	zinc finger protein-coding
chr20-47c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr20	47635558	47636508	+	0 NA	exon (NM exon (NM	134146 NM_001174	8202 Hs. 592142NM_006534	ENSG000002NCOA3	ACTR AIB	nuclear protein-coding
chr22-42c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr22	42592661	42599605	+	0 NA	intron (Nintron (N	-12772 NR_002184	91695 Hs. 534041NR_002184	ENSG000002RRP7BP	RRP7B dJ2	ribosomal pseudo
chr22-45c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr22	45811619	45812076	+	0 NA	intron (Nintron (N	51233 NR_039911	1.01E+08 NR_039911	ENSG000002MIR4762	-	microRNA ncRNA
chr3-146c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr3	14654561	14667632	+	0 NA	intron (Nintron (N	9334 NM_016474	51244 Hs. 517822NM_016474	ENSG000002CCDC174	C3orf19 F	coiled-coil protein-coding
chr3-583c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr3	58309908	58318710	+	0 NA	intron (NAluSx SIN	8064 NM_001348	1.1E+08 Hs. 446323NM_001348	ENSG000002HTD2	-	hydroxyacid protein-coding
chr3-101c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr3	1.02E+08	1.02E+08	+	0 NA	non-coding non-coding	19267 NM_020357	57092 Hs. 732632NM_020357	ENSG000002PCPN	-	PEST protein-coding
chr3-197c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr3	1.98E+08	1.98E+08	+	0 NA	intron (Nintron (N	-18065 NM_001363	84859 Hs. 518414NM_032777	ENSG000002LRCH3	-	leucine protein-coding
chr4-321c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr4	3211908	3216848	+	0 NA	intron (Nintron (N	-29991 NM_001330	345222 Hs. 442291NM_001012	ENSG000002MSANTD1	C4orf44	Myb/SANT protein-coding
chr5-136c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr5	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	17762 NM_001350	389332 Hs. 127682NM_001350	ENSG000002SMIM32	-	small intron protein-coding
chr5-150c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr5	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	36482 NR_109966	1436 Hs. 586211NM_005211	ENSG000002CSF1R	C-FMS CDI	colony stromal protein-coding
chr6-410c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr6	41092838	41098949	+	0 NA	intron (Nintron (N	1894 NM_001325	221443 Hs. 227457NM_145063	ENSG000002CARD1	C6orf130 O	acyl-AI protein-coding
chr6-435c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr6	43586078	43592559	+	0 NA	intron (NLM5 LINE	13133 NM_001291	5429 Hs. 655467NM_006502	ENSG000002POLH	RAD30 RAI	RNA polymerase protein-coding
chr8-991c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chr8	99165988	99166913	+	0 NA	intron (NMERS8 DN	153184 NM_017890	157680 Hs. 191544NM_015242	ENSG000002VPS13B	RAS1 COH	vacuolar protein-coding
chrX-167c	8.67429	0.294362	0.787335	0.373872	0.7085	0.981636	chrX	16740689	16743303	+	0 NA	intron (NAluSx SIN	22384 NM_032796	94056 Hs. 744256NM_032796	ENSG000002SYAP1	BSTA PRO	synapse protein-coding
chr2-4657	11.1367	-0.26574	0.710837	-0.37384	0.708526	0.981636	chr2	46576454	46577164	+	0 NA	intron (NMIR SINE	3429 NR_104182	1.01E+08 Hs. 658541NR_104182	ENSG000002LOC100506	-	uncharacterized ncRNA
chr14-20c	8.210983	0.30726	0.822367	0.373629	0.708681	0.981636	chr14	20354363	20354768	+	0 NA	intron (NAluJb SINE	10958 NM_001042	10038 Hs. 409412NM_005484	ENSG000002PARP2	ADPRT2 A	poly(ADP-ribose) polymerase protein-coding
chr19-571c	8.210983	0.30726	0.822367	0.373629	0.708681	0.981636	chr19	5711048	5714663	+	0 NA	intron (NAluJo SIN	7291 NR_076392	9361 Hs. 350266NM_004793	ENSG000002LONP1	CODASS L	luciferase protein-coding
chr20-321c	8.210983	0.30726	0.822367	0.373629	0.708681	0.981636	chr20	32136887	32137985	+	0 NA	intron (NMIRb SINE	27708 NM_001362	9777 Hs. 654666NM_014742	ENSG000002TM9SF4	dJ836N17	transmembrane protein-coding
chr20-561c	8.210983	0.30726	0.822367	0.373629	0.708681	0.981636	chr20	56480653	56481553	+	0 NA	intron (Nintron (N	12518 NM_001283	51507 Hs. 517134NM_016407	ENSG000002RTF2	C20orf43	replisome protein-coding
chr6-1697c	8.210983	0.30726	0.822367	0.373629	0.708681	0.981636	chr6	1.7E+08	1.7E+08	+	0 NA	intron (NMLT1 J LTF	11651 NM_001278	55780 Hs. 47546 NM_018341	ENSG000002CERMARD	C6orf70 F	ER membrane protein-coding
chr8-4237c	8.210983	0.30726	0.822367	0.373629	0.708681	0.981636	chr8	42371594	42372719	+	0 NA	TTS (NM_C TTS (NM_C	5073 NM_014422	27121 Hs. 159311NM_014422	ENSG000002DKK4	DKK-4	dishevelled protein-coding
chr16-11f	2.469718	-0.53648	1.435908	-0.37361	0.708691	0.981636	chr16	11579200	11580025	+	0 NA	intron (NLM3D3 LIN	66278 NM_004862	9516 Hs. 459944NM_004862	ENSG000002LITAF	PIG7 SIMF	lipophilin protein-coding
chr15-41c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr15	41089519	41093509	+	0 NA	intron (NLMIP10 LI	24732 NR_104038	54617 Hs. 292949NM_017555	ENSG000002IN080	IN080A I	IN080 complex protein-coding
chr16-70c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr16	70300988	70301979	+	0 NA	intron (NHAL LINE	2430 NM_001257	11269 Hs. 221761NM_007242	ENSG000002DDX19B	DBP5 DDX1	DEAD-box protein-coding
chr16-821c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr16	81251549	82151115	+	0 NA	intron (Nintron (N	19419 NR_005792	10200 Hs. 344400NM_005792	ENSG000002MPHOSPH6	MPP MDX	EM-phase protein-coding
chr17-73c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr17	73235010	73235925	+	0 NA	intron (Nintron (N	2806 NR_110105	55028 Hs. 12929 NM_017941	ENSG000002C17orf80	HLC-8 MIC	chromosome protein-coding
chr19-46c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr19	4692149	4693927	+	0 NA	intron (Nintron (N	13756 NM_001242	1E+08 Hs. 678132NM_001242	ENSG000002DPP9-AS1	-	DPP9 antiprotein-coding
chr2-237c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr2	2.37E+08	2.37E+08	+	0 NA	3' UTR (N3' UTR (N	14219 NM_006710	10920 Hs. 531712NM_006710	ENSG000002COP58	COP9 CSNE	COP9 signal protein-coding
chr4-267c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr4	26722661	26723019	+	0 NA	intron (NMIR SINE	137404 NR_134675	1.05E+08 Hs. 548855NR_134675	ENSG000002STIM2-AS1	-	STIM2 antncRNA
chr5-407c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr5	40787937	40788724	+	0 NA	intron (NLM16 LIN	9847 NM_001355	5562 Hs. 43322 NM_006251	ENSG000002PRKAA1	AMPK AMP	protein kinase protein-coding
chr9-1207c	8.367013	-0.30014	0.80364	-0.37348	0.708792	0.981636	chr9	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	5655 NM_021264	26190 Hs. 494982NM_012164	ENSG000002FBXW2	FBW2 Fwz	F-box protein-coding
chr16-75c	11.3384	0.276081	0.73998	0.373092	0.70908	0.981636	chr16	75234920	75235545	+	0 NA	exon (NM exon (NM	3428 NM_001170	9564 Hs. 479747NM_014567	ENSG000002BCAR1	CAS CAS1	BCAR1 subunit protein-coding
chr1-1704c	9.212017	0.287163	0.769725	0.373073	0.709094	0.981636	chr1	17043593	17045012	+	0 NA	intron (Nintron (N	9868 NM_003000	6390 Hs. 465924NM_003000	ENSG000002SDHB	CWS2 IP	fuscinatase protein-coding
chr19-55c	9.212017	0.287163	0.769725	0.373073	0.709094	0.981636	chr19	55662607	55663953	+	0 NA	intron (NLA2 LINE	9230 NM_007275	11338 Hs. 528007NM_007275	ENSG000002U2AF2	U2AF52	U2 small protein-coding
chr20-54c	9.212017	0.287163	0.769725	0.373073	0.709094	0.981636	chr20	540504	541086	+	0 NA	intron (NMLTIE2 LI	2995 NM_001362	1457 Hs. 644056NM_001895	ENSG000002CSNK2A1	CK2A1 CKI	casein kinase protein-coding
chr4-799c	9.212017	0.287163	0.769725	0.373073	0.709094	0.981636	chr4	79905289	79907716	+	0 NA	3' UTR (N3' UTR (N	79031 NR_026555	118425 Hs. 104215NR_026555	ENSG000002PCAT4	GDEP PCA	astrocyte ncRNA
chr5-810c	9.212017	0.287163	0.769725	0.373073	0.709094	0.981636	chr5	81086050	81087591	+	0 NA	intron (Nintron (N	-125913 NR_105015	1.03E+08 Hs. 737155NR_105015	ENSG000002RASGRF2-A	-	RASGRF2 ncRNA
chr6-138c	9.212017	0.287163	0.769725	0.373073	0.709094	0.981636	chr6	1.38E+08	1.38E+08	+							

chr1-161:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	intron (AluSc8 SI	26654 NM_001278	6391 Hs. 444472	ENS00000SDHC	CYB560 Cy succinate protein-coding	
chr1-179:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	exon (NM exon (NM	12907 NM_022371	64222 Hs. 584957	ENS00000TOR3A	ADIR ADIF torsin F protein-coding	
chr10-10:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	13633 NM_014976	22984 Hs. 239495	ENS00000PDCD11	ALG-4 ALC programme protein-coding	
chr10-10:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (AluYb8 SI	25233 NM_014976	22984 Hs. 239495	ENS00000PDCD11	ALG-4 ALC programme protein-coding	
chr11-57:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr11	57552324	57555086	+	0	NA	intron (AluSx SIN	11064 NM_001105	219537 Hs. 68756	ENS00000SMTNL1	CHAS2 smooth like protein-coding	
chr11-61:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr11	61299979	61304641	+	0	NA	exon (NM exon (NM	-6994 NM_152718	220001 Hs. 60640	ENS00000CVWCE	URG11 VWC von Wille protein-coding	
chr11-65:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr11	65402785	65410797	+	0	NA	intron (AluSp SIN	-16007 NR_131012	283131 Hs. 523789	ENS00000NEAT1	LINC00084 nuclear ncRNA	
chr12-64:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr12	6463111	64662366	+	0	NA	3' UTR (3' UTR (N	6004 NM_01683C	6843 Hs. 20021	ENS00000VAMP1	CMS25 SPVA vesicle protein-coding	
chr12-66:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr12	6666881	6679669	+	0	NA	exon (NM exon (NM	-10156 NM_001127	51147 Hs. 52421	ENS00000ING4	my036 p25 inhibitor protein-coding	
chr12-124:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (intron (N	-5524 NR_105914	1.02E+08	NR_10694C	ENS00000MIR6880	hsa-mir-6microRNA ncRNA
chr12-13:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	exon (NM exon (NM	-20619 NM_015114	23141 Hs. 65462	ENS00000ANKLE2	KIAA0692 ankyrin 1 protein-coding	
chr15-76:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr15	76224399	76225849	+	0	NA	intron (intron (N	35028 NR_02851C	7302 Hs. 68488	ENS00000TYRO3P	TYRO3P pseudo	
chr15-77:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr15	77132406	77132647	+	0	NA	intron (AluSq2 LI	-61417 NM_198902	10099 Hs. 74486	ENS00000TSPAN3	TM4-A TM4 tetraspan protein-coding	
chr16-44:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr16	4468082	4469515	+	0	NA	intron (L1PA16 SI	5827 NM_001351	57407 Hs. 28896	ENS00000NMRAL1	HSCARG SE NmrA like protein-coding	
chr16-29:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr16	29858610	29861154	+	0	NA	intron (AluS6 SI	3344 NM_00631E	10423 Hs. 12154	ENS00000CDIPT	PIS PIS1 CDP-diacy protein-coding	
chr17-17:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr17	17216177	17231881	+	0	NA	exon (NM exon (NM	13139 NM_001355	201163 Hs. 31652	ENS00000FLCN	BHD DENN1 follicular protein-coding	
chr17-40:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr17	40274112	40280534	+	0	NA	intron (AluSx3 SI	-10556 NM_001254	990 Hs. 40595	ENS00000CCDC6	CDC18L Hs cell divi protein-coding	
chr17-50:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr17	50057500	50085665	+	0	NA	intron (L2c LINE	-14055 NM_001199	5164 Hs. 25666	ENS00000PK2	PDHK2 PDH pyruvate protein-coding	
chr17-81:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr17	81699870	81701931	+	0	NA	intron (intron (N	-2467 NM_002949	6182 Hs. 10905	ENS00000MRPL12	5c5-2 L12 mitochoon protein-coding	
chr19-38:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr19	38620741	38631570	+	0	NA	intron (intron (N	6967 NM_013234	27335 Hs. 31435	ENS00000EIF3F	ARG134 Eukaryoti protein-coding	
chr2-46:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr2	46621536	46622574	+	0	NA	intron (intron (N	4840 NM_014171	9419 Hs. 13399	ENS00000CRIPT	HSPC139 SCXXC rep protein-coding	
chr2-85:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr2	85598943	85598545	+	0	NA	TTS (NM_TTS (NM_C	1999 NM_016494	51255 Hs. 35618	ENS00000RNF181	HSPC238 ring fing protein-coding	
chr2-160:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (intron (N	-23242 NR_03994E	1.01E+08	NR_03994E	ENS00000MIR4785	mir-4785 microRNA ncRNA
chr20-67:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr20	6778136	6779089	+	0	NA	exon (NM exon (NM	10926 NM_00120C	650 Hs. 73853	ENS00000BMP2	BDA2 BMP2 bone mori protein-coding	
chr20-35:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr20	35471461	35474139	+	0	NA	exon (NM exon (NM	12817 NM_00131E	11190 Hs. 44397	ENS00000CEP250	C-NAP1 CF centroson protein-coding	
chr20-36:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr20	36525817	36528713	+	0	NA	3' UTR (3' UTR (N	-14254 NM_18152E	10398 Hs. 50468	ENS00000MYL9	LC20 MLC- myosin 1 protein-coding	
chr20-49:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr20	49012708	49015946	+	0	NA	intron (intron (N	31729 NR_11062E	1.03E+08	HS. 20900	ENS00000CSEIL-AS1	CSEIL antncRNA
chr20-62:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr20	62125083	62131943	+	0	NA	intron (intron (N	6038 NM_14470E	149986 Hs. 10537	ENS00000LSM14B	C20orf40 LSM famil protein-coding	
chr21-46:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr21	46251863	46280925	+	0	NA	intron (intron (N	19217 NM_00390E	8888 Hs. 38903	ENS00000MCM3AP	GANP MAP6 minichron protein-coding	
chr22-50:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr22	50414021	50424367	+	0	NA	intron (intron (N	11752 NR_16212E	1.13E+08	NR_162128	MIR12114	microRNA ncRNA
chr5-13:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr5	1.33E+08	1.33E+08	+	0	NA	intron (intron (N	3090 NR_132124	1.02E+08	Hs. 59881	ENS00000TH2LCRR	TH2-LCR T helper ncRNA
chr5-140:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr5	1.41E+08	1.41E+08	+	0	NA	intron (intron (N	-3769 NM_14472E	153527 Hs. 35019	ENS00000ZMAT2	Ptg-12 Src zinc fing protein-coding	
chr7-57:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr7	5709425	5716113	+	0	NA	promoter-promoter-	-859 NR_106934	1.02E+08	NR_106934	ENS00000MIR6874	hsa-mir-6microRNA ncRNA
chr7-43:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr7	43865603	43867210	+	0	NA	TTS (NM_TTS (NM_C	3111 NM_032014	64951 Hs. 28428	ENS00000MRPS24	HSPC335 mitochoon protein-coding	
chr7-70:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr7	76056595	76067277	+	0	NA	intron (MERS DNA	13830 NM_00591E	4191 Hs. 52096	ENS00000MDH2	EIEE51 malate de protein-coding	
chr7-102:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (AluJo SIN	6482 NM_017621	54784 Hs. 65859	ENS00000ALKBH4	ABH4 alkB homc protein-coding	
chr7-152:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	Intergeni LIMEc LIN	49837 NM_001371474				
chr8-144:8.682148	0.292628	0.78934	0.370724	0.710843	0.981636	chr8	1.45E+08	1.45E+08	+	0	NA	intron (L1M5 LINE	29765 NM_138367	90987 Hs. 53451	ENS00000ZNF251	zinc fing protein-coding	
chr15-98:7.477381	-0.32081	0.8654	-0.37071	0.710852	0.981636	chr15	98955394	98956017	+	0	NA	intron (intron (N	49951 NM_001102	145814 Hs. 59202	ENS00000PGPEP1L	pyrglut protein-coding	
chr17-49:7.477381	-0.32081	0.8654	-0.37071	0.710852	0.981636	chr17	49311340	49311692	+	0	NA	intron (intron (N	-23062 NR_10674E	1.02E+08	NR_10674E	ENS00000MIR6129	hsa-mir-6microRNA ncRNA
chr1-223:7.00747	0.281157	0.758524	0.370663	0.710888	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (intron (N	16205 NM_00174E	824 Hs. 35089	ENS00000CAPN2	CANP2 CAN calpain 2 protein-coding	
chr11-68:7.639974	0.313211	0.84537	0.370501	0.711009	0.981636	chr11	68899521	68900073	+	0	NA	intron (intron (N	4035 NM_181514	219927 Hs. 50304	ENS00000MRPL21	L21mt MRP mitochoon protein-coding	
chr11-12:7.639974	0.313211	0.84537	0.370501	0.711009	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	intron (intron (N	9755 NM_02476E	79827 Hs. 59194	ENS00000CLMP	ACAM ASAM CXADR 1i protein-coding	
chr16-44:7.639974	0.313211	0.84537	0.370501	0.711009	0.981636	chr16	4463003	4463900	+	0	NA	non-codiron-codir	11174 NM_001351	57407 Hs. 28896	ENS00000NMRAL1	HSCARG SE NmrA like protein-coding	
chr18-21:7.639974	0.313211	0.84537	0.370501	0.711009	0.981636	chr18	21429294	21501110	+	0	NA	intron (MERSA DNA	-6123 NM_13837E	91768 Hs. 11108	ENS00000CABLES1	CABL1 CAE Cdk5 and protein-coding	
chr20-41:7.639974	0.313211	0.84537	0.370501	0.711009	0.981636	chr20	41421740	41422891	+	0	NA	intron (intron (N	-55497 NM_05284E	90187 Hs. 72652	ENS00000EMILIN3	C20orf13C elastin n protein-coding	
chr8-124:7.639974	0.313211	0.84537	0.370501	0.711009	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	TTS (NR_TTS (NR_I	1030 NR_10690E	1.02E+08	NR_10690E	ENS00000MIR6844	hsa-mir-6microRNA ncRNA
chr1-240:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (L1MB3 LIN	32199 NM_02006E	56776 Hs. 24889	ENS00000CFMN2	formin 2 protein-coding	
chr10-60:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr10	60881043	60881922	+	0	NA	intron (intron (N	62703 NM_00135C	9886 Hs. 73737	ENS00000RHOBTB1	Rho relat protein-coding	
chr13-30:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr13	30657146	30657592	+	0	NA	intron (intron (N	23154 NM_001321	10208 Hs. 53383	ENS00000USPL1	C13orf22 ubiquiti r protein-coding	
chr13-11:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	-4749 NM_001267	1E+08	Hs. 64003	ENS00000COL4A2-AS-	COL4A2-AS protein-coding
chr14-10:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr14	1E+08	1E+08	+	0	NA	intron (AluJr4 SI	14431 NM_00135C	28300 Hs. 10826	ENS00000SLC25A47	C14orf68 solute c protein-coding	
chr2-94:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr2	9496417	9497409	+	0	NA	intron (intron (N	21858 NM_00132C	285148 Hs. 66722	ENS00000IAH1	isoamyl e protein-coding	
chr2-113:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	intron (NMSTB LTR	-14958 NR_121187	1.03E+08	Hs. 9015	ENS00000PGM5P4-AS	FAM233C PGM5P4 arncRNA
chr22-36:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr22	36347401	36348789	+	0	NA	intron (L1MC LINE	39972 NM_00247E	4627 Hs. 47475	ENS00000MYH9	BDPLT6 DF myosin protein-coding	
chr22-41:8.408153	-0.29758	0.803417	-0.3704	0.711086	0.981636	chr22	41676988	41680604	+	0	NA	intron (intron (N	10071 NM_00100E	4809 Hs. 18225	ENS00000SNU13	15.5K FA- small nuc protein-coding	



chr1-161	9.749745	0.280932	0.760176	0.369561	0.711709	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	promoter-promoter-	-774	NM_001113	1E+08	Hs.72003CNM_001113	ENSG000002TSTD1	KAT TST	thiosulfate protein-coding	
chr20-411	9.749745	0.280932	0.760176	0.369561	0.711709	0.981636	chr20	41104096	41104573	+	0	NA	intron (L2b LINE	-33209	NM_182811	5335	Hs.268177NM_002666	ENSG00000PLCG1	NCKAP3 PI	phospholipase protein-coding	
chr11-185	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr11	18561471	18563070	+	0	NA	intron (AluSx SIN	17248	NM_001261	55293	Hs.407991NM_018314	ENSG00000CUEVLD	ATTP UEV UEV	and lprotein-coding	
chr11-517	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr11	51715182	51716196	+	0	NA	IntergeniALR Alpha	1306542	NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEX-h box pseudo	
chr12-118	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr12	11847070	11847476	+	0	NA	intron (L2 LINE L	197419	NM_001987	2120	Hs.504766NM_001987	ENSG00000ETV6	TEL TEL AETS	varic protein-coding	
chr13-465	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr13	46010551	46011455	+	0	NA	intron (intron (S	41743	NM_001330	23091	Hs.136102NM_015070	ENSG00000CZC3H13	KIAA0853 zinc	finger protein-coding	
chr13-958	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr13	95876683	95877259	+	0	NA	intron (AluS6 S1	176430	NM_020121	55757	Hs.193222NM_020121	ENSG00000UGGT2	HUGT2 UGC	UDP-glucose protein-coding	
chr14-585	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr14	58368771	58370366	+	0	NA	intron (AluS6 S1	-26362	NM_207377	387990	Hs.592307NM_207377	ENSG00000TOMM20L	UNQ9438	translocase protein-coding	
chr21-455	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr21	45529361	45530149	+	0	NA	intron (GT)n Sin	5001	NM_001205	6573	Hs.84190	NM_003050	ENSG00000SLC19A1	CHMD FOL	soluble c protein-coding
chr3-1367	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr3	1.37E+08	1.37E+08	+	0	NA	intron (AluSq SIN	39315	NM_005862	10274	Hs.412586NM_005862	ENSG00000STAG1	MRD47 SAI	stromal protein-coding	
chr3-1725	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (intron (S	29174	NM_001135	64778	Hs.744886NM_022763	ENSG00000FNDC3B	FAD104 PF	fibronectin protein-coding	
chr4-5271	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr4	52716337	52717277	+	0	NA	intron (MLT1D LTF	3558	NR_003010	677810	Hs.635034NR_003010	ENSG00000SNORA26	HBI-6	small nucleolar RNA	
chr4-7315	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr4	73153966	73155022	+	0	NA	intron (intron (S	68563	NM_001280	26057	Hs.601200NM_015574	ENSG00000ANKRD17	GTAR MASF	ankyrin 1 protein-coding	
chr5-4361	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr5	43618216	43618788	+	0	NA	intron (intron (S	-15272	NR_073113	1.01E+08	Hs.482042NR_073113	NNT-AS1	-	NNT antisense RNA	
chr7-5905	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr7	5909644	5910065	+	0	NA	intron (intron (S	11121	NM_015621	51622	Hs.530000NM_015622	ENSG00000CCZ1	C7orf28A CCZ1	home protein-coding	
chr9-2796	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chr9	2796245	2797924	+	0	NA	IntergeniMER104 DN	46921	NM_014878	9933	Hs.493300NM_014878	ENSG00000PUM3	HA-8 HLA	pumilio 1 protein-coding	
chrX-1184	5.178854	-0.37102	1.004181	-0.36947	0.711775	0.981636	chrX	1.18E+08	1.18E+08	+	0	NA	intron (intron (S	20420	NR_031685	1E+08	NR_031685	ENSG00000CMIR1277	MIRN1277	microRNA ncRNA	
chr1-166	17.3899	0.213956	0.579379	0.369286	0.711915	0.981636	chr1	16605802	16608020	+	0	NA	intron (intron (S	6694	NM_017940	55672	Hs.467587NM_017940	ENSG00000BNPFP1	AB13 AB14 BNPFP	membrane protein-coding	
chr7-668	9.219875	0.285544	0.773285	0.369261	0.711933	0.981636	chr7	66805441	66806321	+	0	NA	intron (AluJr SIN	38945	NR_003934	729156	Hs.709878NR_003934	ENSG00000GTF2IR1DF1	-	GTF2I repeat pseudo	
chr7-1055	9.219875	0.285544	0.773285	0.369261	0.711933	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	non-codiron-codir	13978	NM_001355	1E+08	Hs.719432NM_001355	ENSG00000EFCAB10	-	EF-hand c protein-coding	
chr11-115	7.889841	-0.3088	0.837003	-0.36893	0.712176	0.981636	chr11	1.14E+08	1.14E+08	+	0	NA	intron (NMERSA DNA	32898	NM_0044724	9183	Hs.503886NM_0044724	ENSG00000ZW10	HWZ10 KNI	zinc finger protein-coding	
chr13-455	7.889841	-0.3088	0.837003	-0.36893	0.712176	0.981636	chr13	45031544	45032596	+	0	NA	intron (intron (S	42532	NM_018555	55425	Hs.731811NM_018555	ENSG00000GPALP1	ADQ29 KIA	GPALP1 protein-coding	
chr5-1812	7.889841	-0.3088	0.837003	-0.36893	0.712176	0.981636	chr5	1.81E+08	1.81E+08	+	0	NA	intron (AluY SINE	4186	NM_201627	90933	Hs.441488NM_033545	ENSG00000TRIM41	RINCK	tripartite protein-coding	
chr6-4206	7.889841	-0.3088	0.837003	-0.36893	0.712176	0.981636	chr6	42064267	42064532	+	0	NA	intron (AluSx S1	13875	NM_138572	129685	Hs.520122NM_138572	ENSG00000TAF8	II TAF TAF	TATA-box protein-coding	
chr15-101	11.12885	-0.26441	0.716699	-0.36893	0.712181	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (THE1C LTF	3721	NM_152334	123283	Hs.657163NM_152334	ENSG00000TARSL2	-	threonyl- protein-coding	
chr11-124	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr11	1.24E+08	1.24E+08	+	0	NA	3' UTR (S' UTR (S	31239	NM_001130	4013	Hs.152944NM_014622	ENSG00000CVA5A	BCSC-1 BC	von Willebrand protein-coding	
chr15-644	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr15	64423434	64424739	+	0	NA	exon (NM exon (NM	36250	NM_001321	9325	Hs.500340NM_016210	ENSG00000TRIP4	ASC-1 ASC	thyroid l protein-coding	
chr16-211	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr16	211628	212518	+	0	NA	intron (AluSp SIN	17376	NM_018032	55692	Hs.16803	NM_018032	ENSG00000LUC7L	LUC7B1 Lu	LUC7 like protein-coding
chr19-198	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr19	1988288	1991297	+	0	NA	intron (intron (S	25922	NM_017797	55643	Hs.465542NM_017797	ENSG00000BTBD2	-	BTB domain protein-coding	
chr2-853	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr2	85306329	85307898	+	0	NA	intron (intron (S	20876	NM_001368	10618	Hs.506382NM_006464	ENSG00000TGLN2	TGN38 TG	trans-golgi protein-coding	
chr2-966	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr2	96633503	96633829	+	0	NA	intron (AluSx SIN	4325	NR_047655	55683	Hs.516341NM_017991	ENSG00000KANSL3	KIAA1310 KAT8	regulator protein-coding	
chr2-2414	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr2	2.41E+08	2.41E+08	+	0	NA	intron (L1PA10 L1	-56749	NR_036083	1E+08	NR_036083	ENSG00000MIR3133	-	microRNA ncRNA	
chr22-457	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr22	45702053	45704094	+	0	NA	intron (L2c LINE	31239	NM_013230	25814	Hs.475122NM_013230	ENSG00000ATXN10	E46L HUME	ataxin 10 protein-coding	
chr3-478	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr3	47891334	47892736	+	0	NA	intron (intron (S	42480	NR_031595	1E+08	NR_031595	ENSG00000MIR1226	MIRN1226	microRNA ncRNA	
chr6-1085	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr6	1.09E+08	1.09E+08	+	0	NA	intron (MLT1C LTF	10497	NM_001455	2309	Hs.220950NM_001455	ENSG00000FOX03	AF6q21 PF	forkhead protein-coding	
chr7-273	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr7	2730725	2731573	+	0	NA	3' UTR (S' UTR (S	31991	NM_001282	2768	Hs.487341NM_007355	ENSG00000GNA12	NNX3 RMP	G protein protein-coding	
chr7-1311	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (AluSx SIN	5203	NR_024153	378805	Hs.150555NM_001085	ENSG00000LINC-PIN1	LincRNA-F	long intergenic ncRNA	
chr8-945	8.14442	0.300642	0.815082	0.368849	0.71224	0.981636	chr8	94532101	94532853	+	0	NA	intron (L1MD2 LIN	20989	NM_015496	25962	Hs.202233NM_015496	ENSG00000VIRMA	KIAA1429 vir	like protein-coding	
chr10-294	8.642858	0.301594	0.81799	0.368702	0.71235	0.981636	chr10	29494779	29495767	+	0	NA	intron (intron (S	49824	NR_030335	693189	NR_030335	ENSG00000MIR604	MIRN604	microRNA ncRNA	
chr16-236	7.97027	-0.31438	0.852996	-0.36856	0.712454	0.981636	chr16	23690331	23690984	+	0	NA	TTS (NM_C	11768	NM_005030	5347	Hs.592045NM_005030	ENSG00000PLK1	PLK STPK1	polo like protein-coding	
chrX-464	7.856559	-0.31326	0.850886	-0.36816	0.712753	0.981636	chrX	46451061	46451279	+	0	NA	intron (intron (S	3873	NM_001125	55634	Hs.632800NM_017770	ENSG00000KRBOX4	ZNF673	KRAB box protein-coding	
chr1-1555	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr1	15538850	15540299	+	0	NA	intron (AluSx SIN	-2245	NR_135611	1.07E+08	NR_135611	ENSG00000SCARN2A1E	-	small box ncRNA	
chr1-208	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr1	20808835	20811516	+	0	NA	intron (AluS8 S1	-23487	NM_016287	50809	Hs.142442NM_016287	ENSG00000CHP1BP3	HP1-BP74	heterochromatin protein-coding	
chr1-4634	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr1	46349347	46350805	+	0	NA	intron (MIRc SINE	8898	NM_001255	387338	Hs.163424NM_199044	ENSG00000NSUN4	SHTAP	NOP2/Sun	protein-coding
chr1-1081	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr1	1.08E+08	1.08E+08	+	0	NA	intron (THE1C LTF	19472	NM_213651	29957	Hs.656870NM_013388	ENSG00000SLC25A24	APC1 SCAM	soluble c protein-coding	
chr10-312	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr10	3129886	3141688	+	0	NA	exon (NM exon (NM	1683	NR_132755	1E+08	NR_132755	SNORD142	SNORA85 S	small nucleolar RNA	
chr10-245	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr10	24598837	24602987	+	0	NA	exon (NM exon (NM	21931	NM_001367	57584	Hs.524195NM_020824	ENSG00000ARHGAP21	ARHGAP10	Rho	GTPase protein-coding
chr10-73	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr10	73004761	73012624	+	0	NA	intron (intron (S	-53886	NM_032562	84647	Hs.333175NM_032562	ENSG00000PLA2G12B	FKSG71 G	phospholipase protein-coding	
chr10-74	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr10	74061534	74067492	+	0	NA	intron (AluJo SIN	66397	NM_003373	7414	Hs.643896NM_003373	ENSG00000CVC1	CMD1W CMF	vinculin protein-coding	
chr10-952	8.392437	-0.29442	0.800102	-0.36798	0.712885	0.981636	chr10	95238308	95242017	+	0	NA	intron (L1PA11 L1	45962	NM_207321	142827	Hs.134225NM_207321	ENSG00000ACSM6	C10orf		

chr19-952	17.35662	0.212256	0.577143	0.36777	0.713045	0.981636	chr19	9523588	9536541	+	0	NA	intron (AluSx SIN	8581	NM_00131E	79088	Hs.38647ENM_02410ENSG00000ZNF426	K-RBP	zinc fingprotein-coding	
chr1-6655	8.63315	0.292932	0.796851	0.367612	0.713162	0.981636	chr1	66554321	66560162	+	0	NA	intron (intron (N	23088	NM_032291	84251	Hs.132121NM_032291ENSG00000SGIP1	-	SH3 domaiprotein-coding	
chr15-987	8.63315	0.292932	0.796851	0.367612	0.713162	0.981636	chr15	98707786	98708802	+	0	NA	intron (intron (N	-57073	NR_126455	1.04E+08	Hs.34904ENR_126453	IRAIN	IGF1R-AS IGF1R antncRNA	
chr5-9554	8.63315	0.292932	0.796851	0.367612	0.713162	0.981636	chr5	95524448	95525559	+	0	NA	intron (AluSx SIN	30002	NM_01463E	9652	Hs.48286ENM_01463ENSG00000TTC37	KIAA0372	tetratricprotein-coding	
chr10-124	8.818762	-0.29891	0.813555	-0.36741	0.713331	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	3' UTR (3' UTR (N	20483	NM_00136E	1488	Hs.50134ENM_00132ENSG00000CTBP2	-	C-terminalprotein-coding	
chr10-38E	8.423868	-0.30088	0.819154	-0.36731	0.713387	0.981636	chr10	389864	390260	+	0	NA	exon (NM_exon (NM	210068	NM_00120E	10771	Hs.29226ENM_00662ENSG00000ZMYND11	BRAMI BS	zinc fingprotein-coding	
chr1-5241	7.428384	-0.3218	0.87628	-0.36723	0.713446	0.981636	chr1	52419747	52420070	+	0	NA	3' UTR (3' UTR (N	15307	NM_032864	84950	Hs.5301	NM_032284ENSG00000PRPF38A	PRP38A Pr	pre-mRNA protein-coding
chr4-4302	7.469524	-0.31891	0.868838	-0.36706	0.713577	0.981636	chr4	4302251	4302500	+	0	NA	exon (NM_exon (NM	11224	NM_00133C	166793	Hs.419997NM_145291ENSG00000ZBTB49	ZNF509	zinc fingprotein-coding	
chr22-287	12.08504	-0.24904	0.67857	-0.367	0.713618	0.981636	chr22	28793465	28798704	+	0	NA	exon (NM_exon (NM	4488	NM_00107E	7494	Hs.43763ENM_00508ENSG00000XBP1	TREB-5 TFX	box birprotein-coding	
chr12-19E	8.18556	0.302019	0.823485	0.366757	0.713801	0.981636	chr12	1950859	1956500	+	0	NA	exon (NM_exon (NM	-16653	NR_03654E	1E+08	Hs.737031NR_03654ENSG00000LINC0094C	-	long intncRNA	
chr3-3684	8.18556	0.302019	0.823485	0.366757	0.713801	0.981636	chr3	36845878	36846077	+	0	NA	intron (L1ME3G LI	-23477	NR_147141	1.05E+08	Hs.33386ENR_147141ENSG00000LINC0203E	-	long intncRNA	
chr4-515E	8.18556	0.302019	0.823485	0.366757	0.713801	0.981636	chr4	515247	516449	+	0	NA	intron (intron (N	16638	NM_001127	54872	Hs.7099	NM_01773ENSG00000PIGG	GPI7 LAS	phosphatiprotein-coding
chr6-1437	8.18556	0.302019	0.823485	0.366757	0.713801	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (intron (N	-82378	NM_00132E	83496	Hs.18567ENM_03286ENSG00000LTV1	C6orf93 cLTV1	ribcprotein-coding	
chr9-131E	8.18556	0.302019	0.823485	0.366757	0.713801	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (L2a LINE	2542	NM_03143E	83549	Hs.9597	NM_03143ENSG00000UCK1	URK1	uridine-cprotein-coding
chr9-135E	8.18556	0.302019	0.823485	0.366757	0.713801	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	exon (NM_exon (NM	96193	NM_015447	157922	Hs.52249ENM_015447ENSG00000CAMSAP1	-	calmodulinprotein-coding	
chr19-267	15.4054	0.229286	0.625221	0.366728	0.713822	0.981636	chr19	26734101	26734918	+	0	NA	IntergeniALR Alph	-1058922	NR_14673E	1.02E+08	Hs.567934NR_110687ENSG00000LOC101927	-	uncharactncRNA	
chr11-117	7.681114	0.31454	0.857796	0.366684	0.713855	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	TTS (NM_C TTS (NM_C	5005	NM_03296E	643	Hs.11391ENM_00171ENSG00000CCXCR5	BLR1 CD1E	C-X-C motprotein-coding	
chr14-67E	7.681114	0.31454	0.857796	0.366684	0.713855	0.981636	chr14	67760622	67761735	+	0	NA	intron (intron (N	55412	NM_01534E	23503	Hs.98041	NM_01534ENSG00000ZFYVE26	FYVE-CEN1	zinc fingprotein-coding
chr16-85E	7.681114	0.31454	0.857796	0.366684	0.713855	0.981636	chr16	85661278	85661961	+	0	NA	exon (NM_exon (NM	27335	NM_01609E	51659	Hs.43318CNM_01609ENSG00000GINS2	HSPC037 GINS	comprotein-coding	
chr1-1557	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (AluSp SIN	-16194	NR_132767	1.07E+08	NR_132767	SCARNA26E	-	small Ca_ncRNA
chr15-62E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr15	62835976	62836549	+	0	NA	intron (L2b LINE	12305	NR_02970E	406965	NR_02970ENSG00000MIR190A	MIR190 MI	microRNA ncRNA	
chr17-407	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr17	4074149	4077004	+	0	NA	intron (intron (N	67436	NM_01511E	23140	Hs.277624NM_01511ENSG00000ZZEF1	ZZZ4	zinc fingprotein-coding	
chr17-19E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr17	19292648	19932371	+	0	NA	intron (AluJr SIN	46819	NM_00720E	11216	Hs.64267ENM_00720ENSG00000AKAP10	AKAP-10 A	kinase protein-coding	
chr17-28E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr17	28648038	28649329	+	0	NA	non-codiron-codir	-3524	NM_00136E	9703	Hs.151761NM_01468ENSG00000KIAA0100	BCOX BCO	KIAA0100 protein-coding	
chr17-57E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr17	57975948	57977947	+	0	NA	intron (intron (N	11307	NM_00714E	7716	Hs.46356ENM_00714ENSG00000VEZF1	DB1 ZNF1E	vascular protein-coding	
chr2-885	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr2	88592590	88593164	+	0	NA	intron (intron (N	32052	NM_00131E	9451	Hs.59158ENM_00483ENSG00000EIF2AK3	PEK PERK	ubiquitiprotein-coding	
chr2-17E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr2	17594089	17595092	+	0	NA	intron (intron (N	-17096	NR_14907E	1.11E+08	Hs.60713ENR_14907ENSG00000BTG3-AS1	ASEL	BTG3 antncRNA	
chr3-491E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr3	49126856	49129182	+	0	NA	intron (AluSc SIN	5031	NM_00229E	3913	Hs.43972ENM_00229ENSG00000LAMB2	LAMS NPHS	laminin sprotein-coding	
chr3-101E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr3	1.02E+08	1.02E+08	+	0	NA	intron (AluJo SIN	16522	NM_02035E	57092	Hs.73263ENM_02035ENSG00000PCNP	-	PEST protprotein-coding	
chr6-128E	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr6	1.28E+08	1.28E+08	+	0	NA	intron (THE1B-int	144259	NM_001291	5796	Hs.15591ENM_002844ENSG00000PTPRK	R-PTP-ka	protein tprotein-coding	
chr8-6707	8.648866	0.289478	0.789753	0.366542	0.71396	0.981636	chr8	67077657	67078975	+	0	NA	intron (MIR SINE	-5532	NM_001291	79848	Hs.370147NM_02479ENSG00000CSPP1	CSPP JBT	centrosonprotein-coding	
chr11-53	9.724321	0.276387	0.754414	0.366359	0.714097	0.981636	chr11	532443	534148	+	0	NA	exon (NM_exon (NM	2272	NM_16799E	3265	Hs.37003	NM_00534ENSG00000HRAS	C-BAS HAS	HRAS protprotein-coding
chr11-117	9.683182	0.275036	0.750879	0.366286	0.714152	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (L1PA7 LIN	77556	NM_01495E	22897	Hs.50400ENM_01495ENSG00000CEP164	NPHP15	centrosonprotein-coding	
chr2-6127	9.683182	0.275036	0.750879	0.366286	0.714152	0.981636	chr2	61277320	61278422	+	0	NA	intron (THE1B LTF	100453	NR_152211	130872	Hs.65560ENM_15239ENSG00000AHS2P	AHA1 AHS	activatorpseudo	
chr14-301	8.844185	-0.29289	0.799848	-0.36618	0.714228	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	exon (NM_exon (NM	-70021	NM_00137E	1778	Hs.61408CNM_00137ENSG00000DYNCH1	CMT20 DHC	dynein cyprotein-coding	
chr1-1221	7.923122	-0.3044	0.831479	-0.36609	0.714298	0.981636	chr1	32216714	32216916	+	0	NA	TTS (NM_C TTS (NM_C	-4769	NM_00375E	8668	Hs.53009ENM_00375ENSG00000EIF3E	EIF3E2 PF	eukaryotiprotein-coding	
chr16-14E	7.923122	-0.3044	0.831479	-0.36609	0.714298	0.981636	chr16	14260782	14261116	+	0	NA	exon (NM_exon (NM	-41339	NR_13298E	1E+08	Hs.19074ENR_13298E	MIR193BHC	-	MIR193B lncRNA
chr5-3697	7.923122	-0.3044	0.831479	-0.36609	0.714298	0.981636	chr5	36975953	36977331	+	0	NA	intron (intron (N	99873	NM_015384	25836	Hs.481922NM_015384ENSG00000NIPBL	CDLS CDLS	NIPBL cofprotein-coding	
chr11-77E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr11	77632714	77633121	+	0	NA	intron (AluSx SI	4874	NM_001311	1207	Hs.43073ENM_00129ENSG00000CLNS1A	CLC1 CLNS	chloride protein-coding	
chr19-36E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr19	36840524	36842166	+	0	NA	intron (AluSx SIN	-2958	NM_206894	388536	Hs.282067NM_206894ENSG00000ZNF790	-	zinc fingprotein-coding	
chr2-364E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr2	36400613	36401426	+	0	NA	intron (intron (N	45264	NM_016441	51232	Hs.699247NM_016441ENSG00000CRIM1	CRIM-1 SE	cysteine protein-coding	
chr1-159E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr1	15926115	15927122	+	0	NA	intron (L2a LINE	49518	NM_001324	7709	Hs.433764NM_00344ENSG00000ZBTB17	MIZ-1 ZNF	zinc fingprotein-coding	
chr1-950E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr1	95063004	95064075	+	0	NA	intron (L1PA11 LI	1943	NR_13278E	1.02E+08	Hs.73009ENR_13278ENSG00000LOC10192E	-	uncharactncRNA	
chr11-481	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr11	48130799	48131718	+	0	NA	intron (AluS6 SI	34476	NR_03611E	1E+08	NR_03611ENSG00000MIR3161	-	microRNA ncRNA	
chr12-45E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr12	45900290	45900785	+	0	NA	intron (HAL LINE	90037	NR_00471E	9169	Hs.210367NM_00471ENSG00000SCAF11	CASP11 SF	SFR-relateprotein-coding	
chr13-42E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr13	42952915	42953455	+	0	NA	intron (MIR SINE	39056	NM_00100E	94240	Hs.546467NM_03325ENSG00000EPST11	BRES11	epitheliEprotein-coding	
chr13-10E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr13	1.06E+08	1.06E+08	+	0	NA	3' UTR (3' UTR (N	43227	NM_00409E	1948	Hs.14923ENM_00409ENSG00000EFNB2	EPLG5 HTF	ephrin B2protein-coding	
chr14-99E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr14	99458441	99459671	+	0	NA	intron (intron (N	21803	NM_19912E	84193	Hs.510407NM_03223ENSG00000CETD3	C14orf154	SET domainprotein-coding	
chr14-101	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	intron (intron (N	-63483	NM_00137E	1778	Hs.61408CNM_00137ENSG00000DYNCH1	CMT20 DHC	dynein cyprotein-coding	
chr17-54E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr17	5446107	5446820	+	0	NA	intron (MIR SINE	-7308	NM_00121E	708	Hs.55586ENM_00121ENSG00000C1QP	COXPD33 C	complexerprotein-coding	
chr17-35E	5.137715	-0.37548	1.025796	-0.36604	0.714336	0.981636	chr17	5547682	5549577	+	0	NA	intron (L2b LINE	35880	NM_033004	22861	Hs.65227ENM_01492ENSG00000NLRP1	ATADK CAF	NLR familprotein-coding	
chr17-574	5																			



chr7-103: 8.384579	-0.29285	0.802902	-0.36474	0.715308	0.981636	chr7	1.03E+08	1.03E+08	+	0 NA	intron (N L2c LINE	3891 NM_014377	27000 Hs. 55847ENR_014377	ENSG000002DNAJ2C2	MPHOSPH11DnaJ	heatprotein-coding	
chr7-107: 8.384579	-0.29285	0.802902	-0.36474	0.715308	0.981636	chr7	1.08E+08	1.08E+08	+	0 NA	intron (N intron (N	3764 NM_002291	3912 Hs. 65058ENR_002291	ENSG000002LAMB1	CLM LIS5	laminin sprotein-coding	
chr7-124: 8.384579	-0.29285	0.802902	-0.36474	0.715308	0.981636	chr7	1.25E+08	1.25E+08	+	0 NA	intron (N AluJb SIN	6668 NM_005302	2861 Hs. 406094NM_005302	ENSG000002GPR37	EDNRBL PAG	protein-coding	
chr8-117: 8.384579	-0.29285	0.802902	-0.36474	0.715308	0.981636	chr8	1.18E+08	1.18E+08	+	0 NA	intron (N intron (N	86249 NR_145799	1.1E+08	NR_145799	SNORD168	small nucsnRNA	
chr9-110: 8.384579	-0.29285	0.802902	-0.36474	0.715308	0.981636	chr9	1.11E+08	1.11E+08	+	0 NA	intron (N L1P1 LINE	104836 NM_001351	1902 Hs. 126667NR_001401	ENSG000002LPAR1	EDG2 GPR2	lysophosphprotein-coding	
chr12-11: 8.152278	0.298722	0.819329	0.364594	0.715414	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	intron (N intron (N	25999 NM_016238	51434 Hs. 71993ENR_016238	ENSG000002CANAP7	APC7	anaphase protein-coding	
chr12-11: 8.152278	0.298722	0.819329	0.364594	0.715414	0.981636	chr12	1.18E+08	1.18E+08	+	0 NA	intron (N L1ME3Cz L	-38297 NM_001346	51347 Hs. 644422NR_016281	ENSG000002TAOK3	DPK JIK VTAO	kinasprotein-coding	
chr15-90: 8.152278	0.298722	0.819329	0.364594	0.715414	0.981636	chr15	90625923	90627170	+	0 NA	intron (N intron (N	-33688 NR_120371	1.02E+08	Hs. 61534ENR_120371	ENSG000002LINC0158E	-	long intencRNA
chr5-119: 8.152278	0.298722	0.819329	0.364594	0.715414	0.981636	chr5	1.19E+08	1.19E+08	+	0 NA	intron (N intron (N	11302 NR_049892	1.01E+08	NR_049892	ENSG000002MIR5706	-	microRNA ncRNA
chr20-50: 9.145454	0.281159	0.771581	0.364393	0.715564	0.981636	chr20	50933977	50936564	+	0 NA	intron (N intron (N	-3833 NM_181442	23394 Hs. 29373ENR_01533E	ENSG000002ADNP	ADNP1 HV	actinprotein-coding	
chr17-67: 4.6684	-0.40084	1.100371	-0.36428	0.715651	0.981636	chr17	67105175	67105726	+	0 NA	intron (N L1MB7 LIN	60896 NM_000727	786 Hs. 14798ENR_000727	ENSG000002CACNG1	CACNLG	calcium vprotein-coding	
chr4-8807	4.6684	-0.40084	1.100371	-0.36428	0.715651	chr4	88077886	88078149	+	0 NA	TTS (NM_C	70382 NR_156488	5311 Hs. 18127ENR_000297	ENSG000002PKD2	APKD2 PC2	polycystinprotein-coding	
chr1-234: 7.14395	0.317942	0.872942	0.364129	0.715694	0.981636	chr1	2.34E+08	2.34E+08	+	0 NA	intron (N (GA)n Sin	3383 NM_001301	388753 Hs. 23198 NR_001012	ENSG000002COA6	Clorf31 C	cytochrome protein-coding	
chr1-168: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr1	1.68E+08	1.68E+08	+	0 NA	intron (N intron (N	5381 NR_031702	1E+08	NR_031702	ENSG000002MIR1255B2	MIR1255B	microRNA ncRNA
chr10-12: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr10	1.26E+08	1.26E+08	+	0 NA	exon (NM exon (NM	28765 NM_07846E	56647 Hs. 37029ENR_016567	ENSG000002BCC1P	TOK-1 TOK	BRCA2 ancprotein-coding	
chr12-12: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr12	1.2E+08	1.2E+08	+	0 NA	TTS (NR_C	12177 NR_038924	1.01E+08	Hs. 56920ENR_038924	ENSG000002PXN-AS1	EyeLinc4	PXN antisncRNA
chr13-11: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	exon (NM exon (NM	-39147 NM_00136E	1.01E+08	Hs. 704267NM_00136E	ENSG000002C13orf46	-	chromosonprotein-coding
chr15-84: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr15	84541387	84543058	+	0 NA	non-codirnon-codir	-25375 NM_001267	643707 Hs. 49834ENR_001267	ENSG000002GOLG6L4	-	golgin A protein-coding	
chr17-72: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr17	7254870	7256349	+	0 NA	intron (N intron (N	3183 NR_14551E	23587 Hs. 41702ENR_01536E	ENSG000002ELP5	C17orf81 e	elongator protein-coding	
chr17-30: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr17	39918996	39923491	+	0 NA	3' UTR (N3' UTR (N	-2593 NM_00116E	55876 Hs. 306777NM_01853C	ENSG000002GSDMB	GSDML PP4	gasdermir protein-coding	
chr19-19: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr19	5722 NR_03990E	10790447	+	0 NA	intron (N AluXl SI	5722 NR_03990E	1.01E+08	NR_03990E	ENSG000002MIR4748	mir-4748	microRNA ncRNA
chr19-38: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr19	38906935	38908437	+	0 NA	non-codirnon-codir	4472 NM_00124C	643669 Hs. 355357NM_00124C	ENSG000002CCER2	-	coiled-c protein-coding	
chr19-49: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr19	49791984	49797431	+	0 NA	intron (N AluSq2 SI	2841 NR_106857	1.02E+08	NR_106857	ENSG000002MIR6799	hsa-mir-6	microRNA ncRNA
chr20-40: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr20	4009729	4010446	+	0 NA	intron (N L2 LINE L	5971 NM_001134	11237 Hs. 54757ENR_000721E	ENSG000002RNF24	G1L	ring fingprotein-coding	
chr3-5247	9.194452	0.280879	0.771343	0.364142	0.981636	chr3	52479314	52481568	+	0 NA	exon (NM exon (NM	-14897 NM_01513E	23166 Hs. 30198ENR_01513E	ENSG000002STAB1	CLEVER1 s	stabilin protein-coding	
chr5-957: 9.194452	0.280879	0.771343	0.364142	0.715752	0.981636	chr5	95787825	95788960	+	0 NA	intron (N intron (N	34334 NM_002064	2745 Hs. 28988 NR_002064	ENSG000002GLRX	GRX GRX1	glutaredc protein-coding	
chr11-434: 7.143386	0.324966	0.819329	0.363983	0.715871	0.981636	chr11	43414275	43414806	+	0 NA	intron (N intron (N	55620 NM_01825E	55761 Hs. 19118ENR_01825E	ENSG000002TTC17	-	tetratric protein-coding	
chr6-146: 4.701682	-0.39329	1.080624	-0.36395	0.715898	0.981636	chr6	1.47E+08	1.47E+08	+	0 NA	intron (N intron (N	6944 NM_006834	10981 Hs. 287714NM_006834	ENSG000002RAB32	-	RAB32, meprotein-coding	
chr16-30: 2.11832	-0.24617	0.676577	-0.36385	0.715974	0.981636	chr16	30265792	30267448	+	0 NA	Intergeni Intergeni	-18207 NM_001321	613037 Hs. 58573ENR_001321	ENSG000002NPIP13	-	nuclear f protein-coding	
chr1-211: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr1	21104924	21105487	+	0 NA	intron (N AluXl SIN	6178 NM_00376E	8672 Hs. 467084NM_00376E	ENSG000002EIF4G3	eIF-4G 3 e	ukaryotiprotein-coding	
chr1-217: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr1	21753032	21756460	+	0 NA	intron (N LTRA1 LTF	28403 NM_00135C	84196 Hs. 467524NM_03223E	ENSG000002CUP48	RAP1GA1 u	ubiquitiprotein-coding	
chr1-3934: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr1	39345083	39355783	+	0 NA	intron (N intron (N	-58640 NM_01503E	643314 Hs. 65876ENR_01503E	ENSG000002KIAA0754	-	KIAA0754 protein-coding	
chr1-167: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr1	-5330 NR_031702	1.68E+08	+	0 NA	exon (NM exon (NM	8057 NR_03990E	1.01E+08	NR_03990E	ENSG000002MIR1255B2	MIR1255B	microRNA ncRNA
chr1-2351: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr1	2.35E+08	2.35E+08	+	0 NA	exon (NM exon (NM	14826 NM_00602E	8872 Hs. 41284ENR_00602E	ENSG000002CDC123	C10orf7 C	ell diviprotein-coding	
chr15-99: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr15	99599722	99600815	+	0 NA	intron (N intron (N	-32710 NM_00113C	4205 Hs. 26867ENR_005587	ENSG000002MEF2A	ADCAD1 RS	myocyte e protein-coding	
chr19-16: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr19	16389409	16392539	+	0 NA	intron (N intron (N	66148 NM_01627C	10365 Hs. 68513ENR_01627C	ENSG000002KLF2	LKLF	Kruppel lprotein-coding	
chr19-37: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr19	37634133	37640119	+	0 NA	intron (N intron (N	18339 NM_00132C	22835 Hs. 686737NM_01489E	ENSG000002ZFP30	ZNF745	ZFP30 zirprotein-coding	
chr2-3654	9.153312	0.279521	0.768394	0.363774	0.981636	chr2	36547146	36548426	+	0 NA	intron (N intron (N	50382 NM_00104E	9637 Hs. 25857ENR_00510E	ENSG000002FEZ2	HUM3CL	fascicul protein-coding	
chr2-101: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr2	1.02E+08	1.02E+08	+	0 NA	intron (N Mirb SINE	-116708 NR_103791	1.01E+08	Hs. 51624ENR_103791	LINC01127-	long intencRNA	
chr20-44: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr20	44902638	44903598	+	0 NA	intron (N intron (N	-6942 NR_13498E	80336 Hs. 641481NM_001124	ENSG000002PABPC1L	C20orf15 p	oly(A) t protein-coding	
chr3-426: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr3	-20566 NM_14516E	1.4516E	+	0 NA	intron (N AluJr4 SI	92999 Hs. 409561NM_14516E	ENSG000002ZBT47	ZNF651	zinc fingprotein-coding		
chr4-488: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr4	48833791	48837992	+	0 NA	intron (N intron (N	4585 NM_00116E	54940 Hs. 51875ENR_01783C	ENSG000002OCIAD1	ASRJ1 OCI	OClA dom protein-coding	
chr6-315: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr6	31509296	31511535	+	0 NA	3' UTR (N3' UTR (N	12270 NM_00128E	4277 Hs. 73144ENR_005931	ENSG000002MIBC	PERB1L.2	MHC class protein-coding	
chr8-384: 9.153312	0.279521	0.768394	0.363774	0.716027	0.981636	chr8	38456969	38457436	+	0 NA	intron (N intron (N	10522 NM_001174	2260 Hs. 264887NM_01585E	ENSG000002FGFR1	BFGFR CD	fibrolas protein-coding	
chr2-2004	10.19734	0.274546	0.755371	0.63459	0.716262	chr2	2E+08	2E+08	+	0 NA	intron (N LTRID1 LI	33493 NM_001321	130535 Hs. 60577ENR_152387	ENSG000002KCTD18	6530404F	Ipotassium protein-coding	
chr1-2312	9.153312	0.279521	0.768394	0.363774	0.981636	chr1	2.31E+08	2.31E+08	+	0 NA	exon (NM exon (NM	32783 NM_00131E	8443 Hs. 49802ENR_01423E	ENSG000002GNPAT	DAP-AT D	glyceron protein-coding	
chr1-155: 8.656724	0.287722	0.791765	0.363393	0.716311	0.981636	chr1	1.55E+08	1.55E+08	+	0 NA	intron (N AluXs SIN	18706 NR_03418E	645682 Hs. 63248ENR_03418E	ENSG000002POU5F1P4	OC3 OC4	POU class pseudo	
chr11-434	7.143386	0.324966	0.819329	0.363983	0.715871	chr11	1.75E+08	1.75E+08	+	0 NA	intron (N intron (N	5677 NM_02210C	643931 Hs. 65485ENR_02210C	ENSG000002MRP514	COXP238 I	mitochonc protein-coding	
chr11-29: 8.656724	0.287722	0.791765	0.363393	0.716311	0.981636	chr11	2964095	2966577	+	0 NA	intron (N Tigger3a	-1443 NR_00298E	677833 Hs. 68969ENR_00298E	ENSG000002SNORA54	ACA54	small nucsnRNA	
chr14-21: 8.656724	0.287722	0.791765	0.363393	0.716311	0												

chr15-746	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr15	74619669	74631090	+	0	NA	intron (Nintron (N	10385 NM_00113C	1198 Hs. 51179CNM_001292	ENSG00000CLK3	PHCLK3 PFCD3 like protein-coding
chr15-754	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr15	75408753	75413730	+	0	NA	intron (NAluSx3 SI	40449 NM_015477	25942 Hs. 513039NM_015477	ENSG00000SIN3A	WITKOS SIN3 trarprotein-coding
chr15-847	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr15	84798161	84802514	+	0	NA	intron (NMIRc SINE	-16343 NM_020778	57538 Hs. 459189NM_020778	ENSG00000CALPK3	CMH27 MAKalpha kirprotein-coding
chr16-443	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr16	4437090	4447243	+	0	NA	intron (Nintron (N	16298 NM_00113E	9093 Hs. 459779NM_005147	ENSG00000DNAJA3	HCA57 TII DnaJ heatprotein-coding
chr16-15C	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr16	15038820	15041433	+	0	NA	intron (Nintron (N	15948 NM_017347	123803 Hs. 592049NM_173474	ENSG00000NTAN1	PNA1 PNAI-N-terminus protein-coding
chr16-15E	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr16	15631345	15632530	+	0	NA	intron (NLIPA8 LIN	11217 NM_014647	9665 Hs. 173524NM_014647	ENSG00000CMARF1	KIAA0430 meiosis I protein-coding
chr16-574	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr16	57468917	57471384	+	0	NA	intron (Nintron (N	7471 NM_03294C	5432 Hs. 79402 NM_002694	ENSG00000POLR2C	RPP3 RPBc RNA polynprotein-coding
chr17-408	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr17	4084199	4088752	+	0	NA	intron (Nintron (N	56555 NM_015113	23140 Hs. 277624NM_015113	ENSG00000ZZEF1	ZZZ4 zinc fingprotein-coding
chr17-13C	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr17	13007359	13016306	+	0	NA	intron (Nintron (N	6195 NM_018127	60528 Hs. 434232NM_018127	ENSG00000ELAC2	COXP17 FeLaC ribcprotein-coding
chr17-212	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr17	21299604	21305900	+	0	NA	intron (NL4_A_Mam)	14716 NM_00275E	5606 Hs. 514012NM_00275E	ENSG00000MAP2K3	MAPK3 MEIinogen-ε protein-coding
chr17-313	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr17	31348972	31350700	+	0	NA	intron (Nintron (N	-28214 NM_001003	-2123 Hs. 591199NM_01421C	ENSG00000EVI2A	EVD4 EVI-ecotopicprotein-coding
chr17-478	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr17	47823382	47827282	+	0	NA	intron (NAluSq2 SI	-3538 NM_14579E	114881 Hs. 463322NM_017731	ENSG00000OSBPL7	ORP7 oxysterolprotein-coding
chr2-4661	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr2	46619634	46621077	+	0	NA	intron (NAluJb SIN	3140 NM_014171	9419 Hs. 133999NM_014171	ENSG00000CRIPT	HSPC139 CXCC reprotein-coding
chr2-110E	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr2	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	-49583 NR_02714E	1E+08 Hs. 535619NR_027144	ENSG00000LIMS3-LOC	LIMS3-L3LOCncRNA
chr21-462	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr21	46250587	46251456	+	0	NA	non-codiron-codir	21790 NR_11056E	114044 Hs. 655099NR_00277C	ENSG00000MCM3AP-AS	C21orf85 MCM3AP arncRNA
chr22-24C	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr22	24084336	24086682	+	0	NA	intron (Nintron (N	74139 NM_00119E	23523 Hs. 517478NM_01229E	ENSG00000CABIN1	CAIN KB-ε calcineurinprotein-coding
chr3-1224	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	17218 NR_12540E	1.03E+08 Hs. 675059NR_12540E	ENSG00000CLOC10272E	uncharactncRNA
chr4-122A	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	exon (NM exon (NM	53962 NM_015312	84162 Hs. 408142NM_015312	ENSG00000KIAA1109	ALKKUCS FKIAA1109 protein-coding
chr5-1387	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr5	13877523	13885158	+	0	NA	intron (NLIM3de LI	63140 NM_00136E	1767 Hs. 212366NM_00136E	ENSG00000DNAH5	CILD3 DNA dynein α protein-coding
chr5-1191	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr5	1.19E+08	1.19E+08	+	0	NA	intron (NLIPA4 LINE	43893 NR_04989E	1.01E+08 NR_04989E	ENSG00000CIR5706	microRNA ncRNA
chr6-2487	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr6	24871638	24875692	+	0	NA	exon (NM exon (NM	3605 NM_015864	9750 Hs. 559459NM_01472E	ENSG00000RIPOR2	C6orf32 RHO fami protein-coding
chr7-613E	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr7	6139077	6140224	+	0	NA	intron (Nintron (N	32487 NM_001367	9265 Hs. 487479NM_004227	ENSG00000CYTH3	ARN03 GRF cytohesin protein-coding
chr7-1023	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (NLIME3D LI	15712 NM_001347	1E+08 Hs. 406399NM_001242713	LOC10028E	uncharactprotein-coding
chr8-2302	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr8	23022153	23030648	+	0	NA	intron (Nintron (N	26821 NM_01517E	23221 Hs. 372688NM_01517E	ENSG00000RHOBTB2	DBC2 EIEE Rho relatprotein-coding
chr9-3433	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chr9	34338918	34339227	+	0	NA	intron (Nintron (N	9353 NM_147173	318 Hs. 493767NM_001161	ENSG00000NUD2T	APAH1 nudix hycprotein-coding
chrX-1674	9.16117	0.277884	0.768579	0.361555	0.717685	0.981636	chrX	16746929	16748616	+	0	NA	intron (NLIMC5a LI	28160 NM_03279E	94056 Hs. 744255NM_03279E	ENSG00000SYAP1	BSTA PRO: synapse ε protein-coding
chr20-41C	12.11047	-0.24504	0.678112	-0.36135	0.717835	0.981636	chr20	41099700	41102771	+	0	NA	exon (NM exon (NM	-36308 NM_182811	5335 Hs. 268177NM_00266C	ENSG00000PLCG1	NCKAP3 PI phospholiprotein-coding
chr9-137E	12.11047	-0.24504	0.678112	-0.36135	0.717835	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	TTS (NM_C TTS (NM_C	1557 NM_00608E	10383 Hs. 433619NM_00608E	ENSG00000TUBB4B	Beta2 LCβ tubulin tprotein-coding
chr1-1552	8.11138	0.29718	0.822757	0.3612	0.71795	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (NAluSc SIN	2177 NM_052837	10067 Hs. 200609NM_00569E	ENSG00000SCAMP3	Clorf3 secretoryprotein-coding
chr4-8307	5.21994	-0.36674	0.1016283	-0.36665	0.718202	0.981636	chr4	83076598	83077426	+	0	NA	IntergeniLIMCa LIN	32877 NM_00113C	51316 Hs. 546392NM_01661E	ENSG00000PLAC8	C15 DGC placenta protein-coding
chr1-150E	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (NAluY SINE	21090 NM_00128E	405 Hs. 632449NM_00166E	ENSG00000CARNT	HIF-1-βetaryl hydriprotein-coding
chr10-312	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr10	32284580	32287732	+	0	NA	intron (Nintron (N	61002 NM_00127E	80314 Hs. 16780E NM_02520E	ENSG00000EPC1	Ep11 enhancer protein-coding
chr10-92E	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr10	91833798	91835523	+	0	NA	intron (NMERSA DNA	36234 NM_02523E	80351 Hs. 329327NM_02523E	ENSG00000TNK52	ARTD6 PAF thnkyrase protein-coding
chr14-52C	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr14	52065865	52067963	+	0	NA	intron (Nintron (N	2145 NM_007361	22795 Hs. 369844NM_007361	ENSG00000CNID2	NID-2 nidogen 2 protein-coding
chr17-81E	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr17	81685643	81689631	+	0	NA	intron (Nintron (N	3626 NM_00471E	9146 Hs. 66105E NM_00471E	ENSG00000HGS	HRS hepatocytprotein-coding
chr2-232E	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (Nintron (N	-21292 NM_00134E	389084 Hs. 65750E NM_20689E	ENSG00000SNORC	ASCL830 c secondaryprotein-coding
chr5-1343	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr5	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	18488 NM_003337	7320 Hs. 61209E NM_003337	ENSG00000CUBE2B	E2-17kDa ubiquitin protein-coding
chr7-358E	9.657758	0.27061	0.750279	0.36068	0.718339	0.981636	chr7	35832716	35833975	+	0	NA	intron (Nintron (N	3622 NM_00136E	989 Hs. 19134E NM_00178E	ENSG00000SEPTIN7	CDC10 CDC septin 7 protein-coding
chr1-433E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr1	43360262	43365518	+	0	NA	TTS (NM_C TTS (NM_C	1643 NR_10679E	1.02E+08 NR_10679E	ENSG00000MIR6734	hsa-mir-ε microRNA ncRNA
chr10-14E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr10	14906945	14909344	+	0	NA	non-codiron-codir	29244 NM_02467C	79723 Hs. 55488E NM_02467C	ENSG00000SUV39H2	KMT1B suppresscprotein-coding
chr10-67E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr10	67983434	67988774	+	0	NA	intron (Nintron (N	24779 NR_131184	1E+08 NR_131184	POU5F1P5	Oc14-pg5 POU classpseudo
chr12-10E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (NATATATAI	46719 NM_001251	55198 Hs. 50660E NM_018171	ENSG00000APPL2	DIP13B adaptor iprotein-coding
chr14-60E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr14	60991391	60995043	+	0	NA	intron (NMIR SINE	-11527 NM_00135C	57570 Hs. 38015E NM_02081C	ENSG00000TRMT5	COXP26 tRNA meti protein-coding
chr16-16E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr16	1698229	1698449	+	0	NA	intron (Nintron (N	-7844 NM_00131E	23162 Hs. 20776E NM_01513E	ENSG00000MAPK8IP3	JIP-3 JIPinogen-ε protein-coding
chr17-59C	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr17	59087666	59088261	+	0	NA	intron (Nintron (N	18917 NR_148347	4591 Hs. 579079NM_015294	ENSG00000TRIM37	MUL POBI tripartitprotein-coding
chr17-673	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr17	67341154	67344362	+	0	NA	intron (NAluJr4 SI	23819 NM_00281E	5718 Hs. 4295 NM_00281E	ENSG00000PSMD12	Rpn5 STIS proteasone protein-coding
chr2-9457	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	9457961	9458209	+	0	NA	intron (Nintron (N	-16469 NM_00132C	285148 Hs. 66722E NM_00103E	ENSG00000IAH1	isoamyl ε protein-coding
chr2-364E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	36458300	36458493	+	0	NA	intron (Nintron (N	102621 NM_016441	51232 Hs. 699247NM_016441	ENSG00000CRIM1	CRIM-1 Sε cysteine protein-coding
chr2-664E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	66481802	66485751	+	0	NA	intron (Nintron (N	-43446 NR_04662E	1.01E+08 Hs. 73469E NR_04662E	ENSG00000MEI51-AS2	MEI51-AS1 MEI51 antncRNA
chr2-1597	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	6123 NM_02282E	64844 Hs. 52927E NM_02282E	ENSG000007-Mar	AXO AXOT membrane protein-coding
chr2-172E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	1.73E+08	1.73E+08	+	0	NA	intron (NLTR33 LTF	33304 NM_00261C	5163 Hs. 47063E NM_00261C	ENSG00000CPDK1	pyruvate protein-coding
chr2-2034	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	3' UTR (N3' UTR (N	77081 NM_00128E	10152 Hs. 47115E NM_00575E	ENSG00000ABI2	ABI-2 ABIab1 interprotein-coding
chr2-41E	8.41786	-0.28873	0.800597	-0.36065	0.718362	0.981636	chr2	41214740	41215674	+	0	NA	intron (Nintron (N	2420 NR			



chr6-3166	9.665616	0.269057	0.748934	0.359253	0.719406	0.981636	chr6	31666725	31673574	+	0	NA	promoter-promoter-	-802	NM_021221	58496	Hs.70871	ENM_021221	ENSG000004LY665B	C6orf19 Clymphocytprotein-coding
chr9-125	9.665616	0.269057	0.748934	0.359253	0.719406	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	non-codnon-codir	101980	NM_00133C	26130	Hs.42376	NM_01563F	ENSG000004GAPVD1	GAPX5 GAGTase acprotein-coding
chr9-1308	9.665616	0.269057	0.748934	0.359253	0.719406	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	21689	NM_19818C	347148	Hs.660704	NM_19818C	ENSG000004QRFP	26RFA P51pyroglutεprotein-coding
chr17-601	8.615584	0.286241	0.796917	0.359186	0.719456	0.981636	chr17	60189413	60191065	+	0	NA	intron (NMSTB LTF	40266	NM_000717	762	Hs.89485	NM_000717	ENSG000004CA4	CA1V Car4carbonic protein-coding
chr9-6922	8.615584	0.286241	0.796917	0.359186	0.719456	0.981636	chr9	69227855	69228326	+	0	NA	exon (NM_exon (NM	22935	NM_00136E	9414	Hs.50382	NM_004817	ENSG000004TJP2	C9DU P21.tight jur protein-coding
chr1-247	8.697864	0.289022	0.804948	0.359056	0.719553	0.981636	chr1	2.47E+08	2.47E+08	+	0	NA	intron (Nintron (N	2737	NM_00132E	84838	Hs.168677	NM_03275Z	ENSG000004ZNF496	NIZP1 ZFF zinc fingprotein-coding
chr20-46	8.697864	0.289022	0.804948	0.359056	0.719553	0.981636	chr20	46371829	46373297	+	0	NA	intron (NAluSq2 S1	-8105	NM_001281	51006	Hs.593344	NM_01594F	ENSG000004SLC35C2	BA39402. Isolute εprotein-coding
chr8-1302	7.61455	0.307402	0.85615	0.359051	0.719557	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	82725	NR_00276E	29065	Hs.63931	NR_00276E	ASAP1-IT1 ASAP1 intrncRNA	
chr15-844	8.607726	0.287946	0.802386	0.358862	0.719698	0.981636	chr15	84483361	84483560	+	0	NA	intron (Nintron (N	-19115	NR_033787	440299	Hs.454641	NR_033787	DNM1P41	DNM1DN11-dynamin lpseudo
chr2-319	8.607726	0.287946	0.802386	0.358862	0.719698	0.981636	chr2	31902042	31902338	+	0	NA	intron (NAluS6 S1	-98210	NR_146994	1.05E+08	Hs.58038	NR_146994	ENSG000004LINC0194E	- long intencRNA
chr9-976	9.20231	0.279208	0.778431	0.358668	0.719834	0.981636	chr9	97669845	97670200	+	0	NA	intron (NAluSx1 S1	27387	NR_149094	7507	Hs.654364	NM_00038C	ENSG000004XPA	XP1 XPAC XPA, DNA protein-coding
chr10-687	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr10	68723258	68726559	+	0	NA	intron (NAluSp SIN	3669	NM_00128E	55749	Hs.49853	NM_018237	ENSG000004CCAR1	- cell diviprotein-coding
chr11-14	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr11	14506285	14507980	+	0	NA	intron (NMLTIH LI	-7237	NM_001144	1315	Hs.33927	NR_016451	ENSG000004COPB1	COPB
chr12-114	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr12	1.14E+08	1.14E+08	+	0	NA	intron (N) (N)  S1	45418	NM_18148E	6910	Hs.38171	ENM_00019Z	ENSG000004TBX5	HOS
chr14-39	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr14	39029480	39033835	+	0	NA	TTS (NM_TTS (NM_C	-71483	NR_14654E	1.05E+08	NR_14654E	ENSG000004SEC23A-AS	- SEC23A arncRNA	
chr15-944	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr15	94401605	94403163	+	0	NA	intron (Nintron (N	46454	NM_00115E	55784	Hs.33368	NM_01834E	ENSG000004MCTP2	- multiple protein-coding
chr16-563	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr16	56408350	56408993	+	0	NA	intron (Nintron (N	16318	NM_00132E	267	Hs.295137	NM_001144	ENSG000004CAMFR	GP78 RNFA4autocrincprotein-coding
chr19-217	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr19	21726382	21728397	+	0	NA	exon (NM_exon (NM	-23356	NR_02452Z	641367	Hs.68012	NR_02452Z	ENSG000004LOC641367	- cyclin Y pseudo
chr2-174	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr2	1.75E+08	1.75E+08	+	0	NA	intron (Nintron (N	25125	NM_00120E	1123	Hs.38013	NM_00182Z	ENSG000004CHN1	ARHGAP2 Chimerin protein-coding
chr5-137	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (NAluSx SIN	58190	NM_01438E	27039	Hs.716884	NM_01438E	ENSG000004PKD2L2	TRPP5
chr7-101	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr7	1.01E+08	1.01E+08	+	0	NA	exon (NM_exon (NM	3005	NM_030961	81844	Hs.521092	NM_030961	ENSG000004TRIM56	TRIP109
chr7-105	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr7	1.05E+08	1.05E+08	+	0	NA	intron (NAluS6 S1	27861	NM_182931	55904	Hs.59226	NM_01868Z	ENSG000004KMT2E	HDCMC04 lysine mcprotein-coding
chr7-134	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr7	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	21710	NM_03282E	84912	Hs.490181	NM_03282E	ENSG000004SLC35B4	YEA YEA4 solute εprotein-coding
chr8-143	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	-4683	NM_00044E	5339	Hs.43424	NR_00044E	ENSG000004PLEC	EBS1 EBSN plectin protein-coding
chr9-657	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chr9	65700251	65701509	+	0	NA	intron (Nintron (N	24952	NM_00136E	220869	Hs.35595	NM_00102Z	ENSG000004CBWD5	CBWD3 DC3COB mcprotein-coding
chrX-271	8.887175	-0.28012	0.78136	-0.3585	0.719967	0.981636	chrX	271452	2721181	+	0	NA	intron (Nintron (N	28021	NM_002414	4267	Hs.65334	NR_002414	ENSG000004CD99	HBA71 MICCD99 mcprotein-coding
chr12-194	12.1516	-0.24328	0.678621	-0.3585	0.719972	0.981636	chr12	1945200	1946990	+	0	NA	TTS (NM_TTS (NM_L	-9179	NR_03654E	1E+08	Hs.737031	NR_03654E	ENSG000004LINC0094C	- long intencRNA
chr7-100	8.895033	-0.28166	0.785696	-0.35849	0.719979	0.981636	chr7	1E+08	1E+08	+	0	NA	intron (NAluJr SIN	-7535	NR_03656E	1.02E+08	Hs.52107	NR_03656E	ENSG000004TAG3L5P	FDFACT LC3TAG3L5P-ncRNA
chr11-63	8.664582	0.285904	0.79755	0.358478	0.719986	0.981636	chr11	63990944	63991669	+	0	NA	intron (Nintron (N	5453	NR_00308E	55611	Hs.47378	NM_01767C	ENSG000004OTUB1	HSPC263 COTU deubiprotein-coding
chr15-504	8.664582	0.285904	0.79755	0.358478	0.719986	0.981636	chr15	50471988	50471859	+	0	NA	intron (NAluSx SIN	47682	NM_00112E	9101	Hs.443731	NM_005154	ENSG000004USP8	HumORF8 Fubiquitin protein-coding
chr19-88	8.664582	0.285904	0.79755	0.358478	0.719986	0.981636	chr19	8806994	8807527	+	0	NA	3' UTR (N3' UTR (N	14803	NM_001304	148156	Hs.349444	NM_14469Z	ENSG000004ZNF558	- zinc fingprotein-coding
chr9-954	8.664582	0.285904	0.79755	0.358478	0.719986	0.981636	chr9	95455464	95456847	+	0	NA	intron (Nintron (N	-7454	NR_03898Z	1.01E+08	Hs.661847	NR_03898Z	LOC100507	- uncharactncRNA
chr16-197	8.160136	0.296698	0.82791	0.35837	0.720066	0.981636	chr16	1976834	1976834	+	0	NA	exon (NM_exon (NM	4206	NM_09645E	10607	Hs.513267	NM_00645E	ENSG000004TBL3	SAZD UTP1 transduciprotein-coding
chr2-134	8.160136	0.296698	0.82791	0.35837	0.720066	0.981636	chr2	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	16907	NM_00241C	4249	Hs.4988	NM_00241C	ENSG000004MGAT5	GNT-V GNT1alpha-1,εprotein-coding
chr4-1027	8.160136	0.296698	0.82791	0.35837	0.720066	0.981636	chr4	1.03E+08	1.03E+08	+	0	NA	intron (N) (N)  LI	41667	NM_00590E	4126	Hs.48041	NR_00590E	ENSG000004MANBA	MANB1
chr22-362	12.61306	-0.23805	0.665317	-0.35781	0.720489	0.981636	chr22	36279776	36301624	+	0	NA	intron (N) (N)  Ret	-3793	NR_106877	1.02E+08	NR_106877	ENSG000004MIR6819	hsa-mir-εmicroRNA ncRNA	
chr5-5451	12.61306	-0.23805	0.665317	-0.35781	0.720489	0.981636	chr5	54518523	54522735	+	0	NA	3' UTR (N3' UTR (N	2870	NM_00110Z	112574	Hs.43275	NR_05287C	ENSG000004SNX18	SH3PX2 SF sorting rprotein-coding
chr12-534	8.623442	0.284511	0.795241	0.357767	0.720518	0.981636	chr12	5340008	53402037	+	0	NA	intron (N) (N)  LMB8 LIN	19463	NM_00310E	6667	Hs.620754	NM_00310E	ENSG000004SP1	- Spl transprotein-coding
chr17-81	8.623442	0.284511	0.795241	0.357767	0.720518	0.981636	chr17	81911827	81913022	+	0	NA	exon (NM_exon (NM	-1030	NM_00133C	5833	Hs.56984	NM_002861	ENSG000004PCYT2	ET
chr3-160	8.623442	0.284511	0.795241	0.357767	0.720518	0.981636	chr3	1.61E+08	1.61E+08	+	0	NA	promoter-promoter-	-668	NR_003001	677767	Hs.67595	NR_003001	ENSG000004SCARNA7	U90
chr1-193	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr1	19305323	19308423	+	0	NA	intron (Nintron (N	5269	NM_00368E	8574	Hs.57188	NM_00368E	ENSG000004AKR7A2	AFAR AFAlaldo-ketεprotein-coding
chr1-179	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	exon (NM_exon (NM	42336	NM_01481C	9857	Hs.41304	NM_01481C	ENSG000004CEP350	CAP350 Gε centroson protein-coding
chr1-225	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (Nintron (N	20355	NM_01469E	9725	Hs.119387	NM_01469E	ENSG000004TMEM63A	KIAA0792
chr11-63	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr11	63818104	63825791	+	0	NA	intron (NAluJo SIN	8491	NM_138471	144097	Hs.50279	NM_138471	ENSG000004SPINDOC	C1lorf84 spindin protein-coding
chr11-77	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr11	77309044	77731852	+	0	NA	intron (N) (N)  int	89436	NM_01657E	51773	Hs.42022	NR_01657E	ENSG000004RSF1	HXBXP RSF remodεlir protein-coding
chr12-53	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr12	53074208	53075903	+	0	NA	intron (Nintron (N	4335	NM_03284C	84926	Hs.343334	NM_03284C	ENSG000004SPRYD3	- SPRY domε protein-coding
chr12-54	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr12	54345510	54350489	+	0	NA	intron (Nintron (N	-5692	NR_12048E	1.03E+08	Hs.670941	NR_12048E	ENSG000004LOC102724	- uncharactncRNA
chr13-48	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr13	48001451	4801650	+	0	NA	TTS (NM_TTS (NM_C	3824	NR_01828Z	55270	Hs.144407	NM_01828Z	ENSG000004NUDT15	MTH2 NUDT1nudix hycprotein-coding
chr15-78	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr15	78041257	78063227	+	0	NA	exon (NM_exon (NM	-7467	NR_02699E	91450	Hs.40676	NR_02699E	LOC91450	- uncharactncRNA
chr15-84	9.169028	0.276217	0.772138	0.357731	0.720545	0.981636	chr15	84186664	84189201	+	0	NA	IntergeniMamGypL TF	-3916	NR_03373E	440300	Hs.54656	NR_03373E	LOC44030C	- chondroitpseudo
chr17-78	9.169028	0.276217	0.772138	0.357731	0.720545</															

chr2-1175	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr2	1.18E+08	1.18E+08	+	0 NA	intron (NLIPA4 LIN	90149 NR_158155	1.08E+08	NR_158150	LOC10798E-	uncharactncRNA	
chr2-1282	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr2	1.28E+08	1.28E+08	+	0 NA	intron (NLIMB3 LIN	20681 NM_004807	9394 Hs. 512841	NR_004807	ENSG000004HS6ST1	HHL15 HSGS heparan s protein-coding	
chr2-1615	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr2	1.61E+08	1.61E+08	+	0 NA	intron (Nintron (N	-47915 NM_006593	10716 Hs. 210862	NR_006593	ENSG00000CTBR1	IDDAS TBFT-box br protein-coding	
chr20-184	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr20	18471032	18471997	+	0 NA	TTS (NR_CTS (NR_C	899 NR_03616C	1E+08	NR_03616C	ENSG00000MIR3192	mir-3192 microRNA ncRNA	
chr22-457	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr22	45733554	45733941	+	0 NA	intron (NALuSx1 SI	-26777 NR_03991E	1.01E+08	NR_03991E	ENSG00000MIR4762	microRNA ncRNA	
chr3-3784	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr3	37843728	37844645	+	0 NA	intron (NLIPA6 LIN	17594 NR_110532	1.02E+08	Hs. 657314	NR_110532	ENSG00000ITGA9-AS1	ITGA9 antncRNA
chr3-4705	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr3	47052554	47053829	+	0 NA	intron (Nintron (N	41649 NR_02404C	1E+08	Hs. 201522	NR_02404C	NRADDP	neurotropseudo
chr3-5140	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr3	51402095	51403651	+	0 NA	intron (NMERS5A DN	11588 NM_01328E	29890 Hs. 11873E	NR_01328E	ENSG00000RBM15B	HUMAGGGB RNA bindi protein-coding	
chr3-5758	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr3	57585101	57585859	+	0 NA	intron (Nintron (N	11864 NM_00166C	378 Hs. 65218E	NR_00166C	ENSG00000CARF4	ARF2 ADP ribos protein-coding	
chr3-1422	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (Nintron (N	14235 NM_00103E	256356 Hs. 135904	NR_15277E	ENSG00000CGK5	glycerol protein-coding	
chr4-309C	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr4	3090911	3093563	+	0 NA	intron (NALuSx3 SI	17556 NM_00211E	3064 Hs. 51845C	NR_00211E	ENSG00000HHT	HD IT15 Luntingtiprotein-coding	
chr5-7357	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr5	73571409	73572973	+	0 NA	intron (Nintron (N	6448 NM_03217E	84135 Hs. 40670E	NR_03217E	ENSG00000UTP15	NET21 UTP15 sm protein-coding	
chr5-1025	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr5	1.03E+08	1.03E+08	+	0 NA	intron (NLIM4A LI	116945 NM_00091E	5066 Hs. 36943C	NR_00091E	ENSG00000PAM	PAL PHM peptidyl protein-coding	
chr7-3301	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr7	33017029	33018858	+	0 NA	intron (Nintron (N	22963 NM_00135E	51251 Hs. 48793E	NR_00135E	ENSG00000NT5C3A	NT5C3 P5' 5' nucle protein-coding	
chr7-1574	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr7	1.57E+08	1.57E+08	+	0 NA	intron (NALuSp SIN	64388 NM_05824E	10049 Hs. 49074E	NR_00549E	ENSG00000DNAJB6	DJ4 DnaJ DnaJ heat protein-coding	
chr9-1908	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr9	19080862	19081624	+	0 NA	intron (Nintron (N	-17457 NR_00300E	677776 Hs. 68963E	NR_00300E	ENSG00000SCARN28	U92 small Ca ncRNA	
chr9-2201	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr9	22016084	22016740	+	0 NA	intron (NLIP1 LINE	-7099 NM_07848E	1030 Hs. 72901	NR_00493E	ENSG00000CDKN2B	CDK4I INK cyclin d protein-coding	
chrX-1685	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chrX	16853268	16854530	+	0 NA	intron (NALuSx SIN	15964 NM_00119E	5931 Hs. 49575E	NR_00289E	ENSG00000RBPB7	RbAp46 Rb bindi protein-coding	
chr10-245	5.19642	-0.35935	1.007005	-0.35685	0.721201	0.981636	chr10	24590256	24590455	+	0 NA	non-codir non-codir	32488 NM_001367	57584 Hs. 52419E	NR_02082E	ENSG00000ARHGAP21	ARHGAP10 Rho GTPas protein-coding	
chr17-401	10.17006	0.261115	0.73221	0.356612	0.721382	0.981636	chr17	40167563	40168372	+	0 NA	intron (Nintron (N	6034 NR_10692E	1.02E+08	NR_10692E	ENSG00000MIR6866	hsa-mir-6866 microRNA ncRNA	
chr17-1681	10.17006	0.261115	0.73221	0.356612	0.721382	0.981636	chr17	1.68E+08	1.68E+08	+	0 NA	intron (Nintron (N	20910 NM_001031	261726 Hs. 209431	NR_15290E	ENSG00000TIPRL	TIP TIP41TOR sign protein-coding	
chr15-671	10.17006	0.261115	0.73221	0.356612	0.721382	0.981636	chr15	67164807	67167187	+	0 NA	promoter-promoter-	-158 NM_00114E	4088 Hs. 72798E	NR_00590E	ENSG00000SMAD3	HSPC193 SMAD fami protein-coding	
chr19-167	10.17006	0.261115	0.73221	0.356612	0.721382	0.981636	chr19	36744912	36753847	+	0 NA	exon (NM exon (NM	23428 NM_00119E	342892 Hs. 406307	NR_00119E	ENSG00000ZNF850	ZNF850P zinc fing protein-coding	
chr5-368	10.17006	0.261115	0.73221	0.356612	0.721382	0.981636	chr5	1.69E+08	1.69E+08	+	0 NA	intron (NFRAM SINE	-11111 NM_00135E	345630 Hs. 16626E	NR_00135E	ENSG00000FBLL1	fibillar protein-coding	
chr1-2085	10.70779	0.25661	0.71968	0.356561	0.721421	0.981636	chr1	20892353	20893591	+	0 NA	intron (NALuJr LI	95460 NR_03165E	1E+08	NR_03165E	ENSG00000MIR1256	MIRN1256 microRNA ncRNA	
chr16-875	5.640311	-0.34801	0.976241	-0.35648	0.72148	0.981636	chr16	87978545	87978545	+	0 NA	intron (NLIME4a LI	8155 NM_00117E	54971 Hs. 46170E	NR_01786E	ENSG00000BANP	BENDI SM BTG3 ass protein-coding	
chr17-365	5.640311	-0.34801	0.976241	-0.35648	0.72148	0.981636	chr17	36969067	36969999	+	0 NA	intron (NHAL LINE	20579 NM_01213E	26574 Hs. 19574C	NR_01213E	ENSG00000AATF	BFR2 CHE apoptos protein-coding	
chr1-1444	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr1	1.44E+08	1.44E+08	+	0 NA	intron (NLIP2 LINE	20699 NR_10407E	1.02E+08	NR_10407E	ENSG00000RNVU1-15	RNU1-121 RNA, varisnRNA	
chr1-1542	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr1	1.54E+08	1.54E+08	+	0 NA	intron (NALuSg4 SI	-5299 NM_00611E	10456 Hs. 19962E	NR_00611E	ENSG00000HAX1	HCLSBP1 HCLSL1 ass protein-coding	
chr1-1629	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr1	1.63E+08	1.63E+08	+	0 NA	intron (Nintron (N	-20541 NM_00130A	51478 Hs. 49292E	NR_00130A	ENSG00000HSD17B7	PRP1 SDR hydroxost protein-coding	
chr1-2195	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (Nintron (N	-57945 NR_046437	55532 Hs. 28445C	NR_01871E	ENSG00000SLC30A10	HMDPC HMM solute c protein-coding	
chr10-588	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr10	5881608	5886510	+	0 NA	exon (NM exon (NM	-5513 NM_00125E	84893 Hs. 49854E	NR_03280E	ENSG00000FBH1	GYLO18 PF F-box DN protein-coding	
chr11-455	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr11	45978509	45979247	+	0 NA	intron (Nintron (N	56222 NM_00130C	120071 Hs. 86543	NR_15231E	ENSG00000LARGE2	FBLTL BL LARGE xy protein-coding	
chr11-722	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr11	72228292	72235877	+	0 NA	intron (Nintron (N	7317 NM_001567	3636 Hs. 52387E	NR_001567	ENSG00000INPPL1	OPSM SHI inositol protein-coding	
chr12-488	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr12	48853210	48856636	+	0 NA	promoter-promoter-	-393 NR_03162E	1E+08	NR_03162E	ENSG00000MIR1291	MIRN1291 microRNA ncRNA	
chr12-108	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	8920 NM_00707E	11153 Hs. 661891	NR_00707E	ENSG00000FICD	HIP13 HYF FIC domai protein-coding	
chr12-118	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr12	1.18E+08	1.18E+08	+	0 NA	intron (NL2b LINE	14463 NM_00134E	51347 Hs. 64442C	NR_01628E	ENSG00000TAOK3	DPK JIK VTAO kinas protein-coding	
chr14-102	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (NLIM5c LI	39333 NM_03094E	81693 Hs. 534494	NR_03094E	ENSG00000AMN	PR01028 eamion as protein-coding	
chr16-89	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr16	89882253	89891449	+	0 NA	intron (NALuSx1 SI	12359 NM_01497E	22890 Hs. 41533C	NR_01497E	ENSG00000TCF25	FKSG26 Hx transcrip protein-coding	
chr17-155	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr17	15625940	15636711	+	0 NA	intron (NLIMC4a LI	-11621 NM_00128E	374286 Hs. 548021	NR_00638E	ENSG00000CDRT1	C17ORF1 CCMT1A dup protein-coding	
chr17-67	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr17	67236518	67238977	+	0 NA	intron (NALuSx SIN	-7029 NR_13639E	1.02E+08	NR_13639E	LOC10192E-	uncharactncRNA	
chr19-982	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr19	9809611	9811938	+	0 NA	3' UTR (N3' UTR (N	8305 NM_00131E	54850 Hs. 12439	NR_01770E	ENSG00000FBXL12	Fbl12 F-box anc protein-coding	
chr19-435	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr19	43991427	43997463	+	0 NA	intron (NMER77B LI	8425 NR_110727	1.02E+08	NR_110727	ENSG00000LOC10192E-	uncharactncRNA	
chr19-535	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr19	53571660	53579819	+	0 NA	intron (NALuSx1 SI	20432 NM_00107E	55422 Hs. 185674	NR_01855E	ENSG00000ZNF331	RITA ZNF2 zinc fing protein-coding	
chr20-385	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr20	3854181	3866109	+	0 NA	intron (Nintron (N	1331 NR_03792E	57506 Hs. 57036E	NR_02074E	ENSG00000CMV5	CARDIF IFI mitocho protein-coding	
chr22-302	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr22	30240893	30246086	+	0 NA	3' UTR (N3' UTR (N	-2721 NR_14894E	91370 Hs. 65899E	NR_05285E	ENSG00000LOC91370	uncharactncRNA	
chr3-4905	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr3	49098713	49103196	+	0 NA	intron (NALuSx SIN	-1040 NR_10695E	1.02E+08	NR_10695E	ENSG00000MIR6890	hsa-mir-6890 microRNA ncRNA	
chr4-289	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr4	2896485	2901017	+	0 NA	intron (Nintron (N	35486 NM_00112C	10227 Hs. 632581	NR_00112C	ENSG00000MFSD10	TETRA NF major fac protein-coding	
chr7-2361	9.673474	0.267502	0.750669	0.356351	0.721578	0.981636	chr7	2361895	2367632	+	0 NA	intron (Nintron (N	14436 NM_001037	8662 Hs. 371001	NR_00375E	EN		



chr2-6912	9.135746	0.273203	0.772142	0.353825	0.72347	0.981636	chr2	69128489	69129365	+	0	NA	intron (Nintron (N	25245	NR_036073	1E+08	NR_036073	ENSG000003MIR3126	mir-3126	microRNA	ncRNA	
chr6-432	9.135746	0.273203	0.772142	0.353825	0.72347	0.981636	chr6	43205881	43206924	+	0	NA	exon (NM exon (NM	23079	NR_199184	10591	Hs.109752	NR_006443	ENSG000003DNPH1	G6orf108 2'	-deoxyribose protein-coding	
chr1-1804	9.624476	0.267732	0.756728	0.353802	0.723487	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (NCharlieLz	4041	NR_032366	84320	Hs.200051	NR_032366	ENSG000003ACBD6	-	acyl-CoA protein-coding	
chr6-443	9.624476	0.267732	0.756728	0.353802	0.723487	0.981636	chr6	44392674	44392851	+	0	NA	intron (NMER21B LI	9556	NR_001252	988	Hs.485471	NR_001252	ENSG000003CDC5L	CDC5 CDC5	cell divi protein-coding	
chr18-736	10.617451	0.25395	0.717935	0.353723	0.723546	0.981636	chr18	736333	736605	+	0	NA	intron (NMER20 DN	-23805	NR_148705	55556	Hs.658551	NR_017512	ENSG000003ENOSF1	FDCU RTS	enolase protein-coding	
chr19-174	4.487132	0.383317	1.085066	0.353266	0.723889	0.981636	chr19	17422841	17423733	+	0	NA	intron (NAluSq SI	3240	NR_138401	93343	Hs.515242	NR_138401	ENSG000003MVB12A	CFBP FAM1	multivesi protein-coding	
chr1-284	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr1	28466259	28467614	+	0	NA	intron (NAluSc8 SI	28786	NR_002392	65979	Hs.225641	NR_002392	ENSG000003PHACTR4	PPP1R124	phosphatase protein-coding	
chr13-415	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr13	41340221	41342360	+	0	NA	intron (Nintron (N	-29252	NR_001354	9617	Hs.381276	NR_004294	ENSG000003MTRF1	MRF1 MTTF	mitochondr protein-coding	
chr13-728	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr13	72895815	72896974	+	0	NA	intron (NLIPB1 LIN	114261	NR_146205	10464	Hs.441922	NR_006346	ENSG000003PIBF1	C13orf24	progester protein-coding	
chr2-1278	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (NAluSx1 SI	7058	NR_001354	5433	Hs.715342	NR_004805	ENSG000003POLR2D	HSRBP4 HS	RNA polymer protein-coding	
chr4-849	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr4	849384	849583	+	0	NA	3' UTR (N3' UTR (N	-23354	NR_006651	10815	Hs.478933	NR_006651	ENSG000003CPLX1	CPX-1 CPX	complexir protein-coding	
chr4-1216	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	8291	NR_001154	308	Hs.480652	NR_001154	ENSG000003ANXA5	ANX5 ENX	anexin protein-coding	
chr7-9278	8.402144	-0.28547	0.809278	-0.35275	0.724278	0.981636	chr7	92788419	92789201	+	0	NA	intron (NLIM4 LINE	45149	NR_001252	1021	Hs.119882	NR_001252	ENSG000003CDK6	MCPH12 PI	cyclin deprotein-coding	
chr1-178	8.592011	0.291408	0.826186	0.352715	0.724302	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (Nintron (N	4312	NR_022371	64222	Hs.584952	NR_022371	ENSG000003TOR3A	ADIR ADIF	torsin protein-coding	
chr1-2468	9.640192	0.264631	0.750877	0.35243	0.724516	0.981636	chr1	2.47E+08	2.47E+08	+	0	NA	intron (NAluJr4 SI	42498	NR_015446	25909	Hs.300887	NR_015446	ENSG000003AHCTF1	ELYS MST1	AT-hook protein-coding	
chr11-628	9.640192	0.264631	0.750877	0.35243	0.724516	0.981636	chr11	62813492	62827912	+	0	NA	intron (NAluJ SINE	11349	NR_003164	6811	Hs.654602	NR_003164	ENSG000003STX5	SED5 STX	syntaxis protein-coding	
chr12-104	9.640192	0.264631	0.750877	0.35243	0.724516	0.981636	chr12	1.04E+08	1.04E+08	+	0	NA	intron (NMLT1H LTF	6971	NR_013322	29915	Hs.510655	NR_013322	ENSG000003HCF2	HCF-2 HCF	host cell protein-coding	
chr1-75	9.640192	0.264631	0.750877	0.35243	0.724516	0.981636	chr15	75684417	75685620	+	0	NA	intron (NMLTB SINE	27830	NR_001897	1464	Hs.513044	NR_001897	ENSG000003CSPG4	HMW-MAA H	chondroitin protein-coding	
chr2-8612	9.640192	0.264631	0.750877	0.35243	0.724516	0.981636	chr2	86125377	86129156	+	0	NA	exon (NM exon (NM	-8604	NR_004378	692225	Hs.723087	NR_004378	ENSG000003SNORD94	U94	small nucsnRNA	
chr9-324	9.640192	0.264631	0.750877	0.35243	0.724516	0.981636	chr9	32433174	32434250	+	0	NA	intron (Nintron (N	49069	NR_001362	48	Hs.567222	NR_002197	ENSG000003CACO1	ACONS HEL	aconitase protein-coding	
chr1-455	10.68237	0.252531	0.716824	0.352292	0.724619	0.981636	chr1	45509859	45519980	+	0	NA	exon (NM exon (NM	6965	NR_181697	5052	Hs.180909	NR_002574	ENSG000003PRDX1	MSP23 NKF	peroxidase protein-coding	
chr1-2038	10.68237	0.252531	0.716824	0.352292	0.724619	0.981636	chr1	2.04E+08	2.04E+08	+	0	NA	intron (NLIMC4 LIN	22940	NR_001174	1E+08	NR_001174	ENSG000003ZBED6	MGR	zinc fing protein-coding		
chr14-747	10.68237	0.252531	0.716824	0.352292	0.724619	0.981636	chr14	74723999	74724812	+	0	NA	intron (NAluJb SIN	11261	NR_001318	51077	Hs.579822	NR_015962	ENSG000003FCF1	Bka C14orf	FCF1 rRNA protein-coding	
chr19-457	10.68237	0.252531	0.716824	0.352292	0.724619	0.981636	chr19	45775949	45779571	+	0	NA	exon (NM exon (NM	1859	NR_001288	1760	Hs.631596	NR_004405	ENSG000003DMPK	DM1 DM1	DM1 prote protein-coding	
chr22-40	9.176886	0.274495	0.779235	0.352262	0.724641	0.981636	chr22	40365558	40366342	+	0	NA	intron (NL2c LINE	-4644	NR_146413	27352	Hs.474914	NR_015705	ENSG000003SGSM3	CIP85 MAF	small G protein-coding	
chr10-741	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr10	74113848	74122984	+	0	NA	3' UTR (N3' UTR (N	32412	NR_001322	26985	Hs.500104	NR_012095	ENSG000003APM3	-	adaptor protein-coding	
chr11-671	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr11	67133881	67135361	+	0	NA	intron (NAluSx1 SIN	11538	NR_012308	22992	Hs.124147	NR_012308	ENSG000003KDM2A	CXXC8 FBL	lysine deprotein-coding	
chr12-105	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (NAluSc5 SI	25303	NR_001034	160428	Hs.42572	NR_001034	ENSG000003ALDH1L2	mtFHD	aldehyde protein-coding	
chr12-11	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	13021	NR_001347	28981	Hs.528382	NR_014055	ENSG000003IFT81	CDV-1 CDV	intraflag protein-coding	
chr12-124	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr12	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	28921	NR_003265	57647	Hs.107382	NR_032656	ENSG000003DHX37	DDX37 Dhr	DEAH-box protein-coding	
chr13-11	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (NCpG	-42917	NR_02658C	7027	Hs.79353	NR_007111	ENSG000003TFDP1	DILC DP1	transcrip protein-coding	
chr14-95	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr14	95093585	95094113	+	0	NA	intron (Nintron (N	39654	NR_001199	23405	Hs.87889	NR_030621	ENSG000003DICER1	DCR1 Dicer	dicer 1, protein-coding	
chr14-951	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr14	95124044	95125079	+	0	NA	exon (NM exon (NM	8942	NR_001199	23405	Hs.87889	NR_030621	ENSG000003DICER1	DCR1 Dicer	dicer 1, protein-coding	
chr20-63	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr20	63557724	63562532	+	0	NA	intron (NCpG	5969	NR_001319	79025	Hs.197755	NR_024055	ENSG000003FNDC11	C20orf19	fibronect protein-coding	
chr22-45	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr22	45541057	45544891	+	0	NA	intron (NMTR SINE	40091	NR_001999	2192	Hs.24601	NR_001999	ENSG000003FBLN1	FBLN FBL	fibulin 1 protein-coding	
chr3-5205	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr3	52055051	52052120	+	0	NA	intron (Nintron (N	5236	NR_001947	1849	Hs.591664	NR_001947	ENSG000003DUSP7	MKPX PYS	tubal spec protein-coding	
chr5-1321	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr5	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	10378	NR_04747C	1.01E+08	Hs.519562	NR_04747C	ENSG000003P4HA2-AS1	-	P4HA2 antncRNA	
chr6-315	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr6	3152608	3156016	+	0	NA	TTS (NM_TTS (NM_C	3232	NR_00131C	7280	Hs.654542	NR_001069	ENSG000003TUBB2A	ORC5M5 T	tubulin protein-coding	
chr7-104	8.912599	-0.27474	0.780076	-0.35219	0.724692	0.981636	chr7	1.04E+08	1.04E+08	+	0	NA	intron (NMSTD LTR	8185	NR_002555	5001	Hs.432942	NR_002555	ENSG000003ORC5	ORC5L ORC	ubiquitin protein-coding	
chr19-11	8.920456	-0.27624	0.784405	-0.35216	0.724716	0.981636	chr19	1107946	1110386	+	0	NA	exon (NM exon (NM	4516	NR_001035	2879	Hs.433951	NR_002085	ENSG000003GPX4	GPX-4 GSF	glutathic protein-coding	
chr19-18	8.920456	-0.27624	0.784405	-0.35216	0.724716	0.981636	chr19	18538235	18538472	+	0	NA	exon (NM exon (NM	5220	NR_012181	23770	Hs.173464	NR_012181	ENSG000003FKBP8	FKBP38 FK	FKBP prol protein-coding	
chr5-129	8.920456	-0.27624	0.784405	-0.35216	0.724716	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-52523	NR_001257	1E+08	Hs.582534	NR_001257	ENSG000003MINAR2	KIAA1024	membrane protein-coding	
chr1-236	9.681332	0.26592	0.755552	0.351954	0.724873	0.981636	chr1	2.36E+08	2.36E+08	+	0	NA	intron (NAluSq SIN	36104	NR_002508	4811	Hs.356624	NR_002508	ENSG000003CNID1	NID	nidogen 1 protein-coding	
chr11-67	9.681332	0.26592	0.755552	0.351954	0.724873	0.981636	chr11	67226694	67230092	+	0	NA	intron (Nintron (N	-11621	NR_001255	22992	Hs.124147	NR_012308	ENSG000003KDM2A	CXXC8 FBL	lysine deprotein-coding	
chr19-161	9.681332	0.26592	0.755552	0.351954	0.724873	0.981636	chr19	16126366	1616306	+	0	NA	exon (NM exon (NM	10009	NR_00683C	10975	Hs.8372	NR_00683C	ENSG000003UCR11	U10008D	ubiquinol protein-coding	
chr7-939	9.681332	0.26592	0.755552	0.351954	0.724873	0.981636	chr7	93997643	93998906	+	0	NA	intron (Nintron (N	6081	NR_001317	10282	Hs.489132	NR_005865	ENSG000003BET1	HBET1	Bet1 golg protein-coding	
chr9-1314	9.681332	0.26592	0.755552	0.351954	0.724873	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	14806	NR_013318	84726	Hs.743955	NR_013318	ENSG000003PRRC2B	BAT2L BAT	proline protein-coding	
chr1-170	5.665734	-0.33939	0.964488	-0.35188	0.724926	0.981636	chr1	17037321	17037772	+	0	NA	intron (NAluS6 SI	16624	NR_00300C	6390	Hs.465924	NR_00300C	ENSG000003SDHB	IP1 F	succinate protein-coding	
chr1-																						



chr7-1051 8.904741	-0.27325	0.778525	-0.35098	0.725602	0.981636	chr7	1.05E+08	1.05E+08	0	NA	intron (Nintron (N	96936 NM_182931	55904 Hs. 592262	ENSG00000CKMT2E	HDCMC04P lysine mεprotein-coding	
chr9-9208 8.904741	-0.27325	0.778525	-0.35098	0.725602	0.981636	chr9	92088847	92089349	0	NA	intron (NLMed LIN	26495 NM_00641E	10558 Hs. 90458	ENSG00000SPTLC1	HSAN1 HsN serine εprotein-coding	
chr14-582 9.340773	-0.26973	0.768835	-0.35083	0.725713	0.981636	chr14	58286387	58286702	0	NA	intron (NAluSx1 SI	-1489 NR_14659E	55451	NR_14659E	ENSG00000CLINC0021E	C14orf107 long intεncRNA
chr7-9277 10.12892	0.259875	0.741057	0.350682	0.725827	0.981636	chr7	92777376	92777370	0	NA	intron (NLIPIA7 LIN	56406 NM_00125E	1021 Hs. 119882	ENSG00000CDK6	MCPH12 PI cyclin εprotein-coding	
chr22-502 12.63063	-0.23314	0.664962	-0.35062	0.725885	0.981636	chr22	50275200	50277661	0	NA	intron (Nintron (N	-6050 NR_110887	5600 Hs. 57732	ENSG00000MAPK11	P38E myotogen-εprotein-coding	
chr1-193C 10.14464	0.256896	0.732277	0.350582	0.725902	0.981636	chr1	1.93E+08	1.93E+08	0	NA	intron (NSVA_F Ret	21617 NM_19796E	51022 Hs. 45828E	ENSG00000GLRX2	CGI-133 Cglutaredεprotein-coding	
chr11-33C 10.14464	0.256896	0.732277	0.350582	0.725902	0.981636	chr11	33098533	33099137	0	NA	intron (Nintron (N	22685 NR_015451	283267 Hs. 533701	ENSG00000LINC0029A	NCRN0029 long intεncRNA	
chr13-497 10.14464	0.256896	0.732277	0.350582	0.725902	0.981636	chr13	49714586	49722493	0	NA	intron (Nintron (N	-27052 NM_00127E	84650 Hs. 43327E	ENSG00000EBPL	EBRPA EBP like protein-coding	
chr14-52C 10.14464	0.256896	0.732277	0.350582	0.725902	0.981636	chr14	52003719	52013060	0	NA	3' UTR (N3' UTR (N	18843 NM_01603E	51637 Hs. 534457	ENSG00000CTRAF	C14orf16εRNA transprotein-coding	
chr7-754C 10.14464	0.256896	0.732277	0.350582	0.725902	0.981636	chr7	75427134	75439695	0	NA	intron (NAluY SINE	23092 NR_10401E	155400 Hs. 436034	ENSG00000NSUN5P1	NSUN5B WE NSUN5 pεpseudo	
chr11-434 9.143604	0.271502	0.775716	0.350002	0.726337	0.981636	chr11	43491850	43492776	0	NA	intron (Nintron (N	-67343 NR_031577	1E+08	NR_031577	ENSG00000MIR670	hsa-mir-εmicroRNA ncRNA
chr17-602 9.143604	0.271502	0.775716	0.350002	0.726337	0.981636	chr17	60218738	60219515	0	NA	intron (Nintron (N	12519 NR_00299E	677681	NR_00299E	ENSG00000SCARNA20	ACA66 small Ca_ncRNA
chr18-205 9.143604	0.271502	0.775716	0.350002	0.726337	0.981636	chr18	20967934	20969308	0	NA	intron (Nintron (N	143192 NM_00540E	6093 Hs. 306307	ENSG00000ROCK1	P16OROCK Rho assocprotein-coding	
chr20-137 9.143604	0.271502	0.775716	0.350002	0.726337	0.981636	chr20	13769361	13769743	0	NA	intron (NAluSz6 SI	15334 NM_01664E	51575 Hs. 369284	ENSG00000CESF1	ABTAP C2CESF1 nucleprotein-coding	
chr5-7841 9.143604	0.271502	0.775716	0.350002	0.726337	0.981636	chr5	78416617	78416996	0	NA	intron (Nintron (N	56189 NM_00486E	9522 Hs. 482587	ENSG00000SCAMP1	SCAMP SCεsecretory protein-coding	
chr3-1014 5.624595	-0.34348	0.981582	-0.34992	0.726398	0.981636	chr3	10143204	10143520	0	NA	intron (NAluSx SIN	1584 NM_19815E	7428 Hs. 517792	ENSG00000VHL	HRCAL RCεvon Hippεprotein-coding	
chr1-162F 11.18681	0.246091	0.703484	0.349817	0.726476	0.981636	chr1	1.63E+08	1.63E+08	0	NA	intron (NAluSq SIN	15155 NM_17586E	127933 Hs. 12731C	ENSG00000UHMK1	KIS KIST U2AF homεprotein-coding	
chr9-8367 11.18681	0.246091	0.703484	0.349817	0.726476	0.981636	chr9	83677059	83678186	0	NA	intron (Nintron (N	-30213 NR_13583E	1.05E+08	NR_13583E	ENSG00000LOC10537E	uncharactεncRNA
chr11-12E 8.639158	0.280562	0.803083	0.349717	0.726551	0.981636	chr11	1.26E+08	1.26E+08	0	NA	intron (NHAL LINE	26730 NM_02455E	79607 Hs. 27631E	ENSG00000FAM118B	- family wiprotein-coding	
chrX-1307 7.940688	-0.29613	0.847043	-0.34961	0.726633	0.981636	chrX	13751528	13751766	0	NA	intron (NAluSx1 SI	16899 NM_00361E	8481 Hs. 6483	ENSG00000CFD1	71-7A CXCFD1 centprotein-coding	
chr3-100C 10.69022	0.251129	0.718354	0.349589	0.726647	0.981636	chr3	1E+08	1E+08	0	NA	intron (NLIPIA3 LIN	16429 NM_02020E	56954 Hs. 43915E	ENSG00000CNT2	HEL-5-8a nitrilaseprotein-coding	
chr1-625E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr1	62537945	62539058	0	NA	intron (NLa2 LINE	-59019 NM_01449E	27329 Hs. 20915E	ENSG00000ANGPTL3	ANG-5 ANG angiopoicεprotein-coding	
chr11-69C 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr11	69094091	69092112	0	NA	TTS (NM_TTS (NM_C	8125 NR_03612E	1E+08	NR_03612E	ENSG00000MIR3164	- microRNA ncRNA
chr11-702 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr11	70205235	70205736	0	NA	intron (NMLT1D LTF	2322 NM_003824	8772 Hs. 86131	ENSG00000FADD	GIG3 MORT1Fas assocprotein-coding	
chr11-902 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr11	90205612	90206650	0	NA	intron (Nintron (N	16918 NM_012124	26973 Hs. 22857	ENSG00000CHORDC1	CHP1 cysteine protein-coding	
chr15-80E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr15	80555957	80556899	0	NA	non-codirnon-codir	6516 NR_12036E	1.02E+08	NR_12036E	ENSG00000LOC10192E	uncharactεncRNA
chr15-82E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr15	82540328	82241062	0	NA	intron (Nintron (N	21833 NM_00132E	79631 Hs. 459114	ENSG00000EFL1	EFTUD1 Fεelongaticεprotein-coding	
chr17-29E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr17	29672355	29673505	0	NA	TTS (NM_TTS (NM_C	-51507 NM_032854	84940 Hs. 14304E	ENSG00000COR06	- coronin εprotein-coding	
chr17-42E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr17	42616190	42416653	0	NA	IntergeniAluYJ4 SI	6740 NM_00107E	7283 Hs. 27966E	ENSG00000TUBG1	CDCBM4 GC tubulin εprotein-coding	
chr17-49E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr17	49833870	49835098	0	NA	3' UTR (N3' UTR (N	11426 NM_00124E	729220 Hs. 43413E	ENSG00000FLJ45513	- uncharactεprotein-coding	
chr18-351 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr18	35102052	35102509	0	NA	intron (Nintron (N	60867 NM_01426E	10982 Hs. 532824	ENSG00000MAPRE2	CSCSC2 Eεmicrotubεprotein-coding	
chr2-1117 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr2	1.12E+08	1.12E+08	0	NA	3' UTR (N3' UTR (N	2307 NR_03992E	1.01E+08	NR_03992E	ENSG00000MIR4771-1	- microRNA ncRNA
chr20-367 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr20	36791590	36791974	0	NA	intron (NMLT10 LTF	-18019 NM_00114E	79980 Hs. 63226E	ENSG00000DSN1	C20orf172 DSN1 comεprotein-coding	
chr22-38E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr22	38263880	38264444	0	NA	intron (Nintron (N	8502 NM_00119E	25829 Hs. 18262E	ENSG00000TMEM184B	C22orf5 F transmemtεprotein-coding	
chr3-138E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr3	1.39E+08	1.39E+08	0	NA	intron (NMER1A LI	46100 NM_00132C	80321 Hs. 53196E	ENSG00000CEPT0	BITE centrosomεprotein-coding	
chr5-321E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr5	32132917	32135347	0	NA	intron (NAluJr4 SI	40187 NM_02213C	64083 Hs. 40890E	ENSG00000GOLPH3	GOPPI GFP golgi phεprotein-coding	
chr5-129E 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr5	1.3E+08	1.3E+08	0	NA	intron (NLIPI3 LINE	-63271 NR_12574E	1.04E+08	NR_12574E	ENSG00000ADAMTS19-	ADAMTS19 ncRNA
chr9-5027 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr9	5027421	5028244	0	NA	intron (NTigger1 E	-13861 NM_00132E	3717 Hs. 65621E	ENSG00000JAK2	JTK10 THCJanus kirεprotein-coding	
chr9-3507 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr9	35076463	35077287	0	NA	intron (Nintron (N	3141 NM_00462E	2189 Hs. 591084	ENSG00000FANGC	FAG XRCC5 FA comεprotein-coding	
chr9-1347 5.657877	-0.33711	0.964439	-0.34953	0.726688	0.981636	chr9	1.35E+08	1.35E+08	0	NA	intron (Nintron (N	78762 NR_039691	1.01E+08	NR_039691	ENSG00000MIR3689C	- microRNA ncRNA
chr1-150E 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr1	1.51E+08	1.51E+08	0	NA	exon (NM exon (NM	2988 NM_00120E	1893 Hs. 81071	ENSG00000ECM1	URBWD extracellεprotein-coding	
chr1-214E 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr1	2.14E+08	2.14E+08	0	NA	intron (Nintron (N	112423 NM_020197	56950 Hs. 66170	ENSG00000SMDY2	HSKM-B KMT SET and εprotein-coding	
chr1-227C 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr1	2.27E+08	2.27E+08	0	NA	intron (Nintron (N	150647 NM_020247	56997 Hs. 118241	ENSG00000COQ8A	ADCK3 ARCoenzymε protein-coding	
chr10-102 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr10	1.02E+08	1.02E+08	0	NA	intron (Nintron (N	-40799 NM_00128E	4791 Hs. 73090	ENSG00000NFKB2	CVI10 Hεnuclear fεprotein-coding	
chr11-11E 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr11	1.19E+08	1.19E+08	0	NA	exon (NM exon (NM	-2419 NM_00210E	3014 Hs. 47787E	ENSG00000H2AFX	H2A.X H2A histεprotein-coding	
chr12-12C 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr12	1.2E+08	1.2E+08	0	NA	exon (NM exon (NM	-18622 NR_03971E	1.01E+08	NR_03971E	ENSG00000MIR4498	mir-4498 microRNA ncRNA
chr14-731 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr14	73120200	73120440	0	NA	3' UTR (N3' UTR (N	-16187 NM_000021	5663 Hs. 3260	ENSG00000PSEN1	ACIN1V3 Aεpreseniliprotein-coding	
chr14-747 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr14	74778921	74783567	0	NA	intron (Nintron (N	17928 NM_01958E	56252 Hs. 531111	ENSG00000CYLPM1	C14orf17 CYLP motifεprotein-coding	
chr19-441 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr19	44117245	44125297	0	NA	intron (NLIPIB1 LIN	7872 NM_01336E	7768 Hs. 27956E	ENSG00000ZNF225	- zinc fingεprotein-coding	
chr19-45E 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr19	45610633	45614300	0	NA	intron (NAluJb SIN	-10254 NM_00528E	2828 Hs. 17170	ENSG00000GPR4	- GPR5εprotein-coding	
chr22-451 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr22	45132567	45136157	0	NA	non-codirnon-codir	18274 NR_038957	1.01E+08	NR_038957	ENSG00000NUP50-DT	NUP50-AS1 NUP50 divεncRNA
chr3-48E 9.64805	0.263059	0.752616	0.349526	0.726695	0.981636	chr3	48629627	48633687	0	NA	intron (N(CCTG)n	2091 NR_10688E	1.02E+08	NR_10688E	ENSG00000MIR6824	hs



chr13-414	10.65694	0.248489	0.716184	0.346962	0.72862	0.981636	chr13	41463233	41471697	+	0 NA	intron (Nintron (N	9915 NM_01405E	28984 Hs. 507866NM_01405E	ENSG00000CRGCC	C13orf15	regulator protein-coding
chr22-411	10.65694	0.248489	0.716184	0.346962	0.72862	0.981636	chr22	41145450	41159470	+	0 NA	intron (Nintron (N	45041 NR_110514	1.02E+08 Hs. 517517NR_110514	EP300-AS1	EP300 antncRNA	
chr4-412f	10.65694	0.248489	0.716184	0.346962	0.72862	0.981636	chr4	41260199	41265728	+	0 NA	intron (NMIR SINE	6035 NM_004181	7345 Hs. 518731NM_004181	ENSG00000UCHL1	HEL-117	ubiquitin protein-coding
chr15-61f	9.102465	0.270084	0.778433	0.346959	0.728622	0.981636	chr15	61967091	61967327	+	0 NA	intron (Nintron (N	93238 NM_017684	54832 Hs. 511668NM_017684	ENSG00000VPS13C	PARR23	vacuolar protein-coding
chr6-441f	9.102465	0.270084	0.778433	0.346959	0.728622	0.981636	chr6	44152741	44153101	+	0 NA	intron (Nintron (N	-5899 NM_00705E	11131 Hs. 225955NM_00705E	ENSG00000CAPN11	calpainII calpain I	protein-coding
chr16-864	9.366197	-0.26451	0.762549	-0.34688	0.728681	0.981636	chr16	86481264	86487435	+	0 NA	intron (MLTI LTF	24511 NR_03392E	400550 Hs. 448822NR_03392E	ENSG00000FENDRR	FOXF1-AS1 FOXF1 ad_ncRNA	
chr3-124f	9.366197	-0.26451	0.762549	-0.34688	0.728681	0.981636	chr3	1.25E+08	1.25E+08	+	0 NA	3' UTR (N3' UTR (N	-34753 NM_03304E	56667 Hs. 5940 NM_03304E	ENSG00000MUC13	DRCC1	MUC mucin 13, protein-coding
chr5-988f	9.366197	-0.26451	0.762549	-0.34688	0.728681	0.981636	chr5	98869497	98870560	+	0 NA	intron (Nintron (N	56506 NM_00127C	1105 Hs. 64346E NM_00127C	ENSG00000CHD1	CHD-1	PII chromodomain protein-coding
chr9-137f	9.366197	-0.26451	0.762549	-0.34688	0.728681	0.981636	chr9	1.38E+08	1.38E+08	+	0 NA	intron (Nintron (N	-20986 NR_03033E	693187 NR_03033E	ENSG00000MIR602	MIRN602	microRNA ncRNA
chr1-775f	8.394287	-0.28374	0.818466	-0.34667	0.72884	0.981636	chr1	77577735	77578904	+	0 NA	intron (Nintron (N	104339 NM_015534	26009 Hs. 48050E NM_015534	ENSG00000ZZZ3	ATAC1	zinc finger protein-coding
chr17-40f	8.394287	-0.28374	0.818466	-0.34667	0.72884	0.981636	chr17	4090142	4090341	+	0 NA	intron (Nintron (N	52789 NM_01511E	23140 Hs. 277624NM_01511E	ENSG00000ZZEF1	ZZZA	zinc finger protein-coding
chr9-131f	8.394287	-0.28374	0.818466	-0.34667	0.72884	0.981636	chr9	1.31E+08	1.31E+08	+	0 NA	intron (Nintron (N	2540 NM_00131E	8021 Hs. 654533NM_00508E	ENSG00000NUP214	CAIN CAN	nucleoporin protein-coding
chr7-166f	8.855743	-0.27412	0.791864	-0.34617	0.729218	0.981636	chr7	16606086	16606404	+	0 NA	intron (Nintron (N	39509 NM_02031E	57037 Hs. 15737E NM_02031E	ENSG00000ANKMY2	ZMYND20	ankyrin I protein-coding
chr15-75f	10.19364	0.256659	0.741507	0.346131	0.729244	0.981636	chr15	75521576	75524336	+	0 NA	intron (Nintron (N	56359 NM_00283E	5780 Hs. 44577E NM_00283E	ENSG00000PTPN9	MEG2	PTP protein-coding
chr22-20f	10.19364	0.256659	0.741507	0.346131	0.729244	0.981636	chr22	20564702	20564992	+	0 NA	intron (Nintron (N	56800 NM_00129E	51586 Hs. 517421NM_01588E	ENSG00000MED15	ARC105 C	mediator protein-coding
chr11-67f	9.68919	0.264287	0.763786	0.346022	0.729326	0.981636	chr11	67397770	67399552	+	0 NA	TTS (NM_CTS (NM_C	3197 NM_20687E	5499 Hs. 183994NM_00270E	ENSG00000PPP1CA	PP-1A	PP1 protein-coding
chr12-58f	9.68919	0.264287	0.763786	0.346022	0.729326	0.981636	chr12	58880104	58880789	+	0 NA	intron (Nintron (N	39100 NM_00113E	121227 Hs. 25373E NM_15337E	ENSG00000CLRIG3	LIG3	leucine I protein-coding
chr16-19f	9.68919	0.264287	0.763786	0.346022	0.729326	0.981636	chr16	16829297	19842321	+	0 NA	intron (Nintron (N	-32842 NM_00130E	124152 Hs. 460217NM_15320E	ENSG00000IQCK	-	IQ motif protein-coding
chr9-128f	9.68919	0.264287	0.763786	0.346022	0.729326	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	exon (NM_exon (NM_	-14147 NR_03611E	1E+08 NR_03611E	ENSG00000MIR3154	mir-3154	microRNA ncRNA
chr6-334f	4.461708	0.374116	1.081422	0.345948	0.729381	0.981636	chr6	33449082	33449401	+	0 NA	intron (Nintron (N	-5335 NM_15273E	221504 Hs. 59180E NM_15273E	ENSG00000ZBTB9	ZNF199	zinc finger protein-coding
chr16-214	12.61491	-0.23094	0.667851	-0.3458	0.729494	0.981636	chr16	21438849	21438849	+	0 NA	Intergeni LIPA5 LIN	-4215 NR_02445E	1E+08 Hs. 64843E NR_02445E	LOC10019C	-	uncharacterized ncRNA
chr11-974	9.606911	0.261694	0.756797	0.345791	0.7295	0.981636	chr11	9749773	9750240	+	0 NA	3' UTR (N3' UTR (N	-8287 NR_03648E	283104 Hs. 63215E NR_03648E	ENSG00000SBF2-AS1	-	SBF2 antncRNA
chr11-12f	10.69808	0.249723	0.722571	0.345603	0.729641	0.981636	chr11	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	3268 NM_001301	7753 Hs. 11255E NM_00345E	ENSG00000ZNF202	ZKSCAN10	zinc finger protein-coding
chr1-183f	11.14567	0.244955	0.708842	0.34557	0.729666	0.981636	chr1	1.84E+08	1.84E+08	+	0 NA	intron (Nintron (N	57126 NM_00043E	4688 Hs. 58755E NM_00043E	ENSG00000NCF2	NCF-2	NOX2 neuropeptide protein-coding
chr17-15f	11.14567	0.244955	0.708842	0.34557	0.729666	0.981636	chr17	15544965	15546889	+	0 NA	intron (Nintron (N	17556 NM_001204	1.01E+08 Hs. 16459E NM_001204	ENSG00000TVP23C-CI	FAM18B2 F	TVP23C-CI protein-coding
chrX-5364	9.389771	-0.26907	0.778851	-0.34548	0.729737	0.981636	chrX	53640116	53640349	+	0 NA	intron (Nintron (N	46487 NM_031407	10075 Hs. 13690E NM_031407	ENSG00000CHUWE1	ARF-BP1	FHECT, UB1 protein-coding
chr4-168f	8.739003	0.29021	0.84017	0.345428	0.729773	0.981636	chr4	1.68E+08	1.68E+08	+	0 NA	intron (Nintron (N	37276 NM_017631	55601 Hs. 59171E NM_017631	ENSG00000DDX60	-	DexD/Hc-box protein-coding
chr14-75f	9.391838	0.397966	1.15225	0.345381	0.729808	0.981636	chr14	75021546	75022143	+	0 NA	intron (Nintron (N	18923 NM_01423E	8892 Hs. 409137NM_01423E	ENSG00000EIF2B2	EIF-2B2	eukaryotic protein-coding
chr1-379f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr1	37963279	37964264	+	0 NA	intron (Nintron (N	-16714 NR_15862E	3633 Hs. 44994E NM_00554E	ENSG00000INPP5B	5PTase	inositol protein-coding
chr1-426f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr1	42693356	42694863	+	0 NA	intron (Nintron (N	10973 NR_132737	4904 Hs. 47358E NM_00455E	ENSG00000YBX1	BP-8 CBF-	Y-box bir protein-coding
chr1-565f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr1	56526017	56527164	+	0 NA	intron (Nintron (N	52973 NM_00371E	8613 Hs. 40515E NM_00371E	ENSG00000PLPP3	Dri42 LPF	phospholipid protein-coding
chr1-923f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr1	92352092	92352965	+	0 NA	intron (Nintron (N	53469 NM_02481E	79871 Hs. 444421NM_02481E	ENSG00000RPAP2	Clorf82	RNA polymer protein-coding
chr1-173f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr1	1.74E+08	1.74E+08	+	0 NA	intron (Nintron (N	38983 NM_01445E	27252 Hs. 49503E NM_01445E	ENSG00000KHLH20	KHLHX	KLH kelch like protein-coding
chr10-60f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr10	60890891	60892768	+	0 NA	intron (Nintron (N	52356 NM_00135E	9886 Hs. 737374NM_01483E	ENSG00000RHOTB1	-	Rho relat protein-coding
chr12-45f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr12	45823965	45824741	+	0 NA	intron (Nintron (N	94644 NM_001347	196528 Hs. 317304NM_15264E	ENSG00000ARID2	BAF200	CSAT-rich iprotein-coding
chr14-54f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr14	54431261	54431966	+	0 NA	intron (Nintron (N	9761 NM_00577E	10175 Hs. 29460E NM_00577E	ENSG00000CNH1	CNH1	CNH1 cornichon protein-coding
chr14-64f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr14	64425302	64427362	+	0 NA	intron (Nintron (N	37979 NM_001364	4522 Hs. 65230E NM_00595E	ENSG00000MTHFD1	CIMAH	MTF methylene protein-coding
chr17-47f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr17	47563820	47565101	+	0 NA	intron (Nintron (N	33352 NM_00631E	9520 Hs. 443837NM_00631E	ENSG00000NPEPPS	ARP-5	IMP1 aminopept protein-coding
chr17-49f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr17	49031593	49033398	+	0 NA	intron (Nintron (N	35110 NM_00116E	10642 Hs. 14493E NM_00654E	ENSG00000IGF2BP1	CADP-BP	CF insulin I protein-coding
chr18-12f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr18	12974419	12974999	+	0 NA	intron (Nintron (N	-16653 NM_03214E	55125 Hs. 100914NM_01806E	ENSG00000CEP192	PPP1R62	centrosome protein-coding
chr19-34f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr19	34496568	34497430	+	0 NA	intron (Nintron (N	15241 NM_00108E	126374 Hs. 58501E NM_00108E	ENSG00000WTIP	-	WT1 interprotein-coding
chr2-154f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr2	15460961	15461202	+	0 NA	intron (Nintron (N	100253 NM_00108E	51594 Hs. 46775E NM_01590E	ENSG00000CNBAS	ILF52	NAC neurobasal protein-coding
chr2-133f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr2	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	-109698 NR_110294	1.02E+08 Hs. 661917NR_110294	ENSG00000CNKAP5-AS	-	NCKAP5 arncRNA
chr3-390f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr3	39097427	39098069	+	0 NA	non-codiron-codir	9879 NM_00127E	64689 Hs. 72194E NM_03189E	ENSG00000GORASP1	GOLPH5	GF golgi ree protein-coding
chr3-195f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr3	1.7E+08	1.7E+08	+	0 NA	3' UTR (N3' UTR (N	29286 NM_00326E	7095 Hs. 74485E NM_00326E	ENSG00000SEC62	Dtrp1	HEC62 hom protein-coding
chr3-195f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr3	1.96E+08	1.96E+08	+	0 NA	intron (Nintron (N	4861 NM_00130E	10188 Hs. 51851E NM_005781	ENSG00000TNK2	ACK1	tyrosine protein-coding
chr6-354f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr6	35455736	35456301	+	0 NA	exon (NM_exon (NM_	3657 NM_02192E	2178 Hs. 30200E NM_02192E	ENSG00000FANCE	FACE	FAE Fae complex protein-coding
chr6-148f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr6	1.49E+08	1.49E+08	+	0 NA	intron (Nintron (N	18726 NM_00134E	23328 Hs. 19313E NM_01527E	ENSG00000CSASH1	CAPOK	DUF SAM and S protein-coding
chr7-149f	5.650019	-0.33485	0.969746	-0.3453	0.72987	0.981636	chr7	-19369 NM_01225E	7988 Hs. 49051E NM_01225E	ENSG00000ZNF212	C2H2-150	zinc finger protein-coding					
chr8-586f	5.650019	-0.33485	0.9														

chr11-621	11.16925	0.24085	0.702006	0.343088	0.731532	0.981636	chr11	62792380	62803877	+	0	NA	intron (AluSz SIN	-5357 NR_106766	1.02E+08	NR_106766	ENSG000002MIR6514	hsa-mir-6microRNA ncRNA	
chr16-756	11.16925	0.24085	0.702006	0.343088	0.731532	0.981636	chr16	75654271	75657285	+	0	NA	intron (L2a LINE	8005 NM_018975		54386 Hs. 301415	ENSG000002TERF2IP	DRIP5 RAF TERF2 intron protein-coding	
chr2-1866	11.16925	0.24085	0.702006	0.343088	0.731532	0.981636	chr2	1.87E+08	1.87E+08	+	0	NA	intron (L1MB7 LIN	-22431 NM_177454		165215 Hs. 28872	NM_177454	ENSG000002FAM171B	KIAA1946 family wiprotein-coding
chr17-204	8.682098	0.281952	0.821937	0.343034	0.731573	0.981636	chr17	30498521	30498746	+	0	NA	intron (intron (N	121225 NM_001007		9527 Hs. 462628	NM_004871	ENSG000002GOSR1	GOLM2 GC golgi SN protein-coding
chr1-307	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr1	26840 NR_125345			0	NA	intron (L1PA15 LI	26840 NR_125345		1604 Hs. 126517	NM_000574	ENSG000002CD55	CHAPLE CF CD55 moleprotein-coding
chr14-242	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr14	24200877	24203614	+	0	NA	IntergeniMER11C LI	-3451 NM_001184		283629 Hs. 314432	NM_174944	ENSG000002TSSK4	C14orf20 testis sf protein-coding
chr16-84	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr16	84466409	84466539	+	0	NA	promoter-promoter-	-113 NR_146503	1.05E+08	Hs. 610979	NR_146503	ENSG000002ATP2C2-AS-	ATP2C2 arncRNA
chr17-302	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr17	30265867	30266838	+	0	NA	intron (AluV SINE	25592 NM_000386		642 Hs. 371914	NM_000386	ENSG000002BLMH	BH BMH bleomycin protein-coding
chr3-1792	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (L2a LINE	40732 NM_014407		27094 Hs. 59128	NM_014407	ENSG000002KCNMB3	BKBETA3 f potassium protein-coding
chr3-1964	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	intron (intron (N	20335 NM_152617		165918 Hs. 250642	NM_152617	ENSG000002RNF168	hRNF168 ring fing protein-coding
chr7-1491	8.930164	-0.26786	0.780887	-0.34302	0.731584	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (LOR1a LTF	4345 NM_020781		57541 Hs. 632032	NM_020781	ENSG000002ZNF398	P51 P71 Zzinc fing protein-coding
chr2-2332	8.647016	0.278858	0.813001	0.342999	0.731599	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	exon (NM exon (NM	-2736 NR_003008		677775 Hs. 66361	NR_003008	ENSG000002SCARNA5	U87 small Ca_ncRNA
chr1-1456	8.484424	-0.28011	0.817315	-0.34272	0.731811	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	intron (intron (N	41124 NM_001097		653519 Hs. 504322	NM_001097	ENSG000002GPR89A	GPHR GPR8G proteir protein-coding
chr11-661	5.180704	-0.35395	1.032933	-0.34267	0.731847	0.981636	chr11	66199106	66199991	+	0	NA	intron (L1MA3 LIN	-57746 NM_001134		64837 Hs. 280792	NM_022822	ENSG000002KLC2	- kinesin l protein-coding
chr3-2391	13.57896	-0.22064	0.644253	-0.34247	0.732	0.981636	chr3	23917860	23920695	+	0	NA	exon (NM exon (NM	2145 NM_001255		6138 Hs. 38121	NM_002948	ENSG000002RPL15	DBA12 EC4 ribosomal protein-coding
chr11-86C	7.93283	-0.29406	0.859158	-0.34227	0.732149	0.981636	chr11	86014688	86014976	+	0	NA	intron (intron (N	54252 NM_007166		8301 Hs. 16389	NM_007166	ENSG000002PICALM	CALM CLTF phosphat i protein-coding
chr17-824	7.93283	-0.29406	0.859158	-0.34227	0.732149	0.981636	chr17	82465900	82466099	+	0	NA	intron (intron (N	7258 NM_012336		26502 Hs. 25652	NM_012336	ENSG000002NCARF	IOP2 nuclear i protein-coding
chr1-1175	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr1	11795643	11796671	+	0	NA	intron (intron (N	7520 NM_001033		4524 Hs. 214142	NM_005957	ENSG000002MTHFR	- methylene protein-coding
chr1-5145	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr1	51458398	51459395	+	0	NA	intron (intron (N	-36801 NM_001155		2060 Hs. 83722	NM_001981	ENSG000002EPS15	AF-1P AF1 epidermal protein-coding
chr1-8672	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr1	86728800	86730536	+	0	NA	intron (intron (N	25092 NM_016009		51100 Hs. 13630	NM_016009	ENSG000002CSH3GLB1	Bif-1 CG1SH3 domaiprotein-coding
chr1-2201	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (intron (N	37261 NR_031705		11E+08	NR_031705	ENSG000002MIR664A	MIR664 MimicroRNA ncRNA
chr10-285	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr10	28555978	28557500	+	0	NA	intron (L1M3 LINE	23621 NM_016628		51322 Hs. 743224	NM_016628	ENSG000002WAC	BM-016 DFW domair protein-coding
chr10-124	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr10	1.25E+08	1.25E+08	+	0	NA	intron (AluSx SIN	7134 NM_121554		399818 Hs. 72081	NM_121554	ENSG000002EEF1AKMT2	C10orf13 EEF1A lys protein-coding
chr11-122	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr11	12215884	12216673	+	0	NA	exon (NM exon (NM	52595 NR_106733	1.02E+08	NR_106733	ENSG000002MIR6124	hsa-mir-6microRNA ncRNA	
chr11-33C	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr11	33077682	33079156	+	0	NA	non-codirnon-codir	-2269 NR_015451		283267 Hs. 533701	NR_015451	ENSG000002LINC00294	NCRNA0029 long intncRNA
chr11-684	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr11	68427735	68428558	+	0	NA	intron (AluSq2 SI	-32606 NM_001355		55291 Hs. 503022	NM_018312	ENSG000002PPP6R3	C1orf273 protein i protein-coding
chr11-102	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr11	171047 NM_001195			0	NA	intron (intron (N	171047 NM_001195		10413 Hs. 503692	NM_006109	ENSG000002YAP1	COB1 YAP Yes assoc protein-coding
chr11-124	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr11	1.25E+08	1.25E+08	+	0	NA	TTS (NR TTS (NR C	13978 NR_016021		84897 Hs. 43641	NM_032811	ENSG000002TBRG1	NIAM TB-ε transform protein-coding
chr14-214	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr14	21480365	21481400	+	0	NA	intron (AluSp SIN	3687 NM_001303		9878 Hs. 55591	NR_014828	ENSG000002TOX4	C14orf92 TOX4 high protein-coding
chr14-313	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr14	517664	51363818	+	0	NA	intron (AluSx SIN	57564 NM_015473		25938 Hs. 74497	NR_015473	ENSG000002HEATR5A	MIR664 MimicroRNA ncRNA
chr14-601	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr14	60132215	60134388	+	0	NA	intron (L1MB7 LIN	32097 NM_016025		51635 Hs. 59719	NM_016025	ENSG000002DHRS7	CGI-86 SE dehydroge protein-coding
chr15-417	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr15	41754811	41755738	+	0	NA	intron (intron (N	-19210 NM_001265		23005 Hs. 51366	NM_014994	ENSG000002MAPKBP1	JNKBP-1 Jmi toe protein-coding
chr15-515	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr15	51955561	51956780	+	0	NA	intron (AluSx SIN	19210 NM_001322		123169 Hs. 567662	NM_001322	ENSG000002LEO1	RDL LEO1 homc protein-coding
chr15-712	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr15	71232830	71235211	+	0	NA	intron (MamGypLTF	-44961 NR_120345	1.02E+08	Hs. 680472	NR_120348	THSD4-AS1-	THSD4 antncRNA
chr16-676	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr16	67616684	67618830	+	0	NA	intron (L1M5 LINE	-27387 NR_001013		142606 Hs. 611432	NM_001013	ENSG000002CARMIL2	CARMIL2 capping i protein-coding
chr16-727	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr16	72795845	72796253	+	0	NA	exon (NM exon (NM	-131079 NR_126333	1.02E+08	Hs. 637255	NR_126333	ENSG000002LINC01572	long intncRNA
chr16-892	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr16	89297120	89298331	+	0	NA	non-codirnon-codir	1597 NR_136335	1.05E+08	Hs. 657381	NR_136335	ENSG000002LOC105371	uncharactncRNA
chr17-307	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr17	30773989	30776812	+	0	NA	intron (intron (N	49292 NM_015986		51379 Hs. 649372	NM_015986	ENSG000002CRLF3	CREME-9 Ccytokine protein-coding
chr17-375	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr17	37541941	37542964	+	0	NA	exon (NM exon (NM	52561 NM_007026		11072 Hs. 91448	NM_007026	ENSG000002DUSP14	MKP-L MKF dual spec protein-coding
chr17-475	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr17	47546326	47551606	+	0	NA	intron (intron (N	17858 NM_006310		9520 Hs. 443837	NM_006310	ENSG000002NPEPPS	AAP-S M aminopept protein-coding
chr18-13C	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr18	13019744	13020354	+	0	NA	intron (AluSz SIN	28687 NM_032142		55125 Hs. 100914	NM_018069	ENSG000002CEP192	PPP1R26 centroson protein-coding
chr19-49F	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr19	4950726	4953958	+	0	NA	intron (AluSx1 SI	-16771 NM_015015		23030 Hs. 65481	NM_015015	ENSG000002KDM4B	JMJD2B TI lysine de protein-coding
chr19-344	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr19	34440900	34441295	+	0	NA	intron (L1M5 LINE	12716 NM_005499		10054 Hs. 63158	NM_005499	ENSG000002UBA2	ARX HRH7 ubiquitir protein-coding
chr2-3237	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	32371620	32373923	+	0	NA	intron (AluJb SIN	15743 NM_016252		57448 Hs. 150107	NM_016252	ENSG000002BTRC6	APOLLON Ebaculovir protein-coding
chr2-370C	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	37005495	37006364	+	0	NA	intron (intron (N	-39393 NM_003162		6801 Hs. 12748	NM_003162	ENSG000002CSTRN	PPP2R6A S triatin protein-coding
chr2-538E	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	53854264	53854773	+	0	NA	exon (NM exon (NM	-5313 NR_037455	1.01E+08	NR_037455	ENSG000002MIR3682	mir-3682 microRNA ncRNA	
chr2-860S	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	86092273	86094448	+	0	NA	intron (L1M4C LIN	12526 NM_015422		25885 Hs. 53181	NM_015422	ENSG000002POLR1A	A190 AFDCRNA poly protein-coding
chr2-171S	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	1.72E+08	1.72E+08	+	0	NA	intron (L1M8 LIN	4762 NM_003642		8520 Hs. 632532	NM_003642	ENSG000002CHAT1	KAT1 histone ε protein-coding
chr2-230C	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (L1H5 LINE	13708 NM_001352		93349 Hs. 589661	NM_138402	ENSG000002SP140L	- SP140 nuc protein-coding
chr2-2311	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	IntergeniIntergeni	-22325 NM_025135		80210 Hs. 162411	NM_025135	ENSG000002ARMC9	ARM JBTS armadill i protein-coding
chr20-367	5.6833	-0.32876	0.960747	-0.34219	0.73221	0.981636	chr20	36756779	36758538	+	0	NA	intron (intron (N	-11568 NM_032013		57446 Hs. 43733	NM_022477	ENSG000002CNDRG3	- NDRG fami protein-coding
chr20-37E	5.6833																		



chr4-1222	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	93617	NM_015312	84162	Hs.408142NM_015312	ENSG00000KIAA1109	ALKKUCS FKIAA1109	protein-coding				
chr5-3852	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr5	38521232	38524225	+	0	NA	intron (Nintron (N	33918	NM_001127	3977	Hs.133421NM_00231	ENSG00000LIFR	CD118 LIFLIF	receptor protein-coding				
chr5-128	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	184839	NM_001995	2201	Hs.519294NM_001995	ENSG00000FBN2	CCA DA9 E	fibrillin protein-coding				
chr7-728	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr7	72890205	72894352	+	0	NA	intron (Nintron (N	1651	NM_17202C	9833	Hs.655217NM_17202C	ENSG00000POM121	P145 POM1	POM121	protein-coding			
chr7-1432	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr7	1.43E+08	1.43E+08	+	0	NA	intron (NAluX S	3415	NM_001224	855	Hs.368982NM_001224	ENSG00000CASP2	CASP-2 C	caspace 2	protein-coding			
chr8-1197	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr8	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	29917	NM_003184	6873	Hs.122752NM_003184	ENSG00000TAF2	CIF150 MT	TATA-box	protein-coding			
chr9-122	9.391621	-0.25941	0.759771	-0.34143	0.732779	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (NAluJr S N	2478	NM_005388	5082	Hs.271749NM_005388	ENSG00000PDCL	PHLP	phosphudic	protein-coding			
chr12-125	10.12707	0.25116	0.735928	0.341283	0.73289	0.981636	chr12	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	8717	NR_03892C	1.01E+08	Hs.127718NR_03892C	ENSG00000GPRC5D-AS-	GPRC5D	arncRNA				
chr16-582	10.12707	0.25116	0.735928	0.341283	0.73289	0.981636	chr16	58578884	58579261	+	0	NA	intron (NLMC5a L	-1914	NR_00298C	677830	Hs.677518NR_00298C	ENSG00000SNORA50A	ACA50 SNC	small	nucsnRNA			
chr17-146	10.12707	0.25116	0.735928	0.341283	0.73289	0.981636	chr17	48848231	48850437	+	0	NA	exon (NM exon (NM	18299	NM_001261	10241	Hs.514922NM_005831	ENSG00000CALCOCO2	NDP52	calcium	protein-coding			
chr17-168	10.922306	-0.26634	0.782075	-0.34056	0.733434	0.981636	chr17	16091371	16091631	+	0	NA	TTS (NM_C TTS (NM_C	61695	NR_145787	1.1E+08	NR_145787	SNORD163	-	small	nucsnRNA			
chr2-2298	8.922306	-0.26634	0.782075	-0.34056	0.733434	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (Nintron (N	-91887	NM_13907Z	92737	Hs.234074NM_13907Z	ENSG00000CDNER	UNQ26 bet	delta/not	protein-coding			
chr3-2741	8.922306	-0.26634	0.782075	-0.34056	0.733434	0.981636	chr3	27414065	27415052	+	0	NA	intron (NTiger2 I	42220	NM_00125E	9497	Hs.250072NM_00361E	ENSG00000SLC4A7	NBC2 NBC2	solute	carrier	protein-coding		
chr7-2295	8.922306	-0.26634	0.782075	-0.34056	0.733434	0.981636	chr7	22959048	22960909	+	0	NA	intron (Nintron (N	54152	NM_032581	84668	Hs.85603	NM_032581	ENSG00000FAM126A	DRCTNNB1 family	wiprotein-coding			
chr11-118	10.63152	0.24444	0.717762	0.340559	0.733436	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	-5972	NM_00134E	143941	Hs.653444NM_00108C	ENSG00000TTC36	HBP21	tetracy	protein-coding			
chr16-302	10.63152	0.24444	0.717762	0.340559	0.733436	0.981636	chr16	30241056	30245434	+	0	NA	intron (Nintron (N	2656	NM_00135E	440353	NM_001355401	NPIPBI2	-	nuclear	protein-coding			
chr7-5474	10.63152	0.24444	0.717762	0.340559	0.733436	0.981636	chr7	54748357	54748800	+	0	NA	Intergeni Intergeni	10633	NM_01430Z	23480	Hs.488282NM_01430Z	ENSG00000SEC61G	SSS1	SEC1	tr	protein-coding		
chr11-578	10.961596	-0.27377	0.80444	-0.34032	0.733616	0.981636	chr11	5703100	5703800	+	0	NA	intron (NAluY S N	13660	NM_006074	10346	Hs.501778NM_006074	ENSG00000TRIM22	GPSTAF50 tripartit	protein-coding				
chr2-5523	13.10179	-0.2227	0.654389	-0.34031	0.733621	0.981636	chr2	55233992	55236595	+	0	NA	TTS (NR_C TTS (NR_C	1129	NR_039624	1.01E+08	NR_039624	ENSG00000MIR4426	-	microRNA	ncRNA			
chr22-364	10.70594	0.248294	0.729616	0.340308	0.733625	0.981636	chr22	36475634	36476876	+	0	NA	intron (Nintron (N	5385	NM_01247Z	25828	Hs.211925NM_01247Z	ENSG00000TXN2	COXP29 D	thiorodopsin	protein-coding			
chr1-1567	10.67266	0.245646	0.72193	0.340264	0.733658	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (NAluSz S N	20386	NM_00597Z	5546	Hs.516948NM_00597Z	ENSG00000PRCC	RCP1 TPF	proline	protein-coding			
chr1-161	10.67266	0.245646	0.72193	0.340264	0.733658	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	exon (NM exon (NM	-2695	NM_00111Z	1E+08	Hs.720033NM_00111Z	ENSG00000TSTD1	KAT TST	thiosulfate	protein-coding			
chr19-347	10.67266	0.245646	0.72193	0.340264	0.733658	0.981636	chr19	34762380	34770777	+	0	NA	intron (Nintron (N	6637	NM_001007	148103	Hs.590961NM_001007	ENSG00000ZNF599	-	zinc	finger	protein-coding		
chr20-94	10.67266	0.245646	0.72193	0.340264	0.733658	0.981636	chr20	9436912	9439768	+	0	NA	intron (NAluYk4 S	-76018	NM_00119E	21411	Hs.22920	NM_012261	ENSG00000LAMP5	BAD-LAMP lysosomal	protein-coding			
chr4-1187	11.12811	0.239667	0.704429	0.340228	0.733685	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	20141	NM_020961	57721	Hs.596872NM_020961	ENSG00000METTL14	hMETTL14	methyltra	protein-coding			
chr5-1295	8.14257	0.288947	0.849479	0.340146	0.733746	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-139261	NR_12574E	1.04E+08	Hs.628635NR_12574E	ENSG00000ADAMTS19-	ADAMTS19	ncRNA				
chr4-676	10.16821	0.252374	0.742076	0.340091	0.733788	0.981636	chr4	67667894	67668493	+	0	NA	intron (Nintron (N	32962	NM_018227	55236	Hs.212774NM_018227	ENSG00000UBA6	E1-L2 MOF	ubiquitin	protein-coding			
chr3-197	19.30414	0.189126	0.556134	0.340073	0.733802	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (Nintron (N	4421	NR_00326E	220729	Hs.478854NR_00326E	ENSG00000LOC220729-	-	succinate	pseudo			
chr15-65	9.415195	-0.26381	0.776026	-0.33996	0.73389	0.981636	chr15	65674383	65674796	+	0	NA	intron (NAluJb S N	22347	NR_14575E	1.1E+08	NR_14575E	ENSG00000SNORD13E	-	small	nucsnRNA			
chr2-691	9.415195	-0.26381	0.776026	-0.33996	0.73389	0.981636	chr2	69155994	69156906	+	0	NA	intron (Nintron (N	52768	NR_03607Z	1E+08	NR_03607Z	ENSG00000MIR3126	mir-3126	microRNA	ncRNA			
chr10-105	10.10535	0.264742	0.77882	0.339927	0.733911	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	62066	NM_001351	22978	Hs.97439	NM_01222E	ENSG00000CNT5C2	GMP NT5B 5'	-nuclec	protein-coding		
chr1-225	11.1771	0.239503	0.704689	0.33987	0.733955	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	exon (NM exon (NM	6805	NM_15260E	163859	Hs.520192NM_15260E	ENSG00000SDE2	Clorf55 SDE2	telc	protein-coding			
chr13-327	11.1771	0.239503	0.704689	0.33987	0.733955	0.981636	chr13	32712541	32714879	+	0	NA	intron (NLM6 LINE	127258	NM_01503Z	23047	Hs.744901NM_01503Z	ENSG00000PDS5B	APRIN ASE	PDS5	cohc	protein-coding		
chr1-3754	8.881167	-0.26865	0.790559	-0.33982	0.733989	0.981636	chr1	37542504	37542786	+	0	NA	intron (NAluJb S N	11648	NM_02470C	79753	Hs.47232	NM_02470C	ENSG00000CSNIP1	PML1 PMRE	Smad	nucl	protein-coding	
chr13-41	8.881167	-0.26865	0.790559	-0.33982	0.733989	0.981636	chr13	41358834	41359278	+	0	NA	TTS (NM_C TTS (NM_C	-47018	NM_001354	9617	Hs.382177NM_004294	ENSG00000MTRF1	MRF1 MTTF	mitochon	protein-coding			
chr1-149	12.17814	0.229896	0.676897	0.339765	0.734033	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	TTS (NM_C TTS (NM_C	2687	NM_001277	400818	Hs.445082NM_001037	ENSG00000NBPF9	MBP1	NBPF	memt	protein-coding		
chr1-2271	9.84337	-0.25997	0.765403	-0.33965	0.73412	0.981636	chr1	2.27E+08	2.27E+08	+	0	NA	intron (NMIR S N E	171525	NM_020247	56997	Hs.118241NM_020247	ENSG00000COQ8A	ADCK3 ARC	coenzyme	protein-coding			
chr10-954	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr10	95256055	95265022	+	0	NA	intron (Nintron (N	30280	NM_02099Z	9124	Hs.368522NM_02099Z	ENSG00000PDL1M1	CLM1 CLF	PDZ	and I	protein-coding		
chr10-97	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr10	97429625	97434554	+	0	NA	intron (NAluJr S N	4127	NM_001317	5223	Hs.632918NM_00262E	ENSG00000NBPF9	HEL1-S-35 phosphog	protein-coding				
chr11-112	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	3075	NM_00108Z	55216	Hs.195062NM_01819E	ENSG00000CNKAPD1	C1lorf57	NKAP	dom	protein-coding		
chr12-51	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr12	51053741	51054707	+	0	NA	intron (Nintron (N	5897	NR_04502C	25875	Hs.655272NM_01541E	ENSG00000LETMD1	111001901 LETM1	don	protein-coding			
chr12-56	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr12	56663661	56662753	+	0	NA	intron (NAluSq2 S	19880	NR_10421E	10728	Hs.50425	NM_006601	ENSG00000PTGES3	P23 TEBP	prostagl	protein-coding		
chr12-123	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	8259	NM_001321	10959	Hs.733403NM_00681E	ENSG00000TMED2	P24A RNP2	transgl	protein-coding			
chr14-504	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr14	50455460	50457527	+	0	NA	intron (Nintron (N	-59195	NM_001367	8814	Hs.280881NM_00419E	ENSG00000CDKL1	KKIALRE Cyc	clin	de	protein-coding		
chr15-44	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr15	44645193	44648288	+	0	NA	intron (NLM1A15 L	16922	NM_00116C	80208	Hs.656273NM_025137	ENSG00000SPG11	ALS5 CMT2	SPG11	ves	protein-coding		
chr15-59	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr15	59650211	59652764	+	0	NA	intron (Nintron (N	5818	NM_00132C	2958	Hs.512934NM_00449Z	ENSG00000GTF2A2	HS18745 general	protein-coding				
chr17-62	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr17	62536135	62537891	+	0	NA	intron (Nintron (N	55900	NM_001284	11011	Hs.445078NM_00685E	ENSG00000TLK2	HsHPK MRE	tousled	l	protein-coding		
chr18-93	9.383763	-0.25799	0.759579	-0.33964	0.734125	0.981636	chr18	9337455	9346636	+	0	NA	intron (Nintron (N	7272	NM_02064E	57045	Hs.514688NM_02064E	ENSG00000TWSG1	TSG	twisted	protein-coding			
chr18-93	9.383763	-0.25799	0.759579	-0.3396																				

chr22-365	11.14382	0.23697	0.702388	0.337377	0.735833	0.981636	chr22	36510669	36527488	+	0	NA	intron (Nintron (N	10088	NM_003753	8664	Hs.	55682	NM_003753	ENSG00000EIF3D	EIF3S7 eukaryotic protein-coding
chr3-1251	11.14382	0.23697	0.702388	0.337377	0.735833	0.981636	chr3	1.26E+08	1.26E+08	+	0	NA	intron (NAluSq SIN	10966	NM_003794	8723	Hs.	50724E	NM_003794	ENSG00000SNX4	ATG24B sorting rprotein-coding
chr3-1254	12.25256	0.23701	0.692976	0.337242	0.735934	0.981636	chr3	1.25E+08	1.25E+08	+	0	NA	intron (NAluY SINE	64409	NM_003794	8723	Hs.	50724E	NM_003794	ENSG00000SNX4	ATG24B sorting rprotein-coding
chr1-1645	9.630484	0.25688	0.762104	0.337067	0.736066	0.981636	chr1	16455386	16457452	+	0	NA	intron (Nintron (N	-4529	NR_14721C	1.08E+08	Hs.	52831E	NR_14721C	ENSG00000LINC01772	- long intencRNA
chr1-4029	6.930484	0.25688	0.762104	0.337067	0.736066	0.981636	chr1	40291896	40294001	+	0	NA	exon (NM exon (NM	24838	NM_001852	1298	Hs.	41801E	NM_001852	ENSG00000COL9A2	DJ39G22.4 collagen protein-coding
chr12-489	6.930484	0.25688	0.762104	0.337067	0.736066	0.981636	chr12	48825032	48825700	+	0	NA	intron (Nintron (N	6870	NM_001206	784	Hs.	25071E	NM_00072E	ENSG00000CACNB3	CAB3 CAC calcium vprotein-coding
chr19-525	8.46085	-0.27529	0.816798	-0.33704	0.736087	0.981636	chr19	52388596	52389178	+	0	NA	TTS (NR_1TTS (NR_1	8870	NR_12534F	1.03E+08	Hs.	18868E	NR_12534F	ENSG00000ZNF528-AS	- ZNF528 arnRNA
chr8-5397	8.46085	-0.27529	0.816798	-0.33704	0.736087	0.981636	chr8	53978027	53978578	+	0	NA	TTS (NR_1TTS (NR_1	44146	NM_201437	6917	Hs.	49174E	NM_00675E	ENSG00000TCEA1	GTf25 SII transcript protein-coding
chr17-765	8.109289	0.285526	0.847636	0.336849	0.73623	0.981636	chr17	7695548	7695773	+	0	NA	intron (Nintron (N	7183	NM_001143	55135	Hs.	40831E	NM_018081	ENSG00000WRAP53	DKCB3 TC WD repeat protein-coding
chr17-152	8.914448	-0.26478	0.786048	-0.33685	0.736233	0.981636	chr17	15261777	15243472	+	0	NA	intron (NLM3 LINE	9072	NR_03988A	1.01E+08	Hs.	03988A	ENSG00000MIR4731	- microRNA ncRNA	
chr3-1414	8.914448	-0.26478	0.786048	-0.33685	0.736233	0.981636	chr3	1.41E+08	1.41E+08	+	0	NA	intron (NLM3 SINE	1994	NM_00135C	253461	Hs.	518301E	NM_15253E	ENSG00000ZBTB38	CIBZ PPP zinc fing protein-coding
chr17-406	9.853077	-0.25189	0.747831	-0.33682	0.73625	0.981636	chr17	4069122	4071598	+	0	NA	intron (NMIR3 SINE	72670	NM_015113	23140	Hs.	277624E	NM_015113	ENSG00000ZZEF1	ZZZ4 zinc fing protein-coding
chr10-732	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr10	73241362	73244431	+	0	NA	3' UTR (N3' UTR (N	4359	NM_01519C	23234	Hs.	408577E	NM_01519C	ENSG00000DNAJ9C	HDJ9C JDE DnaJ heat protein-coding
chr11-122	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	5924	NR_029671	406911	NR	029671	ENSG00000MIR125B1	MIRN125B1 microRNA ncRNA	
chr11-123	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	intron (NMLT1F2 LI	-53819	NM_006597	3312	Hs.	180414E	NM_006597	ENSG00000HSPA8	HEL-33 HE heat shock protein-coding
chr13-272	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr13	27253553	27260287	+	0	NA	TTS (NM_1TTS (NM_C	1519	NR_00257E	619499	Hs.	68971E	NR_00257E	ENSG00000SNORA27	ACN27 small nucsnRNA
chr16-667	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr16	66742426	66743826	+	0	NA	intron (NAluS2 SIN	8483	NM_006141	1783	Hs.	36906E	NM_006141	ENSG00000DYNCL1L2	DNCL2 LD dyallin cyprotein-coding
chr2-1135	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	-21367	NR_148507	440900	Hs.	66220E	NR_03412E	ENSG00000LINC019191	VIN Inc-? long intencRNA
chr3-1565	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	intron (NLA_C Mam	7050	NM_00130E	6747	Hs.	51834E	NM_007107	ENSG00000SSR3	TRAPG signal se protein-coding
chr4-379	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr4	1.38E+08	1.38E+08	+	0	NA	intron (Nintron (N	9586	NM_014331	23657	Hs.	390594E	NM_014331	ENSG00000CLC7A11	CCBR1 X solute c protein-coding
chr5-755	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr5	75560679	75560919	+	0	NA	intron (NLIPA7 LIN	-48818	NM_00113C	10087	Hs.	270437E	NM_00571E	ENSG00000CERT1	CERT CER ceramide protein-coding
chr7-1308	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	Intergeni THEIA LTF	14552	NR_02950C	407021	NR	02950C	ENSG00000MIR29A	MIRN29 MI microRNA ncRNA	
chr8-3907	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr8	39077149	39078891	+	0	NA	intron (NMLT1M LTF	-29509	NM_001313	203102	Hs.	52154E	NM_145004	ENSG00000ADAM32	- ADAM meta protein-coding
chr8-720	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr8	72060632	72069149	+	0	NA	intron (Nintron (N	10698	NM_007332	8989	Hs.	71681E	NM_007332	ENSG00000TRPA1	ANKMT1 FE transient protein-coding
chr8-998	9.375905	-0.25656	0.761939	-0.33672	0.73633	0.981636	chr8	99885300	99887546	+	0	NA	intron (NLM2B LIN	7284	NM_004374	1345	Hs.	35187E	NM_004374	ENSG00000COX6C	- cytochron protein-coding
chr16-281	11.64827	0.231441	0.68784	0.336475	0.736513	0.981636	chr16	28155455	28156577	+	0	NA	intron (Nintron (N	55949	NM_015171	23214	Hs.	46046E	NM_015171	ENSG00000XPO6	EXP6 RANE exportin protein-coding
chr17-165	11.64827	0.231441	0.68784	0.336475	0.736513	0.981636	chr17	16504547	16507432	+	0	NA	intron (Nintron (N	-9078	NM_03143C	83547	Hs.	534497E	NM_03143C	ENSG00000RILP	PIP10141 Rab interprotein-coding
chr17-167	11.64827	0.231441	0.68784	0.336475	0.736513	0.981636	chr17	16703000	16834479	+	0	NA	intron (Nintron (N	7978	NM_00644E	10594	Hs.	18136E	NM_00644E	ENSG00000PRPF8	HPRP8 PRF pre-mRNA protein-coding
chr20-358	11.64827	0.231441	0.68784	0.336475	0.736513	0.981636	chr20	35842343	35844420	+	0	NA	intron (NAluSx3 SI	71366	NM_01643C	51230	Hs.	517044E	NM_01643C	ENSG00000PHF20	AROF10 PHD finger protein-coding
chr5-3938	11.64827	0.231441	0.68784	0.336475	0.736513	0.981636	chr5	39385498	39394645	+	0	NA	intron (Nintron (N	-25576	NM_001737	735	Hs.	65444E	NM_001737	ENSG00000C	CARM15 5C compleher protein-coding
chr6-2597	11.64827	0.231441	0.68784	0.336475	0.736513	0.981636	chr6	25972338	25977333	+	0	NA	intron (Nintron (N	12033	NM_00635E	10475	Hs.	584851E	NM_00635E	ENSG00000TRIM38	RNF15 ROF tripartit protein-coding
chr19-405	9.077041	0.265156	0.788075	0.33646	0.736524	0.981636	chr19	40320780	40321070	+	0	NA	TTS (NM_1TTS (NM_C	27472	NR_046202	126526	Hs.	631557E	NM_17883C	ENSG00000C19orf47	- chromoson protein-coding
chr16-717	9.581487	0.257096	0.764152	0.336446	0.736535	0.981636	chr16	71742564	71742778	+	0	NA	intron (Nintron (N	15816	NR_00305E	692111	NR	00305E	ENSG00000SNORD71	HBI1-239 small nucsnRNA	
chr6-1252	9.581487	0.257096	0.764152	0.336446	0.736535	0.981636	chr6	1.25E+08	1.25E+08	+	0	NA	intron (NHALIM8 LI	16581	NM_01606E	51020	Hs.	3282E	NM_01606E	ENSG00000HDDC2	C6orf74 CHD domair protein-coding
chr2-1124	4.436284	0.364958	1.085765	0.33613	0.736773	0.981636	chr2	11242048	11242744	+	0	NA	intron (Nintron (N	86929	NM_00128E	130814	Hs.	27441E	NM_152391	ENSG00000CLC66A3	C2orf22 f solute c protein-coding
chr5-1771	4.436284	0.364958	1.085765	0.33613	0.736773	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (NAluYh3 SI	46874	NM_00136E	64324	Hs.	106861E	NM_02245E	ENSG00000NSD1	ARA267 K nuclear rprotein-coding
chr3-1884	6.152615	-0.31299	0.93231	-0.33571	0.737089	0.981636	chr3	1.88E+08	1.88E+08	+	0	NA	intron (Nintron (N	126152	NR_04662E	1.01E+08	Hs.	67499E	NR_04662E	ENSG00000LPP-AS1	- LPP antisncRNA
chr5-1504	6.152615	-0.31299	0.93231	-0.33571	0.737089	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	TTS (NM_1TTS (NM_C	12258	NR_157074	972	Hs.	43656E	NM_00435E	ENSG00000CD74	DHLAG HLA CD74 molc protein-coding
chr4-1234	4.966154	0.347077	1.034051	0.335648	0.737137	0.981636	chr4	1.23E+08	1.23E+08	+	0	NA	intron (NMLT2B3 LI	129654	NM_00134E	166378	Hs.	70964E	NM_145207	ENSG00000SPATA5	AFG2 EHL spermatog protein-coding
chr17-406	6.160473	-0.31526	0.939662	-0.3355	0.737245	0.981636	chr17	40019772	40020360	+	0	NA	intron (Nintron (N	4626	NM_17221E	1440	Hs.	2233	NM_00075E	ENSG00000CSF3	C17orf33 colony st protein-coding
chr19-465	6.160473	-0.31526	0.939662	-0.3355	0.737245	0.981636	chr19	4697533	4698102	+	0	NA	intron (NMLT1C LTF	18535	NM_00124E	1E+08	Hs.	67813E	NM_001242901	DPP9-AS1	- DPP9 anti protein-coding
chr17-81	9.126038	0.26483	0.789383	0.33483	0.737255	0.981636	chr17	81249618	81249937	+	0	NA	intron (Nintron (N	9863	NR_14842E	28184	Hs.	35654E	NM_00108E	ENSG00000NDUFAF8	C17orf89 NADH ubic protein-coding
chr21-394	12.15271	0.22638	0.675297	0.33523	0.737451	0.981636	chr21	39405330	39406823	+	0	NA	exon (NM exon (NM	18313	NR_14661E	7485	Hs.	19830E	NM_004627	ENSG00000GET1	CHD5 WRB guided er protein-coding
chr9-324	12.15271	0.22638	0.675297	0.33523	0.737451	0.981636	chr9	32405210	32412469	+	0	NA	intron (Nintron (N	24196	NM_00136E	48	Hs.	56722E	NM_002197	ENSG00000AC01	ACONS HEL aconitase protein-coding
chr15-422	9.424902	-0.25574	0.763089	-0.33514	0.737519	0.981636	chr15	42251536	42253218	+	0	NA	intron (NLIPA6 LIN	21056	NM_015497	259663	Hs.	51113E	NM_015497	ENSG00000TMEM87A	- transmemt protein-coding
chr20-455	9.424902	-0.25574	0.763089	-0.33514	0.737519	0.981636	chr20	45938728	45940132	+	0	NA	intron (NLA2B LINE	4747	NM_022104	63935	Hs.	47285E	NM_022104	ENSG00000PCIP1	C20orf67 PDX1 C-? protein-coding
chr3-9967	9.424902	-0.25574	0.763089	-0.33514	0.737519	0.981636	chr3	9967539	9969524	+	0	NA	intron (NLM1B7 LIN	-16116	NM_00131E	285368	Hs.	598147E	NM_207351	ENSG00000PRRT3	- proline r protein-coding
chr3-191	10.09379	0.24832	0.741176	0.335035	0.737599	0.981636	chr3	1.91E+08	1.91E+08	+	0	NA	intron (Nintron (N	-31922	NM_19815E	257313	Hs.	51849E	NM_19815E	ENSG00000UTS2B	U2B URP t urotensin protein-coding
chr14-501	6.68147	-0.2253	0.672861	-0.33484	0.737743	0.981636	chr14	50112939	50113138	+	0	NA	intron (NAluSg SIN	3534	NR_04973E	79609	Hs.	558541E	NM_02455E	ENSG00000VCPKMT	C14orf138



chr8-1124	11.61499	0.228996	0.690061	0.331849	0.740003	0.981636	chr8	71841675	71842550	+	0 NA	3' UTR (N3' UTR (N	-1011 NR_033652	1E+08 Hs. 137674NR_033651	ENSG000000MSC-AS1	-	MSC antisenseRNA	
chr10-876	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr10	87683821	87684118	+	0 NA	intron (NAluJr SIN	24091 NM_001015	9060 Hs. 524491NM_004676	ENSG000000PAPSS2	-	ATPSK2 BC3'-phospho protein-coding	
chr13-95	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr13	95076644	95077353	+	0 NA	intron (NAluJo SIN	116957 NR_047487	1.01E+08 Hs. 48706 NR_047487	ENSG000000CLINCO0557-	-	long introncRNA	
chr17-55	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr17	5566552	5567304	+	0 NA	intron (NLM1A1 LIN	17581 NM_033004	22861 Hs. 652277NM_014922	ENSG000000NLRP1	-	AIADK CAF NLR fam1 protein-coding	
chr2-158	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr2	159E+08	1.59E+08	+	0 NA	intron (Nintron (N	56889 NR_135242	8008 Hs. 630724NR_135242	ENSG000000PKP4-AS1	-	PKP4 anticRNA	
chr2-177	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr2	1.77E+08	1.77E+08	+	0 NA	intron (NLM5 LINE	40364 NM_003655	8540 Hs. 516545NM_003655	ENSG000000CAGPS	-	ADAP-S AI alkylglyc protein-coding	
chr20-414	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr20	41486441	41486790	+	0 NA	intron (Nintron (N	-191797 NR_052844	90187 Hs. 726522NM_052844	ENSG000000EMILIN3	-	C20orf13 elastin n protein-coding	
chr3-157	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr3	15740607	15742136	+	0 NA	intron (NL3 LINE C	15176 NM_001195	23243 Hs. 335235NM_015199	ENSG000000ANKRD28	-	PITK PPP1lankyrin r protein-coding	
chr3-130	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr3	1.31E+08	1.31E+08	+	0 NA	intron (NLTR87 LTF	65871 NM_001001	27032 Hs. 584884NM_014382	ENSG000000ATP2C1	-	ATP2C1A EATPase s e protein-coding	
chr3-142	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (NAluSq2 SI	45643 NM_001282	54464 Hs. 435103NM_019001	ENSG000000XRN1	-	1-Sep 5'-3' exc protein-coding	
chr5-35	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr5	356127	356889	+	0 NA	intron (NCPg	52332 NM_020731	57491 Hs. 50823	NM_020731	ENSG000000AHR	-	AHH AHH aryl-hyd protein-coding
chr6-87	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr6	87525626	87526531	+	0 NA	intron (NLM1A7 LIN	53104 NM_006416	10559 Hs. 423163NM_006416	ENSG000000SLC35A1	-	CDG2F CMF solute c e protein-coding	
chr6-159	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr6	1.6E+08	1.6E+08	+	0 NA	intron (NLM1E7 LIN	7933 NR_002966	677806 Hs. 689705NR_002966	ENSG000000SNORA20	-	ACA20 small nucRNA	
chr9-12	5.667584	-0.32405	0.977239	-0.3316	0.740191	0.981636	chr9	1.22E+08	1.22E+08	+	0 NA	intron (NLM1TIK LTF	8355 NM_014222	4702 Hs. 495035NM_014222	ENSG000000NDUF8	-	CI-19KD CNADH:ubiq protein-coding	
chr13-72	5.496024	0.333189	1.005769	0.331278	0.740435	0.981636	chr13	72833105	72834020	+	0 NA	intron (NLM1PA7 LIN	51429 NR_146205	10464 Hs. 441922NM_006344	ENSG000000PIBF1	-	C13orf24 progester protein-coding	
chr10-72	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr10	72235061	72235377	+	0 NA	non-codirnon-codir	-18085 NR_045564	51008 Hs. 500007NM_015947	ENSG000000ASCC1	-	ASC1p50 cactivat r protein-coding	
chr16-24	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr16	24917595	24918651	+	0 NA	IntergeniIntergeni	71892 NM_052944	115584 Hs. 164115NM_052944	ENSG000000CLSC5A11	-	KST1 RKST1 solute c e protein-coding	
chr17-37	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr17	37472254	37473716	+	0 NA	intron (NAluJr SIN	-16906 NM_007026	11072 Hs. 91448 NM_007026	ENSG000000DUSP14	-	MKP-L MKF dual spec protein-coding	
chr2-85	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr2	85759126	85759667	+	0 NA	intron (Nintron (N	5405 NM_032827	84913 Hs. 135566NM_032827	ENSG000000ATOH8	-	HATH6 bHL atonal b protein-coding	
chr2-186	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr2	1.86E+08	1.86E+08	+	0 NA	intron (Nintron (N	11537 NM_018471	55854 Hs. 74118CNM_018471	ENSG000000ZC3H15	-	HTO10 LEF zinc b protein-coding	
chr3-48	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr3	48173831	48176013	+	0 NA	intron (Nintron (N	13495 NM_001785	993 Hs. 437705NM_001785	ENSG000000CDC25A	-	CDC25A2 cell divi protein-coding	
chr4-73	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr4	73122681	73123420	+	0 NA	intron (Nintron (N	-53291 NM_001300	285521 Hs. 356697NM_173827	ENSG000000COX18	-	COX18HS cytochron protein-coding	
chr8-10	6.136899	-0.30872	0.932146	-0.33119	0.740498	0.981636	chr8	1.03E+08	1.03E+08	+	0 NA	promoter-promoter-	-437 NR_145795	1.1E+08 NR_145795	SNORD173	-	small nucRNA	
chr22-40	9.638342	0.255124	0.770392	0.331161	0.740523	0.981636	chr22	40431079	40431301	+	0 NA	intron (Nintron (N	32250 NM_001282	57591 Hs. 654688NM_020831	ENSG000000MRFTA	-	BSAC MAL myocardir protein-coding	
chr9-16	9.638342	0.255124	0.770392	0.331161	0.740523	0.981636	chr9	16552441	16552754	+	0 NA	exon (NM exon (NM	-174217 NR_151723	1.11E+08 Hs. 609215NR_151723	ENSG000000BNC2-AS1	-	BNC2 anticRNA	
chr3-98	9.707798	-0.25676	0.775374	-0.33114	0.740538	0.981636	chr3	98580586	98580785	+	0 NA	exon (NM exon (NM	12926 NM_000097	1371 Hs. 476982NM_000097	ENSG000000CPOX	-	COX CPO copropor r protein-coding	
chr19-44	9.74773	-0.26081	0.788192	-0.3309	0.740724	0.981636	chr19	44754846	44755464	+	0 NA	intron (Nintron (N	-3502 NR_107052	1.02E+08 NR_107052	ENSG000000MIR8085	-	hsa-mir-5 microRNA ncRNA	
chr1-180	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr1	1800957	1805747	+	0 NA	intron (NAluJr SIN	-23321 NM_001353	65220 Hs. 654792NM_023018	ENSG000000NADK	-	dJ283E3.1NAD kinase protein-coding	
chr11-37	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr11	3729901	3731993	+	0 NA	intron (NLM1E4a LI	-59565 NM_001303	57053 Hs. 732805NM_020402	ENSG000000CHRNA10	-	choliner g protein-coding	
chr11-37	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr11	3776575	3779688	+	0 NA	intron (NAluY SINE	19442 NR_157591	4928 Hs. 524755NM_005387	ENSG000000NUP98	-	ADIR2 NUF nucleor protein-coding	
chr11-47	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr11	47716012	47726215	+	0 NA	intron (NAluY SINE	-5744 NM_024783	79841 Hs. 147377NM_024783	ENSG000000AGBL2	-	CCP2 ATP/GTP t protein-coding	
chr18-7	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr18	76894006	76898232	+	0 NA	intron (Nintron (N	71959 NM_007345	7776 Hs. 719137NM_007345	ENSG000000ZNF236	-	ZNF236A zinc fing protein-coding	
chr19-45	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr19	45522491	4552833	+	0 NA	intron (NAluJr4 SI	17683 NM_003337	7408 Hs. 515466NM_003337	ENSG000000VASP	-	vasodilat protein-coding	
chr2-19	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr2	1.91E+08	1.91E+08	+	0 NA	intron (NL2a LINE	119435 NM_001161	4430 Hs. 439622NM_012222	ENSG000000MYO1B	-	MMI-alpha myosin II protein-coding	
chr3-12	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	-23483 NR_046622	1.01E+08 Hs. 667315NR_046622	ENSG000000MYLK-AS2	-	MYLK anticRNA	
chr5-12	9.870643	-0.24562	0.742384	-0.33086	0.740754	0.981636	chr5	1.27E+08	1.27E+08	+	0 NA	intron (N (A)n Simp	-13323 NM_020740	389320 Hs. 177983NM_207405	ENSG000000TEX43	-	C5orf48 12testis e protein-coding	
chr1-26	9.870643	-0.33025	0.998895	-0.33061	0.740938	0.981636	chr1	26844336	26844602	+	0 NA	intron (NLM1E3a LI	17781 NM_032283	84243 Hs. 52371CNM_032283	ENSG000000ZDHC18	-	DHHC-18 Zinc fing protein-coding	
chr13-3	9.870643	-0.33025	0.998895	-0.33061	0.740938	0.981636	chr13	32042850	32043057	+	0 NA	intron (Nintron (N	11179 NM_023037	10129 Hs. 507666NM_023037	ENSG000000FRY	-	LINC0A73 FRY micr protein-coding	
chr3-19	13.62195	-0.2125	0.642801	-0.33059	0.740957	0.981636	chr3	1.96E+08	1.96E+08	+	0 NA	intron (NLM1C5a LI	1430 NR_122105	440993 Hs. 708995NM_01013714	MIR570HG	-	LINC00966 MIR570 hncRNA	
chr2-10	11.62284	0.227707	0.689129	0.330427	0.741077	0.981636	chr2	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	14035 NM_001318	2274 Hs. 443687NM_001455	ENSG000000FHL2	-	AAG11 DR4 four and protein-coding	
chr6-3	10.61395	0.238986	0.72315	0.330355	0.741132	0.981636	chr6	36059764	36060111	+	0 NA	intron (Nintron (N	32133 NM_139013	1432 Hs. 485233NM_001318	ENSG000000MAPK14	-	CSBP CSBF mitogen-e protein-coding	
chr3-27	10.61395	-0.31472	0.953075	-0.33022	0.741233	0.981636	chr3	27472641	27473528	+	0 NA	intron (NAluSx SIN	11300 NM_001321	9497 Hs. 250072NM_003615	ENSG000000SLCAA7	-	NBC2 NBC1 solute c e protein-coding	
chr8-1	10.61395	-0.31472	0.953075	-0.33022	0.741233	0.981636	chr8	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	-14718 NR_031611	1E+08 NR_031611	ENSG000000MIR1206	-	MIRN1206 microRNA ncRNA	
chr5-6	10.61395	-0.31472	0.953075	-0.33022	0.741233	0.981636	chr5	61533809	61534877	+	0 NA	intron (Nintron (N	-103402 NR_161251	285668 Hs. 683866NR_126522	ENSG000000C5orf64	-	chromosomncRNA	
chr1-150	9.829504	-0.2478	0.750843	-0.33003	0.74138	0.981636	chr1	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	4084 NM_001304	51177 Hs. 438822NM_016274	ENSG000000PLEKH01	-	CKIP-1 Ck pleckstri protein-coding	
chr8-10	8.411852	-0.27582	0.835971	-0.32994	0.741445	0.981636	chr8	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	25743 NM_015420	25879 Hs. 532265NM_015420	ENSG000000DCAF13	-	GM83 HSPCDB1 and protein-coding	
chr1-17	12.12729	0.22279	0.67554	0.329795	0.741555	0.981636	chr1	1.72E+08	1.72E+08	+	0 NA	exon (NM exon (NM	-53143 NM_001368	1.11E+08 NM_001368164	MYOCOS	-	myocilin protein-coding	
chr15-6	12.12729	0.22279	0.67554	0.329795	0.741555	0.981636	chr15	65876993	65880779	+	0 NA	intron (Nintron (N	9395 NM_001206	8766 Hs. 321541NM_004665	ENSG000000CRAB11A	-	YL8 RAB11A, n protein-coding	
chr12-6	9.401329	-0.25146	0.762514	-0.32977	0.741571	0.981636	chr12	6457896	6458095	+	0 NA	intron (Nintron (N	5953 NM_001351	55080 Hs. 504597NM_018005	ENSG00000			

chr1-2036	12.13515	-0.22155	0.675762	0.327852	0.743024	0.981636	chr1	2.04E+08	2.04E+08	+	0	NA	intron (Nintron (N	-26505 NM_003094	6635 Hs. 334612NM_003094	ENSG000003NRPE	HYPT11 SM small nucprotein-coding
chr1-2175	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr1	21732289	21732940	+	0	NA	intron (NCharlie2E	50535 NM_00135C	84196 Hs. 467524NM_03223E	ENSG00000USP48	RAP1GA1 ubiquitin protein-coding
chr1-3547	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr1	35473722	35474929	+	0	NA	intron (NMIRB SINE	83078 NM_024874	79932 Hs. 456507NM_024874	ENSG00000KIAA03191	AAVR AAVF KIAA0319 protein-coding
chr11-434	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr11	43452722	43454470	+	0	NA	intron (NLIM8 LINE	94676 NM_01825E	55761 Hs. 191188NM_01825E	ENSG00000TTC17	- tetraatric protein-coding
chr18-205	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr18	20957449	20958723	+	0	NA	intron (NLIME2 LIN	153727 NM_00540E	6093 Hs. 306307NM_00540E	ENSG00000ROCK1	P16OROCK Rho assoc protein-coding
chr2-4235	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr2	42335870	42336353	+	0	NA	intron (Nintron (N	23927 NR_13494E	9167 Hs. 339635NM_00471E	ENSG00000COX7A2L	COX7AR CC cytochron protein-coding
chr2-1215	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr2	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-6436 NR_02334E	1E+08 Hs. 689635NR_02334E	ENSG00000RNU4ATAC	MOPD1 RFM RNA, 4eat snRNA
chr2-1827	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr2	1.83E+08	1.83E+08	+	0	NA	intron (NLIPA6 LIN	53480 NR_073367	54431 Hs. 516632NM_018981	ENSG00000DNAJC10	ERJ5 JPE DnaJ heat protein-coding
chr3-475	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr3	47505699	47507116	+	0	NA	intron (NMER11C LI	6938 NM_00136E	54859 Hs. 31110CNM_01771E	ENSG00000CELP6	C3orf75 Telongator protein-coding
chr3-4935	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr3	49394119	49394951	+	0	NA	intron (NALuSz SIN	17441 NM_00131E	387 Hs. 247077NM_001664	ENSG00000RHOA	ARH12 ARF ras homol protein-coding
chr3-1305	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr3	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	60457 NM_01406E	28990 Hs. 100878NM_01406E	ENSG00000ASTE1	HT001 asteroid protein-coding
chr5-131E	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr5	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	-12165 NM_001164	51735 Hs. 483325NM_01634C	ENSG00000CRAPGEF6	KIA0011B Rap guani protein-coding
chr6-875E	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr6	87584801	87585546	+	0	NA	non-codiron-codir	4814 NM_02032E	57038 Hs. 485914NM_02032E	ENSG00000RARS2	ArgRS DAL arginyl-t protein-coding
chr6-8975	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr6	89730399	89732480	+	0	NA	intron (NLIPA8 LIN	8835 NM_01461E	23195 Hs. 459666NM_01461E	ENSG00000MDN1	ReagL midasin f protein-coding
chr8-474	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr8	47400952	47401842	+	0	NA	intron (NLIPA5 LIN	140459 NM_00108C	23514 Hs. 381055NM_00108C	ENSG00000SPIDR	KIAA0146 scaffold protein-coding
chr8-1095	5.700866	-0.31798	0.969939	-0.32784	0.743035	0.981636	chr8	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	7274 NR_03647E	56943 Hs. 492555NM_02018E	ENSG00000ENY2	DC6 Susi ENY2 trar protein-coding
chr15-664	4.948588	0.335699	1.02511	0.327476	0.743308	0.981636	chr15	66446899	66447880	+	0	NA	intron (Nintron (N	49645 NR_039737	1.01E+08 NR_039737	ENSG00000MIR4512	- microRNA ncRNA
chr7-6674	4.948588	0.335699	1.02511	0.327476	0.743308	0.981636	chr7	66721015	66722288	+	0	NA	intron (NMLT1D LTF	-19082 NM_001367	27342 Hs. 530052NM_014504	ENSG00000RABGEF1	RABEX5 RAB guani protein-coding
chr9-9634	4.948588	0.335699	1.02511	0.327476	0.743308	0.981636	chr9	96348628	96349681	+	0	NA	intron (NLTRA8B LI	34556 NR_104627	11046 Hs. 494556NM_007001	ENSG00000SLC35D2	HFRFC1 SQV solute c protein-coding
chr9-1302	4.948588	0.335699	1.02511	0.327476	0.743308	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	3175 NM_00112E	23413 Hs. 642944NM_01428E	ENSG00000NCNS1	FLU1 FRE neuronal protein-coding
chr1-1101	4.63959	0.21708	0.663008	0.327416	0.743353	0.981636	chr1	11013689	11023851	+	0	NA	exon (NM exon (NM	6148 NM_00737E	23435 Hs. 300624NM_00737E	ENSG00000TARDBP	ALU10 TDF TAR DNA t protein-coding
chr1-2306	6.193754	-0.30966	0.945917	-0.32737	0.743389	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	intron (Nintron (N	34476 NM_00002E	183 Hs. 19383 NM_00002E	ENSG00000AGT	ANHU SERF angiotens protein-coding
chr18-797	5.478458	0.32224	0.984474	0.327322	0.743424	0.981636	chr18	79722520	79723412	+	0	NA	intron (Nintron (N	41536 NM_00120E	9150 Hs. 46549CNM_00471E	ENSG00000CTDP1	CCFDN CFCD2 phosph protein-coding
chr19-185	5.478458	0.32224	0.984474	0.327322	0.743424	0.981636	chr19	18312905	18315558	+	0	NA	intron (NALuJo SIN	7845 NM_012321	25804 Hs. 512555NM_012321	ENSG00000LSM4	GRP1 YER11LSM4 homc protein-coding
chr3-1264	5.478458	0.32224	0.984474	0.327322	0.743424	0.981636	chr3	1.26E+08	1.26E+08	+	0	NA	intron (Nintron (N	11886 NM_02511E	79364 Hs. 440045NM_02511E	ENSG00000ZXDC	ZXDL ZXD famil protein-coding
chr7-128	5.478458	0.32224	0.984474	0.327322	0.743424	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	7000 NR_030324	693178 NR_030324	ENSG00000MIR593	MIRN593 t microRNA ncRNA
chr3-1974	4.752529	-0.36986	1.13028	-0.32723	0.743497	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (Nintron (N	57119 NM_00136E	84859 Hs. 518414NM_03277E	ENSG00000LRCH3	- leucine r protein-coding
chr19-458	8.939872	-0.25919	0.792187	-0.32719	0.743525	0.981636	chr19	45824779	45825182	+	0	NA	intron (Nintron (N	-9672 NM_03078E	81492 Hs. 146544NM_03078E	ENSG00000RSPH6A	RSHL1 RSF radial s protein-coding
chr6-8751	8.939872	-0.25919	0.792187	-0.32719	0.743525	0.981636	chr6	87510141	87512114	+	0	NA	intron (Nintron (N	38153 NM_00641E	10559 Hs. 423162NM_00641E	ENSG00000SLC35A1	CDGF2 CF solute c protein-coding
chr9-9764	6.133996	-0.24503	0.735268	-0.32713	0.743568	0.981636	chr9	97647054	97648266	+	0	NA	intron (Nintron (N	14064 NM_00248E	4686 Hs. 595666NM_00248E	ENSG00000NCBP1	CBP80 NCF nuclec c protein-coding
chr14-954	4.989728	0.338018	1.033875	0.326943	0.743711	0.981636	chr14	95466829	95467686	+	0	NA	intron (NMIRB SINE	8578 NM_00136E	161176 Hs. 41502 NM_02463E	ENSG00000CYNE3	C14orf13 spectrin protein-coding
chr7-6804	4.989728	0.338018	1.033875	0.326943	0.743711	0.981636	chr7	6804507	6806148	+	0	NA	intron (Nintron (N	20968 NM_198097	221960 Hs. 567775NM_198097	ENSG00000CCZ1B	SP7orf28A CCZ1 homc protein-coding
chr9-1101	14.06769	-0.20695	0.633509	-0.32668	0.743912	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (NALuJb SIN	-61809 NM_00128E	255220 Hs. 143766NM_00100E	ENSG00000TXND8	CPTXorf3 S thioeredox protein-coding
chr2-2015	12.68073	0.21817	0.668224	0.326492	0.744052	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	exon (NM exon (NM	-23228 NM_13916E	130540 Hs. 107944NM_13916E	ENSG00000FLACC1	ALS2CR12 flagellun protein-coding
chr11-171	6.129041	-0.30665	0.93934	-0.32646	0.74408	0.981636	chr11	17119135	17119987	+	0	NA	intron (Nintron (N	-41894 NM_001017	6207 Hs. 446588NM_001017	ENSG00000RPS13	S13 ribosomal protein-coding
chr4-3986	6.129041	-0.30665	0.93934	-0.32646	0.74408	0.981636	chr4	39878279	39879102	+	0	NA	intron (Nintron (N	99221 NM_00110C	23244 Hs. 331431NM_01520C	ENSG00000PDS5A	P1G54 SCC PDS5 cohe protein-coding
chr6-8395	6.129041	-0.30665	0.93934	-0.32646	0.74408	0.981636	chr6	83936555	83937226	+	0	NA	intron (Nintron (N	77201 NM_01623C	51167 Hs. 5741 NM_01623C	ENSG00000CYB5R4	NCB50R ct cytochron protein-coding
chr9-9591	6.129041	-0.30665	0.93934	-0.32646	0.74408	0.981636	chr9	95918602	95919024	+	0	NA	intron (Nintron (N	42804 NM_00101C	375748 Hs. 432364NM_020207	ENSG00000ERCC6L2	BMF52 C9c ERCC exciprotein-coding
chr1-7975	8.445134	-0.27158	0.831986	-0.32643	0.744099	0.981636	chr1	79757635	7979844	+	0	NA	intron (NALuJr4 SI	18028 NM_00726E	11315 Hs. 41964CNM_00726E	ENSG00000PARK7	DJ-1 DJ1 Parkinson protein-coding
chr14-512	5.4706	0.325193	0.996412	0.326364	0.744149	0.981636	chr14	51245676	51246622	+	0	NA	intron (Nintron (N	5902 NM_03075E	81542 Hs. 125221NM_03075E	ENSG00000TMX1	PDIA11 TV thioeredox protein-coding
chr9-124	9.424268	-0.24919	0.764279	-0.32604	0.744392	0.981636	chr9	1.24E+08	1.24E+08	+	0	NA	intron (NLIME3 LIN	-15526 NR_02740E	1E+08 Hs. 65498CNR_02740E	LOC10012E	- uncharactncRNA
chr1-1185	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr1	11838617	11839875	+	0	NA	intron (Nintron (N	-1073 NR_03780E	1E+08 Hs. 710015NR_03780E	NPPA-AS1	NPPA-AS1 NPPA antncRNA
chr3-1695	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (NALuY SINE	11232 NM_00326E	7095 Hs. 744855NM_00326E	ENSG00000SEC62	Dtrp1 HTF SEC62 hon protein-coding
chr5-692E	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr5	69267568	69270525	+	0	NA	intron (NALuS6 SI	34160 NM_00179E	1022 Hs. 184298NM_00179E	ENSG00000CDK7	CAC CAC1 cyclin d protein-coding
chr5-1285	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	17774 NM_00104E	6558 Hs. 162588NM_00104E	ENSG00000SLC12A2	BASC BASC2 solute c protein-coding
chr5-1285	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (NALuS2 SI	193491 NM_00199E	2201 Hs. 519294NM_00199E	ENSG00000PBN2	CCA DA9 Fibrillin protein-coding
chr6-7905	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr6	79052778	79053588	+	0	NA	intron (NALuSz SIN	25071 NM_017934	55023 Hs. 511817NM_017934	ENSG00000PHIP	BRWD2 DC pleckstri protein-coding
chr7-7765	9.903925	-0.24216	0.742837	-0.32599	0.74443	0.981636	chr7	77620672	77622729	+	0	NA	intron (NTigger3b	74565 NR_134254	1.01E+08 Hs. 72451 NR_038361	ENSG00000CAPTR	RSBN1L-AS1 u-medicncRNA
chr2-1137	10.57821	0.237562	0.728978	0.325884	0.744512	0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	non-codiron-codir	8817 NR_038942	1.01E+08 NR_038942	ENSG00000MIR4782	- microRNA ncRNA
chr22-505	5.486316	0.319471	0.980716	0.325752	0.744612	0.981636	chr22	50303530	50304360	+	0	NA	intron (Nintron (N	3701 NM_012401	23654 Hs. 3989 NM_012401	ENSG00000PLXNB2	MM1 Nbla cplexin B2 protein-coding
chr5-1105	5.486316	0.319471	0.980716	0.325752	0.744612	0.981636	chr5	71059127	71059675	+	0	NA	intron (NALuSc SIN	8251 NM_00109E	728340 Hs. 191355NM_00109E	ENSG00000GTF2H2C	GTF2H2C_2 GTF2H2 f2 protein-coding
chr15-797	25.23823	0.16098	0.49419	0.325744	0.744618	0.981636	chr15	79775509	79779864	+	0	NA	IntergeniALR/Alpha	-505058 NR_03883E	646096 Hs. 448789NR_03883E	ENSG00000CHEK2P2	- checkpoi pseudo
chr1-9995	9.821646	-0.24646	0.756763	-0.32568	0.744669	0.981636	chr1	99991598	99992028	+	0	NA	intron (NALuSc SIN	21296 NM			



chr3-9452 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr3	9452893	9458812	+ 0 NA	intron (Nintron (N	58152 NM_00108C	55209 Hs. 288164NM_018187	ENSG000000CSETD5	-	SET domain protein-coding
chr3-1837 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr3	1.84E+08	1.84E+08	+ 0 NA	intron (NLMB7 LIN	23565 NR_046727	1.01E+08 NR_046727	YEATS2-AS-	YEATS2 arncRNA	
chr4-7701 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr4	77014127	77016297	+ 0 NA	intron (NMIR3 SINE	59698 NM_00134E	10983 Hs. 518827NM_00683E	ENSG000000CCNI	CCNI1 CYC cyclin I protein-coding	
chr5-2544 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr5	254427	262975	+ 0 NA	IntergeniCpG	12823 NR_10461E	1.02E+08 Hs. 36832ENR_104613	HRAT5	heart tiscrRNA	
chr5-1711 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr5	1.71E+08	1.71E+08	+ 0 NA	intron (NAluSx SIN	13319 NM_00135E	4869 Hs. 55755ENR_00252C	ENSG000000NP1M	B23 NPM nucleoph protein-coding	
chr6-404 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr6	4040106	4045177	+ 0 NA	intron (Nintron (N	21341 NM_00391E	8899 Hs. 159014NM_00391E	ENSG000000PRPF4B	PR4H PRP4pre-mRNA protein-coding	
chr7-8734 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr7	87348710	87355828	+ 0 NA	intron (NLOR1-int)	6605 NM_00114E	54677 Hs. 12503ENR_021151	ENSG000000CROT	COT carnitine protein-coding	
chr7-1124 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr7	1.12E+08	1.12E+08	+ 0 NA	intron (Nintron (N	12026 NM_001134	286006 Hs. 39618ENR_182597	ENSG000000LSMEM1	C7orf53 leucine protein-coding	
chr7-1395 9.896067	-0.2408	0.741454	-0.32477	0.745354	0.981636	chr7	1.4E+08	1.4E+08	+ 0 NA	intron (Nintron (N	80380 NM_00108C	154790 Hs. 57806 NM_00108C	ENSG000000CLEC2L	- C-type Ie protein-coding	
chr11-107 10.32244	-0.23785	0.732617	-0.32465	0.745445	0.981636	chr11	10761115	10761321	+ 0 NA	intron (Nintron (N	9972 NM_00134E	9646 Hs. 725151NM_01463E	ENSG000000CT9R	SH2BP1 TSCR9 homc protein-coding	
chr16-84 9.956446	0.332715	1.02505	0.324585	0.745495	0.981636	chr16	84054539	84055112	+ 0 NA	intron (Nintron (N	-12668 NM_00108C	146167 NM_00108C	ENSG000000SLC38A8	FVH2 solute c protein-coding	
chr9-125 9.956446	0.332715	1.02505	0.324585	0.745495	0.981636	chr9	1.25E+08	1.25E+08	+ 0 NA	intron (NLMIP3 LIN	-71133 NM_002077	2800 Hs. 59504 NM_002077	ENSG000000GOLGA1	golgin-97 golgin A1 protein-coding	
chr14-305 10.11736	0.243615	0.750558	0.324578	0.7455	0.981636	chr14	30949389	30949924	+ 0 NA	intron (NAluSx3 SI	-59848 NR_03835E	1.01E+08 Hs. 72919ENR_03835E	ENSG000000LOC10050E	uncharactercncRNA	
chr13-455 9.43461	-0.24776	0.764087	-0.32425	0.745746	0.981636	chr13	45531771	45352192	+ 0 NA	intron (NAluJb SIN	10636 NR_02445E	1E+08 Hs. 37576ENR_02445E	TPT1-AS1	TPT1 antncRNA	
chr17-598 6.606213	-0.29618	0.916471	-0.32317	0.746565	0.981636	chr17	59812342	59812695	+ 0 NA	intron (Nintron (N	-28748 NR_02949E	406991 Hs. 44456ENR_02949E	ENSG000000MIR21	MIRN21 hs microRNA ncRNA	
chr6-3091 8.98887	-0.2581	0.798736	-0.32314	0.746589	0.981636	chr6	3091904	3092472	+ 0 NA	intron (NCpG	23694 NM_00135E	8737 Hs. 51984ENR_003804	ENSG000000R1PK1	IMP57 RIE receptor protein-coding	
chr17-461 12.60631	0.214803	0.664854	0.323083	0.746632	0.981636	chr17	46170086	46172222	+ 0 NA	exon (NM exon (NM	21628 NM_00119E	284058 Hs. 648744NM_01544E	ENSG000000CKANSL1	ENSP-36 KAT8 regt protein-coding	
chr2-3554 10.36538	-0.23581	0.730084	-0.32298	0.746708	0.981636	chr2	3554863	3556150	+ 0 NA	intron (Nintron (N	2827 NM_00128E	246243 Hs. 56800ENR_00293E	ENSG000000RNASEH1	HIRNA PEC ribonucle protein-coding	
chr10-151 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr10	15126127	15128402	+ 0 NA	intron (Nintron (N	28083 NR_03650E	1E+08 Hs. 714691NR_03650E	ENSG000000PPIAP30	- peptidyl pseudo	
chr12-437 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr12	43793079	43795579	+ 0 NA	non-codir non-codir	11988 NM_00124E	5756 Hs. 18907ENR_00282E	ENSG000000TWF1	A6 PTK9 twinfilr protein-coding	
chr12-111 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr12	1.1E+08	1.1E+08	+ 0 NA	intron (Nintron (N	10337 NM_17066E	488 Hs. 50675ENR_001681	ENSG000000ATP2A2	ATP2B DAF ATPase s protein-coding	
chr14-921 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr14	92154477	92156371	+ 0 NA	intron (Nintron (N	33455 NM_00132E	53981 Hs. 65763ENR_017437	ENSG000000CPSF2	CPSF100 cleavage protein-coding	
chr16-75 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr16	75240634	75243257	+ 0 NA	intron (Nintron (N	-3285 NM_00117E	9564 Hs. 479747NM_014567	ENSG000000BCAR1	CAS CAS1 BCAR1 sc protein-coding	
chr3-123 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr3	1.24E+08	1.24E+08	+ 0 NA	intron (Nintron (N	-6549 NM_05303E	4638 Hs. 47737ENR_00596E	ENSG000000MYLK	AAL7 KRP myosin I1 protein-coding	
chr5-141 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr5	14162761	14164878	+ 0 NA	intron (Nintron (N	20477 NM_00711E	7204 Hs. 130031NM_00711E	ENSG000000TR10	ARHGEF23 trio Rho protein-coding	
chr8-130 9.888209	-0.23944	0.74244	-0.3225	0.747072	0.981636	chr8	1.3E+08	1.3E+08	+ 0 NA	intron (NTigger12c	-5247 NR_04538E	1.01E+08 Hs. 10601ENR_04538E	ENSG000000ASAP1-IT2	ASAP1 intncRNA	
chr1-1461 14.66524	0.20137	0.624833	0.322279	0.747242	0.981636	chr1	1.46E+08	1.46E+08	+ 0 NA	intron (NLMIP8 LIN	41890 NM_001364	388677 Hs. 65515ENR_20345E	ENSG000000NOTCH2NL2 N2N	NOTCH2 notch 2 protein-coding	
chr1-551 10.31638	-0.23656	0.734654	-0.322	0.747455	0.981636	chr1	55154007	55154206	+ 0 NA	intron (Nintron (N	61258 NM_01530E	23358 Hs. 47700ENR_01530E	ENSG000000USP24	- ubiquitin protein-coding	
chr7-6497 13.15976	0.210667	0.654333	0.321957	0.747485	0.981636	chr7	64978273	64982801	+ 0 NA	intron (Nintron (N	10499 NM_01585E	51351 Hs. 25069ENR_01585E	ENSG000000ZNF117	H-p1k HPF zinc finger protein-coding	
chr12-12 8.981012	-0.25661	0.797164	-0.32191	0.747523	0.981636	chr12	8233 NR_14574E	1.1E+08	+ 0 NA	intron (Nintron (N	8233 NR_14574E	1.1E+08	ENSG000000SNORA9B	small nucsnoRNA	
chr14-74 10.58853	0.234676	0.729397	0.32174	0.74765	0.981636	chr14	74666910	74667255	+ 0 NA	intron (Nintron (N	45998 NM_00103E	9870 Hs. 497417NM_014821	ENSG000000AREL1	FIEL1 KI apoptosis protein-coding	
chr1-384 5.693008	-0.31545	0.981023	-0.32155	0.747794	0.981636	chr1	3849967	3850785	+ 0 NA	intron (Nintron (N	6835 NM_014704	9731 Hs. 13308ENR_014704	ENSG000000CEP104	CFAP256 centrosom protein-coding	
chr3-1237 5.693008	-0.31545	0.981023	-0.32155	0.747794	0.981636	chr3	1.24E+08	1.24E+08	+ 0 NA	intron (Nintron (N	66928 NR_04662E	1.01E+08 Hs. 66731ENR_04662E	ENSG000000MYLK-AS2	- MYLK antncRNA	
chr6-1167 5.693008	-0.31545	0.981023	-0.32155	0.747794	0.981636	chr6	1.17E+08	1.17E+08	+ 0 NA	intron (Nintron (N	35185 NM_00136E	3841 Hs. 182971NM_00226E	ENSG000000KPN5A5	IPOA6 SRF karyopher protein-coding	
chr8-144 5.693008	-0.31545	0.981023	-0.32155	0.747794	0.981636	chr8	1.45E+08	1.45E+08	+ 0 NA	intron (NAluSq2 SI	18645 NM_138367	90987 Hs. 53451ENR_138367	ENSG000000ZNF251	zinc finger protein-coding	
chr16-595 6.203462	-0.29756	0.925957	-0.32135	0.747943	0.981636	chr16	599326	599994	+ 0 NA	intron (NCpG	9583 NM_00117E	57799 Hs. 45963ENR_02116E	ENSG000000RAB40C	RARL RASL RAB40C, n protein-coding	
chr2-857 6.203462	-0.29756	0.925957	-0.32135	0.747943	0.981636	chr2	85782725	85783391	+ 0 NA	TTS (NR_TTS (NR_1	619 NR_10671E	1.02E+08	NR_10671E	ENSG000000MIR6071	hsa-mir-6 microRNA ncRNA
chr2-2377 6.203462	-0.29756	0.925957	-0.32135	0.747943	0.981636	chr2	2.38E+08	2.38E+08	+ 0 NA	intron (NLMED LIN	-22078 NM_00108C	375316 Hs. 60726ENR_19885E	ENSG000000RBM44	- RNA bindi protein-coding	
chr6-160 6.203462	-0.29756	0.925957	-0.32135	0.747943	0.981636	chr6	1.6E+08	1.6E+08	+ 0 NA	intron (Nintron (N	-24849 NR_047511	1E+08 Hs. 74216ENR_047511	ENSG000000A1RN	AIR IGF2F antisense ncRNA	
chr4-388 9.426752	-0.24628	0.766456	-0.32132	0.747967	0.981636	chr4	38887804	38888476	+ 0 NA	intron (Nintron (N	20108 NR_03030C	693159 NR_03030C	ENSG000000MIR574	MIR574-3 microRNA ncRNA	
chr9-717 9.426752	-0.24628	0.766456	-0.32132	0.747967	0.981636	chr9	71724851	71725050	+ 0 NA	intron (Nintron (N	43563 NM_00113E	23670 Hs. 49414ENR_01339E	ENSG000000CEM1P2	TMEM2 cell migr protein-coding	
chr12-37 13.60735	0.208189	0.648565	0.320999	0.748211	0.981636	chr12	37236154	37236174	+ 0 NA	IntergeniALR Alphe	-1080975 NM_00130E	144245 Hs. 25930ENR_00101E	ENSG000000ALG10B	ALG10 KCFALG10 al protein-coding	
chr11-364 6.639495	-0.29066	0.905682	-0.32093	0.748264	0.981636	chr11	36485378	36486205	+ 0 NA	3' UTR (N3' UTR (N	24481 NM_14580E	7189 Hs. 44417ENR_00462C	ENSG000000TRAF6	MGC:3310 TNF rece protein-coding	
chr12-661 9.847069	-0.24153	0.752658	-0.32069	0.748288	0.981636	chr12	66122669	66125074	+ 0 NA	exon (NM exon (NM	6879 NM_03233E	84298 Hs. 50482ENR_03233E	ENSG000000LLPH	C12orf31 LLP homol protein-coding	
chr1-205 11.60528	0.222612	0.693791	0.320863	0.748314	0.981636	chr1	2.05E+08	2.05E+08	+ 0 NA	3' UTR (N3' UTR (N	-3601 NM_20337E	388730 Hs. 14692ENR_20337E	ENSG000000TMEM81	HC3107 KV transmem protein-coding	
chr13-111 5.453034	0.314589	0.981445	0.320536	0.748562	0.981636	chr13	1.13E+08	1.13E+08	+ 0 NA	intron (NAluSx SIN	84712 NM_00632E	10426 Hs. 22415ENR_00632E	ENSG000000TUBGCP3	104P ALPF tubulin g protein-coding	
chr17-185 5.453034	0.314589	0.981445	0.320536	0.748562	0.981636	chr17	18977971	18978940	+ 0 NA	exon (NM exon (NM	26290 NM_00127E	125206 Hs. 46241ENR_152351	ENSG000000SLC5A10	SGLT-5 SC solute c protein-coding	
chr7-650 5.453034	0.314589	0.981445	0.320536	0.748562	0.981636	chr7	65069425	65070221	+ 0 NA	promoter-promoter-	-715 NR_14571E	1.1E+08	NR_14571E	ENSG000000SNORA15B-SNORA15C	small nucsnoRNA
chr8-117 5.453034	0.314589	0.981445	0.320536	0.748562	0.981636	chr8	1.18E+08	1.18E+08	+ 0 NA	intron (Nintron (N	32113 NR_14579E	1E+08	NR_14579E	SNORD168	small nucsnoRNA
chr2-613 10.34967	-0.23316	0.727445	-0.32052	0.748572	0.981636	chr2	61354633	61354938	+ 0 NA	intron (Nintron (N	62592 NR_00370E	1E+08 Hs. 67582ENR_00370E	ENSG000000SNORA70B	small nucsnoRNA	
chr1-246 6.154465	-0.29886	0.932765	-0.3204	0.748663	0.981636	chr1	2.47E+08	2.47E+08	+ 0 NA	intron (NAluS6 SI	20369 NM_01600E	51097 Hs. 498397NM_01600E	ENSG000000SCCPD4	CGI-49 NF sacchar protein-coding	
chr11-437 6.154465	-0.29886	0.932765	-0.3204	0.748663	0.981636	chr11	43898686	43899312	+ 0 NA	non-codir non-codir	1696 NR_02695E	729799 Hs. 36892ENR_02695E	ENSG000000SEC14L1P1	SEC14 lip pseudo	
chr12-62 6.154465	-0.29886	0.932765	-0.3204	0.748663											

chr9-9445 5.460892	0.311866	0.977698	0.31898	0.749742	0.981636	chr9	94453642	94455598	+	0 NA	intron (AluSx1 SI	80051 NM_032558	84641 Hs.555999NM_032558	ENSG000003MFS14B	HIATL1	major facprotein-coding	
chr2-9225 14.17651	0.202447	0.634846	0.318892	0.749808	0.981636	chr2	92235686	92236549	+	0 NA	IntergeniALR Alpha	294984 NR_027714	440888 Hs.730236NM_001032412	ACTR3BP2	FKSG73	ACTR3B pseudo	
chr12-125 4.964304	0.329655	1.033997	0.318816	0.749866	0.981636	chr12	1.25E+08	1.25E+08	+	0 NA	intron (intron (N	22257 NM_023928	65985 Hs.656072NM_023928	ENSG00000CAACS	ACSF1 SUF	acetoacetprotein-coding	
chr2-2636 4.964304	0.329655	1.033997	0.318816	0.749866	0.981636	chr2	26369768	26370497	+	0 NA	intron (NSVA_D Ret	-23343 NM_001321	165082 Hs.631878NM_153835	ENSG00000ADGRF3	GPR13 PC	adhesion protein-coding	
chr2-7385 4.964304	0.329655	1.033997	0.318816	0.749866	0.981636	chr2	73850599	73851237	+	0 NA	intron (intron (N	21950 NM_001352	10617 Hs.469018NM_006463	ENSG00000STAMPB	AMH MICC	STAM bincprotein-coding	
chr3-4693 4.964304	0.329655	1.033997	0.318816	0.749866	0.981636	chr3	46937569	46938191	+	0 NA	intron (intron (N	38621 NR_102266	151903 Hs.631918NM_144716	ENSG00000CCDC12	-	coiled-co protein-coding	
chr4-1254 4.964304	0.329655	1.033997	0.318816	0.749866	0.981636	chr4	1.25E+08	1.25E+08	+	0 NA	intron (intron (N	-25801 NR_031746	1E+08	NR_031746	ENSG00000MIR2054	hsa-mir-2	miRNA ncRNA
chr18-576 9.937206	-0.23865	0.748769	-0.31872	0.749937	0.981636	chr18	57641703	57642865	+	0 NA	intron (LTR12C LI	11953 NM_001242	1.01E+08	Hs.660646NM_001242804	LOC100505E	-	uncharacter protein-coding
chr2-1572 9.937206	-0.23865	0.748769	-0.31872	0.749937	0.981636	chr2	1.57E+08	1.57E+08	+	0 NA	intron (AluSx1 SI	23532 NM_001322	11227 Hs.269027NM_014568	ENSG00000GALNT5	GALNAC-T	polypeptiprotein-coding	
chr11-182 9.929348	-0.23731	0.744979	-0.31855	0.750068	0.981636	chr11	18348860	18349243	+	0 NA	intron (AluS6 SI	26484 NM_005316	29655 Hs.577202NM_005316	ENSG00000GTF2H1	BTF2 P62	general tprotein-coding	
chr16-506 6.623779	-0.28657	0.901151	-0.318	0.750482	0.981636	chr16	50217756	50218963	+	0 NA	intron (AluSx4 SI	-48192 NM_001114	113 Hs.513578NM_001114	ENSG00000ADCY7	AC7	adenylate protein-coding	
chr3-1968 6.623779	-0.28657	0.901151	-0.318	0.750482	0.981636	chr3	1.97E+08	1.97E+08	+	0 NA	intron (intron (N	18776 NM_152699	205564 Hs.240777NM_152699	ENSG00000SENP5	-	SUMO specprotein-coding	
chr12-103 10.34181	-0.23187	0.72947	-0.31786	0.750592	0.981636	chr12	1.04E+08	1.04E+08	+	0 NA	intron (AluJr SIN	15972 NM_003211	6996 Hs.584809NM_003211	ENSG00000TDG	htDG	thymine lprotein-coding	
chr2-2-111 10.34181	-0.23187	0.72947	-0.31786	0.750592	0.981636	chr2	1.11E+08	1.11E+08	+	0 NA	intron (NMIRc SINE	-9960 NR_039634	1.01E+08	NR_039634	ENSG00000MIR4435-1	mir-4435	microRNA ncRNA
chr1-4664 10.39081	-0.23117	0.727859	-0.31761	0.750783	0.981636	chr1	46649503	46651923	+	0 NA	intron (NLIMA5 LIN	15165 NM_001256	64756 Hs.100874NM_022745	ENSG00000ATPAF1	ATP11 ATF	ATP syntp protein-coding	
chr1-1596 10.39081	-0.23117	0.727859	-0.31761	0.750783	0.981636	chr1	1.6E+08	1.6E+08	+	0 NA	exon (NM exon (NM	4419 NM_001277	8407 Hs.517168NM_003564	ENSG00000TAGLN2	HA1756	transgeliprotein-coding	
chr14-35 10.39081	-0.23117	0.727859	-0.31761	0.750783	0.981636	chr14	35028398	35029300	+	0 NA	intron (NMIR SINE	-16058 NM_001075	283635 Hs.446357NM_173607	ENSG00000CFAM177A1	C14orf24	family wiprotein-coding	
chr16-294 10.39081	-0.23117	0.727859	-0.31761	0.750783	0.981636	chr16	29483141	29484068	+	0 NA	TTS (NM_C TTS (NM_C	-16026 NR_002557	613038 Hs.569588NR_002557	ENSG00000LOC613038	-	SAGA compseudo	
chr6-312 10.39081	-0.23117	0.727859	-0.31761	0.750783	0.981636	chr6	31267845	31270930	+	0 NA	intron (intron (N	2705 NM_002117	3107 Hs.656022NM_002117	ENSG00000CHLA-C	D6S204 HL	major hisprotein-coding	
chr16-151 4.426577	0.348766	1.098371	0.31753	0.750841	0.981636	chr16	1513021	1514481	+	0 NA	intron (AluY SINE	-14927 NM_001256	79652 Hs.459652NM_024600	ENSG00000TMEM204	C16orf30	transmem protein-coding	
chr10-112 9.175036	0.263609	0.830447	0.31743	0.750917	0.981636	chr10	1.12E+08	1.12E+08	+	0 NA	intron (intron (N	24024 NM_020918	57678 Hs.572262NM_020918	ENSG00000GPAM	GPAT GPA1	glycerol -protein-coding	
chr12-108 9.921491	-0.23596	0.743593	-0.31733	0.750995	0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	intron (intron (N	16605 NM_001161	54434 Hs.199763NM_018984	ENSG00000SSH1	SSH1L	slingshotprotein-coding	
chr14-609 9.921491	-0.23596	0.743593	-0.31733	0.750995	0.981636	chr14	60997679	60998913	+	0 NA	intron (LTRIF1 LI	-16606 NM_001335	57570 Hs.380155NM_020810	ENSG00000TRMT5	COXP26 k	trRNA metp protein-coding	
chr5-1387 9.921491	-0.23596	0.743593	-0.31733	0.750995	0.981636	chr5	13870338	13870973	+	0 NA	intron (intron (N	73825 NM_001366	1767 Hs.212362NM_001366	ENSG00000DNAH5	C1LD3 DN	dynein aprotein-coding	
chr5-1798 9.921491	-0.23596	0.743593	-0.31733	0.750995	0.981636	chr5	1.8E+08	1.8E+08	+	0 NA	intron (intron (N	23796 NM_198866	23061 Hs.155822NM_015043	ENSG00000TBC1D9B	GRAMD9B	TBC1 domain protein-coding	
chr1-1505 13.63878	0.203708	0.642162	0.317222	0.751075	0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	intron (intron (N	4612 NM_001366	9869 Hs.643565NM_012432	ENSG00000SETDB1	ESET H3-K	SET domain protein-coding	
chr12-133 13.63878	0.203708	0.642162	0.317222	0.751075	0.981636	chr12	1.33E+08	1.33E+08	+	0 NA	intron (NLIMC1 LIN	9445 NM_001300	7699 Hs.181552NM_003440	ENSG00000ZNF140	PHZ-39	zinc fingerprotein-coding	
chr16-285 4.915307	0.330301	1.04131	0.317198	0.751094	0.981636	chr16	28952634	28952991	+	0 NA	intron (AluSq2 SI	1815 NM_032815	84901 Hs.513477NM_032815	ENSG00000NFATC21P	ESCC NIP4	nuclear fprotein-coding	
chr7-1566 4.915307	0.330301	1.04131	0.317198	0.751094	0.981636	chr7	1.57E+08	1.57E+08	+	0 NA	intron (LTR12C LI	20058 NM_001335	64327 Hs.209988NM_022458	ENSG00000LMBR1	ACHP C7c	limb devp protein-coding	
chr4-1694 4.923165	0.327348	1.032155	0.31715	0.75113	0.981636	chr4	1.7E+08	1.7E+08	+	0 NA	intron (intron (N	38025 NM_001243	1182 Hs.481188NM_001825	ENSG00000CLNC3	CLNC3 C7c	chloride protein-coding	
chr5-1464 11.17525	0.23123	0.729144	0.317125	0.751149	0.981636	chr5	1.46E+08	1.46E+08	+	0 NA	intron (intron (N	33366 NM_194251	134391 Hs.483732NM_194251	ENSG00000GPR151	GALR4 GALG	protein-coding	
chr20-317 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr20	31706524	31707776	+	0 NA	intron (intron (N	-14357 NR_131907	1.03E+08	NR_131907	ENSG00000ABALON	INXS	apoptoticncRNA
chr12-67 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr12	67304697	67306164	+	0 NA	exon (NM exon (NM	36072 NM_001325	55832 Hs.546407NM_018448	ENSG00000CAND1	TIP120 TI	cellular protein-coding	
chr14-497 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr14	49787246	49788635	+	0 NA	intron (intron (N	19787 NM_014315	23588 Hs.509264NM_014315	ENSG00000KLHDC2	HCLP-1 H	kelch domprotein-coding	
chr14-68 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr14	68999987	68912377	+	0 NA	intron (NLIMB3 LIN	73120 NM_001102	87 Hs.235755NM_001102	ENSG00000ACTN1	BDPLT15	actinin eprotein-coding	
chr15-64 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr15	64153965	64162275	+	0 NA	TTS (NM_C TTS (NM_C	5035 NM_000942	5479 Hs.434937NM_000942	ENSG00000PP1B	B CYP-S1	peptidylp protein-coding	
chr19-145 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr19	1439066	1442547	+	0 NA	TTS (NM_C TTS (NM_C	2381 NM_001308	6209 Hs.406683NM_001018	ENSG00000CRPS15	RIG S15	ribosomal protein-coding	
chr2-371 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr2	37105946	37109674	+	0 NA	intron (intron (N	23359 NM_001278	253635 Hs.592525NM_174931	ENSG00000GPATCH11	CCDC75 CF	patch cprotein-coding	
chr20-564 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr20	56458482	56459820	+	0 NA	3' UTR (3' UTR (N	-9434 NM_016407	51507 Hs.517134NM_016407	ENSG00000CAND1	C2orf43 C	replicatiprotein-coding	
chr5-1428 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr5	14286288	14291274	+	0 NA	intron (intron (N	145439 NM_007118	7204 Hs.130031NM_007118	ENSG00000TRIO	ARHGEP23	trio Rho protein-coding	
chr5-1774 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (intron (N	8691 NR_103804	9260 Hs.533040NM_005451	ENSG00000PDLIM7	LMP1 LMP2	PDZ and lprotein-coding	
chr6-3162 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr6	31622679	31640535	+	0 NA	exon (NM exon (NM	-2180 NR_106890	1.02E+08	NR_106890	ENSG00000MIR6832	hsa-mir-6	microRNA ncRNA
chr9-2717 10.38295	-0.22986	0.72543	-0.31686	0.751346	0.981636	chr9	27177189	27178520	+	0 NA	intron (NLIMA9 LIN	68713 NM_000455	7010 Hs.89640 NM_000455	ENSG00000TEK	CD202B G	TEK recep protein-coding	
chr1-1808 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr1	1808163	1809961	+	0 NA	intron (intron (N	-29031 NM_001353	65220 Hs.654792NM_023018	ENSG00000NADK	dJ283E3	INAD kinase protein-coding	
chr1-6702 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr1	67027296	67028371	+	0 NA	intron (AluS6 SI	26315 NM_015135	23169 Hs.213642NM_015135	ENSG00000SLCS35D1	SHNKND	INAD solute cprotein-coding	
chr1-7785 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr1	77855443	77856315	+	0 NA	intron (NLIPB1 LIN	-32636 NM_144573	91624 Hs.612388NM_144573	ENSG00000NEXN	CMH20 NEL	nexlin lprotein-coding	
chr1-1546 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr1	1.55E+08	1.55E+08	+	0 NA	intron (intron (N	434 NM_001193	103 Hs.12341 NM_001111	ENSG00000ADAR	ADAR1 AGS	adenosine protein-coding	
chr1-285 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr1	2.26E+08	2.26E+08	+	0 NA	intron (AluSx SIN	53477 NM_001008	55740 Hs.497893NM_018212	ENSG00000ENAH	ENA MENA	ENAH actiprotein-coding	
chr10-336 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr10	38018175	38020640	+	0 NA	intron (NLIP4 LIN	8732 NM_001278	7581 Hs.435747NM_006954	ENSG00000ZNF33A	KOX2 KOX	zinc fingerprotein-coding	
chr10-10 6.187746	-0.29333	0.925788	-0.31685	0.751361	0.981636	chr10	1E+08	1E+08	+	0 NA	intron (Tigger3a	-11224 NR_144755	10613 Hs.150087NM_006455	ENSG00000ERLIN1	C10orf69 ER		



chr14-754	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr14	75445770	75446512	+	0 NA	intron (NLIMB8 LIN	14007 NM_001135	122953 Hs. 196482NM_130466	ENSG000004JDP2	JUNDM2	Jun dimer protein-coding		
chr14-101	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr14	1.01E+08	1.01E+08	+	0 NA	promoter-promoter-	162 NR_029875	494330 NR_029875	ENSG000004MIR381	MIRN381	hmicrorna ncRNA		
chr22-376	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr22	37690189	37691753	+	0 NA	intron (Nintron (N	4628 NM_024313	79159 Hs. 632777NM_024313	ENSG000004NOL12	Nov25 dJ3	nucleolar protein-coding		
chr3-757	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr3	75771234	75772643	+	0 NA	intron (NMERS2A LI	13064 NM_001324	1E+08 Hs. 556877NM_001128	ENSG000004ZNF717	OB1 X17	zinc finger protein-coding		
chr4-5542	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr4	55429640	55431449	+	0 NA	3' UTR (N3' UTR (N	34587 NM_001847	55858 Hs. 479766NM_018477	ENSG000004TMEM165	CD2K FT2	transmembrane protein-coding		
chr5-3745	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr5	37452706	37453629	+	0 NA	intron (NMER9a2 LI	73849 NM_001345	55100 Hs. 21369CNM_018034	ENSG000004WDR70	WD repeat	protein-coding		
chr5-1705	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr5	1.71E+08	1.71E+08	+	0 NA	intron (NLIP2 LINE	39310 NM_0022897	64901 Hs. 41081CNM_022897	ENSG000004RANBP17	RAM bindin	protein-coding		
chr8-1407	6.657061	-0.28133	0.892821	-0.3151	0.752686	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	intron (Nintron (N	-45507 NR_029892	442893 NR_029892	ENSG000004MIR151A	MIR151	microRNA ncRNA		
chr10-111	9.913633	-0.23459	0.74458	-0.31506	0.752718	0.981636	chr10	1.11E+08	1.11E+08	+	0 NA	intron (Nintron (N	10861 NM_005445	9126 Hs. 24485 NM_005445	ENSG000004SMC3	BAM BMH C	structure protein-coding		
chr12-722	9.913633	-0.23459	0.74458	-0.31506	0.752718	0.981636	chr12	72286721	72287435	+	0 NA	intron (Nintron (N	-13569 NR_026836	283392 Hs. 363603NM_001022	ENSG000004TRHDE-AS1	TRHDE	antncRNA		
chr2-3928	9.913633	-0.23459	0.74458	-0.31506	0.752718	0.981636	chr2	39287691	39289163	+	0 NA	intron (Nintron (N	-44444 NR_144521	344387 Hs. 403201NM_001005	ENSG000004CDKL4	CDKL4	cyclin d	protein-coding	
chr10-751	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr10	75176559	75178226	+	0 NA	3' UTR (N3' UTR (N	-32762 NM_003375	7417 Hs. 355927NM_003375	ENSG000004VDAC2	POR	voltage c	protein-coding	
chr12-316	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr12	31682749	31683729	+	0 NA	intron (NAluSz SIN	23551 NM_001133	254013 Hs. 740625NM_173802	ENSG000004ETFBKMT	C12orf72	electron	protein-coding	
chr14-547	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr14	54782104	54783303	+	0 NA	intron (Nintron (N	27870 NM_001161	23034 Hs. 98259 NM_015585	ENSG000004SAMD4A	SAMD4 SMA	struc	protein-coding	
chr14-572	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr14	57213878	57215419	+	0 NA	intron (NL2 LINE I	54257 NM_006544	10640 Hs. 743987NM_006544	ENSG000004EXOC5	HSEC10 PF	exocyst	protein-coding	
chr15-988	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr15	98828315	98828993	+	0 NA	intron (Nintron (N	44228 NR_039864	1.01E+08 NR_039864	ENSG000004MIR4714	MIR4714	microRNA ncRNA		
chr16-465	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr16	463008	463878	+	0 NA	intron (NAluSp SIN	-11481 NM_001142	9727 Hs. 531642NM_01470C	ENSG000004RAB11FIP5	CART1 FIF	RAB11 fan	protein-coding	
chr17-364	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr17	36492202	36492968	+	0 NA	intron (Nintron (N	5904 NM_001281	9326 Hs. 2210 NM_004477	ENSG000004ZNHT3	PEHO TRIF	zinc	finger protein-coding	
chr7-2256	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr7	2256828	2257556	+	0 NA	TTS (NR_1TTS (NR_1	385 NR_106895	1.02E+08 NR_106895	ENSG000004MIR6836	hsa-mir-6836	microRNA ncRNA		
chr8-3065	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr8	30693811	30694480	+	0 NA	intron (Nigger19e	33701 NM_000637	2936 Hs. 27151CNM_000637	ENSG000004GCSR	GR HEL-75	glutathion	protein-coding	
chr9-134	5.46875	0.309163	0.98145	0.315006	0.752757	0.981636	chr9	1.34E+08	1.34E+08	+	0 NA	intron (Nintron (N	-10283 NR_135122	1E+08 Hs. 671095NR_135122	ENSG000004LOC100130C	uncharact	ncRNA		
chr2-1205	5.72629	-0.30918	0.98163	-0.31497	0.752785	0.981636	chr2	1.21E+08	1.21E+08	+	0 NA	intron (NAluJo SIN	186758 NM_00527C	2736 Hs. 111867NM_00527C	ENSG000004GLI2	CJ5 HP59	GLI fami	protein-coding	
chr6-8892	5.72629	-0.30918	0.98163	-0.31497	0.752785	0.981636	chr6	88922925	88923523	+	0 NA	intron (NLIMC5a LI	40394 NM_00128C	8732 Hs. 567377NM_00380C	ENSG000004RNGTT	CAP1A HCF	RNA guan	protein-coding	
chr1-220	10.02723	0.24214	0.768843	-0.31494	0.752807	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (Nintron (N	17118 NM_00608E	10380 Hs. 406134NM_00608E	ENSG000004BPNT1	HEL20 PIF 3' (2')	epsilon	protein-coding	
chr1-1561	14.65553	0.196229	0.623163	0.314893	0.752843	0.981636	chr1	1.56E+08	1.56E+08	+	0 NA	intron (Nintron (N	8928 NM_001257	4000 Hs. 594444NM_005572	ENSG000004LMNA	CDCD1 CDE	lamin A/C	protein-coding	
chr19-50	14.15108	0.199295	0.633391	0.314648	0.753029	0.981636	chr19	50042316	50046922	+	0 NA	intron (Nintron (N	-5970 NR_027257	400710 Hs. 628965NR_027257	ENSG000004LOC40071C	uncharact	ncRNA		
chr16-581	6.615921	-0.28463	0.905356	-0.31439	0.753225	0.981636	chr16	58195933	58196525	+	0 NA	intron (Nintron (N	1877 NM_00189E	1459 Hs. 82201 NM_00189E	ENSG000004CSNK2A2	CK2A2 CK2	casein	kinase protein-coding	
chr5-1545	6.615921	-0.28463	0.905356	-0.31439	0.753225	0.981636	chr5	1.55E+08	1.55E+08	+	0 NA	exon (NM exon (NM	30437 NM_01546E	25929 Hs. 483921NM_01546E	ENSG000004GEMIN5	GEMIN-5	gem nucl	protein-coding	
chr19-444	7.983677	-0.2799	0.89056	-0.31423	0.753296	0.981636	chr19	44438255	44438483	+	0 NA	intron (NLIME3G LI	10103 NR_103551	7772 Hs. 709345NM_01451E	ENSG000004ZNF229	zinc	finger protein-coding		
chr20-58	4.931023	0.324336	1.032092	0.314251	0.75333	0.981636	chr20	58697757	58699585	+	0 NA	intron (Nintron (N	5871 NM_02466E	79716 Hs. 654868NM_02466E	ENSG000004NPEPL1	ba261P9	zaminogen	protein-coding	
chr4-868	4.931023	0.324336	1.032092	0.314251	0.75333	0.981636	chr4	86886147	86887160	+	0 NA	TTS (NM_1TTS (NM_C	5769 NM_00136E	132989 Hs. 339645NM_14464E	ENSG000004Corf36	chromosom	protein-coding		
chr5-572	10.33395	-0.23057	0.733779	-0.31423	0.753349	0.981636	chr5	57250342	57251429	+	0 NA	intron (Nintron (N	36831 NR_001127	65056 Hs. 444275NM_02291E	ENSG000004GPBP1	GPBP SSH6	GC-rich	protein-coding	
chr1-1657	12.0843	0.214266	0.681883	0.314227	0.753349	0.981636	chr1	16573298	16575069	+	0 NA	intron (Nintron (N	25249 NR_03744E	1.01E+08 NR_03744E	ENSG000004MIR3675	MIR3675	microRNA ncRNA		
chr4-122	10.85226	-0.22569	0.718374	-0.31417	0.753392	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (NAluY SINE	96544 NM_01531E	84162 Hs. 408142NM_01531E	ENSG000004KIAA1109	ALKKUCS FK	IAA1109	protein-coding	
chr5-1501	10.85226	-0.22569	0.718374	-0.31417	0.753392	0.981636	chr5	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	-15670 NM_005211	1436 Hs. 586215NM_005211	ENSG000004CSF1R	C-FMS CD1	colony st	protein-coding	
chr1-2241	5.95748	0.297144	0.946417	0.313967	0.753546	0.981636	chr1	2.24E+08	2.24E+08	+	0 NA	non-codirnon-codir	-23847 NM_001321	8560 Hs. 299878NM_00367E	ENSG000004DEGS1	DEGS DEGS	delta 4-c	protein-coding	
chr15-908	5.95748	0.297144	0.946417	0.313967	0.753546	0.981636	chr15	90879067	90880461	+	0 NA	exon (NM exon (NM	-4740 NM_001143	2242 Hs. 7636 NM_00200E	ENSG000004CFES	FPS	FES protc	protein-coding	
chr17-354	5.95748	0.297144	0.946417	0.313967	0.753546	0.981636	chr17	35418452	35419168	+	0 NA	intron (NLIME4E LIN	13690 NM_01804E	55106 Hs. 663545NM_01804E	ENSG000004SLFN12	SLFN3	schlafen	protein-coding	
chr6-1325	5.95748	0.297144	0.946417	0.313967	0.753546	0.981636	chr6	1.82E+08	1.82E+08	+	0 NA	intron (NLIM2 LINE	5404 NM_01552E	26002 Hs. 6909 NM_01552E	ENSG000004MOXD1	MOX PRO57	monooxyg	protein-coding	
chr7-1284	10.8444	-0.22438	0.715007	-0.31382	0.753661	0.981636	chr7	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	2821 NM_01839E	55798 Hs. 433215NM_01839E	ENSG000004METTL2B	METL METI	methyltr	protein-coding	
chr20-365	6.146607	-0.29666	0.945442	-0.31378	0.753688	0.981636	chr20	36910219	36910862	+	0 NA	intron (NAluSx SIN	34402 NM_08062E	140711 Hs. 472623NM_08062E	ENSG000004TLCDC2	C20orf11E	TBC/LysM	protein-coding	
chr4-143	6.146607	-0.29666	0.945442	-0.31378	0.753688	0.981636	chr4	14359108	1435938	+	0 NA	exon (NM exon (NM	29836 NM_00129C	84640 Hs. 480845NM_032557	ENSG000004USP38	HP43	KBD ubiquit	protein-coding	
chr6-4355	6.146607	-0.29666	0.945442	-0.31378	0.753688	0.981636	chr6	43594875	43595544	+	0 NA	intron (NAluSx3 SI	19024 NM_001291	5429 Hs. 655467NM_00650E	ENSG000004POLH	RAD30 RAI	DNA polyn	protein-coding	
chr8-1334	6.146607	-0.29666	0.945442	-0.31378	0.753688	0.981636	chr8	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	71322 NM_003033	6482 Hs. 374257NM_003033	ENSG000004ST3GAL1	Gal-1	Nac6S	T3 beta	protein-coding
chr10-598	8.637308	0.268828	0.857086	0.313654	0.753784	0.981636	chr10	59811680	59811895	+	0 NA	intron (NMER8 DNA	-58332 NM_001304	1.01E+08 Hs. 64879CNM_001304	ENSG000004MRLN	LINC0094E	myoregulin	protein-coding	
chr1-2302	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr1	2.3E+08	2.3E+08	+	0 NA	intron (Nintron (N	175426 NM_00125E	79605 Hs. 520465NM_024554	ENSG000004PGDB5	pyggyBac	protein-coding		
chr12-135	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr12	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	20248 NM_006231	5426 Hs. 524871NM_006231	ENSG000004POLE	CRCS12 F1D	NA polyn	protein-coding	
chr16-165	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr16	16344610	16345445	+	0 NA	intron (NAluSx SIN	9097 NM_00698E	9284 Hs. 672625NM_00698E	ENSG000004NP1PA1	NP1 NP1F	nuclear f	protein-coding	
chr22-245	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr22	24379891	24380952	+	0 NA	intron (Nintron (N	38313 NM_001254	23384 Hs. 474388NM_01533C	ENSG000004SPECC1L	CYTSA GFE	sperm ant	protein-coding	
chr4-351	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr4	3510857	3512422	+	0 NA	non-codirnon-codir	20510 NR_11000E	4043 Hs. 40966 NM_002337	ENSG000004LRPAP1	A2MRAP A2	LDL recep	protein-coding	
chr6-855	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr6	85532347	85533422	+	0 NA	intron (Nintron (N	60974 NM_15381E	57231 Hs. 485871NM_02046E	ENSG000004SNX14	RGS-PX2	Sorting r	protein-coding	
chr8-4227	5.965338	0.294584	0.939737	0.313475	0.75392	0.981636	chr8	42279258	42280174	+	0 NA	intron (NMRB SINE	8414 NR_03381E	3551 Hs. 597664NM_00155E	ENSG000004IKKBK				

chr9-1275	5.427611	0.306975	0.984384	0.311844	0.755159	0.981636	chr9	1.28E+08	1.28E+08	0	NA	intron (NMIRb SINE	25141	NM_022833	64855	Hs.522401NM_022833	ENSG000002CNBAN2	C9orf88	Fniban apc protein-coding	
chr12-121	9.905775	-0.23317	0.747974	-0.31173	0.755245	0.981636	chr12	1.21E+08	1.21E+08	0	NA	exon (NM exon (NM	18971	NM_00127C	10645	Hs.297344NM_006544	ENSG000002CAMKK2	CAMKK1	CAV calcium/c protein-coding	
chr3-1137	9.905775	-0.23317	0.747974	-0.31173	0.755245	0.981636	chr3	1.14E+08	1.14E+08	0	NA	3' UTR (N3' UTR (N	-24323	NR_111981	205717	Hs.63257CNM_001005	ENSG000002USF3	KIAA2018	upstream protein-coding	
chr5-968	3.443478	-0.3839	1.231589	-0.31171	0.755263	0.981636	chr5	9.6885042	9.6885757	0	NA	intron (Nintron (N	9466	NR_137637	64167	Hs.48291CNM_02235C	ENSG000002ERAP2	L-RAP1	LR1 endoplasmic protein-coding	
chr14-391	6.503066	0.28442	0.913663	0.311296	0.755575	0.981636	chr14	9.313849	9.3132658	0	NA	intron (NAluSx1 SI	17969	NM_00361E	8487	Hs.652307NM_00361E	ENSG000002GEMIN2	SIP1	SIP1em nucleprotein-coding	
chr15-925	13.65708	-0.20313	0.652558	-0.31129	0.755583	0.981636	chr15	92901198	92901434	0	NA	intron (Nintron (N	992	NM_001271	1106	Hs.220864NM_001271	ENSG000002CHD2	EEOC	chromodon protein-coding	
chr11-977	10.41623	-0.22656	0.728488	-0.31101	0.755796	0.981636	chr11	9779847	9782080	0	NA	intron (Nintron (N	-21430	NR_033972	440028	Hs.677541NR_033972	ENSG000002LINC02705	-	long intencRNA	
chr13-114	10.41623	-0.22656	0.728488	-0.31101	0.755796	0.981636	chr13	1.14E+08	1.14E+08	0	NA	promoter-promoter-	-785	NR_039724	1.01E+08	NR_039724	ENSG000002MIR4502	-	microRNA ncRNA	
chr1-155	5.419753	0.309706	0.996342	0.310843	0.75592	0.981636	chr1	15534319	15535366	0	NA	intron (Nintron (N	-7324	NR_135613	1.07E+08	NR_135613	ENSG000002SCARNA21E	-	small Ca_ncRNA	
chr10-871	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr10	87108276	87109198	0	NA	intron (Nintron (N	13531	NM_019054	54537	Hs.500415NM_019054	ENSG000002SHLD2	FAM35A	F3shieldin protein-coding	
chr15-641	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr15	64184544	64185590	0	NA	intron (Nintron (N	-21912	NM_000942	5479	Hs.434937NM_000942	ENSG000002PPIB	B/CYP-51	peptidylr protein-coding	
chr16-735	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr16	735284	737654	0	NA	intron (Nintron (N	4528	NM_022493	64428	Hs.513247NM_022493	ENSG000002CIAO3	HPRN	IOP1 cytosolic protein-coding	
chr2-2804	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr2	280452	280947	0	NA	intron (Nintron (N	7392	NM_001002	285016	Hs.355207NM_001002	ENSG000002ALKAL2	AUGA	FAM1ALK and I protein-coding	
chr20-344	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr20	34423760	34424197	0	NA	intron (Nintron (N	-42347	NR_030374	93229	NR_030374	ENSG000002MIR644A	MIR644	M1microRNA ncRNA	
chr3-125	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr3	1.26E+08	1.26E+08	0	NA	intron (Nintron (N	27798	NM_02277E	114885	Hs.47744CNM_02277E	ENSG000002OSBPL11	ORP-11	OF oxysterol protein-coding	
chr4-1027	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr4	1.03E+08	1.03E+08	0	NA	intron (Nintron (N	9747	NM_00590E	4126	Hs.480415NM_00590E	ENSG000002MANBA	MANB1	mannoside protein-coding	
chr4-109	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr4	1.1E+08	1.1E+08	0	NA	intron (NAluJb SIN	30231	NR_030302	693161	NR_030302	ENSG000002MIR576	MIRN576	I microRNA ncRNA	
chr6-316	5.973196	0.292108	0.939786	0.310824	0.755935	0.981636	chr6	31686281	31687351	0	NA	TTS (NM_CTS (NM_C	-6443	NM_025262	80741	Hs.25738	NM_025262	ENSG000002L1665C	C6orf20	C lymphocyt protein-coding
chr15-735	10.82869	-0.22186	0.714587	-0.31047	0.756202	0.981636	chr15	73559647	73559896	0	NA	TTS (NM_CTS (NM_C	9772	NR_103844	1.01E+08	Hs.656678NR_103844	ENSG000002NPTN-IT1	lncRNA-LE	NPTN intrncRNA	
chr3-444	14.63011	0.193187	0.622452	0.310364	0.756284	0.981636	chr3	44446869	44451279	0	NA	intron (Nintron (N	21502	NR_14443E	1.01E+08	Hs.180744NR_14443E	ENSG000002LINC0198E	-	long intencRNA	
chr1-188	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr1	18907678	18908198	0	NA	3' UTR (N3' UTR (N	-5182	NM_00131E	8659	Hs.77448	NM_00374E	ENSG000002ALDHA1A	ALDHA4	P5C aldehyde protein-coding
chr1-3634	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr1	36345522	36346217	0	NA	intron (Nintron (N	-21715	NM_01816E	55194	Hs.87016	NM_01816E	ENSG000002EVA1B	Clorf78	Feva-1 hon protein-coding
chr1-146	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr1	1.47E+08	1.47E+08	0	NA	intron (N (TTCC)n S	6377	NM_00127E	149013	Hs.666981NM_00127E	ENSG000002NBPF12	COAS1	KI/NBPF memt protein-coding	
chr1-2344	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr1	2.34E+08	2.34E+08	0	NA	intron (Nintron (N	13310	NM_00564E	6894	Hs.498127NM_00564E	ENSG000002TARBP1	TRM3	TRM1TAR (HIV- protein-coding	
chr12-12	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr12	1.23E+08	1.23E+08	0	NA	intron (Nintron (N	-1259	NR_036187	1E+08	NR_036187	ENSG000002MIR4304	-	microRNA ncRNA	
chr14-527	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr14	52747053	52747762	0	NA	intron (Nintron (N	17241	NM_145251	6815	Hs.36498CNM_145251	ENSG000002STYX	-	serine/tR protein-coding	
chr15-434	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr15	43433844	43436995	0	NA	intron (Nintron (N	57737	NM_001141	7158	Hs.440962NM_005657	ENSG000002TP53BP1	53BP1	TDF tumor prc protein-coding	
chr16-70	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr16	70006208	70006794	0	NA	intron (NMERIB DNA	-23845	NR_03626E	1E+08	NR_03626E	ENSG000002MIR1972-2	-	microRNA ncRNA	
chr18-31	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr18	31874723	31875532	0	NA	intron (Nintron (N	68001	NM_01493E	22878	Hs.202001NM_01493E	ENSG000002TRAPPC8	GSG1	HsT2 traffickin protein-coding	
chr18-48	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr18	48940994	48942311	0	NA	intron (Nintron (N	1155	NM_00119C	4092	Hs.465087NM_005904	ENSG000002SMAD7	CRCS3	MAI SMAD fami protein-coding	
chr2-932	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr2	93209564	93210740	0	NA	IntergeniALR/Alphe	998267	NR_14610E	728034	NR_14610E	BMS1P14	-	BMS1 pset pseudo	
chr3-524	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr3	52467822	52469160	0	NA	intron (Nintron (N	12887	NM_007184	11188	Hs.43529CNM_007184	ENSG000002NISCH	I-1 IR1	I nischari protein-coding	
chr5-312	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chr5	31206414	31207070	0	NA	intron (Nintron (N	13456	NM_004932	1004	Hs.12477E	NM_004932	ENSG000002CDH6	CAD6	KCAL cadherin protein-coding
chrX-106	5.435469	0.304277	0.980619	0.310291	0.75634	0.981636	chrX	1.07E+08	1.07E+08	0	NA	exon (NM exon (NM	21766	NM_020384	9075	Hs.52274E	NM_020384	ENSG000002CLDN2	-	claudin 2 protein-coding
chr17-18	10.40837	-0.22527	0.726058	-0.31027	0.756358	0.981636	chr17	18801185	18806815	0	NA	intron (Nintron (N	14965	NM_00131E	51030	Hs.87295	NM_01607E	ENSG000002TVP23B	CGI-148	F trans-gol protein-coding
chr18-361	10.40837	-0.22527	0.726058	-0.31027	0.756358	0.981636	chr18	36174573	36175617	0	NA	non-codiron-codir	12340	NR_13460E	1.02E+08	Hs.600673NR_13460E	ENSG000002LOC101927-	-	uncharactncRNA	
chr9-954	10.40837	-0.22527	0.726058	-0.31027	0.756358	0.981636	chr9	95453070	95453561	0	NA	intron (NAluSg7 SI	-10294	NR_038982	1.01E+08	Hs.661847NR_038982	LOC100507-	-	uncharactncRNA	
chr5-313	9.96263	-0.23369	0.754067	-0.30991	0.756633	0.981636	chr5	31306101	31306538	0	NA	intron (Nintron (N	112633	NM_004932	1004	Hs.12477E	NM_004932	ENSG000002CDH6	CAD6	KCAL cadherin protein-coding
chr1-284	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr1	28491418	28492854	0	NA	intron (Nintron (N	-13807	NM_00104E	1104	Hs.469722NM_00126E	ENSG000002RCC1	CHC1	RCC1 regulator protein-coding	
chr1-388	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr1	38839708	38840358	0	NA	intron (NAluY SINE	19739	NM_001271	64121	Hs.532461NM_022157	ENSG000002RRAC	GTR2	RAGC Ras relat protein-coding	
chr1-666	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr1	66631448	66633573	0	NA	intron (NFAM SINE	4070	NR_03606E	1E+08	NR_03606E	ENSG000002MIR3117	mir-3117	microRNA ncRNA	
chr11-68	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr11	68527812	68528153	0	NA	intron (Nintron (N	67230	NM_001352	55291	Hs.503022NM_018312	ENSG000002PPP6R3	C1orfF23	protein r protein-coding	
chr12-307	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr12	30737446	30738160	0	NA	intron (NAluY SINE	16711	NM_00131E	65981	Hs.234355NM_02392E	ENSG000002CAPRIN2	C1QDC1	EF caprin f2 protein-coding	
chr12-102	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr12	1.02E+08	1.02E+08	0	NA	intron (Nintron (N	2548	NM_01605E	51019	Hs.405692NM_01605E	ENSG000002WASHC3	CCDC53	CC WASH com protein-coding	
chr12-112	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr12	1.12E+08	1.12E+08	0	NA	intron (Nintron (N	-106543	NR_106921	1.02E+08	NR_106921	ENSG000002MIR6861	hsa-mir-6	microRNA ncRNA	
chr12-124	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr12	1.24E+08	1.24E+08	0	NA	intron (Nintron (N	-18061	NR_10694C	1.02E+08	NR_10694C	ENSG000002MIR6880	hsa-mir-6	microRNA ncRNA	
chr17-47	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr17	47607033	47607885	0	NA	intron (NLa2 LINE	-42460	NM_00226E	3837	Hs.532793NM_00226E	ENSG000002KPNB1	IMB1	IPO1 karyofer protein-coding	
chr19-15	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr19	1583407	1584755	0	NA	intron (NAluSx SIN	8784	NM_001281	53615	Hs.17872E	NM_00392E	ENSG000002CMBD3	-	methyl-Cf protein-coding
chr2-378	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr2	37315765	37316062	0	NA	intron (NAluSx1 SI	1171	NM_00581E	23683	Hs.660757NM_00581E	ENSG000002PRKD3	EPK2	PKC- protein r protein-coding	
chr2-134	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr2	1.34E+08	1.34E+08	0	NA	intron (NLMC5a LI	98407	NM_00241C	4249	Hs.4988	NM_00241C	ENSG000002MGAT5	GNT-V	GN1alpha-1, f protein-coding
chr2-200	6.641345	-0.2774	0.896887	-0.30929	0.757098	0.981636	chr2	2.01E+08	2.01E+08	0	NA	intron (Nintron (N	28036	NM_001142	60491	Hs.145284NM_021824	ENSG000002CN1F3L1	ALS2CR1	I GNG11	



chr9-109C	6.682484	-0.27426	0.89013	-0.30811	0.758	0.981636	chr9	1.09E+08	1.09E+08	+	0	NA	promoter-promoter-	-120 NR_02950E	407036	NR_02950E	ENSG000002MIR32	MIRN32 hs	microRNA	ncRNA		
chr11-59E	6.6982	-0.27824	0.903511	-0.30795	0.758119	0.981636	chr11	59602392	59603056	+	0	NA	intron (Alu)Jb SIN	-7566 NR_03612C	1E+08	NR_03612C	ENSG000002MIR3162	mir-3162	microRNA	ncRNA		
chr5-347E	6.6982	-0.27824	0.903511	-0.30795	0.758119	0.981636	chr5	34755578	34756178	+	0	NA	intron (MIR SINE	68319 NR_00114E	26064	Hs.43140C	NR_015577	ENSG000002CRAI14	NORPEG R	retinoic protein-coding		
chr19-357	6.461926	-0.282536	0.917702	-0.307873	0.758179	0.981636	chr19	35768169	35768561	+	0	NA	intron (intron (N	-7199 NR_005294E	115703	Hs.515364	NR_005294E	ENSG000002ARHGAP33	NOMA-GAP Rho	GTPase protein-coding		
chr1-666G	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr1	66634117	66636946	+	0	NA	intron (intron (N	7091 NR_03606C	1E+08	NR_03606C	ENSG000002MIR3117	mir-3117	microRNA	ncRNA		
chr10-11E	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr10	1.19E+08	1.19E+08	+	0	NA	intron (Alu)Jo SIN	4526 NR_002917	641451	Hs.68865E	NR_002917	ENSG000002CSNORA19	ACA19	small	nucsnRNA	
chr12-56I	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr12	56159335	56164539	+	0	NA	TTS (NM_C TTS (NM_C	3578 NR_002101E	4637	Hs.632717	NR_002101E	ENSG000002MYL6	ESMLC LCI	myosin I protein-coding		
chr12-13C	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr12	1.31E+08	1.31E+08	+	0	NA	intron (intron (N	2708 NR_00632E	5901	Hs.10842	NR_00632E	ENSG000002CRAN	ARA24 GSF	RAN, mem	protein-coding	
chr20-34I	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr20	34100959	34105714	+	0	NA	intron (intron (N	8907 NR_00131E	8894	Hs.42918C	NR_00390E	ENSG000002EIF2S2	EIF2 EIF2	eukaryoti	protein-coding	
chr5-145L	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr5	14506538	14508904	+	0	NA	intron (intron (N	43738 NR_14581E	1.1E+08	NR_14581E	SNORD170	-	small	nucsnRNA		
chr5-728E	10.86197	-0.21869	0.710412	-0.30783	0.75821	0.981636	chr5	72880616	72899056	+	0	NA	exon (NM_exon (NM	11245 NR_03996E	1.01E+08	NR_03996E	ENSG000002MIR4804	-	microRNA	ncRNA		
chr9-111E	15.10016	-0.18872	0.613633	-0.30755	0.758425	0.981636	chr9	1.12E+08	1.12E+08	+	0	NA	intron (Alu)Sc SIN	32176 NR_01221E	22949	Hs.584864	NR_01221E	ENSG000002PTGR1	LTB4DH PC	prostagla	protein-coding	
chr2-159E	9.897917	-0.23169	0.753869	-0.30733	0.758589	0.981636	chr2	1.59E+08	1.59E+08	+	0	NA	TTS (NM_C TTS (NM_C	48295 NR_10694E	1.02E+08	NR_10694E	ENSG000002MIR6888	hsa-mir-ε	microRNA	ncRNA		
chr21-49E	9.897917	-0.23169	0.753869	-0.30733	0.758589	0.981636	chr21	46656205	46656419	+	0	NA	intron (MSTB1 LTF	20638 NR_20696E	3275	Hs.15416E	NR_00153E	ENSG000002PRMT2	HRMT1L L	protein α	protein-coding	
chr11-92C	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr11	9202329	9203012	+	0	NA	intron (NL2a LINE	62656 NR_14596E	23258	Hs.501857	NR_01521E	ENSG000002DENND5A	EIEE49 R	DENN dom	protein-coding	
chr11-65E	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr11	65044330	65044810	+	0	NA	TTS (NM_C TTS (NM_C	3360 NR_01329E	29901	Hs.23642	NR_01329E	ENSG000002SAC3D1	HSU7926E SAC3	dom	protein-coding	
chr14-96E	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr14	96211313	96233501	+	0	NA	intron (MIR113 DN	-23503 NR_00071C	623	Hs.52557E	NR_00071C	ENSG000002BDRKB1	B1BKR B1F	bradykin	protein-coding	
chr16-23A	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr16	23414865	23416152	+	0	NA	intron (intron (N	37681 NR_15360C	91949	Hs.185807	NR_15360E	ENSG000002COG7	CDG2E	component	protein-coding	
chr18-13C	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr18	13077512	13079391	+	0	NA	intron (NLIP47 LIN	87089 NR_03214E	55125	Hs.100914	NR_01806E	ENSG000002CEP192	PPP1R62	centrosom	protein-coding	
chr19-35E	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr19	3509025	3510711	+	0	NA	intron (NLIMB5 LIN	3557 NR_01626E	51343	Hs.41313E	NR_01626E	ENSG000002FZRI	CDC20C C	fizzy anc	protein-coding	
chr2-157E	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chr2	1.58E+08	1.58E+08	+	0	NA	intron (MER20B DN	39398 NR_001347	90	Hs.47031E	NR_00110E	ENSG000002ACVR1	ACTRI AC	activin β	protein-coding	
chrX-123E	5.932057	0.290078	0.946242	0.306558	0.75918	0.981636	chrX	1.24E+08	1.24E+08	+	0	NA	intron (Alu)Sc8 SI	28944 NR_001167	331	Hs.35607E	NR_001167	ENSG000002XIAP	API3 BIRC	X-linked	protein-coding	
chr11-12E	6.477642	0.27751	0.906076	0.306542	0.759192	0.981636	chr11	1.3E+08	1.3E+08	+	0	NA	intron (NLIME3Cz I	2471 NR_00616E	4798	Hs.53053E	NR_00616E	ENSG000002NFRKB	IN080G	nuclear f	protein-coding	
chr12-50E	6.477642	0.27751	0.906076	0.306542	0.759192	0.981636	chr12	50722434	50723519	+	0	NA	intron (intron (N	-4125 NR_00517I	466	Hs.64856E	NR_00517I	ENSG000002ATF1	EWS-ATF1	activati	protein-coding	
chr13-11E	6.477642	0.27751	0.906076	0.306542	0.759192	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (intron (N	-65494 NR_04666I	1.01E+08	Hs.65869E	NR_04666I	ENSG000002ATP11A-AS-	ATP11A	anc	ncRNA	
chr14-29E	6.477642	0.27751	0.906076	0.306542	0.759192	0.981636	chr14	29665090	29665806	+	0	NA	intron (NLIPB3 LIN	261648 NR_00134E	5587	Hs.50899E	NR_00274E	ENSG000002PRKD1	CHDED PKC	protein-coding		
chr16-25E	6.477642	0.27751	0.906076	0.306542	0.759192	0.981636	chr16	25142942	25143578	+	0	NA	intron (PRIMA41-i	7772 NR_03999E	1.01E+08	Hs.65757E	NR_03999E	ENSG000002LCMT1-AS2-	LCMT1	ant	ncRNA	
chr8-103E	6.477642	0.27751	0.906076	0.306542	0.759192	0.981636	chr8	1.04E+08	1.04E+08	+	0	NA	intron (NLIMC1 LIN	145012 NR_00134E	9699	Hs.655271	NR_01467E	ENSG000002RIMS2	OBOE RAB	regulati	protein-coding	
chr8-670A	11.32943	-0.22389	0.730372	-0.30654	0.759192	0.981636	chr8	67045551	67045899	+	0	NA	intron (intron (N	16408 NR_006837	10987	Hs.49191E	NR_006837	ENSG000002COPS5	CSN5 JAB1	COP9 sig	protein-coding	
chr9-606E	16.62247	0.180472	0.58893	0.30644	0.759269	0.981636	chr9	60625264	60626506	+	0	NA	Intergeni ALR Alpha	-288522 NR_00111E	727905	Hs.64549E	NR_00111E	ENSG000002SPATA31A	FAM75A5	SPATA31	s	protein-coding
chr14-35A	15.61357	0.184978	0.603758	0.306377	0.759318	0.981636	chr14	35400380	35403856	+	0	NA	intron (intron (N	2636 NR_02052E	4792	Hs.81328	NR_02052E	ENSG000002NFKBIA	EDAID2 I	NFKB	inh	protein-coding
chr1-323E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr1	32392188	32392842	+	0	NA	intron (intron (N	1926 NR_00130C	55108	Hs.353454	NR_01804E	ENSG000002BSCD1	-	BSD	dom	protein-coding
chr11-10E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (Alu)Y SINE	13247 NR_00001E	38	Hs.23237E	NR_00001E	ENSG000002ACAT1	ACAT MAT	acetyl-C	protein-coding	
chr12-12E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (Alu)Sx1 SI	2185 NR_00114E	91574	Hs.31912E	NR_15226E	ENSG000002C12orf65	COXPD7 S	F	chromosom	protein-coding
chr12-12E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (MIR SINE	13864 NR_13070G	196383	Hs.48817E	NR_14505E	ENSG000002RILPL2	RLP2	Rab	int	protein-coding
chr12-12E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr12	1.25E+08	1.25E+08	+	0	NA	intron (NL2a LINE	13575 NR_00239E	65985	Hs.65607E	NR_00239E	ENSG000002AACS	ACSF1 SUF	acetoac	protein-coding	
chr16-88E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr16	88698016	88700057	+	0	NA	exon (NM_exon (NM	4545 NR_00117I	115992	Hs.513804	NR_17884I	ENSG000002CRNF166	-	ring	ring	protein-coding
chr17-74E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr17	74793732	74795638	+	0	NA	intron (intron (N	18186 NR_01772E	54868	Hs.37026E	NR_01772E	ENSG000002MEM104	-	transmem	protein-coding	
chr19-621E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr19	6210986	6212898	+	0	NA	3' UTR (3' UTR (N	68033 NR_005934	4298	Hs.10095	NR_005934	ENSG000002MLL17	ENL L	TLG1 MLL1	sup	protein-coding
chr19-44E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr19	44984390	44986693	+	0	NA	intron (intron (N	-15923 NR_00650E	5971	Hs.65440E	NR_00650E	ENSG000002RELB	I-REL IM	RELB	prot	protein-coding
chr19-45E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr19	45003446	45004376	+	0	NA	intron (Alu)Sx1 SI	2447 NR_00650E	5971	Hs.65440E	NR_00650E	ENSG000002RELB	I-REL IM	RELB	prot	protein-coding
chr19-55E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr19	55298563	55299766	+	0	NA	intron (Alu)Sx3 SI	15167 NR_03243C	84446	Hs.12081N	NR_03243C	ENSG000002BRSK1	hSAD1	BR	serine	protein-coding
chr21-37E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr21	37239143	37239758	+	0	NA	intron (intron (N	27884 NR_00605E	10311	Hs.36948E	NR_00605E	ENSG000002VPS26C	DCRA DSCF	VPS26	enc	protein-coding
chr22-23E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr22	23821274	23822075	+	0	NA	intron (Alu)Sx1 SI	17327 NR_00113E	91319	Hs.59367E	NR_19844C	ENSG000002DERL3	C22orf14 d	erlin 3	protein-coding	
chr4-573E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr4	5737039	5737789	+	0	NA	intron (Tigger1 I	26208 NR_15371I	2121	Hs.64689E	NR_01455E	ENSG000002CEC1	DWF-1 EVC	EVC cili	protein-coding	
chr4-169A	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr4	1.69E+08	1.7E+08	+	0	NA	intron (NLPI1 LINE	112219 NR_00119E	4750	Hs.48118E	NR_01222E	ENSG000002NEK1	ALS24 NY	NIMA	rel	protein-coding
chr5-173E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (NLIME1 LIN	-32755 NR_00120E	662	Hs.14572E	NR_00120E	ENSG000002BNIP1	NIP1 SEC	E	int	protein-coding
chr9-107E	5.443327	0.301526	0.984386	0.306309	0.75937	0.981636	chr9	1.07E+08	1.07E+08	+	0	NA	intron (intron (N	93736 NR_12602E	340512	Hs.43252E	NR_12602E	ENSG000002LOC34051E-	-	uncharact	ncRNA	
chr16-21E	3.69897	-0.24505	0.800382	-0.30616	0.759482	0.981636	chr16	21898106	21898370	+	0	NA	Intergeni Alu Jb SIN	-31503 NR_02445E	1E+08	Hs.64843E	NR					

chr3-881f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr3	88153495	88159567	+	0 NA	exon (NM exon (NM	6572 NM_173824	285237 Hs. 476944NM_173824	ENSG000003orf38	-	chromosomprotein-coding	
chr3-1424 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (AluJr4 SI	-34782 NM_001282	5464 Hs. 435103NM_019001	ENSG000003XRN1	-	1-Sep 5'-3' exc protein-coding	
chr4-4271 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	4271522	4274445	+	0 NA	intron (Nintron (N	17038 NM_00114f	55646 Hs. 425427NM_01781f	ENSG000003LYAR	ZC2HC2 ZlLyl	antit protein-coding	
chr4-2642 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	26421660	26426915	+	0 NA	intron (Nintron (N	66199 NM_00073C	886 Hs. 129	NM_00073C	ENSG000003CKAR	CCR-A CCR	cholecyst protein-coding
chr4-3888 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	38884677	38885989	+	0 NA	intron (AluJr4 SI	17301 NR_03003C	693159	NR_03003C	ENSG000003MIR574	MIR574-3f	microRNA ncRNA
chr4-3991 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	39915719	39916582	+	0 NA	intron (AluJo SIN	61761 NM_00110C	23244 Hs. 331431NM_01520C	ENSG000003PDS5A	PIG54 SCC	PDS5 cohe protein-coding	
chr4-5262 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	52603841	52606096	+	0 NA	intron (Nintron (N	51571 NM_001134	64854 Hs. 7966	NM_02283f	ENSG000003USP46	-	ubiquitin protein-coding
chr4-7315 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	73133968	73134890	+	0 NA	intron (Nintron (N	-64670 NM_00130C	285521 Hs. 356697NM_17382f	ENSG000003COX18	COX18HS	cytochom protein-coding	
chr4-7891 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	78910685	78912029	+	0 NA	TTS (NR_TTS (NR_I	28081 NM_00104C	152559 Hs. 657312NM_17745f	ENSG000003PAQR3	RKTG	progestr protein-coding	
chr4-8676 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	86764507	86767070	+	0 NA	intron (Nintron (N	83821 NM_19796f	345274 Hs. 452999NM_19796f	ENSG000003SLC10A6	SOAT	solute c protein-coding	
chr4-1451 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr4	1.45E+08	1.45E+08	+	0 NA	intron (Nintron (N	-8035 NM_00125f	10393 Hs. 48087fNM_01488f	ENSG000003ANAPC10	APC10 DOC	anaphase protein-coding	
chr5-7044 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr5	70446972	70448603	+	0 NA	TTS (NM_TTS (NM_C	32413 NM_00151f	2966 Hs. 19135fNM_00151f	ENSG000003GTF2H2	BTF2 BTF2	general t protein-coding	
chr5-7776 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr5	77766728	77767951	+	0 NA	intron (Nintron (N	9000 NM_00129f	6902 Hs. 29121fNM_00460f	ENSG000003TBCA	-	tubulin f protein-coding	
chr5-1322 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr5	1.33E+08	1.33E+08	+	0 NA	intron (NLM2D LIN	31524 NM_00573f	10111 Hs. 63350fNM_00573f	ENSG000003RAD50	NBSLD RAD	RAD50 dot protein-coding	
chr5-140f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr5	1.41E+08	1.41E+08	+	0 NA	intron (Nintron (N	-6227 NM_00373f	8637 Hs. 594084NM_00373f	ENSG000003EIF4EBP3	4E-BP3 4E	eukaryoti protein-coding	
chr5-160C 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr5	1.6E+08	1.6E+08	+	0 NA	intron (Nintron (N	26657 NM_003314	7265 Hs. 51971fNM_003314	ENSG000003TTC1	TPR1	tetratric protein-coding	
chr5-178f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr5	1.79E+08	1.79E+08	+	0 NA	intron (Nintron (N	-18291 NM_17346f	91522 Hs. 66002fNM_17346f	ENSG000003COL23A1	-	collagen protein-coding	
chr6-244C 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr6	24405401	24406429	+	0 NA	intron (AluV SINE	2979 NR_10442f	57380 Hs. 65861fNM_02066f	ENSG000003MRS2	HPT MRS2	magnesium protein-coding	
chr6-5714 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr6	57142405	57146546	+	0 NA	intron (AluSzl SIN	27738 NR_110742	1.02E+08 Hs. 70571fNR_110742	ZNF451-AS-	ZNF451	rencRNA	
chr6-147f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr6	1.47E+08	1.47E+08	+	0 NA	intron (Nintron (N	-145513 NM_00103C	389432 Hs. 56797fNM_00103C	ENSG000003SAMD5	dJ875H10	sterile e protein-coding	
chr6-149f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr6	1.5E+08	1.5E+08	+	0 NA	exon (NM exon (NM	52600 NM_00136C	5110 Hs. 27925fNM_00538f	ENSG000003PCMT1	P1MT	protein-l protein-coding	
chr6-166f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr6	1.66E+08	1.66E+08	+	0 NA	intron (NMLT1A LTF	13734 NM_14516f	113402 Hs. 48714fNM_14516f	ENSG000003SFT2D1	C6orf83 SFT2	dom protein-coding	
chr7-2474 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr7	24748544	24749277	+	0 NA	intron (NLTR52 LTF	8554 NM_00112f	1687 Hs. 52070fNM_00440f	ENSG000003GSDME	DFNA5 ICF	gasderm protein-coding	
chr7-6654 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr7	66546595	66548684	+	0 NA	intron (AluSx1 SI	44768 NR_111974	493754 Hs. 73240fNR_02093f	ENSG000003GS1-124fE	-	RAB guanipseudo	
chr7-135f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr7	1.36E+08	1.36E+08	+	0 NA	exon (NM exon (NM	-39690 NM_00113C	647087 Hs. 20002fNM_00113C	ENSG000003TMTP1	C7orf73 F	short tr protein-coding	
chr8-388C 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr8	38809802	38812470	+	0 NA	intron (Nintron (N	5686 NM_00135f	6867 Hs. 27924fNM_00628f	ENSG000003TACC1	Gas5	transform protein-coding	
chr9-282f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	2825291	2829741	+	0 NA	intron (NChar1e E	16579 NM_01487f	9933 Hs. 49330fNM_01487f	ENSG000003PUM3	HA-5 HLA	pumilio f protein-coding	
chr9-324f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	32453397	32455383	+	0 NA	TTS (NM_TTS (NM_C	69747 NM_00136f	48 Hs. 56722fNM_00219f	ENSG000003ACO1	ACONS HEI	aconitase protein-coding	
chr9-362f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	36239515	36240872	+	0 NA	intron (NLIPIA17 LI	18255 NM_00119f	10020 Hs. 5920	NM_00547f	ENSG000003GNE	DMRV GLCN	glucosamin protein-coding
chr9-982C 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	98201173	98202555	+	0 NA	intron (Nintron (N	-9227 NM_05282f	7464 Hs. 113094NM_00338f	ENSG000003CORO2A	CLIP INB I	conon e protein-coding	
chr9-111f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	2828 NM_00101f	2790 Hs. 53419fNM_00101f	ENSG000003GNG10	-	G protei protein-coding	
chr9-114f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	1.14E+08	1.14E+08	+	0 NA	intron (NFLAM_A SI	-24973 NM_00060f	5004 Hs. 52235fNM_00060f	ENSG000003ORM1	AGP-A AGF	orosomucc protein-coding	
chr9-127f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	1.27E+08	1.27E+08	+	0 NA	intron (NLIPIA16 LI	7248 NM_000713f	7633 Hs. 52239fNM_000713f	ENSG000003ZNF79	p17	zinc fng protein-coding	
chr9-1284 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	intron (NMIR SINE	4315 NM_15343f	4957 Hs. 12905fNM_00254f	ENSG000003ODF2	CT134 ODF	outer der protein-coding	
chr9-130f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	1.31E+08	1.31E+08	+	0 NA	intron (NLA2A LINE	3205 NM_01428f	23404 Hs. 65464fNM_01428f	ENSG000003EXOSC2	RRP4 Rrp4	exosome c protein-coding	
chr9-132f 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chr9	1.33E+08	1.33E+08	+	0 NA	intron (NLIPIA LINE	27868 NM_00136f	7248 Hs. 370854NM_00036f	ENSG000003TSC1	LAM TSC	compl protein-coding	
chrX-7811 6.674626	-0.27229	0.890018	-0.30594	0.759652	0.981636	chrX	78117472	78119961	+	0 NA	intron (NLTR33 LTF	14468 NM_000291	5230 Hs. 78771	NM_000291	ENSG000003CPGK1	HEL-S-68f	phosphogl protein-coding
chr11-10f 6.6121	0.229772	0.751086	0.305919	0.759666	0.981636	chr11	1.08E+08	1.08E+08	+	0 NA	intron (Nintron (N	48143 NM_001351	472 Hs. 367437NM_000051	ENSG000003ATM	ATI ATA ATM	seri protein-coding	
chr16-224 10.39265	-0.22265	0.727873	-0.30589	0.759691	0.981636	chr16	22479264	22483357	+	0 NA	intron (Nintron (N	-23139 NR_02445f	1E+08 Hs. 64843fNR_02445f	LOC10019C-	-	uncharactcRNA	
chr5-7021 15.65471	0.185906	0.607893	0.305821	0.759741	0.981636	chr5	70218959	70220106	+	0 NA	non-codiron-codir	6263 NR_024054	11039 Hs. 58250fNM_006780	SMA4	SMA3 b55c	glucuronipseudo	
chr11-73 10.85411	-0.21744	0.711243	-0.30572	0.759819	0.981636	chr11	73366447	73366820	+	0 NA	intron (AluJb SIN	-9756 NM_15222f	84957 Hs. 53372fNM_032871	ENSG000003RELT	A13C TNF	RELT TNF protein-coding	
chr12-437 10.85411	-0.21744	0.711243	-0.30572	0.759819	0.981636	chr12	43744212	43746386	+	0 NA	intron (THEIC LINE	13491 NM_00109f	83448 Hs. 23554	NM_03129f	ENSG000003PUSL7	-	pseudouri protein-coding
chr2-365f 10.85411	-0.21744	0.711243	-0.30572	0.759819	0.981636	chr2	36586622	36586943	+	0 NA	intron (AluJr SIN	11386 NM_00104f	9637 Hs. 25856fNM_00510f	ENSG000003FEZ2	HUM3CL	fascicul protein-coding	
chr20-35f 10.85411	-0.21744	0.711243	-0.30572	0.759819	0.981636	chr20	35653075	35655316	+	0 NA	promoter-promoter-	-287 NM_00391f	8904 Hs. 24641fNM_00391f	ENSG000003CPNE1	COPN1 CPN	copine l protein-coding	
chr20-44f 10.85411	-0.21744	0.711243	-0.30572	0.759819	0.981636	chr20	44904086	44907836	+	0 NA	intron (Nintron (N	-4099 NR_13498f	80336 Hs. 641481NM_00112f	ENSG000003PABPCL	C2orf11f	poly (A) t protein-coding	
chr21-33f 10.85411	-0.21744	0.711243	-0.30572	0.759819	0.981636	chr21	33549189	33563094	+	0 NA	intron (Nintron (N	5479 NR_10675f	1.02E+08 NR_10675f	ENSG000003MIR6501	hosa-mir-	microRNA ncRNA	
chr14-601 7.110659	-0.26759	0.875448	-0.30566	0.759863	0.981636	chr14	60146944	60147834	+	0 NA	3' UTR (N3' UTR (N	-18009 NM_01602f	51635 Hs. 59719	NM_01602f	ENSG000003DHR57	CGI-86 SE	dehydrog protein-coding
chr2-112f 7.110659	-0.26759	0.875448	-0.30566	0.759863	0.981636	chr2	1.13E+08	1.13E+08	+	0 NA	intron (NAluSx SIN	-12738 NR_136321	1.05E+08 Hs. 59954fNR_136321	LOC10537f-	-	uncharactcRNA	
chr1-410f 3.427762	-0.3765	1.232251	-0.30554	0.759956	0.981636	chr1	41065369	41066259	+	0 NA	intron (NLM1C LIN	-44059 NM_00116f	200172 Hs. 19460fNM_14499f	ENSG000003SLFN11	-	schlafen protein-coding	
chr15-637 6.17203	-0.28878	0.945592	-0.30539	0.760066	0.981636	chr15	63729277	63729856	+	0 NA	exon (NM exon (NM	104382 NM_00392f	89				



chr3-1395	10.43379	-0.22063	0.72954	-0.30242	0.762331	0.981636	chr3	1.39E+08	1.39E+08	+	0	NA	intron (NL2a LINE)	8113	NM_004766	9276	Hs.68161ENM_004766	ENSG00000COPB2	MCPH19	beoatomer protein-coding
chr1-1081	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr1	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	53437	NM_213651	29957	Hs.656877NM_01338E	ENSG00000SLC25A24	APC1 SCAM	solute cεprotein-coding
chr11-20C	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr11	20077955	20078809	+	0	NA	intron (Nintron (N	-29079	NR_046672	1.01E+08	Hs.55791ENR_046672	ENSG00000NAV2-AS2	NAV2	antincRNA
chr11-102	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr11	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	-99346	NM_001166	330	Hs.127799NM_001166	ENSG00000BIRC3	AIP1 AP2	baculovir protein-coding
chr12-62	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr12	62537225	62539880	+	0	NA	intron (Nintron (N	64882	NR_121682	283416	Hs.375881NM_17589E	ENSG00000LINC01465	C12orf61	long intencRNA
chr13-484	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr13	48478586	48479223	+	0	NA	intron (Nintron (N	-34235	NM_005767	10161	Hs.123464NM_005767	ENSG00000CLPAR6	ARWH1 HYF	lysofosf protein-coding
chr14-605	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr14	60956507	60958063	+	0	NA	intron (THE1B LTF	23794	NM_00135C	57570	Hs.380159NM_02081C	ENSG00000TRMT5	CPXD26 K	tRNA methyl protein-coding
chr18-275	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr18	2750130	2753877	+	0	NA	intron (NMER33 DNA	-95003	NM_032048	84034	Hs.53281ENM_03204E	ENSG00000EMILIN2	EMILIN-2 elastin	nprotein-coding
chr19-515	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr19	51576758	51578833	+	0	NA	intron (NALuY SINE	6512	NM_007147	7728	Hs.119014NM_007147	ENSG00000ZNF175	OTK18	zinc fing protein-coding
chr2-652	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr2	65235650	65235606	+	0	NA	intron (Nintron (N	7398	NM_00100E	10097	Hs.643727NM_00572E	ENSG00000ACTR2	ARP2	actin relprotein-coding
chr2-6915	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr2	69158431	69158722	+	0	NA	intron (NMER47A DN	54894	NR_036073	1E+08	NR_036073	ENSG00000MIR3126	mir-3126	microRNA ncRNA
chr3-4728	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr3	47288400	47288928	+	0	NA	intron (Nintron (N	5720	NM_02501C	23276	Hs.51794ENM_02501C	ENSG00000KLHL18	-	kelch lik protein-coding
chr3-5756	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr3	57565660	57566897	+	0	NA	3' UTR (N3' UTR (N	10004	NM_00132E	201626	Hs.57299ENM_17796E	ENSG00000PDEL2	2'-PDE 2-	phosphodi protein-coding
chr3-1565	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	3' UTR (N3' UTR (N	13103	NM_00130E	6747	Hs.51834ENM_00710E	ENSG00000CSSR3	TRAP3	signal sεprotein-coding
chr4-121C	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr4	1210469	1211373	+	0	NA	TTS (NM_TTS (NM_C	801	NR_104331	285463	Hs.707614NR_104331	ENSG00000CTBP1-AS	PCAT10	CTBP1 antncRNA
chr4-287E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr4	2876352	2876970	+	0	NA	intron (NALuY SINE	32511	NM_00128E	118	Hs.18370ENM_00111E	ENSG00000ADD1	ADDA	adducin lprotein-coding
chr4-128E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr4	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	9878	NM_00632C	10424	Hs.50791ENM_00632C	ENSG00000PGRMC2	DG6 PMBP	progester protein-coding
chr5-150E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr5	13768945	13769662	+	0	NA	intron (NALuYc SIN	175177	NM_00136E	1767	Hs.21236ENM_00136E	ENSG00000DNAH5	C1LD3 DN	dynein αprotein-coding
chr5-1341	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr5	1.34E+08	1.34E+08	+	0	NA	3' UTR (N3' UTR (N	25437	NR_17067E	6500	Hs.17162ENM_00693C	ENSG00000SKP1	EMC19 OCF5	-phase lprotein-coding
chr5-150E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	22337	NR_157074	972	Hs.43656ENM_00435E	ENSG00000CD74	DHLAG HLA	CD74 mole protein-coding
chr6-591E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr6	591950	592567	+	0	NA	intron (Nintron (N	64706	NR_14895E	135458	Hs.66903ENM_14895E	ENSG00000HUS1B	-	HUS1 checprotein-coding
chr6-789E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr6	78996132	78996699	+	0	NA	intron (NLTR79 LTF	81839	NM_017934	55023	Hs.511817NM_017934	ENSG00000PHIP	BRWD2 DC	pleckstri protein-coding
chr6-1497	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	intron (NMLT1J LTF	10596	NM_00136E	5110	Hs.279257NM_00538E	ENSG00000PCMT1	P1MT	protein-l protein-coding
chr7-300E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr7	30062967	30064318	+	0	NA	intron (Nintron (N	18557	NM_00136E	84725	Hs.23349ENM_03263E	ENSG00000PLEKH8A	FAPP2	pleckstri protein-coding
chr7-121E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr7	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	-80935	NM_016087	51384	Hs.27237ENM_016087	ENSG00000WNT16	-	Wnt familt protein-coding
chr8-889C	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr8	8890891	8892357	+	0	NA	exon (NM exon (NM	2006	NM_00422E	9258	Hs.379414NM_00422E	ENSG00000MFHAS1	LRRC65	mantant protein-coding
chr8-3044	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr8	30445872	30447144	+	0	NA	intron (Nintron (N	-6107	NR_04620E	1E+08	Hs.12681ENR_04620E	ENSG00000RBPMS-AS1	RBPMS	antncRNA
chr8-123E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr8	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	3652	NM_032847	84933	Hs.707401NM_032847	ENSG00000C8orf76	-	chromoson protein-coding
chr9-773E	6.666769	-0.2703	0.894161	-0.30229	0.762431	0.981636	chr9	77370625	77373038	+	0	NA	intron (NLIPA2 LIN	-75181	NR_121184	1.02E+08	Hs.434324NR_121184	ENSG00000GNA14-AS1	GNA14	antncRNA
chr1-272E	6.820888	0.265549	0.878574	0.302249	0.762462	0.981636	chr1	27264470	27265083	+	0	NA	intron (NALuJr SIN	30144	NM_01502E	23038	Hs.469154NM_01502E	ENSG00000WDC1C	ADP DCAF9	WD and tεprotein-coding
chr16-23E	6.820888	0.265549	0.878574	0.302249	0.762462	0.981636	chr16	23531786	23532204	+	0	NA	intron (NALuSx SIN	-21501	NM_015044	23062	Hs.46033ENM_015044	ENSG00000CGA2	VEAR	golgi ass protein-coding
chr2-170E	6.820888	0.265549	0.878574	0.302249	0.762462	0.981636	chr2	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	-106392	NR_04568E	140469	Hs.67190CNM_13899E	ENSG00000MYO3B	-	myosin lI protein-coding
chr22-42E	6.820888	0.265549	0.878574	0.302249	0.762462	0.981636	chr22	42890237	42891001	+	0	NA	intron (NALuSx SIN	-33346	NM_001142	26286	Hs.68522ENM_01457C	ENSG00000ARFGAP3	ARFGAP1	ADP ribos protein-coding
chr5-149E	6.820888	0.265549	0.878574	0.302249	0.762462	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	intron (NALuS6 SI	18346	NM_001271	1452	Hs.52986ENM_00189E	ENSG00000CSNK1A1	CK1 CK1a	casein kiprotein-coding
chr4-1187	10.3848	-0.22129	0.732171	-0.30223	0.762475	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	54498	NM_020961	57721	Hs.59687ENM_020961	ENSG00000METTL14	hMETTL14	methyltrε protein-coding
chr1-320E	9.43646	-0.23764	0.786753	-0.30205	0.762613	0.981636	chr1	32022142	32022399	+	0	NA	intron (NALuSc SIN	8403	NM_001271	10657	Hs.44589ENM_00655E	ENSG00000KHDRB51	Sam68 p62	KH RNA bε protein-coding
chr12-98E	10.88739	-0.21431	0.709745	-0.30195	0.762687	0.981636	chr12	98596157	98604421	+	0	NA	TTS (NR_TTS (NR_C	654	NR_00301E	677832	Hs.69325ENR_00301E	ENSG00000SNORA53	ACA53	small nuc snoRNA
chr18-35E	10.88739	-0.21431	0.709745	-0.30195	0.762687	0.981636	chr18	35331853	35340534	+	0	NA	3' UTR (N3' UTR (N	8227	NM_00130E	7572	Hs.51480ENM_00696E	ENSG00000ZNF24	KOX17 RSC	zinc fing protein-coding
chr19-52E	10.88739	-0.21431	0.709745	-0.30195	0.762687	0.981636	chr19	52015322	52025861	+	0	NA	intron (NMER77B LI	7788	NM_02504C	80110	Hs.29233ENM_02504C	ENSG00000ZNF614	-	zinc fing protein-coding
chr2-324E	10.88739	-0.21431	0.709745	-0.30195	0.762687	0.981636	chr2	32466664	32469777	+	0	NA	intron (Nintron (N	-63933	NR_03028E	693143	NR_03028E	ENSG00000MIR558	MIRN558	microRNA ncRNA
chr2-3927	10.88739	-0.21431	0.709745	-0.30195	0.762687	0.981636	chr2	39276275	39279215	+	0	NA	intron (NALuS2 SI	-33762	NR_144521	344387	Hs.403201NM_00100E	ENSG00000CDKL4	-	cyclin dε protein-coding
chr9-577E	10.88739	-0.21431	0.709745	-0.30195	0.762687	0.981636	chr9	5776554	5780651	+	0	NA	Intergeni LIMB7 LI	54515	NM_02489E	79956	Hs.59107ENM_02489E	ENSG00000CERMP1	FXNA KIAA	endoplasm protein-coding
chr1-154E	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (NL2a LINE)	-2844	NM_01865E	55891	Hs.27239ENM_01865E	ENSG00000LENEP	LEP503	lens epit protein-coding
chr11-96E	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr11	96382019	96382975	+	0	NA	3' UTR (N3' UTR (N	7319	NM_00136E	79780	Hs.52508ENM_01414E	ENSG00000CCDC82	HSPC048	coiled-cε protein-coding
chr16-10E	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr16	105570	106321	+	0	NA	intron (Nintron (N	27720	NM_00101E	4350	Hs.45959ENM_00243C	ENSG00000MPG	AAG ADPG	N-methyl l protein-coding
chr16-13E	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr16	132416	1325161	+	0	NA	3' UTR (N3' UTR (N	-8757	NM_00119E	8938	Hs.458427NM_00393C	ENSG00000BTAIP3	BAP3	BAN1 assε protein-coding
chr18-947	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr18	9478894	9479414	+	0	NA	intron (NALuJb SIN	3641	NM_00678E	10928	Hs.52899ENM_00678E	ENSG00000RALBP1	RIP1 RLIF	raIA binc protein-coding
chr2-171E	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	intron (NLIMB7 LI	-3291	NM_00113E	9874	Hs.744917NM_01229C	ENSG00000TLK1	PKU-beta	tousled l protein-coding
chr4-106E	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr4	1.06E+08	1.06E+08	+	0	NA	intron (NA-rich Lc	-83122	NM_001142	9255	Hs.59168ENM_00475E	ENSG00000AIMP1	EMAP2 EM	aminoacyl protein-coding
chr5-6124	6.444361	0.273521	0.906217	0.301827	0.762784	0.981636	chr5	61249173	61250543	+	0	NA	TTS (NR_TTS (NR_I	15071	NR_146624	1.05E+08	Hs.62168ENR_146624	ENSG00000LINC02057	-	long intencRNA
chr5-6941																				

chr4-12962	5.451184	0.29863	0.996341	0.299727	0.764385	0.981636	chr4	1299087	1300633	+	0	NA	intron (NL2a LINE)	-9583	NM_001297	10296	Hs.13989	ENM_005882	ENSG000000MAEA	EMLP EMP	macrophag protein-coding	
chr9-1085	5.451184	0.29863	0.996341	0.299727	0.764385	0.981636	chr9	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	13235	NM_001318	8518	Hs.49473	ENM_003642	ENSG000000ELP1	DYS FD Fk	elongator protein-coding	
chr1-8564	5.410045	0.296528	0.989771	0.299592	0.764488	0.981636	chr1	85644701	85645691	+	0	NA	Intergeni LIPA3 LIN	63237	NM_00117C	54680	Hs.5111	NM_017953	ENSG000000ZNHIT6	BCD1 Clor	zinc fing protein-coding	
chr14-100	5.410045	0.296528	0.989771	0.299592	0.764488	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	Intergeni Intergeni	-1216	NM_001134	388015	Hs.298602	NM_001134	ENSG000000RTL1	HUR1 MAR1	retrotrans protein-coding	
chr2-9408	5.410045	0.296528	0.989771	0.299592	0.764488	0.981636	chr2	9408885	9409869	+	0	NA	intron (Nintron (N	13214	NM_00131E	9270	Hs.467662	ENM_004763	ENSG000000ITGB1BP1	ICAP-1A I	integrin protein-coding	
chr2-2034	5.410045	0.296528	0.989771	0.299592	0.764488	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (Nintron (N	83647	NM_21358E	65059	Hs.471162	NM_025252	ENSG000000CRAPH1	ALS2CR18	Ras assoc protein-coding	
chr5-1574	6.428645	0.278402	0.930587	0.299166	0.764812	0.981636	chr5	1.57E+08	1.57E+08	+	0	NA	intron (NMIRb SINE	-32691	NR_13620E	1.03E+08	Hs.57088	NR_13620A	LOC102724-		uncharactncRNA	
chr1-2176	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr1	2.18E+08	2.18E+08	+	0	NA	intron (NLIPA13 LI	82760	NM_001297	55105	Hs.362342	ENM_001804	ENSG000000GPATCH2	CT110 GP	A-parach protein-coding	
chr13-956	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr13	95599216	95600160	+	0	NA	intron (Nintron (N	45018	NM_19896E	22873	Hs.65658	ENM_014934	ENSG000000CDZIP1	DZIP DZIF	DAZ inter protein-coding	
chr15-446	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr15	44521206	44521646	+	0	NA	intron (Nintron (N	15474	NR_03417I	645212	Hs.594287	NR_03417O	E1F3J3-DT	E1F3J3-AS1	E1F3J3	dincRNA
chr18-137	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr18	13734613	13735385	+	0	NA	intron (Nintron (N	8326	NM_00130E	8731	Hs.592347	ENM_003799	ENSG000000CRNMT	CMT1 CMT1	RNA guiv protein-coding	
chr2-1134	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	intron (NLIPA3 LIN	-21779	NM_01218A	200350	Hs.591554	ENM_012184	ENSG000000FOXDL1	FOXD5 ba	forkhead protein-coding	
chr5-1674	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr5	16748932	16749950	+	0	NA	intron (NALuSz SIN	-132383	NM_001034	54463	Hs.481704	NM_01900C	ENSG000000RETRG1	FAM1348 J	reticulo protein-coding	
chr7-9962	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr7	99626518	99627535	+	0	NA	intron (NLIMC5a LI	10080	NM_00135C	221785	Hs.446297	NM_14511E	ENSG000000ZSCAN25	ZNF498	zinc fing protein-coding	
chr9-1284	6.707908	-0.26717	0.893358	-0.29906	0.764896	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	exon (NM exon (NM	-5592	NM_001003	2733	Hs.52241E	ENM_001499	ENSG000000GLE1	CAAHG CA	GLE1 RNA protein-coding	
chr3-1015	11.34099	-0.20849	0.697428	-0.29895	0.76498	0.981636	chr3	1.02E+08	1.02E+08	+	0	NA	exon (NM exon (NM	5633	NM_020357	57092	Hs.732633	NM_020357	ENSG000000PCNP	-	PEST prot	protein-coding
chr19-375	5.988912	0.287119	0.960504	0.298926	0.764997	0.981636	chr19	37352708	37353253	+	0	NA	intron (NALuSz SIN	-18119	NM_032453	84503	Hs.59094	ENM_032453	ENSG000000ZNF527	-	zinc fing protein-coding	
chr2-275	5.988912	0.287119	0.960504	0.298926	0.764997	0.981636	chr2	27594410	27594868	+	0	NA	intron (NSVA_A Ret	11597	NM_032434	84503	Hs.52917E	ENM_032434	ENSG000000ZNF512	-	zinc fing protein-coding	
chr1-199	7.094493	-0.26396	0.883073	-0.29891	0.765011	0.981636	chr1	19904291	19905147	+	0	NA	intron (Nintron (N	18898	NM_01458E	30814	Hs.27237E	NM_01458E	ENSG000000PLA2G2E	GIE	sPLA	phospholip protein-coding
chr6-172	5.751713	-0.29975	1.003085	-0.29882	0.765074	0.981636	chr6	17283095	17283512	+	0	NA	intron (NTrigger19e	602	NM_15302C	221662	Hs.519904	NM_15302C	ENSG000000CRBM24	RNPC6 dJ	RNA bindi protein-coding	
chr1-539	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr1	53967885	53971093	+	0	NA	Intergeni AluJb SIN	23139	NM_00125E	115353	Hs.419004	NM_005294	ENSG000000LRRC42	dJ167A19	leucine i protein-coding	
chr17-534	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr17	5347302	5348485	+	0	NA	intron (Nintron (N	65609	NM_00129I	9135	Hs.584784	NM_00470C	ENSG000000RABEP1	RAB5EP RA	rabaptin, protein-coding	
chr18-57	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr18	57618483	57619941	+	0	NA	intron (NALuJb SIN	2624	NM_00453E	4677	Hs.465224	NM_00453E	ENSG000000CNARS	ASNRs NAF	asparagir protein-coding	
chr4-122	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (NLIPB1 LIN	45120	NM_015312	84162	Hs.408142	NM_015312	ENSG000000K1AA1109	ALFKUCs FK	IAA1109 protein-coding	
chr7-6141	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr7	6141139	6141547	+	0	NA	intron (NALuSx4 SI	30794	NM_001367	9265	Hs.48747E	NM_004227	ENSG000000CYTH3	ARN03 GRF	cytohesir protein-coding	
chr8-1794	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr8	17947654	17951363	+	0	NA	intron (NALuSz SIN	26520	NM_00135E	5108	Hs.49114E	NM_006197	ENSG000000PCMI	PTC4 RET	pericytl protein-coding	
chr9-9808	7.128225	-0.25893	0.867102	-0.29862	0.765231	0.981636	chr9	98087490	98087831	+	0	NA	exon (NM exon (NM	39028	NM_01894E	54187	Hs.522621	ENM_01894E	ENSG000000NANS	HEL-S-10C	N-acetyl protein-coding	
chr11-69	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr11	69078787	69080031	+	0	NA	intron (Nintron (N	-3767	NR_036122	1E+08	NR_036122	ENSG000000MIR3164	-	microRNA	ncRNA	
chr16-177	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr16	17762029	1777622	+	0	NA	TTS (NM_C TTS (NM_C	3597	NM_001257	197342	Hs.7247	NM_00101C	ENSG000000EME2	SLX2B gs	lesential protein-coding	
chr17-537	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr17	5372147	5372462	+	0	NA	intron (NALuSx3 SI	-4737	NM_00116C	84268	Hs.46208E	NM_03230E	ENSG000000RPAIN	HRIP RIP	RPA inter protein-coding	
chr17-438	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr17	43829578	43830165	+	0	NA	intron (Nintron (N	3323	NR_14834E	4356	Hs.39656E	NM_001932	ENSG000000MPP3	DLG3	membrane protein-coding	
chr2-364	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr2	36483423	36484189	+	0	NA	intron (Nintron (N	114362	NM_001042	9637	Hs.25856E	NM_005102	ENSG000000PEZ2	HUM3CL	fasciculE protein-coding	
chr20-63	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr20	63891284	63892752	+	0	NA	TTS (NM_C TTS (NM_C	-3108	NM_02521E	80331	Hs.16441E	NM_02521E	ENSG000000DNAJC5	CLN4 CLN4	DnaJ heat protein-coding	
chr22-497	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr22	49783414	49785733	+	0	NA	intron (NCpG	39758	NR_14633A	23774	Hs.12795	ENM_014577	ENSG000000CBRD1	BRL BRPF1	bromodomE protein-coding	
chr4-488	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr4	48853744	48855510	+	0	NA	intron (Nintron (N	5576	NR_14680E	1.01E+08	Hs.66106E	NR_14680E	ENSG000000OCIAD1-AS	-	OCIAD1	arcncRNA
chr4-128	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr4	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	127506	NM_001287	79960	Hs.12420	NM_02490C	ENSG000000JADE1	PHF17	jade fami protein-coding	
chr4-182	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr4	1.83E+08	1.83E+08	+	0	NA	intron (NMIRc SINE	14181	NM_00135I	1635	Hs.18385	ENM_001921	ENSG000000CDDTD	-	dCMP	dean protein-coding
chr4-184	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr4	1.84E+08	1.84E+08	+	0	NA	intron (NALuSx8 SI	-24070	NR_125933	1.03E+08	Hs.432281	NR_125933	ENSG000000LINC02362	-	long intencRNA	
chr7-146	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr7	1469881	1472008	+	0	NA	exon (NM exon (NM	11474	NM_18292A	79778	Hs.376617	ENM_02472E	ENSG000000MICALL2	JRAB MIC	MICAL2 linc protein-coding	
chr7-254	5.95563	0.282579	0.946387	0.298587	0.765255	0.981636	chr7	2544679	2545532	+	0	NA	intron (NALuSg SIN	10419	NM_00135C	221927	Hs.52062E	ENM_15274E	ENSG000000BRAT1	BAAT1 C7c	BRCA1 asE protein-coding	
chr1-923	6.948807	0.261569	0.878952	0.297591	0.766015	0.981636	chr1	92520397	92321041	+	0	NA	intron (Nintron (N	21660	NM_02481E	79871	Hs.444421	NM_02481E	ENSG000000RPAP2	ClorF82 F	RNA poly protein-coding	
chr12-95	6.948807	0.261569	0.878952	0.297591	0.766015	0.981636	chr12	95508800	95508873	+	0	NA	intron (NMLT1_J-int	34574	NM_001317	10988	Hs.44498E	NM_00683E	ENSG000000MAP2	MAP2 MNP	methionyl protein-coding	
chr15-64	6.948807	0.261569	0.878952	0.297591	0.766015	0.981636	chr15	64694369	64695461	+	0	NA	intron (Nintron (N	8366	NM_00130I	4947	Hs.744924	NM_002537	ENSG000000OAZ2	AZ2	ornithine protein-coding	
chr2-199	6.948807	0.261569	0.878952	0.297591	0.766015	0.981636	chr2	1.99E+08	1.99E+08	+	0	NA	intron (Nintron (N	149336	NR_134967	23314	Hs.516617	NM_01526E	ENSG000000SATB2	GLSS	SATB	home protein-coding
chr3-158	6.948807	0.261569	0.878952	0.297591	0.766015	0.981636	chr3	1.55E+08	1.55E+08	+	0	NA										





chr19-555.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr19	55595356	55597562	+	0	NA	intron (NL2a LINE	3058	NR_032836	84922	Hs.515617NM_032836	ENSG000003FIZ1	ZNF798	FLT3	intcprotein-coding		
chr20-625.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr20	62340833	62342365	+	0	NA	intron (NLIMS LINE	-9042	NR_039911	1.01E+08	NR_039911	ENSG000003MIR4758	-	microRNA	ncRNA		
chr22-298.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr22	29833554	29834439	+	0	NA	intron (NFLAM_C SI	4278	NR_001366	84164	Hs.731754NM_032204	ENSG000003ACC2	ASC1p100	activatir	protein-coding		
chr4-136.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr4	13606039	13606892	+	0	NA	intron (Nintron (N	21260	NR_148894	259282	Hs.744935NM_148894	ENSG000003BOD1L1	BOD1L	IFAM	biorentc	protein-coding	
chr5-3705.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr5	37052938	37054135	+	0	NA	intron (NMER44A DN	176767	NR_015384	25836	Hs.481927NM_015384	ENSG000003NPBL	CDDL3 CDDL3NPBL	col	protein-coding		
chr9-1276.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (NAluSx1 SI	29982	NR_037477	1.01E+08	NR_037477	ENSG000003MIR3911	mir-3911	microRNA	ncRNA		
chr1-193.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr1	19302134	19303321	+	0	NA	TTS (NM_C TTS (NM_C	-6991	NR_037847	1.01E+08	NR_037847	LOC100506	-	uncharactncRNA			
chr10-104.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	intron (Nintron (N	23768	NR_03076C	1E+08	NR_03076C	ENSG000003MIR936	MIRN936	tmicroRNA	ncRNA		
chr11-435.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr11	43397943	43398856	+	0	NA	intron (Nintron (N	39479	NR_01825E	55761	Hs.191186NM_01825E	ENSG000003TTC17	-	tetratric	protein-coding		
chr11-434.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr11	43474918	43477846	+	0	NA	intron (NLIMC5 LIN	-83274	NR_031577	1E+08	NR_031577	ENSG000003MIR670	hsa-mir-670	microRNA	ncRNA		
chr13-282.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr13	28281945	28283253	+	0	NA	intron (N(CACATG) R	-143425	NR_029383	1E+08	Hs.123191NR_029383	PAN3-AS1	-	PAN3	anticrRNA		
chr15-985.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr15	98823763	98825176	+	0	NA	intron (Nintron (N	40043	NR_039864	1.01E+08	NR_039864	ENSG000003MIR4714	-	microRNA	ncRNA		
chr16-274.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr16	27474385	27475696	+	0	NA	intron (Nintron (N	-21647	NR_03125E	283888	Hs.66093E NR_03125E	ENSG000003IL21R-AS1	-	IL21R	anticrRNA		
chr17-756.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr17	75672748	75673496	+	0	NA	intron (Nintron (N	5784	NR_013716C	29115	Hs.65508E NR_013716C	ENSG000003SAP30BP	HNGP HTF	SAP30	bir	protein-coding	
chr18-768.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr18	76879099	76881953	+	0	NA	intron (Nintron (N	56366	NR_00734E	7776	Hs.719137NM_00734E	ENSG000003ZNF236	ZNF236A	Z	zinc	fin	protein-coding
chr19-137.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr19	13738021	13738549	+	0	NA	intron (Nintron (N	6533	NR_00132C	81576	Hs.24998	NR_03081E	ENSG000003CCDC130	-	coiled-c	protein-coding	
chr20-185.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr20	18551863	18552856	+	0	NA	intron (Nintron (N	-15061	NR_00134E	388789	Hs.34909E NR_00134E	ENSG000003SMIM26	LINC00495	small	int	protein-coding	
chr3-144.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr3	14465785	14467091	+	0	NA	intron (NMIRc SINE	63832	NR_001134	6533	Hs.52948E NR_00304E	ENSG000003SLC6A6	TAUT	solute	c	protein-coding	
chr3-142.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr3	1.42E+08	1.42E+08	+	0	NA	intron (Nintron (N	88017	NR_001282	54646	Hs.43510E NR_019001	ENSG000003XRN1	1-Sep 5'-3'	exc	protein-coding		
chr4-2337.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr4	2337964	23395058	+	0	NA	intron (NAluSx1 SI	26303	NR_00117E	57732	Hs.29205E NR_02097E	ENSG000003ZFVE28	LST2 LYST	zinc	fin	protein-coding	
chr4-561.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr4	5613777	5615521	+	0	NA	intron (Nintron (N	89493	NR_126517	10141	Hs.17797E NR_00575E	ENSG000003LINC01587	C4orf6	f	linc	ncRNA	
chr5-1755.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr5	1.76E+08	1.76E+08	+	0	NA	TTS (NM_C TTS (NM_C	36054	NR_022754	94081	Hs.36944E NR_022754	ENSG000003SFXN1	SLC56A1	l	siderofl	protein-coding	
chr6-995.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr6	99533437	99535375	+	0	NA	IntergeniLIMEg LIN	13412	NR_00119E	1E+08	Hs.63450E NR_00119E	ENSG000003TSTD3	-	thiosulf	protein-coding		
chr6-1116.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chr6	11162081	11164729	+	0	NA	intron (NMIRb SINE	68431	NR_15304E	2534	Hs.39056E NR_002037	ENSG000003FYN	SLK SYN	f	YFN	prot	protein-coding
chrX-5341.6.964522	0.257269	0.874094	0.294327	0.768508	0.981636	chrX	53412301	53413380	+	0	NA	intron (Nintron (N	-7075	NR_10691E	1.02E+08	NR_10691E	ENSG000003MIR6857	hsa-mir-6857	microRNA	ncRNA		
chr13-321.7.59754	-0.25118	0.853981	-0.29413	0.768658	0.981636	chr13	32171214	32171895	+	0	NA	intron (NAluSx6 SI	139780	NR_023037	10129	Hs.50766E NR_023037	ENSG000003FRY	13CDNA73	FRY	micr	protein-coding	
chr1-3924.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr1	39249828	39251196	+	0	NA	intron (Nintron (N	-15857	NR_01503E	643314	Hs.65876E NR_01503E	ENSG000003KIAA0754	-	KIAA0754	protein-coding		
chr1-1656.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr1	1.66E+08	1.66E+08	+	0	NA	intron (NAluJr SIN	-1295	NR_037431	1.01E+08	NR_037431	ENSG000003MIR3658	-	microRNA	ncRNA		
chr1-2276.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr1	2.27E+08	2.27E+08	+	0	NA	intron (Nintron (N	158838	NR_00136E	8476	Hs.35433	NR_003607	ENSG000003CDC42BPA	MRCK MRCKC	CD42	bir	protein-coding
chr10-421.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr10	42816453	42818310	+	0	NA	exon (NM exon (NM	34586	NR_01475E	9790	Hs.10848	NR_01475E	ENSG000003BMS1	ACC BMS1	BMS1	rib	protein-coding
chr11-134.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr11	1.34E+08	1.34E+08	+	0	NA	3' UTR (N3' UTR (N	2170	NR_14579C	1.1E+08	NR_145790	SNORD153	-	small	nuc	snoRNA	
chr12-881.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr12	88179851	88181145	+	0	NA	intron (NHERVK22-i	38191	NR_00136E	160418	Hs.33126E NR_18178E	ENSG000003TMTC3	LIS8 SMI1	trans	protein-coding		
chr12-108.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr12	36722	NR_001161	54434	Hs.19976E	NR_001161	ENSG000003SSH1	SSH1L	slingshot	protein-coding							
chr15-415.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr15	41908729	41910530	+	0	NA	intron (Nintron (N	-11788	NR_12033E	1.02E+08	Hs.68019E NR_12033E	EHD4-AS1	-	EHD4	anticrRNA		
chr15-525.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr15	52553938	52554782	+	0	NA	intron (Nintron (N	14472	NR_00133C	10776	Hs.51290E NR_00662E	ENSG000003ARPP19	ARPP-16	ac	AMP	reg	protein-coding
chr16-252.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr16	1658	NR_00104E	752014	Hs.43349E NR_00104E	ENSG000003CEMP1	CP-23 CP2	ce	mentum	protein-coding							
chr16-185.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr16	18361875	18364214	+	0	NA	intron (NLIMEg LIN	-10599	NR_14633E	1.1E+08	Hs.63615E NR_14633E	PKD1P4-NF	-	PKD1P4-NF	pseudo		
chr17-601.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr17	60180110	60182081	+	0	NA	intron (NAluJb SIN	31122	NR_000717	762	Hs.89485	NR_000717	ENSG000003CA4	CAIV Car4	car	protein-coding	
chr19-402.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr19	40281639	40282226	+	0	NA	TTS (NR_C TTS (NR_C	7099	NR_030371	693226	NR_030371	ENSG000003MIR641	MIRN641	tmicroRNA	ncRNA		
chr2-2017.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (NMIRb SINE	27946	NR_02091E	57679	Hs.47109E NR_02091E	ENSG000003CALS2	ALS2CR6	al	sin	Rhc	protein-coding
chr20-621.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr20	62133341	62133811	+	0	NA	intron (Nintron (N	9818	NR_00279E	5688	Hs.23395E NR_00279E	ENSG000003PSMA7	C6 HEL-5	pro	teaso	protein-coding	
chr3-136.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr3	1.36E+08	1.36E+08	+	0	NA	intron (NAluSx2 SI	69414	NR_181897	5523	Hs.51815E NR_00271E	ENSG000003PPP2R3A	PPP2R3	PF	pro	tein	protein-coding
chr4-266.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr4	26632748	26634140	+	0	NA	intron (NTiger2 I	49360	NR_018317	55296	Hs.47940E NR_018317	ENSG000003TBC1D19	-	TBC1	dom	protein-coding	
chr5-159.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr5	1.59E+08	1.59E+08	+	0	NA	exon (NM exon (NM	15058	NR_14504E	134510	Hs.59173E NR_14504E	ENSG000003UBLCP1	CPUB1	ubiquitin	protein-coding		
chr5-1754.6.418937	0.266994	0.908283	0.293955	0.768792	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	-47590	NR_00211E	3101	Hs.41169E NR_00211E	ENSG000003CHK3	HKIII HXK	h	u	kin	protein-coding
chr5-1754.11.83559	-0.20271	0.689647	-0.29393	0.768813																		



chr5-1772.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (N LIMB1 LIN	80830 NM_001365	64324 Hs. 106861NM_022455	ENSG00000CNSD1	ARA267 KV nuclear rprotein-coding	
chr6-2666.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr6	26650007	26657576	+	0 NA	intron (N LIMC4 LIN	5955 NM_024635	79692 Hs. 126289NM_024635	ENSG00000ZNF322	HCG12 ZNF zinc finger protein-coding	
chr7-4725.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr7	47292265	47297711	+	0 NA	intron (N intron (N	169815 NR_145813	1.E+08 NR_145813	SNORD151	small nucleolar RNA	
chr7-5517.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr7	55182575	55184265	+	0 NA	intron (N MLT1C LITF	5529 NR_047551	0.01E+08 Hs. 720489NR_047551	ENSG00000EGFR-AS1	EGFR anticancer	
chr7-1301.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (N LIMB1 LIN	7432 NM_032842	84928 Hs. 267245NM_032842	ENSG00000TMEM209	NET31 transmembrane protein-coding	
chr8-9624.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr8	96241681	96245487	+	0 NA	intron (N intron (N	-7950 NM_006294	7381 Hs. 131255NM_006294	ENSG00000UCRBR	MC3DN3 QCubiquinol protein-coding	
chr9-2691.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr9	26916566	26918738	+	0 NA	intron (N L2a LINE	-24824 NM_001167	79886 Hs. 178357NM_024825	ENSG00000CAAP1	C9orf82 caspase 9 protein-coding	
chr9-111.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr9	1.1E+08	1.1E+08	+	0 NA	intron (N intron (N	32964 NM_001351	1902 Hs. 126667NM_001401	ENSG00000LPAR1	EDG2 GPR2 lysophospholipid protein-coding	
chr9-136.7.153649	-0.25232	0.8624	-0.29258	0.769843	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (N LIMEc LIN	55374 NM_144655	138151 Hs. 112895NM_144655	ENSG00000NACC2	BEND9 BTE NACC famiprotein-coding	
chr1-112.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr1	11235245	11236867	+	0 NA	intron (N L2a LINE	26495 NM_004958	2475 Hs. 338207NM_004958	ENSG00000MTOR	FRAP FRAF mechanistic protein-coding	
chr1-2545.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr1	25496603	25498384	+	0 NA	intron (N intron (N	-46092 NM_015627	26119 Hs. 590911NM_015627	ENSG00000LDLRAP1	ARH ARH1 low density lipoprotein receptor class B type 1 protein-coding	
chr1-514.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr1	51400982	51405871	+	0 NA	exon (NM exon (NM	18669 NM_001155	2060 Hs. 83722 NM_001981	ENSG00000ECP515	AF-1P AF1 epidermal protein-coding	
chr10-12.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr10	72560086	72560671	+	0 NA	intron (N intron (N	-36392 NM_001195	10367 Hs. 524367NM_006077	ENSG00000M1CU1	CALC CBFAf mitochon protein-coding	
chr10-72.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr10	1.27E+08	1.27E+08	+	0 NA	intron (N intron (N	86067 NM_001035	642938 Hs. 613882NM_001035	ENSG00000INSYN2A	C10orf14 inhibitor protein-coding	
chr10-127.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr10	1.27E+08	1.27E+08	+	0 NA	intron (N MER1B DNA	-52416 NM_001035	642938 Hs. 613882NM_001035	ENSG00000INSYN2A	C10orf14 inhibitor protein-coding	
chr11-94.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr11	9499922	9502938	+	0 NA	intron (N intron (N	40418 NM_003442	7702 Hs. 523471NM_003442	ENSG00000ZNF143	SBF STAF zinc finger protein-coding	
chr12-77.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr12	77029853	77031246	+	0 NA	intron (N intron (N	35020 NM_203394	144455 Hs. 416377NM_203394	ENSG00000E2F7	E2F trans protein-coding	
chr12-105.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	3' UTR (N 3' UTR (N	16579 NM_032300	84260 Hs. 410924NM_032300	ENSG00000TCHP	TpMs trichoplein protein-coding	
chr12-112.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr12	1.12E+08	1.12E+08	+	0 NA	intron (N intron (N	-101386 NR_106921	1.02E+08 NR_106921	ENSG00000MIR6861	hsa-mir-61 microRNA ncRNA	
chr13-41.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr13	41748148	41750232	+	0 NA	intron (N LIPA4 LIN	-180795 NR_049803	0.01E+08 NR_049803	ENSG00000MIR5006	miRNA ncRNA	
chr13-117.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr13	1.1E+08	1.1E+08	+	0 NA	intron (N intron (N	13264 NM_01821C	55739 Hs. 408324NM_01821C	ENSG00000NAXD	CARKD LP2(N)HX protein-coding	
chr14-73.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr14	73074709	73075570	+	0 NA	intron (N FAM SINE	16605 NM_021235	58517 Hs. 531106NM_021235	ENSG00000RBM25	NET52 RE1 RNA binding protein-coding	
chr15-44.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr15	44347055	44348809	+	0 NA	intron (N LIMA3 LIN	59213 NR_157845	113201 Hs. 512867NM_138425	ENSG00000CASC4	H63 cancer suppressor protein-coding	
chr16-351.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr16	35189991	3520820	+	0 NA	exon (NM exon (NM	10011 NM_024793	23059 Hs. 155999NM_015041	ENSG00000CLUAP1	CFAP22 CF2 clusterin protein-coding	
chr16-356.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr16	3583205	3584736	+	0 NA	intron (N Alu Jo SIN	-6567 NR_075083	197358 Hs. 592091NM_178844	ENSG00000NLR3C	CLR16.2 NLR family protein-coding	
chr16-25.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr16	2525249	25253759	+	0 NA	intron (N MER102a SIN	4492 NM_001012	342357 Hs. 513451NM_001012	ENSG00000ZKSCAN2	ZNF694 ZS zinc finger protein-coding	
chr17-264.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr17	26242417	2643972	+	0 NA	intron (N Alu Jo SIN	49540 NM_00043C	5048 Hs. 77318 NM_00043C	ENSG00000PAFAH1B1	LISI LIS2 platelet protein-coding	
chr17-662.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr17	6620217	6623159	+	0 NA	intron (N intron (N	19023 NM_001351	9851 Hs. 28070 NM_014804	ENSG00000K1AA0753	MNR OFIP K1AA0753 protein-coding	
chr19-11.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr19	11000534	11001136	+	0 NA	intron (N Alu Sx4 SIN	16683 NM_001125	6597 Hs. 327527NM_003072	ENSG00000SMARCA4	BAF190 BFI SMF1 rprotein-coding	
chr19-161.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr19	16128244	16134019	+	0 NA	intron (N Alu Jo SIN	-2897 NM_032855	84941 Hs. 631617NM_032855	ENSG00000HSH2D	ALX HSH2 hemopoietic protein-coding	
chr2-387.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr2	38732054	38734568	+	0 NA	intron (N CharlielC	18050 NM_001031	6432 Hs. 309099NM_006272	ENSG00000CSRSF7	9G8 AAG3 serine ar protein-coding	
chr2-2004.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr2	2E+08	2E+08	+	0 NA	intron (N intron (N	87379 NM_001321	130535 Hs. 605777NM_152387	ENSG00000KCTD18	6530404F1 potassium protein-coding	
chr2-235.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr2	2.35E+08	2.35E+08	+	0 NA	intron (N intron (N	-11889 NM_001371306	5116 Hs. 474065NM_006031	ENSG00000PCNT	KEN MOPD2 pericentriolar protein-coding	
chr2-21.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr2	21611080	21612980	+	0 NA	intron (N intron (N	17992 NR_163925	3985 Hs. 474599NM_005565	ENSG00000LIMK2	LIM domain protein-coding	
chr22-311.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr22	31186489	31187731	+	0 NA	non-coding-non-coding	-25188 NM_005565	55007 Hs. 265015NM_017911	ENSG00000FAM118A	C22orf8 family wiprotein-coding	
chr22-45.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr22	45338756	45340964	+	0 NA	intron (N intron (N	16271631	16272307	0.01E+08	ENSG00000OXNAD1	oxidoreductase protein-coding
chr3-1627.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr3	43591159	43594059	+	0 NA	intron (N LIP45 LIN	29317 NM_001346	951206 Hs. 656657NM_018075	ENSG00000ANO10	SCAR10 TANoctamer protein-coding	
chr3-172.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr3	1.73E+08	1.73E+08	+	0 NA	intron (N intron (N	-38709 NR_146714	1.05E+08 Hs. 186265NR_146714	ENSG00000LINC02065	long intergenic ncRNA	
chr5-113.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr5	1.14E+08	1.14E+08	+	0 NA	intron (N LIP11 LIN	58840 NM_001346	64848 Hs. 231942NM_022825	ENSG00000YTHDC2	CAHL HYTH YTH domain protein-coding	
chr6-3211.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr6	32117482	32119482	+	0 NA	intron (N Alu Sx3 SIN	-9144 NM_001365	7148 Hs. 485104NM_019105	ENSG00000TNXB	EDS3 EDS3 tenascin protein-coding	
chr7-967.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr7	967829	970292	+	0 NA	3' UTR (N 3' UTR (N	6489 NM_001031	90639 Hs. 121595NM_001031	ENSG00000COX19	cytochrome protein-coding	
chr7-129.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (N L2a LINE	82018 NM_003344	7328 Hs. 643545NM_003344	ENSG00000UBE2H	E2-20K G1ubiquitin protein-coding	
chr8-2874.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr8	28741200	28743320	+	0 NA	intron (N MER63D DN	40759 NR_073465	2137 Hs. 491354NM_00144C	ENSG00000EXTL3	BOTV EXTI extensin protein-coding	
chr8-701.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr8	70137675	70138362	+	0 NA	intron (N intron (N	-66766 NM_024504	63978 Hs. 736039NM_024504	ENSG00000PRDM14	PFM11 PR/SET domain protein-coding	
chr8-9958.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr8	99584099	99585597	+	0 NA	intron (N L2a LINE	-47987 NR_030595	1E+08 NR_030595	ENSG00000MIR875	MIRN875 miRNA ncRNA	
chr8-144.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr8	1.45E+08	1.45E+08	+	0 NA	intron (N Kangald I	2973 NM_001345	7553 Hs. 493215NM_003415	ENSG00000ZNF7	HF.16 K0X zinc finger protein-coding	
chr9-124.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr9	1.25E+08	1.25E+08	+	0 NA	intron (N LIMEg LIN	30490 NM_030978	81873 Hs. 132429NM_030978	ENSG00000ARPC5L	ARL16-2 actin related protein-coding	
chr9-124.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr9	1.25E+08	1.25E+08	+	0 NA	intron (N Alu Sg SIN	3731 NM_002077	2800 Hs. 59504 NM_002077	ENSG00000GOLGA1	golgin-97 golgin A protein-coding	
chr9-131.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr9	1.32E+08	1.32E+08	+	0 NA	TTS (NM TTS (NM C	7497 NM_031432	83549 Hs. 9597 NM_031432	ENSG00000UCK1	URK1 uridine C-protein-coding	
chr9-136.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (N intron (N	-9082 NM_178138	8022 Hs. 148427NM_014564	ENSG00000LHX3	CPHD3 LTM LIM homeobox protein-coding	
chrX-715.6.426795	0.264715	0.905517	0.292336	0.770029	0.981636	chrX	71561									

chr16-234 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr16	23404515	23405653	+	0	NA	intron (Nintron (N	48105 NM_153603	91949 Hs. 185807NM_153603	ENSG000003COG7	CDG2E	componentprotein-coding
chr16-682 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr16	68290453	68296275	+	0	NA	intron (NAluSx SIN	17582 NM_032178	84138 Hs. 729522NM_032178	ENSG000003SLCTA60S	-	solute cprotein-coding
chr16-745 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr16	74920407	74922109	+	0	NA	intron (NLIPIREC2 I	63865 NM_030581	79726 Hs. 280951NM_030581	ENSG000003WDR59	CDW12 FPFWD	repeatprotein-coding
chr16-84 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr16	84306257	84306703	+	0	NA	intron (Nintron (N	11602 NM_021197	58189 Hs. 36688 NM_021197	ENSG000003WFDC1	PS20	WAP four-protein-coding
chr17-756 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr17	75650038	75651614	+	0	NA	3' UTR (N3' UTR (N	4575 NM_001162	1E+08 Hs. 662541NM_001162	ENSG000003SMIM6	C17orf11C	small intronprotein-coding
chr17-822 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr17	82243775	82244283	+	0	NA	non-codingnon-coding	7361 NR_106845	1.02E+08 NR_106845	ENSG000003MIR6787	hsa-mir-ε	microRNA ncRNA
chr19-956 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr19	959504	961453	+	0	NA	intron (Nintron (N	-23850 NM_024100	57418 Hs. 325321NM_024100	ENSG000003WDR18	Ipi3 R321D	repeatprotein-coding
chr19-564 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr19	5642297	5642879	+	0	NA	intron (Nintron (N	19505 NM_002967	6294 Hs. 728802NM_002967	ENSG000003SAFB	HAP HET S	scaffold protein-coding
chr19-105 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr19	10920799	10921763	+	0	NA	TTS (NM_C TTS (NM_C	7358 NM_024025	78992 Hs. 164025NM_024025	ENSG000003YIPF2	FinGER2	Yipl dom protein-coding
chr2-8824 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	8824350	8826514	+	0	NA	intron (NLM2 LIN	12181 NM_001134	57498 Hs. 9873 NM_020738	ENSG000003KIDINS22C	ARMS SINC	kinase D protein-coding
chr2-6355 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	63593648	63596711	+	0	NA	intron (Nintron (N	6028 NM_001195	4190 Hs. 526521NM_005917	ENSG000003MDHI	HEL-S-32	malate deprotein-coding
chr2-9592 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	95923240	95924291	+	0	NA	intron (Nintron (N	68059 NM_001310	400986 Hs. 646315NM_001010	ENSG000003ANKRD36C	-	ankyrin rprotein-coding
chr2-1012 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	1.01E+08	1.01E+08	+	0	NA	3' UTR (N3' UTR (N	3038 NR_003077	692205 Hs. 656503NR_003077	ENSG000003SNORD89	HBII-289	small nucleolar
chr2-162 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	1.62E+08	1.62E+08	+	0	NA	intron (Nintron (N	65485 NR_001935	1803 Hs. 368912NM_001935	ENSG000003DPPP4	ADABP ADC	dipeptid protein-coding
chr2-203 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (NAluSp SIN	80468 NM_001114	65065 Hs. 648844NM_198945	ENSG000003NBEAL1	A530083I	neurohepatic protein-coding
chr2-2161 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (Nintron (N	-50353 NR_037701	150967 Hs. 56876 NM_001195	ENSG000003LINC01965	PKI55	long intncRNA
chr2-233 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (Nintron (N	2618 NR_003005	677775 Hs. 663615NR_003005	ENSG000003SCARNA5	U87	small Ca ncRNA
chr2-2416 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr2	2.42E+08	2.42E+08	+	0	NA	intron (NAluSp SIN	8772 NR_033255	1841 Hs. 471875NM_012145	ENSG000003DTMYK	CDC8 PP37	deoxythymine protein-coding
chr20-487 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr20	4879905	4881333	+	0	NA	intron (NHAL LINE	-57011 NM_014737	9770 Hs. 631504NM_014737	ENSG000003CRASSF2	CENP-34 Fas	assoc protein-coding
chr20-357 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr20	35782694	35783894	+	0	NA	intron (Nintron (N	11279 NM_016435	51230 Hs. 517044NM_016435	ENSG000003PHF20	C20orf104PHD	finger protein-coding
chr20-472 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr20	47212242	47213468	+	0	NA	intron (Nintron (N	45888 NR_037411	1.01E+08 NR_037411	ENSG000003MIR3616	mir-3616	microRNA ncRNA
chr21-392 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr21	39262665	39269404	+	0	NA	intron (NCharlie2C	47598 NM_018962	54014 Hs. 627135NM_018962	ENSG000003BRWD1	C21orf107	bromodomain protein-coding
chr22-18 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr22	18086201	18088157	+	0	NA	intron (NAluS6 SI	9189 NM_017925	55670 Hs. 517400NM_017925	ENSG000003PEX26	PBD7A PBE	peroxisome protein-coding
chr22-426 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr22	42888639	42889869	+	0	NA	intron (NLM2 LINE	-31981 NM_001142	26286 Hs. 685225NM_014570	ENSG000003ARFGAP3	ARFGAP1	ADP ribosome protein-coding
chr3-1341 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr3	1.34E+08	1.34E+08	+	0	NA	IntergeniIntergeni	96304 NM_002955	6259 Hs. 654562NM_002955	ENSG000003CRVK	D3BC3195 Jreceptor	protein-coding
chr3-184 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (NAluY SINE	4409 NM_001275	5437 Hs. 432574NM_006235	ENSG000003POLR2H	RPAC3 RF	RNA polyn protein-coding
chr4-1981 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr4	1981344	1984056	+	0	NA	TTS (NM_C TTS (NM_C	3777 NR_030641	1E+08 NR_030641	ENSG000003MIR943	MIR943 J	microRNA ncRNA
chr4-5725 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr4	5729528	5733929	+	0	NA	intron (NMIRc SINE	20527 NM_153717	2121 Hs. 646895NM_014555	ENSG000003EVC	DWF-1 EVC	cylic protein-coding
chr4-1218 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (NAluJb SIN	-8331 NM_001237	890 Hs. 58974 NM_001237	ENSG000003CCNA2	CCN1 CCN	cyclin A2 protein-coding
chr4-1507 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr4	1.51E+08	1.51E+08	+	0	NA	intron (NAluS6 SI	14878 NM_006435	10586 Hs. 584852NM_006435	ENSG000003MAB21L2	MCN514 J	ubiquitin 1 protein-coding
chr6-303 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr6	30337609	30338739	+	0	NA	intron (NTigger1 I	-6982 NM_001195	79897 Hs. 183232NM_024835	ENSG000003CRPP21	C6orf135 J	ribonucle protein-coding
chr6-875 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr6	87595626	87597319	+	0	NA	intron (Nintron (N	6405 NM_012381	23595 Hs. 410225NM_012381	ENSG000003ORC3	LAT LATH	origin re protein-coding
chr7-7697 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr7	76979805	76979932	+	0	NA	IntergeniAluSx1 SI	-1454 NR_023383	441263 Hs. 675885NR_023383	ENSG000003DTX2P1-UF	PMS2L11	DTX2P1-UF pseudo
chr7-1212 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr7	1.21E+08	1.21E+08	+	0	NA	intron (NLIPIA4 LIN	-76864 NM_016087	51384 Hs. 272375NM_016087	ENSG000003WNT16	-	Wnt famil protein-coding
chr7-1494 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	-15736 NM_015694	27153 Hs. 38512 NM_015694	ENSG000003ZNF777	-	zinc fing protein-coding
chr8-9632 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr8	96330664	96331631	+	0	NA	intron (Nintron (N	55501 NR_125825	1.03E+08 Hs. 571415NR_125825	ENSG000003LOC102724	-	uncharacterncRNA
chr8-1434 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr8	1.43E+08	1.43E+08	+	0	NA	intron (NLM5 LINE	-13819 NM_201585	389692 NM_201585	ENSG000003MAFA	INSDM RF	MFAF bZIP protein-coding
chr9-1101 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (NMIR SINE	25287 NR_001136	445815 Hs. 591905NM_007205	ENSG000003PALM2-AK	AKAP-2 AK	PALM2-AK protein-coding
chr9-1302 6.931241	0.253307	0.873619	0.289952	0.771853	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (NAluSg4 SI	-8750 NR_162144	1.13E+08 NR_162140	MIR12126	-	microRNA ncRNA
chr22-355 11.41541	-0.20369	0.70287	-0.2898	0.771969	0.981636	chr22	35808357	35810285	+	0	NA	intron (Nintron (N	31143 NM_001345	23543 Hs. 282995NM_014305	ENSG000003RFX2	FOX2 F	ox-RNA bindi protein-coding
chr1-268 6.915525	0.257447	0.889066	0.289796	0.771973	0.981636	chr1	26837821	26838180	+	0	NA	intron (NAluSp SIN	11312 NM_032283	84243 Hs. 520311NM_032283	ENSG000003DHHIC18	DHHIC-18 Zinc	fing protein-coding
chr10-871 6.915525	0.257447	0.889066	0.289796	0.771973	0.981636	chr10	87105222	87106282	+	0	NA	intron (NMLTIL LTF	10546 NM_019054	54537 Hs. 500411NM_019054	ENSG000003SHLD2	FAM35A F	shieldin protein-coding
chr1-1567 5.930207	0.275428	0.951552	0.289452	0.772236	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	TTS (NM_C TTS (NM_C	7391 NM_001370	81875 Hs. 301904NM_030980	ENSG000003ISG20L2	HSD38	interferc protein-coding
chr1-2438 5.930207	0.275428	0.951552	0.289452	0.772236	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (NLIPIA10 LI	23901 NM_181696	10000 Hs. 498292NM_005465	ENSG000003AKT3	MPPH MPP	AKT serir protein-coding
chr10-975 5.930207	0.275428	0.951552	0.289452	0.772236	0.981636	chr10	97568304	97569457	+	0	NA	intron (NAluSp SIN	-3561 NM_001291	26287 Hs. 73708 NM_020345	ENSG000003ANKRD2	ARPP	ankyrin rprotein-coding
chr13-112 5.930207	0.275428	0.951552	0.289452	0.772236	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (NAluSx1 SI	-100671 NR_046661	1.01E+08 Hs. 658692NR_046661	ENSG000003ATP11A-AS	-	ATP11A arncRNA
chr14-75 5.930207	0.275428	0.951552	0.289452	0.772236	0.981636	chr14	75095698	75097963	+	0	NA	intron (Nintron (N	27639 NM_001042	79696 Hs. 48642 NM_024645	ENSG000003ZC2H1C1C	C14orf14	zinc fing protein-coding
chr17-765 5.930207	0.275428	0.951552	0.289452	0.772236	0.981636	chr17	76342226	76343752	+	0	NA	intron (NAluSx1 SI	10924 NM_002765	5635 Hs. 77498 NM_002765	ENSG000003PRPSAP1	PAP39	phosphoriprotein-coding
chr19-1																	



chr4-847( 7.145791	-0.25045	0.868109	-0.28851	0.772959	0.981636	chr4	84707435	84708727	+	0	NA	intron (Nintron (N	124954	NM_001263	1040	Hs. 654899	ENSG000001263	ENSG000000CDS1	CDS 1	CDP-diacylprotein-coding
chr5-5305( 7.145791	-0.25045	0.868109	-0.28851	0.772959	0.981636	chr5	53097321	53098634	+	0	NA	3' UTR (N3' UTR (N	11780	NM_17680E	4338	Hs. 16364E	ENSG00000100453	ENSG000000MOC52	MCPBE	MOL molybdenum protein-coding
chr7-801E( 7.145791	-0.25045	0.868109	-0.28851	0.772959	0.981636	chr7	80189171	80189866	+	0	NA	intron (Nintron (N	53734	NM_00125E	2770	Hs. 134587	ENSG00000100206	ENSG000000CGNA11	Gi	G protein protein-coding
chr3-170( 7.615105	-0.24292	0.842266	-0.28841	0.773033	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	exon (NM exon (NM	-27672	NM_00560E	5010	Hs. 31595	ENSG00000100560	ENSG000000CLDN11	OSP	OTM claudin 1 protein-coding
chr7-277E( 7.615105	-0.24292	0.842266	-0.28841	0.773033	0.981636	chr7	27792922	27793728	+	0	NA	intron (Nintron (N	53230	NM_00107E	8887	Hs. 34576	ENSG00000100602	ENSG000000TAX1BP1	CALCOC03	Tax1 binc protein-coding
chr11-592( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr11	59205965	59206341	+	0	NA	3' UTR (N3' UTR (N	6774	NM_00103E	219972	Hs. 74492	ENSG00000100103E	ENSG000000CMPEG1	MPG1	MPS1 macrophage protein-coding
chr15-801( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr15	80159852	80160051	+	0	NA	intron (Nintron (N	6952	NM_000137	2184	Hs. 73875	ENSG000001000137	ENSG000000FAH	FAH	fumarylac protein-coding
chr17-177( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr17	17705503	17705702	+	0	NA	intron (NAluSx SIN	24144	NM_03066E	10743	Hs. 65539E	ENSG00000103066E	ENSG000000RAI1	SMCR	SMS retinoic protein-coding
chr2-134( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr2	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	102166	NM_00241C	4249	Hs. 4988	ENSG00000100241C	ENSG000000MGAT5	GNT-V	GNT1 alpha-1, epsilon protein-coding
chr20-42E( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr20	429067	429541	+	0	NA	intron (NAluSp SIN	21005	NM_00646E	10616	Hs. 29546	ENSG00000100646E	ENSG000000RBCK1	C20orf18	RANBP2-ty protein-coding
chr4-6761( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr4	67619316	67620238	+	0	NA	intron (Nintron (N	61050	NM_001317	26228	Hs. 43557E	ENSG0000010210E	ENSG000000STAP1	BRDG1	ST1 signal t protein-coding
chr4-128E( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chr4	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	37370	NM_001287	79960	Hs. 12420	ENSG00000102490C	ENSG000000JADE1	PHF17	jade fami protein-coding
chrX-5364( 6.684334	-0.26099	0.906084	-0.28804	0.773318	0.981636	chrX	53647311	53647986	+	0	NA	intron (Nintron (N	39071	NM_031407	10075	Hs. 13690E	ENSG000001031407	ENSG000000HUWE1	ARF-BP1	FHECT, UB1 protein-coding
chr1-102E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr1	10262696	10265067	+	0	NA	intron (N(L2a LINE	33416	NM_00136E	23095	Hs. 97858	ENSG00000105074	ENSG000000KIF1B	CMT2	CMT2 kinesin f protein-coding
chr1-9357( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr1	93573894	93576639	+	0	NA	intron (Nintron (N	8986	NM_00130E	8412	Hs. 36958	ENSG000001003567	ENSG000000BCAR3	AND-34	NSBCAR3 adp protein-coding
chr1-1174( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr1	1.17E+08	1.17E+08	+	0	NA	intron (N(LIP47 LIN	108213	NM_00669E	10905	Hs. 43593E	ENSG00000100669E	ENSG000000MAN1A2	MAN1B	mannosidp protein-coding
chr1-1787( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (N(LIM1 LINE	33754	NM_15266E	55103	Hs. 63248E	ENSG00000108037	ENSG000000CRALGPS2	dJ595C2.1	RAL GEF w protein-coding
chr1-225E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (N(X7A LINE	86365	NM_00100E	55740	Hs. 49789E	ENSG00000101821E	ENSG000000ENAH	ENA MEN4	ENAH acti protein-coding
chr10-14E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr10	14866661	14868831	+	0	NA	exon (NM exon (NM	-11037	NM_00119E	79723	Hs. 55488E	ENSG00000102467C	ENSG000000SUV39H2	KMT1B	suppressc protein-coding
chr10-431( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr10	43177314	43178619	+	0	NA	intron (N(LIMB7 LIN	23069	NM_00131E	55454	Hs. 65756E	ENSG00000101859C	ENSG000000CSGALNACT1	CHGN2	Chc chondroit protein-coding
chr10-704( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr10	70427056	70428226	+	0	NA	3' UTR (N3' UTR (N	14040	NM_01805E	4838	Hs. 37041E	ENSG00000101805E	ENSG000000NADAL	HTX5	nodal grc protein-coding
chr10-73E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr10	73863571	73864069	+	0	NA	intron (Nintron (N	10735	NM_001367	818	Hs. 52304E	ENSG00000100122E	ENSG000000CAMK2G	CAMK	CAMM calcium/c protein-coding
chr10-102( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (N(MIRc SINE	15646	NM_00119E	8729	Hs. 29024E	ENSG00000100419E	ENSG000000GBF1	ARF1GEF	golgi brp protein-coding
chr12-11E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	TTS (NM_TTS (NM_C	15832	NM_00737C	5985	Hs. 73190E	ENSG00000100737C	ENSG000000RFC5	RFC36	replicat protein-coding
chr13-20C( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr13	20033807	20034096	+	0	NA	intron (Nintron (N	-68750	NR_12638C	1.04E+08	Hs. 57801E	ENSG00000102638C	ENSG000000LINC01072	-	long intncRNA
chr14-99E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr14	99904518	99905513	+	0	NA	intron (N(MER41-int	-66407	NM_00133C	51466	Hs. 125867	ENSG000001016337	ENSG000000CEVL	RNB6	Enah/Vasf protein-coding
chr15-73E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr15	731916245	73191997	+	0	NA	TTS (NR_TTS (NR_C	-9841	NM_00557E	4016	Hs. 65436	ENSG00000100557E	ENSG000000LOXL1	LNL6	LOXL1 lysyl x protein-coding
chr16-30E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr16	30942761	30945448	+	0	NA	intron (Nintron (N	-4964	NM_15228E	93129	Hs. 745104	ENSG00000105228E	ENSG000000ORAI3	TMEM142C	ORAI cal protein-coding
chr16-534( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr16	53496667	53497062	+	0	NA	intron (Nintron (N	6345	NM_02247E	64400	Hs. 380897	ENSG00000100247E	ENSG000000AKTIP	FT1	FTS AKT inter protein-coding
chr17-10E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr17	1054771	1055577	+	0	NA	intron (N(FLAM_C SI	-23343	NM_00125E	29	Hs. 15930E	ENSG00000100109E	ENSG000000ABR	MFB	ABR acti protein-coding
chr17-62C( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr17	62046715	62048559	+	0	NA	intron (N(LIP48 LIN	17641	NM_005121	9969	Hs. 28267E	ENSG000001005121	ENSG000000MED13	ARC250	DF mediator protein-coding
chr2-4697( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr2	46974808	46976295	+	0	NA	intron (Nintron (N	-3369E	NM_001171	90411	Hs. 66215E	ENSG000001013927E	ENSG000000MCFD2	F5F8D	F5F multiple protein-coding
chr2-702E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr2	70264193	70264608	+	0	NA	intron (NAluSz SIN	6263	NM_016297	51449	Hs. 56750E	ENSG000001016297	ENSG000000PCYOX1	PCL1	prenylcy protein-coding
chr2-971E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr2	97191492	97192984	+	0	NA	intron (Nintron (N	79085	NM_001354	375248	Hs. 541894	ENSG000001019855E	ENSG000000ANKRD36	UNQ2430	ankyrin t protein-coding
chr2-1327( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (N(Tiger3b	-99757	NM_001077	116372	Hs. 43239E	ENSG00000104458E	ENSG000000LYPD1	LYPD1	PLF, PF6, PLAUf protein-coding
chr2-199E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr2	2E+08	2E+08	+	0	NA	intron (NAluJb SIN	7756	NM_15368E	205327	Hs. 154494	ENSG00000105368E	ENSG000000C2orf69	-	chromoson protein-coding
chr2-224E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr2	2.25E+08	2.25E+08	+	0	NA	intron (N(ERV3-16A3	117495	NM_00129C	55619	Hs. 46578	ENSG00000101468E	ENSG000000DOCK10	DRIP2	Nbl dedicator protein-coding
chr20-19E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr20	19935191	19937886	+	0	NA	intron (Nintron (N	46972	NM_01899E	54453	Hs. 47227E	ENSG00000100189E	ENSG000000RIN2	MACS	RARS Ras and F protein-coding
chr20-584( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr20	58443986	58446317	+	0	NA	non-codiron-codir	55372	NR_03663C	9217	Hs. 18262E	ENSG00000100473E	ENSG000000VAPB	ALS8	VAMF VAMP assc protein-coding
chr3-1837( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (N(MIR SINE	18543	NR_046727	1.01E+08	NR_046727	YEATS2-AS-	YEATS2	arncRNA	
chr3-184E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr3	1.85E+08	1.85E+08	+	0	NA	intron (Nintron (N	50640	NM_00134E	23355	Hs. 26926E	ENSG00000101530E	ENSG000000VPS8	KIAA0804	VPS8 sub protein-coding
chr4-1134( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr4	1.13E+08	1.13E+08	+	0	NA	intron (NAluSx1 SI	184817	NM_001354	287	Hs. 620557	ENSG00000100114E	ENSG000000ANK2	ANK-2	LQ1ankyrin z protein-coding
chr4-119E( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (N(LIP42 LIN	25113	NM_001001	401152	Hs. 17370E	ENSG000001001001	ENSG000000C4orf3	ANK-2	LQ1ankyrin z protein-coding
chr4-1684( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (Nintron (N	49412	NM_001291	91351	Hs. 53011E	ENSG00000100101E	ENSG000000DDX60L	-	Ddx6/H-bc protein-coding
chr5-6937( 7.18693	-0.24761	0.860974	-0.2876	0.773656	0.981636	chr5	69374657	69379135	+	0	NA									



chr7-752:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr7	75232134	75233248	+	0 NA	intron (AluSz SIN	-4496 NR_146079	643862	NR_146079	SPDYE10P	-	speedy/R1pseudo
chr7-130C:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	TTS (NM_C TTS (NM_C	33511 NM_001363	51530 Hs.	194157NM_016478	ENSG000002C3HC1	HSPC216	zinc fingprotein-coding
chr7-1491:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr7	1.49E+08	1.49E+08	+	0 NA	intron (N intron (N	-18332 NM_001303	8427 Hs.	729056NM_003575	ENSG000002ZNF282	HUB1	zinc fingprotein-coding
chr8-428:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr8	42837731	42838349	+	0 NA	exon (NM exon (NM	5285 NM_018105	55145 Hs.	7432 NM_018105	ENSG000002THAP1	DY16	THAP dome protein-coding
chr8-5697:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr8	56976856	56979824	+	0 NA	intron (N LIPA13 LI	15527 NM_017813	54928 Hs.	438689NM_017813	ENSG000002IMPAD1	GPAPP	IMF inotop protein-coding
chr8-672C:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr8	67200118	67207333	+	0 NA	intron (N L2 LINE I	119877 NM_001291	79848 Hs.	370147NM_02479C	ENSG000002CSPP1	CSPP	JBT:centrosom protein-coding
chr8-9625:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr8	96259601	96297363	+	0 NA	intron (N AluJ SINE	34310 NM_014754	9791 Hs.	292579NM_014754	ENSG000002PTDSS1	LMHD	PSS1 phosphat i protein-coding
chr9-111F:6.939099	0.251188	0.873732	0.287488	0.773738	0.981636	chr9	1.12E+08	1.12E+08	+	0 NA	intron (N MRB SINE	2721 NM_133464	158399 Hs.	584864NM_133464	ENSG000002ZNF483	ZKSCAN16	zinc fingprotein-coding
chr1-6592:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr1	6592576	6595070	+	0 NA	3' UTR (N3' UTR (N	9046 NM_001324	9903 Hs.	7764 NM_014851	ENSG000002KLHL21	-	kelch lik protein-coding
chr1-254F:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr1	25459031	25461110	+	0 NA	intron (N intron (N	29173 NM_018202	55219 Hs.	179978NM_018202	ENSG000002MACO1	MACO1 IN	macoilin protein-coding
chr1-3302:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr1	33023690	33024596	+	0 NA	intron (N AluSx1 SI	12740 NM_001195	204 Hs.	470907NM_001625	ENSG000002AK2	ADK2	adenylatc protein-coding
chr11-775:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr11	77978037	77981179	+	0 NA	intron (N intron (N	15060 NM_033547	92105 Hs.	533722NM_033547	ENSG000002INTS4	INT4	MSTC integratc protein-coding
chr13-77C:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr13	77920665	77940004	+	0 NA	exon (NM exon (NM	17722 NR_046716	1.01E+08 Hs.	569286NR_046716	ENSG000002MYCBP2-AS	-	MYCBP2 arncRNA
chr13-772:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr13	77020665	77205885	+	0 NA	intron (N LIPA3 LI	123819 NM_015057	23077 Hs.	591221NM_015057	ENSG000002MYCBP2	Myc-bp2	MYC bndiprotein-coding
chr14-761F:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr14	76182277	76184326	+	0 NA	intron (N intron (N	28947 NR_110314	55668 Hs.	410231NM_017925	ENSG000002PATCH2L	C14orf11E	G-patch c protein-coding
chr15-73Z:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr15	73289622	73291879	+	0 NA	intron (N intron (N	-9164 NR_162148	1.13E+08	MIR12135	-	microRNA ncRNA	
chr16-695:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr16	69988151	69988999	+	0 NA	intron (N intron (N	37395 NM_00137C	348174 Hs.	592064NM_182615	ENSG000002CLEC18A	MRCL	MRC1 C-type I c protein-coding
chr2-7017:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr2	70177006	70178776	+	0 NA	intron (N AluJb SIN	12820 NR_145971	54980 Hs.	720045NM_01788C	ENSG000002CP9F42	-	chromosom protein-coding
chr2-1914:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr2	1.91E+08	1.91E+08	+	0 NA	intron (N Tiger1 E	160745 NM_001161	4430 Hs.	439622NM_012225	ENSG000002MYO1B	MMI-1	alpha myosin I f protein-coding
chr2-2182:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr2	2.19E+08	2.19E+08	+	0 NA	TTS (NM_C TTS (NM_C	7190 NM_001366	7701 Hs.	657969NM_001105	ENSG000002ZNF142	HA4654	NE zinc fing protein-coding
chr22-505:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr22	50238986	50239453	+	0 NA	intron (N AluJb SIN	5804 NM_020461	85378 Hs.	336431NM_020461	ENSG000002TUBGCP6	GCP-6	GFC tubulin f protein-coding
chr4-121F:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	exon (NM exon (NM	7248 NM_176824	55212 Hs.	591694NM_01819C	ENSG000002BBS7	BBS2L1	Bardet-Bi protein-coding
chr5-326F:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr5	32604145	32605227	+	0 NA	TTS (NM_C TTS (NM_C	19129 NM_006713	10923 Hs.	229641NM_006713	ENSG000002SUB1	P15 PC4	SUB1 regt protein-coding
chr5-1421:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr5	1.42E+08	1.42E+08	+	0 NA	intron (N intron (N	36827 NM_030571	80762 Hs.	9788 NM_030571	ENSG000002NDF1P1	N4WBFP5	Necdd4 fan protein-coding
chr6-321F:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr6	32156378	32158396	+	0 NA	intron (N AluSz SIN	-3022 NR_037172	1.01E+08 Hs.	549204NR_037165	ENSG000002LOC100507	-	uncharactncRNA
chr7-4008:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr7	40088405	40089896	+	0 NA	intron (N AluS6 SI	45427 NM_138701	136647 Hs.	654989NM_138701	ENSG000002MPLKIP	ABHS	C7orfM-phase s protein-coding
chr7-9208:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr7	92082868	92089210	+	0 NA	intron (N intron (N	49030 NM_00078E	1595 Hs.	417077NM_00078E	ENSG000002CYP51A1	CP51	CYPE cytochrom protein-coding
chr7-139Z:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr7	1.39E+08	1.39E+08	+	0 NA	intron (N AluSz SIN	31257 NM_173565	254048 Hs.	153458NM_173565	ENSG000002UBN2	-	ubnuclei protein-coding
chr8-172Z:7.435687	0.243469	0.847124	0.287406	0.773801	0.981636	chr8	17293456	17295638	+	0 NA	intron (N LIPA7 LI	47589 NM_001363	137492 Hs.	343875NM_152415	ENSG000002VPS37A	HCRPI	PQE VPS37A s protein-coding
chr19-447:11.39184	-0.20011	0.696299	-0.28739	0.773817	0.981636	chr19	47737656	47742428	+	0 NA	intron (N intron (N	-5504 NM_015176	29997 Hs.	4121907NM_015171	ENSG000002NOP53	GLTSCR2	FNOP53 rit protein-coding
chr12-715:5.368905	0.293759	1.022283	0.287356	0.77384	0.981636	chr12	7133844	7134182	+	0 NA	intron (N MRB SINE	3642 NM_014715	9746 Hs.	535377NM_014715	ENSG000002CLSTN3	CDHR14	CS calsynter protein-coding
chr5-179F:5.368905	0.293759	1.022283	0.287356	0.77384	0.981636	chr5	1.8E+08	1.8E+08	+	0 NA	intron (N intron (N	-2252 NR_110566	1.02E+08 Hs.	663255NR_110566	ENSG000002LOC101925	-	uncharactncRNA
chr19-18Z:4.921315	0.308607	1.076327	0.287322	0.774325	0.981636	chr19	1827361	1827711	+	0 NA	exon (NM exon (NM	5447 NR_152847	1E+08 Hs.	662425NR_034114	ENSG000002LOC10028E	-	uncharactncRNA
chr17-211:7.981272	0.236608	0.825226	0.286719	0.774327	0.981636	chr17	21197519	21198147	+	0 NA	TTS (NR_C TTS (NR_C	16762 NR_024547	8834 Hs.	592949NM_003875	ENSG000002TMEM11	C17orf35	transmemt protein-coding
chr19-13Z:7.981272	0.236608	0.825226	0.286719	0.774327	0.981636	chr19	1357382	1358987	+	0 NA	intron (N intron (N	765 NR_163145	84939 Hs.	515015NM_03222C	ENSG000002PWWP3A	EXPAND1	F PWW dome protein-coding
chr14-24Z:7.656245	-0.24201	0.839641	-0.28608	0.774814	0.981636	chr14	24235201	24236673	+	0 NA	intron (N intron (N	3008 NM_016576	51292 Hs.	368855NM_016576	ENSG000002GMPR2	GMPR 2	guanosin protein-coding
chr17-507:7.656245	-0.24201	0.839641	-0.28608	0.774814	0.981636	chr17	50754011	50754626	+	0 NA	3' UTR (N3' UTR (N	13200 NM_001355	55018 Hs.	389466NM_017925	ENSG000002ANKRD40C1	C17orf73	ANKRD40 ( protein-coding
chr19-387:7.656245	-0.24201	0.839641	-0.28608	0.774814	0.981636	chr19	38730796	38731998	+	0 NA	3' UTR (N3' UTR (N	13077 NM_144691	147968 Hs.	731775NM_144691	ENSG000002CAPN12	-	calpain I protein-coding
chr5-178F:7.656245	-0.24201	0.839641	-0.28608	0.774814	0.981636	chr5	1.79E+08	1.79E+08	+	0 NA	intron (N LIME3G LI	3161 NM_001324	6940 Hs.	484324NM_005645	ENSG000002ZNF354A	EZNF	HEL1 zinc fing protein-coding
chr9-893Z:7.656245	-0.24201	0.839641	-0.28608	0.774814	0.981636	chr9	89332597	89334544	+	0 NA	intron (N Charliel	14719 NM_001282	79048 Hs.	59804 NM_024077	ENSG000002SECS1BP2	SBP2	SECS1 bir protein-coding
chr9-974F:7.656245	-0.24201	0.839641	-0.28608	0.774814	0.981636	chr9	97485741	97488943	+	0 NA	intron (N intron (N	62549 NM_001166	7111 Hs.	404289NM_003275	ENSG000002TMD01	D9S57E	ET1 tropomod protein-coding
chr19-571F:5.889067	0.273276	0.955704	0.285942	0.774922	0.981636	chr19	57197821	57198278	+	0 NA	intron (N HERVL-int	-12938 NM_003417	9422 Hs.	515633NM_003417	ENSG000002ZNF264	-	zinc fing protein-coding
chr3-1805:6.156314	-0.28353	0.991992	-0.28582	0.775015	0.981636	chr3	1.81E+08	1.81E+08	+	0 NA	intron (N intron (N	2436 NM_001363	8087 Hs.	478407NM_005087	ENSG000002FXR1	FXR1P	FMR1 autc protein-coding
chr15-731:6.725474	-0.25788	0.902231	-0.28582	0.775016	0.981636	chr15	73184679	73185410	+	0 NA	intron (N LMC1 LI	-114866 NR_162148	1.13E+08	MIR12135	-	microRNA ncRNA	
chr9-976F:6.725474	-0.25788	0.902231	-0.28582	0.775016	0.981636	chr9	97682296	97682746	+	0 NA	intron (N LIME LINE	14888 NR_149094	7507 Hs.	654364NM_00038C	ENSG000002XPA	XP1 XPAC	XPA, DNA protein-coding
chr12-875:6.462145	0.234785	0.821546	0.285785	0.775043	0.981636	chr12	879790	880188	+	0 NA	exon (NM exon (NM	53088 NM_001297	5893 Hs.	410355NM_134422	ENSG000002RAD52	-	RAD52 hon protein-coding
chr5-7151:6.462145	0.234785	0.821546	0.285785	0.775043	0.981636	chr5	71515346	71515825	+	0 NA	intron (N Tiger14a	59934 NM_018425	55814 Hs.	258272NM_018425	ENSG000002BDP1	DFNB112	EB double protein-coding
chr19-191F:6.641103	-0.24205	0.846978	-0.28578	0.775047	0.981636	chr19	1912436	1913553	+	0 NA	exon (NM exon (NM	7595 NM_001325	113178 Hs.	144988NM_079834	ENSG000002SCAMP4	SCAMP-4	secretory protein-coding
chr1-105Z:7.443545	0.241481	0.845008	0.285773	0.775052	0.981636	chr1	1050463	1053157	+								



chr11-108.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr11	1.08E+08	1.08E+08	0	NA	intron (AluSc SIN	25391 NM_000019	38 Hs. 232375NM_000019	ENSG00000ACAT1	ACAT MAT acetyl-Ccprotein-coding	
chr11-117.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr11	1.17E+08	1.17E+08	0	NA	intron (AluJb SIN	11506 NM_001077	257160 Hs. 591934NM_20734	ENSG00000RNF214	- ring fingprotein-coding	
chr14-305.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr14	30998053	30999717	+	0	NA	intron (FLAM_A SI	15857 NR_030354	693209 NR_030354	ENSG00000MIR624	MIRN624 microRNA ncRNA
chr14-104.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr14	1.01E+08	1.01E+08	0	NA	intron (NA-rich LC	-7580 NR_030528	768222 NR_030528	ENSG00000MIR770	MIRN770 microRNA ncRNA	
chr15-430.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr15	40360737	40361902	+	0	NA	intron (AluJb SIN	31837 NM_001141	7158 Hs. 440966NM_005657	ENSG00000TP53BP1	53BP1 TDF tumor prcprotein-coding
chr19-49C.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr19	49096324	49097701	+	0	NA	intron (AluSx SIN	11561 NM_001301	6625 Hs. 467097NM_00308	ENSG00000SNRNP70	RNPUIZ RF small nucprotein-coding
chr2-333C.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr2	33306463	33308063	+	0	NA	intron (L1ME2 LIN	-111253 NR_039628	1.01E+08 NR_039628	ENSG00000MIR4430	- microRNA ncRNA
chr2-365E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr2	36537126	36538956	+	0	NA	intron (intron (N	60127 NM_001042	9637 Hs. 258566NM_00510	ENSG00000FEZ2	HUM3CL fasciculaprotein-coding
chr2-174E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr2	1.75E+08	1.75E+08	+	0	NA	intron (L3 LINE C	-40754 NM_00103E	1134 Hs. 434479NM_00007	ENSG00000CHRNA1	ACHRA ACF cholinerprotein-coding
chr20-472.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr20	47226460	47229142	+	0	NA	intron (intron (N	60834 NR_037411	1.01E+08 NR_037411	ENSG00000MIR3616	mir-3616 microRNA ncRNA
chr3-1327.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	exon (NM exon (NM	-13494 NR_002811	348808 Hs. 586111NR_002811	ENSG00000NPHP3-AS1	NCRNA0011NPHP3 antncRNA
chr3-136E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr3	1.37E+08	1.37E+08	+	0	NA	intron (L1MB3 LIN	28661 NM_00615E	4690 Hs. 126889NM_00615E	ENSG00000CNCK1	NCK NCKa NCK adaptprotein-coding
chr4-7141.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr4	71418184	71420232	+	0	NA	intron (L1PA3 LIN	80155 NM_00375E	8671 Hs. 5462 NM_00375E	ENSG00000SLC44A	HNBC1 KNE solute cprotein-coding
chr5-7475.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr5	74736362	74739324	+	0	NA	intron (L2a LINE	29274 NR_10400E	84340 Hs. 277154NM_03238	ENSG00000GFM2	EF-G2nt EG elongatprotein-coding
chr5-1404.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr5	1.4E+08	1.4E+08	+	0	NA	exon (NM exon (NM	-61936 NM_00373E	8637 Hs. 594084NM_00373E	ENSG00000EIF4EBP3	4E-BP3 4Eukaryotiiprotein-coding
chr7-765E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr7	76561255	76562548	+	0	NA	intron (L1PA4 LIN	12560 NR_029411	1E+08 Hs. 712837NR_029411	ENSG00000LOC100103E	- uncharactncRNA
chr7-1211.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr7	1.21E+08	1.21E+08	+	0	NA	intron (L1MA4 LIN	166929 NM_00110E	79974 Hs. 189656NM_02491E	ENSG00000CCPED1	C7orf58 cadherin protein-coding
chr7-128E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (intron (N	33764 NM_001364	3663 Hs. 521181NM_03264E	ENSG00000IRF5	SLEB10 interfercprotein-coding
chr7-139E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	3' UTR (3' UTR (N	45224 NM_00108C	154790 Hs. 57806 NM_00108C	ENSG00000CLEC2L	- C-type lprotein-coding
chr8-173E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr8	17303757	17304832	+	0	NA	intron (intron (N	57336 NM_00136E	137492 Hs. 343877NM_15241E	ENSG00000VPS37A	HCRP1 PQE VPS37A st protein-coding
chr8-265E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr8	26584003	26587305	+	0	NA	intron (intron (N	7249 NM_001244	1808 Hs. 593187NM_00138E	ENSG00000KIFAP5L2	CRMP-2 CF dihydroyprotein-coding
chr9-3624.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr9	36244763	36247013	+	0	NA	intron (intron (N	12560 NM_00119C	10020 Hs. 5920 NM_00547E	ENSG00000CNE	DMRV GLCN glucosamiprotein-coding
chr9-9684.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr9	96843778	96844719	+	0	NA	intron (L1ME1 LIN	10266 NM_00134E	158431 Hs. 30567NM_001001	ENSG00000ZNF782	- zinc fingprotein-coding
chr9-128E.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (intron (N	-4170 NM_00135E	883 Hs. 49525NM_00405E	ENSG00000KYAT1	CCBL1 GTR kynureniniprotein-coding
chrX-242C.7.648387	-0.23843	0.835975	-0.28521	0.775484	0.981636	chrX	24207409	24209146	+	0	NA	exon (NM exon (NM	58548 NM_00117E	7543 Hs. 336681NM_00341C	ENSG00000ZFX	ZNF926 zinc fingprotein-coding
chr15-632.11.38398	-0.19889	0.698047	-0.28492	0.775706	0.981636	chr15	63258429	63258662	+	0	NA	intron (NMER51A LI	-19005 NM_00114E	83464 Hs. 51170NM_031301	ENSG00000APH1B	APH-1B PF aph-1 honprotein-coding
chr19-477.11.38398	-0.19889	0.698047	-0.28492	0.775706	0.981636	chr19	47276906	47278893	+	0	NA	intron (AluSx1 SI	14477 NM_014601	30846 Hs. 744966NM_014601	ENSG00000EHD2	PAST2 EF domainiprotein-coding
chr2-971E.11.38398	-0.19889	0.698047	-0.28492	0.775706	0.981636	chr2	97194901	97195165	+	0	NA	intron (MERS5A DN	81880 NM_001354	375248 Hs. 541894NM_19855E	ENSG00000ANKRD36	UNQ2430 ankryn iprotein-coding
chr1-900C.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr1	90005202	90006004	+	0	NA	3' UTR (3' UTR (N	10493 NM_181781	284695 Hs. 306221NM_181781	ENSG00000ZNF326	ZAN75 ZIF zinc fingprotein-coding
chr1-170C.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr1	1.7E+08	1.7E+08	+	0	NA	intron (intron (N	52801 NM_001204	22920 Hs. 433442NM_01497C	ENSG00000KIFAP3	FLA3 KAP-kinesin iprotein-coding
chr11-115.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr11	11905398	11906389	+	0	NA	intron (intron (N	64470 NM_00133C	55031 Hs. 57725NM_01794E	ENSG00000CUSP47	TRFP ubiquitiiprotein-coding
chr15-784.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr15	78445377	78446154	+	0	NA	intron (intron (N	7344 NM_00132C	3658 Hs. 436031NM_00413E	ENSG00000IREB2	AC03 IRE-iron resiprotein-coding
chr16-21E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr16	21888886	21890583	+	0	NA	Intergeni Intergeni	-22999 NR_02445E	LOC100109C	- uncharactncRNA	
chr17-46E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr17	46209084	46209910	+	0	NA	intron (AluSz SIN	15877 NM_00119E	284058 Hs. 648744NM_01544E	ENSG00000KANSL1	CENP-36 KAT8 regiprotein-coding
chr2-261E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr2	26134796	26135733	+	0	NA	3' UTR (3' UTR (N	-37824 NM_00116E	150946 Hs. 187912NM_00116E	ENSG00000GAREM2	FAM59B GARGB2 ascprotein-coding
chr2-737E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr2	37251362	37256394	+	0	NA	non-codiron-codir	28220 NR_14640E	55471 Hs. 433466NM_01860E	ENSG00000NDUFAF7	C2orf56 WADH:ubiciprotein-coding
chr2-390C.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr2	39005143	39006679	+	0	NA	intron (intron (N	-45567 NR_02838E	375196 Hs. 65903NR_02838E	ENSG00000LOC37519E	- uncharactncRNA
chr2-130C.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr2	1.3E+08	1.3E+08	+	0	NA	intron (intron (N	-2581 NM_001321	84317 Hs. 10420E	ENSG00000CCDC115	CDG20 ccpcolide-cprotein-coding
chr22-297.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr22	29794325	29795183	+	0	NA	intron (L1ME3G LI	27385 NM_013387	29796 Hs. 284292NM_013387	ENSG00000UCRQ10	HSPC051 H ubiquinoliprotein-coding
chr22-414.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr22	41438931	41441118	+	0	NA	intron (intron (N	6777 NM_01627E	10766 Hs. 47497E	ENSG00000TOB2	APRO5 TOE transducepprotein-coding
chr3-187E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr3	1.87E+08	1.87E+08	+	0	NA	intron (intron (N	-7049 NR_135551	1.02E+08 NR_135551	ENSG00000LOC10192E	- uncharactncRNA
chr3-191E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr3	1.91E+08	1.91E+08	+	0	NA	intron (intron (N	-33886 NR_12060E	1.03E+08 NR_12060E	LINC1-00C	- uncharactncRNA
chr4-675E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr4	67538538	67539723	+	0	NA	intron (L1M5 LINE	6373 NM_00181E	1060 Hs. 479867NM_00181E	ENSG00000CENPC	CENP-C CF centromeriprotein-coding
chr4-999C.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr4	99905966	99907712	+	0	NA	intron (intron (N	-12293 NR_02417E	8649 Hs. 433332NM_02197C	ENSG00000LAMTOR3	MAP2K1 IPI late endcprotein-coding
chr5-347E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr5	34723452	34724356	+	0	NA	intron (intron (N	36345 NM_00114E	26064 Hs. 431403NM_01557E	ENSG00000CRAI14	NORPEG Rretinoic protein-coding
chr5-657E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr5	65701739	65702130	+	0	NA	intron (MER3 DNA	20155 NM_01907E	54557 Hs. 482301NM_01907E	ENSG00000SGTB	SGT2 small gltprotein-coding
chr6-1224.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr6	1.22E+08	1.22E+08	+	0	NA	Intergeni L1PA14 LI	33127 NM_02075E	57515 Hs. 146666NM_02075E	ENSG00000SERINC1	TDEL1 TDE serine irprotein-coding
chr6-149E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	promoter-promoter-	-146 NR_077247	645958 Hs. 632614NR_077247	RPS18P9	RPS18_6_7ribosomalpseudo
chr8-557E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr8	55794743	55797715	+	0	NA	intron (intron (N	22783 NM_00136E	96764 Hs. 335066NM_024831	ENSG00000TGS1	NCOA61P T trimethyliprotein-coding
chr9-105E.7.179072	-0.24575	0.862754	-0.28484	0.775766	0.981636	chr9	1.06E+08	1.06E+08	+	0	NA	intron (intron (N	15597 NR_10426E	26134 Hs. 11315CNR_10426E	ENSG00000CALGAP1E	GARNL2 GaRAL GTPaspseudo
chr13-491.7.940133	0.234932	0.825042	0.284751</													

chr11-77: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr11	77330405	77331505	+	0	NA	intron (N)LP4A LIN	-29289	NM_182833	220032	Hs. 249799	ENSG000002GDPD4	GDE6	glycerolp protein-coding			
chr12-22: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr12	22678730	22679484	+	0	NA	intron (N)MLT2B3 LI	53936	NM_001035	55500	Hs. 29464	NM_018633	ENSG000002ETNK1	EKI1 EKI1	lethanolan protein-coding		
chr12-48: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr12	48139780	48141301	+	0	NA	intron (N)intron (N)	7743	NR_106766	1.02E+08	NR_106766	ENSG000002MIR6505	hsa-mir-6	microRNA ncRNA			
chr12-11: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (N)intron (N)	-12267	NR_106921	1.02E+08	NR_106921	ENSG000002MIR6861	hsa-mir-6	microRNA ncRNA			
chr12-11: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr12	1.13E+08	1.13E+08	+	0	NA	intron (N)MER58A DN	-11173	NR_106956	1.02E+08	NR_106956	ENSG000002MIR7106	hsa-mir-7	microRNA ncRNA			
chr12-12: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (N)intron (N)	-23520	NM_207437	196385	Hs. 622654	NM_207437	ENSG000002DNAH10	-	dynein a	protein-coding	
chr15-42: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr15	62723503	62727131	+	0	NA	intron (N)intron (N)	11811	NM_138477	146059	Hs. 599232	NM_138477	ENSG000002CDAM1	CDAI1 CDAI1	codanin 1	protein-coding	
chr16-68: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr16	68254068	68256154	+	0	NA	intron (N)intron (N)	-9415	NM_003983	9057	Hs. 679582	NM_003983	ENSG000002SLCTA6	LAT-2 LAT1	solute c	protein-coding	
chr16-69: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr16	69876493	69877352	+	0	NA	intron (N)Tiger1 I	38185	NM_001270	11060	Hs. 408458	NM_007014	ENSG000002WWP2	WWP2 WWP2	WW domain	protein-coding	
chr16-71: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr16	71476098	71478550	+	0	NA	intron (N)intron (N)	12000	NM_006961	7567	Hs. 660070	NM_006961	ENSG000002ZNF19	KOX12	zinc finger	protein-coding	
chr16-82: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr16	89277873	89283169	+	0	NA	exon (NM)exon (NM)	-15607	NR_136333	1.05E+08	Hs. 657381	NR_136333	ENSG000002LOC105371	-	uncharacter	ncRNA	
chr17-76: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr17	76328798	76329405	+	0	NA	intron (N)AluJo SIN	-21421	NM_032134	84074	Hs. 252733	NM_032134	ENSG000002QRICH2	SPGF35	glutamine	protein-coding	
chr17-77: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr17	77167403	77168578	+	0	NA	intron (N)LTR10B1 I	-17223	NM_001144	6397	Hs. 464184	NM_003003	ENSG000002SECI4L1	PRELID4A SECI4	lik	protein-coding	
chr18-23: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr18	23244119	23247608	+	0	NA	intron (N)intron (N)	90038	NM_138373	91768	Hs. 11108	NM_138373	ENSG000002CABLES1	CABL1 CAF	Cdk5 and	protein-coding	
chr19-184: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr19	18435439	18435992	+	0	NA	intron (N)CpG-14071	1594	NM_001255	51477	Hs. 405873	NM_016368	ENSG000002ISYNA1	INO1 INOS	inositol-	protein-coding	
chr2-201: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	intron (N)intron (N)	15042	NM_033355	841	Hs. 599762	NM_001228	ENSG000002CASP8	ALPS2B CASP8	caspase	protein-coding	
chr2-239: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr2	2.39E+08	2.39E+08	+	0	NA	promoter-promoter-	-518	NR_039948	1.01E+08	NR_039948	ENSG000002MIR2467	mir-2467	microRNA ncRNA			
chr20-94: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr20	9435917	9436706	+	0	NA	intron (N)intron (N)	-78047	NM_001199	24141	Hs. 22920	NM_012261	ENSG000002LAMP5	BAD-LAMP	lysosomal	protein-coding	
chr20-414: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr20	41414356	41416080	+	0	NA	exon (NM)exon (NM)	-48400	NM_052846	90187	Hs. 726522	NM_052846	ENSG000002EMILIN3	C20orf130	elastin	protein-coding	
chr21-39: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr21	39308254	39311584	+	0	NA	intron (N)LMC5a LI	3713	NM_018963	54014	Hs. 627135	NM_018963	ENSG000002BRWD1	C21orf107	bromodomain	protein-coding	
chr21-35: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr22	35389836	35394701	+	0	NA	intron (N)Charlie2	-7872	NM_006733	4174	Hs. 517582	NM_006733	ENSG000002MCM5	CD46 MG	minichrom	protein-coding	
chr22-501: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr22	50193330	50194930	+	0	NA	intron (N)intron (N)	3543	NM_001320	80305	Hs. 517731	NM_025204	ENSG000002TRABD	LP6054 PF	TraB domain	protein-coding	
chr3-488: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr3	48837882	48839069	+	0	NA	intron (N)AluSx SIN	9399	NM_001321	5576	Hs. 631922	NM_004157	ENSG000002PRKAR2A	PKR2 PRK2	protein	protein-coding	
chr5-1067: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr5	10679713	10683101	+	0	NA	intron (N)intron (N)	79823	NM_004394	1611	Hs. 75189	NM_004394	ENSG000002DAP	-	death	protein-coding	
chr7-2214: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr7	2214821	2218330	+	0	NA	intron (N)LMC1 LIN	16370	NM_001304	8379	Hs. 654838	NM_003550	ENSG000002MAD1L1	MAD1 PIG6	mitotic	protein-coding	
chr7-102: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (N)LP4A LIN	78562	NM_001144	222234	Hs. 202543	NM_147194	ENSG000002FAM185A	-	family w	protein-coding	
chr8-277: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr8	27750881	27752583	+	0	NA	intron (N)intron (N)	20908	NR_156432	55246	Hs. 445512	NM_018240	ENSG000002CCDC25	-	coiled-c	protein-coding	
chr8-1334: 6.946957	0.249036	0.878933	0.283338	0.776917	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (N)intron (N)	75539	NM_003033	6482	Hs. 374257	NM_003033	ENSG000002ST3GAL1	Gal-1 Nac6S	ST3 beta-	protein-coding	
chrX-155: 5.896259	0.270743	0.955749	0.282378	0.776964	0.981636	chrX	1.55E+08	1.55E+08	+	0	NA	intron (N)LMIEc LIN	6453	NM_001242	79184	Hs. 558537	NM_024332	ENSG000002BRCC3	BRCC36 C	BRCA1/BRC	protein-coding	
chr1-244: 6.946957	0.23669	0.835824	-0.28318	0.777041	0.981636	chr1	24466030	24467263	+	0	NA	TTS (NM)_TTS (NM)_C	-35698	NM_001251	11123	Hs. 656799	NM_013441	ENSG000002RCAN3	DISCR1L2 N	RCAN1	protein-coding	
chr1-108: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	3' UTR (N)3' UTR (N)	20246	NM_001278	23155	Hs. 658485	NM_015127	ENSG000002CLCC1	MCLC	chloride	protein-coding	
chr10-87: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr10	87665651	87667590	+	0	NA	intron (N)intron (N)	6742	NM_001016	9060	Hs. 524491	NM_004670	ENSG000002PAPSS2	ATPSK2 BC3	3'-phosph	protein-coding	
chr10-88: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr10	88936891	88943119	+	0	NA	TTS (NR)_TTS (NR)_I	7321	NR_125373	1E+08	NR_125373	ENSG000002ACTA2-AS1	UC001kfo ACTA2	ant	ncRNA		
chr10-10: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (N)AluSq4 SI	-15141	NM_017893	57715	Hs. 591922	NM_017893	ENSG000002SEMA4G	-	semaphori	protein-coding	
chr10-10: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr10	1.1E+08	1.1E+08	+	0	NA	exon (NM)exon (NM)	34668	NM_001324	7511	Hs. 390622	NM_020383	ENSG000002XPNP1	APPI SAMF	X-prolyl	protein-coding	
chr10-11: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr10	1.2E+08	1.2E+08	+	0	NA	intron (N)LMIE4b LI	27318	NM_007190	19116	Hs. 435004	NM_007190	ENSG000002SEC23IP	MPT053 F	SEC23	intron	protein-coding
chr11-29: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr11	2953475	2955216	+	0	NA	intron (N)intron (N)	9548	NR_002982	677833	Hs. 689696	NR_002982	ENSG000002SNORA54	ACA54	small	nucsnRNA	
chr11-33: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr11	3308474	33088262	+	0	NA	intron (N)intron (N)	9636	NR_015451	283267	Hs. 533701	NR_015451	ENSG000002LINC00294	hsa-miR-6	microRNA ncRNA		
chr12-53: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr12	53055164	53059730	+	0	NA	TTS (NR)_TTS (NR)_I	503	NR_106811	1.02E+08	NR_106811	ENSG000002MIR6757	hsa-mir-6	microRNA ncRNA			
chr12-111: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr12	1.11E+08	1.11E+08	+	0	NA	3' UTR (N)3' UTR (N)	15043	NM_001291	10019	Hs. 506784	NM_005477	ENSG000002SH2B3	IDDM20 L	SH2B adaf	protein-coding	
chr14-96: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr14	96521603	96522455	+	0	NA	intron (N)AluSz SIN	19114	NM_001293	10914	Hs. 253722	NM_032632	ENSG000002PAPOLA	PAP PAP	-poly (A)	protein-coding	
chr14-10: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr14	1.11E+08	1.01E+08	+	0	NA	TTS (NR)_TTS (NR)_C	116	NR_003198	767582	NR_003198	ENSG000002SNORD114-14q	(11-6)	small	nucsnRNA		
chr14-101: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	promoter-promoter-	-900	NR_029874	494331	NR_029874	ENSG000002MIR382	MIRN382	microRNA ncRNA			
chr15-28: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr15	28311053	28313054	+	0	NA	intron (N)intron (N)	10099	NM_004667	8924	Hs. 434893	NM_004667	ENSG000002HERC2	D15F37S1	HECT and	protein-coding	
chr16-89: 7.640529	-0.23669	0.835824	-0.28318	0.777041	0.981636	chr16	8929543</															



chr6-3033	8.990164	0.22243	0.787552	0.282432	0.777612	0.981636	chr6	30335992	30336931	+	0	NA	intron (N)Tigger1 I	7150 NM_001199	202658 Hs. 413495NM_001199	ENSG000003TRIM39- RF TRIM39R	TRIM39- RF protein-coding
chr14-73C	6.717616	-0.25576	0.906427	-0.28217	0.777817	0.981636	chr14	73082081	73082304	+	0	NA	intron (N)HAL LINE	23658 NM_021235	58517 Hs. 531106NM_021235	ENSG000003RBM25	NET52 REI RNA bindi protein-coding
chr14-102	6.717616	-0.25576	0.906427	-0.28217	0.777817	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	3' UTR (N)3' UTR (N)	-49741 NM_001199	7187 Hs. 510525NM_00330C	ENSG000003TRAF3	CAP-1 CAITNF rece protein-coding
chr20-945	6.717616	-0.25576	0.906427	-0.28217	0.777817	0.981636	chr20	9455657	9456041	+	0	NA	intron (N)intron (N)	-58509 NM_001199	24141 Hs. 22920 NM_012261	ENSG000003LAMP5	BAD-LAMP lysosomal protein-coding
chr9-125	6.717616	-0.25576	0.906427	-0.28217	0.777817	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (N)L1P43 LIN	-69303 NM_002077	2800 Hs. 59504 NM_002077	ENSG000003GOLGA1	golgin-97 golgin Al protein-coding
chr17-604	8.966591	0.228067	0.808311	0.282152	0.777827	0.981636	chr17	60478900	60479220	+	0	NA	intron (N)intron (N)	47180 NM_001282	10513 Hs. 84084 NM_00638C	ENSG000003APPBP2	APP-BP2 Famlyoid t protein-coding
chr4-867	8.444579	0.227485	0.806545	0.282049	0.777906	0.981636	chr4	86750901	86751100	+	0	NA	intron (N)intron (N)	98384 NM_197966	345274 Hs. 452996NM_197966	ENSG000003SLC10A6	SOAT solute c protein-coding
chr6-358	8.444579	0.227485	0.806545	0.282049	0.777906	0.981636	chr6	35863942	35864956	+	0	NA	intron (N)L1MA2 LIN	56649 NM_003137	6732 Hs. 443861NM_003137	ENSG000003SRPK1	SFRSK1 SRSF protein-coding
chr9-999	8.444579	0.227485	0.806545	0.282049	0.777906	0.981636	chr9	99923864	99924327	+	0	NA	intron (N)MER21A LI	17441 NM_017919	55014 Hs. 704031NM_017919	ENSG000003STX17	- syntaxin protein-coding
chr1-394	11.87872	-0.19227	0.682233	-0.28182	0.778083	0.981636	chr1	39435046	39450893	+	0	NA	intron (N)intron (N)	33896 NM_015038	643314 Hs. 658766NM_015038	ENSG000003KIAA0754	- KIAA0754 protein-coding
chr1-2431	11.87872	-0.19227	0.682233	-0.28182	0.778083	0.981636	chr1	2.43E+08	2.43E+08	+	0	NA	exon (NM)exon (NM)	-63312 NR_029401	731275 Hs. 722353NR_029401	ENSG000003LINC01347	- long intncRNA
chr21-466	11.87872	-0.19227	0.682233	-0.28182	0.778083	0.981636	chr21	46643466	46646622	+	0	NA	intron (N)AluJr SIN	9370 NM_206962	3275 Hs. 154163NM_001535	ENSG000003PRMT2	HRMT1L1 protein protein-coding
chr22-363	11.87872	-0.19227	0.682233	-0.28182	0.778083	0.981636	chr22	36325537	36327193	+	0	NA	intron (N)intron (N)	-39458 NR_106877	1.02E+08 NR_106877	ENSG000003MIR6819	hpa-mir-6819 ncRNA
chr3-519	11.87872	-0.19227	0.682233	-0.28182	0.778083	0.981636	chr3	51991623	51994870	+	0	NA	TTS (NM)TTS (NM)C	2649 NM_000992	6159 Hs. 425125NM_000992	ENSG000003RPL29	HIS HMR1 ribosomal protein-coding
chr2-3867	8.493576	0.227325	0.806778	0.281769	0.778121	0.981636	chr2	38675846	38676412	+	0	NA	intron (N)intron (N)	10015 NM_138801	130589 Hs. 435012NM_138801	ENSG000003GALM	BLOCK25 Galactose protein-coding
chr1-3547	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr1	35477702	35479021	+	0	NA	intron (N)L1MA2 LIN	79042 NM_024874	79932 Hs. 456507NM_024874	ENSG000003KIAA03191	AAVR AAVKIAA0319 protein-coding
chr1-426	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr1	42666204	42667055	+	0	NA	intron (N)intron (N)	8206 NM_006347	10465 Hs. 256635NM_006347	ENSG000003CPII	CYP-20 Cpeptidyl protein-coding
chr10-375	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr10	375065	376046	+	0	NA	intron (N)intron (N)	195561 NM_001202	10771 Hs. 292265NM_006624	ENSG000003MYND11	BRAM1 BS5 zinc finger protein-coding
chr11-75	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr11	75983498	75984151	+	0	NA	intron (N)Tigger3a	168614 NM_003366	7405 Hs. 202477NM_003366	ENSG000003UVRAG	DHTX VPS5UV radiat protein-coding
chr12-481	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr12	48123803	48125376	+	0	NA	intron (N)intron (N)	1942 NM_001166	5213 Hs. 75160 NM_000285	ENSG000003PFKM	ATP-PFK1 Cphospho protein-coding
chr13-64	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr13	64154379	64154738	+	0	NA	intron (N)THE1B LTF	-49178 NM_001278	84650 Hs. 433278NM_032565	ENSG000003EBPL	EBP EB like protein-coding
chr14-10C	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	intron (N)intron (N)	1655 NR_146000	79104 Hs. 118101NR_024149	MEG8	Bsr Irm maternal ncRNA
chr16-195	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr16	19500109	19501445	+	0	NA	TTS (NM)TTS (NM)C	21321 NR_136688	51573 Hs. 512607NM_016641	ENSG000003GDE1	363E6.2 glycerol protein-coding
chr17-85	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr17	8512147	8512566	+	0	NA	intron (N)intron (N)	76472 NM_030808	81565 Hs. 372122NM_030808	ENSG000003NDEL1	EOPA MIT1 nudE protein-coding
chr20-334	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr20	33412008	33412433	+	0	NA	intron (N)MIR3 SINE	-10651 NM_016082	51654 Hs. 435952NM_016082	ENSG000003CDK5RAP1	C20orf34 CDK5 reg protein-coding
chr3-370	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr3	37022172	37022448	+	0	NA	intron (N)MER21A LI	29860 NM_001258	4292 Hs. 195364NM_000245	ENSG000003MLH1	COCA2 FCCmutL home protein-coding
chr3-641	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr3	64154379	64154738	+	0	NA	intron (N)AluY SINE	-32986 NR_046702	1.01E+08 Hs. 670843NR_046702	ENSG000003PRICKLE2-	PRICKLE2 ncRNA
chr3-149	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr3	1.5E+08	1.5E+08	+	0	NA	intron (N)intron (N)	86015 NM_001168	25937 Hs. 477921NM_015475	ENSG000003WVTR1	TAZ WW domair protein-coding
chr4-133	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr4	1330742	1331248	+	0	NA	intron (N)intron (N)	-16213 NM_020894	57654 Hs. 380475NM_020894	ENSG000003UVSSA	KIAA1530 UV stimu protein-coding
chr7-994	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr7	99426636	99429799	+	0	NA	intron (N)AluY SINE	10581 NM_015545	26024 Hs. 632313NM_015545	ENSG000003PTCD1	- pentatric protein-coding
chr7-115	6.905817	0.247196	0.877495	0.281706	0.778169	0.981636	chr7	1.12E+08	1.12E+08	+	0	NA	intron (N)AluY SINE	130866 NR_103800	1.01E+08 Hs. 677515NR_103800	ENSG000003DOCK4-AS1-	DOCK4 antncRNA
chr17-44	6.222878	-0.27225	0.966455	-0.2817	0.778171	0.981636	chr17	44064249	44064514	+	0	NA	intron (N)intron (N)	2290 NM_001371445	146057 Hs. 646511NM_17350C	ENSG000003TTBK2	SCA11 TTE tau tubul protein-coding
chr15-42	8.452437	0.225641	0.801071	0.281674	0.778193	0.981636	chr15	42946157	42947443	+	0	NA	intron (N)intron (N)	-26022 NM_173500	146057 Hs. 646511NM_17350C	ENSG000003TTBK2	SCA11 TTE tau tubul protein-coding
chr19-17	8.452437	0.225641	0.801071	0.281674	0.778193	0.981636	chr19	17577696	17578957	+	0	NA	intron (N)MIR3 SINE	22677 NM_024655	79709 Hs. 418795NM_024655	ENSG000003COLGALT1	BVSD3 Colcollagen protein-coding
chr2-2067	8.452437	0.225641	0.801071	0.281674	0.778193	0.981636	chr2	2.07E+08	2.07E+08	+	0	NA	intron (N)LM1B LIN	-7258 NR_036078	NR_036078	ENSG000003MIR3130-2	MIR3130-4 microRNA ncRNA
chr20-45	8.452437	0.225641	0.801071	0.281674	0.778193	0.981636	chr20	45961945	45962377	+	0	NA	exon (NM)exon (NM)	10042 NR_022095	63925 Hs. 174193NM_022095	ENSG000003ZNF335	MCPH10 Nizinc finger protein-coding
chr7-147	8.452437	0.225641	0.801071	0.281674	0.778193	0.981636	chr7	1473412	1473953	+	0	NA	exon (NM)exon (NM)	-14212 NM_182924	79778 Hs. 376617NM_024725	ENSG000003MICALL2	JRAB MIC MICAL lik protein-coding
chr7-149	8.452437	0.225641	0.801071	0.281674	0.778193	0.981636	chr7	1.5E+08	1.5E+08	+	0	NA	intron (N)AluJr4 SI	-54417 NM_152557	155061 Hs. 24643 NM_152557	ENSG000003ZNF746	PARIS zinc finger protein-coding
chr5-957	11.37612	-0.19674	0.7018	-0.28161	0.778239	0.981636	chr5	95737227	95740432	+	0	NA	intron (N)L2c LINE	-6727 NM_001345	83890 Hs. 50499 NM_031955	ENSG000003SPATA9	ND5-SP16 spermatog protein-coding
chr12-45	6.890101	0.251432	0.89302	0.281552	0.778287	0.981636	chr12	45932011	45932595	+	0	NA	intron (N)intron (N)	58271 NM_004715	9169 Hs. 210367NM_004715	ENSG000003SCAF11	CASP11 SFR-relate protein-coding
chr12-101	6.890101	0.251432	0.89302	0.281552	0.778287	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (N)L2c LINE	-27473 NR_049838	1.01E+08 NR_049838	ENSG000003MIR548A	microRNA ncRNA
chr2-105	6.890101	0.251432	0.89302	0.281552	0.778287	0.981636	chr2	1.06E+08	1.06E+08	+	0	NA	exon (NM)exon (NM)	30421 NM_001004	8440 Hs. 529244NM_003581	ENSG000003CNCK2	GRB4 NCK1NCK adapt protein-coding
chr22-26	6.890101	0.251432	0.89302	0.281552	0.778287	0.981636	chr22	26527722	26528377	+	0	NA	intron (N)intron (N)	15517 NR_144525	1.01E+08 Hs. 405877NR_144529	LOC100507-	uncharacterncRNA
chr10-294	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr10	29468157	29470746	+	0	NA	TTS (NR)TTS (NR)1	59208 NR_110928	1.03E+08 Hs. 499205NR_00393C	ENSG000003SVIL-AS1	SVIL antincRNA
chr10-84	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr10	84442206	84443853	+	0	NA	intron (N)L1P47 LIN	17863 NM_001284	54462 Hs. 461985NM_018995	ENSG000003CCSER2	FAM190B Coiled-cc protein-coding
chr10-924	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr10	92468085	92470493	+	0	NA	intron (N)intron (N)	28472 NM_001322	3416 Hs. 500545NM_004965	ENSG000003IDE	INSULYSIN insulin protein-coding
chr10-97	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr10	97394768	97397701	+	0	NA	exon (NM)exon (NM)	5106 NM_015175	23223 Hs. 434251NM_015175	ENSG000003RRP12	KIAA0690 ribosomal protein-coding
chr12-90	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr12	900037	906523	+	0	NA	intron (N)intron (N)	29796 NM_001297	5893 Hs. 410355NM_134422	ENSG000003RAD52	- RAD52 hon protein-coding
chr12-11	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (N)LTR10C LI	25777 NM_025247	80724 Hs. 331141NM_025247	ENSG000003ACAD10	- acyl-CoA protein-coding
chr14-234	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr14	23470962	23477872	+	0	NA	intron (N)intron (N)	4714 NM_001042	25983 Hs. 9043 NM_015514	ENSG000003NGDN	C14orf12C neurogic protein-coding
chr17-42	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr17	42500434	42505352	+	0	NA	intron (N)intron (N)	7924 NR_049845	1.01E+08 NR_049845	ENSG000003MIR548AT	microRNA ncRNA
chr19-37	7.955849	0.231176	0.821256	0.28149	0.778334	0.981636	chr19	37090264	37096453	+	0	NA	intron (N)AluSg SIN	14925 NM_001325	147923 Hs. 444992NM_1446		



chr9-1114	8.460295	0.223867	0.799392	0.280047	0.779441	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	44682	NM_001364	23392	Hs.368255	ENSG000002ECPAS	ECM29 KIF23	prcprotein-coding
chr1-1554	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr1	15544599	15546772	+	0	NA	intron (N2 LINE L	3519	NR_135611	1.07E+08	NR_135611	ENSG000002SCARNA21E	-	small Ca <sub>v</sub> ncRNA
chr1-9678	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr1	96786366	96787786	+	0	NA	intron (NAluSx SIN	64438	NR_125356	58155	Hs.596061	ENSG000002PTBP2	PTBLP brf	polypyriminprotein-coding
chr10-15c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr10	15671419	15671618	+	0	NA	intron (Nintron (N	48404	NM_003638	8516	Hs.171311	ENSG000002ITGA8	-	integrin protein-coding
chr10-10c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (Nintron (N	13817	NR_144755	10613	Hs.150087	ENSG000002ERL1N1	C10orf69 ER	lipid protein-coding
chr11-124	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr11	12479925	12480668	+	0	NA	intron (Nintron (N	102725	NM_018222	55742	Hs.432914	ENSG000002PARVA	CH-ILKBP parv	alprotein-coding
chr12-10c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr12	1.06E+08	1.06E+08	+	0	NA	intron (NMIR SINE E	5741	NM_006822	10970	Hs.74368	ENSG000002CKAP4	CLMP6-63 cyto	skeletalprotein-coding
chr14-69c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr14	69383648	69387376	+	0	NA	intron (N2a LINE E	12787	NM_00445C	2079	Hs.599791	ENSG000002ERH	DROER	ERH mRNA protein-coding
chr18-234	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr18	23428541	23430447	+	0	NA	intron (NAluSp SIN	8467	NM_03293C	85019	Hs.137562	ENSG000002MEM241	C18orf45 trans	memt protein-coding
chr19-357	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr19	35760177	35761211	+	0	NA	intron (NAluSq SIN	2518	NM_001039	148137	Hs.527982	ENSG000002PROSER3	C19orf55	proline ε protein-coding
chr19-44c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr19	44301701	44302583	+	0	NA	intron (Nintron (N	2883	NM_004234	9310	Hs.613424	ENSG000002ZNF235	ANF270 HZ	zinc fing protein-coding
chr2-179c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr2	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	55058	NM_02094C	57703	Hs.31136C	ENSG000002CWC22	EIF4GL NC	CWC22 spl protein-coding
chr2-2161	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (NMER49 LTF	-47523	NR_037701	150967	Hs.56876	ENSG000002LINC0196C	PKI55	long intencRNA
chr2-2384	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	3' UTR (N3' UTR (N	21740	NM_00104C	51665	Hs.516788	ENSG000002ASB1	ASB-1	ankyrin i protein-coding
chr20-46c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr20	46685163	46686873	+	0	NA	3' UTR (N3' UTR (N	-1533	NM_00119C	64849	Hs.65549E	ENSG000002SLC13A3	ARLIAK N	solute ε protein-coding
chr20-50c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr20	50092822	50097511	+	0	NA	TTS (NR_TTS (NR_1	17984	NM_001257	7335	Hs.42052E	ENSG000002UBE2V1	CIR1 CROC	ubiquitin protein-coding
chr21-24c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr21	24649133	24649180	+	0	NA	intron (Nintron (N	29185	NR_04640C	1.01E+08	Hs.73716E	ENSG000002DIP2A-IT1	-	DIP2A intncRNA
chr22-264	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr22	24334657	24335775	+	0	NA	intron (N2c LINE E	-6892	NM_001254	23384	Hs.474384	ENSG000002SPECC1L	CYTSA G	BE sperm ant protein-coding
chr3-5254	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr3	52547981	52550691	+	0	NA	intron (NAluJr4 SI	12731	NM_001124	440957	Hs.660577	ENSG000002SMIM4	C3orf78	small intprotein-coding
chr3-138c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr3	1.38E+08	1.38E+08	+	0	NA	intron (NAluSc SIN	37762	NM_001127	25852	Hs.74486E	ENSG000002ARMC8	GID5 HSP	cardiil protein-coding
chr6-289c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr6	28901229	28902112	+	0	NA	IntergeniIntergeni	5140	NR_104117	414767	Hs.21100E	ENSG000002HCG14	dJ111M5.4HLA	complncRNA
chr6-107c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr6	1.08E+08	1.08E+08	+	0	NA	intron (Nintron (N	-51624	NM_00128E	256380	Hs.48610E	ENSG000002SCML4	dJ47M23.1Scm	polycprotein-coding
chr7-481c	7.632671	-0.23495	0.839188	-0.27998	0.779494	0.981636	chr7	48101759	48103532	+	0	NA	intron (Nintron (N	13380	NM_003364	7378	Hs.48824C	ENSG000002UPP1	UDRPASE urid	ine protein-coding
chr1-239c	7.187086	-0.19111	0.682938	-0.27983	0.779608	0.981636	chr1	23969094	23963998	+	0	NA	3' UTR (N3' UTR (N	2668	NM_017761	55629	Hs.7862	ENSG000002PNRC2	-	proline i protein-coding
chr3-526c	11.87086	-0.19111	0.682938	-0.27983	0.779608	0.981636	chr3	52687458	52696670	+	0	NA	promoter-promoter-	-672	NR_003057	692109	NR_003057	ENSG000002SNORD69	HBII-210	small nucsnRNA
chr8-122c	12.33232	-0.18781	0.671274	-0.27977	0.779651	0.981636	chr8	12205494	12206704	+	0	NA	IntergeniIntergeni	-11967	NR_14887E	653333	Hs.45841E	ENSG000002FAM86B2	-	family wiprotein-coding
chr18-48c	7.22807	-0.24457	0.874441	-0.27969	0.779718	0.981636	chr18	4827349	4827746	+	0	NA	intron (NTigger1 E	19741	NM_03256E	84656	Hs.38725E	ENSG000002GLYR1	BM045 HIF	glyoxylat protein-coding
chr20-35c	7.22807	-0.24457	0.874441	-0.27969	0.779718	0.981636	chr20	35852187	35852758	+	0	NA	intron (Nintron (N	80457	NM_01643E	51230	Hs.517044	ENSG000002PHF20	C20orf104 PHD	fingc protein-coding
chr6-149c	7.22807	-0.24457	0.874441	-0.27969	0.779718	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	intron (NLMIMEf LIN	-12625	NM_001204	11104	Hs.45017E	ENSG000002KATNA1	-	katanin c protein-coding
chr14-54c	7.220212	-0.24278	0.868438	-0.27956	0.779813	0.981636	chr14	54754924	54754920	+	0	NA	promoter-promoter-	-76	NM_001161	23034	Hs.98259	ENSG000002SAMD4A	SAMD4 SM	sterile ε protein-coding
chr19-47c	7.220212	-0.24278	0.868438	-0.27956	0.779813	0.981636	chr19	47208852	47209285	+	0	NA	intron (NMER20 DNA	-17874	NR_03615E	1E+08	NR_03615E	ENSG000002MIR3190	mir-3190	microRNA ncRNA
chr2-160c	8.949025	-0.22096	0.791007	-0.27934	0.779984	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	-9563	NR_10377E	1.01E+08	Hs.72953E	ENSG000002LINC0247E	-	long intencRNA
chr6-147c	8.949025	-0.22096	0.791007	-0.27934	0.779984	0.981636	chr6	1.47E+08	1.47E+08	+	0	NA	intron (NLPAP7 LIN	-47374	NR_03411E	29178	Hs.55760E	ENSG000002STXBP5-AS-	STXBP5-AS-	arncRNA
chr1-846c	7.681669	-0.23403	0.837819	-0.27934	0.779987	0.981636	chr1	84653631	84656462	+	0	NA	intron (Nintron (N	-20026	NR_02737E	439927	Hs.407054	ENSG000002LINC0155E	C1orf180	long intencRNA
chr10-59c	7.681669	-0.23403	0.837819	-0.27934	0.779987	0.981636	chr10	5934872	5936186	+	0	NA	intron (Nintron (N	33399	NM_001351	3601	Hs.445124	ENSG000002IL15RA	CD215	interleuk protein-coding
chr13-75c	7.681669	-0.23403	0.837819	-0.27934	0.779987	0.981636	chr13	75836671	75837151	+	0	NA	intron (Nintron (N	-34127	NM_001257	729420	Hs.58682C	ENSG000002LM07DN	C13orf45	LM07 dowr protein-coding
chr17-351	7.681669	-0.23403	0.837819	-0.27934	0.779987	0.981636	chr17	35132114	35138590	+	0	NA	exon (NM exon (NM	6899	NM_001014	54475	Hs.85570	ENSG000002CNLE1	NLE	notchless protein-coding
chr5-7151	7.681669	-0.23403	0.837819	-0.27934	0.779987	0.981636	chr5	71516851	71518743	+	0	NA	intron (NAluJo SIN	62146	NM_01842E	55814	Hs.25827E	ENSG000002BDP1	DFNB112 EB	double protein-coding
chr6-166c	7.681669	-0.23403	0.837819	-0.27934	0.779987	0.981636	chr6	1.67E+08	1.67E+08	+	0	NA	intron (Nintron (N	5688	NR_031734	1E+08	NR_031734	ENSG000002MIR1913	MIRN1913 micro	RNA ncRNA
chr1-100c	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr1	1E+08	1E+08	+	0	NA	intron (Nintron (N	35575	NM_00191E	1629	Hs.709187	ENSG000002CBT	BCATE2 BC	dihydroliprotein-coding
chr12-101	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr12	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	28742	NM_01837C	55332	Hs.526564	ENSG000002DRAM1	DRAM	DNA damag protein-coding
chr16-68c	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr16	68073755	68074945	+	0	NA	intron (Nintron (N	-11020	NR_17316E	4775	Hs.43658E	ENSG000002NFATC3	NF-AT4C	nuclear f protein-coding
chr18-76c	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr18	76910532	76911507	+	0	NA	intron (Nintron (N	86859	NM_00734E	7776	Hs.719137	ENSG000002ZNF236	ZNF236A z	zinc fing protein-coding
chr20-32c	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr20	32702830	32703768	+	0	NA	3' UTR (N3' UTR (N	-29358	NM_182584	284805	Hs.35326E	ENSG000002C20orf20C	-	chromoson protein-coding
chr3-515c	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr3	51590873	51591267	+	0	NA	intron (Nintron (N	49481	NM_001322	23132	Hs.10539E	ENSG000002RAD54L2	ARIP4 HSF	RAD54 L1k protein-coding
chr6-116c	6.409229	0.255732	0.915514	0.279332	0.77999	0.981636	chr6	1.16E+08	1.16E+08	+	0	NA	intron (Nintron (N	-6325	NM_00108C	29940	Hs.45835E	ENSG000002DSE	DS-epil1 D	ermatan protein-coding
chr1-662c	6.913675	0.245063	0.877608	0.27924	0.780061	0.981636	chr1	6627853	6632116	+	0	NA	intron (Nintron (N	4834	NM_00119E	90326	Hs.68900E	ENSG000002THAP3	-	THAP domε protein-coding
chr1-102c	6.913675	0.245063	0.877608	0.27924	0.780061	0.981636	chr1	10282049	10285073	+	0	NA	intron (Nintron (N	-15405	NR_104084	1.02E+08	NR_104084	ENSG000002CRNU6-7	U6-7	RNA, u6 ε snRNA
chr1-109c	6.913675	0.245063	0.877608	0.27924	0.780061	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	42286	NM_00120E	6272	Hs.48519E	ENSG000002SORT1	Gp95 LDL	C sirtilin protein-coding
chr12-12c	6.913675	0.245063	0.877608	0.27924	0.780061	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	3' UTR (N3' UTR (N	-10337	NM_00108C	84747	Hs.12761C	ENSG000002UNC119B	POC7B	unc-119 l protein-coding
chr12-121	6.913675	0.245063	0.877608	0.27924	0.780061	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	10943	NM_00127C	10645	Hs.29734E	ENSG000002CAMK2C	CAMKK CA	calcium/c protein-coding
chr15-24c	6.913675	0.245063	0.																	



chr22-504	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr22	50426581	50433032	+	0	NA	intron (NMIR SINE	22364	NR_162128	1.13E+08	NR_162128	MIR12114	-	microRNA ncRNA		
chr3-1136	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr3	11360197	11362757	+	0	NA	intron (NALuSg SIN	89080	NM_001144	10533	Hs. 38032	NR_006399	ENSG00000	ATG7	APG7-LIKE autophagy protein-coding	
chr3-1198	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr3	1.2E+08	1.2E+08	+	0	NA	intron (NTigger1 I	75011	NM_022002	8856	Hs. 7303	NR_003889	ENSG00000	CNR12	BXR ONR1 nuclear rprotein-coding	
chr3-1224	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	42078	NR_125405	1.03E+08	Hs. 675059	NR_125405	ENSG00000	LOC102722	-	uncharacterncRNA
chr4-1234	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr4	1234901	1237596	+	0	NA	intron (Nintron (N	12882	NR_001328	1487	Hs. 208597	NM_001328	ENSG00000	CTBP1	BARS HADE C-terminus protein-coding	
chr4-2625	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr4	2629859	2632494	+	0	NA	intron (Nintron (N	5744	NR_046335	8603	Hs. 652364	NM_003704	ENSG00000	FAM193A	C4orf8 RF family wiprotein-coding	
chr4-8288	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr4	82887363	82890297	+	0	NA	intron (Nintron (N	2323	NM_001077	22872	Hs. 370024	NM_014933	ENSG00000	SEC31A	ABP125 AF SEC31 honprotein-coding	
chr4-1585	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr4	1585908	1592950	+	0	NA	intron (NLIM45 LIN	56796	NM_001322	57600	Hs. 652441	NM_020844	ENSG00000	FNIP2	FNIP1 MAF follicular protein-coding	
chr5-1384	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr5	13847961	13850090	+	0	NA	intron (NL4_A_Mam	95455	NM_001366	1767	Hs. 21236	NM_001366	ENSG00000	CNAH5	CILD3 DN dynein a protein-coding	
chr5-9675	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr5	96796290	96797501	+	0	NA	intron (NALuJr SIN	11050	NM_00104C	51752	Hs. 666524	NM_016442	ENSG00000	ERAP1	A-LAP AL endoplasm protein-coding	
chr5-1597	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr5	1597508	1597508	+	0	NA	exon (NM exon (NM	21616	NM_14504A	134510	Hs. 59173	NM_14504A	ENSG00000	UBLCP1	CPUB1 ubiquitin protein-coding	
chr5-1798	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	15523	NM_19886E	23061	Hs. 15582	NM_015043	ENSG00000	TBC1D9B	GRAMD9B TBC1 dom protein-coding	
chr6-1166	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr6	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	16512	NM_14506E	221302	Hs. 29857	NM_14506E	ENSG00000	ZUP1	C6orf113 zinc fing protein-coding	
chr7-1667	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr7	16600302	16602673	+	0	NA	intron (Nintron (N	44267	NM_02031E	57037	Hs. 15737	NM_02031E	ENSG00000	ANKMY2	ZMYND20 ankyrin rprotein-coding	
chr7-1392	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (NALuSp SIN	43492	NM_17356E	254048	Hs. 15345	NM_17356E	ENSG00000	UBN2	-	ubiquitin protein-coding
chr8-6482	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr8	6482099	6483096	+	0	NA	intron (Nintron (N	75444	NM_001322	79648	Hs. 593807	NM_02459E	ENSG00000	MCPH1	BRIT1 MC microcep protein-coding	
chr8-4317	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr8	43188070	43189057	+	0	NA	intron (NLIPA5 LIN	48099	NM_15241E	138050	Hs. 600384	NM_15241E	ENSG00000	HGSNAT	HGNAT MP speran-ε protein-coding	
chr8-9484	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr8	94843090	94845792	+	0	NA	intron (NALuSj SIN	21151	NR_073444	55656	Hs. 72760	NM_00113E	ENSG00000	INTS8	C8orf52 I integrat protein-coding	
chr9-9652	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr9	96521017	96523589	+	0	NA	intron (Nintron (N	44528	NM_001351	8555	Hs. 40582	NM_003671	ENSG00000	CDC14B	CDC14B3 Cell divi protein-coding	
chr9-9765	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr9	97688317	97688773	+	0	NA	intron (Nintron (N	8864	NR_149094	7507	Hs. 654364	NM_00038C	ENSG00000	XPA	XPI XPAC XPA, DNA protein-coding	
chr9-1257	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (NALuSc8 SI	12150	NM_001174	10244	Hs. 19012	NM_005833	ENSG00000	RABEPK	RAB9P40 t Bab9 eff protein-coding	
chr9-1281	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	-4424	NR_033374	1E+08	Hs. 69379	NR_033374	SLC25A25	-	SLC25A25 ncRNA	
chr9-1347	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	59778	NR_039691	1.01E+08	NR_039691	ENSG00000	MIR3689C	-	microRNA ncRNA	
chrX-4721	7.418121	0.235774	0.846484	0.278533	0.780603	0.981636	chrX	47215296	47216677	+	0	NA	TTS (NM_C TTS (NM_C	-2317	NM_03301E	5127	Hs. 49606	NM_006201	ENSG00000	CDK16	PCTAIRE F cyclin d protein-coding	
chr20-397	5.904783	0.268044	0.962493	0.278489	0.780637	0.981636	chr20	397217	397499	+	0	NA	3' UTR (N3' UTR (N	-10692	NM_001322	10616	Hs. 29546	NM_00646E	ENSG00000	RBCK1	C20orf18 RANBP2-ty protein-coding	
chr3-1567	5.904783	0.268044	0.962493	0.278489	0.780637	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	3' UTR (N3' UTR (N	29203	NM_00118A	25976	Hs. 74405	NM_01550E	ENSG00000	TIPARP	ARTD14 P T CD  ind protein-coding	
chr1-4481	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr1	44813774	44814837	+	0	NA	TTS (NM_C TTS (NM_C	5823	NM_00113E	149478	Hs. 63240	NM_00113E	ENSG00000	BTBD19	-	BTB dom protein-coding
chr1-8445	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr1	84490368	84491761	+	0	NA	intron (Nintron (N	11798	NM_02506E	80135	Hs. 48120	NM_02506E	ENSG00000	RPF1	BXDC5 ribosome protein-coding	
chr1-9117	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr1	91319785	93120180	+	0	NA	intron (Nintron (N	40699	NM_00735E	22823	Hs. 31016	NM_00735E	ENSG00000	MTF2	M96 PCL2 metal res protein-coding	
chr10-111	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr10	1.11E+08	1.11E+08	+	0	NA	intron (NMIR SINE	25123	NM_00544E	9126	Hs. 24485	NM_00544E	ENSG00000	SMC3	BAM BMH c structure protein-coding	
chr11-115	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr11	11961536	11968146	+	0	NA	intron (Nintron (N	43798	NM_00101E	27122	Hs. 29215	NM_01325E	ENSG00000	DKK3	REIC RIG dickkopf protein-coding	
chr11-671	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr11	67193555	67194505	+	0	NA	intron (Nintron (N	-45984	NM_00125E	22992	Hs. 12414	NM_01230E	ENSG00000	KDM2A	CXXC8 FBL lysine d protein-coding	
chr13-244	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr13	24437067	24440134	+	0	NA	intron (NChap1_Man	14788	NM_006437	143	Hs. 74485	NM_006437	ENSG00000	PARP4	ADPRTL1 A poly (ADP- protein-coding	
chr14-105	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (NALuSp SIN	28510	NM_00182E	1152	Hs. 17372	NM_00182E	ENSG00000	CKKB	B-CK BCK creatine protein-coding	
chr15-226	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr15	22852111	22852474	+	0	NA	intron (Nintron (N	14555	NM_00100E	81614	Hs. 59100	NM_03092E	ENSG00000	NIP2A	SLC57A2 NIP4 magr protein-coding	
chr15-666	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr15	66328860	66330235	+	0	NA	intron (Nintron (N	17795	NR_00438E	692149	NR_00438E	ENSG00000	SCARNA14	U100 small Ca ncRNA		
chr15-706	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr15	70670294	70670665	+	0	NA	intron (NMER50 LTF	31803	NM_00100E	55075	Hs. 10804	NM_01800E	ENSG00000	CUACA	NUCLING uveal aut protein-coding	
chr17-307	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr17	30751997	30754619	+	0	NA	intron (NALuSj SIN	43700	NR_14439E	440423	Hs. 62888	NR_024187	SUZ12P1	SUZ12P SUZ12 pse pseud		
chr19-467	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr19	46841586	46845683	+	0	NA	intron (NALuSj SIN	6680	NM_001301	1175	Hs. 11959	NM_00406E	ENSG00000	AP2S1	AP17 CLAF adaptor r protein-coding	
chr2-1078	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr2	10780947	10786629	+	0	NA	3' UTR (N3' UTR (N	28997	NM_00574E	10130	Hs. 21210	NM_00574E	ENSG00000	PDIA6	ERP5 P5 I protein c protein-coding	
chr2-1137	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	intron (NALuSc5 SI	7763	NM_00133E	80255	Hs. 35565	NM_025181	ENSG00000	SLC35F5	-	solute c protein-coding
chr2-1275	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (NLIMB7 LIN	8600	NM_01796E	55677	Hs. 46987	NM_01796E	ENSG00000	IWS1	-	interact protein-coding
chr20-467	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr20	46718167	46720313	+	0	NA	intron (Nintron (N	9591	NM_030777	81031	Hs. 30597	NM_030777	ENSG00000	SLC2A10	ATORS ATS solute c protein-coding	
chr22-187	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr22	18083286	18085522	+	0	NA	intron (NALu SINE	6414	NM_01792E	55670	Hs. 51740	NM_01792E	ENSG00000	PEX26	PBD7A PBE peroxisom protein-coding	
chr3-1255	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr3	12599623	12601873	+	0	NA	intron (NALuSx SIN	43661	NM_01416C	23609	Hs. 59166	NM_01416C	ENSG00000	MKRN2	HSPC070 Fmakorin protein-coding	
chr3-1267	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr3	12603618	12604417	+	0	NA	intron (Nintron (N	46930	NM_01416C	23609	Hs. 59166	NM_01416C	ENSG00000	MKRN2	HSPC070 Fmakorin protein-coding	
chr3-1465	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr3	1.47E+08	1.47E+08	+	0	NA	intron (NLIM45 LIN	17378	NM_00136E	5359	Hs. 13075	NM_02110E	ENSG00000	PLSCR1	MMTRA1B phospholip protein-coding	
chr3-1687	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr3	1.68E+08	1.68E+08	+	0	NA	intron (Nintron (N	73215	NM_01449E	27333	Hs. 14360	NM_01449E	ENSG00000	GOLIM4	GIMPC GOL golgi int protein-coding	
chr4-8467	7.673811	-0.23229	0.834161	-0.27848	0.780647	0.981636	chr4	84678173	84680312	+	0	NA	exon (NM exon (									



chr16-905.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr16	9099802	9102162	+	0	NA	intron (Nintron (N	9338 NM_014117	29035 Hs. 221497NM_014117	ENSG00000160r72	PR00149	chromosonprotein-coding	
chr16-157.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr16	15073991	15077926	+	0	NA	intron (NLTR16A1 L	18377 NM_001301	54700 Hs. 460077NM_018427	ENSG000000RRN3	A-270G1.2RRN3	homcprotein-coding	
chr16-157.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr16	15595637	15597672	+	0	NA	3' UTR (N3' UTR (N	14441 NR_106761	1.02E+08	NR_106761	ENSG000000MIR6506	hsa-mir-6microRNA ncRNA	
chr16-896.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr16	89980169	89986539	+	0	NA	intron (Nintron (N	-10522 NM_145039	92806 Hs. 513832NM_145039	ENSG000000CENPBD1	-	CENPB DN/protein-coding	
chr17-697.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr17	690125	690667	+	0	NA	intron (NMER102b L	24453 NM_00112F	55275 Hs. 461819NM_018289	ENSG000000VPS53	HCCS1 PCFVPS53	snr-protein-coding	
chr17-404.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr17	4042431	4046980	+	0	NA	intron (NAluSc SIN	67602 NR_146884	1.05E+08	Hs. 579239NR_146884	LINC0197F	-	long intencRNA
chr17-307.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr17	30504695	30506242	+	0	NA	intron (NTigger1 L	28060 NM_001007	9527 Hs. 462688NM_004871	ENSG000000GOSR1	GOLIM2 GC golgi SNr	protein-coding	
chr17-597.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr17	59945680	59946797	+	0	NA	intron (NLa2a LINE	18502 NM_01612F	51136 Hs. 531701NM_01612F	ENSG000000CRNFT1	PTD016	ring fingprotein-coding	
chr17-627.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr17	62599319	62603071	+	0	NA	intron (Nintron (N	-26475 NM_00603E	9902 Hs. 7835 NM_00603E	ENSG000000MRC2	CD280 CLFmannose r	protein-coding	
chr19-167.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr19	16831430	16837499	+	0	NA	intron (Nintron (N	5066 NM_001297	23309 Hs. 13999 NM_01526E	ENSG000000SIN3B	-	SIN3 trnprotein-coding	
chr19-574.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr19	57442584	57446834	+	0	NA	exon (NM exon (NM	9384 NM_001321	388567 Hs. 467355NM_00102E	ENSG000000ZNF749	-	zinc fingerprotein-coding	
chr2-162C.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr2	1.62E+08	1.62E+08	+	0	NA	intron (Nintron (N	30588 NM_00193E	1803 Hs. 368912NM_00193E	ENSG000000DPP4	ADABP ADC dipeptid	protein-coding	
chr2-178.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr2	1.78E+08	1.79E+08	+	0	NA	intron (NTigger16a	-20512 NR_03827E	1.01E+08	Hs. 710694NR_03827E	ENSG000000TTN-AS1	-	TTN antiscRNA
chr20-454.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr20	45801190	45811299	+	0	NA	intron (NAluSp SIN	-6332 NM_001281	11065 Hs. 93002 NM_00701E	ENSG000000UBE2C	UBCH10 DjubiQuitin r	protein-coding	
chr22-238.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr22	23816973	23819383	+	0	NA	intron (NAluV SINE	20828 NM_00113E	91319 Hs. 593679NM_19844C	ENSG000000DERL3	C2orf14 delrin 3	protein-coding	
chr22-247.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr22	24064318	24065680	+	0	NA	intron (NSVA_D Ret	53629 NM_00119E	23523 Hs. 517478NM_01229E	ENSG000000CABIN1	CAIN KB-3	calcineurin protein-coding	
chr22-296.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr22	29667471	29669719	+	0	NA	intron (Nintron (N	-51408 NM_182527	164633 Hs. 643608NM_182527	ENSG000000CABP7	CALN2	calcium tprotein-coding	
chr3-152.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr3	15230711	15237337	+	0	NA	intron (Nintron (N	-20160 NR_046084	1.01E+08	Hs. 745022NR_046084	ENSG000000SH3BP5-AS	-	SH3BP5 arncRNA
chr3-1541.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr3	15413074	15417423	+	0	NA	intron (NMIRc SINE	12296 NM_00133C	131965 Hs. 149487NM_15239E	ENSG000000METTL6	-	methyltra protein-coding	
chr3-475.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr3	47501189	47503683	+	0	NA	intron (NAluSz SIN	10909 NM_00136E	54859 Hs. 31110CNM_01771E	ENSG000000CELP6	C3orf75 Telangorin r	protein-coding	
chr3-5187.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr3	51886854	51889308	+	0	NA	intron (Nintron (N	59511 NM_003794	8723 Hs. 50724E NM_003794	ENSG000000SNX4	ATG24B	sorting rprotein-coding	
chr3-1297.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (NAluJo SIN	11969 NM_00137C	56941 Hs. 45832CNM_02018E	ENSG000000HMCE5	C3orf37 E5-hydroxy	protein-coding	
chr4-3157.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr4	3155770	3158189	+	0	NA	intron (Nintron (N	82298 NM_002111	3064 Hs. 51845CNM_002111	ENSG000000CHTT	HD IT15 L	huntingtprotein-coding	
chr4-5187.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr4	51886854	51889308	+	0	NA	intron (Nintron (N	44502 NM_001287	23142 Hs. 605388NM_01511E	ENSG000000DCUN1D4	-	defectiveprotein-coding	
chr4-1227.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (NLM1 LINE	81507 NM_01531E	84162 Hs. 408142NM_01531E	ENSG000000K1AA1109	ALKKUCS FK1AA1109	protein-coding	
chr5-172E.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr5	17260876	17261800	+	0	NA	intron (Nintron (N	43707 NM_006317	10409 Hs. 201641NM_006317	ENSG000000BASP1	CAP-23 C	brain abt protein-coding	
chr5-371E.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr5	37156284	37157888	+	0	NA	intron (Nintron (N	-91960 NR_13426E	1.05E+08	Hs. 170999NR_13426E	ENSG000000LOC105374	-	uncharactncRNA
chr5-9674.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr5	96747652	96750895	+	0	NA	intron (Nintron (N	5671 NR_10428E	831 Hs. 43618CNM_00175E	ENSG000000CAST	BS-17 PLA	calpastatprotein-coding	
chr5-1384.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (Nintron (N	-9234 NR_07344E	51308 Hs. 41609CNM_01660E	ENSG000000REEP2	C5orf19 I	receptor protein-coding	
chr5-160.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr5	1.6E+08	1.6E+08	+	0	NA	intron (NLM1E2 LIN	3734 NM_003314	7265 Hs. 519718NM_003314	ENSG000000TTC1	TPR1	tetratric protein-coding	
chr6-9657.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr6	96532043	96532753	+	0	NA	intron (NMSTAI LTF	10592 NM_01532E	23376 Hs. 149367NM_01532E	ENSG000000UFL1	K1AA0776 UFM1	specprotein-coding	
chr6-1112.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (NMER11B LI	41238 NM_15336E	91749 Hs. 400572NM_15336E	ENSG000000MFSFD4B	K1AA1919 major	facprotein-coding	
chr6-1121.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr6	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	-70124 NR_12119E	1.02E+08	Hs. 510007NR_12119E	LOC101927	-	uncharactncRNA
chr6-1387.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr6	1.39E+08	1.39E+08	+	0	NA	intron (NMER58C DN	80213 NM_00112E	85021 Hs. 33460E NM_03192E	ENSG000000CREP51	NBIA7 RALRALBP1	asprotein-coding	
chr6-1402.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr6	1.42E+08	1.42E+08	+	0	NA	intron (NMSTA-int	66102 NM_01648E	51534 Hs. 431367NM_01648E	ENSG000000VTA1	C6orf55 I	vesicle tprotein-coding	
chr7-7307.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr7	73096778	73098817	+	0	NA	IntergeniAluJr SIN	-11763 NR_003664	728524 Hs. 57127E NM_00102356E	SPDYEP	-	speedy/RJ pseudo	
chr7-7457.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr7	74597078	74598173	+	0	NA	intron (NAluSz SIN	1657 NR_16211E	1.13E+08	NR_16211E	MIR10525	-	microRNA ncRNA
chr7-801E.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr7	80169986	80170756	+	0	NA	intron (NLM1B8 LIN	34587 NM_00125E	2770 Hs. 134587NM_00206E	ENSG000000GNA11	Gi	G rprotein-coding	
chr7-101E.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr7	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	49756 NM_182931	55904 Hs. 59226E NM_01868E	ENSG000000KMT2E	HDHC04P I	lysine mprotein-coding	
chr7-1287.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	exon (NM exon (NM	28892 NM_018077	55131 Hs. 27426E NM_018077	ENSG000000CRBM28	ANES	RNA bindiprotein-coding	
chr8-2021.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr8	20211237	20213751	+	0	NA	intron (Nintron (N	15113 NM_00169E	526 Hs. 295917NM_00169E	ENSG000000ATPGV1B2	ATPG61B2 ATPase	Hprotein-coding	
chr8-6721.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr8	67218997	67227606	+	0	NA	intron (NAluJr SIN	120480 NM_006421	10565 Hs. 65690E NM_006421	ENSG000000ARFGF1	ARFGF1 EADP	Rprotein-coding	
chr8-1238.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr8	1.24E+08	1.24E+08	+	0	NA	intron (N(TA)n Sin	40420 NM_14496E	157769 Hs. 459174NM_14496E	ENSG000000FAM91A1	-	family wiprotein-coding	
chr9-921E.7.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr9	92105121	92109037	+	0	NA	intron (NLM1S LINE	8334 NM_00641E	10558 Hs. 90458 NM_00641E	ENSG000000SPTLC1	HSAN1 HS	serine rprotein-coding	
chr9-1087.9.922567	0.227651	0.820622	0.277413	0.781463	0.981636	chr9	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	28700 NM_006687	10881 Hs. 12353CNM_006687	ENSG000000ACTL7A	-	actin lprotein-coding	
chr9-706E.9.461329	0.213431	0.770019	0.277177	0.781644	0.981636	chr9	70658547	70659404	+	0	NA	intron (NAluSx3 SI	10210 NM_016027	51110 Hs. 118554NM_016027	ENSG000000LACTB2	CGI-83	lactamase protein-coding	
chr11-112.8.468153	0.222132	0.801411	0.277176	0.781645	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	3' UTR (N3' UTR (N	-5613 NM_001931	1737 Hs. 335551NM_001931	ENSG000000DLAT	DLTA E2 F	dihydroliprotein-coding	
chr17-305.8.468153	0.222132	0.801411	0.277176	0.781645	0.981636	chr17	30507347	30507546	+	0	NA	intron (NAluSx SIN	30038 NM_001007	9527 Hs. 462688NM_004871	ENSG000000GOSR1	GOLIM2 GC gol		



chr1-1612	8.972599	0.215772	0.78118	0.276213	0.782384	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	TTS (NM_C	1687	NR_049815	1.01E+08	NR_049815	ENSG000002MIR5187	mir-5187	microRNA	ncRNA
chr21-334	8.972599	0.215772	0.78118	0.276213	0.782384	0.981636	chr21	33421463	33422572	+	0	NA	intron (MER58A)DN	19121	NR_001325	3460	Hs.634632	NR_005534	ENSG000001FNGR2	AF-1 IFG	interferon protein-coding
chr14-102	8.094128	-0.22728	0.822854	-0.27621	0.782386	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	intron (intron)	40463	NR_005348	3320	Hs.525600	NR_005348	ENSG000002HSP90AA1	EL52 HEL-	heat shock protein-coding
chr2-2332	8.094128	-0.22728	0.822854	-0.27621	0.782386	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (intron)	5387	NR_003008	677775	Hs.663615	NR_003008	ENSG000002SCARNA5	U87	small Ca_ncRNA
chr16-300	12.3656	-0.18506	0.67003	-0.27619	0.7824	0.981636	chr16	30727255	30821052	+	0	NA	Intergeni Intergeni	-30740	NR_001321	613037	Hs.585737	NR_001321	ENSG000002NPIP13	U87	nuclear protein-coding
chr1-1565	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr1	1.57E+08	1.57E+08	+	0	NA	intron (intron)	3987	NR_015599	54865	Hs.193832	NR_015599	ENSG000002CPATCH4	GPATC4	G-patch protein-coding
chr1-213	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	intron (NLTR41B)LI	37034	NR_012424	26750	Hs.59141	NR_012424	ENSG000002RPS6K1	RPK118 RS	ribosomal protein-coding
chr10-11	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr10	1.11E+08	1.11E+08	+	0	NA	exon (NM exon)	14916	NR_005444	9126	Hs.24485	NR_005444	ENSG000002SMC3	BAM BMH	cytoskeletal protein-coding
chr10-124	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr10	1.24E+08	1.24E+08	+	0	NA	intron (intron)	13712	NR_001322	4942	Hs.523332	NR_000274	ENSG000002OAT	GACR HOG	ornithine protein-coding
chr12-644	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr12	6.04E+08	6.04E+08	+	0	NA	intron (ALuSc8)SI	37449	NR_013254	29110	Hs.505874	NR_013254	ENSG000002TBK1	FTDAL54 ITANK	bin protein-coding
chr12-105	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (intron)	15756	NR_001251	55198	Hs.506602	NR_018171	ENSG000002APPL2	DIP13B	adaptor protein-coding
chr13-302	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr13	30275040	30276270	+	0	NA	intron (LIMA9)LIN	31356	NR_001014	84056	Hs.243599	NR_032111	ENSG000002KATNAL1	-	katanin protein-coding
chr14-92	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr14	92012967	92014356	+	0	NA	intron (intron)	26318	NR_004233	9321	Hs.632332	NR_004233	ENSG000002TRIP11	ACG14 CEV	thyroid l protein-coding
chr14-101	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	3' UTR (3' UTR)	-39128	NR_001376	1778	Hs.614089	NR_001376	ENSG000002DYNCH1H	CGM20 DHC	dynein cy protein-coding
chr16-158	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr16	15870360	15871216	+	0	NA	intron (ALuJr)SIN	-13758	NR_022844	4629	Hs.460109	NR_002474	ENSG000002MYH11	AAT4 FAA	myosin he protein-coding
chr18-62	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr18	62574430	62575483	+	0	NA	exon (NM exon)	51931	NR_126534	54877	Hs.114191	NR_017742	ENSG000002ZCHC2	C18orf49	zinc finger protein-coding
chr22-378	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr22	37858703	37861477	+	0	NA	intron (ML2a)LINE	10721	NR_001363	51386	Hs.446852	NR_016091	ENSG000002EIF3F	EIF3EIP E	leukaryot protein-coding
chr4-267	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr4	2671027	2674605	+	0	NA	intron (intron)	47384	NR_046333	8603	Hs.652364	NR_003704	ENSG000002FAM193A	C4orf8 RF	family w protein-coding
chr7-473	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr7	47300850	47305154	+	0	NA	exon (NM exon)	161801	NR_145811	1.1E+08	NR_145813	SNORD151	-	small nucsnoRNA	
chr7-994	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr7	99457740	99458864	+	0	NA	TTS (NM_C	7865	NR_001198	1.01E+08	NR_001198	ENSG000002ATP5MF-P1	PIATP5J2 PIATP5	5MF-P1 protein-coding	
chr8-538	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr8	53826669	53829520	+	0	NA	intron (NLIPREC2)I	14948	NR_213623	51606	Hs.491737	NR_015941	ENSG000002ATP6V1H	CGI-11 MS	ATPase H protein-coding
chr9-111	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr9	1.12E+08	1.12E+08	+	0	NA	non-codiron-codir	-8129	NR_001198	2790	Hs.534199	NR_001017	ENSG000002CNG10	-	G protein protein-coding
chr9-1308	8.427013	0.22052	0.798955	0.27601	0.78254	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Tiger11a	29702	NR_005157	25	Hs.431048	NR_005157	ENSG000002CABL1	ABL CHDS	ABL protc protein-coding
chr13-41	8.143125	-0.2264	0.820315	-0.27599	0.782558	0.981636	chr13	41081317	41081722	+	0	NA	intron (ALuJb)SIN	19581	NR_036127	1E+08	NR_036127	ENSG000002MIR3168	-	microRNA	ncRNA
chr17-568	8.143125	-0.2264	0.820315	-0.27599	0.782558	0.981636	chr17	56899953	56901543	+	0	NA	intron (L2b)LINE	-9393	NR_037408	1.01E+08	NR_037408	ENSG000002MIR3614	mir-3614	microRNA	ncRNA
chr20-365	8.143125	-0.2264	0.820315	-0.27599	0.782558	0.981636	chr20	36518994	36519240	+	0	NA	intron (ALuSg)SIN	-22402	NR_181522	10398	Hs.504687	NR_006097	ENSG000002MYL9	LCN20 MLC	myosin I protein-coding
chr9-935	7.898993	0.23344	0.846034	-0.27599	0.782602	0.981636	chr9	93529379	93530962	+	0	NA	3' UTR (3' UTR)	-46414	NR_005392	5253	Hs.211441	NR_005392	ENSG000002PHF2	PCN-35 CPHD	finger protein-coding
chr1-278	7.624813	-0.23321	0.846228	-0.27559	0.782866	0.981636	chr1	27833434	27833708	+	0	NA	promoter-promoter	-830	NR_002997	677774	Hs.689694	NR_002997	ENSG000002SCARNA1	ACA35	small Ca_ncRNA
chr13-771	7.624813	-0.23321	0.846228	-0.27559	0.782866	0.981636	chr13	77193652	77193983	+	0	NA	intron (intron)	118258	NR_046711	1.01E+08	Hs.569288	NR_046711	ENSG000002MYCBP2-AS1	-	MYCBP2 arncRNA
chr16-302	7.624813	-0.23321	0.846228	-0.27559	0.782866	0.981636	chr16	3027294	3028229	+	0	NA	TTS (NM_C	-3475	NR_001288	54985	Hs.423103	NR_017888	ENSG000002HCFC1R1	HP1P	host cell protein-coding
chr2-995	7.624813	-0.23321	0.846228	-0.27559	0.782866	0.981636	chr2	99933593	99933900	+	0	NA	intron (LIPA8)LIN	171837	NR_001025	3899	Hs.444414	NR_002288	ENSG000002AFF3	LAF4 MLL1	AFA/FMR2 protein-coding
chr3-729	7.624813	-0.23321	0.846228	-0.27559	0.782866	0.981636	chr3	72967565	72968046	+	0	NA	intron (intron)	-28938	NR_001318	51987	Hs.431092	NR_174907	ENSG000002PPP4R2	PP4R2	protein f protein-coding
chr1-518	7.135267	-0.22467	0.815269	-0.27557	0.782877	0.981636	chr1	51818494	51919933	+	0	NA	3' UTR (3' UTR)	-40276	NR_002522	4898	Hs.584782	NR_002522	ENSG000002NRDC	NRD1 hNR	nardylis protein-coding
chr16-305	7.135267	-0.22467	0.815269	-0.27557	0.782877	0.981636	chr16	30936183	30936561	+	0	NA	intron (MIR SINE)	11797	NR_001095	54620	Hs.152149	NR_019088	ENSG000002FBXL19	CXXC11 Ft	F-box anc protein-coding
chr2-382	7.135267	-0.22467	0.815269	-0.27557	0.782877	0.981636	chr2	38229247	38231710	+	0	NA	intron (intron)	-5758	NR_132774	1.07E+08	NR_132774	SNORA92	-	small nucsnoRNA	
chr4-766	7.135267	-0.22467	0.815269	-0.27557	0.782877	0.981636	chr4	766664	768428	+	0	NA	3' UTR (3' UTR)	14302	NR_036511	1E+08	Hs.731759	NR_036511	ENSG000002LOC10010225	-	uncharactercna
chr4-207	7.135267	-0.22467	0.815269	-0.27557	0.782877	0.981636	chr4	20722008	20722344	+	0	NA	intron (LIPA5)LIN	21718	NR_001333	133015	Hs.479299	NR_145048	ENSG000002PACRGL	C4orf28	parkin cc protein-coding
chr4-731	7.135267	-0.22467	0.815269	-0.27557	0.782877	0.981636	chr4	73168461	73169977	+	0	NA	intron (Tiger17a	53838	NR_001288	26057	Hs.601209	NR_015574	ENSG000002ANKRD17	G17AR MAS	ankyrin I protein-coding
chr2-289	7.386689	0.243956	0.88548	0.275507	0.782927	0.981636	chr2	28902029	28902831	+	0	NA	intron (LTR50)LIT	7763	NR_001123	23160	Hs.622982	NR_015131	ENSG000002WDR43	NET12 UTF	WD repeat protein-coding
chr8-382	7.411297	-0.22419	0.813982	0.275423	0.782991	0.981636	chr8	38262921	38264100	+	0	NA	TTS (NM_C	5710	NR_032483	84513	Hs.567619	NR_032483	ENSG000002PLPP5	DPPL1 HTF	phospholipid protein-coding
chr1-152	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr1	1525174	1526634	+	0	NA	intron (ALuJb)SIN	13374	NR_001177	55210	Hs.23413	NR_018188	ENSG000002ATAD3A	HAYOS	ATPase f protein-coding
chr1-269	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr1	26933789	26934736	+	0	NA	intron (THEIC)LIT	12519	NR_006607	10726	Hs.263812	NR_006607	ENSG000002NUDC	NUDC MN	nuclear c protein-coding
chr1-434	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr1	43420327	43421870	+	0	NA	intron (intron)	-27441	NR_106799	1.02E+08	NR_106799	ENSG000002MIR6735	hsa-mir-6	microRNA	ncRNA
chr1-446	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr1	44638419	44640902	+	0	NA	intron (intron)	31396	NR_145811	1.1E+08	NR_145811	SNORD145	-	small nucsnoRNA	
chr1-165	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr1	1.66E+08	1.66E+08	+	0	NA	intron (intron)	32645	NR_004528	4259	Hs.191734	NR_004528	ENSG000002MGST3	GST-III	microsome protein-coding
chr10-13	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr10	13652950	13654067	+	0	NA	intron (intron)	54059	NR_001318	55691	Hs.330462	NR_018027	ENSG000002PRMD4A	CCAFCA FF	FERM dom protein-coding
chr10-13	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr10	1.33E+08	1.33E+08	+	0	NA	intron (intron)	-7953	NR_001164	101	Hs.501574	NR_001109	ENSG000002ADAM8	CD156 CD1	ADAM metc protein-coding
chr11-11	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	exon (NM exon)	13018	NR_138785	120379	Hs.420662	NR_138785	ENSG000002PIH1D2	-	PIH1 dom protein-coding
chr12-90	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr12	9067936	9070726	+	0	NA	intron (intron)	4154	NR_137424	144571	Hs.592432	NR_026971	ENSG000002A2M-AS1	-	A2M antiscRNA
chr12-65	7.425979	0.233774	0.848878	0.275391	0.783016	0.981636	chr12	65218918	65219878	+	0	NA	in								



chr1-2402	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (N)LP1A7 LIN	132129	NM_020066	56776	Hs.24889	ENSG0000020066	formin 2 protein-coding
chr1-2488	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr1	2.49E+08	2.49E+08	+	0	NA	intron (N)LM1E4a LI	10246	NM_001322	80851	Hs.29857	ENSG0000020064	SH3 binding protein-coding
chr10-122	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	12217303	12219074	+	0	NA	intron (N)(TATA)n S	22000	NM_006023	8872	Hs.41284	ENSG0000020062	C10orf71 cell divi protein-coding
chr10-451	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	45769439	45774758	+	0	NA	intron (N)LM1B7 LIN	44832	NM_001367	253725	Hs.36528	ENSG0000020062	FAM21A FAM21A protein-coding
chr10-507	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	50106354	50112424	+	0	NA	intron (N)intron (N)	41435	NM_001005	387680	Hs.36528	ENSG0000020062	FAM21A FAM21A protein-coding
chr10-507	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	50342905	50344332	+	0	NA	exon (NM)exon (NM)	-95008	NM_001143	56624	Hs.51264	ENSG0000020062	BCDase HIN-acyl spl protein-coding
chr10-685	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	68917251	68920786	+	0	NA	intron (N)Tiger3 c	17703	NM_024045	79009	Hs.52298	ENSG0000020062	GU2 GUB FDBX-d box protein-coding
chr10-877	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	87060323	87064036	+	0	NA	intron (N)AluSx SIN	31908	NM_001318	2746	Hs.50040	ENSG0000020062	GDH GDH1 glutamate protein-coding
chr10-918	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	91854755	91861409	+	0	NA	intron (N)intron (N)	51404	NM_152425	143282	Hs.46612	ENSG0000020062	C10orf13 fibroblas protein-coding
chr10-105	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr10	1.1E+08	1.1E+08	+	0	NA	intron (N)intron (N)	50137	NM_001324	7511	Hs.39062	ENSG0000020062	APP1 SAMF-X-prolyl protein-coding
chr11-871	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	8710153	8716230	+	0	NA	intron (N)intron (N)	27752	NR_002977	677826	Hs.74555	ENSG0000020062	ACA3-2 SN small nucsnRNA
chr11-125	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	12936990	12941146	+	0	NA	3' UTR (N)3' UTR (N)	50480	NR_038904	1.01E+08	Hs.15340	ENSG0000020062	BLACAT2 long intencRNA
chr11-182	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	18554308	18558546	+	0	NA	intron (N)intron (N)	23091	NM_001261	55293	Hs.40799	ENSG0000020062	ATTP UEV2 UEV and lprotein-coding
chr11-626	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	62699135	62699505	+	0	NA	intron (N)AluY SINE	-2290	NM_203422	221091	Hs.42744	ENSG0000020062	LRRN4 C-tprotein-coding
chr11-672	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	67231103	67232753	+	0	NA	exon (NM)exon (NM)	-8086	NM_001255	22992	Hs.12414	ENSG0000020062	CXXC8 FBI lysine deprotein-coding
chr11-703	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	70320265	70338339	+	0	NA	intron (N)intron (N)	48997	NR_031262	1E+08	NR_031262	ENSG0000020062	MIRN548K microRNA ncRNA
chr11-756	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr11	75055550	75060031	+	0	NA	exon (NM)exon (NM)	16857	NM_001367	10825	Hs.19107	ENSG0000020062	SIAL3 neuramin protein-coding
chr12-195	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	1961524	1967547	+	0	NA	intron (N)LM1E5 LINE	-27959	NR_036545	1E+08	Hs.73703	ENSG0000020062	long intencRNA
chr12-908	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	9087318	9095734	+	0	NA	intron (N)intron (N)	24703	NM_001347	2	Hs.88556	ENSG0000020062	A2M CPAM alpha-2-n protein-coding
chr12-144	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	14470216	14473400	+	0	NA	intron (N)THE1C LTF	86347	NM_181355	55729	Hs.50485	ENSG0000020062	AM ATF-1 activator protein-coding
chr12-195	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	19357608	19359897	+	0	NA	intron (N)intron (N)	-80740	NM_001114	121536	Hs.12649	ENSG0000020062	AE bindin protein-coding
chr12-276	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	27678988	27680570	+	0	NA	intron (N)intron (N)	-16668	NM_001025	387849	Hs.26983	ENSG0000020062	RAB15EP RAB15 eff protein-coding
chr12-767	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	76363664	76370591	+	0	NA	intron (N)LM1M4 LINE	-18712	NM_024685	79738	Hs.96322	ENSG0000020062	C12orf58 Bardet-Bi protein-coding
chr12-773	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	77023423	77026158	+	0	NA	intron (N)intron (N)	40779	NM_203394	144455	Hs.41637	ENSG0000020062	E2F transprotein-coding
chr12-132	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (N)intron (N)	19944	NR_107035	1.02E+08	NR_107035	ENSG0000020062	hsa-mir-5 microRNA ncRNA
chr12-132	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (N)AluSx1 SI	28266	NR_003292	347918	Hs.12211	ENSG0000020062	EP400L EP400 pse pseudo
chr13-244	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr13	24450423	24457534	+	0	NA	intron (N)AluSx1 SI	58800	NM_006437	143	Hs.74485	ENSG0000020062	ADPRTL1 poly (ADP- protein-coding
chr13-244	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr13	24474803	24481162	+	0	NA	intron (N)intron (N)	34796	NM_006437	143	Hs.74485	ENSG0000020062	ADPRTL1 poly (ADP- protein-coding
chr13-321	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr13	32179215	32179931	+	0	NA	intron (N)intron (N)	132381	NM_001136	646799	Hs.56925	ENSG0000020062	Z3CXXC Zzygote ar protein-coding
chr13-793	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr13	79395600	79397160	+	0	NA	intron (N)LM1E6 LIN	941	NM_001288	64062	Hs.55825	ENSG0000020062	ARRS2 C1C1R bindin protein-coding
chr14-505	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr14	50904263	50915542	+	0	NA	exon (NM)exon (NM)	34581	NM_002863	5836	Hs.28241	ENSG0000020062	GSD6 glycogen protein-coding
chr14-928	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr14	92824220	92830286	+	0	NA	intron (N)Tiger1 I	32948	NM_005113	9950	Hs.10432	ENSG0000020062	GOLGA5 Golgin A5 protein-coding
chr14-102	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (N)intron (N)	19419	NM_030942	81693	Hs.53449	ENSG0000020062	PRO1028 eamion as protein-coding
chr15-421	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr15	42171022	42179000	+	0	NA	intron (N)L2b LINE	-18375	NM_213600	255189	Hs.23187	ENSG0000020062	PLA2G4F phospholipid protein-coding
chr15-421	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr15	42179828	42185633	+	0	NA	intron (N)L2b LINE	16932	NR_030357	933212	NR_030357	ENSG0000020062	MIRN627 microRNA ncRNA
chr15-425	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr15	42958728	42959273	+	0	NA	intron (N)AluSx1 SI	-8222	NM_173500	646057	Hs.64651	ENSG0000020062	SCA11 TTE tau tubul protein-coding
chr15-848	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr15	84804845	84805120	+	0	NA	3' UTR (N)3' UTR (N)	-11698	NM_020778	57538	Hs.45918	ENSG0000020062	CMH27 MAK alpha kir protein-coding
chr15-943	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr15	94313233	94317833	+	0	NA	exon (NM)exon (NM)	17332	NM_001155	55784	Hs.33368	ENSG0000020062	multiple protein-coding
chr16-374	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	37420665	37452641	+	0	NA	intron (N)intron (N)	-26140	NM_016292	10131	Hs.30345	ENSG0000020062	HSP 75 HSP75 recep protein-coding
chr16-444	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	4448184	4453966	+	0	NA	intron (N)intron (N)	23550	NM_001351	57407	Hs.28896	ENSG0000020062	HSCARG SEMrA like protein-coding
chr16-156	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	15622651	15625751	+	0	NA	intron (N)AluY SINE	-13106	NR_106761	1.02E+08	NR_106761	ENSG0000020062	hsa-mir-5 microRNA ncRNA
chr16-185	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	18554155	18556796	+	0	NA	intron (N)LM1E3G LI	6137	NM_001004	283820	Hs.46014	ENSG0000020062	NOMO PMS5 NODAL moc protein-coding
chr16-252	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	25245852	25247563	+	0	NA	exon (NM)exon (NM)	11138	NM_001012	342357	Hs.51345	ENSG0000020062	ZNF694 Zs zinc fing protein-coding
chr16-275	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	27507688	27511047	+	0	NA	intron (N)intron (N)	40546	NM_001125	2975	Hs.37171	ENSG0000020062	TFIIIC TF general t protein-coding
chr16-286	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	28099324	28103334	+	0	NA	intron (N)intron (N)	-37615	NM_001105	146395	Hs.91910	ENSG0000020062	PRO19651 GSG1 like protein-coding
chr16-295	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	29987336	29991811	+	0	NA	intron (N)(CTC)n SI	6044	NM_003605	8479	Hs.56737	ENSG0000020062	HIRA inte protein-coding
chr16-702	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	70511545	70515110	+	0	NA	intron (N)intron (N)	10227	NM_001365	25839	Hs.20868	ENSG0000020062	CDGJ COE component protein-coding
chr16-722	7.930425	0.225796	0.820776	0.2751	0.783239	0.981636	chr16	72087922	72090326	+	0	NA	exon (NM)exon (NM)	4496					



chr20-21: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr20	21334976	21337709	+	0	NA	intron (AluSx1 SI	32844	NM_001317	22803	Hs. 255932NM_012255	ENSG00000XRN2	-	5'-3'	excprotein-coding		
chr22-31: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr22	31201294	31202139	+	0	NA	intron (intron (N	-10582	NM_005566	3985	Hs. 474596NM_005566	ENSG00000LIMK2	-		LIM domainprotein-coding		
chr22-387: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr22	38716264	38717245	+	0	NA	exon (NM_exon (NM	10810	NM_004288	9567	Hs. 276922NM_004288	ENSG00000GTPBP1	-	GP-1 GP1 GTP	bindiprotein-coding		
chr22-46: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr22	46350388	46352836	+	0	NA	intron (intron (N	15898	NM_001282	55687	Hs. 439524NM_018006	ENSG00000TRMU	-	LCAL3 MT cRNA	5-mcprotein-coding		
chr3-179: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (L1PA6 LIN	27121	NM_152244	64393	Hs. 371606NM_022477	ENSG00000ZMAT3	-	PAG608 Wlinc	fm-protein-coding		
chr5-377: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr5	37726926	37728317	+	0	NA	intron (AluJr4 SI	107201	NM_001278	2668	Hs. 248114NM_000514	ENSG00000GDNF	-	ATF ATF1 glial	cellprotein-coding		
chr8-127: 6.921533	0.242854	0.882834	0.275085	0.783251	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (intron (N	-13493	NR_031611	1E+08	Hs. 031611NM_000000	MIR1206	-	MIRN1206 microRNA	ncRNA		
chr3-185: 12.35774	-0.18394	0.66981	-0.27462	0.783607	0.981636	chr3	1.86E+08	1.86E+08	+	0	NA	exon (NM_exon (NM	16883	NM_004599	6434	Hs. 533122NM_004599	ENSG00000TRA2B	-	Htra2-beta	transformprotein-coding		
chr17-31: 8.931459	0.214237	0.780707	0.274415	0.783766	0.981636	chr17	31373745	31374709	+	0	NA	3' UTR (3' UTR (N	-17448	NM_032932	84440	Hs. 406788NM_032932	ENSG00000CRAB11FIP4	-	FIP4-Rab1	RAB11 fanprotein-coding		
chr2-443: 8.931459	0.214237	0.780707	0.274415	0.783766	0.981636	chr2	44336417	44336752	+	0	NA	intron (L1PA15 LI	23165	NM_001042	9581	Hs. 444349NM_006036	ENSG00000PREPL	-	CMS22	prolyl erprotein-coding		
chr5-1327: 8.931459	0.214237	0.780707	0.274415	0.783766	0.981636	chr5	1.33E+08	1.33E+08	+	0	NA	intron (intron (N	-19359	NR_134248	1.05E+08	Hs. 73917	NR_134248	-	LOC105375	uncharacterncRNA		
chr7-103: 8.931459	0.214237	0.780707	0.274415	0.783766	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (AluSp SIN	9025	NM_004279	9512	Hs. 184211NM_004279	ENSG00000PMPCB	-	Beta-MPP	peptidaseprotein-coding		
chr9-122: 8.931459	0.214237	0.780707	0.274415	0.783766	0.981636	chr9	1.22E+08	1.22E+08	+	0	NA	non-codiron-codir	-12127	NM_014368	26468	Hs. 103137NM_014368	ENSG00000LHX6	-	LHX6.1	LIM homeprotein-coding		
chr1-174: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr1	1714962	1722336	+	0	NA	intron (AluYml SI	5708	NM_024011	728642	Hs. 651228NM_024011	ENSG00000CDK11A	-	CDK2L2 C	cyclin deprotein-coding		
chr1-163: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr1	16307533	16309826	+	0	NA	intron (AluJb SIN	43801	NM_018994	54455	Hs. 522384NM_018994	ENSG00000FBX042	-	Fbx42 JFK	box prcprotein-coding		
chr1-2694: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr1	26941500	26947238	+	0	NA	intron (AluJb SIN	16099	NM_15236E	126695	Hs. 188881NM_15236E	ENSG00000KDF1	-	Clorf172	keratinocprotein-coding		
chr1-393: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr1	39360927	39373287	+	0	NA	intron (AluSz SIN	41696	NM_01503E	643314	Hs. 658766NM_01503E	ENSG00000KIAA0754	-	KIAA0754	protein-coding		
chr1-240: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (intron (N	247273	NM_02246E	64388	Hs. 98206	NM_02246E	-	GREM2	CTKTSF1B2	gremlin 2protein-coding	
chr11-93: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr11	9369812	93698729	+	0	NA	exon (NM_exon (NM	-23744	NR_00256E	619383	Hs. 66066E	NR_00256E	-	ENSG00000SCARN9	Z32 mqU2-	small Ca <sub>v</sub> ncRNA	
chr11-11: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr11	1.18E+08	1.18E+08	+	0	NA	intron (HALI LINE	-13936	NR_03375E	10632	Hs. 486366NM_00647E	ENSG00000ATP5MG	-	ATP5JG A1ATP	syntfprotein-coding		
chr12-29: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr12	291221	298084	+	0	NA	intron (intron (N	-13779	NM_00119C	6540	Hs. 504398NM_01661E	ENSG00000SLC6A13	-	GAT-2 GAI	solute cprotein-coding		
chr12-48: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr12	48937306	48941068	+	0	NA	intron (intron (N	-13640	NM_001143	51303	Hs. 655103NM_016594	ENSG00000FKBP11	-	FKBP19	FKBP proprotein-coding		
chr12-53: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr12	53406306	53412813	+	0	NA	exon (NM_exon (NM	-14294	NM_001164	269	Hs. 659889NM_020547	ENSG00000AMHR2	-	AMHR MISF	anti-Mullprotein-coding		
chr12-624: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr12	62554471	62557329	+	0	NA	intron (intron (N	47534	NR_121682	283416	Hs. 375881NM_17589E	ENSG00000LINC0146E	-	C12orf61	long intncRNA		
chr12-12: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (AluSc5 SI	32830	NR_10703E	1.02E+08	NR_10703E	ENSG00000MIR8072	-	hsa-mir-5	microRNA ncRNA		
chr14-49: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr14	49842832	49851146	+	0	NA	intron (AluSg SIN	5799	NM_00471E	9147	Hs. 655964NM_00471E	ENSG00000CNEMF	-	NY-CO-1 S	nuclear cprotein-coding		
chr14-73: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr14	73920707	73930751	+	0	NA	intron (intron (N	-24205	NM_18248C	51004	Hs. 13155E	NM_18247E	-	ENSG00000COQ6	CG1-10 C	nuclease protein-coding	
chr15-42: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr15	42948352	42954355	+	0	NA	intron (AluSg SIN	-30575	NM_17350C	146057	Hs. 646511NM_17350C	ENSG00000TTBR2	-	SCA11 TTE	tau tubulprotein-coding		
chr15-65: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr15	65695392	65697335	+	0	NA	TTS (NR_TTS (NR_C	573	NR_14575E	1.1E+08	NR_14575E	ENSG00000SNORD13E	-	small nucsnRNA			
chr15-94: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr15	94476793	94479733	+	0	NA	intron (intron (N	122353	NM_00115E	55784	Hs. 33368	NM_01834E	-	ENSG00000MCTP2	-	multiple	protein-coding
chr16-88: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr16	88714474	88717687	+	0	NA	TTS (NM_TTS (NM_C	257	NR_03987E	1.01E+08	NR_03987E	ENSG00000MIR4722	-	microRNA	ncRNA		
chr17-76: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr17	7616416	778927	+	0	NA	intron (L1ME4a LI	10735	NM_00136C	51031	Hs. 279061NM_01608E	ENSG00000GLOD4	-	C17orf25	glyoxalaseprotein-coding		
chr17-18: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr17	18208512	18208711	+	0	NA	3' UTR (3' UTR (N	-17024	NM_00414C	3996	Hs. 51398E	NM_00414C	-	ENSG00000LLGL1	DLG4 HUGL	LLGL scriprotein-coding	
chr17-42: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr17	42494050	42497014	+	0	NA	TTS (NR_TTS (NR_C	759	NR_04984E	1.01E+08	NR_04984E	ENSG00000MIR548AT	-	microRNA	ncRNA		
chr17-67: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr17	67295592	67309877	+	0	NA	intron (intron (N	65372	NM_18165E	284018	Hs. 90790	NM_18165E	-	ENSG00000C17orf58	-	chromoson	protein-coding
chr18-23: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr18	23530502	23534404	+	0	NA	TTS (NM_TTS (NM_C	28942	NM_01332E	29919	Hs. 46477E	NM_01332E	-	ENSG00000RMC1	-	C18orf8 F	regulatorprotein-coding
chr19-84: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr19	8455458	8456819	+	0	NA	intron (intron (N	11163	NM_03120E	4670	Hs. 46580E	NM_00596E	-	ENSG00000HNRNPM	-	CEAR HNR	heteroger protein-coding
chr19-12: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr19	12284346	12285876	+	0	NA	intron (intron (N	9700	NM_00135E	51710	Hs. 296731NM_016264	ENSG00000ZNF44	-	GIOT-2 Kc	zinc fingprotein-coding		
chr19-19: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr19	19005561	19012172	+	0	NA	intron (MLTIH LTF	24651	NR_14791E	10147	Hs. 77876	NM_014884	-	ENSG00000SUGP2	SFRS14 SF	SURP and protein-coding	
chr19-19: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr19	19500487	19503488	+	0	NA	exon (NM_exon (NM	13561	NM_032037	83983	Hs. 532711NM_032037	ENSG00000TSSK6	-	CT72 FKS	testis sprotein-coding		
chr19-24: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr19	24116415	24124006	+	0	NA	intron (THEIB LTF	33223	NM_00127E	9534	Hs. 43440E	NM_00487E	-	ENSG00000ZNF254	BMFZ-5 Hc	zinc fingprotein-coding	
chr19-43: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr19	43508410	43512204	+	0	NA	intron (intron (N	-5474	NM_19885E	653583	Hs. 631581NM_19885E	ENSG00000PHLDB3	-	pleckstri	protein-coding		
chr2-653: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr2	65311803	65313812	+	0	NA	3' UTR (3' UTR (N	53971	NM_00112E	200734	Hs. 59332	NM_181784	-	ENSG00000SPRED2	-	Spred-2	sprouty iprotein-coding
chr2-86: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr2	86169978	86171592	+	0	NA	exon (NM_exon (NM	22323	NR_03993E	1.01E+08	NR_03993E	ENSG00000MIR4779	-	microRNA	ncRNA		
chr2-174: 8.434871	0.218765	0.792728	0.27439	0.783785	0.981636	chr2	1.74E+08	1.74E+08	+	0	NA	intron (intron (N	35379	NR_00193E	1803	Hs. 368912NM_00193E	ENSG00000DPP4	-	ADABP ADC	diptidylprotein-coding		
chr2-162: 8.434871																						



chr2-4358 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	43584457	43585153	+ 0 NA	intron (HAL1 LINE	11169 NM_001083	63892 Hs. 369592NM_022066	ENSG000003THADA	ARMC13 GIT1THADA	arnprotein-coding
chr2-4395 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	43955628	43958070	+ 0 NA	intron (L1MC4 LIN	40140 NM_133255	10128 Hs. 368084NM_133255	ENSG000003LRPPRC	CLONE-239	leucine i protein-coding
chr2-8758 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	87584410	87585038	+ 0 NA	Intergeni Intergeni	-45031 NR_039634	1.01E+08 NR_039634	ENSG000003MIR4435-1	mir-4435	microRNA ncRNA
chr2-1011 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	1.02E+08	1.02E+08	+ 0 NA	intron (intron (N	141536 NM_145687	9448 Hs. 701013NM_004834	ENSG000003MAP4K4	FLH21957 mitogen- $\alpha$	protein-coding
chr2-1711 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	1.71E+08	1.71E+08	+ 0 NA	intron (intron (N	44197 NM_001136	9874 Hs. 744919NM_012299	ENSG000003TLK1	PKU-beta	tousled l protein-coding
chr2-2182 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	2.18E+08	2.18E+08	+ 0 NA	intron (intron (N	3602 NM_005731	10109 Hs. 529303NM_005731	ENSG000003CARPC2	ARC34 PN $\beta$	actin rel protein-coding
chr2-2411 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr2	2.42E+08	2.42E+08	+ 0 NA	intron (intron (N	22078 NM_178322	23192 Hs. 282613NM_013327	ENSG000003ATG4B	APG4B AU1	autophagy protein-coding
chr3-1806 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr3	1.81E+08	1.81E+08	+ 0 NA	intron (intron (N	2533 NM_001042	151613 Hs. 432133 NM_133462	ENSG000003TTC14	DRDL5813	tetratric protein-coding
chr3-1895 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr3	1.9E+08	1.9E+08	+ 0 NA	intron (AluSx SIN	141485 NM_018192	55214 Hs. 374191NM_018192	ENSG000003CP3H2	LEPREL1  $\beta$	prolyl 3- protein-coding
chr4-5203 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr4	52031860	52032495	+ 0 NA	intron (HAL1 LINE	6142 NM_000232	6443 Hs. 122875NM_000232	ENSG000003SGCB	A3b LGM2 $\beta$	sarcoglyc protein-coding
chr4-1588 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr4	1.59E+08	1.59E+08	+ 0 NA	intron (L1PA7 LIN	91522 NM_001323	57600 Hs. 652441NM_020848	ENSG000003FNIP2	FNIP1 MAF	follicular protein-coding
chr5-1135 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr5	1.14E+08	1.14E+08	+ 0 NA	intron (HAL1 LINE	36257 NM_001345	64848 Hs. 231942NM_022828	ENSG000003YTHDC2	CAHL HYTF	YTH domain protein-coding
chr5-134 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr5	1.34E+08	1.34E+08	+ 0 NA	intron (intron (N	3595 NM_003337	7320 Hs. 612096NM_003337	ENSG000003UBE2B	E2-17kDa	ubiquitin protein-coding
chr6-1287 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr6	7275584	7288849	+ 0 NA	non-codir-non-codir	24983 NM_001292	6745 Hs. 114033NM_003144	ENSG000003SSR1	TRAPA	signal se protein-coding
chr7-7471 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr7	74718328	74719937	+ 0 NA	intron (intron (N	9786 NR_110044	1.02E+08 Hs. 654772NR_110044	ENSG000003LOC101926	-	uncharactercncRNA
chr7-1503 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr7	1.5E+08	1.5E+08	+ 0 NA	exon (NM exon (NM	-8103 NR_027237	728743 Hs. 650365NM_001080852	LOC278743	-	zinc fingpseudo
chr8-1194 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr8	41940424	41942336	+ 0 NA	TTS (NM TTS (NM C	-44639 NM_001142	286 Hs. 654433NM_000037	ENSG000003CANK1	ANK SPH1	ankyrin l protein-coding
chr8-1197 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr8	1.2E+08	1.2E+08	+ 0 NA	exon (NM exon (NM	44495 NM_003184	6873 Hs. 122755NM_003184	ENSG000003TAF2	CIF150 MF	TATA-box protein-coding
chr9-2184 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr9	21840357	21841825	+ 0 NA	intron (L1PBI LIN	38455 NM_002451	4507 Hs. 193266NM_002451	ENSG000003MTAP	BDMF DMSF	methylthi protein-coding
chr9-7034 7.658095	-0.2288	0.837364	-0.27324	0.784672	0.981636	chr9	70347155	70349861	+ 0 NA	intron (AluS6 SI	66149 NM_001206	687 Hs. 150557NM_001206	ENSG000003KLF9	BTEB BTEK	Kruppel l protein-coding
chr1-8875 3.932208	-0.31499	1.1531	-0.27317	0.784723	0.981636	chr1	88751500	88752021	+ 0 NA	intron (intron (N	99807 NM_001514	2959 Hs. 481852NM_001514	ENSG000003GTF2B	TF2B TF1	general t protein-coding
chr2-1344 3.932208	-0.31499	1.1531	-0.27317	0.784723	0.981636	chr2	1.34E+08	1.34E+08	+ 0 NA	intron (intron (N	163939 NM_00241C	4249 Hs. 4988 NM_00241C	ENSG000003MGAT5	GNT-V GNT	$\alpha$ 1,6 protein-coding
chr1-1558 8.403439	0.226172	0.828227	0.27308	0.784792	0.981636	chr1	1.56E+08	1.56E+08	+ 0 NA	intron (AluS6 SI	-26919 NR_132767	1.07E+08 NR_132767	SCARNA26F	-	small Ca <sub>n</sub> cRNA
chr1-1231 8.476011	0.220404	0.807227	0.273039	0.784823	0.981636	chr1	12311773	12312788	+ 0 NA	intron (intron (N	82250 NM_015378	55187 Hs. 439381NM_015378	ENSG000003VPS13D	SCAR4	vacuolar protein-coding
chr22-428 8.476011	0.220404	0.807227	0.273039	0.784823	0.981636	chr22	42838803	42839443	+ 0 NA	intron (AluV SINE	18150 NM_01457C	26286 Hs. 685222NM_01457C	ENSG000003ARFGAP3	ARFGAP1	ADP ribos protein-coding
chr4-8802 8.476011	0.220404	0.807227	0.273039	0.784823	0.981636	chr4	88025790	88026708	+ 0 NA	intron (THE1D-int	18614 NR_156488	5311 Hs. 181272NM_000297	ENSG000003PKD2	APKD2 PC2	polycysti protein-coding
chr3-1970 8.476011	-0.19997	0.732707	-0.27291	0.78492	0.981636	chr3	1.97E+08	1.97E+08	+ 0 NA	intron (AluV SINE	29300 NM_003316	4241 Hs. 184727NM_005925	ENSG000003MELTF	CD228 MAF	melanotr protein-coding
chr14-756 6.872536	0.243036	0.890916	0.272793	0.785012	0.981636	chr14	75650186	75650842	+ 0 NA	3' UTR (3' UTR (N	10362 NM_00717E	11161 Hs. 15106 NM_00717E	ENSG000003ERG28	C14orf11	ergosterc protein-coding
chr11-862 8.08627	-0.22568	0.827613	-0.27269	0.785092	0.981636	chr11	86306529	86306918	+ 0 NA	intron (intron (N	4431 NM_001322	5950 Hs. 283322NM_016401	ENSG000003HIKESHI	HI1orf73	heat shoc protein-coding
chr12-105 8.08627	-0.22568	0.827613	-0.27269	0.785092	0.981636	chr12	1.09E+08	1.09E+08	+ 0 NA	intron (intron (N	15722 NM_130466	8190 Hs. 374067NM_130466	ENSG000003UBE3B	C11orf3	KOsubiquitir protein-coding
chr1-2081 9.435905	0.208686	0.765294	0.272687	0.785094	0.981636	chr1	20812749	20813116	+ 0 NA	intron (intron (N	-26244 NM_016287	50809 Hs. 142442NM_016287	ENSG000003HP1BP3	HP1-BP74	heteroch protein-coding
chr1-1195 9.435905	0.208686	0.765294	0.272687	0.785094	0.981636	chr1	1.2E+08	1.2E+08	+ 0 NA	exon (NM exon (NM	-19656 NM_021794	11085 Hs. 283011NM_021794	ENSG000003ADAM30	svch1	ADAM met $\alpha$ protein-coding
chr15-425 12.34988	-0.18283	0.617139	-0.27263	0.785368	0.981636	chr15	42955698	42957931	+ 0 NA	intron (L1MC4 LIN	-36036 NR_02984E	146057 Hs. 646511NM_17350C	ENSG000003TTBK2	SCVA11 TTE	tua tubul protein-coding
chr17-312 9.443763	0.207043	0.760764	0.272151	0.785506	0.981636	chr17	31229100	31231026	+ 0 NA	intron (intron (N	67176 NM_002544	4974 Hs. 113874NM_002544	ENSG000003COMG	OMGP	oligodenc protein-coding
chr3-1002 9.443763	0.207043	0.760764	0.272151	0.785506	0.981636	chr3	1E+08	1E+08	+ 0 NA	intron (intron (N	-35375 NM_002020	50754 Hs. 439152NM_002020	ENSG000003NIT2	MLR-5-8a	nitrilase protein-coding
chr1-4074 6.880393	0.240944	0.885866	0.271987	0.785632	0.981636	chr1	40749564	40749853	+ 0 NA	intron (intron (N	-4647 NR_02984E	469334 NR_02984E	ENSG000003MIR30E	MIRN30E	microRNA ncRNA
chr12-652 6.880393	0.240944	0.885866	0.271987	0.785632	0.981636	chr12	6525287	6525857	+ 0 NA	intron (intron (N	-8945 NM_00128E	2597 Hs. 544577NM_00204C	ENSG000003GAPDH	G3PD GAP1	glyceralc protein-coding
chr13-114 6.880393	0.240944	0.885866	0.271987	0.785632	0.981636	chr13	1.14E+08	1.14E+08	+ 0 NA	intron (intron (N	41858 NM_00132C	22821 Hs. 593076NM_00736E	ENSG000003RASA3	GAP1IP4B	RAF Ras p21 i protein-coding
chr2-4395 6.880393	0.240944	0.885866	0.271987	0.785632	0.981636	chr2	43959387	43961037	+ 0 NA	intron (AluS6 SIN	36227 NM_133255	10128 Hs. 368084NM_133255	ENSG000003LRPPRC	CLONE-239	leucine i protein-coding
chr2-9937 6.880393	0.240944	0.885866	0.271987	0.785632	0.981636	chr2	99376662	99377164	+ 0 NA	intron (intron (N	39524 NM_015904	9669 Hs. 158688NM_015904	ENSG000003EIF5B	IF2	eukaryoti protein-coding
chr16-224 11.02366	0.199665	0.73476	0.271742	0.78582	0.981636	chr16	22444278	22445205	+ 0 NA	intron (NL2 LINE L	-7251 NR_02746C	1E+08 Hs. 709576NR_02746C	RRN3P3	-	RRN3 hompseudo
chr11-677 7.376982	0.233919	0.860842	0.271733	0.785828	0.981636	chr11	67501276	67502675	+ 0 NA	intron (intron (N	2938 NM_00491E	9600 Hs. 37229E NM_00491C	ENSG000003PTPMM1	DRES9 NIF	phosphat i protein-coding
chr16-155 7.376982	0.233919	0.860842	0.271733	0.785828	0.981636	chr16	15972462	15972843	+ 0 NA	intron (MLT1J LTF	23036 NM_00499E	4363 Hs. 391464NM_00499E	ENSG000003ABCC1	ABC29 ABC	ATP bindi protein-coding
chr20-321 7.376982	0.233919	0.860842	0.271733	0.785828	0.981636	chr20	3215230	3215429	+ 0 NA	intron (intron (N	5831 NM_18149E	3704 Hs. 415299NM_00345E	ENSG000003ITPA	C20orf37	inosine t protein-coding
chr16-84 7.467119	0.235421	0.866657	0.271643	0.785897	0.981636	chr16	84083817	84084467	+ 0 NA	intron (AluSx1 SI	32800 NM_003791	8702 Hs. 75890 NM_003791	ENSG000003MBTPS1	PCSK8 SIF	membrane protein-coding
chr17-624 7.467119	0.235421	0.866657	0.271643	0.785897	0.981636	chr17	62672250	62672494	+ 0 NA	intron (MIR SINE E	-33834 NR_14788E	1.05E+08 Hs. 446268NR_14788E	ENSG000003LOC105371	-	uncharactercncRNA
chr1-3128 8.119551	-0.22135	0.814938	-0.27162	0.785913	0.981636	chr1	31280343	31281786	+ 0 NA	intron (intron (N	15724 NM_004814	9410 Hs. 33962 NM_004814	ENSG000003SNRP40	40K HPRP	small nuc protein-coding
chr10-118 8.119551	-0.22135	0.814938	-0.27162	0.785913	0.981636	chr10	18668355	18669994	+ 0 NA	intron (intron (N	9716 NM_17881E	221079 Hs. 25362 NM_17881E	ENSG000003CARL5B	ARL8	ADP ribos protein-coding
chr10-411 8.119551	-0.22135	0.814938	-0.27162	0.785913	0.981636	chr10	1.11E+08	1.11E+08	+ 0 NA	intron (intron (N	21213 NM_00544E	9126 Hs. 24485 NM_00544E	ENSG000003SMC3	BAM BMH	C structure $\alpha$ protein-coding
chr12-585 8.119551	-0.22135	0.814938	-0.27162	0.785913	0.981636	chr12	58911892	58912370	+ 0 NA	intron (intron (N	7415 NM_001136	121227 Hs. 25373E NM_153377	ENSG000003LRIG3	LIG3	leucine i protein-coding
chr13-445 8.119551	-0.22135	0.814938	-0.27162	0.785913	0.981636	chr13	44985741	44986512	+ 0 NA	intron (Tigger1 E					



chr17-412.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr17	4120601	4124089	+	0	NA	intron (Nintron (N	20685	NM_015113	23140	Hs. 277624NM_015113	ENSG000003ZEF1	ZZZA	zinc_fingprotein-coding		
chr18-244.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr18	24438842	24439125	+	0	NA	intron (NMLT2D LTF	12313	NM_018435	55364	Hs. 515317NM_018435	ENSG000003IMPACT	RWDD5	impact_RWprotein-coding		
chr18-765.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr18	76359589	76360171	+	0	NA	3' UTR (N3' UTR (N	-131772	NR_136504	1.02E+08	Hs. 665186NR_136504	ENSG000003LOC101927	-	uncharactncRNA		
chr19-211.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr19	2105054	2119375	+	0	NA	intron (NLTMS LINE	15299	NM_001039	113177	Hs. 424045NM_002878	ENSG000003IZUM04	C19orf36 IZUM04	fanprotein-coding		
chr19-101.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr19	10133028	10133298	+	0	NA	TTS (NMT_C NM_C	-13264	NM_003755	8666	Hs. 529055NM_003755	ENSG000003EIF3G	EIF3-P42 eukaryotprotein-coding			
chr19-105.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr19	10987060	10993701	+	0	NA	intron (NAluSx SIN	6228	NM_001128	6597	Hs. 327527NM_003072	ENSG000003SMARCA4	BAF190 BAF190 SNF1	protein-coding		
chr19-204.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr19	24049553	24051555	+	0	NA	intron (NBSR Beta)	17105	NM_001278	9534	Hs. 434400NM_004878	ENSG000003ZNF254	BMZF5-5 Hh zinc_fingprotein-coding			
chr2-603.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr2	60785548	60790641	+	0	NA	intron (NLM4EAb LI	31826	NM_022894	64895	Hs. 387471NM_022894	ENSG000003PAPOLG	-	poly(A) protein-coding		
chr20-362.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr20	36243961	36248972	+	0	NA	intron (Nintron (N	9988	NM_001271	25980	Hs. 11314	NM_015511	ENSG000003CAAR2	C20orf4 CAAR2	spliprotein-coding	
chr20-632.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr20	63275493	63283824	+	0	NA	intron (Nintron (N	-4652	NR_104022	55738	Hs. 25584	NM_018209	ENSG000003ARFGAP1	ARFGAP1 EADP	ribosprotein-coding	
chr22-305.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr22	30292909	30297854	+	0	NA	exon (NM_exon (NM	-5319	NM_001037	652968	Hs. 444955NM_001037	ENSG000003CASTOR1	CASTOR1	cytosolicprotein-coding		
chr3-5312.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr3	53120424	53120840	+	0	NA	intron (Nintron (N	9803	NM_052855	91869	Hs. 631911NM_052855	ENSG000003CRFT1	CDG1N	RFT1	homprotein-coding	
chr5-1815.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr5	1813378	1816942	+	0	NA	intron (Nintron (N	13753	NM_004552	4726	Hs. 408257NM_004552	ENSG000003NDUFS6	NDUFS6	cytosolicprotein-coding		
chr5-615.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr5	61537303	61539539	+	0	NA	intron (Nintron (N	-99339	NR_161251	285668	Hs. 683866NR_126522	ENSG000003C5orf64	-	chromosomncRNA		
chr5-7815.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr5	78153901	78156404	+	0	NA	intron (NLM1 LINE	139546	NM_001271	8546	Hs. 532091NM_003664	ENSG000003AP3B1	ADTB3 AD1	adaptor protein-coding		
chr5-1462.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (NAluSx SIN	34160	NM_018988	54439	Hs. 61441	NM_018988	ENSG000003RBM27	ARRS1 Psc	RNA bindiprotein-coding	
chr6-4265.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr6	42636067	42637906	+	0	NA	intron (Nintron (N	72957	NM_001184	23304	Hs. 529922NM_015255	ENSG000003CUBR2	C6orf133 ubiquitin	protein-coding		
chr6-1275.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr6	1.28E+08	1.28E+08	+	0	NA	intron (NAluSx3 SI	-47882	NR_125849	1.02E+08	Hs. 656775NR_125849	LOC101928	-	uncharactncRNA		
chr7-7764.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr7	77646032	77647113	+	0	NA	IntergeniAluSg7 SI	49693	NR_134254	1.01E+08	Hs. 72451	NR_038361	ENSG000003APTR	RSNBL-AS	Alu-medicncRNA	
chr7-1565.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr7	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	15129	NM_138400	64434	Hs. 15825	NM_138400	ENSG000003NOM1	C7orf3 PF	nucleolar protein-coding	
chr8-4217.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr8	42176284	42181581	+	0	NA	exon (NM_exon (NM	25865	NM_006803	10947	Hs. 654522NM_006803	ENSG000003AP3M2	AP47B CL	adaptor protein-coding		
chr8-9485.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr8	94853880	94855194	+	0	NA	intron (Nintron (N	31247	NR_073444	55656	Hs. 727666NM_017864	ENSG000003INTS8	C8orf52 Integratc	protein-coding		
chr9-3461.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr9	34616987	34618269	+	0	NA	intron (Nintron (N	2867	NM_007234	11258	Hs. 511768NM_007234	ENSG000003DCTN3	DCTN-22 Dyadnatin	protein-coding		
chr9-9646.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chr9	96465814	96472706	+	0	NA	intron (Nintron (N	19091	NM_014282	22927	Hs. 494566NM_014282	ENSG000003HABP4	IHABP-4 Hyaluron	protein-coding		
chrX-1402.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chrX	1402236	1408108	+	0	NA	intron (N(TGGA)n S	4641	NR_026710	80161	Hs. 521855NM_025091	ASMTL-AS1 ASMTL	ASMTL	antncRNA		
chrX-1547.7.938283	0.223918	0.825028	0.271407	0.786078	0.981636	chrX	1.54E+08	1.54E+08	+	0	NA	intron (Nintron (N	8989	NM_006014	8270	Hs. 444615NM_006014	ENSG000003LAGE3	CVG5 DXS	L	antigen protein-coding	
chrX-137.7.938283	-0.23706	0.873907	-0.27127	0.786184	0.981636	chr11	13726772	13728804	+	0	NA	intron (Nintron (N	-56598	NR_149108	1.05E+08	Hs. 577257NR_149108	ENSG000003LINC02548	-	long intncRNA		
chr3-3814.7.938283	-0.23706	0.873907	-0.27127	0.786184	0.981636	chr3	38141403	38141781	+	0	NA	3' UTR (N3' UTR (N	2931	NM_001172	4615	Hs. 82116	NM_002468	ENSG000003MYD88	MYD88	MYD88	inrprotein-coding
chr5-1711.7.938283	-0.23706	0.873907	-0.27127	0.786184	0.981636	chr5	1.71E+08	1.71E+08	+	0	NA	intron (NTigger1 I	-123581	NM_021025	30012	Hs. 249125NM_021025	ENSG000003TLX3	HFN11L2 FT	cell l1	protein-coding	
chr6-7568.7.938283	-0.23706	0.873907	-0.27127	0.786184	0.981636	chr6	75687941	75688373	+	0	NA	intron (NLI1PA6 LIN	-61082	NM_001368	4646	Hs. 149387NM_004996	ENSG000003MYO6	DFX22 DF	myosin VI	protein-coding	
chrX-1415.7.938283	-0.23706	0.873907	-0.27127	0.786184	0.981636	chrX	1413482	1413759	+	0	NA	TTS (NR_C TTS (NR_C	13089	NR_026710	80161	Hs. 521855NM_025091	ASMTL-AS1 ASMTL	ASMTL	antncRNA		
chr1-1627.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (Nintron (N	73741	NM_006182	4921	Hs. 275757NM_006182	ENSG000003DDR2	MIG20a MI	discoidin	protein-coding	
chr1-2225.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (Nintron (N	-13248	NM_024746	79802	Hs. 665666NM_024746	ENSG000003HHIPL2	KIAA1822 HHIP	like	protein-coding	
chr1-2355.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr1	2.35E+08	2.35E+08	+	0	NA	intron (Nintron (N	7239	NR_036605	9453	Hs. 730766NM_004837	ENSG000003GGPS1	GGPPS GGF	geranyl	protein-coding	
chr10-136.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr10	13693550	13694388	+	0	NA	exon (NM_exon (NM	13598	NM_001318	55691	Hs. 330462NM_018027	ENSG000003FRMD4A	CCAFCA FF	FERM	domain	protein-coding
chr11-134.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr11	35489855	35490668	+	0	NA	intron (NTHEI1 LTF	35355	NM_001001	25891	Hs. 55044	NM_015430	ENSG000003PAMR1	DKFZP586E	peptidase	protein-coding
chr11-118.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr11	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	-42749	NM_001346	143941	Hs. 653445NM_001080	ENSG000003TTC36	HBP21	tetratric	protein-coding	
chr12-51.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr12	51063516	51069132	+	0	NA	intron (NAluSc SIN	17272	NR_045072	81566	Hs. 524422NM_030809	ENSG000003CSRNP2	C12orf2 C	cysteine	protein-coding	
chr12-135.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	19362	NM_175066	317781	Hs. 445168NM_175066	ENSG000003DDX51	-	DEAD-box	protein-coding	
chr13-321.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr13	32184724	32187690	+	0	NA	intron (Nintron (N	125747	NM_001136	646799	Hs. 569254NM_001136	ENSG000003ZARIL	Z3CXXC7 z	zygote	protein-coding	
chr13-497.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr13	49558593	49559875	+	0	NA	intron (NLM1B3 LIN	26324	NM_001352	55213	Hs. 508021NM_018191	ENSG000003RCBTB1	CLLD7 CL	RCC1	and	protein-coding
chr15-575.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr15	57121211	57115949	+	0	NA	intron (NAluY SINE	7321	NM_015532	81488	Hs. 437255NM_015532	ENSG000003POLR2M	GCOM1 GR	RNA	polynprotein-coding	
chr15-906.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr15	90631805	90637191	+	0	NA	intron (Nintron (N	-25736	NR_120371	1.02E+08	Hs. 615345NR_120371	ENSG000003LINC01585	-	long intncRNA		
chr16-353.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr16	3530164	3531367	+	0	NA	intron (Nintron (N	20871	NM_024793	23059	Hs. 155995NM_015041	ENSG000003CTUAP1	CFAP22 F	clusterin	protein-coding	
chr16-225.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr16	22529923	22530455	+	0	NA	intron (Nintron (N	-15509	NR_003676	653786	Hs. 564945NR_003676	ENSG000003OIAOP1	-	OTOA	pseudoprotein-coding	
chr16-581.8.947175	0.210899	0.777675	0.271192	0.786244	0.981636	chr16															





chr1-110.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	3' UTR (N3' UTR (N	-8938 NM_00127C	85369 Hs. 584999NM_033088	ENSG000003STRIP1	FAM40A F	striatin protein-coding
chr1-110.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	exon (NM exon (NM	11838 NM_018372	55791 Hs. 25245 NM_018372	ENSG000003LRIF1	C1orf103	ligand deprotein-coding
chr1-112.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (NL2c LINE	22101 NM_138727	54879 Hs. 201921NM_017744	ENSG000003ST7L	FAM4B ST7	suppressin protein-coding
chr10-51.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr10	50129582	50132313	+	0	NA	exon (NM exon (NM	62993 NM_00100E	387680 Hs. 365288NM_018232	ENSG000003WASHC2A	FAM21A F	WASH comp protein-coding
chr10-60.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr10	61960725	61961963	+	0	NA	intron (NMER11 DN	59645 NM_03219E	84159 Hs. 535297NM_03219E	ENSG000003ARID5B	DESK2 MR	AT-rich protein-coding
chr10-93.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr10	93305049	93308467	+	0	NA	3' UTR (N3' UTR (N	175576 NM_013451	26509 Hs. 602088NM_013451	ENSG000003MYOF	FER1L3	myoferlin protein-coding
chr11-10.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr11	10686358	10688665	+	0	NA	intron (NLTR79 LTF	6063 NM_00110C	10335 Hs. 501898NM_13038E	ENSG000003MRV11	TRAG JAW	murine rprotein-coding
chr11-43.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr11	43415087	43415508	+	0	NA	intron (NLTR79 LTF	56377 NM_01825E	55761 Hs. 191188NM_01825E	ENSG000003TTC17	-	triatric protein-coding
chr11-47.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr11	47632998	47637304	+	0	NA	intron (NALuJb SIN	7408 NM_01434E	23788 Hs. 269944NM_01434E	ENSG000003MTCH2	HSPC032	mitochondr protein-coding
chr11-11.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (NL2a LINE	-10778 NM_00134E	143941 Hs. 653445NM_00108C	ENSG000003TTC36	HBP21	triatric protein-coding
chr11-11.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (NALuSx1 SI	35858 NR_106814	NR_106814	ENSG000003MIR6756	hsa-mir-6	microRNA ncRNA
chr12-45.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr12	45922501	45930948	+	0	NA	exon (NM exon (NM	63850 NM_00471E	9169 Hs. 210367NM_00471E	ENSG000003SCAF11	CASP11 S	FRS-related protein-coding
chr12-56.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr12	56566505	56577726	+	0	NA	intron (NALuSx1 SI	50295 NM_00289E	5939 Hs. 505725NM_00289E	ENSG000003RBMS2	SCR3	RNA bindin protein-coding
chr12-64.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr12	64741529	6473922	+	0	NA	intron (Nintron (N	16681 NM_00207E	2799 Hs. 334534NM_00207E	ENSG000003GNS	G6S	glucosamin protein-coding
chr12-76.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr12	76389362	76390474	+	0	NA	intron (Nintron (N	33367 NM_00131E	114882 Hs. 430845NM_020841	ENSG000003OSBPL8	MST120	MS oxysterol protein-coding
chr12-10.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	-5284 NR_03035C	693204 NR_03035C	ENSG000003MIR619	MIRN619	microRNA ncRNA
chr12-11.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (NALuJo SIN	55530 NM_080601	5781 Hs. 506852NM_002834	ENSG000003PTPN1	BTP3	CF protein-coding
chr13-49.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr13	49919075	49921861	+	0	NA	intron (Nintron (N	15872 NM_02045E	57213 Hs. 44235 NM_02045E	ENSG000003SPRYD7	C13orf11	CSPRY dom protein-coding
chr13-11.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	36768 NR_148221	1.05E+08 Hs. 134725NR_148221	LOC10537C	-	uncharactncRNA
chr14-23.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr14	23309142	23312942	+	0	NA	3' UTR (N3' UTR (N	4182 NM_00119E	599 Hs. 410025NM_00405C	ENSG000003BCL2L2	BCL-2 BCL2	like protein-coding
chr14-31.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr14	31107870	31123512	+	0	NA	intron (NALuJb SIN	89048 NM_001254	11154 Hs. 293411NM_007077	ENSG000003AP4S1	AP47B CL	adaptor protein-coding
chr14-52.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr14	52027096	52029771	+	0	NA	intron (NALuJo SIN	38887 NM_01603E	51637 Hs. 534457NM_01603E	ENSG000003RTRAF	C14orf16	RNA trans protein-coding
chr14-73.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr14	52723873	52728737	+	0	NA	intron (Nintron (N	-3861 NM_00113C	6815 Hs. 364988NM_145251	ENSG000003STYX	-	serine/t protein-coding
chr14-52.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr14	73419881	73420798	+	0	NA	intron (Nintron (N	38241 NM_00100E	8650 Hs. 525445NM_003744	ENSG000003NUMB	C14orf41	NUMB dom protein-coding
chr15-29.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr15	29738713	29742917	+	0	NA	intron (NMER20 DNA	65880 NR_135221	1E+08 Hs. 525725NR_135221	ENSG000003LOC10013C	-	uncharactncRNA
chr15-29.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr15	29764618	29765853	+	0	NA	intron (NL2b LINE	55439 NM_00135E	7082 Hs. 743999NM_003257	ENSG000003TJP1	ZO-1	tight jur protein-coding
chr15-78.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr15	78492542	78499082	+	0	NA	intron (NMER106A E	-11752 NM_00108E	123688 Hs. 307962NM_00101E	ENSG000003HYKK	AGPHD1	hydroxyl protein-coding
chr16-53.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr16	53685328	53686248	+	0	NA	intron (NLIPA1 LI	18071 NM_001127	23322 Hs. 298382NM_01527E	ENSG000003RPRGIP1L	CORS3	FTV RPRGRI1 protein-coding
chr17-7.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr17	7935858	7937902	+	0	NA	intron (Nintron (N	4674 NM_00135E	116840 Hs. 348012NM_053051	ENSG000003CNTROB	LIP8	PP12 centrobri protein-coding
chr17-32.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr17	32451356	32458095	+	0	NA	intron (Nintron (N	10215 NM_002281E	5717 Hs. 443375NM_002281E	ENSG000003PSMD11	Rpn6 S9	proteasom protein-coding
chr17-66.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr17	66321124	66322187	+	0	NA	intron (NALuSx SIN	19042 NM_002737	5578 Hs. 531704NM_002737	ENSG000003PRKCA	AAG6	PKC- protein protein-coding
chr17-67.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr17	67734502	67742768	+	0	NA	intron (NPLAM_C SI	-2080 NR_00370E	1E+08 Hs. 693445NR_00370E	ENSG000003SNORA38B	-	small ncsnoRNA
chr17-77.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr17	76742759	76747359	+	0	NA	intron (Nintron (N	7558 NM_024311	79157 Hs. 73965 NM_024311	ENSG000003MFSD11	ET	major fac protein-coding
chr18-29.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr18	2921947	2925935	+	0	NA	intron (Nintron (N	22682 NR_02665E	727896 Hs. 673125NR_02665E	LOC72789E	-	cysteine pseudo
chr19-23.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr19	23221734	23231409	+	0	NA	intron (Nintron (N	23823 NM_00135E	440519 Hs. 657814NM_00135E	ENSG000003ZNF724	ZNF724P	zinc fing protein-coding
chr19-54.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr19	54459935	54462423	+	0	NA	TTS (NM_C TTS (NM_C	2599 NM_19899E	94059 Hs. 590977NM_19899E	ENSG000003LENG9	-	leucocyte protein-coding
chr19-58.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr19	58229713	58239479	+	0	NA	intron (Nintron (N	5682 NM_00132C	27300 Hs. 438994NM_01448C	ENSG000003ZNF544	-	zinc fing protein-coding
chr2-27.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr2	27684903	27689488	+	0	NA	intron (NLIMA4a LI	-23355 NM_00128E	9913 Hs. 6232 NM_01486C	ENSG000003SUPT7L	SPT7L	ST7SPT7 like protein-coding
chr2-17.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr2	1.75E+08	1.75E+08	+	0	NA	intron (NSVA_C Ret	59668 NR_03063C	NR_03063C	ENSG000003MIR933	MIRN933	microRNA ncRNA
chr2-18.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (NALuSx SIN	11772 NM_001321	5378 Hs. 111745NM_000534	ENSG000003PMS1	HNPCC3	ML PMS1 homc protein-coding
chr2-21.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (NLIPA5 LI	-43035 NM_00099E	6168 Hs. 433701NM_00099E	ENSG000003RPL37A	L37A	ribosomal protein-coding
chr20-31.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr20	31544748	31556862	+	0	NA	intron (Nintron (N	21108 NR_04685E	1.01E+08 Hs. 373741NR_04685E	ENSG000003HM13-AS1	-	HM13 antncRNA
chr22-27.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr22	27894020	27899698	+	0	NA	intron (Nintron (N	22355 NM_001284	23760 Hs. 705325NM_01239E	ENSG000003PITPNB	PI-TP-	betphosphati protein-coding
chr3-16.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr3	16469860	16472773	+	0	NA	intron (NMIR SINE	42383 NM_01515E	23180 Hs. 98910 NM_01515E	ENSG000003RFTN1	MIG2	P1B1 raftlin, protein-coding
chr3-33.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr3	33384173	33388060	+	0	NA	non-codirnon-codir	54262 NM_00112E	7342 Hs. 729125NM_014517	ENSG000003UBP1	LBP-1	UPstream protein-coding
chr3-37.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr3	37057946	37058988	+	0	NA	intron (NALuSx1 SI	65117 NM_00125E	4292 Hs. 195368NM_00024E	ENSG000003MLH1	COCA2	FLC mutl homc protein-coding
chr3-47.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr3	47845966	47848801	+	0	NA	intron (Nintron (N	-2172 NR_03159E	1E+08 NR_03159E	ENSG000003MIR1226	MIRN1226	microRNA ncRNA
chr3-53.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr3	53317304	53320297	+	0	NA	intron (Nintron (N	14327 NR_14571E	1.1E+08 NR_14571E	ENSG000003SNORD38C	-	small ncsnoRNA
chr3-56.8.152833	-0.21721	0.809909	-0.26819	0.788551	0.981636	chr3	56645420	56648541	+	0	NA	exon (NM exon (NM	17066 NM_015224	23272 Hs. 116877NM_015224</			

chr18-295 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr18	2950327	2955799	+	0	NA	intron (Nintron (N	-6440 NR_026655	727896 Hs. 67312cNR_026659	LOC727896	-	cysteine pseudo	
chr19-488 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr19	48863796	48865418	+	0	NA	intron (NAluJb SIN	4010 NM_001161	57664 Hs. 9469	NM_020904	ENSG00000.PLEKHA4	PEPPI	pleckstrinprotein-coding
chr2-9481 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr2	9481503	9494777	+	0	NA	TTS (NM_C TTS (NM_C	13085 NM_00132c	285148 Hs. 66722cNM_00103c	ENSG00000.IAH1	-	isoamylase protein-coding	
chr2-2101 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr2	26194531	26202960	+	0	NA	intron (N L3 LINE C	18029 NM_001191	150946 Hs. 187912cNM_00116c	ENSG00000.GAREM2	FAM59B GA GRB2	ascp protein-coding	
chr2-2108 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr2	2.1E+08	2.1E+08	+	0	NA	exon (NM_exon (NM_	-12410 NR_110291	1.02E+08 Hs. 124091c	ENSG00000.LOC10192c	-	uncharacterized RNA	
chr21-366 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr21	36043407	36046090	+	0	NA	intron (Nintron (N	15616 NM_001007	54093 Hs. 60620cNM_01743c	ENSG00000.CSETD4	C21orf18 SET	domain protein-coding	
chr21-436 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr21	43802762	43803036	+	0	NA	intron (Nintron (N	9668 NR_026961	284837 Hs. 59215cNM_19431c	ENSG00000.AATBC	-	apoptosis ncRNA	
chr22-196 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr22	19850454	19852221	+	0	NA	exon (NM_exon (NM_	3537 NM_053004	54584 Hs. 105642cNM_053004c	ENSG00000.GNBL1	DGCRK3 FBX	protein-coding	
chr22-382 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr22	38290961	38294634	+	0	NA	intron (Nintron (N	-19787 NM_00119c	25829 Hs. 18262cNM_01226c	ENSG00000.TMEM184B	C22orf5 F	transmembrane protein-coding	
chr22-462 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr22	46209421	46209845	+	0	NA	intron (N LIME1 LIN	40660 NM_207327	150383 Hs. 10311cNM_207327c	ENSG00000.CDPF7	C22orf40	cysteine protein-coding	
chr3-1136 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr3	11307401	11310863	+	0	NA	intron (Nintron (N	36735 NM_001144	10533 Hs. 38032	NM_00639c	ENSG00000.APG7	APG7-LIKE	autophagy protein-coding
chr3-1126 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	-9429 NR_10977c	1.01E+08 Hs. 86538	NR_10977c	LINC0127c	-	long intergenic RNA
chr4-2196 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr4	2693482	2698153	+	0	NA	intron (NAluJo SIN	60519 NM_02430c	79155 Hs. 368551cNM_02430c	ENSG00000.TNIP2	ABIN2 FLI1 TNFAIP3	iprotein-coding	
chr4-519 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr4	51908729	51910386	+	0	NA	intron (N MamRTE L S	65978 NM_001287	23142 Hs. 60538cNM_01511c	ENSG00000.DCUN1D4	-	defective protein-coding	
chr4-1451 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr4	1.45E+08	1.45E+08	+	0	NA	intron (NAluY SINE	15826 NM_01749c	54726 Hs. 270851cNM_01749c	ENSG00000.OTUD4	DUBA6 HINOTU	deubiquitinase protein-coding	
chr5-6556 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr5	65598074	65605014	+	0	NA	intron (N THEIA L TF	22789 NM_00165c	373 Hs. 792	NM_00165c	ENSG00000.TRIM23	ARD1 ARF1	tripartite protein-coding
chr6-4267 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr6	42673246	42688025	+	0	NA	intron (N MR3 SINE	41962 NM_00032c	5961 Hs. 65448cNM_00032c	ENSG00000.CPRH2	AOFM6 AVM	peripherin protein-coding	
chr6-4358 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr6	43568099	43570889	+	0	NA	intron (NAluSx1 S S	6544 NM_02075c	57510 Hs. 20320cNM_02075c	ENSG00000.XP05	exp5	exportin protein-coding	
chr6-158 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	74457 NM_032861	84947 Hs. 15470cNM_032861c	ENSG00000.SERAC1	-	serine acetyltransferase protein-coding	
chr7-1058 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	intron (Nintron (N	11412 NM_02193c	60561 Hs. 53138cNM_02193c	ENSG00000.CRINT1	RINT-1	rad50 protein-coding	
chr7-1314 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr7	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	102206 NM_001321	4289 Hs. 44693	NM_01325c	ENSG00000.MKLN1	TWA2	muskelin protein-coding
chr9-5074 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr9	5074691	5075444	+	0	NA	intron (N Tigger1 E	33374 NM_001322	3717 Hs. 65621cNM_00497c	ENSG00000.JAK2	JTK10 THC	Janus kinase protein-coding	
chr9-872 8.409447	0.21368	0.798347	0.267653	0.788967	0.981636	chr9	87272556	87731953	+	0	NA	intron (Nintron (N	3635 NM_00191c	1514 Hs. 731507cNM_00191c	ENSG00000.CTSL	CATL CTSL	cathepsin protein-coding	
chr16-295 11.92957	-0.18413	0.688214	-0.26755	0.789045	0.981636	chr16	29537327	29538343	+	0	NA	Intergeni Intergeni	-31961 NM_00135c	440353	NR_001355401	NPIPBI2	-	nuclear protein-coding
chr1-3785 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr1	37837167	37839631	+	0	NA	intron (Nintron (N	21193 NM_00595c	4520 Hs. 471991cNM_00595c	ENSG00000.MTF1	MTF-1 ZRF	metal regulatory protein-coding	
chr1-2367 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (Nintron (N	13062 NM_01807c	55127 Hs. 708114cNM_01807c	ENSG00000.CHEATR1	BAP28 UTF	heat shock protein-coding	
chr15-437 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr15	43761218	43761852	+	0	NA	intron (Nintron (N	15097 NM_00531c	2923 Hs. 59109cNM_00531c	ENSG00000.PDIA3	ER60 ERp	protein-coding	
chr16-211 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr16	21173480	21174685	+	0	NA	exon (NM_exon (NM_	-14641 NM_01753c	55567 Hs. 52650cNM_01753c	ENSG00000.DNAH3	DNAH3C-3 dynein	alpha protein-coding	
chr16-58 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr16	58564139	58565570	+	0	NA	intron (NAluS2 S S	-4923 NR_00298c	677830 Hs. 67751cNR_00298c	ENSG00000.SNORA50A	ACU50 SNC	small nucleolar RNA	
chr16-744 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr16	74461539	74463690	+	0	NA	exon (NM_exon (NM_	41144 NM_001011	497190 Hs. 45467cNM_001011c	ENSG00000.CLEC18B	MRC2L2	C-type lectin protein-coding	
chr17-17 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr17	17246921	17248959	+	0	NA	intron (Nintron (N	-10772 NM_14460c	201163 Hs. 31652	NM_14460c	ENSG00000.FCLN	BHD DENN	follicular protein-coding
chr17-394 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr17	39474630	39474906	+	0	NA	intron (Nintron (N	13282 NM_01508c	51755 Hs. 34502cNM_01508c	ENSG00000.CDK12	CRK7 CRKF	cyclin dependent protein-coding	
chr19-94 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr19	9494307	948433	+	0	NA	intron (N CpG	21655 NM_005224	1820 Hs. 50129cNM_005224c	ENSG00000.ARID3A	BRIGHT DFAT	rich protein-coding	
chr19-465 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr19	4656506	4660795	+	0	NA	intron (Nintron (N	11753 NM_019107	56005 Hs. 46564cNM_019107c	ENSG00000.CMYDG	C19orf10 myeloid	protein-coding	
chr19-171 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr19	17183116	17190135	+	0	NA	intron (Nintron (N	-28732 NM_018467	55850 Hs. 16187	NM_018467c	ENSG00000.USE1	D12 MSD5	unconvent protein-coding
chr19-458 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr19	45858294	45860695	+	0	NA	intron (NAluS26 S S	3653 NM_00481c	8189 Hs. 51547cNM_00481c	ENSG00000.SYMPK	SPK SYM	sympkin protein-coding	
chr2-6908 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr2	69081007	69082330	+	0	NA	intron (N MRB SINE	-22014 NR_03607c	1E+08	NR_03607c	ENSG00000.MIR3126	mir-3126	microRNA ncRNA
chr2-9628 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr2	96286163	96286648	+	0	NA	exon (NM_exon (NM_	19142 NM_014014	23020 Hs. 24611cNM_014014c	ENSG00000.SNRNP200	ASCC3L1 Esmal	nucleo protein-coding	
chr2-1605 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	-40599 NR_10377c	1.01E+08 Hs. 72953cNR_10377c	ENSG00000.LINC0247c	-	long intergenic RNA	
chr2-1796 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr2	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	34260 NM_02094c	57703 Hs. 31136cNM_02094c	ENSG00000.CWC22	EIF4GL NC	CWC22 sp1 protein-coding	
chr20-248 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr20	2485964	2486808	+	0	NA	intron (Nintron (N	-15597 NM_19821c	6628 Hs. 83753	NM_003091c	ENSG00000.SNRPB	CCMS COD	small nucleo protein-coding
chr21-316 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr21	31682463	31684795	+	0	NA	intron (Nintron (N	24007 NM_000454	6647 Hs. 443914cNM_000454c	ENSG00000.COD1	ALS ALS1	superoxide protein-coding	
chr22-215 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr22	21928385	21931413	+	0	NA	intron (Nintron (N	-8338 NR_14762c	1E+08 Hs. 65918cNR_14762c	LOC10028c	-	uncharacterized RNA	
chr22-295 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr22	29510389	29512553	+	0	NA	intron (Nintron (N	31253 NM_02107c	4744 Hs. 19876cNM_02107c	ENSG00000.NEFH	CMT2CC NF	neurofilament protein-coding	
chr22-427 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr22	42797564	42803619	+	0	NA	intron (Nintron (N	56682 NM_01457c	26286 Hs. 68522cNM_01457c	ENSG00000.ARFGAP3	ARFGAP1	ADP ribosyl protein-coding	
chr5-327 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr5	37236661	37240701	+	0	NA	intron (NAluJo SIN	-10365 NR_13426c	1.05E+08 Hs. 17099cNR_13426c	ENSG00000.LOC10537c	-	uncharacterized RNA	
chr5-1774 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	7002 NM_00208c	2870 Hs. 23511cNM_00208c	ENSG00000.GRKB	GRPK6	G protein protein-coding	
chr7-6807 7.905001	0.220387	0.82379	0.267528	0.789062	0.981636	chr7	6808867	6812206	+	0	NA	intron (NAluJr SIN	15759 NM_198097	22196 Hs. 56777cNM_198097c	ENSG00000.CCZ1B	C7orf28A CCZ1	homoc protein-coding	
chr7-1001 7.905001	0.220387	0.823																



chr3-1559.9.418339	0.202421	0.758817	0.266759	0.789655	0.981636	chr3	15598801	15599345	+	0	NA	intron (NL2c LINE	-2279	NM_001281	686	Hs.444197NM_001281	ENSG000000CBTD	-	biotinidase protein-coding	
chr3-6415.9.418339	0.202421	0.758817	0.266759	0.789655	0.981636	chr3	64196646	64198816	+	0	NA	intron (NLP1A13 LI	10187	NR_046702	1.01E+08	Hs.67084CNR_046702	ENSG000000PRICKLE2-	-	PRICKLE2 ncRNA	
chr4-1229.9.418339	0.202421	0.758817	0.266759	0.789655	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-61297	NM_139243	132612	Hs.518957NM_139243	ENSG000000CADAD1	Tenr	adenosine protein-coding	
chr5-1341.9.418339	0.202421	0.758817	0.266759	0.789655	0.981636	chr5	1.34E+08	1.34E+08	+	0	NA	intron (NL2 LINE I	7969	NM_170675	6500	Hs.17162CNM_00693C	ENSG000000SKP1	EMC19 OCF5-phase I	protein-coding	
chr7-1487.9.418339	0.202421	0.758817	0.266759	0.789655	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	87152	NM_00137C	8454	Hs.14680CNM_00359E	ENSG000000CULL1	-	cullin 1 protein-coding	
chr8-9915.9.418339	0.202421	0.758817	0.266759	0.789655	0.981636	chr8	99150457	99151696	+	0	NA	intron (NLMC1 LIN	137810	NM_01789C	157680	Hs.19154CNM_01524E	ENSG000000CVPS13B	CHS1 COH1	vacuolar protein-coding	
chr1-1864.9.402624	0.205692	0.771232	0.266705	0.789696	0.981636	chr1	1.86E+08	1.86E+08	+	0	NA	intron (NL2c LINE	9406	NM_02237F	10896	Hs.67923CNM_02237F	ENSG000000OCLM	TISR	oculomedial protein-coding	
chr16-572.8.630005	-0.21426	0.804033	-0.26648	0.789871	0.981636	chr16	57230163	57230921	+	0	NA	intron (NMER104 DN	-14717	NM_01210E	23568	Hs.63287CNM_01210E	ENSG000000ARL2BP	BART BARTADP	ribos protein-coding	
chr12-123.8.622147	-0.21256	0.797793	-0.26643	0.789909	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	18618	NM_00151E	2967	Hs.35534CNM_00151E	ENSG000000GTF2H3	BT2F P34	general t protein-coding	
chr15-327.6.424945	0.250509	0.940284	0.266418	0.789917	0.981636	chr15	32727818	32728043	+	0	NA	intron (NLP13 LINE	-9065	NR_109767	1E+08	Hs.61054ENR_109767	ENSG000000LOC100131	-	uncharacterized ncRNA	
chr9-1365.6.424945	0.250509	0.940284	0.266418	0.789917	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	7038	NM_00308E	6621	Hs.11326CNM_00308E	ENSG000000SNAPC4	PTFalpha small	nuc protein-coding	
chr16-214.12.37531	-0.17896	0.67203	-0.26629	0.790016	0.981636	chr16	21451480	21453763	+	0	NA	non-codirnon-codir	-18166	NR_02445E	1E+08	Hs.64843ENR_02445E	LOC10019C-	-	uncharacterized ncRNA	
chr5-4057.12.37531	-0.17896	0.67203	-0.26629	0.790016	0.981636	chr5	40826544	40834722	+	0	NA	3' UTR (N3' UTR (N	2102	NR_00258E	619564	NR_00258E	ENSG000000SNORD72	HBII-240	small nuc snRNA	
chr1-1582.7.946141	0.221981	0.833626	0.266283	0.790021	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (NAluSg7 SI	-26035	NR_024117	1E+08	Hs.656361NR_024117	MSTO2P	misato f pseudo		
chr13-102.7.946141	0.221981	0.833626	0.266283	0.790021	0.981636	chr13	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	17302	NM_00101C	196541	Hs.50862CNM_00101C	ENSG000000METTL21C	C13orf39	methyltra protein-coding	
chr15-731.7.946141	0.221981	0.833626	0.266283	0.790021	0.981636	chr15	73132706	73132905	+	0	NA	intron (NLP1B1 LIN	80321	NM_00117E	4756	Hs.38861CNM_00249E	ENSG000000NE01	IGDC2C Nc	neogenin protein-coding	
chr19-172.7.946141	0.221981	0.833626	0.266283	0.790021	0.981636	chr19	17231454	17232487	+	0	NA	3' UTR (N3' UTR (N	5790	NM_02457E	79629	Hs.42267CNM_02457E	ENSG000000CECEL1	FWP009 SE	occludin/ protein-coding	
chr6-1601.7.946141	0.221981	0.833626	0.266283	0.790021	0.981636	chr6	1.6E+08	1.6E+08	+	0	NA	exon (NM exon (NM	11765	NR_00328E	729603	Hs.67481CNR_00328E	ENSG000000LOC72960E	-	calcineur pseudo	
chr17-595.7.979423	0.225521	0.847599	0.266071	0.790185	0.981636	chr17	59931602	59932336	+	0	NA	intron (Nintron (N	32771	NM_01612E	51136	Hs.531701NM_01612E	ENSG000000RNFT1	PTD106	ring fing protein-coding	
chr5-3395.9.914927	0.199266	0.749098	0.266007	0.790233	0.981636	chr5	33988134	33988604	+	0	NA	non-codirnon-codir	-3676	NM_01618C	51151	Hs.27896CNM_01618C	ENSG000000SLC45A2	1A1 AIM1	solute c protein-coding	
chr6-3611.9.914927	0.199266	0.749098	0.266007	0.790233	0.981636	chr6	36107518	36108511	+	0	NA	intron (NMIR1 Am	-22499	NR_07299E	5603	Hs.17869CNM_002754	ENSG000000MAPK13	MAPK 13	mitogen e protein-coding	
chr2-2391.13.76754	-0.17277	0.649546	-0.26599	0.790246	0.981636	chr2	2.39E+08	2.39E+08	+	0	NA	intron (NLMB7 LIN	-39169	NR_03964E	1.01E+08	NR_03964E	ENSG000000MIR4441	-	microRNA ncRNA	
chr14-348.9.922785	0.197966	0.743435	0.265922	0.790299	0.981636	chr14	34802399	34803333	+	0	NA	exon (NM exon (NM	-71325	NR_16077E	1.12E+08	Hs.50914CNR_16077E	LOC11226E-	-	uncharacterized ncRNA	
chr9-6925.6.458227	0.254624	0.95761	0.265896	0.790332	0.981636	chr9	69254129	69254554	+	0	NA	exon (NM exon (NM	49186	NM_00136E	9414	Hs.50382	NM_00481E	ENSG000000TJP2	C9DUPq21.2	tight jur protein-coding
chr12-292.7.18878	-0.23494	0.8839	-0.2658	0.790394	0.981636	chr12	2927948	2928365	+	0	NA	intron (Nintron (N	-31241	NM_00321E	7004	Hs.94865	NM_00321E	ENSG000000TEAD4	EFTR-2 RTTEA	doma protein-coding
chr12-292.7.18878	-0.23494	0.8839	-0.2658	0.790394	0.981636	chr12	29280801	29281702	+	0	NA	intron (Nintron (N	-121563	NM_00135E	341350	Hs.67458CNM_18337E	ENSG000000OVCHI	OVCH	ovochymas protein-coding	
chr15-615.7.18878	-0.23494	0.8839	-0.2658	0.790394	0.981636	chr15	61982093	61982142	+	0	NA	intron (Nintron (N	79275	NM_01768A	54832	Hs.51166CNM_01768A	ENSG000000VPS13C	PARK23	vacuolar protein-coding	
chr3-1491.7.18878	-0.23494	0.8839	-0.2658	0.790394	0.981636	chr3	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	45695	NM_00009E	1356	Hs.558314NM_00009E	ENSG000000CP	CP-2	cerulopl protein-coding	
chr1-6701.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr1	67010364	67012900	+	0	NA	intron (NAluJb SIN	5410	NM_01513E	23169	Hs.21364CNM_01513E	ENSG000000SLC35D1	SHNKND UC	solute c protein-coding	
chr1-1531.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr1	1.50E+08	1.54E+08	+	0	NA	exon (NM exon (NM	759	NM_01462A	6277	Hs.27524CNM_01462A	ENSG000000S100A6	OAG9 5B10 S100	calc protein-coding	
chr1-2431.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr1	2.43E+08	2.43E+08	+	0	NA	intron (Nintron (N	58328	NM_01481E	9859	Hs.53363CNM_01481E	ENSG000000CEP170	FAM68A K	centrosom protein-coding	
chr10-125.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr10	12236966	12237377	+	0	NA	intron (Nintron (N	41174	NM_00602E	8872	Hs.41284CNM_00602E	ENSG000000CDC123	C10orf7 I	cell div protein-coding	
chr10-68.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr10	68912599	68915794	+	0	NA	exon (NM exon (NM	12881	NM_02404E	79009	Hs.522984NM_02404E	ENSG000000DDX50	GU2 GUB F	DEX-hv protein-coding	
chr11-671.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr11	67180321	67183044	+	0	NA	intron (NLMIME4a LI	-58332	NM_00125E	22992	Hs.124147NM_01230E	ENSG000000KDM2A	CXXC8 FBI	lysine de protein-coding	
chr11-117.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (NAluSx SIN	5635	NR_16040C	26521	Hs.27991CNM_01245E	ENSG000000TIMM8B	DDP2 TIM	transloc protein-coding	
chr11-112.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	non-codirnon-codir	-9227	NM_00104C	51092	Hs.712144NM_01599E	ENSG000000SIDT2	CGI-40	SIDI tra protein-coding	
chr12-487.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr12	48710316	48712487	+	0	NA	intron (N(AAAT)n S	5306	NM_00124C	904	Hs.92308	NM_00124C	ENSG000000CCNT1	CCNT CYC1	cyclin T1 protein-coding
chr12-927.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr12	92793881	92797572	+	0	NA	intron (NLP1A6 LIN	58327	NM_00100A	440107	Hs.59101CNM_00100A	ENSG000000PLEKHG7	-	pleckstrin protein-coding	
chr13-946.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr13	94621163	946125200	+	0	NA	exon (NM exon (NM	21324	NM_18098E	160897	Hs.43936CNM_18098E	ENSG000000GPR180	ITR	G protein protein-coding	
chr14-602.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr14	60291858	60292810	+	0	NA	intron (Nintron (N	-30862	NR_146481	1.02E+08	NR_146481	ENSG000000LINC02322-	-	long intencRNA	
chr14-602.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr14	60984879	60990242	+	0	NA	intron (NMR1b SINE	-5870	NM_00135E	57570	Hs.38015CNM_02081C	ENSG000000TRMT5	COXP26 K	RNA meth protein-coding	
chr14-761.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr14	76177386	76179467	+	0	NA	3' UTR (N3' UTR (N	24072	NM_11031A	55668	Hs.410231NM_01792E	ENSG000000GPATCH2L	C14orf11E	G-patch protein-coding	
chr15-503.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr15	50302915	50303654	+	0	NA	intron (NAluJb SIN	-37558	NM_00211E	3067	Hs.1481	NM_00211E	ENSG000000CHDC	-	histidine protein-coding
chr17-535.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr17	5399631	5401386	+	0	NA	intron (NAluSg SIN	-19133	NM_00116E	84268	Hs.46208CNM_03230E	ENSG000000RPA1N	HRIP RIP	RPA inter protein-coding	
chr17-545.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr17	54961709	54964971	+	0	NA	exon (NM exon (NM	5314	NR_13567E	1353	Hs.591171NM_00437E	ENSG000000COX11	COX11P	cytochon protein-coding	
chr19-343.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr19	34389802	34392044	+	0	NA	intron (Nintron (N	-13475	NM_00135E	84306	Hs.515344NM_03234E	ENSG000000PDCD2L	-	programme protein-coding	
chr2-6385.8.144975	-0.21557	0.811342	-0.2657	0.790474	0.981636	chr2	63857925	63859347	+	0	NA	intron (Nintron (N</								







chr4-1478	8.137117	-0.21391	0.816037	-0.26213	0.793219	0.981636	chr4	1.48E+08	1.48E+08	+	0	NA	intron (Nkangal DN	50397 NR_039962	1.01E+08	NR_039962	ENSG00000MIR4799	-	microRNA	ncRNA	
chr5-4361	8.137117	-0.21391	0.816037	-0.26213	0.793219	0.981636	chr5	43619762	43620114	+	0	NA	intron (NMSTB1 LTF	-16708 NR_073111	1.01E+08	Hs.482045	NR_073111	NNT-AS1	-	NNT antisenseRNA	
chr5-1158	8.137117	-0.21391	0.816037	-0.26213	0.793219	0.981636	chr5	1.16E+08	1.16E+08	+	0	NA	intron (NMADE2 DN	5390 NM_004707	9140	Hs.264482	NM_004707	ENSG00000CATG12	APG12 APC	autophagy protein-coding	
chr6-8748	8.137117	-0.21391	0.816037	-0.26213	0.793219	0.981636	chr6	87483579	87484712	+	0	NA	intron (NHERY1P OF	11171 NM_006416	10559	Hs.423162	NM_006416	ENSG00000SLC35A1	CDG2F CM	solute carrier protein-coding	
chr8-1188	8.137117	-0.21391	0.816037	-0.26213	0.793219	0.981636	chr8	1.81E+08	1.81E+08	+	0	NA	intron (Nintron (N	18355 NM_000127	2131	Hs.492618	NM_000127	ENSG00000EXT1	EXT LGC	extosin protein-coding	
chr15-648	8.20183	-0.21638	0.825665	-0.26207	0.793269	0.981636	chr15	64866718	64867981	+	0	NA	3' UTR (N3' UTR (N	25434 NM_025201	80301	Hs.709337	NM_025201	ENSG00000PLEKH02	PLEKHQ1 F	pleckstrin protein-coding	
chr1-7741	4.426947	-0.28376	1.082835	-0.26205	0.793282	0.981636	chr1	77412731	77413572	+	0	NA	intron (Nintron (N	130064 NM_012093	26289	Hs.559718	NM_012093	ENSG00000AK5	AK6	adenylate protein-coding	
chr2-5534	4.426947	-0.28376	1.082835	-0.26205	0.793282	0.981636	chr2	55349399	55349987	+	0	NA	intron (Nintron (N	67374 NR_027258	344405	Hs.445292	NR_027258	ENSG00000PRORSD1P	NCRNA0011	prolyl-tf pseudo	
chr3-6416	4.426947	-0.28376	1.082835	-0.26205	0.793282	0.981636	chr3	64165747	64166915	+	0	NA	intron (Nintron (N	-21213 NR_046702	1.01E+08	Hs.67084	CNR_046702	ENSG00000PRICKLE2-	PRICKLE2	ncRNA	
chr5-6236	4.426947	-0.28376	1.082835	-0.26205	0.793282	0.981636	chr5	62368529	62369119	+	0	NA	intron (Nintron (N	27292 Hs.73166	NM_014473	ENSG00000DIMT1	DIM1 DIM1	DIMT1 rRNA	protein-coding		
chr11-767	7.863862	0.218585	0.834295	0.261999	0.793322	0.981636	chr11	76546095	76546380	+	0	NA	exon (NM exon (NM	101212 NM_020134	56946	Hs.35258	NM_020134	ENSG00000EMSY	C1orf30 EMSY	trp protein-coding	
chr21-288	7.863862	0.218585	0.834295	0.261999	0.793322	0.981636	chr21	28881148	28882199	+	0	NA	intron (NAluJb SIN	3694 NM_013240	29104	Hs.16384	CNM_013240	ENSG00000N6AMT1	C21orf127	N-6 adenylate protein-coding	
chr4-422	7.863862	0.218585	0.834295	0.261999	0.793322	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (NHSMAR2 DN	-100479 NM_139243	132612	Hs.51895	NM_139243	ENSG00000ADAD1	Tenr	adenosine protein-coding	
chr13-194	12.86219	-0.17255	0.658683	-0.26197	0.793345	0.981636	chr13	49460861	49464154	+	0	NA	intron (NMER21C LI	18233 NM_001320	83852	Hs.63178	NM_001320	ENSG00000SETDB2	C3orf41 CSET	domain protein-coding	
chr2-2314	12.86219	-0.17255	0.658683	-0.26197	0.793345	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (Nintron (N	1853 NR_004398	25826	NR_004398	ENSG00000SNORD82	RNU82 U82	small nucleolar RNA		
chr5-1796	12.86219	-0.17255	0.658683	-0.26197	0.793345	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	2532 NM_001364	3187	Hs.604001	NM_005520	ENSG00000HNRNPH1	HNRPH HNF	heterolog protein-coding	
chr5-1812	12.86219	-0.17255	0.658683	-0.26197	0.793345	0.981636	chr5	1.81E+08	1.81E+08	+	0	NA	exon (NM exon (NM	2348 NR_002592	619571	NR_002592	ENSG00000SNORD96A	U96A	small nucleolar RNA		
chr12-101	7.351558	0.227946	0.870544	0.261843	0.793442	0.981636	chr12	1E+08	1E+08	+	0	NA	intron (Nintron (N	-19435 NM_001146	246213	Hs.116871	NM_139319	ENSG00000SLC17A8	DFNA25 VC	solute carrier protein-coding	
chr1-1612	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr1	16123301	16134900	+	0	NA	intron (NMIRb SINE	26969 NM_001325	1969	Hs.17159	NM_004431	ENSG00000EPHA4	ARCC2 CTF	EPH receptor protein-coding	
chr1-5868	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr1	58693114	58695381	+	0	NA	intron (NML2c LINE	5815 NM_001088	114803	Hs.744921	NM_001088	ENSG00000MYSM1	2A-DUB 2Myb	like, protein-coding	
chr11-958	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr11	959673	961465	+	0	NA	intron (NAluSp SIN	34699 NM_012305	161	Hs.19121	NM_012305	ENSG00000AP2A2	ADTAB CLF	adaptor protein-coding	
chr11-188	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr11	18500017	18502804	+	0	NA	intron (NLMMA4A LI	25532 NM_006292	7251	Hs.52351	NM_006292	ENSG00000TSG101	TSG10 VPS	tumor suppressor protein-coding	
chr13-978	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr13	97993030	97995554	+	0	NA	intron (NAluSq2 SI	40617 NM_002271	3843	Hs.71259	NM_002271	ENSG00000IPO5	IMB3 KPNE	importin protein-coding	
chr14-94	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr14	94058062	94062343	+	0	NA	exon (NM exon (NM	21000 NM_020414	57062	Hs.51032	NM_020414	ENSG00000DDX24	-	DEAD-box protein-coding	
chr15-238	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr15	23009104	23011211	+	0	NA	intron (Nintron (N	-29259 NM_001324	23191	Hs.26704	NM_014608	ENSG00000CYFIP1	P140SR	A-lycopolysaccharide protein-coding	
chr16-518	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr16	55579	59142	+	0	NA	TTS (NM_CTTT	3532 NM_024571	79622	Hs.15277	NM_024571	ENSG00000SNRNP25	C16orf33	small nucleolar protein-coding	
chr16-255	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr16	21981487	21984560	+	0	NA	TTS (NM_CTTT	18093 NM_001363	255762	Hs.98244	NM_173800	ENSG00000PDZD9	C16orf65	PDZ domain protein-coding	
chr16-848	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr16	84319759	84329026	+	0	NA	intron (Nintron (N	29514 NM_021197	58189	Hs.36688	NM_021197	ENSG00000WFD1	W20	WAP four-protein-coding	
chr17-402	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr17	40232673	40234999	+	0	NA	intron (NAluSp SIN	14532 NM_133264	147179	Hs.42162	NM_133264	ENSG00000WIPF2	WICH WIRE	WAS/WASL protein-coding	
chr17-628	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr17	62674334	62674334	+	0	NA	exon (NM exon (NM	-30320 NR_147888	1.01E+08	Hs.44626	NR_147888	ENSG00000LOC105371	-	uncharacterized RNA	
chr19-398	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr19	39393591	39394405	+	0	NA	intron (Nintron (N	2620 NR_133918	55588	Hs.61154	NM_017592	ENSG00000MED29	IXL MED2	mediator protein-coding	
chr2-1608	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (NAluJo SIN	-30466 NR_103777	1.01E+08	Hs.72953	NR_103777	ENSG00000LINC02478	-	long intergenic RNA	
chr20-388	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr20	38500330	38501344	+	0	NA	intron (NTigger L	-15726 NR_039608	1.01E+08	NR_039608	ENSG00000MIR54802	-	microRNA	ncRNA	
chr22-208	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr22	20582579	20585246	+	0	NA	intron (Nintron (N	75865 NM_001292	51586	Hs.51742	NM_015888	ENSG00000MED15	ARC105 C	mediator protein-coding	
chr3-1708	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (NAluSz SIN	67412 NM_002744	5584	Hs.47819	NM_002744	ENSG00000PRKCI	DXS1179E	protein kinase protein-coding	
chr7-4984	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr7	4984187	4990936	+	0	NA	intron (Nintron (N	13576 NR_023388	441191	Hs.52063	NR_023388	ENSG00000RNF216P1	RNF216L	tring finger pseudo	
chr7-4404	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr7	44049707	44051167	+	0	NA	intron (Nintron (N	-1329 NR_106898	1.02E+08	NR_106898	ENSG00000MIR6837	-	hsa-mir-6	microRNA	ncRNA
chr7-994	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr7	99401766	99403516	+	0	NA	intron (NAluSc8 SI	5956 NM_004891	11333	Hs.63229	NM_014891	ENSG00000PDAP1	HASPP28 T	PDGFA as protein-coding	
chr8-4218	8.929609	0.204403	0.780694	0.261823	0.793458	0.981636	chr8	42188134	42188738	+	0	NA	intron (NTCATCTA	20686 NM_009033	5327	Hs.49105	NM_009033	ENSG00000PLAT	T-PA TPA	plasminogen protein-coding	
chr16-568	8.368308	0.212012	0.809857	0.261789	0.793484	0.981636	chr16	56395572	56397659	+	0	NA	intron (NLMIPA5 LI	28374 NM_001322	267	Hs.29513	NM_001144	ENSG00000CAMFR	GP78 RNF	4 autocrine protein-coding	
chr19-320	8.368308	0.212012	0.809857	0.261789	0.793484	0.981636	chr19	32635911	32636170	+	0	NA	intron (Nintron (N	-27571 NR_145718	1.1E+08	NR_145718	ENSG00000SNORA68B	-	small nucleolar RNA		
chr5-160	7.359416	0.226016	0.863637	0.261702	0.793551	0.981636	chr5	1.6E+08	1.6E+08	+	0	NA	intron (NLA_C_Mam	29326 NM_000314	7265	Hs.51971	NM_000314	ENSG00000TTC1	TPR1	tetratricopeptide-coding	
chr18-488	6.694042	-0.24834	0.949113	-0.26166	0.793586	0.981636	chr18	48559701	48560024	+	0	NA	intron (NLMIPB4 LI	20831 NM_001142	9811	Hs.14523	CNM_014772	ENSG00000CTIF	Gm672 KI	cap binding protein-coding	
chr7-3254	7.856004	0.220404	0.842673	0.261553	0.793666	0.981636	chr7	32548905	32550070	+	0	NA	intron (NAluJb SIN	53998 NM_015066	23080	Hs.12805	NM_015066	ENSG00000AVL9	KIAA0241	AVL9 cell protein-coding	
chr12-428	6.847112	0.236528	0.904424	0.261523	0.793689	0.981636	chr12	42356273	42356494	+	0	NA	intron (NLTR40b LI	24585 NM_001364	51535	Hs.44415	NM_016488	ENSG00000PPHLN1	CR HSPC2	periplakin protein-coding	
chr1-2368	8.376166	0.210282	0.804353	0.26143	0.793761	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (NLMIME3B LI	55729 NM_001291	4548	Hs.49818	NM_000254	ENSG00000MTR	HMG MS C	5-methyl protein-coding	
chr16-288	8.376166	0.210282	0.804353	0.26143	0.793761	0.981636	chr16	28960090	28960787	+	0	NA	intron (NMLT1C-int	1855 NR_039742	1.01E+08	NR_039742	ENSG00000MIR4517	-	mir-4517	microRNA	ncRNA
chr17-568	8.376166	0.210282	0.804353	0.26143	0.793761	0.981636	chr17	56985422	56986255	+	0	NA	intron (Nintron (N	7841 NM_021622	59342	Hs.51495	CNM_021622	ENSG00000SCPEP1	HSCP1 RI	Serine protease protein-coding	
chr2-2248	8.376166	0.210282	0.804353	0.26143	0.793761	0.981636	chr2	2.25E+08	2.25E+08	+	0	NA	exon (NM exon (NM	66947 NM_001257	8452	Hs.37228	NM_003590	ENSG00000CUL3	CUL-3 PH	cullin 3 protein-coding	
chr5-134	8.376166	0.210282	0.804353	0.26143	0.793761	0.981636	chr5	1.34E+08	1.34E+08	+	0	NA	intron (NLMIME3G LI	5849 NM_003337	7320	Hs.61209	NM_003337	ENSG00000UBEZB	E2-17kDa	ubiquitin protein-coding	
chr																					



chr10-89c	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr10	89007362	89012871	+	0	NA	intron (Nintron (N	-17141	NR_028371	1E+08	Hs.24413cNR_028371	FAS-AS1	FAS-AS1 FAS antisncRNA	
chr11-117	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	exon (NM exon (NM	-11293	NM_00104C	51092	Hs.712144NM_01599c	ENSG00000	S1D1 trarprotein-coding	
chr15-40f	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr15	40978716	40981212	+	0	NA	non-codiron-codir	26493	NM_00114Z	79094	Hs.15556c	ENSG00000	CHAC1 - ChaC glutprotein-coding	
chr17-43f	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr17	43521399	43524234	+	0	NA	intron (NAluXs SI	7619	NM_001261	2118	Hs.43405c	ENSG00000	ETV4 E1A-F E1A/ETS variaprotein-coding	
chr2-1914	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	exon (NM exon (NM	168682	NM_001161	4110	Hs.43962c	ENSG00000	MYO1B MMI-alpha myosin I protein-coding	
chr2-2267	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr2	2.27E+08	2.27E+08	+	0	NA	intron (Nintron (N	49083	NM_005544	3667	Hs.47150c	ENSG00000	IRS1 HIRS-2 insulin I protein-coding	
chr5-139f	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr5	1.39E+08	1.39E+08	+	0	NA	3' UTR (N3' UTR (N	-11679	NR_10983C	51247	Hs.396644NM_01648c	ENSG00000	PAIP2 PAIP-2 P poly(A) t protein-coding	
chr5-7104	9.392916	0.197823	0.759589	0.260434	0.794529	0.981636	chr5	71040932	71041347	+	0	NA	intron (NMER63B DN	-16025	NM_02289Z	4671	Hs.646951NM_00453c	ENSG00000	NAIP BIRC1 N FLNLR faml protein-coding	
chr17-187	10.95525	0.185483	0.712352	0.260381	0.79457	0.981636	chr17	18797497	18800080	+	0	NA	intron (Nintron (N	9753	NM_00131f	51030	Hs.87295	NR_01607c	ENSG00000	TVP23B CGI-148 F trans-gol protein-coding
chr11-202	8.88847	0.202882	0.779325	0.260331	0.794609	0.981636	chr11	202834	205717	+	0	NA	3' UTR (N3' UTR (N	3147	NM_00109E	51272	Hs.41441c	ENSG00000	BET1L BET1L GC bet1 gol protein-coding	
chr11-122	8.88847	0.202882	0.779325	0.260331	0.794609	0.981636	chr11	1.22E+08	1.22E+08	+	0	NA	intron (NAluJr SIN	40719	NR_029671	406911	NR_029671	ENSG00000	MIR125B1	MIRN125B1 microRNA ncRNA
chr13-331	8.88847	0.202882	0.779325	0.260331	0.794609	0.981636	chr13	33158252	33159179	+	0	NA	intron (Nintron (N	27376	NM_00124z	90627	Hs.156551NM_052851	ENSG00000	STARD13 ARHGAP37 StAR relaprotein-coding	
chr20-354	8.88847	0.202882	0.779325	0.260331	0.794609	0.981636	chr20	35462371	35462974	+	0	NA	intron (Nintron (N	2689	NM_00131E	11190	Hs.44397c	ENSG00000	CEP250 C-NAP1 CE centrosome protein-coding	
chr20-45f	8.88847	0.202882	0.779325	0.260331	0.794609	0.981636	chr20	45896629	45897259	+	0	NA	intron (Nintron (N	-5657	NM_00074E	140825	Hs.517094NM_08074c	ENSG00000	NEURL2 C20orf16 neuralize protein-coding	
chr9-122f	8.88847	0.202882	0.779325	0.260331	0.794609	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	3' UTR (N3' UTR (N	5304	NR_003071	692206	Hs.69325c	NR_003071	ENSG00000	SNORD90 HBII-295 small nucsnRNA
chr3-167f	8.209688	-0.21808	0.837969	-0.26024	0.794676	0.981636	chr3	1.68E+08	1.68E+08	+	0	NA	IntergeniL1MC4 LIN	-18891	NM_00134E	511790	Hs.21376c	NM_17882c	ENSG00000	WDR49 - WD repeat protein-coding
chr1-354f	9.897362	0.193293	0.742823	0.260214	0.794699	0.981636	chr1	35403344	35403560	+	0	NA	intron (NAluXs SI	-37375	NR_04665f	1.01E+08	Hs.585397NR_04665c	ENSG00000	ZMY4-AS1-ZMY4A antncRNA	
chr6-5714	9.897362	0.193293	0.742823	0.260214	0.794699	0.981636	chr6	57147577	57148679	+	0	NA	exon (NM exon (NM	57147577	NR_11074Z	1.02E+08	Hs.70571c	NR_11074Z	ZNF451-AC-ZNF451 rencRNA	
chr1-666f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr1	66698268	66700588	+	0	NA	intron (N L2 LINE L	-53031	NM_15266E	200132	Hs.47922c	NM_15266E	ENSG00000	TCTEX1D1 - Tctex1 d protein-coding
chr10-121	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr10	12156952	12159887	+	0	NA	intron (Nintron (N	-27603	NR_03969f	1.01E+08	NR_03969f	ENSG00000	MIR548A	- microRNA ncRNA
chr10-131	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr10	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	11649	NM_00405Z	664	Hs.14487c	NR_00405Z	ENSG00000	BNI3P3 NIP3 - BCL2 int protein-coding
chr12-69f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr12	6965003	6969328	+	0	NA	TTS (NR_C TTS (NR_C	441	NR_00301C	677777	Hs.68963c	NR_00301C	ENSG00000	SCARNA12 U89 small Ca ncRNA
chr12-881	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr12	88108322	88108826	+	0	NA	intron (Nintron (N	33642	NM_025114	80184	Hs.150444NM_025114	ENSG00000	CEP290 3H11Ag BE centrosome protein-coding	
chr12-132	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	intron (N Kangal L	-28696	NM_015114	23141	Hs.65462c	NM_015114	ENSG00000	ANKLE2 KIAA0692 ankyrin I protein-coding
chr14-311	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr14	31104789	31106832	+	0	NA	intron (Nintron (N	79167	NM_001254	11154	Hs.293411NM_00707c	ENSG00000	AP451 AP47B CL adaptor I protein-coding	
chr14-54f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr14	54789049	54791126	+	0	NA	3' UTR (N3' UTR (N	35255	NM_001161	23034	Hs.98259	NR_01558c	ENSG00000	SAMD4A SAMD4 SM sterile ep protein-coding
chr2-3654	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr2	36544183	36544161	+	0	NA	intron (Nintron (N	55846	NM_00104Z	9637	Hs.25856c	ENSG00000	FEZ2 5846 SM fasciculation protein-coding	
chr2-127f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr2	1.27E+08	1.27E+08	+	0	NA	intron (NAluJo SIN	23991	NM_00130z	-2071	Hs.46987c	NR_00012c	ENSG00000	ERC33 BTF2 GTF ERC3 exciprotein-coding
chr20-331	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr20	3310710	3312021	+	0	NA	intron (NAluJo SIN	-72175	NM_001174	83959	Hs.105607NM_03203c	ENSG00000	SLC4A11 BTRP1 CDP solute ep protein-coding	
chr20-17f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr20	17613859	17619815	+	0	NA	exon (NM exon (NM	46762	NM_00687C	11034	Hs.30419c	NR_00687C	ENSG00000	CALD1 ACD ATP destrin, protein-coding
chr4-113f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr4	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	222391	NM_001354	287	Hs.620557NM_00114c	ENSG00000	ANK2 ANK-2 LQ ankyrin 2 protein-coding	
chr4-122	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-45003	NM_13924Z	132612	Hs.518957NM_13924c	ENSG00000	ADADD Tenr adenosine protein-coding	
chr4-168f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N	88514	NM_001367	23022	Hs.15122c	NM_016081	ENSG00000	PALLD CGI-151 cadallan, protein-coding
chr5-1284	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (NAluY SINE	68896	NM_00199f	2201	Hs.519294NM_00199c	ENSG00000	FBN2 CCA DA9 F fibrillin I protein-coding	
chr7-102f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (NAluJb SIN	8487	NM_00114E	729597	Hs.48944c	NR_00114c	ENSG00000	SPDYE6 speedy RI protein-coding
chr7-134f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr7	1.35E+08	1.35E+08	+	0	NA	exon (NM exon (NM	42309	NM_003314C	800	Hs.49020c	NR_003314C	ENSG00000	CALD1 CDM H-CAL caldesmon protein-coding
chr7-139f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N	58327	NM_00108C	154790	Hs.57806	NR_00108C	ENSG00000	CLEC2L - C-type I protein-coding
chr7-140f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr7	1.41E+08	1.41E+08	+	0	NA	intron (Nintron (N	29134	NR_13447f	27147	Hs.6385	NR_01568c	ENSG00000	DENN2DA FAM3D1 D DENN2 protein-coding
chr9-697f	8.639713	-0.20542	0.789557	-0.26017	0.794729	0.981636	chr9	69722611	69724578	+	0	NA	exon (NM exon (NM	36417	NR_15951f	375743	Hs.74419c	NR_00109c	ENSG00000	PTAR1 - protein I protein-coding
chr20-35f	7.367274	0.224029	0.861474	0.260053	0.794823	0.981636	chr20	3591250	3591937	+	0	NA	intron (NMER76 LTF	71806	NM_02213c	64096	Hs.30202c	NR_02213c	ENSG00000	GFR4 - GDNF fami protein-coding
chr7-128f	7.367274	0.224029	0.861474	0.260053	0.794823	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	IntergeniAluJb SIN	-77248	NR_02436E	402483	Hs.72235c	NR_00103968Z	LINC0100C - long intencRNA	
chr1-153f	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (N L1MC4 LIN	-12514	NR_024117	1E+08	Hs.656361NR_024117	MSTO2P - MSTO2 misato f pseudo		
chr11-43f	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr11	43320683	43321467	+	0	NA	intron (Nintron (N	9079	NM_00114Z	8539	Hs.435771NM_00659c	ENSG00000	API5 AAC-11 A apoptosis protein-coding	
chr11-77f	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr11	77921547	77921906	+	0	NA	intron (Nintron (N	72942	NM_00354f	92103	Hs.53372c	NR_00354f	ENSG00000	INTS4 INT4 MSTC integrat protein-coding
chr12-48f	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr12	48922045	48924191	+	0	NA	TTS (NM_C TTS (NM_C	1875	NM_00114z	51035	Hs.65510c	NR_016594c	ENSG00000	FKBP11 FKBP19 FKBP prol protein-coding
chr13-45f	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr13	45966802	45968934	+	0	NA	exon (NM exon (NM	84878	NM_00133C	23091	Hs.13610c	NR_01507c	ENSG00000	CZCH13 KIAA0853 zinc fing protein-coding
chr15-654	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr15	65488977	65490287	+	0	NA	intron (NAluY SINE	27642	NM_19796C	54878	Hs.45860c	NR_01774c	ENSG00000	DPP8 DP8 DPRP- dipeptidyl protein-coding
chr16-111	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr16	11732272	11734494	+	0	NA	intron (NAluYf1 SI	9474	NM_00130z	51061	Hs.313847NM_015914	ENSG00000	TXNDC11 EFP1 thiredoxin protein-coding	
chr18-307	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr18	3010781	3011739	+	0	NA	intron (Nintron (N	687	NM_01464c	9663	Hs.13234c	NR_01464c	ENSG00000	LPIN2 - lipin 2 protein-coding
chr5-737f	8.384024	0.208537	0.802663	0.259807	0.795013	0.981636	chr5	73780194	73781366	+	0	NA	intron (Nintron (N	-32766	NM_001244	64283	Hs.482521NM_00108c	ENSG00000	ARHGEP28 RGNF RF Rho guan protein-coding	
chr6-433f	8.384024	0.208537	0.802663	0.259807																



chr19-361.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr19	3611054	3612416	+ 0 NA	3' UTR (N3' UTR (N	4488 NR_038866	404665 Hs. 719722	ENSG000003CACTIN-AS1	C9orf29-CTACTIN	ar ncRNA
chr2-5395.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr2	53930109	53932791	+ 0 NA	intron (Nintron (N	39543 NM_014614	23198 Hs. 413801	ENSG000003PSMF4	PA200	proteasome protein-coding
chr2-1357.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr2	1.36E+08	1.36E+08	+ 0 NA	intron (NAluJb SIN	-6394 NR_163478	1.08E+08 Hs. 591242	ENSG000003LOC107985		uncharacterized ncRNA
chr2-1717.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr2	1.72E+08	1.72E+08	+ 0 NA	intron (Nintron (N	42787 NM_00132C	1781 Hs. 546256	ENSG000003DYNCL12	DIC74 DNC	dynein cy protein-coding
chr20-444.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr20	44488091	44491069	+ 0 NA	3' UTR (N3' UTR (N	13706 NM_001261	79183 Hs. 283866	ENSG000003TTPAL	C2orf121	alpha cy protein-coding
chr20-588.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr20	58902783	58905456	+ 0 NA	intron (Nintron (N	11956 NR_132272	2778 Hs. 125898	ENSG000003GNAS	AHO C2orf	GNAS comp protein-coding
chr3-1014.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr3	10146483	10147941	+ 0 NA	intron (NAluSc8 S1	5434 NM_198156	7428 Hs. 517792	ENSG000003VHL	HRAA1 RCV	Hippe protein-coding
chr6-1511.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr6	1.51E+08	1.51E+08	+ 0 NA	intron (NAluSg7 S1	9541 NM_00135C	25902 Hs. 591342	ENSG000003MTHFD1L	HTF5FDC1	methylenase protein-coding
chr7-1786.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr7	17867621	17868130	+ 0 NA	intron (Nintron (N	72619 NM_00135C	23161 Hs. 487648	ENSG000003SNX13	RGS-PX1	sorting r protein-coding
chr7-4366.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr7	43680054	43612051	+ 0 NA	intron (Nintron (N	26944 NM_00476C	9263 Hs. 709482	ENSG000003STK17A	DRAK1	serine/th protein-coding
chr7-7506.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr7	75062761	75064643	+ 0 NA	intron (NAluSx1 S1	10100 NM_00136C	81554 Hs. 529622	ENSG000003RCC1L	WBSRCR16	RCC1 like protein-coding
chr7-1514.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr7	1.51E+08	1.51E+08	+ 0 NA	intron (NMER58B DN	30203 NM_005614	6009 Hs. 283521	ENSG000003RHEB	RHEB2	Ras homol protein-coding
chr8-1188.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr8	1.19E+08	1.19E+08	+ 0 NA	intron (Nintron (N	6228 NM_00254E	4982 Hs. 81791	ENSG000003TNFRSF11E	OC1F OPC	TNF recee protein-coding
chr9-3758.8.170399	-0.20981	0.811822	-0.25844	0.796067	0.981636	chr9	37588103	37588702	+ 0 NA	TTS (NM_C TTS (NM_C	4195 NM_001001	401505 Hs. 130774	ENSG000003TOMM5	C9orf105	translocat protein-coding
chr1-8882.4.419089	-0.28086	1.086927	-0.2584	0.796096	0.981636	chr1	88835064	88837025	+ 0 NA	3' UTR (N3' UTR (N	55523 NM_001514	2959 Hs. 481852	ENSG000003GTF2B	TF2B TF1I	general t protein-coding
chr3-1805.4.419089	-0.28086	1.086927	-0.2584	0.796096	0.981636	chr3	1.81E+08	1.81E+08	+ 0 NA	intron (NMLT1D LTF	24022 NM_00119C	131118 Hs. 230601	ENSG000003DNAJC19	PAM18 TJM	DnaJ heat protein-coding
chr6-8558.4.419089	-0.28086	1.086927	-0.2584	0.796096	0.981636	chr6	85583263	85584285	+ 0 NA	intron (NLIPTA7 LTF	10084 NM_15381E	57231 Hs. 485871	ENSG000003SNX14	RGS-PX2	Sorting r protein-coding
chr7-1007.4.419089	-0.28086	1.086927	-0.2584	0.796096	0.981636	chr7	1.01E+08	1.01E+08	+ 0 NA	TTS (NM_C TTS (NM_C	1628 NM_005837	10248 Hs. 416993	ENSG000003POPT7	OG61003	POPT7 homc protein-coding
chrX-1542.7.7168	-0.21808	0.843973	-0.2584	0.796102	0.981636	chrX	1.54E+08	1.54E+08	+ 0 NA	intron (Nintron (N	17583 NM_00111C	2316 Hs. 195464	ENSG000003FLNA	ABP-280	filamin A protein-coding
chr3-1134.11.41856	-0.20982	0.700296	-0.258351	0.796136	0.981636	chr3	11348165	11349130	+ 0 NA	intron (NLTR12 LTF	76250 NM_001144	10533 Hs. 38032	ENSG000003ATG7	APG7-LIKE	autophagy protein-coding
chr1-2331.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr1	23315796	23321583	+ 0 NA	exon (NM_exon (NM	25595 NM_001102	10236 Hs. 373736	ENSG000003HNRNP	HNRNP	hnf heterog protein-coding
chr1-5181.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr1	51804915	51809810	+ 0 NA	intron (Nintron (N	29040 NR_03158C	1E+08 NR_03158C	ENSG000003MIR761	hsa-mir-7	microRNA ncRNA
chr1-1001.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr1	1E+08	1E+08	+ 0 NA	intron (Nintron (N	6075 NR_13507E	54488 Hs. 729098	ENSG000003TRMT13	CCDC76	tRNA met protein-coding
chr1-2237.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr1	2.24E+08	2.24E+08	+ 0 NA	TTS (NM_C TTS (NM_C	64050 NM_00174E	824 Hs. 350898	ENSG000003CAPN2	CANP2 CAM	calpain 2 protein-coding
chr11-373.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr11	3733490	3736593	+ 0 NA	intron (Nintron (N	62505 NR_157591	4928 Hs. 524756	ENSG000003NUP98	ADIR2 NUF	nucleopor protein-coding
chr11-330.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr11	33058089	33059181	+ 0 NA	intron (Nintron (N	-17514 NR_015451	283267 Hs. 533701	ENSG000003LINC00294	NCRNA0025	long intncRNA
chr15-596.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr15	5966240	59666503	+ 0 NA	intron (NAluV SINE	-6955 NM_00132C	2958 Hs. 512934	ENSG000003GTF2A2	HS118745	general t protein-coding
chr16-587.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr16	58715214	58716436	+ 0 NA	intron (NAluSp SIN	18491 NM_00128E	2806 Hs. 599477	ENSG000003GOT2	KAT4 KATI	glutamic protein-coding
chr19-441.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr19	44144665	44145969	+ 0 NA	intron (Nintron (N	3663 NM_001144	10780 Hs. 235992	ENSG000003ZNF234	HZF4 ZNF2	zinc fing protein-coding
chr2-6816.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr2	68160191	68164980	+ 0 NA	exon (NM_exon (NM	4697 NM_020143	56902 Hs. 262858	ENSG000003PNO1	KHRBP1	RFP partner c protein-coding
chr2-1053.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr2	1.05E+08	1.05E+08	+ 0 NA	intron (Nintron (N	8751 NM_00131E	2274 Hs. 443687	ENSG000003FHL2	AAG11 DRA	four and protein-coding
chr2-414.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr2	41432221	41437866	+ 0 NA	3' UTR (N3' UTR (N	11758 NM_01627Z	10766 Hs. 474978	ENSG000003TOB2	APRO5	TOE transduce protein-coding
chr3-3335.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr3	33391282	33392636	+ 0 NA	intron (NLa2 LINE	48419 NM_00112E	7342 Hs. 729122	ENSG000003UBP1	LBP-1B	LE upstre protein-coding
chr3-1237.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr3	1.24E+08	1.24E+08	+ 0 NA	intron (Nintron (N	32370 NR_04662E	1.01E+08 Hs. 667318	ENSG000003MYLK-AS2	MYLK	antincRNA
chr3-1321.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr3	1.33E+08	1.33E+08	+ 0 NA	intron (NAluYk4 S1	-67671 NM_016557	51554 Hs. 310512	ENSG000003ACKR4	CK-CR	-11atypical protein-coding
chr3-1438.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr3	1.43E+08	1.43E+08	+ 0 NA	intron (NLM1B7 LIN	16760 NM_00132C	23350 Hs. 596572	ENSG000003USURP	SRI401	f5A12 snRNP protein-coding
chr5-5688.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr5	56880346	56884114	+ 0 NA	exon (NM_exon (NM	-27030 NR_13655E	133383 Hs. 85950	ENSG000003SETD9	C5orf35	SET doma protein-coding
chr5-1316.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr5	1.32E+08	1.32E+08	+ 0 NA	intron (NLM1J LINE	-34607 NM_001164	51735 Hs. 483328	ENSG000003RAPGEF6	KIA0011B	Rap guaniprotein-coding
chr5-1733.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr5	1.73E+08	1.73E+08	+ 0 NA	intron (NCPg	2394 NM_003714	8614 Hs. 233166	ENSG000003STC2	STC-2	STC stannic protein-coding
chr6-5658.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr6	56597043	56598818	+ 0 NA	exon (NM_exon (NM	44959 NM_01554E	667 Hs. 604918	ENSG000003COST	BP240	BP dystonin protein-coding
chr7-3588.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr7	35882332	35884817	+ 0 NA	intron (Nintron (N	82355 NM_00136C	989 Hs. 191346	ENSG000003SEPTIN7	CDC10	CDC septin 7 protein-coding
chr7-7298.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr7	72980420	72982152	+ 0 NA	Intergeni MLT1H2 LI1	11604 NR_104007	1E+08 Hs. 695008	ENSG000003LOC100101		FKBP prolpseudo
chr7-7648.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr7	76482253	76482859	+ 0 NA	exon (NM_exon (NM	2046 NM_001102	113878 Hs. 187058	ENSG000003CDTX2	RNF58	deltex E3 protein-coding
chr7-1212.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr7	1.21E+08	1.21E+08	+ 0 NA	intron (Nintron (N	-87864 NM_016087	51384 Hs. 272378	ENSG000003WNT16	Wnt	famil protein-coding
chr8-6712.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr8	67122926	67123754	+ 0 NA	intron (NLM1B3 LIN	39492 NM_001291	79848 Hs. 370147	ENSG000003CSPPI1	CSPP	JBT centroson protein-coding
chr8-1301.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr8	1.3E+08	1.3E+08	+ 0 NA	intron (Nintron (N	-33949 NR_04538E	1.01E+08 Hs. 106018	ENSG000003ASAP1-IT2	ASAP1	intncRNA
chr9-3332.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr9	33321588	33325523	+ 0 NA	intron (NAluSg SIN	33039 NM_147134	4799 Hs. 413074	ENSG000003NFX1	NFX2	TEG-nuclear t protein-coding
chr9-1011.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr9	1.01E+08	1.01E+08	+ 0 NA	3' UTR (N3' UTR (N	-5436 NM_001701	570 Hs. 284712	ENSG000003BAAT	BACAT	BATbile acic protein-coding
chr9-1313.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chr9	1.31E+08	1.31E+08	+ 0 NA	intron (Nintron (N	8021 Hs. 654538	ENSG000003NUP214	CAIN CAN	nucleopor protein-coding	
chrX-4511.8.631855	-0.20386	0.78938	-0.25826	0.796209	0.981636	chrX	45107928	45108446	+ 0 NA	intron (NL2c LINE	92689 NM_17681E	79742 Hs. 98321	ENSG000003DIPK2B	4930578C1	divergent protein-coding
chr5-1606.8.628228	-0.23223	0.899412	-0.258203	0.796251	0.981636	chr5	1.6E+08	1.6E+08	+ 0 NA	3' UTR (N3' UTR (N	54337 NR_146217	114825 Hs. 744968	ENSG000003PWWP2A	MST101	PWWP dome protein-coding
chr1-3797.8.896328	-0.201223	0.779506	-0.258142	0.796297	0.981636	chr1	37971016	37987790	+ 0 NA	intron (Nintron (N	10619 NM_00680Z	10946 Hs. 77899	ENSG000003F3A3	PRP9	PRPF splicing protein-coding
chr1-1241.8.896328	-0.201223	0.779506	-0.258142	0.796297	0										



chr6-3057 9.913078	0.190306	0.740345	0.25705	0.79714	0.981636	chr6	30576517	30588913	+	0	NA	intron (AluJb SIN	-1617 NR_03061E	1E+08	NR_03061E	ENSG00000MIR877	MIRN877 lmiRNA	ncRNA				
chr6-1587 9.913078	0.190306	0.740345	0.25705	0.79714	0.981636	chr6	1.59E+08	1.59E+08	+	0	NA	intron (intron (N	-4547 NR_037482	1.01E+08	NR_037482	ENSG00000MIR3918	mir-3918	microRNA	ncRNA			
chrX-532C 9.913078	0.190306	0.740345	0.25705	0.79714	0.981636	chrX	53202688	53220685	+	0	NA	intron (intron (N	-12741 NR_106954	1.02E+08	NR_106954	ENSG00000MIR6894	hsa-mir-ε	microRNA	ncRNA			
chr17-441 8.391882	0.206747	0.804691	0.256927	0.797235	0.981636	chr17	44195176	44195944	+	0	NA	intron (intron (N	2601 NM_0010098	56970	Hs.512651NM_02021E	ENSG00000ATXN7L3	ataxin 7	protein-coding				
chr2-2312 8.391882	0.206747	0.804691	0.256927	0.797235	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (AluSzl SIN	1060 NM_001352	80210	Hs.162411NM_02513E	ENSG00000ARMC9	ARM JBT5 armadillo	protein-coding				
chr4-828C 8.391882	0.206747	0.804691	0.256927	0.797235	0.981636	chr4	82832333	82833369	+	0	NA	intron (LIPA6 LIN	-33994 NM_02490E	79966	Hs.379191NM_02490E	ENSG00000CSD5	ACOD4 FAI	stearoyl- protein-coding				
chr7-358E 8.391882	0.206747	0.804691	0.256927	0.797235	0.981636	chr7	35888819	35889920	+	0	NA	intron (intron (N	88150 NM_00136C	989	Hs.19134NM_00178E	ENSG00000SEPTIN7	CDCl0 CDC	septin 7	protein-coding			
chr7-927F 8.391882	0.206747	0.804691	0.256927	0.797235	0.981636	chr7	92705253	92705950	+	0	NA	intron (intron (N	-115211 NM_00104C	257415	Hs.18346NM_15278E	ENSG00000FAMI33B	-	family wiprotein-coding				
chr1-230C 7.375132	0.221946	0.863906	0.25691	0.797249	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	3' UTR (3' UTR (N	20351 NM_00002E	183	Hs.19383	NR_00002E	ENSG00000CAGT	ANHU SERF	angiotensin	protein-coding		
chr19-46E 8.590716	-0.20629	0.803151	-0.25685	0.797296	0.981636	chr19	46674474	46674873	+	0	NA	intron (intron (N	13295 NR_040041	1.01E+08	Hs.434327NR_040041	ENSG00000DACT3-AS1	-	DACT3	antncRNA			
chr2-1217 6.432803	0.247501	0.965032	0.25647	0.797588	0.981636	chr2	1.22E+08	1.22E+08	+	0	NA	intron (MER1B DNA	4707 NM_004622	7247	Hs.75066	NR_004622	ENSG00000TSN	BCLF1 C	translin	protein-coding		
chr1-230C 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr1	2306590	2308560	+	0	NA	3' UTR (3' UTR (N	45086 NR_02448E	1E+08	Hs.65531E	NR_001127	ENSG00000CLOC10012E	-	small nucpseudo			
chr1-669E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr1	66981723	66984088	+	0	NA	intron (intron (N	52649 NM_0010077	57708	Hs.60543E	NR_02094E	ENSG00000MIER1	ERI MI-EMFIER1	trε	protein-coding		
chr11-344 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr11	34470983	34473177	+	0	NA	TTS (NM TTS (NM C	33146 NM_001175Z	847	Hs.50230E	NR_001175Z	ENSG00000CAT	-	catalase	protein-coding		
chr11-73C 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr11	73358623	73366456	+	0	NA	exon (NM exon (NM	-13860 NM_15222Z	84957	Hs.53372C	NR_032871	ENSG00000CRELT	AI3C TNFF	RELT	TNF	protein-coding	
chr12-10E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	37762 NM_03230C	84260	Hs.410924NM_03230C	ENSG00000TCHP	TpMs	trichople	protein-coding			
chr12-12C 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr12	1.2E+08	1.2E+08	+	0	NA	exon (NM exon (NM	16792 NR_03971E	1.01E+08	NR_03971E	ENSG00000MIR4498	mir-4498	microRNA	ncRNA			
chr13-11C 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr13	1.3E+08	1.3E+08	+	0	NA	intron (intron (N	-17053 NR_10704Z	1.02E+08	NR_10704Z	ENSG00000MIR8075	hsa-mir-ε	microRNA	ncRNA			
chr15-904 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr15	90496895	90500653	+	0	NA	intron (AluSxl SIN	-31149 NM_02276E	64784	Hs.56752E	NR_02276E	ENSG00000CRTC3	TORC-3 TC	CREB	reg	protein-coding	
chr17-84F 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr17	8459873	8463038	+	0	NA	intron (AluJo SIN	25571 NM_03080E	81565	Hs.37212E	NR_03080E	ENSG00000CNDEL1	EOPA MITA	nudE	neur	protein-coding	
chr2-958F 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr2	95874286	95875215	+	0	NA	intron (LIPA3 LIN	-47769 NR_103734	150759	Hs.50346E	NR_103734	LINC0034Z	NCRNA0034	long	intncRNA		
chr2-215F 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr2	2.15E+08	2.15E+08	+	0	NA	intron (AluSxl SIN	14273 NM_004044	471	Hs.90280	NR_004044	ENSG00000ATIC	AICAR AIC	5-aminoin	protein-coding		
chr20-35E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr20	35627882	35631212	+	0	NA	intron (MIR SINE	13663 NM_001317	6676	Hs.12315E	NR_00311E	ENSG00000CPAG4	CT127 SUN	sperm	ass	protein-coding	
chr20-50E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr20	50574351	50680104	+	0	NA	intron (NL2b LINE	-8559 NR_03037E	693230	NR_03037E	ENSG00000MIR645	MIRN645 lmiRNA	ncRNA				
chr20-50E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr20	50598835	50606217	+	0	NA	non-codir non-codir	12259 NR_031634	1E+08	NR_031634	ENSG00000MIR1302-ε	MIRN1302-ε	microRNA	ncRNA			
chr3-155E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr3	15588251	15589517	+	0	NA	intron (intron (N	-12428 NM_001281	686	Hs.444197NM_001281	ENSG00000CMTD	-	biotinidε	protein-coding			
chr3-583C 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr3	58394401	58401457	+	0	NA	intron (intron (N	583903	5162	Hs.161357NM_00092E	ENSG00000PDHB	PDHBD PDF	pyruvate	protein-coding			
chr3-869F 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr3	86977194	86978096	+	0	NA	intron (MER5A DNA	13504 NM_00132C	389136	Hs.606507NM_01620E	ENSG00000VGLL3	VGL-3 VGL	vestigial	protein-coding			
chr4-716F 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr4	76167496	76170733	+	0	NA	intron (intron (N	-20599 NR_103781	53371	Hs.43043E	NR_01742E	ENSG00000CNP54	-	nucleopor	protein-coding		
chr5-113C 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr5	1.14E+08	1.14E+08	+	0	NA	intron (AluSp SIN	19720 NM_00134E	64848	Hs.23194E	NR_02282E	ENSG00000YTHDC2	CAHL HYT	YTH	doma	protein-coding	
chr6-306E 9.408632	0.19468	0.759972	0.256168	0.797821	0.981636	chr6	30628766	30631829	+	0	NA	intron (AluJb SIN	3423 NM_001031	79969	Hs.65479E	NR_02490E	ENSG00000CATAT1	C6orf134 α	tul	protein-coding		
chr6-3061 11.43427	0.178256	0.696075	0.256087	0.797883	0.981636	chr6	30619656	30621966	+	0	NA	intron (AluSx3 SI	2971 NM_01404E	28973	Hs.65532E	NR_01404E	ENSG00000MRP51B	C6orf14 f	mitochnc	protein-coding		
chr1-1097 10.92983	0.181432	0.709492	0.255721	0.798166	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	3726 NR_024537	2947	Hs.20008E	ENSG00000CSTM3	GST5 GSTE	glutathion	protein-coding			
chr1-212F 10.92983	0.181432	0.709492	0.255721	0.798166	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	intron (intron (N	2909 NM_00120E	467	Hs.460	NR_001674	ENSG00000CATF3	-	activatir	protein-coding		
chr12-96E 10.92983	0.181432	0.709492	0.255721	0.798166	0.981636	chr12	96241712	96247742	+	0	NA	exon (NM exon (NM	-8071 NM_00130C	2004	Hs.46523	NR_00523C	ENSG00000ELK3	ERP NET SETS	trans	protein-coding		
chr16-31E 10.92983	0.181432	0.709492	0.255721	0.798166	0.981636	chr16	31912891	31918524	+	0	NA	exon (NM exon (NM	41900 NM_003414	10308	Hs.46064E	NR_003414	ENSG00000ZNF267	HFZ2	zinc	protein-coding		
chr5-134E 10.92983	0.181432	0.709492	0.255721	0.798166	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (AluSq2 SI	32528 NM_02198Z	10802	Hs.59554C	NR_02198Z	ENSG00000SEC24A	-	SEC24	hon	protein-coding	
chr8-431F 9.954217	0.191712	0.750102	0.255581	0.798274	0.981636	chr8	43183114	43185019	+	0	NA	intron (LIPA5 LIN	43602 NM_15241E	138050	Hs.600384NM_15241E	ENSG00000HGSNAT	HGNAT MP	heparan-ε	protein-coding			
chr1-196E 4.460228	-0.27622	1.080887	-0.25555	0.798302	0.981636	chr1	19689726	19690518	+	0	NA	intron (LITR2B LIN	25247 NM_000871	3362	Hs.22180	NR_000871	ENSG00000CHTR6	5-HTf5-1-5	-hydroxy	protein-coding		
chr17-47E 4.460228	-0.27622	1.080887	-0.25555	0.798302	0.981636	chr17	47572069	47573004	+	0	NA	intron (HAL1 LINE	41428 NM_00631C	9520	Hs.443837NM_00631C	ENSG00000NPEPPS	AAP-S MP	laminopept	protein-coding			
chr4-169E 4.460228	-0.27622	1.080887	-0.25555	0.798302	0.981636	chr4	1.7E+08	1.7E+08	+	0	NA	intron (intron (N	17917 NM_00182E	1182	Hs.48118E	NR_00182E	ENSG00000CLCN3	CLC3 CIC	-chloride	protein-coding		
chr1-353E 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr1	35385482	35388234	+	0	NA	intron (L2a LINE	-20781 NR_04665E	1.01E+08	NR_04665E	ENSG00000ZMYM4-AS1	-	ZMYM4	antncRNA			
chr10-10C 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (AluSxl SI	-27601 NM_01789E	57715	Hs.59192E	NR_01789E	ENSG00000SEMA4G	-	semaphor	protein-coding		
chr10-11C 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr10	1.11E+08	1.11E+08	+	0	NA	intron (intron (N	11291 NM_00441E	1847	Hs.2128	NR_00441E	ENSG00000DUSP5	DUSP HVH	dual	spec	protein-coding	
chr11-62E 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr11	62700904	62702058	+	0	NA	intron (MER47A DN	4834 NM_00113C	26580	Hs.53370E	NR_03266E	ENSG00000BSC12	GN3LG HM	BSC12	lε	protein-coding	
chr13-331 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr13	33129098	33131098	+	0	NA	exon (NM exon (NM	55993 NM_00124Z	90627	Hs.156551NM_052851	ENSG00000STARD13	ARHGAP37 StAR	relε	protein-coding			
chr15-58E 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr15	58618959	58620984	+	0	NA	intron (intron (N	73636 NR_07341E	664618	Hs.670224NR_002927	HSP90ABF4	HSP90b	heat	shoc	pseudo		
chr15-61E 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr15	61753067	61756545	+	0	NA	intron (intron (N	-11349 NM_00114E	4088	Hs.72798E	NR_00590E	ENSG00000CSMAD3	HSPC193 F	SMAD	famiprotein-coding		
chr2-131C 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr2	1.31E+08	1.31E+08	+	0	NA	intron (AluSc5 SI	18875 NM_001321	130074	Hs.53467E	NR_00100E	ENSG00000FAMI68B	MAN1	family	wiprotein-coding		
chr3-1231 8.623997	-0.20231	0.792165	-0.25539	0.798423	0.981636	chr3	12315028	12315668	+	0	NA	intron (L1MA5 LIN										

chr2-951	0.449771	0.196088	0.77239	0.253872	0.799594	0.981636	chr2	95107841	95109780	+	0	NA	intron (N LIME3G LI	12747	NM_001321	64969	Hs. 655259	ENSG00000MRP55	MRP-55 SE mitochondrial protein-coding
chr4-5542	0.449771	0.196088	0.77239	0.253872	0.799594	0.981636	chr4	55426612	55426919	+	0	NA	TTS (NM_C TTS (NM_C	30808	NM_018475	55858	Hs. 479766	ENSG00000TMEM165	CDGK2 FT2 transmembrane protein-coding
chr16-351	8.211538	-0.20726	0.816716	-0.25378	0.799667	0.981636	chr16	3515886	3516545	+	0	NA	intron (N intron (N	6321	NM_024793	23059	Hs. 155999	ENSG00000CLUAP1	CFAP22 FA clusterin protein-coding
chr1-5655	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr1	56557317	56558163	+	0	NA	intron (N intron (N	21813	NM_003713	8613	Hs. 405156	ENSG00000PLPP3	DR142 LFP phospholipid protein-coding
chr10-895	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr10	89598178	89599036	+	0	NA	intron (N intron (N	-5795	NR_029524	406901	NR_029524	ENSG00000MIR107	MIRN107 miR microRNA ncRNA
chr10-125	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	TTS (NM_C TTS (NM_C	26747	NM_01818C	55760	Hs. 370292	ENSG00000DXH32	DDX32 DHL DEAH-box protein-coding
chr11-685	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr11	68568560	68569255	+	0	NA	intron (N intron (N	108490	NM_001352	55291	Hs. 503022	ENSG00000PPP6R3	C1orf23 protein [protein] protein-coding
chr15-628	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr15	62820498	62821481	+	0	NA	intron (N intron (N	-2968	NR_029705	406965	NR_029705	ENSG00000MIR190A	MIR190 miR microRNA ncRNA
chr19-104	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr19	10456333	10457162	+	0	NA	intron (N intron (N	3815	NM_006202	5141	Hs. 89901	ENSG00000PDE4A	DPDE2 PDF phosphodiesterase protein-coding
chr7-7511	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr7	75112161	75112689	+	0	NA	exon (NM exon (NM	18393	NM_001368	389524	Hs. 647017	ENSG00000GTF21RD2E	GTF21RD2 GTF2I repressor protein-coding
chr9-1145	4.45237	-0.27331	1.077019	-0.25376	0.799668	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	exon (NM exon (NM	-12450	NM_000607	5004	Hs. 522356	ENSG00000CORM1	AGP-A AGF orosomucoid protein-coding
chr12-716	10.37638	0.185016	0.729094	0.253761	0.799668	0.981636	chr12	71649828	71650349	+	0	NA	intron (N AluY SINE	13760	NM_144982	196441	Hs. 245799	ENSG00000ZFC3H1	CCDC131 Zinc finger protein-coding
chr1-5645	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr1	56499813	56501003	+	0	NA	intron (N L2c LINE	79155	NM_003713	8613	Hs. 405156	ENSG00000PLPP3	DR142 LFP phospholipid protein-coding
chr1-8674	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr1	86741706	86744049	+	0	NA	intron (N AluJb SIN	38301	NM_016005	51100	Hs. 136305	ENSG00000SH3GLB1	Bif-1 CGI SH3 domain protein-coding
chr1-1472	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr1	1.47E+08	1.47E+08	+	0	NA	non-coding non-coding	52435	NM_001348	9557	Hs. 191164	ENSG00000CHD1L	ALC1 CHD1 chromatin protein-coding
chr11-104	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr11	1.05E+08	1.05E+08	+	0	NA	intron (N intron (N	14904	NM_003306	837	Hs. 138378	ENSG00000CASP4	ICE (rel1) caspase 4 protein-coding
chr12-682	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr12	6836770	6839558	+	0	NA	intron (N intron (N	-2761	NM_001297	2784	Hs. 631657	ENSG00000GNB3	CSNB1H G protein-coding
chr12-125	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (N AluSx1 SI	-23537	NR_045382	1.01E+08	Hs. 624255	ENSG00000CLIP1-AS1	CLIP1-AS1 CLIP1 antcncRNA
chr14-505	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr14	50922685	50924074	+	0	NA	intron (N AluSx1 SI	21104	NM_002862	5836	Hs. 282417	ENSG00000PYGL	GSD6 glycogen protein-coding
chr14-512	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr14	51256980	51258405	+	0	NA	TTS (NM_C TTS (NM_C	17445	NM_030755	81542	Hs. 152221	ENSG00000TMX1	PDIA11 Thioredoxin protein-coding
chr14-812	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr14	81214575	81216317	+	0	NA	intron (N Charlie1E	5513	NM_015855	2957	Hs. 592334	ENSG00000GTF2A1	TF2A1 TFII general transcription factor
chr14-921	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr14	92161343	92165074	+	0	NA	3' UTR (N3' UTR (N	41239	NM_001322	53981	Hs. 657632	ENSG00000CPSF2	CPSF100 cleavage factor protein-coding
chr16-728	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr16	72950403	72950774	+	0	NA	exon (NM exon (NM	97540	NM_006885	463	Hs. 598297	ENSG00000ZFHX3	ATBF1 ATF zinc finger protein-coding
chr17-304	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr17	30491838	30497388	+	0	NA	intron (N AluSx1 SI	17205	NM_001007	9527	Hs. 462688	ENSG00000GOSR1	GOLM2 Golggi SNAP protein-coding
chr17-511	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr17	51169803	51172206	+	0	NA	intron (N intron (N	4282	NM_001018	4831	Hs. 463456	ENSG00000NME2	NDBK NDP/NME/NM23 protein-coding
chr17-565	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr17	56948860	56950787	+	0	NA	intron (N intron (N	11227	NM_004645	8161	Hs. 532795	ENSG00000COIL	CLN80 p8 coilin protein-coding
chr17-618	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr17	61959780	61962807	+	0	NA	intron (N AluSx1 SI	-33311	NM_001133C	57508	Hs. 279645	ENSG00000INTS2	INT2 KIAF integrator protein-coding
chr17-675	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr17	67352618	67356459	+	0	NA	intron (N intron (N	12039	NM_002818	5718	Hs. 4295	ENSG00000PSMD12	Rpn5 ST15 proteasome protein-coding
chr18-127	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr18	12706532	12709414	+	0	NA	intron (N intron (N	4931	NM_020232	56984	Hs. 464652	ENSG00000PSMG2	CLAST3 HC proteasome protein-coding
chr19-215	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr19	12367174	12374455	+	0	NA	intron (N intron (N	11814	NM_001355	148203	Hs. 124384	ENSG00000ZNF738	ZNF738 zinc finger protein-coding
chr19-475	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr19	47364725	47368039	+	0	NA	intron (N AluSz SIN	17067	NM_014681	9704	Hs. 151706	ENSG00000DXH34	DDX34 HRE DEXH-box protein-coding
chr2-3924	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr2	39249916	39255759	+	0	NA	intron (N intron (N	-8874	NR_144521	344387	Hs. 403201	ENSG00000CDKL4	cyclin D6 protein-coding
chr2-8503	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr2	85037189	85037859	+	0	NA	intron (N intron (N	29823	NR_146455	1.01E+08	Hs. 434398	ENSG00000LINC01964	long intcncRNA
chr2-1105	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr2	1.11E+08	1.11E+08	+	0	NA	intron (N intron (N	44914	NM_005054	84220	Hs. 469633	ENSG00000CRGPD5	BS-63 BSR/RANBP2 lip protein-coding
chr2-2395	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr2	2.4E+08	2.4E+08	+	0	NA	intron (N LIMEF LIN	-27199	NR_039944	1.01E+08	NR_039944	ENSG00000MIR4786	miR-4786 microRNA ncRNA
chr2-2416	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr2	2.42E+08	2.42E+08	+	0	NA	intron (N intron (N	4550	NM_001192	51078	Hs. 435755	ENSG00000THAP4	CGI-36 NE THAP domain protein-coding
chr3-937	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr3	9370512	9378927	+	0	NA	intron (N intron (N	11665	NM_015453	25917	Hs. 443081	ENSG00000THUMP3	THUMP domain protein-coding
chr3-1007	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr3	1.01E+08	1.01E+08	+	0	NA	intron (N intron (N	35635	NM_001192	10342	Hs. 518122	ENSG00000TFG	HMSNP SPC trafficking protein-coding
chr3-1055	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr3	1.06E+08	1.06E+08	+	0	NA	intron (N intron (N	175957	NM_001167	214	Hs. 591293	ENSG00000ALCAM	CD166 MEM activator protein-coding
chr4-3908	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr4	39081518	39083421	+	0	NA	intron (N intron (N	20237	NM_199035	51088	Hs. 272251	ENSG00000KLHL5	kelch like protein-coding
chr4-3925	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr4	39296119	39297638	+	0	NA	intron (N LIP2 LIN	69184	NM_001204	5981	Hs. 507475	ENSG00000RFC1	A1 CANVAS replicator protein-coding
chr4-825	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr4	1.83E+08	1.83E+08	+	0	NA	intron (N AluSx1 SI	3164	NM_001351	1635	Hs. 138355	ENSG00000CDDT	dCMP deaminase protein-coding
chr5-1282	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (N intron (N	206396	NM_001046	6558	Hs. 162558	ENSG00000SLC12A2	BSC BSC2 soluble cytochrome protein-coding
chr5-1775	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr5	1.78E+08	1.78E+08	+	0	NA	intron (N intron (N	-3938	NM_016222	51428	Hs. 484288	ENSG00000DDX41	NBS MLPF DEAD-box protein-coding
chr6-8722	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr6	87223016	87224703	+	0	NA	intron (N LMC3 LIN	68294	NM_015021	23036	Hs. 44480C	ENSG00000ZNF292	Nbla00365 zinc finger protein-coding
chr6-1437	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (N LIMD2 LIN	47623	NM_001100	9749	Hs. 102471	ENSG00000PACTR2	C6orf35 phosphatase protein-coding
chr7-4796	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr7	47963079	47967261	+	0	NA	3' UTR (N3' UTR (N	14445	NM_001363	3364	Hs. 152983	ENSG00000HUS1	hHUS1 HUS1 checr protein-coding
chr7-7438	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr7	74386486	74391206	+	0	NA	intron (N AluJo SIN	-65060	NM_005685	9569	Hs. 647055	ENSG00000GTF21RD1	BEN CREAM/GTF2I repressor protein-coding
chr8-3841	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr8	38412257	38415065	+	0	NA	exon (NM exon (NM	26530	NM_001199	137994	Hs. 696457	ENSG00000LETM2	SLC55A2 leucine zipper protein-coding
chr9-5716	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr9	5716894	5717546	+	0	NA	intron (N LIMEF LIN	88101	NM_001206	57589	Hs. 21152C	ENSG00000R1C1	CIP150 K1R1C1 home protein-coding
chr9-1122	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr9	1.12E+08	1.12E+08	+	0	NA	intron (N intron (N	-52364	NM_001282	64420	Hs. 494827	ENSG00000SUSD1	sushi domain protein-coding
chr9-1228	8.665137	-0.2	0.788246	-0.25373	0.799706	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (N AluSx1 SI	11997	NM_018833	54542	Hs. 533492	ENSG00000C3H2	MNAB RNFringer finger protein-coding
chr7-1378	9.359634	0.194742	0.767675	0.253677	0.799745	0.981636	chr7	1.38E+08	1.38E+08	+	0	NA	intron (N						



chr13-11: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr13	1.13E+08	1.13E+08	+	0 NA	intron (NLMC1 LIN	-6097 NR_107042	1.02E+08	NR_107042	ENSG000002MIR8075	hsa-mir-ε microRNA	ncRNA
chr14-23: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr14	23087070	23091246	+	0 NA	intron (NLMC1 LIN	-9529 NR_017924	55017 Hs.	525238 NR_017924	ENSG000002C14orf119	-	chromosom protein-coding
chr14-307: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr14	30734939	30736856	+	0 NA	TTS (NM_1TTS (NM_1	113578 NR_016106	23256 Hs.	369168 NR_016106	ENSG000002SCFD1	C14orf16: secl	famiprotein-coding
chr14-35: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr14	35029858	35033601	+	0 NA	Intergeni Intergeni	-13178 NR_001075	283635 Hs.	446357 NR_173607	ENSG000002FAM177A1	C14orf24	famly wiprotein-coding
chr14-60: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr14	60811290	60813841	+	0 NA	intron (NLTR28 LTF	77804 NR_002431	4331 Hs.	509525 NR_002431	ENSG000002MNAT1	CAP35 MA1MNAT1	con protein-coding
chr14-69: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr14	69388220	69396353	+	0 NA	intron (Nintron (N	6013 NR_00445C	2079 Hs.	509791 NR_00445C	ENSG000002CERH	DROER ERH mRNA	protein-coding
chr14-73: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr14	73097434	73103620	+	0 NA	intron (Nintron (N	-35980 NR_000021	5663 Hs.	3260 NR_000021	ENSG000002PSEN1	ACIN1V3 Ppresenil1	protein-coding
chr15-65: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr15	65025392	65027023	+	0 NA	intron (Nintron (N	3432 NR_139242	123263 Hs.	531615 NR_139242	ENSG000002MTFMT	COPXD15 Fmitohonc	protein-coding
chr16-50: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr16	50318446	50322060	+	0 NA	exon (NM exon (NM	27637 NR_10682E	1.02E+08	NR_10682E	ENSG000002MIR6771	hsa-mir-ε microRNA	ncRNA
chr16-69: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr16	69663448	69672487	+	0 NA	intron (NALuSj SIN	40708 NR_14575E	1.1E+08	NR_145753	SNORD13H	-	small nucsnRNA
chr17-16: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr17	16052169	16059851	+	0 NA	intron (NLMC5 LIN	56186 NR_01777E	54902 Hs.	462316 NR_01777E	ENSG000002TTC19	201020401	tetratric protein-coding
chr17-161: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr17	16144905	16145411	+	0 NA	intron (NSVA_B Ret	8038 NR_145787	1.1E+08	NR_145787	SNORD163	-	small nucsnRNA
chr18-93: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr18	9307608	9370249	+	0 NA	intron (NALuSj SIN	33885 NR_02064E	57045 Hs.	514685 NR_02064E	ENSG000002TWSG1	TSG	twisted protein-coding
chr18-21: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr18	21808966	21810285	+	0 NA	intron (NLMB3 LIN	11660 NR_02967E	406922	NR_02967E	ENSG000002MIR133A1	MIR133A1	microRNA
chr19-18: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr19	18864563	18868165	+	0 NA	intron (Nintron (N	29794 NR_001492	2657 Hs.	412355 NR_001492	ENSG000002GDF1	CERS1 CHI	growth diprotein-coding
chr2-55: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr2	55866615	55868984	+	0 NA	intron (Nintron (N	55983 NR_00103E	2202 Hs.	76224 NR_00410E	ENSG000002EFEMP1	DHRD DRAI	EGF cont protein-coding
chr2-61: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr2	61477651	61485095	+	0 NA	intron (NALuSc SIN	-10339 NR_01470E	9736 Hs.	644705 NR_01470E	ENSG000002CUSP34	-	ubiquit protein-coding
chr2-74: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr2	74877015	74877569	+	0 NA	exon (NM exon (NM	-31839 NR_125792	1.03E+08	Hs. 70864E NR_125792	ENSG000002LINC01291	-	long intncRNA
chr2-86: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr2	86160890	86161974	+	0 NA	intron (NALuSj SIN	25562 NR_00437E	692225 Hs.	723087 NR_00437E	ENSG000002SNORD94	U94	small nucsnRNA
chr2-171: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr2	1.71E+08	1.71E+08	+	0 NA	intron (NALuSj SIN	38828 NR_00113E	9874 Hs.	744917 NR_01229C	ENSG000002TLK1	PKU-beta	talled lprotein-coding
chr20-34: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr20	34486037	34497996	+	0 NA	intron (Nintron (N	-24368 NR_00131E	83658 Hs.	59392C NR_01418E	ENSG000002DYNLRB1	BITH BLP	dynein l1protein-coding
chr21-34: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr21	34870734	34875558	+	0 NA	intron (Nintron (N	15553 NR_001001	861 Hs.	149261 NR_00175E	ENSG000002RUNX1	AML1 AML1	RUNX famiprotein-coding
chr22-42: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr22	42632514	42635177	+	0 NA	intron (NALuJo SIN	6756 NR_00116E	267020 Hs.	664737 NR_00116E	ENSG000002ATP5MGL	ATP5K2 A1ATP	syntf protein-coding
chr3-170: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr3	1.7E+08	1.7E+08	+	0 NA	intron (Nintron (N	45814 NR_021497	80012 Hs.	529592 NR_024947	ENSG000002PHC3	EDR3 HPH	polyhomec protein-coding
chr3-183: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr3	1.84E+08	1.84E+08	+	0 NA	intron (NALuJr SIN	18226 NR_001351	55689 Hs.	632575 NR_01802E	ENSG000002YEATS2	-	YEATS dom protein-coding
chr3-197: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr3	1.98E+08	1.98E+08	+	0 NA	intron (Nintron (N	8005 NR_02784C	84248 Hs.	27553E NR_03228E	ENSG000002FYTDD1	UIF	forty-two protein-coding
chr4-68: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr4	68322637	68325054	+	0 NA	intron (Nintron (N	26245 NR_00133C	91746 Hs.	17595E NR_13337C	ENSG000002YTHDC1	YTS21 YTE	YTH dom protein-coding
chr4-118: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (NSVA_B Ret	43239 NR_01482E	9871 Hs.	189641 NR_01482E	ENSG000002SEC24D	CLCRP2	SEC24 hom protein-coding
chr5-103: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr5	10390504	10393364	+	0 NA	intron (Nintron (N	-10430 NR_16210E	1.13E+08	NR_16210E	MIR10397	-	microRNA
chr5-104: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr5	10414969	10417534	+	0 NA	intron (Nintron (N	13887 NR_16210E	1.13E+08	NR_16210E	MIR10397	-	microRNA
chr5-95: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr5	95920046	95925090	+	0 NA	intron (Nintron (N	39283 NR_012081	22936 Hs.	192221 NR_012081	ENSG000002CELL2	MRCRAT1	elongatic protein-coding
chr5-140: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr5	1.12E+08	1.12E+08	+	0 NA	non-codir non-codir	2307 NR_002922	654322 Hs.	68970E NR_002922	ENSG000002SNORA13	ACA13	small nucsnRNA
chr5-142: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr5	1.4E+08	1.4E+08	+	0 NA	exon (NM exon (NM	47419 NR_01797E	54882 Hs.	594084 NR_017747	ENSG000002ANKHD1	MASK MAS5	ankyrin protein-coding
chr5-174: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (Nintron (N	3609 NR_001364	1627 Hs.	13031E NR_00439E	ENSG000002DBN1	DOS117E	drebrin l1protein-coding
chr6-28: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr6	28902563	28906887	+	0 NA	intron (Nintron (N	8240 NR_104117	414760 Hs.	21100E NR_104117	ENSG000002HCG14	dJ111M5.4HLA	complncRNA
chr6-170: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr6	1.7E+08	1.7E+08	+	0 NA	intron (Nintron (N	-6755 NR_039787	1.01E+08	NR_039787	ENSG000002MIR4644	-	microRNA
chr7-29: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr7	29930344	29931796	+	0 NA	intron (Nintron (N	58731 NR_01476E	9805 Hs.	52074C NR_01476E	ENSG000002SCRNI	SES1	secernin protein-coding
chr7-45: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr7	45724147	45729232	+	0 NA	intron (NMER9a2 LI	42329 NR_024271	641977 Hs.	723477 NR_024271	ENSG000002SEPT13	SEPT13	7 pseudo
chr7-75: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr7	75479993	75484322	+	0 NA	intron (NLMC5 LIN	4142 NR_16030E	1E+08	NR_16030E	ENSG000002POM121C	POM121-2	POM121 tr protein-coding
chr7-100: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr7	1E+08	1E+08	+	0 NA	TTS (NM_1TTS (NM_1	14358 NR_00136E	7589 Hs.	632294 NR_145914	ENSG000002ZSCAN21	NY-REN-21	zinc fing protein-coding
chr7-139: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr7	1.39E+08	1.39E+08	+	0 NA	intron (Nintron (N	30979 NR_02011E	56829 Hs.	13351E NR_02011E	ENSG000002C3HAV1	ARTD13 FLI	zinc fing protein-coding
chr7-139: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (NALuSx SIN	99850 NR_00108C	154790 Hs.	57806 NR_00108C	ENSG000002CLEC2L	-	C-type l1protein-coding
chr8-23: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr8	23378989	23379902	+	0 NA	intron (NLIPA5 LIN	24675 NR_00231E	4017 Hs.	626637 NR_00231E	ENSG000002CLOXL2	LOR LOR2	lysyl oxiprotein-coding
chr8-58: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr8	58578966	58582637	+	0 NA	intron (Nintron (N	27540 NR_00562E	6386 Hs.	200804 NR_00562E	ENSG000002SDCBP	MDA-9 MDA9	syndecan protein-coding
chr8-108: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr8	108E+08	1.08E+08	+	0 NA	intron (NALuSx SIN	14477 NR_00156E	3646 Hs.	405594 NR_00156E	ENSG000002EIF3E	EIF3-4 8	eukaryot iprotein-coding
chr8-133: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr8	1.33E+08	1.33E+08	+	0 NA	intron (NMER58A DN	14513 NR_00113E	10397 Hs.	372914 NR_00609E	ENSG000002NDRG1	CAP43 CMI	myc dow protein-coding
chr9-730: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr9	730170	732720	+	0 NA	intron (Nintron (N	24768 NR_001354	23189 Hs.	306764 NR_01515E	ENSG000002KANK1	ANKRD15 CKN	motif protein-coding
chr9-65: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr9	65683089	65683908	+	0 NA	intron (Nintron (N	7570 NR_00136E	220869 Hs.	35595C NR_001024	ENSG000002CBWD5	CBWD3 C5C	COBW dom protein-coding
chr9-70: 8.657279	-0.19844	0.788068	-0.25181	0.801187	0.981636	chr9	70264242	70269609	+	0 NA	intron (NMIR SINE	7947 NR_001511C	23137 Hs.	53418E NR_01511C	ENSG000002SMC5	SMC5L1	structure protein-coding
chr9-11: 8.657279	-0.19844	0.788068															

chr1-2481 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr1	24812478	24813270	+	0	NA	intron (AluSc SIN	67427	NM_013943	25932	Hs. 440544NM_013943	ENSG00000CLIC4	CLIC4L Hichloride protein-coding		
chr1-1147 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr1	1.15E+08	1.15E+08	+	0	NA	non-codirnon-codir	9249	NM_025073	80143	Hs. 709277NM_025073	ENSG00000SIKE1	SIKE suppressor protein-coding		
chr12-754 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr12	75483028	75484285	+	0	NA	intron (NL2c LINE	2901	NM_006851	11010	Hs. 205555NM_006851	ENSG00000GLIPR1	CRISP7 GLI pathc protein-coding		
chr12-76 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr12	76381772	76382848	+	0	NA	intron (NLIME1 LIN	-33895	NM_024688	79738	Hs. 96322NM_024688	ENSG00000BBS10	C12orf58 Bardet-Bi protein-coding		
chr13-973 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr13	97379137	97380050	+	0	NA	intron (NMIR SINE	-54576	NM_021033	5911	Hs. 508489NM_021033	ENSG00000RAP2A	K-REV1 KRF RAP2A, m protein-coding		
chr14-951 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr14	95101697	95102394	+	0	NA	intron (Nintron (N	31458	NM_001195	23405	Hs. 87889NM_030621	ENSG00000DCICER1	DCR1 Dicer 1, protein-coding		
chr15-806 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr15	80591769	80592570	+	0	NA	intron (Nintron (N	11066	NR_049837	1.01E+08	NR_049837	ENSG00000MIR5572	- microRNA ncRNA		
chr16-568 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr16	56822221	56823771	+	0	NA	intron (Nintron (N	-35522	NR_029688	406930	NR_029688	ENSG00000MIR138-2	MIRN138-2 microRNA ncRNA		
chr16-716 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr16	71676457	71678572	+	0	NA	intron (Nintron (N	21187	NR_033337	1.07E+08	Hs. 725111NR_033337	ENSG00000SNORA70D	U70D small nucsnoRNA		
chr17-372 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr17	37235278	37235850	+	0	NA	intron (Nintron (N	-9215	NR_132772	1.07E+08	NR_132772	SNORA90	- small nucsnoRNA		
chr17-825 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr17	82564336	82565001	+	0	NA	intron (NMIR LIR	44936	NM_004514	3607	Hs. 591144NM_004514	ENSG00000FOXK2	ILF1 ILF-1 forkhead protein-coding		
chr19-365 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr19	36509887	36510313	+	0	NA	TTS (NM_C	18171	NM_001166	339324	Hs. 18103NM_001011	ENSG00000ZNF260	OZRP1 PEX zinc fing protein-coding		
chr2-2247 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr2	2.25E+08	2.25E+08	+	0	NA	intron (NMLTIK LTF	151585	NM_00129C	55619	Hs. 46578NM_014688	ENSG00000DOCK10	DRIP2 Nbl dedicator protein-coding		
chr3-7352 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr3	73522493	73523264	+	0	NA	intron (Nintron (N	1556	NR_121666	1.02E+08	Hs. 662045NR_121666	LOC101927-	uncharactercncRNA		
chr5-3151 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr5	31515281	31516773	+	0	NA	intron (NAluJb SIN	16066	NM_013235	29102	Hs. 97997NM_013235	ENSG00000CDROSHA	ETOHI2 HS drosha riprotein-coding		
chr6-1456 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr6	1.46E+08	1.46E+08	+	0	NA	intron (NLMIG LIN	48735	NM_173082	257218	Hs. 723297NM_173082	ENSG00000SHPRH	ba54515.2 SNP2 hist protein-coding		
chr6-147 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr6	1.47E+08	1.47E+08	+	0	NA	intron (NMIR SINE	-115152	NR_132444	1.06E+08	Hs. 57539CNR_132444	ENSG00000LUAD1	- lung adncRNA		
chr7-9954 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr7	99508900	99510381	+	0	NA	intron (NAluY SINE	3635	NM_001318	23660	Hs. 110833NM_014568	ENSG00000ZKSCAN5	ZFP-95 ZF zinc fing protein-coding		
chr7-151 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	intron (NAluSx SIN	6838	NM_001363	51667	Hs. 647082NM_016118	ENSG00000NUIB1	BS4 NUIB1 negative protein-coding		
chr7-151f 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	6755	NM_024425	51422	Hs. 647072NM_016203	ENSG00000PRKAG2	AAKG AAK protein f protein-coding		
chr8-5397 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr8	53971280	53974044	+	0	NA	intron (Nintron (N	49786	NM_0201437	6917	Hs. 491745NM_006758	ENSG00000TCEA1	GTF2S SII transcrip protein-coding		
chr9-1252 4. 444512	-0.27038	1.081078	-0.2501	0.802511	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (NAluSx SIN	8074	NM_00133C	26130	Hs. 42376NM_015633	ENSG00000GAPVD1	GAPX5 GATPase ac protein-coding		
chr17-418 8. 870904	0.196289	0.784952	0.250065	0.802537	0.981636	chr17	4183031	4185312	+	0	NA	intron (Nintron (N	40474	NM_001254	124936	Hs. 513871NM_144611	ENSG00000CYB5D2	- cytochro protein-coding		
chr2-2005 8. 870904	0.196289	0.784952	0.250065	0.802537	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	3' UTR (N3' UTR (N	-17325	NM_00619C	4999	Hs. 44487CNM_00619C	ENSG00000ORC2	ORC2L origin re protein-coding		
chr3-1125 8. 870904	0.196289	0.784952	0.250065	0.802537	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	IntergeniSATR2 Sat	-30055	NM_18178C	151888	Hs. 445162NM_18178C	ENSG00000BTLA	BTLA1 CD2B and T l protein-coding		
chr3-1962 8. 870904	0.196289	0.784952	0.250065	0.802537	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	intron (NAluSx SIN	30920	NM_001312	5130	Hs. 135997NM_005017	ENSG00000PCYT1A	CCTA CT C phosphate protein-coding		
chr4-3984 8. 870904	0.196289	0.784952	0.250065	0.802537	0.981636	chr4	39840302	39841672	+	0	NA	intron (NAluSx SIN	136924	NM_00110C	23244	Hs. 331431NM_01520C	ENSG00000PDS5A	PIG54 SCC PDS5 coe protein-coding		
chr7-661f 8. 870904	0.196289	0.784952	0.250065	0.802537	0.981636	chr7	66158060	66158878	+	0	NA	IntergeniMSTL LIR	43622	NM_014475	27297	Hs. 300684NM_014475	ENSG00000CRCP	CGRP-RCP CGRP recep protein-coding		
chr13-197 7. 895294	0.210797	0.843442	0.249925	0.802645	0.981636	chr13	19738232	19738703	+	0	NA	intron (NMER2 DNA	44478	NM_001354	55269	Hs. 213198NM_001042	ENSG00000PSPC1	PSP1 paraspecl protein-coding		
chr9-1344 7. 895294	0.210797	0.843442	0.249925	0.802645	0.981636	chr9	1.34E+08	1.34E+08	+	0	NA	intron (NAluY SINE	23582	NM_001291	6256	Hs. 590886NM_002957	ENSG00000XRRA	NR2B1 retinoid protein-coding		
chr10-131 9. 928793	0.187269	0.749489	0.249862	0.802694	0.981636	chr10	13115814	13118732	+	0	NA	intron (NAluY SINE	17110	NM_001005	10133	Hs. 332706NM_02198C	ENSG00000OPTN	ALS12 FIF opt neur iprotein-coding		
chr20-381 9. 928793	0.187269	0.749489	0.249862	0.802694	0.981636	chr20	38147373	38151804	+	0	NA	intron (NAluY SINE	15682	NM_001322	7052	Hs. 517033NM_004613	ENSG00000TGM2	GTG TG translu protein-coding		
chr14-717 7. 75794	-0.21494	0.860282	-0.24985	0.802705	0.981636	chr14	71735337	71735900	+	0	NA	intron (NTiger15e	149320	NM_001284	26037	Hs. 654657NM_015556	ENSG00000SIPALL1	E6TP1 SP signal iprotein-coding		
chr12-121 4. 880545	-0.26368	1.055397	-0.24984	0.802715	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	TTS (NM_C	26692	NM_00256C	5025	Hs. 321705NM_00256C	ENSG00000P2RX4	P2X4 P2X4 purinergi protein-coding		
chr13-191 4. 880545	-0.26368	1.055397	-0.24984	0.802715	0.981636	chr13	19989919	19989816	+	0	NA	intron (NAluSx SIN	29553	NR_148366	7750	Hs. 507433NM_003455	ENSG00000ZMYM2	FIM MYM f zinc fing protein-coding		
chr1-731f 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chr1	731035	732077	+	0	NA	IntergeniAluJr SIN	-1205	NR_028327	1E+08	Hs. 728864NR_028327	LOC1010135-	uncharactercncRNA		
chr1-938f 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chr1	93882628	93883750	+	0	NA	IntergeniLIME2 LIN	-3983	NM_014597	30836	Hs. 85769NM_014597	ENSG00000DNTTIP2	ERBP FCF2 deoxy nucl protein-coding		
chr10-887 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chr10	68726776	68729591	+	0	NA	intron (Nintron (N	6944	NM_001282	55749	Hs. 49853NM_018237	ENSG00000CCAR1	cell divi protein-coding		
chr10-84 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chr10	84458966	84459716	+	0	NA	intron (NLMIE1 LIN	34170	NM_001284	54642	Hs. 461988NM_01899C	ENSG00000CCSER2	FAM190B c cell dc protein-coding		
chr2-5393 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chr2	53933699	53934511	+	0	NA	intron (NMLTID LTF	36888	NM_014614	23198	Hs. 413801NM_014614	ENSG00000PSME4	PA200 proteason protein-coding		
chr2-207 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chr2	2.08E+08	2.08E+08	+	0	NA	intron (NMLTID LTF	30416	NM_001371428	-7504	NR_026645	670	Hs. 10136NM_004332	ENSG00000BPPL	BPH-RP MC biphenyl protein-coding
chrX-291f 8. 195822	-0.20396	0.816382	-0.24983	0.802719	0.981636	chrX	291324	291645	+	0	NA	intron (Nintron (N	8006	NM_00137C	55344	Hs. 522568NM_01839C	ENSG00000PLCXD1	LLOXNC01-phosphati protein-coding		
chr7-1497 43. 93386	0.100128	0.400986	0.249703	0.802817	0.981636	chr7	1.5E+08	1.5E+08	+	0	NA	exon (NM exon (NM	8121	NM_20733C	168544	Hs. 726477NM_20733C	ENSG00000ZNF467	EZ1 Zfp467 zinc fing protein-coding		
chr1-1627 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (Nintron (N	-3461	NM_001304	51478	Hs. 492925NM_016371	ENSG00000HSD17B7	MIR3 SDR hydroxyst protein-coding		
chr1-2242 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (NAluJb SIN	7948	NR_031574	1E+08	NR_031574	ENSG00000MIR320B2	MIR320B-2 microRNA ncRNA		
chr11-354 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr11	35448216	35449885	+	0	NA	intron (NLIPIA10 LI	-28992	NM_001195	6506	Hs. 502338NM_004171	ENSG00000SLCIA2	EAAT2 EIE solute c protein-coding		
chr12-62 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr12	62393233	62394335	+	0	NA	intron (NAluSx SIN	-73042	NM_001275	23041	Hs. 389378NM_01502C	ENSG00000MON2	- MON2 homc protein-coding		
chr17-802 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr17	80287439	80131462	+	0	NA	intron (NAluSx SIN	39948	NM_020954	57674	Hs. 195642NM_020914	ENSG00000RNF213	ALO17 C17 ring fing protein-coding		
chr3-4935 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr3	49396200	49396821	+	0	NA	intron (NAluSx SIN	15466	NM_001313	387	Hs. 247077NM_001664	ENSG00000RHOA	ARH12 ARF ras homol protein-coding		
chr5-166 10. 39996	0.18074	0.725682	0.249062	0.803313	0.981636	chr5	16692730	16695158	+	0	NA	intron (Nintron (N	-76886	NM_001034	54463	Hs. 481704NM_01900C	ENSG00000RETREG1	FAM134B J reticulof protein-coding		
chr10-622 7. 750082	-0.21325	0.856558	-0.24986	0.803393	0.981636	chr10	62005988	62006456	+	0	NA	intron (NAluSx SIN	41335	NM_001244	84159	Hs. 535297NM_032199	ENSG00000ARID5B	DESRT MRF AT-rich iprotein-coding		
chr1-8901 8. 649421	-0.19687	0.790847	-0.24893	0.8																



chr14-212 8.878762	0.194548	0.78856	0.246713	0.805131	0.981636	chr14	21257662	21257959	+	0 NA	intron (NA)uJr4 SI	11669 NM_031314	3183 Hs. 50884ENM_00450C	ENSG00000CHNRNPC	C1 C2 HNF	heteroger protein-coding	
chr19-196 8.878762	0.194548	0.78856	0.246713	0.805131	0.981636	chr19	19658522	19659447	+	0 NA	intron (N)intron (N)	4692 NM_02041C	57130 Hs. 501794NM_02041C	ENSG00000ATP13A1	ATP13A CCATPase 1	protein-coding	
chr10-322 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr10	32290096	32291084	+	0 NA	intron (N)intron (N)	56568 NM_001272	80314 Hs. 16780ENM_02520E	ENSG00000CEPC1	Epl1	enhancer protein-coding	
chr10-736 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr10	73674374	73675969	+	0 NA	exon (NM)exon (NM)	-19142 NM_001114	79933 Hs. 64527ENM_02487E	ENSG00000SYNP02L	-	synaptoz protein-coding	
chr11-65 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr11	65920814	65923981	+	0 NA	TTS (NM_C)TTS (NM_C)	2971 NM_006442	10589 Hs. 356742NM_006442	ENSG00000DRAP1	NC2-alphaDR1	assoc protein-coding	
chr12-164 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr12	1645873	1648996	+	0 NA	TTS (NM_C)TTS (NM_C)	12946 NR_037422	1.01E+08	NR_037422	ENSG00000CIR3649	-	microRNA ncRNA
chr12-132 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr12	1.32E+08	1.32E+08	+	0 NA	intron (N)intron (N)	10054 NR_003299	347918 Hs. 12211ENM_18261E	ENSG00000EP400P1	EP400NL	EP400 pscpseudo	
chr12-139 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr12	1.33E+08	1.33E+08	+	0 NA	intron (N)intron (N)	10912 NM_015114	23141 Hs. 65462ENM_015114	ENSG00000ANKLE2	KIAA0692 ankyrin	intron protein-coding	
chr13-113 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr13	1.13E+08	1.14E+08	+	0 NA	exon (NM)exon (NM)	9023 NM_00134E	55002 Hs. 31759ENM_01790E	ENSG00000TMC03	C13orf11	transmemt protein-coding	
chr15-51 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr15	15920916	15903716	+	0 NA	intron (N)intron (N)	28084 NR_10977E	1E+08 Hs. 66478ENR_10977E	LOC100422-	LE01	homopseudo	
chr15-56 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr15	56093014	56095896	+	0 NA	exon (NM)exon (NM)	95477 NM_00137C	64864 Hs. 74508ENM_02284E	ENSG00000CRFX7	RFXC2	regulator protein-coding	
chr15-632 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr15	63588596	63590544	+	0 NA	intron (N)HALIME LI	-7817 NM_001367	283807 Hs. 63116ENM_20337E	ENSG00000FBXL22	Fb122	F-box anc protein-coding	
chr15-96 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr15	96334008	96336742	+	0 NA	intron (N)intron (N)	1610 NM_00114E	7026 Hs. 347991NM_02100E	ENSG00000NR2F2	ARP-1 ARF	nucleic acid protein-coding	
chr17-424 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr17	42469658	42472721	+	0 NA	intron (N)AluY SINE	12311 NM_001547	535 Hs. 463074NM_005177	ENSG00000ATP6VOA1	ATP6N1 A1ATPase H	protein-coding	
chr19-324 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr19	324230	332427	+	0 NA	intron (N)LMC LINE	16513 NM_00134E	54531 Hs. 101891NM_01755E	ENSG00000MIER2	KIAA1193 MIER	famiprotein-coding	
chr2-1044 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr2	10440084	10444830	+	0 NA	intron (N)intron (N)	4392 NR_028374	1E+08 Hs. 73052ENR_028374	ENSG00000SNORA80B	ACA67B	small nucsnoRNA	
chr2-438 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr2	43887764	43889863	+	0 NA	intron (N)intron (N)	49842 NM_022437	64241 Hs. 413931NM_022437	ENSG00000ACBC68	GBD4 STSL	ATP bindiprotein-coding	
chr2-860 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr2	86032909	86034005	+	0 NA	intron (N)intron (N)	72429 NM_01542E	25885 Hs. 53181ENM_01542E	ENSG00000POLR1A	A190 AFDC	RNA polynprotein-coding	
chr3-1031 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr3	10311014	10319341	+	0 NA	intron (N)intron (N)	5864 NM_00113E	6396 Hs. 166924NM_03067E	ENSG00000SEC13	D3S1231E SEC13	homprotein-coding	
chr3-581 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr3	5818050	58115146	+	0 NA	intron (N)intron (N)	59037 NR_135534	1.05E+08 Hs. 613914NR_135534	ENSG00000FLNB-AS1	-	FLNB anticrRNA	
chr3-155 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr3	1.56E+08	1.56E+08	+	0 NA	intron (N)LMBB LIN	45739 NM_00387E	8833 Hs. 591314NM_00387E	ENSG00000GMP5	GATD7	guanine nprotein-coding	
chr4-580 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr4	5808426	5812928	+	0 NA	intron (N)intron (N)	77136 NM_00128E	1400 Hs. 13527NM_00131E	ENSG00000CRMP1	CRMP-1 DF	collapsir protein-coding	
chr6-154 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr6	1.55E+08	1.55E+08	+	0 NA	exon (NM)exon (NM)	-21139 NR_03610C	NR_03610C	ENSG00000MIR1273C	-	microRNA ncRNA	
chr7-139 9.152017	-0.18979	0.769471	-0.24666	0.805175	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (N)LMBA LIN	63107 NM_00108C	154790 Hs. 57806 NM_00108C	ENSG00000CLEC2L	-	C-type 1e protein-coding	
chr1-156 11.88787	0.167928	0.681258	0.246498	0.805297	0.981636	chr1	1.56E+08	1.56E+08	+	0 NA	intron (N)L3 LINE C	-17130 NM_001004	391104 Hs. 53237ENM_001004	ENSG00000VHLL	VHLP VLP	VHL like protein-coding	
chr11-66 11.88787	0.167928	0.681258	0.246498	0.805297	0.981636	chr11	66054034	66068084	+	0 NA	intron (N)AluSx1 SI	7915 NR_145738	1.1E+08	NR_145738	SNORD13F	-	small nucsnoRNA
chr19-344 11.88787	0.167928	0.681258	0.246498	0.805297	0.981636	chr19	34943418	34944318	+	0 NA	exon (NM)exon (NM)	16965 NR_02401E	90075 Hs. 657402NM_19432E	ENSG00000ZNF30	KOX28	zinc fingprotein-coding	
chr3-1841 9.572334	-0.18778	0.762104	-0.2464	0.805371	0.981636	chr3	1.84E+08	1.84E+08	+	0 NA	3' UTR (N)3' UTR (N)	-3025 NM_001311	1173 Hs. 51846CNM_00406E	ENSG00000AP2M1	AP50 CLAF	adaptor r protein-coding	
chr15-305 8.187964	-0.2022	0.821098	-0.24625	0.805486	0.981636	chr15	30923460	30923785	+	0 NA	intron (N)intron (N)	19707 NM_014967	22909 Hs. 58486ENM_014967	ENSG00000CFAN1	KIAA1018 FANCD2	ar protein-coding	
chr14-311 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr14	31126335	31127940	+	0 NA	intron (N)AluSx1 SI	80656 NM_01538E	25831 Hs. 708017NM_01538E	ENSG00000HECTD1	EULR	HECT dom protein-coding	
chr15-827 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr15	82754707	82756413	+	0 NA	promoter-promoter-	-385 NR_003011	677778 Hs. 74389ENR_003011	ENSG00000SCARNA15	ACA45	small Ca_ncRNA	
chr3-1697 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr3	1.7E+08	1.7E+08	+	0 NA	intron (N)intron (N)	11902 NM_00118E	55892 Hs. 50702ENM_01865E	ENSG00000MYNN	OSZF SBB1	myoneurir protein-coding	
chr4-533 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr4	53397916	53401505	+	0 NA	intron (N)intron (N)	22057 NM_001134	81608 Hs. 55510ENM_030917	ENSG00000FIP1L1	FIP1 Rhe	factor ir protein-coding	
chr6-365 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr6	36505070	36506739	+	0 NA	intron (N)Charlie2C	41575 NM_007271	11329 Hs. 40957ENM_007271	ENSG00000CTK38	NDR NDR1	serine/tf protein-coding	
chr8-263 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr8	26394902	26396436	+	0 NA	intron (N)LIPI2 LIN	5256 NM_00133C	665 Hs. 13122ENM_00433E	ENSG00000BNIP3L	BNIP3a NBCL2	inte protein-coding	
chr8-144 8.690561	-0.19456	0.790611	-0.24609	0.805615	0.981636	chr8	1.45E+08	1.45E+08	+	0 NA	intron (N)intron (N)	6491 NR_00695E	7564 Hs. 49322ENM_00695E	ENSG00000ZNF16	HZF1 KOX	zinc fingprotein-coding	
chr14-32 4.872687	-0.2611	0.062587	-0.24572	0.805896	0.981636	chr14	32095694	32096062	+	0 NA	intron (N)intron (N)	18574 NM_00117E	394 Hs. 59231ENM_00117E	ENSG00000CARHGAP5	GF12 RhoC	Rho GTPas protein-coding	
chr1-201 12.40018	0.164343	0.66883	0.245717	0.805901	0.981636	chr1	2.02E+08	2.02E+08	+	0 NA	intron (N)intron (N)	6437 NM_00633E	10440 Hs. 20716 NM_00633E	ENSG00000TIMM17A	TIM17 TIM	translocac protein-coding	
chr19-444 12.40018	0.164343	0.66883	0.245717	0.805901	0.981636	chr19	44477193	44487672	+	0 NA	intron (N)intron (N)	18090 NM_01325E	7733 Hs. 22305 NM_01325E	ENSG00000ZNF180	HZH168	zinc fing protein-coding	
chr17-213 10.40782	0.179281	0.729923	0.245616	0.805979	0.981636	chr17	21308058	21312300	+	0 NA	intron (N)AluSp SIN	22143 NM_00275E	5606 Hs. 51401ENM_00275E	ENSG00000MAP2K3	MAPKK3 MF	mitogen-ε protein-coding	
chr2-1018 10.40782	0.179281	0.729923	0.245616	0.805979	0.981636	chr2	1.02E+08	1.02E+08	+	0 NA	intron (N)intron (N)	-112727 NR_103791	1.01E+08 Hs. 51624ENR_103791	LINC01127-	-	long intncRNA	
chr20-354 10.40782	0.179281	0.729923	0.245616	0.805979	0.981636	chr20	35406987	35410053	+	0 NA	intron (N)LMB3 LIN	3453 NM_018244	55245 Hs. 72629CNM_018244	ENSG00000UQC1	BFZB C20c	ubiquitin protein-coding	
chr22-502 10.40782	0.179281	0.729923	0.245616	0.805979	0.981636	chr22	50278142	50282043	+	0 NA	intron (N)intron (N)	-9712 NR_110887	5600 Hs. 57732 NM_002751	ENSG00000MAPK11	P38B P38E	mitogen-ε protein-coding	
chr7-7541 10.40782	0.179281	0.729923	0.245616	0.805979	0.981636	chr7	75416792	75419161	+	0 NA	3' UTR (N)3' UTR (N)	7654 NR_10401E	155400 Hs. 436034NM_00103E	ENSG00000NSUN5P1	NSUN5B WE	NSUN5 pscpseudo	
chr7-128 10.40782	0.179281	0.729923	0.245616	0.805979	0.981636	chr7	1.29E+08	1.29E+08	+	0 NA	intron (N)intron (N)	15966 NR_14905E	1.11E+08 Hs. 73592ENR_14905E	ENSG00000FLNC-AS1	-	FLNC anticrRNA	
chr2-691 11.42457	0.171786	0.699463	0.245597	0.805994	0.981636	chr2	69101989	69105597	+	0 NA	TTS (NR_C)TTS (NR_C)	111 NR_03607E	NR_03607E	ENSG00000MIR3126	mir-3126	microRNA ncRNA	
chr12-306 9.10302	-0.19051	0.775874	-0.24554	0.806038	0.981636	chr12	30630486	30631002	+	0 NA	3' UTR (N)3' UTR (N)	46500 NM_00119C	10526 Hs. 50513ENM_00639C	ENSG00000IPOS	RANBP8	importin protein-coding	
chr1-2017 11.38343	0.170538	0.694747	0.245468	0.806094	0.981636	chr1	2.02E+08	2.02E+08	+	0 NA	intron (N)TGn Sin	-1563 NR_03159E	1E+08	NR_03159E	ENSG00000MIR1231	MIRN1231	microRNA ncRNA
chr11-281 11.38343	0.170538	0.694747	0.245468	0.806094	0.981636	chr11	28173004	28174453	+	0 NA	intron (N)LMC3 LIN	65340 NM_15263E	196074 Hs. 24332ENM_15263E	ENSG00000METTL15	METT5D1	methyltr protein-coding	
chr13-422 11.38343	0.170538	0.694747	0.245468	0.806094	0.981636	chr13	42298644	42300029	+	0 NA	intron (N)intron (N)						

chr15-41	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr15	41094636	41095959	+	0	NA	intron (AluSq2 SI	20949	NR_10403E	54617	Hs.29294ENM_01755	ENSG00000	IN080	IN080A IN	IN080	conprotein-coding
chr15-807	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr15	80724979	80726313	+	0	NA	intron (AluJo SIN	30336	NM_021214	58489	Hs.459072NM_021214	ENSG00000	ABHD17C	FAM108C1	abhydrolase protein-coding	
chr19-374	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr19	37462500	37465139	+	0	NA	intron (Tigger3b	3625	NM_00133C	148266	Hs.51184ENM_152484	ENSG00000	ZNF569	ZAP1 ZNF	zinc finger protein-coding	
chr2-993	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr2	99390460	99391534	+	0	NA	intron (Tigger2a	53608	NM_015904	9669	Hs.15868ENM_015904	ENSG00000	E1F5B	IF2	eukaryotic protein-coding	
chr4-308	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr4	30890800	30892524	+	0	NA	intron (AluY SINE	14622	NM_002111	3064	Hs.51845ENM_002111	ENSG00000	CTH	HD IT15 I	huntingtin protein-coding	
chr6-1091	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr6	1.09E+08	1.09E+08	+	0	NA	intron (LIPA3 LIN	-17472	NR_15243E	221262	Hs.373914NM_173671	ENSG00000	CCDC162P	C6orf183	coiled-co pseudo	
chr9-9501	0.682703	-0.193	0.790432	-0.24417	0.8071	0.981636	chr9	95019731	95022140	+	0	NA	intron (AluJb SIN	-44415	NR_106722E	1.02E+08	NR_106722ENSG00000	MIR6081	hsa-mir-6	microRNA ncRNA		
chr10-500	0.87898	0.173391	0.710403	0.244075	0.807173	0.981636	chr10	50097763	50101968	+	0	NA	intron (intron (N	31911	NM_00100E	387680	Hs.36528ENM_01823E	ENSG00000	WASHC2A	FAM21A F	WASH comp protein-coding	
chr14-754	0.605616	-0.18416	0.754847	-0.24397	0.807253	0.981636	chr14	75444223	75444952	+	0	NA	intron (MIRc SINE	12453	NM_00113E	122953	Hs.19648ENM_13046E	ENSG00000	JDP2	JUNDM2	Jun dimer protein-coding	
chr14-819	0.605616	-0.18416	0.754847	-0.24397	0.807253	0.981636	chr14	81527480	81527488	+	0	NA	intron (L1MC5a LI	9289	NM_00506E	6400	Hs.18130ENM_00506E	ENSG00000	SEELL	Hrd3 PRO1	SEELL adex protein-coding	
chr7-1001	0.605616	-0.18416	0.754847	-0.24397	0.807253	0.981636	chr7	1E+08	1E+08	+	0	NA	intron (AluJo SIN	7771	NM_001364	6800	Hs.48930ENM_00564E	ENSG00000	TAF6	ALYUS MG	CATATA-box protein-coding	
chr14-607	0.564476	-0.18639	0.764484	-0.24381	0.807379	0.981636	chr14	60718908	60720545	+	0	NA	intron (intron (N	4625	NM_01742C	51804	Hs.97849	NM_01742C	ENSG00000	SIX4	AREC3	SIX homec protein-coding
chr3-494	0.374316	0.199505	0.818363	0.243786	0.807397	0.981636	chr3	49403115	49403727	+	0	NA	intron (intron (N	8555	NM_00131E	387	Hs.247077NM_001664	ENSG00000	RHOA	ARH12 AR	ras homol protein-coding	
chr1-210	0.92012	0.174657	0.716792	0.243665	0.80749	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (L1PA7 LIN	128848	NM_00206E	56776	Hs.24889	NM_00206E	ENSG00000	FMN2	-	formin 2 protein-coding
chr12-13	12.40803	0.163146	0.670071	0.243476	0.807637	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	intron (L1MA6 LIN	22969	NM_00130C	7699	Hs.181552NM_00344C	ENSG00000	ZNF140	pHZ-39	zinc finger protein-coding	
chr20-33	9.349926	0.186889	0.768186	0.243286	0.807784	0.981636	chr20	33381711	33382106	+	0	NA	intron (L1MD3 LIN	19611	NM_01640E	51654	Hs.435952NM_01608E	ENSG00000	CDK5RAP1	C20orf34	CDK5 regu protein-coding	
chr1-1557	9.90337	0.1828	0.751431	0.24327	0.807797	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (intron (N	5962	NR_024117	1E+08	Hs.656361NR_024117	MSTO21P	MSTO2	misato f pseudo		
chr11-10	9.90337	0.1828	0.751431	0.24327	0.807797	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (AluJr SIN	-41300	NR_00001E	38	Hs.23237ENM_00001E	ENSG00000	ACAT1	ACAT MAT	acetyl-Cc protein-coding	
chr1-151	11.39128	0.169231	0.69612	0.243107	0.807923	0.981636	chr1	1.52E+08	1.52E+08	+	0	NA	intron (L1MA2 LIN	46483	NM_00117E	11189	Hs.26047	NM_00718E	ENSG00000	CELF3	BRUNOL1	CUGBP E1e protein-coding
chr19-52	11.39128	0.169231	0.69612	0.243107	0.807923	0.981636	chr19	52543596	52560999	+	0	NA	intron (AluY SINE	-17976	NM_01826C	55762	Hs.235167NM_01826C	ENSG00000	ZNF701	-	zinc finger protein-coding	
chr20-10	11.39128	0.169231	0.69612	0.243107	0.807923	0.981636	chr20	10639060	10649648	+	0	NA	intron (intron (N	5341	NR_10693C	1.02E+08	NR_10693CENSG00000	MIR6870	hsa-mir-6	microRNA ncRNA		
chr7-102	11.39128	0.169231	0.69612	0.243107	0.807923	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (intron (N	4286	NM_001097	548644	Hs.61025ENM_00101E	ENSG00000	POLR2J3	POLR2J2 F	RNA polyn protein-coding	
chr20-50	8.837622	0.192897	0.793507	0.243095	0.807932	0.981636	chr20	50923389	50923851	+	0	NA	intron (AluSx SIN	-7364	NR_11000E	1.02E+08	Hs.30189ENR_11000E	ENSG00000	ADNP-AS1	-	ADNP anticRNA	
chr2-3327	9.86223	0.181445	0.746797	0.242965	0.808033	0.981636	chr2	33276249	33277194	+	0	NA	intron (AluS6 SI	-141745	NR_03962E	1.01E+08	NR_03962ENSG00000	MIR4430	-	microRNA ncRNA		
chr22-387	9.86223	0.181445	0.746797	0.242965	0.808033	0.981636	chr22	38727984	38729345	+	0	NA	intron (intron (N	22720	NM_00428E	9567	Hs.27692ENM_00428E	ENSG00000	GTPBP1	GP-1 GPI	GTP bindi protein-coding	
chr6-756	9.86223	0.181445	0.746797	0.242965	0.808033	0.981636	chr6	75627114	75627324	+	0	NA	intron (AluSx SIN	25339	NM_015571	26054	Hs.485784NM_015571	ENSG00000	SENP6	SSP1 SUS	SUMO spec protein-coding	
chr12-11	4.477794	-0.26283	1.081833	-0.24295	0.808046	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	TTS (NR_1TTS (NR_1	396	NR_106921	1.02E+08	NR_106921ENSG00000	MIR6861	hsa-mir-6	microRNA ncRNA		
chr22-451	4.477794	-0.26283	1.081833	-0.24295	0.808046	0.981636	chr22	45151164	45151729	+	0	NA	intron (Charlie1E	1138	NR_038957	1.01E+08	Hs.18990ENR_03895E	NUP50-DT	NUP50-AS1 NUP50	divncRNA		
chr4-107	4.477794	-0.26283	1.081833	-0.24295	0.808046	0.981636	chr4	1.08E+08	1.08E+08	+	0	NA	intron (L1PA4 LIN	43749	NR_00544E	9061	Hs.36861ENM_00544E	ENSG00000	PAPSS1	ATL3 P3'	phosph protein-coding	
chr1-8494	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr1	8494816	8496146	+	0	NA	promoter-promoter-	-568	NR_13275E	1.07E+08	NR_13275E	SNORD128	Z3K3	small nucsnRNA		
chr1-269	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr1	26924080	26927208	+	0	NA	intron (intron (N	3901	NM_00660C	10726	Hs.26381ENM_00660C	ENSG00000	NUDC	HNUDC MN	nuclear c protein-coding	
chr1-394	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr1	39432533	39434744	+	0	NA	intron (intron (N	24565	NM_01503E	643314	Hs.65876ENM_01503E	ENSG00000	KIAA0754	-	KIAA0754 protein-coding	
chr11-11	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr11	1.1E+08	1.1E+08	+	0	NA	intron (intron (N	62985	NM_00126C	5962	Hs.263671NM_00290E	ENSG00000	RDX	DFNB24	radixin protein-coding	
chr11-11	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (AluSg SIN	3931	NM_00102E	6230	Hs.51267ENM_00102E	ENSG00000	CRPS25	S25	ribosomal protein-coding	
chr11-12	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr11	1.25E+08	1.25E+08	+	0	NA	intron (intron (N	3416	NR_016021	84897	Hs.43641ENM_03281E	ENSG00000	TBRG1	NIAM TB	E-growth protein-coding	
chr12-55	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr12	55757348	55761134	+	0	NA	intron (intron (N	16119	NM_005811	10220	Hs.60088ENM_00581E	ENSG00000	GDF11	BMP-11 B	growth di protein-coding	
chr12-13	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (AluJb SIN	7603	NR_00329C	347918	Hs.12211ENM_18261E	ENSG00000	CEP400P1	EP400NL	EP400 pse pseudo	
chr13-49	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr13	49923581	49926980	+	0	NA	intron (AluSx4 SI	11060	NM_00204E	57213	Hs.44235	NM_02045E	ENSG00000	SPRYD7	C13orf1	(SPRYD) protein-coding
chr13-11	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	exon (NM exon (NM	-11035	NM_00127E	8451	Hs.33973ENM_00358E	ENSG00000	CUL4A	-	cullin 4 protein-coding	
chr15-484	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr15	48441377	48448493	+	0	NA	intron (intron (N	112738	NM_00194E	1854	Hs.52798ENM_00194E	ENSG00000	CDUT	dUTPase	deoxyuric protein-coding	
chr16-7	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr16	75021304	75021435	+	0	NA	intron (AluSq2 SI	22210	NM_003226E	84937	Hs.427284NM_03226E	ENSG00000	ZNRF1	NIN283	zinc and protein-coding	
chr17-41	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr17	41912731	41939112	+	0	NA	intron (intron (N	48895	NM_001254	124936	Hs.513871NM_14461E	ENSG00000	CYB5D2	-	cytochon protein-coding	
chr17-54	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr17	5476525	5482565	+	0	NA	intron (intron (N	6633	NM_016041	51009	Hs.286131NM_016041	ENSG00000	CERL2	CGI-101 E	derlin 2 protein-coding	
chr17-16	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr17	16029433	16031313	+	0	NA	TTS (NM_1TTS (NM_C	30549	NM_01777E	54902	Hs.46231ENM_01777E	ENSG00000	TTC19	201020401	tetratric protein-coding	
chr17-68	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr17	68515424	68519726	+	0	NA	intron (THEIC LTF	2181	NM_00127E	5573	Hs.28034ENM_002734	ENSG00000	PRKARIA	ACRDY51 A	protein k protein-coding	
chr18-27	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr18	27575529	2778895	+	0	NA	intron (intron (N	-69760	NM_03204E	84034	Hs.53281ENM_03204E	ENSG00000	EMILIN2	EMILIN-2 E	elastin protein-coding	
chr19-47	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr19	4710601	4713270	+	0	NA	intron (MLT1D LTF	11907	NR_15869E	91039	Hs.515081NM_13915E	ENSG00000	DP9P	DP9 DPLP	di peptide protein-coding	
chr2-324	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr2	32405525	32409508	+	0	NA	intron (intron (N	50538	NM_01625E	57448	Hs.150107NM_01625E	ENSG00000	BIRC6	APOLLON E	baculovir protein-coding	
chr2-674	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr2	67402850	67406452	+	0	NA	exon (NM exon (NM	7318	NM_019002	54465	Hs.35302ENM_01900E	ENSG00000	ETAA1	ETAA1E	act protein-coding	
chr2-127	9.136301	-0.18683	0.769096	-0.24292	0.808068	0.981636	chr2	1.28E+08														



chr15-49c	10.8457	0.170685	0.714017	0.239049	0.811068	0.981636	chr15	49042345	49043093	+	0	NA	intron (Nintron (N	3727	NM_001193	9728	Hs.9997	NM_014701	ENSG000003SECISBP2 SBP2L SLF SECIS	bir protein-coding			
chr6-130s	10.8457	0.170685	0.714017	0.239049	0.811068	0.981636	chr6	1.31E+08	1.31E+08	+	0	NA	intron (NMLT1A LI	16696	NM_00135C	2037	Hs.48647C	NM_001431	ENSG000003EPB41L2	4.1-G 4.lerythrocyprotein-coding			
chr1-262f	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr1	26268335	26270166	+	0	NA	promoter-promoter-	-29	NM_001281	64793	Hs.63795	NM_02277E	ENSG000003CEP85	CCDC21 centrosonprotein-coding			
chr1-518z	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr1	51822965	51823183	+	0	NA	intron (Nintron (N	13013	NR_03158C	1E+08	NR_03158C	ENSG000003MIR761	hsa-mir-761	miRNA ncRNA			
chr1-846e	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr1	84650296	84652166	+	0	NA	intron (NAluJo SIN	-1621	NR_027375	439927	Hs.407054	NM_001033	ENSG000003LINC01555E	ClaMir180 long	intcncRNA		
chr11-62f	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr11	62516782	62538745	+	0	NA	exon (NM_exon (NM_	17901	NM_00134E	79026	Hs.50275E	NM_00162C	ENSG000003AHNAK	AHNAK FAHNAK	nucprotein-coding		
chr12-57f	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr12	57530107	57530534	+	0	NA	TTS (NM_CTS (NM_C	7496	NM_052897	114785	Hs.52425E	NM_052897	ENSG000003MBD6	methy1-Cp	protein-coding		
chr17-26f	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr17	2669555	2678961	+	0	NA	exon (NM_exon (NM_	18661	NR_106834	1.02E+08	NR_106834	ENSG000003MIR6776	hsa-mir-6776	miRNA ncRNA			
chr19-56z	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr19	56372856	56377780	+	0	NA	intron (Nintron (N	-6935	NM_001322	79149	Hs.17768E	NM_02430E	ENSG000003ZSCAN5A	ZNF495 Z	zinc fing	protein-coding	
chr4-770C	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr4	77003952	77006858	+	0	NA	intron (Nintron (N	55653	NM_00130C	55752	Hs.128199	NM_01824E	ENSG000003SEPTIN11	11-Sep	septin 11	protein-coding	
chr5-128f	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr5	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	18266	NM_001199E	2201	Hs.519294	NM_001199E	ENSG000003FBN2	CCA DA9 F	fibrillir	protein-coding	
chr8-130C	9.63104	-0.17924	0.750746	-0.23874	0.811304	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	28455	NR_04538E	1.01E+08	Hs.10601E	NR_04538E	ENSG000003ASAP1-IT2	ASAP1	intcncRNA		
chr19-21C	11.87031	0.162967	0.682754	0.238691	0.811345	0.981636	chr19	21054762	21057931	+	0	NA	intron (NAluSx SIN	-25801	NR_117087	148206	Hs.72918E	NM_18251E	ENSG000003ZNF714	zinc	fing	protein-coding	
chr16-21C	10.33339	0.175072	0.733626	0.238639	0.811385	0.981636	chr16	21054958	21835238	+	0	NA	exon (NM_exon (NM_	-14613	NM_018427	54700	Hs.46007E	NM_018427E	ENSG000003RRN3	A-270G1.2	RRN3	home	protein-coding
chr1-330I	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr1	33012299	33014703	+	0	NA	intron (Nintron (N	23382	NM_001119E	204	Hs.470907	NM_00162E	ENSG000003CAK2	ADK2	adenylate	protein-coding	
chr1-113E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr1	1.14E+08	1.14E+08	+	0	NA	intron (NLM1A1 LIN	-11814	NM_00128E	56944	Hs.9315	NM_02019C	ENSG000003OLFML3	HNOEL-isc	olfactome	protein-coding	
chr10-30C	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr10	30032984	30034652	+	0	NA	intron (Nintron (N	25768	NM_00135E	57608	Hs.53395E	NM_02084E	ENSG000003JCAD	KIAA1462	junctione	protein-coding	
chr10-74I	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr10	74111066	74113538	+	0	NA	intron (Nintron (N	38256	NM_00132C	26985	Hs.500104	NM_01209E	ENSG000003AP3M1	-	adaptor	r	protein-coding
chr11-337E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr11	33732251	33733380	+	0	NA	intron (NMLT1E2 LI	3664	NM_203331	966	Hs.27857E	NM_000611	ENSG000003CD59	16.3A5 F	CD59	mole	protein-coding
chr12-64E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr12	64050825	64051379	+	0	NA	intron (NLMC5a LI	171194	NM_00130C	144577	Hs.444671	NM_15244C	ENSG000003C12orf66	-	chromoson	protein-coding	
chr13-327E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr13	32761070	32762004	+	0	NA	intron (NLM1E4b LI	150565	NR_04702C	1.01E+08	Hs.40629C	NR_04702C	LINC0042E	-	long	intcncRNA	
chr13-99E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr13	99508721	99509626	+	0	NA	intron (NMSTA-int	7701	NM_00480C	9375	Hs.60789E	NM_00480C	ENSG000003TM9SF2	P76	transmem	protein-coding	
chr15-42E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr15	42258303	42268608	+	0	NA	intron (NLM1B4 LIN	9978	NM_015497	25963	Hs.51113E	NM_015497E	ENSG000003TMEM87A	-	transmem	protein-coding	
chr15-42E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr15	42972070	42973528	+	0	NA	intron (NLM1C1 LIN	-52021	NM_17350C	146057	Hs.646511	NM_17350C	ENSG000003TTRK2	SCA11 TTE	tau	tubul	protein-coding
chr17-84E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr17	8466751	8468871	+	0	NA	3' UTR (N3' UTR (N	31927	NM_03080E	81565	Hs.37212E	NM_03080E	ENSG000003NDEL1	EOPA MIT	nude	nu	protein-coding
chr17-304I	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr17	30479583	30481014	+	0	NA	intron (NAluSx SIN	2890	NM_001007	9527	Hs.46268C	NM_004871	ENSG000003GOSR1	GOLM12 G	golgi	SN	protein-coding
chr2-365I	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr2	36514690	36519541	+	0	NA	intron (NLM1C1 LIN	81053	NM_001042	9637	Hs.25856E	NM_00510E	ENSG000003FEZ2	HUM3CL	fascicul	protein-coding	
chr2-203A	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	exon (NM_exon (NM_	45606	NM_21358E	65059	Hs.47116E	NM_02525E	ENSG000003CRAPH1	ALS2CR18	Ras	assoc	protein-coding
chr5-150E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	38299	NM_00154E	3340	Hs.22205E	NM_00154E	ENSG000003NDST1	HSST MR74	N-deacety	protein-coding	
chr7-540E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr7	5405618	5406632	+	0	NA	intron (NLM1B3 LIN	17421	NM_00108C	84629	Hs.52063E	NM_00101E	ENSG000003CAGL8	C1879 T	triacetyl	protein-coding	
chr7-871E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr7	87164553	87175244	+	0	NA	intron (NLM2a LINE	17344	NM_02114E	9988	Hs.19612E	NM_02114E	ENSG000003DMTF1	DMP1 DMT	cyclin D	protein-coding	
chr8-1447E	9.169583	-0.18319	0.768484	-0.23837	0.811591	0.981636	chr8	1.45E+08	1.45E+08	+	0	NA	intron (NMLT1A LTI	10990	NM_138367	90987	Hs.53451E	NM_138367E	ENSG000003ZNF251	-	zinc	fing	protein-coding
chr12-19E	8.382174	0.197439	0.828394	0.23834	0.811617	0.981636	chr12	1912536	19512913	+	0	NA	intron (NAluS6 SI	72125	NM_001267	121536	Hs.52457E	NM_153207E	ENSG000003AEBP2	-	Ae	bindir	protein-coding
chr15-56C	8.382174	0.197439	0.828394	0.23834	0.811617	0.981636	chr15	56097308	56097516	+	0	NA	intron (Nintron (N	92520	NM_00137C	64864	Hs.74508E	NM_022841E	ENSG000003CRFX7	RFXDC2	regulator	protein-coding	
chr9-1377E	8.382174	0.197439	0.828394	0.23834	0.811617	0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	3' UTR (N3' UTR (N	25273	NR_14750E	651337	Hs.60319E	NR_14750E	ENSG000003LOC651337	-	uncharact	ncRNA	
chr6-736I	8.723842	-0.19052	0.799909	-0.23818	0.811742	0.981636	chr6	73614112	73615271	+	0	NA	intron (NMER21B LI	39301	NM_012434	26503	Hs.59742E	NM_012434E	ENSG000003SLC17A5	AST ISSD	solute c	protein-coding	
chr15-101I	14.82727	-0.14708	0.617593	-0.23815	0.811768	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (NLM2c LINE	3555	NR_00365E	374666	Hs.45957E	NM_199163	WASH3P	FAM39DP	WASP	famipse	pseudo
chr11-87E	9.112228	0.181143	0.760736	0.238115	0.811792	0.981636	chr11	8729957	8730197	+	0	NA	exon (NM_exon (NM_	-38701	NR_12059E	1.03E+08	Hs.61327E	NR_12059E	LOC102724	-	uncharact	ncRNA	
chr13-99E	9.662471	-0.18527	0.778135	-0.2381	0.811804	0.981636	chr13	99521304	99521601	+	0	NA	intron (Nintron (N	19980	NM_00480C	9375	Hs.60789E	NM_00480C	ENSG000003TM9SF2	P76	transmem	protein-coding	
chr1-103C	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr1	1036313	1037121	+	0	NA	intron (Nintron (N	2724	NM_001364	375790	Hs.27333C	NM_19857E	ENSG000003AGRN	AGRN C	agrin	protein-coding	
chr10-294	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr10	29425142	29426118	+	0	NA	intron (Nintron (N	15387	NR_11092E	1.03E+08	Hs.49920E	NR_00393C	ENSG000003SVIL-AS1	-	SVIL	antinc	RNA
chr11-43C	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr11	43381936	43383810	+	0	NA	intron (NLM1C5 LIN	23953	NM_01825E	55761	Hs.19118E	NM_01825E	ENSG000003TTC17	-	tetratric	protein-coding	
chr15-66C	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr15	66333288	66335777	+	0	NA	TTS (NM_CTS (NM_C	12810	NR_00438E	692149	NR_00438E	ENSG000003SCARNA14	U100	small	Ca <sub>v</sub>	ncRNA	
chr16-74E	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr16	74899403	74900514	+	0	NA	intron (Nintron (N	85165	NM_030581	79726	Hs.280951	NM_030581E	ENSG000003WDR59	CDW12 FP	WD	repeate	protein-coding
chr17-41E	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr17	4164425	4164934	+	0	NA	non-codiron-codir	20982	NM_001254	124936	Hs.513871	NM_144611E	ENSG000003CYB5D2	-	cytochro	n	protein-coding
chr18-13E	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr18	13665816	13668130	+	0	NA	intron (Nintron (N	25215	NM_00127E	753	Hs.697787	NM_00433E	ENSG000003DLR4D4	C18orf1	low	densip	protein-coding
chr18-57E	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr18	57697455	57698453	+	0	NA	intron (Nintron (N	67623	NM_001242	1.01E+08	Hs.66064E	NM_001242804	LOC10050E	-	uncharact	protein-coding	
chr19-214	4.931393	-0.24421	0.126031	-0.23801	0.81187	0.981636	chr19	2149120	2150139	+	0	NA	intron (Nintron (N	1937	NM_00393E	8943	Hs.51281E	NM_00393E	ENSG00000				

chr4-527.9.615324	-0.17641	0.752899	-0.23431	0.814743	0.981636	chr14	52708978	52710311	+	0 NA	5' UTR (N5' UTR (N	2444 NR_158967	5706 Hs. 156171NM_002806	ENSG000003PCMC6	SUG2 p42	proteasome protein-coding	
chr7-776.9.615324	-0.17641	0.752899	-0.23431	0.814743	0.981636	chr7	77635044	77636611	+	0 NA	exon (NM exon (NM	60438 NR_134254	1.01E+08 Hs. 72451 NR_038361	ENSG000003APTR	RSBN1L-AS	Alu-mediated ncRNA	
chr8-172.9.615324	-0.17641	0.752899	-0.23431	0.814743	0.981636	chr8	17226954	17235381	+	0 NA	TTS (NM_TTS (NM_C	15291 NM_001322	29883 Hs. 58746NM_013354	ENSG000003CN077	CAF-1 CAFCCR4-NOT	protein-coding	
chr8-937.9.615324	-0.17641	0.752899	-0.23431	0.814743	0.981636	chr8	93708934	93713708	+	0 NA	intron (Nintron (N	10771 NR_156452	137392 Hs. 125038NM_145266	ENSG000003FAM92A	FAM92A1 F	family wiprotein-coding	
chr22-42.8.625847	-0.19182	0.818654	-0.23431	0.814746	0.981636	chr22	42846965	42847448	+	0 NA	intron (NAluJr SIN	10676 NR_01457C	26326 Hs. 68522NM_01457C	ENSG000003ARFGAP3	ARFGAP1	ADP ribosprotein-coding	
chr5-493.17.87882	0.134234	0.573232	0.234171	0.814852	0.981636	chr5	49385351	49385556	+	0 NA	IntergeniALR/Alpha	1055835 NM_19844E	133418 Hs. 561411NM_19844E	ENSG000003CEMB	GP70	embigin protein-coding	
chr1-922.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr1	92267441	92268400	+	0 NA	exon (NM exon (NM	31067 NM_053274	11146 Hs. 49105 NM_00707C	ENSG000003GLMN	FAP FAP4E	glomulin, protein-coding	
chr10-90.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr10	90886408	90887232	+	0 NA	intron (Nintron (N	14846 NM_001104	10556 Hs. 13912NM_00641E	ENSG000003RPP30	TSG15	ribonucleprotein-coding	
chr13-21.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr13	21040123	21040800	+	0 NA	intron (Nintron (N	21125 NM_01457E	26524 Hs. 78960 NM_01457E	ENSG000003CLATS2	KPM	large tunprotein-coding	
chr15-25.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr15	25679853	25680818	+	0 NA	intron (Nintron (N	168490 NR_03986E	1.01E+08 Hs. NR_03986E	ENSG000003MIR4715	-	microRNA ncRNA	
chr2-694.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr2	69422764	69423438	+	0 NA	intron (NAluJb SIN	14334 NR_04563Z	27247 Hs. 43043NM_01570C	ENSG000003NFU1	CGI-33 HNF1U	iror protein-coding	
chr2-1311.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr2	1.31E+08	1.31E+08	+	0 NA	intron (NAluSq SIN	4865 NM_00130E	55041 Hs. 469944NM_01795E	ENSG000003PLEKHB2	EVT2	pleckstriprotein-coding	
chr20-247.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr20	2476136	2476749	+	0 NA	IntergeniIntergeni	-5653 NM_19821E	6628 Hs. 83753 NM_003091	ENSG000003SNRPB	CCOR3 COD	small ncprotein-coding	
chr20-44.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr20	44945269	44946020	+	0 NA	intron (NMLTIG LTF	14082 NR_13498E	80336 Hs. 641481NM_001124	ENSG000003PABPCIL	CCorf11E poly (A)	tprotein-coding	
chr3-2397.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr3	23973944	23976536	+	0 NA	intron (NAluJo SIN	29119 NM_00114E	9975 Hs. 37288 NM_00512C	ENSG000003NR1D2	BD73 EAR	nuclear lprotein-coding	
chr3-141.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	exon (NM exon (NM	-82030 NR_13619C	646730 Hs. 570677NR_136190	LINC0261E	-	long intncRNA	
chr4-904.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr4	904450	905411	+	0 NA	intron (NMER51A LI	27386 NM_00525E	2580 Hs. 36907NM_00525E	ENSG000003CGAK	DNAJ26 DN	cyclin G protein-coding	
chr5-170.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr5	1.71E+08	1.71E+08	+	0 NA	intron (Nintron (N	35242 NM_022897	64901 Hs. 41081NM_022897	ENSG000003RANBP17	-	RAN bindi protein-coding	
chr6-365.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr6	36528812	36529583	+	0 NA	intron (NLMC5a LI	18282 NM_007271	11329 Hs. 40957NM_007271	ENSG000003STK38	NDR NDR1	serine/tprotein-coding	
chr6-116.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr6	1.16E+08	1.16E+08	+	0 NA	3' UTR (N3' UTR (N	-4955 NM_00108C	29940 Hs. 45835NM_01335E	ENSG000003DSE	DS-epil E	dermatan protein-coding	
chr7-128.4.923535	-0.24156	1.032974	-0.23384	0.815106	0.981636	chr7	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	18112 NM_018077	55131 Hs. 27426NM_018077	ENSG000003RBM28	ANES	RAN bindi protein-coding	
chr17-75.9.672179	-0.17721	0.757885	-0.23382	0.815122	0.981636	chr17	7565477	7567279	+	0 NA	intron (NAluXs SI	4386 NR_03792E	1.01E+08 Hs. 129677NR_03792E	SEN3-EIF	-	SEN3-EIF ncRNA	
chr5-372.9.672179	-0.17721	0.757885	-0.23382	0.815122	0.981636	chr5	37225177	37225568	+	0 NA	intron (NAluJb SIN	-23674 NR_13426E	1.05E+08 Hs. 17099E	NR_13426E	ENSG000003LOC105374	-	uncharactncRNA
chr1-1461.13.37394	0.151345	0.64752	0.23373	0.815195	0.981636	chr1	1.46E+08	1.46E+08	+	0 NA	intron (NLIPI4 LIN	14258 NM_00130Z	1E+08 Hs. 714127NM_00103E	ENSG000003NBPF10	AB6 AG1 NBPF	memt protein-coding	
chr1-220.9.664321	-0.17578	0.752533	-0.23359	0.815304	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	exon (NM exon (NM	-16415 NM_00444E	2058 Hs. 49778NM_00444E	ENSG000003EPRS	EAR5 GLUF	glutamyl-protein-coding	
chr14-34.9.664321	-0.17578	0.752533	-0.23359	0.815304	0.981636	chr14	34581434	34586938	+	0 NA	intron (Nintron (N	-2779 NR_00440C	26863 NR_00440C	ENSG000003RNVU1-18	RNU1-25 FRNA,	varisnRNA	
chr16-89.9.664321	-0.17578	0.752533	-0.23359	0.815304	0.981636	chr16	8904082	8904840	+	0 NA	exon (NM exon (NM	32178 NM_00128E	7874 Hs. 38693NM_00347C	ENSG000003USP7	HAUSP TEF	ubiquitir protein-coding	
chr12-48.4.462078	-0.25661	1.098717	-0.23355	0.815333	0.981636	chr12	48071710	48072823	+	0 NA	intron (NTigger7 E	-32987 NM_001354	5213 Hs. 75160 NM_00028E	ENSG000003PFKM	ATP-PFK1 C	phosphofr protein-coding	
chr7-101.7.836588	0.201016	0.860817	0.233517	0.81536	0.981636	chr7	1.01E+08	1.01E+08	+	0 NA	intron (Nintron (N	-1846 NM_00118E	24146 Hs. 38738 NM_01434E	ENSG000003CLDN15	-	small lncsnoRNA	
chr1-244.14.34955	0.146341	0.626761	0.233488	0.815382	0.981636	chr1	2.45E+08	2.45E+08	+	0 NA	intron (NAluXs SI	-3076 NR_13278E	1.07E+08 Hs. NR_13278E	SNORA100	-	small nucsnRNA	
chr3-4871.10.12578	-0.17249	0.739849	-0.23314	0.815649	0.981636	chr3	48714191	48715529	+	0 NA	intron (NAluYc3 SI	2361 NM_00100E	51447 Hs. 59598NM_016291	ENSG000003IP6K2	IHPK2 Ins	inositol protein-coding	
chr7-5602.10.12578	-0.17249	0.739849	-0.23314	0.815649	0.981636	chr7	5602372	5606434	+	0 NA	intron (Nintron (N	11587 NM_00308E	6624 Hs. 11840NM_00308E	ENSG000003PSCN1	FAN1 HSN	fascin acprotein-coding	
chr9-944.5.392489	-0.23161	0.994247	-0.23295	0.815803	0.981636	chr9	94461242	94462768	+	0 NA	TTS (NM_TTS (NM_C	87436 NM_03255E	84641 Hs. 55599NM_03255E	ENSG000003MFSD14B	HATL1 C11c	A-kinase protein-coding	
chr1-156.9.153867	-0.18016	0.773604	-0.23289	0.815849	0.981636	chr1	15651743	15652211	+	0 NA	intron (Nintron (N	-7736 NM_006511	6248 Hs. 23945NM_006511	ENSG000003RSC1A1	RS1	regulator protein-coding	
chr1-159.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr1	1.59E+08	1.59E+08	+	0 NA	intron (NAluXs SI	7717 NM_00120E	3428 Hs. 38025NM_005531	ENSG000003IF116	IFNGIP1 F	interferc protein-coding	
chr11-89.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr11	8918049	8922961	+	0 NA	TTS (NR_TTS (NR_C	9316 NM_00120E	56672 Hs. 13118NM_02064E	ENSG000003AKIP1	BCA3 C11c	A-kinase protein-coding	
chr13-97.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr13	97985428	97989276	+	0 NA	intron (NCharlie7	33677 NM_002271	3843 Hs. 71259NM_002271	ENSG000003IPO5	IMB3 KPNE	importin protein-coding	
chr14-61.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr14	61767256	61770850	+	0 NA	intron (Nintron (N	6633 NM_00308E	6617 Hs. 17931NM_00308E	ENSG000003SNAPC1	PTFGamma small	nucprotein-coding	
chr17-19.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr17	19966713	19969545	+	0 NA	intron (NAluY SINE	9699 NM_00720E	11216 Hs. 64267NM_00720E	ENSG000003AKAP10	AKAP-10 IA	kinase protein-coding	
chr17-30.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr17	30521968	30524278	+	0 NA	3' UTR (N3' UTR (N	45715 NM_001007	9527 Hs. 46268NM_004871	ENSG000003GOSR1	GOLIM2 GC	golgi SNr protein-coding	
chr17-35.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr17	35600487	35611574	+	0 NA	intron (Nintron (N	22488 NM_00103C	163 Hs. 51481NM_00128E	ENSG000003AP2B1	ADTB2 AP1	adaptor rprotein-coding	
chr18-95.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr18	9579613	9584668	+	0 NA	intron (NLM4b LIN	32411 NR_05200C	9989 Hs. 74323NM_005134	ENSG000003PPP4R1	ADT1 PP4	protein rprotein-coding	
chr19-227.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr19	2271262	2273491	+	0 NA	intron (NAluSq4 SI	2890 NM_00415E	4946 Hs. 446427NM_00415E	ENSG000003OAZ1	AZ1 AZI	Cornithine protein-coding	
chr2-699.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr2	69905625	69906231	+	0 NA	TTS (NM_TTS (NM_C	-9113 NM_00120E	4084 Hs. 46890NM_00235E	ENSG000003MXD1	BHLHC58 MAX	dimer protein-coding	
chr3-435.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr3	43595380	43598337	+	0 NA	intron (NLIPIA5 LIN	24968 NM_00134E	55129 Hs. 65665NM_01807E	ENSG000003ANO10	SCAR10 T	anactimr protein-coding	
chr3-124.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr3	1.25E+08	1.25E+08	+	0 NA	intron (Nintron (N	59297 NM_02073E	57493 Hs. 47422NM_02073E	ENSG000003HEG1	HEG MS11	heart dev protein-coding	
chr4-395.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr4	39502933	39513529	+	0 NA	intron (NAluJr SIN	19008 NM_00335E	7358 Hs. 57251NM_00335E	ENSG000003UGDH	GDH UDP-C	UDP-gluc protein-coding	
chr4-570.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr4	57009423	57013543	+	0 NA	intron (NAluXs SIN	32587 NM_00093E	5431 Hs. 602757NM_00093E	ENSG000003POLR2B	POLR2B RF	RNA polyn protein-coding	
chr4-800.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr4	80066687	80069261	+	0 NA	intron (NLIPIA10 LI	5255 NM_00128E	118429 Hs. 16296NM_05817E	ENSG000003ANTXR2	CMG-2 CMK	ANTXR cel protein-coding	
chr5-347.9.656463	-0.17437	0.749796	-0.23256	0.816103	0.981636	chr5	34793499	34806528	+	0 NA	intron (Nintron (N	-39151 NM_14472E	153657 Hs. 43574NM_14472E	ENSG000003TTC23L			



chr4-451.9.187149	-0.17649	0.773608	-0.22813	0.819542	0.981636	chr14	45107461	45108128	+	0 NA	intron (AluSx SIN	-3081 NR_003691	1E+08	Hs. 712501NR_003691	ENSG00000SNORD127	-	small	nucsnRNA
chr2-2017.9.187149	-0.17649	0.773608	-0.22813	0.819542	0.981636	chr2	2.02E+08	2.02E+08	+	0 NA	exon (NM exon (NM	19786 NM_020919	57679	Hs. 471096NM_020919	ENSG00000ALS2	-	ALS2CR6	Aalsin Rhcprotein-coding
chr4-7594.9.187149	-0.17649	0.773608	-0.22813	0.819542	0.981636	chr4	75946603	75948075	+	0 NA	IntergeniKangalb I	-6326 NM_001042	27163	Hs. 43736NM_01443	ENSG00000CNA	-	ASAH PLTN	acyletfprotein-coding
chr8-1066.9.187149	-0.17649	0.773608	-0.22813	0.819542	0.981636	chr8	1.07E+08	1.07E+08	+	0 NA	intron (NL1PBI LI	28050 NM_181354	55074	Hs. 12728NM_01800	ENSG00000CXR1	-	NblA00307	oxidatorprotein-coding
chr1-2255.9.640747	-0.17153	0.751945	-0.22812	0.819552	0.981636	chr1	2.26E+08	2.26E+08	+	0 NA	intron (NL1ME3A LI	96261 NM_001006	55740	Hs. 49789NR_001006	ENSG00000ENAH	-	ENA MENA ENAH	actiprotein-coding
chr12-955.9.640747	-0.17153	0.751945	-0.22812	0.819552	0.981636	chr12	95308224	95308690	+	0 NA	promoter-promoter-	37 NR_029895	442903	NR_029895	ENSG00000CIR331	-	MIRN331	microRNA ncRNA
chr2-1894.9.640747	-0.17153	0.751945	-0.22812	0.819552	0.981636	chr2	1.89E+08	1.89E+08	+	0 NA	intron (Nintron (N	27777 NM_032166	84128	Hs. 399984NM_032166	ENSG00000WDR75	-	NET16 UTF	repeatprotein-coding
chr3-1895.9.640747	-0.17153	0.751945	-0.22812	0.819552	0.981636	chr3	1.9E+08	1.9E+08	+	0 NA	exon (NM exon (NM	143060 NR_030642	1E+08	NR_030642	ENSG00000CIR944	-	MIRN944	microRNA ncRNA
chr17-766.4.915677	-0.23882	0.1047828	-0.22792	0.819706	0.981636	chr17	7665672	7666598	+	0 NA	IntergeniAluSx SIN	9109 NM_001276	7157	Hs. 43746NM_00054	ENSG00000TP53	-	BCC7 BMF5	tumor prcprotein-coding
chr18-205.4.915677	-0.23882	0.1047828	-0.22792	0.819706	0.981636	chr18	20974817	20975383	+	0 NA	intron (NL2a LINE	136713 NM_005406	6093	Hs. 306307NM_005406	ENSG00000ROCK1	-	P16OROCK	hso assocprotein-coding
chr1-2085.10.1512	-0.1678	0.737591	-0.2275	0.820036	0.981636	chr1	20857597	20859132	+	0 NA	intron (NL2a LINE	-71676 NM_016287	50809	Hs. 14244NM_016287	ENSG00000HP1BP3	-	HP1-BP74	heterochprotein-coding
chr11-301.10.1512	-0.1678	0.737591	-0.2275	0.820036	0.981636	chr11	3014097	3018928	+	0 NA	intron (AluY SINE	-12882 NR_04658C	1.01E+08	Hs. 27487NR_04658C	ENSG00000CARS-AS1	-	CARS	anticrRNA
chr4-2662.10.1512	-0.1678	0.737591	-0.2275	0.820036	0.981636	chr4	26627280	26628797	+	0 NA	intron (NL1PA3 LIN	43954 NM_018317	55296	Hs. 47940NM_018317	ENSG00000TBC1D19	-	TBC1	domprotein-coding
chr3-7295.8.869054	0.185548	0.815846	-0.2272	0.820175	0.981636	chr3	72928856	72929379	+	0 NA	intron (CpG	41071 NM_00108C	727936	Hs. 71027NM_00108C	ENSG00000GXYLT2	-	GLT8D4	glucosideprotein-coding
chr1-3846.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr1	3846873	3847347	+	0 NA	intron (NMER33 DNA	10101 NM_014704	9731	Hs. 13308NM_014704	ENSG00000CEPT104	-	CFAP256	centrosomeprotein-coding
chr13-452.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr13	45285297	45287536	+	0 NA	IntergeniAluSx1 SI	50031 NR_14598E	1.1E+08	NR_14572f	ENSG00000SNORA31B	-	small	nucsnRNA
chr16-366.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr16	3660787	3661641	+	0 NA	intron (NL1ME3B LI	6420 NM_001351	1773	Hs. 62963ENM_00522	ENSG00000CDNAE1	-	DNL1 DRN1	deoxyribonucleaseprotein-coding
chr17-752.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr17	75223023	75224126	+	0 NA	intron (NL1AluSx SIN	17895 NM_024844	79902	Hs. 36281NM_024844	ENSG00000NUP85	-	FRONT NF	neocyporprotein-coding
chr19-108.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr19	10830202	10830917	+	0 NA	intron (NMIRb SINE	1586 NR_106851	1.02E+08	NR_106851	ENSG00000MIR6793	-	hsa-mir-6	microRNA ncRNA
chr5-955.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr5	95507844	95508520	+	0 NA	intron (Nintron (N	46823 NM_014635	9652	Hs. 48286ENM_014635	ENSG00000TTC37	-	KIAA0372	tetratricprotein-coding
chr6-1705.5.418273	-0.22286	0.982254	-0.22689	0.820509	0.981636	chr6	1.7E+08	1.7E+08	+	0 NA	intron (NL1PA8 LIN	9987 NR_039787	1.01E+08	NR_039787	ENSG00000MIR4644	-	microRNA	ncRNA
chr11-112.10.14334	-0.16643	0.733815	-0.2268	0.820576	0.981636	chr11	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	21216 NM_001931	1737	Hs. 335551NM_001931	ENSG00000CDLAT	-	DLTA E2 F	dihydroliprotein-coding
chr15-491.10.14334	-0.16643	0.733815	-0.2268	0.820576	0.981636	chr15	49126454	49130300	+	0 NA	intron (Nintron (N	27222 NM_001143	9318	Hs. 369614NM_00423	ENSG00000COPS2	-	ALIEN CSN	COP9 sigrprotein-coding
chr17-384.10.14334	-0.16643	0.733815	-0.2268	0.820576	0.981636	chr17	38487958	38494662	+	0 NA	intron (Nintron (N	62846 NM_001199	57636	Hs. 37444NM_02087	ENSG00000ARHGAP23	-	Rho	GTPasprotein-coding
chr2-651.10.14334	-0.16643	0.733815	-0.2268	0.820576	0.981636	chr2	65103091	65104746	+	0 NA	intron (NAluSc8 SI	26188 NM_004161	5861	Hs. 31064NM_004161	ENSG00000RAB1A	-	RAB1 YPT1 RAB1A,	mcprotein-coding
chr3-1237.10.14334	-0.16643	0.733815	-0.2268	0.820576	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	4814 NR_04662E	1.01E+08	Hs. 66731cNR_04662E	ENSG00000MYLK-AS2	-	MYLK	anticrRNA
chr5-4191.10.14334	-0.169206	0.745452	-0.22643	0.820623	0.981636	chr5	41917084	41917435	+	0 NA	exon (NM exon (NM	-7993 NM_001297	26272	Hs. 16557NM_001217	ENSG00000FBX04	-	FBX4	F-box prcprotein-coding
chr10-105.10.6048	-0.16375	0.723494	-0.22633	0.820948	0.981636	chr10	1.1E+08	1.1E+08	+	0 NA	3' UTR (N3' UTR (N	58251 NM_001324	7511	Hs. 39062NM_02038	ENSG00000XPNPEP1	-	APP1 SAMFX	prolyl protein-coding
chr17-644.14.82912	-0.14097	0.62299	-0.22628	0.820987	0.981636	chr17	64498485	64505373	+	0 NA	promoter-promoter-	-616 NR_03996E	1.01E+08	NR_03996E	ENSG00000MIR5047	-	microRNA	ncRNA
chr16-581.10.93435	-0.16703	0.739039	-0.22601	0.821192	0.981636	chr16	58113588	58114951	+	0 NA	intron (NAluSx1 SI	15112 NM_013242	29105	Hs. 53275NM_013242	ENSG00000CFAP20	-	BUG22 Clc	cilicia ancrprotein-coding
chr1-844.10.62837	-0.16809	0.744976	-0.22563	0.821486	0.981636	chr1	84483402	84483604	+	0 NA	intron (NAluSx1 SI	4237 NM_02506E	80135	Hs. 48120NM_02506E	ENSG00000CRPF1	-	BXD5C	ribosome protein-coding
chr20-136.4.49536	-0.24876	1.102706	-0.22559	0.821519	0.981636	chr20	1316432	1316980	+	0 NA	intron (Nintron (N	31678 NR_14798E	79133	Hs. 47216NM_02412	ENSG00000NDUFAP5	-	C20orf7 w	NADH:ubiq protein-coding
chr1-1657.15.82775	-0.13529	0.600147	-0.22548	0.821646	0.981636	chr1	16578067	16579272	+	0 NA	intron (Nintron (N	29755 NR_03744E	1.01E+08	NR_03744E	ENSG00000MIR3675	-	microRNA	ncRNA
chr17-294.9.681887	-0.16949	0.751936	-0.2254	0.821664	0.981636	chr17	29498457	29500637	+	0 NA	intron (Nintron (N	67490 NM_198147	116236	Hs. 10651NM_198147	ENSG00000ABHD15	-	abhydrol	protein-coding
chr22-379.9.681887	-0.16949	0.751936	-0.2254	0.821664	0.981636	chr22	37886883	37887208	+	0 NA	intron (NAluS2 SIN	-19252 NM_00338E	85377	Hs. 51761NM_00338E	ENSG00000MICALL1	-	MICAL-L1	MICAL likprotein-coding
chr11-367.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr11	3675032	3676934	+	0 NA	non-codiron-codir	-4599 NM_00130C	57053	Hs. 73280NM_02040	ENSG00000CHRNA10	-	cholinerg	protein-coding
chr11-34C.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr11	34076252	34101444	+	0 NA	intron (Nintron (N	-16781 NM_02466E	55226	Hs. 57728NM_02466E	ENSG00000CNAT10	-	ALP Kre3 N	acetylprotein-coding
chr12-501.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr12	50176260	50182010	+	0 NA	intron (NAluS26 SI	-11602 NM_001281	91012	Hs. 27052NM_14719	ENSG00000CERS5	-	LASS5 T	tricaramide protein-coding
chr12-644.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr12	64409893	64437191	+	0 NA	intron (NAluS26 SI	19195 NM_00723E	11260	Hs. 85951NM_00723E	ENSG00000XPOT	-	XPO3	expotin protein-coding
chr12-12C.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr12	1.2E+08	1.2E+08	+	0 NA	exon (NM exon (NM	21333 NR_038924	1.01E+08	Hs. 56920ENR_038924	ENSG00000CPXN-AS1	-	EyeLine4	PXN anticrRNA
chr16-705.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr16	70554222	70573053	+	0 NA	intron (Nintron (N	-16258 NM_15245E	146433	Hs. 461214NM_15245E	ENSG00000IL34	-	C16orf77	interleukprotein-coding
chr17-415.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr17	41908089	41911063	+	0 NA	intron (Nintron (N	9826 NM_00109E	47	Hs. 387567NM_00109E	ENSG00000ACLY	-	ACL ATPCI	ATP citrprotein-coding
chr17-816.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr17	81604128	81607247	+	0 NA	intron (Nintron (N	-28254 NR_13013E	55666	Hs. 46433NM_017921	ENSG00000CNPLOC4	-	NPL4	NPL4 homprotein-coding
chr19-412.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr19	41230975	41262044	+	0 NA	intron (NAluS26 SI	-16048 NM_14473E	11100	Hs. 15521NM_00704	ENSG00000HNRNPUL1	-	E1B-AP5 E	heterogerprotein-coding
chr2-549.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr2	54980643	54982711	+	0 NA	intron (Nintron (N	28595 NM_00700E	57142	Hs. 63785NM_00700E	ENSG00000CRTN4	-	ASY N122	Creticularprotein-coding
chr21-461.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr21	46110884	46132336	+	0 NA	exon (NM exon (NM	23491 NM_05817E	1292	Hs. 42026NM_00184	ENSG00000COL6A2	-	BTHLM1 P	collagen protein-coding
chr3-522C.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr3	52265741	52270119	+	0 NA	TTS (NR_C	431 NR_02966E	406890	NR_02966E	ENSG00000MIRLET7G	-	LET7G MIF	microRNA ncRNA
chr3-142C.10.13549	-0.16508	0.732431	-0.22539	0.821678	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (NL1PA16 LI	92889 NM_00128E	54464	Hs. 43510ENM_019001	ENSG00000CXRN1	-	1-Sep 5'-3'	excrprotein-coding
chr4-7082.10.13549	-																	

chr18-876	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr18	8761041	8763618	+ 0 NA	intron (Nintron (N	4498	NM_01521C	23255	Hs.70792C	ENSG00000MTCL1	CCDC165	microtubul	protein-coding			
chr19-555	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr19	55386564	55390376	+ 0 NA	TTS (NR_1TTS (NR_1	289	NR_10686E	1.02E+08	NR_10686E	ENSG00000MIR6805	hsa-mir-ε	microRNA	ncRNA			
chr22-411	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr22	41117011	41117897	+ 0 NA	exon (NM_exon (NM_	24862	NM_00136E	2033	Hs.157157	ENSG00000CEP300	KAT3B	MEK1E1A	bindiprotein-coding			
chr3-172	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr3	1.72E+08	1.72E+08	+ 0 NA	intron (NL2c LINE	100375	NM_00412E	2693	Hs.130212	ENSG00000GHSR	GHPD	major h	protein-coding			
chr6-2994	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr6	29943354	29946219	+ 0 NA	intron (Nintron (N	2254	NM_00211E	3105	Hs.181244	ENSG00000HLA-A	HLLA	major h	protein-coding			
chr6-135C	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr6	1.35E+08	1.35E+08	+ 0 NA	exon (NM_exon (NM_	17695	NM_00114E	10767	Hs.378532	ENSG00000CHBS1L	EF-1a	ERF	HBS1 like	protein-coding		
chr7-748E	10.16877	-0.1618	0.734435	-0.2203	0.825636	0.981636	chr7	7488857	7488616	+ 0 NA	intron (Nintron (N	4526	NR_04058A	442582	Hs.63231	ENSG00000STAG3L2	STAG3L1	Sstromal	ε	pseudogene		
chr11-764	5.46727	-0.22182	1.007145	-0.22024	0.825682	0.981636	chr11	76464062	76464903	+ 0 NA	intron (Nintron (N	19457	NM_02019E	56946	Hs.352588	ENSG00000EMSY	C11orf30	EMSY	trarp	protein-coding		
chr1-702	10.62237	-0.15795	0.717688	-0.22008	0.825808	0.981636	chr1	70235633	70238060	+ 0 NA	intron (NAluSc8 SI	15466	NM_00135C	9295	Hs.47969E	ENSG00000CSRF11	NET2	SFRS	serine ar	protein-coding		
chr1-1092	10.62237	-0.15795	0.717688	-0.22008	0.825808	0.981636	chr1	1.09E+08	1.09E+08	+ 0 NA	intron (Nintron (N	14101	NM_00140E	1952	Hs.57652	ENSG00000CELSR2	ADGR2	C	cadherin	protein-coding		
chr14-528	10.62237	-0.15795	0.717688	-0.22008	0.825808	0.981636	chr14	52867079	52873400	+ 0 NA	intron (NTrigger3b	78632	NM_19806E	64841	Hs.47802E	ENSG00000GNPNAT1	GNAI1	GNP	glucosamin	protein-coding		
chr17-422	4.907819	-0.23594	1.072229	-0.22005	0.825833	0.981636	chr17	42223539	42223892	+ 0 NA	intron (Nintron (N	29221	NM_00114E	84514	Hs.38039	ENSG00000GHDC	D11LGP1	I	GH3	domain	protein-coding	
chr13-326	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr13	32509346	32509985	+ 0 NA	promoter-promoter-	270	NR_02692E	116828	Hs.658751	ENSG00000N4BP2L2-1	CG3030	N4BP2	lincRNA			
chr18-26E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr18	26012244	26013092	+ 0 NA	IntergeniIntergeni	77945	NM_001007	6760	Hs.129261	ENSG00000CSS18	SLX1	SYT	SS18	sub	protein-coding	
chr3-325E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr3	32539630	32541144	+ 0 NA	intron (Nintron (N	30471	NM_01614I	51143	Hs.52949E	ENSG00000DYNCL1L1	DLX-A	DN	dynein	c	protein-coding	
chr4-159E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr4	1.59E+08	1.59E+08	+ 0 NA	intron (NL2a LINE	49578	NM_00135E	9693	Hs.744884	ENSG00000RAPGEF2	CNrasGEF	Rap	guanine	protein-coding		
chr5-863E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr5	863058	864298	+ 0 NA	TTS (NR_1TTS (NR_1	12692	NM_02478E	79844	Hs.654874	ENSG00000ZDHHC11	ZNF399	zinc	fin	protein-coding		
chr5-179E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr5	1.8E+08	1.8E+08	+ 0 NA	intron (NAluSp SIN	20895	NR_10566E	1.02E+08	Hs.66325E	ENSG00000LOC10192E				uncharact	ncRNA	
chr6-342E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr6	34287032	34287876	+ 0 NA	3' UTR (N3' UTR (N	38346	NM_001287	221491	Hs.38130C	ENSG00000SMIM29	G6orf1	LE	small	in	protein-coding	
chr6-897E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr6	89755884	89756649	+ 0 NA	intron (Nintron (N	63528	NM_01461I	23195	Hs.52994E	ENSG00000MDN1	Real	midasin	γ	protein-coding		
chr6-107E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr6	1.08E+08	1.08E+08	+ 0 NA	intron (Nintron (N	56575	NM_00128E	256380	Hs.48610E	ENSG00000SCML4	DJ47M23	15cm	poly	protein-coding		
chr9-108E	5.402557	-0.21804	0.994417	-0.21926	0.826447	0.981636	chr9	1.09E+08	1.09E+08	+ 0 NA	intron (Nintron (N	18381	NM_00668E	10881	Hs.12353C	ENSG00000ACTL7A				actin	lik	protein-coding
chr1-124C	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr1	12403269	12403681	+ 0 NA	intron (Nintron (N	103771	NR_00302E	677885	Hs.65845C	ENSG00000SNORA59A	ACA59	small	nuc	snoRNA		
chr1-466E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr1	46633051	46633975	+ 0 NA	IntergeniMIRb SINE	16622	NM_20140C	148932	Hs.632401	ENSG00000MOB3C	MOBE	MOE	MOB	kinas	protein-coding	
chr11-64E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr11	64237448	64238608	+ 0 NA	intron (Nintron (N	3067	NM_00447C	2286	Hs.22772E	ENSG00000FKBP2	FKBP-13	FKBP	prol	protein-coding		
chr17-161E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr17	160270628	160271396	+ 0 NA	intron (Nintron (N	39367	NR_00299E	677681	NR_00299E	ENSG00000SCARNA20	ACA66	small	Ca	ncRNA		
chr19-160E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr19	162123148	16225241	+ 0 NA	intron (Nintron (N	9834	NM_03285E	84941	Hs.631617	ENSG00000HSH2D	ALX1	HSH2	hemato	protein-coding		
chr2-985E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr2	98595154	98595842	+ 0 NA	IntergeniLIP2 LIN	13014	NM_00100E	493753	Hs.596537	ENSG00000COA5	6330578E1	cyto	chron	protein-coding		
chr2-158E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr2	1.59E+08	1.59E+08	+ 0 NA	intron (Nintron (N	113081	NR_13524E	1E+08	Hs.630724	ENSG00000PKP4-AS1				PKP4	ant	ncRNA
chr20-39E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr20	39008885	39010824	+ 0 NA	intron (Nintron (N	47510	NM_00119C	60625	Hs.44452C	ENSG00000DHX35	C20orf15	DEAH	h	protein-coding		
chr3-390E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr3	39099040	39100844	+ 0 NA	intron (Nintron (N	7685	NM_00127E	64689	Hs.72194E	ENSG00000GORASP1	GOLPH5	G	golgi	rec	protein-coding	
chr3-412E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr3	41240921	41241493	+ 0 NA	TTS (NM_CTTS (NM_C	41702	NM_00109E	1499	Hs.47601E	ENSG00000CTNNB1	CTNBB1	EVF	catenin	γ	protein-coding	
chr4-558E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr4	55888777	55890023	+ 0 NA	intron (Nintron (N	35750	NM_01826I	55763	Hs.26966E	ENSG00000EXOC1	BM-102	SE	exocyt	c	protein-coding	
chr5-129E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr5	1.3E+08	1.3E+08	+ 0 NA	intron (NLIPIA13 LI	113245	NM_001257	1E+08	Hs.582534	ENSG00000CMINAR2	KIAA1024	membrane	protein-coding			
chr5-141E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr5	1.42E+08	1.42E+08	+ 0 NA	IntergeniLMC3 LIN	21628	NM_00547I	10007	Hs.63385E	ENSG00000GNPDA1	GNP1	GNP1	glucosami	protein-coding		
chr6-205E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr6	20595947	20596423	+ 0 NA	intron (NLIPIA7 LIN	61728	NM_01777A	54901	Hs.657604	ENSG00000CDKAL1				CDK5	reg	protein-coding
chr7-446E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr7	44666803	44667508	+ 0 NA	intron (NAluJb SIN	60528	NM_00100C	406886	Hs.488181	ENSG00000COGDH	AKGHD1	E	oxoglutar	protein-coding		
chr9-941E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chr9	94182735	94183665	+ 0 NA	intron (NAluJb SIN	4366	NR_02948I	406886	NR_02948I	ENSG00000MIRLET7D	LET7D	M	micro	ncRNA		
chrX-714E	5.443697	-0.21438	0.978456	-0.2191	0.826575	0.981636	chrX	71455246	71455877	+ 0 NA	intron (NMIIRb SINE	36888	NR_00222E	27160	Hs.72180E	ENSG00000INGX	ING1	like	inhibitor	pseudo		
chr20-39E	9.212572	-0.17112	0.781107	-0.21907	0.826592	0.981636	chr20	3989107	3989613	+ 0 NA	intron (NAluY SINE	26198	NM_00113A	11237	Hs.54757E	ENSG00000CRNF24	GIL	ring	fin	protein-coding		
chr13-20E	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr13	20972815	20977469	+ 0 NA	exon (NM_exon (NM_	25714	NR_10405E	1.02E+08	Hs.63763E	ENSG00000LINC00367-				long	int	ncRNA
chr13-491	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr13	49136632	49137563	+ 0 NA	intron (NAluJo SIN	26780	NM_01492E	22862	Hs.50801C	ENSG00000FND3A	FND3	HUC	fibronect	protein-coding		
chr14-21E	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr14	21351408	21355079	+ 0 NA	intron (Nintron (N	30776	NM_00719E	11198	Hs.213724	ENSG00000SUPT16H	CDC68	FAC	SPT16	hon	protein-coding	
chr16-224	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr16	22467332	22471153	+ 0 NA	intron (Nintron (N	31527	NR_02746E	1E+08	Hs.70957E	ENSG00000RRN3P3				RRN3	hom	pseudo
chr16-554	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr16	55495443	55498364	+ 0 NA	intron (Nintron (N	12169	NM_01783E	54947	Hs.460857	ENSG00000LPCAT2	AGPAT11	γ	lysophos	ph	protein-coding	
chr2-331E	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr2	33186393	33190349	+ 0 NA	intron (NAluSq2 SI	53775	NM_00116E	4052	Hs.61931E	ENSG00000LTBP1				latent	γ	protein-coding
chr2-650E	10.16091	-0.16045	0.733051	-0.21889	0.826739	0.981636	chr2	65085606	65086690	+ 0 NA	TTS (NM_CTTS (NM_C	29732	NM_00131E	23177	Hs.709257	ENSG00000CEP68	KIA					



chr9-2721 5.435839	-0.21194	0.981398	-0.21596	0.829022	0.981636	chr9	27200261	27201010	+	0 NA	intron (Nintron (N	82158 NR_026675	158035 Hs. 201554NR_026675	ENSG000003C9orf14	long intencRNA
chr9-8841 5.435839	-0.21194	0.981398	-0.21596	0.829022	0.981636	chr9	88416367	88417308	+	0 NA	intron (NAluSp SIN	28393 NM_006717	10927 Hs. 146804NM_006717	ENSG000003SPIN1	SPIN TDRE spindlin protein-coding
chr9-9205 5.435839	-0.21194	0.981398	-0.21596	0.829022	0.981636	chr9	92055769	92056319	+	0 NA	intron (NLMC5a LI	59369 NM_006415	10558 Hs. 90458 NM_006415	ENSG000003PTLC1	HSAN1 HNS serine pε protein-coding
chr9-1284 5.435839	-0.21194	0.981398	-0.21596	0.829022	0.981636	chr9	1.28E+08	1.28E+08	+	0 NA	intron (NAluSq2 SI	19447 NM_153437	4957 Hs. 129055NM_00254C	ENSG000003ODF2	CT134 ODF outer der protein-coding
chr10-32 10.60665	-0.15536	0.71949	-0.21594	0.829036	0.981636	chr10	32025889	32039459	+	0 NA	intron (Nintron (N	23751 NM_004521	3799 Hs. 327735NM_004521	ENSG000003K1F5B	HEL-S-61 kinesin f protein-coding
chr2-1772 10.60665	-0.15536	0.71949	-0.21594	0.829036	0.981636	chr2	1.77E+08	1.77E+08	+	0 NA	intron (Nintron (N	19517 NR_13847C	220988 Hs. 516535NM_194247	ENSG000003HNRNP3	2610510D1 heteroger protein-coding
chr19-154 10.66351	-0.15613	0.724124	-0.21561	0.829288	0.981636	chr19	15422425	15426324	+	0 NA	exon (NM exon (NM	-5386 NM_001291	26993 Hs. 399800NM_014371	ENSG000003AKAP8L	HA95 HAPK-A-kinase protein-coding
chr2-2312 10.66351	-0.15613	0.724124	-0.21561	0.829288	0.981636	chr2	2.31E+08	2.31E+08	+	0 NA	intron (NAluSx4 SI	-71035 NR_039937	1.01E+08 NR_039937	ENSG000003MIR4777	- microRNA ncRNA
chr9-4105 10.66351	-0.15613	0.724124	-0.21561	0.829288	0.981636	chr9	41050329	41051167	+	0 NA	intron (NLM2 LINE	23877 NR_00283C	595135 Hs. 571595NR_00283C	ENSG000003PGM5P2	- phosphogl pseudo
chr12-214 9.699453	-0.16309	0.757038	-0.21543	0.829432	0.981636	chr12	21483003	21483361	+	0 NA	intron (Nintron (N	18453 NM_002907	5965 Hs. 235065NM_002907	ENSG000003RECQL	RECQL1 ReCq like protein-coding
chr11-445 5.830732	-0.21551	1.000665	-0.21537	0.829448	0.981636	chr11	44934009	44934411	+	0 NA	non-codirnon-codir	15950 NM_001255	9537 Hs. 554791NM_006034	ENSG000003TP53I11	PIG11 tumor pr protein-coding
chr10-501 10.67136	-0.15746	0.731199	-0.21535	0.829495	0.981636	chr10	50128003	50128550	+	0 NA	intron (Nintron (N	60322 NM_001005	387680 Hs. 365285NM_018232	ENSG000003WASHC2A	FAM21A FβWASH com protein-coding
chr11-105 10.65565	-0.15483	0.719429	-0.21521	0.829606	0.981636	chr11	10579214	10580597	+	0 NA	intron (Nintron (N	-11240 NM_006691	10894 Hs. 655332NM_006691	ENSG000003LYVE1	CRSBP-1 F lymphatic protein-coding
chr14-306 10.65565	-0.15483	0.719429	-0.21521	0.829606	0.981636	chr14	30663705	30664597	+	0 NA	intron (NLP2 LINE	41932 NM_01610E	23256 Hs. 369165NM_01610E	ENSG000003SCFD1	C14orf163 secl fami protein-coding
chr2-1691 10.65565	-0.15483	0.719429	-0.21521	0.829606	0.981636	chr2	1691430	1693055	+	0 NA	intron (Nintron (N	52273 NM_012293	7837 Hs. 332197NM_012293	ENSG000003PXDN	ASG7D COF peroxidase protein-coding
chr4-3894 10.65565	-0.15483	0.719429	-0.21521	0.829606	0.981636	chr4	38943968	38945630	+	0 NA	non-codirnon-codir	76767 NR_03030C	693159 NR_03030C	ENSG000003MIR574	MIR574-3r microRNA ncRNA
chr15-997 11.10925	-0.15148	0.705006	-0.21487	0.829869	0.981636	chr15	99712580	99712955	+	0 NA	exon (NM exon (NM	20670 NM_001284	145748 Hs. 562565NM_152445	ENSG000003CLYSD4	- LysM dome protein-coding
chr1-5135 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr1	51396907	51398353	+	0 NA	intron (Nintron (N	24465 NM_001155	2060 Hs. 83722 NM_001198	ENSG000003EPS15	AF-1P AF1 epidermal protein-coding
chr1-8425 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr1	84231467	84232691	+	0 NA	intron (NLP3A3 LIN	50447 NM_001242	5567 Hs. 487325NM_002731	ENSG000003PRKACB	PKA C-βet protein f protein-coding
chr1-1656 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr1	1.66E+08	1.66E+08	+	0 NA	intron (NLP3A6 LIN	7231 NM_001365	223 Hs. 2533 NM_000695	ENSG000003ALDH9A1	ALDH4 ALAldehyde protein-coding
chr1-2005 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr1	2.01E+08	2.01E+08	+	0 NA	intron (Nintron (N	-29838 NM_005298	2848 Hs. 534315NM_005298	ENSG000003GPR25	- G protein protein-coding
chr11-101 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr11	10193039	10193673	+	0 NA	intron (NAluV SINE	100851 NM_030962	81846 Hs. 577252NM_030962	ENSG000003SFB2	CMT4B2 DESET bindi protein-coding
chr11-125 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr11	1.23E+08	1.23E+08	+	0 NA	intron (Nintron (N	46482 NM_02476E	79827 Hs. 591945NM_02476E	ENSG000003CLMP	ACAM ASACXADR 1i protein-coding
chr12-252 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr12	25235536	25236039	+	0 NA	intron (NMER1B DNA	15142 NM_001366	3845 Hs. 505035NM_004985	ENSG000003KRAS	C-K-RAS KRAS prot protein-coding
chr17-455 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr17	45026804	45027250	+	0 NA	intron (Nintron (N	24605 NM_001285	79877 Hs. 463145NM_024815	ENSG000003DCAKD	- dephosph protein-coding
chr18-623 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr18	632411768	63242842	+	0 NA	intron (NHAL1 LINE	-22925 NM_000657	596 Hs. 150745NM_000635	ENSG000003BCL2	Bcl-2 PPFBCL2 apor protein-coding
chr19-221 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr19	2231116	2231623	+	0 NA	intron (Nintron (N	20780 NR_03159E	1E+08 NR_03159E	ENSG000003MIR1227	MIRN1227 microRNA ncRNA
chr19-364 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr19	3647663	3648265	+	0 NA	intron (NAluSx SIN	-21149 NM_021231	58509 Hs. 128425NM_021231	ENSG000003CACTIN	C19orf29 cactin, s protein-coding
chr3-1395 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr3	1.39E+08	1.39E+08	+	0 NA	exon (NM exon (NM	2368 NM_001363	56945 Hs. 745001NM_020191	ENSG000003MRPS22	C3orf5 CCmitochon protein-coding
chr4-1548 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr4	1.55E+08	1.55E+08	+	0 NA	exon (NM exon (NM	2669 NM_00266E	5356 Hs. 249999NM_00266E	ENSG000003PLRG1	Cwcl PRL1pleiotro protein-coding
chr6-4367 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr6	43672448	43673355	+	0 NA	TTS (NM_TTS (NM_I	14911 NM_01813E	55168 Hs. 520145NM_01813E	ENSG000003MRPS18A	HumanS18 mt tochon protein-coding
chr8-8794 5.897295	-0.20292	0.94673	-0.21434	0.830282	0.981636	chr8	8794743	8797097	+	0 NA	intron (Nintron (N	93983 NM_194284	137075 Hs. 183617NM_194284	ENSG000003CLDN23	CLDNL hCClaudin 2 protein-coding
chr11-831 10.64779	-0.15354	0.717005	-0.21413	0.830442	0.981636	chr11	83193068	83192261	+	0 NA	intron (NAluSq2 SI	2355 NR_14901C	1.01E+08 Hs. 585502NM_018705	LOC100505C	uncharactncRNA
chr19-164 10.64779	-0.15354	0.717005	-0.21413	0.830442	0.981636	chr19	16417176	16417429	+	0 NA	intron (Nintron (N	54668 NM_001255	58513 Hs. 654635NM_021235	ENSG000003EPL5L1	EPL5R epidermal protein-coding
chr5-1711 10.64779	-0.15354	0.717005	-0.21413	0.830442	0.981636	chr5	1.71E+08	1.71E+08	+	0 NA	intron (Nintron (N	6626 NM_001355	4869 Hs. 557555NM_00252C	ENSG000003NPM1	B23 NPM nucleoph protein-coding
chr9-9214 10.64779	-0.15354	0.717005	-0.21413	0.830442	0.981636	chr9	92142579	92145984	+	0 NA	intron (Nintron (N	2814 NR_027341	158314 Hs. 149944NR_027341	LINC00475C9orf47	long intencRNA
chrX-1176 4.974382	-0.22245	1.041782	-0.21353	0.830916	0.981636	chrX	11761442	11762106	+	0 NA	intron (Nintron (N	2127 NM_00680C	10943 Hs. 655285NM_00680C	ENSG000003MSL3	MSL3L1 MSL compl protein-coding
chr11-274 11.10139	-0.15023	0.703754	-0.21347	0.830962	0.981636	chr11	27498014	27498675	+	0 NA	3' UTR (N3' UTR (N	8425 NM_018362	55327 Hs. 91393 NM_018362	ENSG000003LINC7	LINC7-7 lin-7 hon protein-coding
chr7-5522 11.10139	-0.15023	0.703754	-0.21347	0.830962	0.981636	chr7	55200000	55206672	+	0 NA	TTS (NM_TTS (NM_C	-14432 NR_047551	1.01E+08 Hs. 720485NR_047551	ENSG000003EGFR-AS1	EGFR anticncRNA
chr9-1142 11.10139	-0.15023	0.703754	-0.21347	0.830962	0.981636	chr9	1.14E+08	1.14E+08	+	0 NA	intron (NLM1E1 LIN	-27534 NM_000607	5004 Hs. 522355NM_000607	ENSG000003ORM1	AGP-A AGF orosomu protein-coding
chr3-6744 5.394699	-0.21557	1.010965	-0.21323	0.831147	0.981636	chr3	67400047	67400897	+	0 NA	intron (NMER103C L	175008 NR_036234	1E+08 NR_036234	ENSG000003MIR4272	- microRNA ncRNA
chr8-1868 5.394699	-0.21557	1.010965	-0.21323	0.831147	0.981636	chr8	1868877	1869218	+	0 NA	intron (NA-rich LC	45121 NM_00130E	9639 Hs. 98594 NM_014625	ENSG000003ARHGEF10	GEF10 SNC Rho guaniprotein-coding
chr9-8634 10.19419	-0.15711	0.737928	-0.21291	0.831396	0.981636	chr9	86342141	86342522	+	0 NA	intron (Nintron (N	12079 NM_024617	79670 Hs. 597057NM_024617	ENSG000003TUT7	PAPD6 TEM terminal protein-coding
chr2-9275 20.42878	0.119449	0.56188	0.212588	0.831648	0.981636	chr2	92758961	92759252	+	0 NA	IntergeniALR/Alpha	817960 NR_027714	440888 Hs. 730235NM_001032412	ACTR3BP2	FKSG73 ACTR3B ps pseudo
chr10-351 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr10	28535666	28541462	+	0 NA	intron (NAluSx1 SI	5446 NM_01662E	51322 Hs. 743224NM_01662E	ENSG000003WAC	BM-016 DEWW domain protein-coding
chr11-285 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr11	35175637	35189923	+	0 NA	intron (NLTR101 Me	19830 NR_145794	1.1E+08 NR_145794	SNORD164	small nuc snoRNA
chr11-596 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr11	59663355	59666834	+	0 NA	intron (Nintron (N	3943 NM_15271E	219988 Hs. 591965NM_15271E	ENSG000003PATL1	Pat1b hPePAT1 homc protein-coding
chr2-6985 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr2	69895315	69897652	+	0 NA	exon (NM exon (NM	2527 NM_006857	11017 Hs. 54649 NM_006857	ENSG000003SNRNP27	27K RY1 small nuc protein-coding
chr4-5697 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr4	56970284	56973924	+	0 NA	intron (NAluYf1 SI	5502 NM_03231C	84273 Hs. 8715 NM_03231C	ENSG000003NOA1	C4orf14 vnitric o protein-coding
chr4-7577 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr4	75773697	75781095	+	0 NA	intron (NLMC2 LIN	52874 NM_00129C	8615 Hs. 744877NM_00371E	ENSG000003USO1	P115 TAP USO1 vesi protein-coding
chr4-1382 10.63993	-0.15224	0.716797	-0.2124	0.831798	0.981636	chr4	1.38E+08	1.38E+08	+	0 NA	intron (Nintron (N	25699 NM_014331	23657 Hs. 390594NM_014331	ENSG000003SLC7A11	CCBR1 Xc1solute cε protein-coding

chr17-501.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr17	50184820	50186367	+	0	NA	exon (NM exon (NM	-13117 NR_024192	373861	Hs.25934	NR_194072	HILS1	HI.9	histone Ipseudo	
chr2-1128.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr2	11283688	11285710	+	0	NA	intron (NL3 LINE C	59937 NR_00485C	9475	Hs.68174	ENS0000000485C	ROCK2	ROCK-II	Rho assoc protein-coding	
chr3-189C.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr2	1.89E+08	1.89E+08	+	0	NA	intron (NL2c LINE	64413 NR_037401.1	0.01E+08	NR_037401	ENS000000037401	MIR3606	mir-3606	microRNA ncRNA	
chr3-1236.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	1648 NR_04662E	0.01E+08	Hs.66731	ENS00000004662E	MYLK-AS2	-	MYLK anticRNA	
chr5-1796.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (NAluJb SIN	8982 NR_00390C	8878	Hs.58729	ENS00000000390C	SQSTM1	A170 DMR3	sequestosome1 protein-coding	
chr6-3152.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr6	31529764	31541049	+	0	NA	TTS (NR_C TTS (NR_C	1043 NR_00314C	692233	NR_00314C	ENS00000000314C	SNORD117	U83	small nucleolar RNA	
chr7-2351.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr7	23512135	23522365	+	0	NA	intron (NAluV SINE	14731 NR_00136Z	29896	Hs.44565	ENS00000000136Z	TRAZA	AWMS1 HSU	transform protein-coding	
chr9-9204.11.12681	-0.146	0.701939	-0.208	0.835232	0.981636	chr9	92041105	92045308	+	0	NA	intron (NL2-3 Crp	72207 NR_00641F	10558	Hs.90458	ENS00000000641F	SPTLC1	HSAN1 HSN	serine protease protein-coding	
chr17-424.6.407749	-0.19508	0.93792	-0.208	0.835233	0.981636	chr17	4241604	4242252	+	0	NA	intron (NAluSc8 SI	21919 NR_001257	51479	Hs.69608	ENS00000001257	ANKFY1	ANKHZN BT	ankyrin 1 protein-coding	
chr3-531C.4.966524	-0.21934	0.105656	-0.2076	0.835543	0.981636	chr3	53109180	53109908	+	0	NA	intron (NAluJr SIN	20891 NR_005285E	91869	Hs.63191	ENS000000005285E	RFT1	CDGIN	RFT1	hom protein-coding
chr1-199C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr1	19901624	19903051	+	0	NA	intron (NAluY SINE	19942 NR_015207	23252	Hs.37498	ENS000000015207	OTUD3	DUBA4	OTU	ubiquitin protein-coding
chr1-542F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr1	54250660	54251690	+	0	NA	intron (NMIRc SINE	14732 NR_10354I	619518	Hs.59143	ENS00000000354I	SSBP3-AS1	Clorf191 SSBP3	antncRNA	
chr1-199C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr1	59673414	59674106	+	0	NA	intron (Nintron (N	59536 NR_039861.1	0.01E+08	NR_039861	ENS000000039861	MIR4711	-	microRNA ncRNA	
chr1-110C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	Intergeni Intergeni	13957 NR_00649Z	257	Hs.66995	ENS00000000649Z	ALX3	FND FND1	ALX homeobox protein-coding	
chr10-92C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr10	92311070	92314311	+	0	NA	intron (NCharlie2F	21523 NR_017824	54708	Hs.57349	ENS000000017824	5-Mar	MARCH-V V	membrane protein-coding	
chr11-108.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (NAluSp SIN	25111 NR_00135T	472	Hs.36743	ENS00000000135T	ATM	ATI ATA ATM	serin protein-coding	
chr12-87F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr12	878064	879400	+	0	NA	intron (Nintron (N	54344 NR_00129T	5893	Hs.41035	ENS00000000129T	CRAD52	-	RAD52	hom protein-coding
chr12-62E.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr12	62571474	62572226	+	0	NA	intron (Nintron (N	31584 NR_012168Z	283416	Hs.37588	ENS0000000012168Z	LINC0146E	C12orf61	long intncRNA	
chr12-11C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (NAluJo SIN	61353 NR_001347	28981	Hs.52382	ENS000000001347	IFT81	CDV-1 CDV	intraflagellar protein-coding	
chr14-73F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr14	73352760	73353649	+	0	NA	intron (NAluSp SIN	105376 NR_00100E	8650	Hs.52544	ENS00000000100E	NUMB	C14orf41 NUMB	endc protein-coding	
chr15-64C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr15	64977264	64987121	+	0	NA	intron (Nintron (N	11778 NR_001127	51324	Hs.24245	ENS000000001127	SPG21	ABHD21 AC	SPG21	abf protein-coding
chr15-74C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr15	74014144	74016273	+	0	NA	intron (Nintron (N	20492 NR_033244	5371	Hs.52646	ENS000000033244	PML	MYL PP867	promyeloc protein-coding	
chr16-14F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr16	14580490	14581086	+	0	NA	intron (Nintron (N	49472 NR_00258Z	5073	Hs.25319	ENS00000000258Z	PARN	DAN DKCB	poly(A)-s protein-coding	
chr16-19C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr16	19528925	19530069	+	0	NA	intron (NLMC5a LI	5555 NR_00119E	9738	Hs.27992	ENS00000000119E	CCP110	CP110 C	cytochrome protein-coding	
chr16-281.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr16	28175379	28180980	+	0	NA	intron (Nintron (N	33786 NR_01517I	23214	Hs.46046	ENS00000001517I	XPO6	EXP6 RANE	exportin protein-coding	
chr16-48C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr16	48348165	48352991	+	0	NA	intron (NHALIME LI	15309 NR_00100E	6477	Hs.70682	ENS00000000100E	SIAH1	SIAHA	siah 1 protein-coding	
chr17-62A.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr17	62491912	62493252	+	0	NA	intron (NAluSx1 SI	11469 NR_001284	11011	Hs.44507	ENS000000001284	TLK2	HsHPK MKR	tousled 1 protein-coding	
chr17-72A.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr17	72417722	72418465	+	0	NA	intron (Nintron (N	75282 NR_13522Z	146795	Hs.65174	ENS000000013522Z	LINC0200E	-	long intncRNA	
chr18-95F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr18	9523471	9525152	+	0	NA	intron (Nintron (N	48798 NR_00678E	10928	Hs.52899	ENS00000000678E	RALBP1	RIP1 RLIF	ralA binc protein-coding	
chr18-48E.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr18	48803460	48804946	+	0	NA	intron (Nintron (N	133603 NR_039897.1	0.01E+08	NR_039897	ENS000000039897	MIR4743	-	microRNA ncRNA	
chr19-11F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr19	11553321	11553755	+	0	NA	3' UTR (N3' UTR (N	1929 NR_00136Z	84337	Hs.63163	ENS00000000136Z	CELOF1	ELF1	elongatic protein-coding	
chr2-42F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr2	42350945	42352814	+	0	NA	intron (NAluJb SIN	8159 NR_13494F	9167	Hs.33963	ENS0000000013494F	COX7A2L	COX7AR C	cytochrome protein-coding	
chr2-112C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	intron (NLMIEF LIN	-12669 NR_001304	84269	Hs.37507	ENS000000001304	CHCHD5	C2orf9 C	cytochrome protein-coding	
chr21-15E.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr21	15874714	15877223	+	0	NA	intron (Nintron (N	145986 NR_00135Z	29761	Hs.74399	ENS00000000135Z	USP25	USP21	ubiquitin protein-coding	
chr21-29C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr21	29035906	29036544	+	0	NA	intron (Nintron (N	11557 NR_006447	10600	Hs.99819	ENS000000006447	USP16	UBP-M UBF	ubiquitin protein-coding	
chr21-46F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr21	46505475	46507117	+	0	NA	intron (NAluSz SIN	43825 NR_04640C	0.01E+08	Hs.73716	ENS00000004640C	DIP2A-IT1	-	DIP2A	intncRNA
chr22-29C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr22	29648355	29649332	+	0	NA	intron (NAluJb SIN	45210 NR_18183I	4771	Hs.18789	ENS00000000183I	CNF2	ACN BANF	neurofibr protein-coding	
chr22-31F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr22	31737360	31740055	+	0	NA	exon (NM exon (NM	11425 NR_17356E	253143	Hs.43890	ENS00000007356E	PRR14L	C22orf30	proline 1 protein-coding	
chr22-45T.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr22	45749712	45751046	+	0	NA	intron (NAluJb SIN	-10145 NR_03991E.1	0.01E+08	NR_03991E	ENS00000003991E	MIR4762	-	microRNA ncRNA	
chr3-689T.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr3	68976404	68976816	+	0	NA	non-codiron-codir	37074 NR_10382E	285203	Hs.51805	ENS00000000382E	EOGT	AER61 AOS	EGF domain protein-coding	
chr5-1371.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr5	13716912	13718507	+	0	NA	intron (Nintron (N	226771 NR_00136E	1767	Hs.21236	ENS00000000136E	DNAH5	CILD3 DN	dynein a protein-coding	
chr5-1374.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr5	13747331	13748890	+	0	NA	intron (NLIIP45 LIN	926771 NR_00136E	1767	Hs.21236	ENS00000000136E	DNAH5	CILD3 DN	dynein a protein-coding	
chr5-371F.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr5	37192329	37194180	+	0	NA	intron (NLMC5 LIN	-55792 NR_13426E	0.05E+08	Hs.17099	ENS000000013426E	LINC0105374	-	uncharactncRNA	
chr5-739A.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr5	73941364	73943814	+	0	NA	TTS (NM_C TTS (NM_C	129043 NR_001244	64283	Hs.48252	ENS000000001244	ARHGFB2	RGNEF RFI	Rho guanine protein-coding	
chr6-354T.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr6	35478720	35480921	+	0	NA	intron (Nintron (N	24924 NR_015704	972	Hs.43656	ENS000000015704	CD74	DHA-GL HLA	CD74	mole protein-coding
chr6-535C.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr6	53539947	53542276	+	0	NA	intron (NAluS2 SI	3990 NR_00149E	2729	Hs.65446	ENS00000000149E	GCLC	GCL GCS	glutamate protein-coding	
chr7-222T.5.922719	-0.19509	0.940246	-0.20749	0.835629	0.981636	chr7	2227314	2227900	+	0	NA	intron (Nintron (N	5338 NR_001304	8379	Hs.65483	ENS000000001304	CMAD1L1	MAD1 PIG	epitonic protein-coding	
chr8-526T.5.																				



chr11-685 6.376318	-0.18611	0.917656	-0.20281	0.839282	0.981636	chr11	68576338	68580096	+	0 NA	intron (Nintron (N	-106327 NM_015973	51083 Hs. 278959NM_015973	ENSG000000000000	GAL	ETL8 GAL-galanin ε protein-coding
chr20-327 6.376318	-0.18611	0.917656	-0.20281	0.839282	0.981636	chr20	3273453	3273918	+	0 NA	intron (MSTB LTR	-34495 NM_0011174	83959 Hs. 105607NM_032034	ENSG000000000000	SLC4A11	BTR1 CDPI solute cε protein-coding
chr10-124 5.963858	-0.19179	0.945789	-0.20278	0.839304	0.981636	chr10	1.25E+08	1.25E+08	+	0 NA	intron (Nintron (N	3711 NM_212554	399818 Hs. 720819NM_212554	ENSG000000000000	EEF1AKMT2	C10orf13 EEF1A lys protein-coding
chr1-234 4.230147	-0.223664	1.10466	-0.202473	0.839547	0.981636	chr1	2.34E+08	2.34E+08	+	0 NA	intron (Nintron (N	32661 NM_005646	6894 Hs. 498116NM_005646	ENSG000000000000	TARBP1	TRM3 TRM1 TAR (HIV- protein-coding
chr14-100 6.425315	-0.18516	0.916528	-0.20203	0.839895	0.981636	chr14	1E+08	1E+08	+	0 NA	intron (MIR SINE	4720 NM_004184	7453 Hs. 497599NM_004184	ENSG000000000000	WARS	GAMMA-2 ε tryptophan protein-coding
chr15-228 6.425315	-0.18516	0.916528	-0.20203	0.839895	0.981636	chr15	22899867	22900386	+	0 NA	intron (MLT1C LTF	17187 NM_001033	23191 Hs. 26704 NM_014608	ENSG000000000000	CYFIP1	P140SRA-1 cytoplasm protein-coding
chr20-188 6.425315	-0.18516	0.916528	-0.20203	0.839895	0.981636	chr20	18528376	18529006	+	0 NA	intron (Nintron (N	20751 NM_032988	10843 Hs. 369377NM_006363	ENSG000000000000	SEC23B	CDA-11 C SEC23 hom protein-coding
chr5-684 6.425315	-0.18516	0.916528	-0.20203	0.839895	0.981636	chr5	64844868	64845670	+	0 NA	3' UTR (N3' UTR (N	76339 NM_001364	10283 Hs. 371372NM_005863	ENSG000000000000	CWC27	NY-CO-10 CWC27 spl protein-coding
chr5-1798 6.425315	-0.18516	0.916528	-0.20203	0.839895	0.981636	chr5	1.8E+08	1.8E+08	+	0 NA	intron (NCharlie4ε	6017 NM_001142	8878 Hs. 587292NM_003900	ENSG000000000000	SQSTM1	A170 DMRV sequestos protein-coding
chr1-2255 11.60583	-0.13911	0.688887	-0.20193	0.839969	0.981636	chr1	2.26E+08	2.26E+08	+	0 NA	intron (Nintron (N	-78045 NM_194442	3930 Hs. 435166NM_002229	ENSG000000000000	LBR	C14SR DHC lamin B1 protein-coding
chr19-215 11.60583	-0.13911	0.688887	-0.20193	0.839969	0.981636	chr19	21375148	213800247	+	0 NA	3' UTR (N3' UTR (N	18697 NM_001355	148203 Hs. 124384NM_001355	ENSG000000000000	ZNF738	- zinc finger protein-coding
chr3-1224 11.60583	-0.13911	0.688887	-0.20193	0.839969	0.981636	chr3	1.22E+08	1.22E+08	+	0 NA	intron (Nintron (N	21407 NR_125405	1.03E+08 Hs. 675056NR_125405	ENSG000000000000	LOC102722	- uncharactericnRNA
chr1-2645 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr1	26455500	26456659	+	0 NA	intron (Nintron (N	11333 NR_125952	1.02E+08 Hs. 663256NR_125952	LOC101928	- uncharactericnRNA	
chr1-2645 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr1	2.4E+08	2.4E+08	+	0 NA	intron (NLM5 LINE	210748 NM_020066	56776 Hs. 24889 NM_020066	ENSG000000000000	FMN2	- formin 2 protein-coding
chr3-168 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr3	1.68E+08	1.68E+08	+	0 NA	exon (NM exon (NM	55076 NM_014498	27333 Hs. 143600NM_014498	ENSG000000000000	GOLIM4	GIMPC GOL golgi intr protein-coding
chr5-712 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr5	71257453	71258169	+	0 NA	intron (Nintron (N	1484 NR_033968	1E+08 Hs. 665231NR_033968	GUSBP9	- GUSB pseudo	
chr5-138 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr5	1.39E+08	1.39E+08	+	0 NA	intron (Nintron (N	42866 NM_001323	1495 Hs. 445981NM_001903	ENSG000000000000	CTNNA1	CAP102 ML catenin ε protein-coding
chr6-720 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr6	7203515	7203931	+	0 NA	intron (Nintron (N	95762 NM_001003	6239 Hs. 298248NM_002955	ENSG000000000000	NRBE1	F1NB HNT ras resp protein-coding
chr7-878 5.453404	-0.20075	0.994503	-0.20186	0.840028	0.981636	chr7	87858406	87859498	+	0 NA	intron (Nintron (N	17408 NM_018842	55972 Hs. 208414NM_018842	ENSG000000000000	SLC25A40	MCFP solute cε protein-coding
chr1-180 11.15224	-0.14178	0.702598	-0.2018	0.840076	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (Nintron (N	69406 NM_014810	9857 Hs. 413045NM_014810	ENSG000000000000	CEP350	CAP350 GW centrosome protein-coding
chr1-2098 11.15224	-0.14178	0.702598	-0.2018	0.840076	0.981636	chr1	2.1E+08	2.1E+08	+	0 NA	intron (Nintron (N	14866 NM_014388	27042 Hs. 194754NM_014388	ENSG000000000000	UTP25	Clorf107 UTP25 smε protein-coding
chr2-463 11.15224	-0.14178	0.702598	-0.2018	0.840076	0.981636	chr2	46364789	46386977	+	0 NA	intron (Nintron (N	18284 NR_146999	1.05E+08 Hs. 570163NR_146999	ENSG000000000000	LOC100182	- long intencnRNA
chr7-265 4.718878	0.218058	1.081219	0.201678	0.840169	0.981636	chr7	2658754	2659526	+	0 NA	intron (Nintron (N	-20382 NM_133463	155185 Hs. 42221 NM_133463	ENSG000000000000	CAMZ1	- archaealys protein-coding
chr10-136 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr10	13699506	13700616	+	0 NA	intron (Nintron (N	7506 NM_001318	55691 Hs. 330463NM_018027	ENSG000000000000	FRMD4A	CCAFCA FFFERM domε protein-coding
chr11-938 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr11	93813644	93815022	+	0 NA	3' UTR (N3' UTR (N	30051 NM_004266	9440 Hs. 444931NM_004266	ENSG000000000000	MED17	CRSP6 CRS mediator protein-coding
chr12-87 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr12	8754702	8755348	+	0 NA	intron (NAluSx1 SI	57034 NR_147946	57494 Hs. 504677NM_020734	ENSG000000000000	RIMKLB	FAM80B Nε ribosomal protein-coding
chr13-95 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr13	95613790	95614979	+	0 NA	intron (NAluSx1 SI	30322 NM_198968	22873 Hs. 656588NM_014934	ENSG000000000000	DZIP1	DZIP DZIP DAZ inter protein-coding
chr13-111 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr13	1.11E+08	1.11E+08	+	0 NA	intron (NLM1 LINE	17901 NM_001354	8874 Hs. 508738NM_003893	ENSG000000000000	ARHGEP7	BETA-PIX Rho guaniprotein-coding
chr19-21 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr19	21365403	21366341	+	0 NA	intron (NAluSx1 SI	6872 NM_001355	148203 Hs. 124384NM_001355	ENSG000000000000	ZNF738	- zinc finger protein-coding
chr19-48 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr19	48850710	48851932	+	0 NA	intron (Nintron (N	-14830 NM_016246	51171 Hs. 18788 NM_016246	ENSG000000000000	HSD17B14	DHR510 SE hydroxyst protein-coding
chr19-55 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr19	55682123	55686688	+	0 NA	intron (Nintron (N	7780 NM_001130	29924 Hs. 279953NM_013333	ENSG000000000000	CEPN1	- epsin 1 protein-coding
chr2-202 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr2	2.02E+08	2.02E+08	+	0 NA	intron (NAluY SINE	10065 NM_001005	7341 Hs. 81424 NM_003335	ENSG000000000000	SUMO1	DAP1 GMP1 small ubi protein-coding
chr3-142 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (Nintron (N	98322 NM_001282	54646 Hs. 435103NM_019001	ENSG000000000000	XRN1	1-Sep 5'-3' ex protein-coding
chr4-67 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr4	67678783	67679388	+	0 NA	intron (NLMC5a LI	22070 NM_018227	55236 Hs. 212774NM_018227	ENSG000000000000	CUBA6	E1-L2 MOF ubiquitir protein-coding
chr4-769 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr4	76942453	76943388	+	0 NA	IntergeniAluSx SIN	-6827 NM_018242	55752 Hs. 128199NM_018242	ENSG000000000000	SEPTIN13	11-Sep septin 11 protein-coding
chr7-647 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr7	64798593	64799839	+	0 NA	exon (NM exon (NM	4813 NM_001271	7697 Hs. 184088NM_006524	ENSG000000000000	ZNF138	pH2-32 zinc finger protein-coding
chr8-900 5.956	-0.18957	0.940431	-0.20158	0.840245	0.981636	chr8	90005608	90006309	+	0 NA	intron (Nintron (N	4481 NM_001355	1666 Hs. 492212NM_001355	ENSG000000000000	DECR1	DECR NDF2, 4-dienε protein-coding
chr1-361 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr1	36138035	36138526	+	0 NA	intron (Nintron (N	11206 NM_014408	27095 Hs. 523131NM_014408	ENSG000000000000	TRAPP3	BET3 traffickiprotein-coding
chr11-68 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr11	68830171	68830750	+	0 NA	intron (Nintron (N	11456 NM_001876	1374 Hs. 50304NM_001876	ENSG000000000000	CPT1A	CPT1 CPT carnitine protein-coding
chr16-23 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr16	23648920	23649700	+	0 NA	intron (NLM2 LINE	7844 NM_032488	84516 Hs. 435941NM_032488	ENSG000000000000	CCTN5	- dynactin protein-coding
chr17-16 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr17	16420721	16421130	+	0 NA	intron (NLM3E3 LI	5354 NM_016113	51393 Hs. 279746NM_016113	ENSG000000000000	TRPV2	VRL VRL-1 transient protein-coding
chr17-62 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr17	62034290	62035926	+	0 NA	intron (NAluSx1 SI	30170 NM_005121	9699 Hs. 282678NM_005121	ENSG000000000000	MED13	ARC250 DF mediator protein-coding
chr19-16 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr19	16433265	16434859	+	0 NA	intron (Nintron (N	37908 NM_001258	58513 Hs. 654633NM_021233	ENSG000000000000	EPS15L1	EPS15R epidermal protein-coding
chr2-320 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr2	32032685	32033700	+	0 NA	intron (NAluSx1 SI	6613 NM_001321	84661 Hs. 531788NM_032574	ENSG000000000000	DPY30	Cps25 HDF dyf-30 hiprotein-coding
chr2-132 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr2	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	43957 NR_135572	1.02E+08 Hs. 680114NR_135572	ENSG000000000000	CNKAP5-AS	- NCKAP5 arncRNA
chr2-135 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr2	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	-19415 NR_029672	406915 NR_029672	ENSG000000000000	MIR128-1	MIR128A vmicroRNA ncRNA
chr2-157 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr2	1.58E+08	1.58E+08	+	0 NA	intron (Nintron (N	77793 NM_001347	90 Hs. 470316NM_001108	ENSG000000000000	ACVR1	ACTR1 ACV activin ε protein-coding
chr3-142 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr3	1.42E+08	1.42E+08	+	0 NA	intron (NAluSx1 SI	78142 NM_001282	54464 Hs. 435103NM_019001	ENSG000000000000	XRN1	1-Sep 5'-3' ex protein-coding
chr4-267 6.417457	-0.18298	0.909101	-0.20127	0.840487	0.981636	chr4	26709782	26710450	+	0 NA	intron (NLM4A LIN	126032 NM_018317	55296 Hs. 479403NM_018317			

chr17-59c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr17	59056447	59057471	+	0	NA	exon (NM exon (NM	49921	NR_148347	4591	Hs.579079	ENM_015294	ENSG000003	TRIM37	MUL POB1	tripartit	protein-coding	
chr18-12c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr18	12333738	12334060	+	0	NA	intron (NMIR SINE	25658	NM_001303	84617	Hs.193491	NM_03252f	ENSG000003	TUBB6	FPVEP Hs	tubulin t	protein-coding	
chr2-177c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr2	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	3660	NR_03607f	1E+08	NR_03607f	ENSG000003	MIR3128	mir-3128	microRNA	ncRNA		
chr3-112f	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr3	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	10869	NM_00134f	55032	Hs.23748C	NM_01794f	ENSG000003	SLC35A5	-	solute c	protein-coding	
chr4-438f	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr4	438972	440905	+	0	NA	TTS (NM_TTS (NM_L	34271	NR_002451	79963	Hs.67749f	NM_02490f	ENSG000003	ABCA11P	ABCA11 ES	ATP bindi	pseudo	
chr4-250c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr4	2503934	2504886	+	0	NA	intron (NLM5 LINE	-30965	NM_00136f	8603	Hs.652364	NM_00370f	ENSG000003	FAM193A	C4orf8 RF	family w	protein-coding	
chr4-531f	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr4	53183117	53183595	+	0	NA	intron (NLIP44 LIN	182705	NM_15254f	152579	Hs.302287	NM_15254f	ENSG000003	SCFD2	STXBPL1 L	secl1	family protein-coding	
chr4-122c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	56655	NM_01531f	84162	Hs.408142	NM_01531f	ENSG000003	KIAA1109	ALKKUCS FK	IAA109	protein-coding	
chr5-131c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr5	1.31E+08	1.31E+08	+	0	NA	intron (NLIP44 LIN	73567	NM_00103f	56990	Hs.50882f	NM_02024f	ENSG000003	CDC42SE2	SPEC2	CDC42 sm	protein-coding	
chr6-110f	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr6	11096936	11097717	+	0	NA	intron (NMLT1B LTF	3492	NM_00113f	221710	Hs.65660C	NM_00113f	ENSG000003	SMIM13	C6orf228	small int	protein-coding	
chr6-831c	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr6	83135882	83137800	+	0	NA	intron (Nintron (N	56424	NM_00119f	5238	Hs.66166f	NM_01559f	ENSG000003	PGM3	AGM1 TMD	2 phospho	protein-coding	
chr7-659f	5.948143	-0.18733	0.940364	-0.19921	0.842096	0.981636	chr7	65970432	65971011	+	0	NA	intron (NALuY SINE	11492	NM_00129f	2990	Hs.25523C	NM_00018f	ENSG000003	GUSB	BG MP57	glucuron	protein-coding	
chr16-74c	5.907003	-0.19054	0.956589	-0.19918	0.842119	0.981636	chr16	74451456	74452090	+	0	NA	non-codir non-codir	-30303	NM_001011	497190	Hs.45467C	NM_001011	ENSG000003	CLEC18B	MRC12	C-type l	protein-coding	
chr6-113c	5.907003	-0.19054	0.956589	-0.19918	0.842119	0.981636	chr6	1.14E+08	1.14E+08	+	0	NA	non-codir non-codir	-30600	NR_12584f	1.02E+08	Hs.12928C	NM_12584f	ENSG000003	HDAC2-AS2	-	HDAC2 anc	ncRNA	
chr8-1334	5.907003	-0.19054	0.956589	-0.19918	0.842119	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	100917	NM_00303f	6482	Hs.374257	NM_00303f	ENSG000003	ST3GAL1	Gal-Nac6S	ST3 beta	protein-coding	
chr9-1131	5.907003	-0.19054	0.956589	-0.19918	0.842119	0.981636	chr9	1.13E+08	1.13E+08	+	0	NA	exon (NM exon (NM	27202	NM_01525f	23307	Hs.522351	NM_01525f	ENSG000003	FKBP15	FKBP133 F	FKBP pro	protein-coding	
chr4-707c	6.36846	-0.18408	0.924819	-0.19905	0.842224	0.981636	chr4	70798200	70798399	+	0	NA	intron (NALuJo SIN	41204	NM_00109f	2926	Hs.30976f	NM_00209f	ENSG000003	GRSF1	-	G-rich R	protein-coding	
chr5-662c	6.36846	-0.18408	0.924819	-0.19905	0.842224	0.981636	chr5	66021068	66022006	+	0	NA	intron (Nintron (N	-75964	NR_028474	1E+08	Hs.60806C	NR_028474	LOC10030f	-	-	LSM3 hom	pseudo	
chr5-785c	6.36846	-0.18408	0.924819	-0.19905	0.842224	0.981636	chr5	78563419	78563618	+	0	NA	intron (NALuSz SIN	85254	NM_00577f	10184	Hs.79299	NM_00577f	ENSG000003	LHFPL2	-	LHFPL	tet	protein-coding
chr5-149f	6.878914	-0.17776	0.893762	-0.19889	0.842349	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	16615	NM_001271	1452	Hs.52986f	NM_00189f	ENSG000003	CSNK1A1	CK1 CK1a	casein k	protein-coding	
chr22-36c	11.63912	-0.13262	0.688626	-0.19787	0.843145	0.981636	chr22	36303783	36324679	+	0	NA	exon (NM exon (NM	-27324	NR_106877	1.02E+08	NR_106877	ENSG000003	MIR6819	hsa-mir-6	microRNA	ncRNA		
chr10-102	6.871056	-0.17566	0.889338	-0.19752	0.843419	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (NALuSg SIN	-48809	NM_00128f	4791	Hs.73090	NM_00250f	ENSG000003	NFKB2	CVID10 H	2 nuclear f	protein-coding	
chr4-730f	6.871056	-0.17566	0.889338	-0.19752	0.843419	0.981636	chr4	73083630	73084270	+	0	NA	intron (N(A)n Simp	-14191	NM_00130f	285521	Hs.356697	NM_17382f	ENSG000003	COX18	COX18HS	cytochro	protein-coding	
chr1-155f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr1	15568857	15569979	+	0	NA	non-codir non-codir	15633	NM_00247f	79814	Hs.46153f	NM_0247f	ENSG000003	AGX18	-	agmatina	protein-coding	
chr1-757c	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr1	75734519	75735690	+	0	NA	intron (NALuSz SIN	9909	NR_13074f	1744	Hs.52545f	NR_13074f	DLSTP1	DLSTP	dihydroli	pseudo		
chr1-204f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr1	2.05E+08	2.05E+08	+	0	NA	intron (NALuY SINE	18819	NM_00239f	4194	Hs.49749f	NM_00239f	ENSG000003	MDM4	HDMX MDM	MDM4 reg	protein-coding	
chr1-236f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr1	2.36E+08	2.36E+08	+	0	NA	exon (NM exon (NM	19505	NM_00250f	4811	Hs.356624	NM_00250f	ENSG000003	ND1	NID	nidogen l	protein-coding	
chr10-934	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr10	93443043	93445001	+	0	NA	intron (Nintron (N	38312	NM_013451	26509	Hs.60208f	NM_013451	ENSG000003	MYOF	FERIL3	myoferli	protein-coding	
chr10-97f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr10	97670576	97673700	+	0	NA	intron (NALuSg SIN	15088	NM_02173f	60370	Hs.23918	NM_02173f	ENSG000003	AVP11	PP5395 V	arginine	protein-coding	
chr11-367	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr11	3672748	3673694	+	0	NA	Intergeni ALuY SINE	-2337	NM_00130f	57053	Hs.73280f	NM_02040f	ENSG000003	CHRNA10	-	choline	protein-coding	
chr11-73f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr11	73684512	73685312	+	0	NA	intron (Nintron (N	35999	NM_00113f	58473	Hs.44548f	NM_02120f	ENSG000003	PLEKHB1	KPL1 PHR	1 pleckst	protein-coding	
chr11-93f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr11	93669528	93672650	+	0	NA	intron (NALuSx1 SI	9407	NM_00339f	85459	Hs.45841f	NM_00339f	ENSG000003	CEP295	KIAA1731	centrosom	protein-coding	
chr11-12f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr11	1.26E+08	1.26E+08	+	0	NA	intron (NALuSz SIN	16097	NM_00313f	6734	Hs.36837f	NM_00313f	ENSG000003	SRPRA	DP SRPR	SRP rec	protein-coding	
chr12-124	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr12	1.25E+08	1.25E+08	+	0	NA	intron (NMLT1C LTF	4110	NM_03265f	57647	Hs.10738f	NM_03265f	ENSG000003	DHX37	DDX37 Dh	DEAH-box	protein-coding	
chr13-49f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr13	49999295	50000433	+	0	NA	intron (NMTR3 SINE	2822	NM_052811	10206	Hs.43692f	NM_00579f	ENSG000003	TRIM13	CAR DLEU	f tripartit	protein-coding	
chr14-69f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr14	69443793	69444796	+	0	NA	intron (NCharlie4	-40434	NM_001161	40224	Hs.50979f	NM_001161	ENSG000003	PLEKHD1	UPF0639	pleckstri	protein-coding	
chr14-10f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	promoter-promoter-	-503	NR_14600f	79104	Hs.11810f	NR_02414f	MEG8	Bsr Irm	maternal	ncRNA		
chr15-79f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr15	79877000	79878730	+	0	NA	intron (NLM14a LI	19132	NR_037654	10588	Hs.194294	NM_00644f	ENSG000003	MTHFS	HsT1926b	methenyl	protein-coding	
chr17-381	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr17	3813743	3815304	+	0	NA	intron (Nintron (N	-13335	NM_00220f	3682	Hs.51386f	NM_00220f	ENSG000003	ITGAE	CD103 HUM	integen	protein-coding	
chr18-361	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr18	36161620	36163146	+	0	NA	intron (NLM1E LIN	25052	NR_13460f	1.02E+08	Hs.60067f	NR_13460f	ENSG000003	LOC101927	-	uncharact	ncRNA	
chr19-13f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr19	13998851	14000626	+	0	NA	intron (NMERS5B DN	6861	NM_00291f	5989	Hs.65521f	NM_00291f	ENSG000003	RFX1	EFC REF	regulator	protein-coding	
chr19-17f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr19	17219541	17219811	+	0	NA	exon (NM exon (NM	4319	NM_01846f	55850	Hs.16187	NM_01846f	ENSG000003	USE1	D12 MDS0	5 uncon	protein-coding	
chr2-991f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr2	99189353	99190147	+	0	NA	intron (Nintron (N	8566	NR_02835f	51263	Hs.34673f	NM_01650f	ENSG000003	MRPL30	L28MT L3	C mitochond	protein-coding	
chr2-171f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr2	1.72E+08	1.72E+08	+	0	NA	intron (NMLT1C LTF	19415	NM_00132f	1781	Hs.54625f	NM_00137f	ENSG000003	DYNC112	DIC74 DNC	dynein c	protein-coding	
chr20-11f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr20	1130626	1133417	+	0	NA	intron (NLM1D LINE	4919	NM_00132f	9791	Hs.47191f	NM_00681f	ENSG000003	PSMF1	P131	proteasom	protein-coding	
chr22-31f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr22	31689721	31690717	+	0	NA	intron (NALuSx2 SI	-27655	NM_00132f	23761	Hs.42055f	NM_01433f	ENSG000003	PISD	DJ858B16	phosphat	protein-coding	
chr22-41f	6.401741	-0.17879	0.908907	-0.19671	0.844055	0.981636	chr22	41575281	41577833	+	0	NA	TTS (NM_TTS (NM_C	13283	NM_00267f	5372	Hs.75835	NM_00267f	ENSG000003	PMM1	PMM 1 PMM	phosphom	protein-coding	
chr3-478f	6.401741	-0																						



chr7-133c 6.442881	-0.17578	0.906479	-0.19392	0.846239	0.981636	chr7	1.33E+08	1.33E+08	+	0	NA	intron (AluY SINE	14014	NM_017812	54927	Hs.65501CNM_017812	ENSG00000CHCHD3	MICOS19	coiled-cc	protein-coding				
chr9-5657 6.442881	-0.17578	0.906479	-0.19392	0.846239	0.981636	chr9	5657464	5658103	+	0	NA	intron (Cheshire	28664	NM_001206	57589	Hs.21152CNM_020822	ENSG00000R1C1	CIP150 KIR1C1	homc	protein-coding				
chr9-1284 6.442881	-0.17578	0.906479	-0.19392	0.846239	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	TTS (NM_TTS (NM_C	-8987	NM_001003	2733	Hs.52241ENM_001495	ENSG00000GLE1	CAAHG CA^GLE1	RNA	protein-coding				
chr15-101 6.912195	-0.17229	0.892308	-0.19377	0.846358	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (MLT1H1 IR	26032	NM_152334	123283	Hs.65716CNM_152334	ENSG00000TARSL2	-	thryonil-	protein-coding				
chr18-362 6.693454	0.208742	1.077444	0.193738	0.846381	0.981636	chr18	36229896	36231586	+	0	NA	intron (L1JMB1 Lin	43244	NM_017947	55034	Hs.40502ENM_017947	ENSG00000MOCOS	HMCS MCS	molybden	protein-coding				
chr6-3644 11.58226	-0.13549	0.700192	-0.19351	0.846559	0.981636	chr6	36448828	36449539	+	0	NA	intron (LTR12 LTF	6183	NM_173562	222658	Hs.188757NM_173562	ENSG00000KCTD20	C6orf69 c	potassium	protein-coding				
chr1-1247 4.204724	0.21376	1.105168	0.193418	0.846631	0.981636	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR Alpha	3182870	NR_003955	647121	Hs.697682NR_003955	ENSG00000EMBP1	10426	Hs.224152NM_006322	ENSG00000TUBGPC3	104p ALP6	ubigin	psuedo	
chr13-112 6.904337	-0.17077	0.883429	-0.19333	0.846721	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (N intron (N	34194	NM_006322	10426	Hs.224152NM_006322	ENSG00000TUBGPC3	104p ALP6	ubigin	psuedo				
chr15-286 6.904337	-0.17077	0.883429	-0.19333	0.846721	0.981636	chr15	28651645	28652294	+	0	NA	IntergeniMLT1C LTF	-2473	NR_036443	440248	Hs.531505NM_199044	ENSG00000CHERC2P9	-	hect dom	psuedo				
chr16-252 6.904337	-0.17077	0.883429	-0.19333	0.846721	0.981636	chr16	25248300	25249238	+	0	NA	intron (NL1MA7 LIN	9036	NM_001012	342357	Hs.513451NM_001012	ENSG00000ZKSCAN2	342357	Hs.513451NM_001012	ENSG00000ZKSCAN2	ZNF694 Z	zinc	finger	protein-coding
chr3-4905 6.904337	-0.17077	0.883429	-0.19333	0.846721	0.981636	chr3	49051767	49053037	+	0	NA	intron (N intron (N	-23004	NM_000084	3615	Hs.654400CNM_000084	ENSG00000LMPDH2	3615	Hs.654400CNM_000084	ENSG00000LMPDH2	IMF	inosine	n	protein-coding
chr9-1363 6.904337	-0.17077	0.883429	-0.19333	0.846721	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (N intron (N	-3648	NM_001145	26086	Hs.23937CNM_015597	ENSG00000GSPSM1	AGS3	G	protein	protein-coding			
chr10-701 5.205758	0.196095	1.0151	0.193178	0.846819	0.981636	chr10	70116799	70117482	+	0	NA	intron (N intron (N	15685	NM_032797	84883	Hs.65068CNM_032797	ENSG00000AIFM2	AMID PRG3	apoptosis	protein-coding				
chr17-351 5.899145	-0.18813	0.974261	-0.19310	0.846883	0.981636	chr17	35009661	35010173	+	0	NA	TTS (NM_TTS (NM_C	29405	NM_013979	3980	Hs.100295NM_002311	ENSG00000LIG3	LIG2 LIG3	DNA	ligas	protein-coding			
chr2-1903 4.70917	0.202312	1.048	0.193046	0.846923	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (N intron (N	12176	NM_014362	26275	Hs.656685NM_014362	ENSG00000HIBCH	HIBYLCOAF3	-3	hydroxy	protein-coding			
chr2-2187 4.70917	0.202312	1.048	0.193046	0.846923	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (N intron (N	29009	NM_014640	9654	Hs.471405NM_014640	ENSG00000TTL4	-	tubulin	protein-coding				
chr4-1358 4.70917	0.202312	1.048	0.193046	0.846923	0.981636	chr4	13582740	13584355	+	0	NA	intron (N intron (N	-35723	NR_015450	285548	Hs.529284NR_015450	LINC01099-	-	long	intencRNA				
chr12-686 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr12	68700756	68701431	+	0	NA	intron (N intron (N	14115	NM_020401	57122	Hs.524574NM_020401	ENSG00000NUP107	NPHS11 N	nucleopor	protein-coding				
chr15-447 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr15	44731623	44732744	+	0	NA	non-codiron-codir	3195	NR_125376	1E+08	Hs.489254NR_125376	LOC100419-	-	ring	finger	psuedo			
chr2-5532 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr2	55320073	55321506	+	0	NA	intron (N intron (N	38470	NR_027255	344405	Hs.445292NM_001080	ENSG00000PRORSD1P	NCRNA0011	prolyl-tf	psuedo				
chr21-392 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr21	39216805	39217321	+	0	NA	intron (N ATn Sin	-33549	NR_203433	8624	Hs.473835NM_003720	ENSG00000PSMG1	C21LRP DS	proteasom	protein-coding				
chr4-1767 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr4	1.77E+08	1.77E+08	+	0	NA	intron (N intron (N	88542	NM_005425	7424	Hs.43521ENM_005425	ENSG00000VEGFC	F14-L L	vascular	protein-coding				
chr4-1832 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr4	1.83E+08	1.83E+08	+	0	NA	intron (N intron (N	30958	NM_001111	53842	Hs.333175NM_001111	ENSG00000CLDN22	CLDN21	claudin	2	protein-coding			
chr5-113 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (NL1PA5 LIN	103243	NM_152624	167227	Hs.443875NM_152624	ENSG00000DCP2	NUTD20	decapping	protein-coding				
chr6-178 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr6	17807707	17808147	+	0	NA	intron (N AACn Si	100884	NR_134611	1.05E+08	Hs.718703NR_134611	ENSG00000LOC105374	-	uncharact	ncRNA				
chr6-1456 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr6	1.46E+08	1.46E+08	+	0	NA	intron (N intron (N	22204	NM_173082	257218	Hs.723297NM_173082	ENSG00000SHPRH	BAS54515.2	SNF2	hist	protein-coding			
chr8-1275 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (N intron (N	17398	NR_031610	1E+08	NR_031610	ENSG00000MIR1205	MIRN1205	microRNA	ncRNA				
chr8-1408 6.393883	-0.17671	0.916145	-0.19289	0.847046	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (NL1PA13 LI	-81583	NR_029892	442893	NR_029892	ENSG00000MIR151A	MIR151 M	microRNA	ncRNA				
chr4-1682 6.466455	-0.18234	0.945505	-0.19285	0.847077	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (N TATGn S	44962	NM_017631	55601	Hs.59171CNM_017631	ENSG00000CDDX60	-	DexH/H-bc	protein-coding				
chr1-2366 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr1	2.36E+08	2.36E+08	+	0	NA	intron (N intron (N	48358	NM_002508	4811	Hs.356624NM_002508	ENSG00000NID1	NID	nidogen	protein-coding				
chr11-122 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr11	12221683	12223439	+	0	NA	intron (N intron (N	58878	NR_106735	1.02E+08	NR_106735	ENSG00000MIR6124	hsa-mir-6	microRNA	ncRNA				
chr12-686 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr12	68697252	68698333	+	0	NA	intron (N AluX1 S1	10813	NM_020401	57122	Hs.524574NM_020401	ENSG00000NUP107	NPHS11 N	nucleopor	protein-coding				
chr13-95 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr13	95089750	95090523	+	0	NA	intron (NL1PB1 LIN	-120208	NR_145733	1.1E+08	NR_145733	SNORD13G	-	small	nucsnRNA				
chr14-102 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	intron (N AluY SINE	53020	NM_001348	122416	Hs.43294ENM_152322	ENSG00000ANKRD9	-	ankyrin	protein-coding				
chr15-444 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr15	44632961	44643883	+	0	NA	intron (N intron (N	30240	NM_001163	80208	Hs.656271NM_025137	ENSG00000SPG11	ALS5 CMT2	SPG11	ves	protein-coding			
chr19-366 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr19	36430111	36431446	+	0	NA	intron (N intron (N	-16763	NM_021126	55809	Hs.12842ENM_021231	ENSG00000CACTIN	C19orf29 c	actin,	protein-coding				
chr2-1175 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr2	1.18E+08	1.18E+08	+	0	NA	intron (N intron (N	64585	NM_019044	54520	Hs.10784ENM_019044	ENSG00000CCDC93	-	coiled-cc	protein-coding				
chr2-1621 5.213616	0.193152	1.002969	0.19258	0.847288	0.981636	chr2	1.62E+08	1.62E+08	+	0	NA	TTS (NR_TTS (NR_1	-21025	NM_002054	2641	Hs.516494NM_002054	ENSG00000CGG	GLP-1 GLF	glucagon	protein-coding				
chr12-574 12.11814	-0.13005	0.675388	-0.19255	0.847308	0.981636	chr12	57489146	57493144	+	0	NA	intron (N ALuG3 SIN	-2321	NM_001319	64333	Hs.43712ENM_032496	ENSG00000ARHGAP9	10C RGL1	Rho	GTPas	protein-coding			
chr18-42c 6.85534	-0.17177	0.893403	-0.19226	0.847537	0.981636	chr18	42029848	42030047	+	0	NA	intron (N MIR SINE	74713	NM_002647	5289	Hs.464971NM_002647	ENSG00000PIK3C3	VPS34 Vps	phosphati	protein-coding				
chr1-8382 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr1	8382168	8383737	+	0	NA	intron (N intron (N	40880	NM_001042	473	Hs.463041NM_012102	ENSG00000RERE	ARG ARP	arginine	protein-coding				
chr1-2876 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr1	28765515	28766233	+	0	NA	intron (NL1MC4 LIN	28934	NM_001172	51441	Hs.53228ENM_016255	ENSG00000YTHDF2	CAHL HGR	CYTH	N6-mc	protein-coding			
chr1-2237 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (N intron (N	54524	NM_001031	7159	Hs.52396ENM_005422	ENSG00000TP53BP2	53BP2 ASF	ythrom	prc	protein-coding			
chr10-186 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr10	18672855	18675724	+	0	NA	intron (N intron (N	14858	NM_178815	221079	Hs.25362	NR_178815	ENSG00000ARL5B	ARL8	ADP	ribos	protein-coding		
chr12-111 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	intron (N intron (N	16885	NM_001346	51347	Hs.64442CNM_016281	ENSG00000TAOK3	DPK JJK W	TAD	kinas	protein-coding			
chr13-118 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (N intron (N	-25445	NR_107042	1.02E+08	NR_107042	ENSG00000MIR8075	hsa-mir-5	microRNA	ncRNA				
chr14-884 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr14	88469069	88470189	+	0	NA	exon (NM exon (NM	83972	NM_018418	55812	Hs.52551ENM_018418	ENSG00000SPATA7	HEL-5-29c	spermatog	protein-coding				
chr15-251 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr15	25107184	25110326	+	0	NA	TTS (NR_TTS (NM_C	487	NR_047032	1.01E+08	NR_047032	ENSG00000SNORD116	HBII-85-2	small	nucsnRNA				
chr15-504 6.435023	-0.17371	0.904047	-0.19214	0.84763	0.981636	chr15	50443126	50444349	+	0	NA	intron (N AluSx4 S1	19332	NM_001128	9101	Hs.443731NM_005154								

chr11-534	5.221474	0.190358	0.999142	0.190522	0.8489	0.981636	chr11	53408632	53409609	+	0	NA	IntergeniALR/Alpha	1194878	NM_001004	119749	Hs.553564NM_001004	ENSG00000404C46	-	olfactoryprotein-coding	
chr17-171	5.221474	0.190358	0.999142	0.190522	0.8489	0.981636	chr17	17133312	17134072	+	0	NA	intron (Nintron (N	72641	NM_178836	201164	Hs.729075NM_178836	ENSG000004PLD6	-	ZUC phospholiprotein-coding	
chr18-685	5.221474	0.190358	0.999142	0.190522	0.8489	0.981636	chr18	6897328	6898079	+	0	NA	intron (NLM2D LIN	32166	NR_034100	400643	Hs.25392CNM_001103	ENSG000004LINC00066	-	long intencRNA	
chr19-161	5.221474	0.190358	0.999142	0.190522	0.8489	0.981636	chr19	16125760	16126353	+	0	NA	intron (Nintron (N	-7972	NM_032855	84941	Hs.631617NM_032855	ENSG000004HSH2D	-	ALX HSH2 hematopoieticprotein-coding	
chr10-804	5.478828	-0.19173	1.00639	-0.19052	0.848906	0.981636	chr10	80469490	80470627	+	0	NA	intron (NMER2 DNA	1795	NM_001351	81619	Hs.30861ENM_030927	ENSG000004TSPAN14	-	DC-TM4F2  tetraspaninprotein-coding	
chr19-444	5.478828	-0.19173	1.00639	-0.19052	0.848906	0.981636	chr19	44444901	44445415	+	0	NA	intron (NLa2 LINE	3314	NR_103551	7772	Hs.70934ENM_014518	ENSG000004ZNF229	-	zinc fingprotein-coding	
chr5-722	5.478828	-0.19173	1.00639	-0.19052	0.848906	0.981636	chr5	72225151	72227131	+	0	NA	intron (NLa3b LINE	46854	NM_001324	4131	Hs.335079NM_005909	ENSG000004MAP1B	-	FUTSCH MAP1BmicroRNA ncRNA	
chr13-111	4.717028	0.199274	1.047917	0.190162	0.849183	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	66336	NR_148221	1.05E+08	Hs.13472ENR_148221	LOC105370	-	uncharacterncRNA	
chr2-232	4.717028	0.199274	1.047917	0.190162	0.849183	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (NAluSx1 SI	-25324	NM_001346	389084	Hs.65750ENM_206899	ENSG000004SNORC	-	ASCL830 Secondaryprotein-coding	
chr5-7357	7.751562	0.162366	0.855223	0.189852	0.849425	0.981636	chr5	73577034	73578137	+	0	NA	intron (Nintron (N	11842	NM_032175	84135	Hs.40670ENM_032175	ENSG000004UTP15	-	NET21 UTP15 smprotein-coding	
chr18-235	11.65668	-0.13101	0.690235	-0.1898	0.849465	0.981636	chr18	23566967	23567679	+	0	NA	intron (NLMC1 LIN	19183	NM_000271	4864	Hs.46477ENM_000271	ENSG000004NPC1	-	NPC POG2 NPC intronprotein-coding	
chr5-134	11.65668	-0.13101	0.690235	-0.1898	0.849465	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (NLMB4 LIN	40357	NM_021982	10802	Hs.59554CNM_021982	ENSG000004SEC24A	-	SEC24 homprotein-coding	
chr1-1447	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr1	1.45E+08	1.45E+08	+	0	NA	intron (NLMec LIN	6841	NR_027354	645166	Hs.74418ENR_027354	LSP1P5	-	LSP1 pseudoprotein-coding	
chr10-965	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr10	96527962	96532440	+	0	NA	intron (Nintron (N	-16275	NM_012465	7093	Hs.15429ENM_012465	ENSG000004TLL2	-	tolloid lprotein-coding	
chr12-100	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (Nintron (N	40992	NM_001286	121601	Hs.58785	NM_178826	ENSG000004CAN04	-	TMEM16D anoctaminprotein-coding
chr14-103	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	exon (NM exon (NM	66564	NM_001122	4140	Hs.35828	NM_002376	ENSG000004MARK3	-	CTAK1 KPT1 microRNA ncRNA
chr15-83	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr15	83054111	83056567	+	0	NA	intron (NAluS6 SI	11913	NM_001101	53339	Hs.45914ENM_025238	ENSG000004BTBD1	-	C15orf1 MTBT domainprotein-coding	
chr16-28	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr16	2896908	2897644	+	0	NA	intron (Nintron (N	14061	NM_138433	114984	Hs.53452ENM_138433	ENSG000004FLYWCH2	-	FLYWCH2 protein-coding	
chr16-564	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr16	56411756	56412986	+	0	NA	intron (Nintron (N	12618	NM_001322	267	Hs.295137NM_001144	ENSG000004AMFR	-	GP78 RNFA4 autocrineprotein-coding	
chr17-302	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr17	30270171	30271106	+	0	NA	intron (Nintron (N	21306	NM_000382	642	Hs.371914NM_000382	ENSG000004BLMH	-	BH BMH bleomycinprotein-coding	
chr17-306	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr17	30800070	30800228	+	0	NA	intron (NAluJr SIN	23543	NM_015986	51379	Hs.649372NM_015986	ENSG000004CRLF3	-	CREME-9 cytokine protein-coding	
chr20-137	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr20	13740737	13742172	+	0	NA	intron (NLM3E3 LI	43432	NM_016645	51575	Hs.369284NM_016645	ENSG000004ESF1	-	ABTAP C2C ESF1 nucleprotein-coding	
chr5-349	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr5	34954041	34955064	+	0	NA	intron (Nintron (N	24959	NM_001348	134218	Hs.131887NM_194288	ENSG000004DNAJC21	-	BMF53 DNAJ heatprotein-coding	
chr6-373	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr6	37386296	37386829	+	0	NA	intron (Nintron (N	32579	NR_046399	9025	Hs.48527ENM_003958	ENSG000004RNF8	-	hRNF8 ring fingprotein-coding	
chr6-107	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr6	1.08E+08	1.08E+08	+	0	NA	intron (NAluJb SIN	36593	NM_007214	11231	Hs.26904	NM_007214	ENSG000004SEC63	-	DNAJC23 SEC63 homprotein-coding
chr8-38	6.888621	-0.16678	0.878929	-0.18976	0.849498	0.981636	chr8	38123841	38125612	+	0	NA	intron (Nintron (N	18933	NM_001105	9070	Hs.52153CNM_004674	ENSG000004ASH2L	-	ASH2 ASH2 likeprotein-coding	
chr21-37	7.793969	-0.16981	0.895215	-0.18969	0.849554	0.981636	chr21	37089942	37090070	+	0	NA	intron (NAluSx SIN	7009	NM_003316	7267	Hs.368214NM_003316	ENSG000004TTC3	-	DCRR1 RNFTetrahelicprotein-coding	
chr10-58	6.206792	0.185489	0.978134	0.189635	0.849595	0.981636	chr10	58233463	58233662	+	0	NA	intron (NLM3A6 LIN	34332	NM_152230	253430	Hs.30280	NM_152230	ENSG000004IPMK	-	inositol protein-coding
chr1-111	5.973566	-0.17943	0.947235	-0.18942	0.849762	0.981636	chr1	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	18031	NM_024901	79961	Hs.55785CNM_024901	ENSG000004DENND2D	-	DENN domainprotein-coding	
chr10-35	5.973566	-0.17943	0.947235	-0.18942	0.849762	0.981636	chr10	35037239	35038381	+	0	NA	intron (NAluSg SIN	36473	NM_001198	8453	Hs.82919	NM_003591	ENSG000004CUL2	-	cullin 2 protein-coding
chr12-11	5.973566	-0.17943	0.947235	-0.18942	0.849762	0.981636	chr12	1.17E+08	1.17E+08	+	0	NA	intron (NAluSx SIN	18046	NM_012174	26259	Hs.624537NM_012174	ENSG000004FBXW8	-	FBW6 FBWF-box anprotein-coding	
chr3-183	5.973566	-0.17943	0.947235	-0.18942	0.849762	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	TTS (NM_C TTS (NM_C	-23416	NR_046577	1.01E+08	Hs.57069ENR_046577	ENSG000004ABCC5-AS1	-	ABCC5 antncRNA	
chr4-143	5.973566	-0.17943	0.947235	-0.18942	0.849762	0.981636	chr4	143759	144303	+	0	NA	intron (NMERS1B LI	15910	NM_001288	255403	Hs.66363ENM_001038	ENSG000004ZNF178	-	zinc fingprotein-coding	
chr11-621	4.212582	0.210322	1.110405	0.18941	0.849771	0.981636	chr11	62128946	62129549	+	0	NA	intron (Nintron (N	5236	NM_001040	3619	Hs.14217ENM_020238	ENSG000004INCENP	-	inner cenprotein-coding	
chr1-259	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr1	25959350	25961986	+	0	NA	3' UTR (N3' UTR (N	37395	NM_000437	5051	Hs.47708ENM_000437	ENSG000004PAFAH2	-	HSD-PLA2 platelet protein-coding	
chr1-3334	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr1	33341708	33343242	+	0	NA	intron (Nintron (N	7374	NM_004427	1912	Hs.524271NM_004427	ENSG000004PHC2	-	EDR2 HPHE polymorphicprotein-coding	
chr1-6814	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr1	68145306	68146840	+	0	NA	intron (Nintron (N	37537	NR_031664	1E+08	NR_031664	ENSG000004MIR1262	-	MIRN1262 microRNA ncRNA	
chr1-200	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (Nintron (N	-20827	NM_005299	2848	Hs.53431ENM_005299	ENSG000004GPR25	-	G proteinprotein-coding	
chr1-2202	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (NAluSx4 SI	-1808	NR_001587	6791	Hs.65484ENR_001587	AURKAP1	-	AURKAP1 aurora kipseudo	
chr10-31	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr10	31337862	31338688	+	0	NA	intron (NMIR SINE	16615	NM_001323	6935	Hs.12450ENM_030751	ENSG000004ZEB1	-	AREB6 BZF zinc fingprotein-coding	
chr11-41	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr11	4119509	4124038	+	0	NA	intron (Nintron (N	5695	NM_001333	6240	Hs.44570ENM_001038	ENSG000004RRM1	-	R1 R1R1 ribonucleprotein-coding	
chr11-11	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	7473	NM_001193	1737	Hs.335551NM_001931	ENSG000004DLAT	-	DLTA E2 Dihydroliprotein-coding	
chr11-12	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr11	1.3E+08	1.3E+08	+	0	NA	TTS (NM_C TTS (NM_C	29219	NM_006165	4798	Hs.53053ENM_006165	ENSG000004NFRKB	-	IN080G nuclear fprotein-coding	
chr12-29	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr12	29602091	29603284	+	0	NA	intron (Nintron (N	-102994	NM_001355	341350	Hs.67458ENM_183378	ENSG000004OVCH1	-	OVCH ovochymaspromtein-coding	
chr12-31	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr12	31295004	31295594	+	0	NA	exon (NM exon (NM	-29017	NR_026806	79857	Hs.53448ENM_024798	ENSG000004FLJ13224	-	uncharacterncRNA	
chr12-53	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr12	53511300	53512364	+	0	NA	TTS (NM_C TTS (NM_C	-2152	NR_046221	1.01E+08	Hs.63360ENR_046221	ENSG000004LOC100655	-	uncharacterncRNA	
chr12-96	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr12	96291446	96294694	+	0	NA	intron (NCharlie S	37572	NM_001303	2004	Hs.46523	NM_005230	ENSG000004ELK3	-	ERP NET1 SETS transprotein-coding
chr14-75	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr14	75036891	75038453	+	0	NA	intron (NFLAM_C SI	13795	NM_014381	27030	Hs.43665CNM_014381	ENSG000004MLH3	-	HNPC27 mutL homprotein-coding	
chr14-91	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr14	91879554	91882053	+	0	NA	intron (NAluSx SIN	-13267	NM_001128	123036	Hs.51026ENM_152338	ENSG000004TC2N	-	C14orf47 tandem C2protein-coding	
chr15-65	6.427165	-0.17162	0.906283	-0.18936	0.849808	0.981636	chr15	65891322	65893121	+	0	NA	TTS (NM_C TTS (NM_C	22730	NM_001206	8766	Hs.321541NM_004665	ENSG000004RAB11A			



chr1-2317 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr1	23070812	23071481	+ 0 NA	intron (Nintron (N	26841 NR_036057	1E+08	NR_036057	ENSG000003MIR3115	mir-3115	microRNA	ncRNA
chr1-3231 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr1	32319665	32320711	+ 0 NA	intron (NAlu SINE	16045 NM_023005	65108	Hs. 75061	NM_023005	ENSG000003MIR3115	F52 MACM MARCKS	liprotein-coding
chr12-111 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr12	1.12E+08	1.12E+08	+ 0 NA	exon (NM_exon (NM	-29958 NM_00069C	217	Hs. 604551	NM_00069C	ENSG000003ALDH2	ALDH-E2	aldehyde protein-coding
chr16-31 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr16	31898153	31900498	+ 0 NA	intron (NLIPI LINE	25518 NM_003414	10308	Hs. 46064E	NM_003414	ENSG000003ZNF267	HZF2	zinc finger protein-coding
chr19-161 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr19	1618921	16190272	+ 0 NA	exon (NM_exon (NM	-13858 NM_00683C	10975	Hs. 8372	NM_00683C	ENSG000003UQR11	071008DC	ubiquitin protein-coding
chr19-468 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr19	4685202	4686699	+ 0 NA	TTS (NM_TTS (NM_C	6668 NM_001242	1E+08	Hs. 67813E	NM_001242901	DPP9-AS1	DPP9	antiprotein-coding
chr19-381 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr19	38110809	38114502	+ 0 NA	intron (NLM3Cz L	-50441 NR_14580C	1.1E+08	NR_14580C	SNORD152		small nucleolar	
chr2-877 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr2	8778591	8779531	+ 0 NA	exon (NM_exon (NM	58552 NM_00134E	57498	Hs. 9873	NM_02073E	ENSG000003KIDIN522C	ARMS SINC	kinase D protein-coding
chr2-157 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr2	1.57E+08	1.57E+08	+ 0 NA	intron (NLIPIA6 LIN	21916 NM_00132E	11227	Hs. 269027	NM_01456E	ENSG000003GALNT5	GALNAC-T	polypeptide protein-coding
chr2-1577 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr2	1.58E+08	1.58E+08	+ 0 NA	intron (Nintron (N	72166 NM_001347	90	Hs. 47031E	NM_00110E	ENSG000003ACVR1	ACTR1 AC	activin $\beta$ protein-coding
chr2-2304 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr2	2.3E+08	2.3E+08	+ 0 NA	intron (Nintron (N	19496 NM_00120E	6672	Hs. 36905E	NM_00311E	ENSG000003SP100	lysp100b	SP100 nucleoprotein-coding
chr2-2396 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr2	2.4E+08	2.4E+08	+ 0 NA	intron (Ntigger3b	25324 NR_136157	4705	Hs. 277677	NM_004544	ENSG000003NDUFA10	CI-42KD C	NADH:ubiquinone protein-coding
chr3-566 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr3	56639236	56641114	+ 0 NA	intron (Nintron (N	23871 NM_015224	23272	Hs. 116877	NM_015224	ENSG000003TASOR	C3orf63 F	transcriptin protein-coding
chr4-3911 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr4	39115919	39119586	+ 0 NA	intron (Nintron (N	55520 NM_199035	51088	Hs. 272251	NM_01599E	ENSG000003KLHL5		kelch like protein-coding
chr5-388 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr5	38895316	38896744	+ 0 NA	intron (NLIPI LINE	50018 NM_00132E	9180	Hs. 12065E	NM_00399E	ENSG000003OSMR	IL-31R-be	oncostatin protein-coding
chr5-126 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr5	1.27E+08	1.27E+08	+ 0 NA	intron (NAluXs1 SI	43869 NM_001201	501	Hs. 48323E	NM_00118E	ENSG000003ALDH7A1	ATQ1 EPD	aldehyde protein-coding
chr7-661 6.929761	-0.16401	0.878632	-0.18667	0.851921	0.981636	chr7	6601972	6603423	+ 0 NA	intron (NMIRc SINE	12676 NM_00130E	79034	Hs. 487511	NM_02406E	ENSG000003Corf26		chromosome protein-coding
chr11-66 6.945477	-0.16817	0.901332	-0.18558	0.851988	0.981636	chr11	66633587	66634280	+ 0 NA	intron (NAluSp SIN	-4684 NM_00289E	5936	Hs. 523822	NM_00289E	ENSG000003RBM4	LARK RBM4	RNA binding protein-coding
chr11-29 6.965708	-0.17704	0.9525	-0.18587	0.852544	0.981636	chr11	2962252	2963135	+ 0 NA	intron (Nintron (N	1200 NR_00298E	67783	Hs. 68969E	NR_00298E	ENSG000003SNORA54	ACA54	small nucleolar
chr12-881 6.965708	-0.17704	0.9525	-0.18587	0.852544	0.981636	chr12	88105141	88105974	+ 0 NA	intron (NLM5Ca LI	36659 NM_025114	80184	Hs. 150444	NM_025114	ENSG000003CEP290	3H11Ag B	epsilon protein-coding
chr2-947 6.965708	-0.17704	0.9525	-0.18587	0.852544	0.981636	chr2	9472804	9473576	+ 0 NA	TTS (NM_TTS (NM_C	-1361 NM_00132C	285148	Hs. 66722E	NM_00103E	ENSG000003TAH1		isoamyl $\epsilon$ protein-coding
chr5-132 6.965708	-0.17704	0.9525	-0.18587	0.852544	0.981636	chr5	1.33E+08	1.33E+08	+ 0 NA	intron (Nintron (N	261 NR_132124	1.02E+08	Hs. 59881E	NR_132124	ENSG000003TH2LCRR	TH2-LCR	T helper ncRNA
chrX-156 6.965708	-0.17704	0.9525	-0.18587	0.852544	0.981636	chrX	15691503	15692791	+ 0 NA	intron (NAluJr SIN	16689 NR_160542	340591	Hs. 732244	NR_026551	ENSG000003CA5BP1	CA5BL CA	epsilon carbonic pseudo
chr8-220 7.34222	-0.16117	0.867365	-0.18581	0.852592	0.981636	chr8	22000407	22001149	+ 0 NA	intron (Ntigger19a	-23356 NM_00128E	10361	Hs. 13105E	NM_18279E	ENSG000003NPM2		nucleophorin-coding
chr9-357 8.784027	0.15148	0.815663	0.185714	0.852669	0.981636	chr9	35737988	35738378	+ 0 NA	intron (Nintron (N	5261 NR_10691E	1.02E+08	NR_10691E	ENSG000003MIR6853	hsa-mir- $\epsilon$	microRNA	ncRNA
chr6-434 8.230584	0.153636	0.827552	0.185651	0.852718	0.981636	chr6	43442958	43443196	+ 0 NA	exon (NM_exon (NM	8535 NR_106894	1.02E+08	NR_106894	ENSG000003MIR6780B	hsa-mir- $\epsilon$	microRNA	ncRNA
chr14-55 6.246082	0.172428	0.928888	0.185628	0.852737	0.981636	chr14	55311879	55312657	+ 0 NA	intron (NTHEID-int	40114 NM_152231	55030	Hs. 52534E	NM_01794E	ENSG000003FBX034	CGI-301 F	-box prc protein-coding
chr17-49 6.724886	0.196203	1.05699	0.185624	0.852739	0.981636	chr17	4900562	4901250	+ 0 NA	exon (NM_exon (NM	1370 NM_00114E	1E+08	Hs. 57924E	NM_00114E	ENSG000003C17orf107		chromosome protein-coding
chr1-217 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr1	21704587	21705538	+ 0 NA	intron (Nintron (N	-35705 NM_00135E	5909	Hs. 14817E	NM_00288E	ENSG000003RAP1GAP	RAP1GAP1	FRAP1 GTP $\epsilon$ protein-coding
chr1-409 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr1	40986164	40987827	+ 0 NA	intron (Nintron (N	-1524 NM_001301	1503	Hs. 473087	NM_00190E	ENSG000003CTPS1	CTPS GATC	CTP synthetase protein-coding
chr1-1081 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr1	1.08E+08	1.08E+08	+ 0 NA	intron (NLMAS8 LIN	14329 NM_213651	29957	Hs. 65687C	NM_01338E	ENSG000003SLC25A24	APC1 SCAM	solute carrier protein-coding
chr10-35 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr10	359833	360492	+ 0 NA	intron (Nintron (N	180168 NM_00120E	10771	Hs. 29226E	NM_00662E	ENSG000003ZMYND11	BRM1 BSE	zinc finger protein-coding
chr11-85 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr11	85656044	85658508	+ 0 NA	TTS (NM_TTS (NM_C	7853 NR_02802E	58487	Hs. 53531E	NM_02121E	ENSG000003CREBZF	SRALE1 Z	CREB/ATF protein-coding
chr11-12 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr11	1.23E+08	1.23E+08	+ 0 NA	intron (Nintron (N	3731 NM_02476E	79827	Hs. 59194E	NM_02476E	ENSG000003CLMP	ACAM ASAX	CXADR like protein-coding
chr12-121 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr12	1.21E+08	1.21E+08	+ 0 NA	intron (Nintron (N	4222 NM_00127C	10645	Hs. 29734E	NM_00654E	ENSG000003CAMKK2	CAMKK CA	calcium/calmodulin protein-coding
chr13-11 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr13	1.1E+08	1.1E+08	+ 0 NA	intron (NLM3 LIN	58034 NM_00184E	1282	Hs. 17441	NM_00184E	ENSG000003COL4A1	BSV BSVI	collagen protein-coding
chr15-494 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr15	49453467	49454797	+ 0 NA	intron (Nintron (N	30890 NM_00200E	2252	Hs. 56726E	NM_00200E	ENSG000003CFG7	HBGF-7 K	C fibroblast protein-coding
chr16-16 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr16	16027955	16028700	+ 0 NA	intron (NLM2 LINE	78711 NM_00499E	4363	Hs. 39146E	NM_00499E	ENSG000003ABCC1	ABC29 ABC	ATP binding protein-coding
chr17-624 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr17	62443610	62444419	+ 0 NA	intron (Nintron (N	20129 NM_18172E	339175	Hs. 381204	NM_18172E	ENSG000003METTL2A	METTL2	methyltransferase protein-coding
chr17-751 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr17	75135532	75136276	+ 0 NA	non-codirnon-codir	-4109 NM_00125E	30833	Hs. 67201	NM_01459E	ENSG000003CNT5C	DNT DNT1	5', 3'-nt protein-coding
chr2-393 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr2	39391643	39392074	+ 0 NA	intron (NMER63B DI	45427 NM_00361E	8491	Hs. 65575E	NM_00361E	ENSG000003MAP4K3	GLK MAPK	mitogen-activated protein-coding
chr2-237 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr2	2.38E+08	2.38E+08	+ 0 NA	intron (NAluXs1 SI	6028 NM_00127E	140739	Hs. 47178E	NM_08067E	ENSG000003UBEZF	NCE2	ubiquitin protein-coding
chr20-167 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr20	16737354	16740128	+ 0 NA	intron (Nintron (N	8715 NM_19822C	6629	Hs. 28037E	NM_00309E	ENSG000003SNRPB2	Msl1 U2B	small nucleoprotein-coding
chr3-1461 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr3	1.46E+08	1.46E+08	+ 0 NA	intron (NMER11B LI	-45060 NR_146297	1.1E+08	NR_146297	ENSG000003LNCsRLR	lncRNA-SF	lncRNA	scncRNA
chr3-195 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr3	1.96E+08	1.96E+08	+ 0 NA	non-codirnon-codir	26837 NR_133014	5504	Hs. 535731	NM_00624E	ENSG000003PPP1R2	IPP-2 IP	protein-coding
chr4-182 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr4	1.83E+08	1.83E+08	+ 0 NA	intron (Nintron (N	18482 NM_001351	1635	Hs. 18385E	NM_00192E	ENSG000003DCTD		dCMP deaminase protein-coding
chr5-149 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr5	1.5E+08	1.5E+08	+ 0 NA	intron (Nintron (N	29570 NM_001271	1452	Hs. 52986E	NM_00189E	ENSG000003CSNK1A1	CK1 CK1a	casein kinase protein-coding
chr7-178 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr7	17855825	17857722	+ 0 NA	intron (NAluJb SIN	83721 NM_00135E	23161	Hs. 48764E	NM_01513E	ENSG000003SNX13	RGS-PX1	sorting receptor protein-coding
chr7-9897 6.419307	-0.16947	0.913497	-0.18552	0.852821	0.981636	chr7	98973548	98975030	+ 0 NA	intron (Nintron (N	-38876 NR_110102						

chr19-342 6.197084	0.172519	0.932074	0.185092	0.853157	0.981636	chr19	34206903	34207492	+	0	NA	intron (Nintron (N	34693 NM_001114	26065 Hs. 744009NM_015577	ENSG000001LSM14A	C19orf13 LSM14A	mfprotein-coding
chr3-3068 6.197084	0.172519	0.932074	0.185092	0.853157	0.981636	chr3	30687569	30688407	+	0	NA	intron (MER106A I	81387 NM_003242	7048 Hs. 82028 NM_003242	ENSG000001TGFR2	AAT3 FAA3	transformprotein-coding
chr1-2308 7.726138	0.156308	0.844787	0.185027	0.853208	0.981636	chr1	23080264	23080823	+	0	NA	intron (ML2b LINE	36238 NR_036057	1E+08 NR_036057	ENSG000001MIR3115	mir-3115	microRNA ncRNA
chr19-501 4.675888	0.19639	1.061474	0.185016	0.853216	0.981636	chr19	5056396	5057112	+	0	NA	intron (MLT1E3 LI	87641 NM_001373	23030 Hs. 654819NM_015017	ENSG000001KDM4B	JMJD2B T	lysine deprotein-coding
chr5-8111 4.675888	0.19639	1.061474	0.185016	0.853216	0.981636	chr5	81119825	81120696	+	0	NA	intron (MLA_Mam	1101826 NM_001822	1160 Hs. 80691 NM_001822	ENSG000001CKMT2	SMTCK	creatine protein-coding
chr14-391 5.180334	0.187807	1.015159	0.185003	0.853227	0.981636	chr14	39157865	39158448	+	0	NA	intron (Nintron (N	12177 NM_001075	122553 Hs. 13303 NM_177452	ENSG000001TRAPPC6B	NEDMEBA T	traffickiprotein-coding
chr6-1421 5.180334	0.187807	1.015159	0.185003	0.853227	0.981636	chr6	1.42E+08	1.42E+08	+	0	NA	intron (NLM1EF LIN	31745 NM_016488	51534 Hs. 431367NM_016488	ENSG000001VTA1	C6orf55 V	vesicle t protein-coding
chr7-1392 5.180334	0.187807	1.015159	0.185003	0.853227	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (NALuJb SIN	13822 NM_173566	254048 Hs. 153458NM_173566	ENSG000001UBN2	-	ubinculeiprotein-coding
chr11-182 7.38336	-0.15832	0.855924	-0.18497	0.853249	0.981636	chr11	18310952	18311312	+	0	NA	intron (Nintron (N	11008 NM_007216	11234 Hs. 437599NM_007216	ENSG000001CHPS5	A1BP63 BI	HP55 bioe protein-coding
chr5-1796 7.38336	-0.15832	0.855924	-0.18497	0.853249	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (Nintron (N	14316 NR_134283	1.01E+08 Hs. 314414NR_134283	ENSG000001LOC100996	-	uncharactncRNA
chr7-5743 5.68478	0.180841	0.977969	0.184914	0.853296	0.981636	chr7	5743573	5745183	+	0	NA	intron (NLIMEg LIN	-32468 NR_106934	1.02E+08 NR_106934	ENSG000001MIR6874	hsa-mir-6	miRNA ncRNA
chr1-4663 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr1	46635945	46636980	+	0	NA	intron (Nintron (N	-19571 NM_201403	148932 Hs. 632401NM_145279	ENSG000001MOB3C	MOB1E MO	MOB kinase protein-coding
chr11-337 6.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr11	452743	453545	+	0	NA	intron (Nintron (N	81490 NM_001325	81490 Hs. 12851 NM_030783	ENSG000001PTDSS2	PSS2	phosphatiprotein-coding
chr14-762 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr14	76007210	76007774	+	0	NA	intron (Nintron (N	21729 NM_001252	112752 Hs. 623622NM_052873	ENSG000001IFT43	C14orf175	intrinflag protein-coding
chr2-551 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr2	55191871	55192368	+	0	NA	intron (NLM1B7 LIN	-39784 NM_001133	6233 Hs. 311642NM_002954	ENSG000001RPS27A	CEP80 HEL	ribosomal protein-coding
chr2-1201 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr2	1.2E+08	1.2E+08	+	0	NA	intron (NLM1E3A LI	53250 NM_024121	79134 Hs. 376722NM_024121	ENSG000001MEM185B	FAM11B	transment protein-coding
chr3-382 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr3	38236982	38238608	+	0	NA	intron (Nintron (N	-28017 NM_004256	9390 Hs. 225941NM_004256	ENSG000001SLC22A13	OAT10 OCI	solute c protein-coding
chr4-676 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr4	67669801	67671033	+	0	NA	intron (Nintron (N	30738 NM_018227	55236 Hs. 212774NM_018227	ENSG000001UBA6	E1-L2 MO	ubiquitir protein-coding
chr4-886 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr4	88606877	88608893	+	0	NA	intron (Nintron (N	15405 NM_001318	8916 Hs. 35804 NM_014600	ENSG000001HERC3	-	HECT and protein-coding
chr5-147 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr5	14707939	14709465	+	0	NA	3' UTR (N3' UTR (N	-3992 NR_046285	1E+08 Hs. 660555NR_046285	LOC100133C	-	uncharactncRNA
chr5-3621 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr5	36219993	36220945	+	0	NA	intron (Nintron (N	20922 NM_001287	133686 Hs. 81907 NM_153013	ENSG000001NADR2	C5orf33 I	NAD kinase protein-coding
chr6-422 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr6	42263938	42264747	+	0	NA	intron (Nintron (N	-46481 NM_018141	55173 Hs. 380887NM_018141	ENSG000001MRP510	MRP-S10 F	mitochonc protein-coding
chr9-965 5.692638	0.178148	0.963761	0.184846	0.85335	0.981636	chr9	96527823	96528244	+	0	NA	intron (NLM1B3 LIN	38798 NM_001351	8555 Hs. 40582 NM_003671	ENSG000001CDC14B	CDC14B3 C	cell diviprotein-coding
chr11-337 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr11	33756135	33757001	+	0	NA	intron (Nintron (N	17952 NM_033406	26273 Hs. 406787NM_012177	ENSG000001FBX03	FBA FBX3	F-box prcprotein-coding
chr14-594 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr14	59471533	59472062	+	0	NA	TTS (NM_C	-6417 NM_022571	64582 Hs. 647573NM_022571	ENSG000001GPR135	-	HECT and protein-coding
chr18-48 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr18	48619544	48620467	+	0	NA	intron (Nintron (N	-50595 NR_039897	1.01E+08 NR_039897	ENSG000001MIR4743	-	microRNA ncRNA
chr2-739 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr2	73932813	73933096	+	0	NA	intron (Nintron (N	6074 NR_134898	1716 Hs. 469022NM_001925	ENSG000001DGUOK	MTDPS3 N	Cdeoxyguar protein-coding
chr3-393 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr3	39392872	39394533	+	0	NA	intron (NALuS6 SI	10332 NM_017875	54977 Hs. 369619NM_017875	ENSG000001SLC25A38	SIDBA2	solute c protein-coding
chr3-526 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr3	52666000	52666712	+	0	NA	intron (NALuSx1 SI	19243 NM_001355	55193 Hs. 189922NM_018167	ENSG000001PBRM1	BAF180 P	polybro protein-coding
chr7-990 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr7	99059705	99060308	+	0	NA	intron (Nintron (N	46841 NR_110102	1.02E+08 Hs. 636663NR_110102	LOC101927	-	uncharactncRNA
chr7-112 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr7	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	25137 NM_152556	154743 Hs. 489734NM_152556	ENSG000001CBMT2	C7orf60 S	base metf protein-coding
chr8-127 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr8	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	-17801 NR_031611	1E+08 NR_031611	ENSG000001MIR1206	MIRN1206	microRNA ncRNA
chr9-363 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr9	36352102	36352733	+	0	NA	intron (Nintron (N	47852 NM_194325	152006 Hs. 333503NM_022781	ENSG000001RNF38	-	ring fingprotein-coding
chr9-132 6.709388	0.165484	0.895363	0.184823	0.853368	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	25187 NM_001316	11092 Hs. 62595 NM_018956	ENSG000001SPACA9	C9orf9 M	sperm acp protein-coding
chr10-89 11.64097	-0.12853	0.965718	-0.18474	0.853429	0.981636	chr10	89017777	89018450	+	0	NA	Intergeni TRI2C LI	-25138 NR_028371	1E+08 Hs. 244139NR_028371	FAS-AS1	FAS-AS1 F	Fas antiscncRNA
chr12-100 5.924569	-0.18	0.974361	-0.18474	0.853432	0.981636	chr12	1E+08	1E+08	+	0	NA	intron (Nintron (N	-22160 NM_001145	246213 Hs. 116871NM_139313	ENSG000001SLC17A8	DFNA25 V	solute c protein-coding
chr14-391 5.924569	-0.18	0.974361	-0.18474	0.853432	0.981636	chr14	39137004	39137215	+	0	NA	TTS (NM_C	22825 NM_003616	8487 Hs. 652307NM_003616	ENSG000001GEMIN2	SIP1 SIP1	gem nucle protein-coding
chr5-112 5.924569	-0.18	0.974361	-0.18474	0.853432	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (NLM1B8 LIN	60066 NM_001354	324 Hs. 158932NM_000038	ENSG000001APC	BTP52 DP2	APC regul protein-coding
chr18-62 8.238442	0.151684	0.821981	0.184534	0.853594	0.981636	chr18	62264224	62265575	+	0	NA	intron (Nintron (N	-60388 NM_001274	8792 Hs. 204044NM_003838	ENSG000001NFRS11A	CD265 F	EC TNF regul protein-coding
chr3-196 8.238442	0.151684	0.821981	0.184534	0.853594	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	3' UTR (N3' UTR (N	-8240 NR_046630	1.01E+08 Hs. 591671NR_046630	NCBP2-AS1	-	NCBP2 antncRNA
chr1-742 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chr1	74202530	74203948	+	0	NA	intron (NTiger 3b	5027 NM_001196	8790 Hs. 480089NM_003838	ENSG000001PPGT	GFPP	fuco-1- protein-coding
chr16-111 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chr16	11039911	11040393	+	0	NA	intron (NALuS6 SI	95808 NM_015226	23274 Hs. 35490 NM_015226	ENSG000001CLEC16A	Gep-1 K1A	C-type I protein-coding
chr17-827 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chr17	82782231	82782762	+	0	NA	intron (Nintron (N	30431 NM_005993	6904 Hs. 464391NM_005993	ENSG000001TBCD	PEBAT S	SE tubulin f protein-coding
chr2-692 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chr2	69204236	69204750	+	0	NA	intron (Nintron (N	100811 NR_036073	1E+08 NR_036073	ENSG000001MIR3126	mir-3126	microRNA ncRNA
chr5-107 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chr5	10755012	10756641	+	0	NA	intron (Nintron (N	5408 NM_004394	1611 Hs. 75189 NM_004394	ENSG000001CDAP	-	death ass protein-coding
chr5-777 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chr5	77733034	77735169	+	0	NA	intron (NTiger1 I	42238 NM_001297	6902 Hs. 291212NM_004607	ENSG000001TBCA	-	tubulin protein-coding
chrX-119 5.188192	0.184986	1.003017	0.18443	0.853676	0.981636	chrX	1.2E+08	1.2E+08	+	0	NA	exon (NM exon (NM	2785 NM_001173	55922 Hs. 437084NM_017544	ENSG000001NKRF	ITBA4 N	RNF NFKB repr protein-coding
chr1-225 6.204942	0.170071	0.9231	0.184239	0.853826	0.981636	chr1	22521748	22522349	+	0	NA	intron (NMIRb SINE	-4144 NM_001006	2046 Hs. 283619NM_020526	ENSG000001EPHA8	EEL EK3 E	EPH recep protein-coding
chr11-182 6.204942	0.170071	0.9231	0.184239	0.853826	0.981636	chr11	18284240	18285442	+	0</							



chr10-798.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr10	79811974	79814641	+ 0 NA	intron (N LIMB4 LIN	-12595 NR_029407	642361 Hs. 164298NR_029407	ENSG000003LOC642361-	uncharactericnRNA	
chr10-876.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr10	87070422	87074293	+ 0 NA	intron (N LIM4 LINE	21730 NM_001318	2746 Hs. 500409NM_005271	ENSG000003GLUD1	GDH GDH1 glutamate protein-coding	
chr11-274.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr11	27499871	27502690	+ 0 NA	intron (N intron (N	5489 NM_018362	55327 Hs. 91393 NM_018362	ENSG000003LIN7C	LIN-7-C lin-7 hon protein-coding	
chr11-436.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr11	43889042	43893376	+ 0 NA	intron (N MRB SINE	-6094 NR_026952	727999 Hs. 368929NR_026952	ENSG000003SEC14L1P1-	SEC14 lik pseudo	
chr11-736.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr11	73676434	73680598	+ 0 NA	intron (N AluSx SIN	29603 NM_00113C	58473 Hs. 445489NM_02120C	ENSG000003PLEKH1	KPL1 PHR1 plekstrin protein-coding	
chr11-117.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr11	1.17E+08	1.17E+08	+ 0 NA	intron (N intron (N	-1047 NR_037803	1E+08 Hs. 73630ENR_037803	BACE1-AS	BACE1-AS1 BACE1 antncRNA	
chr12-651.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr12	6511237	6513220	+ 0 NA	intron (N AluYc SIN	2006 NR_004387	692148 Hs. NR_004387	ENSG000003SCARNA10	U85 small Ca <sub>2</sub> ncRNA	
chr12-295.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr12	29565057	29566426	+ 0 NA	intron (N AluS SIN	-66048 NR_001353	341350 Hs. 674588NM_183378	ENSG000003OVCH1	OVCH ovochymase protein-coding	
chr12-48C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr12	48073685	48074437	+ 0 NA	intron (N Tigger4a	-31192 NM_001354	5213 Hs. 75160 NM_00028E	ENSG000003PFKM	ATP-PFK1 phosphofr protein-coding	
chr12-101.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr12	1.01E+08	1.01E+08	+ 0 NA	intron (N intron (N	-15560 NR_049838	1.01E+08 Hs. NR_049838	ENSG000003MIR548AQ	- microRNA ncRNA	
chr13-46C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr13	46008777	46009470	+ 0 NA	intron (N intron (N	43623 NM_00133C	23091 Hs. 136192NM_01507C	ENSG000003CZ3H13	KIAA0853 zinc fing protein-coding	
chr13-114.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr13	1.14E+08	1.14E+08	+ 0 NA	non-codiron-codir	-9086 NM_03243C	283489 Hs. 7542 NM_03243C	ENSG000003CHAMP1	C13orf8 chromoson protein-coding	
chr14-34C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr14	34612148	34613307	+ 0 NA	intron (N AluSx SIN	17421 NR_15935E	58533 Hs. 27652ENR_02124C	ENSG000003SNX6	MSTP010 sorting r protein-coding	
chr14-35C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr14	35081260	35082585	+ 0 NA	3' UTR (N3' UTR (N	1071 NR_11041E	1.02E+08 Hs. 61713ENR_11041E	ENSG000003LOC101927-	uncharactericnRNA	
chr14-67E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr14	67658714	67659764	+ 0 NA	intron (N intron (N	15393 NM_00637C	10490 Hs. 741177NM_00637C	ENSG000003VTI1B	VTI1 VTI1 vesicle t protein-coding	
chr15-454.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr15	45413436	45417673	+ 0 NA	intron (N intron (N	13218 NR_13664A	79029 Hs. 369657NM_02406C	ENSG000003SPATA5L1	- spermatog protein-coding	
chr15-717.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr15	17171483	17172424	+ 0 NA	intron (N intron (N	-38601 NM_01634E	10002 Hs. 187354NM_01424E	ENSG000003NR2E3	ESCS PNR nuclear l protein-coding	
chr15-774.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr15	77463652	77468627	+ 0 NA	intron (N AluSp SIN	45251 NM_001304	10363 Hs. 69594 NM_01820C	ENSG000003HMG20A	HMGX1 HMC high mob protein-coding	
chr16-89C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr16	89302422	89305379	+ 0 NA	intron (N intron (N	7772 NR_13633E	1.05E+08 Hs. 657381NR_13633E	ENSG000003LOC105371-	uncharactericnRNA	
chr17-17E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr17	17251019	17254642	+ 0 NA	intron (N intron (N	-15662 NM_14460E	201163 Hs. 31652 NM_14460E	ENSG000003FLCN	BHD DENNE folliculiprotein-coding	
chr17-37E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr17	37240170	37247601	+ 0 NA	intron (N LMC LINE	2354 NR_13277E	0.07E+08 NR_13277E	SNORA90	- small nucsnRNA	
chr17-401.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr17	40146031	40147003	+ 0 NA	intron (N AluSx3 SI	5980 NM_00735E	22794 Hs. 743287NM_00735E	ENSG000003CASC3	BTZ MLN51 CASC3 excp protein-coding	
chr17-49C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr17	49052434	49053383	+ 0 NA	3' UTR (N3' UTR (N	55233 NM_00116E	10642 Hs. 14493ENR_00654E	ENSG000003IGF2BP1	CRD-BP CF insulin l protein-coding	
chr17-62E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr17	62608487	62614637	+ 0 NA	intron (N LMC1 LIN	-16108 NM_00603E	9902 Hs. 7835 NM_00603E	ENSG000003MRC2	CD280 CLEmannose l protein-coding	
chr19-32C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr19	32356854	32363323	+ 0 NA	intron (N intron (N	14478 NM_01491C	22847 Hs. 205392NM_01491C	ENSG000003ZNF507	- zinc fing protein-coding	
chr2-173C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	1735018	1735585	+ 0 NA	intron (N Tigger1 I	9214 NM_01229E	7837 Hs. 332197NM_01229E	ENSG000003PXD	ASG7 COF peroxidase protein-coding	
chr2-156E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	15609001	15610841	+ 0 NA	intron (N intron (N	18053 NM_00449E	1653 Hs. 440599NM_00449E	ENSG000003DDX1	DBP-RB UBI DEAD-box protein-coding	
chr2-276C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	27605463	27606027	+ 0 NA	intron (N AluS6 SI	22703 NM_03243A	84450 Hs. 52917ENR_03243A	ENSG000003ZNF512	- zinc fing protein-coding	
chr2-613E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	61381598	61382702	+ 0 NA	intron (N L2a LINE	35227 NR_003707	1E+08 Hs. 67582ENR_003707	ENSG000003SNORA70B	- small nucsnRNA	
chr2-993C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	99392933	99397170	+ 0 NA	intron (N intron (N	57622 NM_015904	9669 Hs. 158688NM_015904	ENSG000003EIF5B	IF2 eukaryot protein-coding	
chr2-127E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	1.27E+08	1.27E+08	+ 0 NA	intron (N HAL1 LINE	16316 NM_001303	2071 Hs. 46987ENR_00012E	ENSG000003ERCC3	BTf2 GTF2 ERCC exciprotein-coding	
chr2-234C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr2	2.35E+08	2.35E+08	+ 0 NA	intron (N intron (N	11545 NM_001371305	25666 NM_00131E	1434 Hs. 90073 NM_00131E	ENSG000003CE1L	CAS CSE1 chromoson protein-coding
chr20-49C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr20	49071555	49072402	+ 0 NA	TTS (NM_C TTS (NM_C	39968 NM_00135C	27352 Hs. 474914NM_01570E	ENSG000003SGSM3	CIP85 MAF small G <sub>1</sub> protein-coding	
chr3-162E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	16258974	16260812	+ 0 NA	3' UTR (N3' UTR (N	5050 NM_001047	285381 Hs. 388087NM_206831	ENSG000003DPH3	DELGIP DE diphthamiprotein-coding	
chr3-4734.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	47344234	47345720	+ 0 NA	3' UTR (N3' UTR (N	-36044 NM_01546E	25930 Hs. 25524 NM_01546E	ENSG000003PTPN23	HD-PTP HE protein t protein-coding	
chr3-525E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	52553792	52555097	+ 0 NA	intron (N intron (N	17839 NM_001124	440957 Hs. 660577NM_001124	ENSG000003SMIM4	C3orf78 small int protein-coding	
chr3-6411.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	64114373	64115595	+ 0 NA	intron (N LIPA13 LI	11514 NR_046701	1.01E+08 Hs. 668874NR_046701	PRICKLE2-	PRICKLE2 ncRNA	
chr3-136E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	1.37E+08	1.37E+08	+ 0 NA	intron (N THE1B LTL	11403 NM_00615E	4690 Hs. 12688ENR_00615E	ENSG000003CNCK1	NCK NCKA NCK adapt protein-coding	
chr3-154E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	1.54E+08	1.54E+08	+ 0 NA	intron (N intron (N	26452 NM_02086E	170506 Hs. 446277NM_02086E	ENSG000003DHX36	DDX36 G4F DEAH-box protein-coding	
chr3-195E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr3	1.95E+08	1.95E+08	+ 0 NA	intron (N AluY SINE	-22983 NM_152531	152002 Hs. 478741NM_152531	ENSG000003XXYL1T	C3orf21 xyloseid protein-coding	
chr4-423C.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr4	4236407	4231229	+ 0 NA	intron (N AluJb SIN	9405 NM_001297	85013 Hs. 12845 NM_032927	ENSG000003TMEM128	- transmemt protein-coding	
chr4-2674.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr4	26743534	26744503	+ 0 NA	intron (N intron (N	116226 NR_13467E	1.05E+08 Hs. 54885ENR_13467E	STIM2-AS1	STIM2 antncRNA	
chr4-526E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr4	52600209	52602405	+ 0 NA	intron (N intron (N	55322 NM_001134	64854 Hs. 7966 NM_02283E	ENSG000003USP46	- ubiquitin protein-coding	
chr4-106E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr4	1.06E+08	1.06E+08	+ 0 NA	intron (N AluSx SIN	-21372 NM_00114E	9255 Hs. 59168CNR_00475E	ENSG000003AIMP1	EMAP2 EM2 aminoacyl protein-coding	
chr5-545E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	5459418	5462247	+ 0 NA	exon (NM exon (NM	38155 NM_01532E	23379 Hs. 44929ENR_01532E	ENSG000003ICE1	KIAA0947 interact protein-coding	
chr5-432E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	43293325	43294770	+ 0 NA	intron (N intron (N	19134 NM_001324	3157 Hs. 39772ENR_00213C	ENSG000003HMGCS1	HMGCS3 3-hydroxy protein-coding	
chr5-695E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	69569919	69574195	+ 0 NA	intron (N Kalgac I	11812 NM_00109E	728340 Hs. 19135ENR_00109E	ENSG000003GTF2H2C	GTF2H2C_2 GTF2H2 f <sub>2</sub> protein-coding	
chr5-7231.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	72311352	72312013	+ 0 NA	intron (N MSTC LTR	8558 NM_00128E	23107 Hs. 482491NM_01508A	ENSG000003MRP527	MRP-527 Smi tohcon protein-coding	
chr5-135E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	1.35E+08	1.35E+08	+ 0 NA	intron (N MRc SINE	12175 NM_13860E	9555 Hs. 42027ENR_00489E	ENSG000003H2AFY	H2A, y H2B H2A haso protein-coding	
chr5-176A.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	1.76E+08	1.76E+08	+ 0 NA	intron (N AluSx1 SI	39718 NM_01461E	23197 Hs. 48424ENR_01461E	ENSG000003FAF2	ETEA UBX1 Fas assoc protein-coding	
chr5-180A.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr5	1.81E+08	1.81E+08	+ 0 NA	exon (NM exon (NM	24310 NM_00137C	57472 Hs. 60838CNR_01545E	ENSG000003CNOT6	CCR4 CCR4-NOT protein-coding	
chr6-282E.6.914045	-0.1601	0.874155	-0.18315	0.854684	0.981636	chr6	28272361	28274047	+ 0 NA	intron (N AluJo SIN</					

chr15-925	12.62258	-0.1206	0.663541	-0.18175	0.855782	0.981636	chr15	92931351	92959875	+	0	NA	intron (AluXs1 SI	41214	NR_036136	1E+08	NR_036136 ENSG000003MIR3175	mir-3175	microRNA	ncRNA		
chr18-494	12.62258	-0.1206	0.663541	-0.18175	0.855782	0.981636	chr18	49487821	49491602	+	0	NA	promoter-promoter-	-387	NR_003701	1E+08	NR_003701	SNORD58C	U58	small	nucsnRNA	
chr20-357	12.62258	-0.1206	0.663541	-0.18175	0.855782	0.981636	chr20	35703073	35740984	+	0	NA	intron (LIMB4 LIN	20232	NR_040723	9584	Hs.282901NM_004902 ENSG000003CRBM39	CAPER CAF	RNA	bindiprotein-coding		
chr8-1308	12.62258	-0.1206	0.663541	-0.18175	0.855782	0.981636	chr8	13082998	13105246	+	0	NA	intron (Nintron (N	22122	NM_001164	10395	Hs.134229NM_006094 ENSG000003DLCL1	ARHGAP7 DLCL1	R30	protein-coding		
chr16-224	13.57878	-0.11728	0.64577	-0.18162	0.855881	0.981636	chr16	22502649	22462848	+	0	NA	intron (AluSc SIN	-25033	NR_027460	1E+08	Hs.709576NR_027460	RRN3P3	RRN3	homo	pseudo	
chr11-741	8.709606	0.145949	0.804304	0.18146	0.856006	0.981636	chr11	74166528	74168236	+	0	NA	intron (Nintron (N	3620	NM_015531	26005	Hs.557938NM_015531 ENSG000003CC2CD3	OFD14	C2	domain	protein-coding	
chr7-356	13.13304	-0.11976	0.660191	-0.1814	0.856053	0.981636	chr7	35664700	35666557	+	0	NA	intron (NLI P45 LIN	29507	NM_0022373	64224	Hs.743051NM_0022373 ENSG000003HERPUD2	HERPUD2	HERPUD2	protein-coding		
chr17-615	7.741854	0.152419	0.840924	0.181251	0.85617	0.981636	chr17	61909238	61910228	+	0	NA	intron (NLI P44 LIN	18249	NM_020748	57508	Hs.269646NM_020748 ENSG000003INTS2	INT2 KIAA	integrated	protein-coding		
chr19-277	5.95785	-0.17449	0.963518	-0.18109	0.856294	0.981636	chr19	2777487	2778052	+	0	NA	intron (AluXs1 SI	5504	NM_003021	6449	Hs.20391CNM_003021 ENSG000003SGTA	SGT alpha	small	glt	protein-coding	
chr1-200	6.725104	0.161092	0.890422	0.180917	0.856433	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (NMER58B DN	10424	NM_001320C	83479	Hs.183983NM_001320C ENSG000003DDX59	DDX59	DDX59	protein-coding		
chr13-111	6.725104	0.161092	0.890422	0.180917	0.856433	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	exon (NM exon (NM	-29960	NM_001320C	121793	Hs.210677NM_001320C ENSG000003TEX29	TEX29	TEX29	protein-coding		
chr2-2194	6.725104	0.161092	0.890422	0.180917	0.856433	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	exon (NM exon (NM	-12446	NM_001177C	10290	Hs.21639	NM_005876 ENSG000003SPEG	SPEG	APEG-1 AF	striated	protein-coding
chr19-153	8.197302	0.15003	0.829585	0.18085	0.856485	0.981636	chr19	15341803	15342058	+	0	NA	Intergeni MER58B DN	-9391	NM_001330C	23476	Hs.187763NM_014299 ENSG000003BRD4	BRD4	HUNK bromodome	protein-coding		
chr1-4601	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr1	46010400	46011322	+	0	NA	exon (NM exon (NM	119780	NM_001328C	8503	Hs.655387NM_003625 ENSG000003PIK3R3	PIK3R3	p55	phosphor	protein-coding	
chr1-2238	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr1	2.24E+08	2.24E+08	+	0	NA	intron (AluXs1 SI	27367	NM_001031	7159	Hs.523968NM_005422 ENSG000003TP53BP2	TP53BP2	ASF	trans	protein-coding	
chr10-738	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr10	73813638	73814622	+	0	NA	non-codirnon-codir	-2310	NR_160743	8509	Hs.654758NM_003633 ENSG000003NDST2	NDST2	HSST2 N-F-N	deacetyl	protein-coding	
chr10-115	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr10	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	-94658	NR_038943	1.01E+08	Hs.604103NR_038943	ADD3-AS1	ADD3	ant	ncRNA	
chr15-225	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr15	22571357	22572044	+	0	NA	intron (Nintron (N	46154	NM_001282C	653073	Hs.574257NM_001282C ENSG000003GOLGA8J	GOLGA8J	golgin	A8	protein-coding	
chr15-412	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr15	41276520	41277390	+	0	NA	intron (NMLT1 L LTF	-7035	NR_152822	729082	Hs.380164NR_026757 ENSG000003OIP5-AS1	OIP5-AS1	cyrano li	OIP5	ant	ncRNA
chr15-851	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr15	85116840	85118431	+	0	NA	intron (Nintron (N	117146	NR_158175	1.02E+08	Hs.681665NR_158175	LOC101929C	golgin	A2	pseudo	
chr17-656	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr17	6580848	6582410	+	0	NA	intron (NLI MC4a LI	-25074	NR_001166	83394	Hs.183983NM_031222 ENSG000003PITPNM3	PITPNM3	ACKR6 COF	PITPNM	protein-coding	
chr18-764	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr18	76432562	76434311	+	0	NA	intron (Nintron (N	-58216	NR_136504	1.02E+08	Hs.665188NR_136504 ENSG000003LOC101927	LOC101927	uncharact	ncRNA		
chr4-8484	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr4	84848183	84850003	+	0	NA	intron (NHAL1 LINE	-116523	NR_152774	404201	Hs.46730	NM_205857 ENSG000003WDFY3-AS2	C4orf12 WDFY3	ant	ncRNA	
chr8-224C	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr8	22404938	22406144	+	0	NA	intron (Nintron (N	12705	NM_001351	23516	Hs.491232NM_015355 ENSG000003SLC39A14	SLC39A14	HCIN ZMNL	solute	protein-coding	
chr9-1298	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	9847	NM_000113	1861	Hs.534312NM_000113 ENSG000003TOR1A	TOR1A	DQ2 DYT1	torsin	protein-coding	
chr9-137	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (Nintron (N	11318	NR_045720C	11253	Hs.279881NM_016215 ENSG000003MAN1B1	MAN1B1	ERMAN EF	mannosid	protein-coding	
chrX-4118	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chrX	4118235	41191362	+	0	NA	intron (Nintron (N	-85941	NR_135611	1.05E+08	Hs.546115NR_135611 ENSG000003LINC02601	LINC02601	long	int	ncRNA	
chrX-1185	5.708354	0.173069	0.957167	0.180814	0.856514	0.981636	chrX	1.18E+08	1.18E+08	+	0	NA	intron (Nigger15e	13096	NR_03168E	1E+08	NR_03168E ENSG000003MIR1277	MIR1277	microRNA	ncRNA		
chr1-664	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr1	6643885	6645466	+	0	NA	intron (Nintron (N	19525	NM_001199E	90326	Hs.689006NM_138355 ENSG000003THAP3	THAP3	THAP	dome	protein-coding	
chr1-151	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr1	1.52E+08	1.52E+08	+	0	NA	intron (NMSTAI1 LTF	48739	NM_001172	11189	Hs.26047	NR_00718E ENSG000003CELF3	CELF3	BRUNOL1 CCUGBP	EL	protein-coding
chr10-332	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr10	33224705	33225836	+	0	NA	intron (Nintron (N	-108463	NR_160030C	1.02E+08	NR_160030	IATPR	TCONS_00C	ITGB1	ad	ncRNA
chr11-74	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr11	74887474	74888716	+	0	NA	intron (NLI P44 LIN	60996	NM_001277C	143570	Hs.370145NM_182966 ENSG000003XRR1A	XRR1A	X	ray	protein-coding	
chr13-197	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr13	19734597	19735355	+	0	NA	intron (NLI P45 LIN	47969	NM_001354	52695	Hs.213198NM_001042 ENSG000003PSPC1	PSPC1	PSP1	parasac	protein-coding	
chr13-215	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr13	21385442	21386454	+	0	NA	intron (NLI MEc LIN	-41089	NR_103841	1.01E+08	Hs.659199NR_103840	LINC0053E	LINC00422	long	int	ncRNA
chr14-505	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr14	50932297	50933131	+	0	NA	intron (NMLT1M LTF	11769	NM_002862C	5836	Hs.282417NM_002862 ENSG000003PYGL	PYGL	GSD6	glycogen	protein-coding	
chr19-586	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr19	58583117	58583928	+	0	NA	non-codirnon-codir	8123	NR_026052	65996	Hs.541177NM_023939 ENSG000003CENPBD1P1	CENPBD1P1	CENPB	DN	pseudo	
chr2-369	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr2	36998970	37002138	+	0	NA	intron (Nintron (N	-34018	NR_003162	6801	Hs.127488NM_003162 ENSG000003STRN	STRN	PPP2R6A S	striatin	protein-coding	
chr3-117	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr3	11798317	11799613	+	0	NA	intron (NAluJo SIN	47920	NM_001321	132001	Hs.475472NM_138807 ENSG000003TAMM41	TAMM41	C3orf31 F	TAMM41	mit	protein-coding
chr4-183	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr4	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	10627	NM_152682	201965	Hs.133337NM_152682 ENSG000003RWDMA	RWDMA	FAM28A RW	RWD	doma	protein-coding
chr5-370	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr5	37078950	37079721	+	0	NA	Intergeni LIPA11 LI	-169711	NR_134263	1.05E+08	Hs.170999NR_134263 ENSG000003LOC105374	LOC105374	uncharact	ncRNA		
chr6-153	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr6	1.53E+08	1.53E+08	+	0	NA	intron (Nintron (N	-40581	NM_001301	54516	Hs.225833NM_019041 ENSG000003MTRF1L	MTRF1L	MMF	mitochon	protein-coding	
chr7-152	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	150662	NM_001371474	159090	Hs.404706NM_145284 ENSG000003FAM122B	FAM122B	SPACIA2	family	wi	protein-coding
chrX-1347	6.452589	-0.1644	0.909524	-0.18075	0.856561	0.981636	chrX	9333	NR_145284	39998	NR_017646	54802	Hs.356554NM_017646 ENSG000003TRIT1	TRIT1	COXP235 C	RNA	iso	protein-coding				
chr1-3984	7.367644	-0.15462	0.855641	-0.18071	0.856596	0.981636	chr1	39843135	39843878	+	0	NA	intron (Nintron (N	2693	NM_001330C	9921	Hs.442798NM_014868 ENSG000003RNF10	RNF10	RIE2	ring	protein-coding	
chr13-427	7.367644	-0.15462	0.855641	-0.18071	0.856596	0.981636	chr13	4053721	40754076	+	0	NA	intron (Nintron (N	17292	NM_005830C	10240	Hs.596607NM_005830C ENSG000003MRP53	MRP53	IMOGN38 mi	tochon	protein-coding	
chr5-103	7.367644	-0.15462	0.855641	-0.18071	0.856596	0.981636	chr5	10381430	10382702	+	0	NA	intron (Nintron (N	-20298	NR_162106	1.13E+08	NR_162106	MIR10397	microRNA	ncRNA		
chr5-323	7.367644	-0.15462	0.855641	-0.18071	0.856596	0.981636	chr5	32381945	32383759	+	0	NA	intron (Nintron (N	11623	NR_030305	693164	NR_030305 ENSG000003MIR579	MIR579	MIRN579	mi	ncRNA	
chr6-9954	7.367644	-0.15462	0.855641	-0.18071	0.856596	0.981636	chr6	99544956	99545484	+	0	NA	exon (NM exon (NM	23440	NM_005199C	892	Hs.430646NM_005199C ENSG000003CCNC	CCNC	CycC SRB1	cyclin	C	protein-coding
chr6-1587	7.367644	-0.15462	0.855641	-0.18071	0.856596	0.981636	chr6	1.59E+08	1.59E+08	+	0	NA</										



chr10-305	7.18841	0.155467	0.867697	0.179172	0.857803	0.981636	chr10	30993940	30994669	+	0	NA	intron (NMSTC LTR)	5213	NM_001143	220929	Hs.660642NM_182755	ENSG000002ZNF438	ba330011.zinc	finger	protein-coding		
chr12-123	7.18841	0.155467	0.867697	0.179172	0.857803	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	3' UTR (3' UTR (N	35072	NM_001304	10335	Hs.114111NM_02514C	ENSG000002CCDC92	-	coiled-coil	protein-coding		
chr14-105	7.18841	0.155467	0.867697	0.179172	0.857803	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	3' UTR (3' UTR (N	10031	NM_017955	55038	Hs.34045	NM_017955	ENSG000002CDCA4	HEPP SEI-cell	divi	protein-coding	
chr19-114	7.18841	0.155467	0.867697	0.179172	0.857803	0.981636	chr19	1.1442778	1.1443219	+	0	NA	intron (NAluX1 S1	-7216	NM_001302	115948	Hs.12401C	NM_145045	ENSG000002CCDC151	CILD30	coiled-coil	protein-coding	
chr3-137	7.18841	0.155467	0.867697	0.179172	0.857803	0.981636	chr3	1.14E+08	1.14E+08	+	0	NA	intron (NLM1E2z L1	-45872	NM_017577	54762	Hs.24583	NM_017577	ENSG000002GRAMD1C	-	GRAM dom	protein-coding	
chr5-8857	7.18841	0.155467	0.867697	0.179172	0.857803	0.981636	chr5	885706	886089	+	0	NA	intron (Nintron (N	6625	NR_134296	65980	Hs.449275NM_023924	ENSG000002BRD9	LAVS3040 bromodome	protein-coding			
chr10-611	6.955185	-0.15733	0.878961	-0.17899	0.857943	0.981636	chr10	61978986	61979702	+	0	NA	intron (Nintron (N	-70013	NM_001244	84159	Hs.535297NM_032199	ENSG000002ARID5B	DESRT MRAT-rich	protein-coding			
chr11-111	6.955185	-0.15733	0.878961	-0.17899	0.857943	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	TTS (NM_1TTS (NM_1	40150	NM_002716	5519	Hs.269125NM_002716	ENSG000002PPP2R1B	PP2A BET-AT-rich	protein-coding			
chr17-365	6.955185	-0.15733	0.878961	-0.17899	0.857943	0.981636	chr17	36574358	36575905	+	0	NA	intron (Nintron (N	-16748	NM_024308	79154	Hs.462855NM_024308	ENSG000002DHRS11	ARPG836 S-dehydroge	protein-coding			
chr19-135	6.955185	-0.15733	0.878961	-0.17899	0.857943	0.981636	chr19	13914638	13915606	+	0	NA	intron (NCharlie2E	8921	NM_017721	54862	Hs.269592NM_017721	ENSG000002CC2D1A	FREUD-1 Coiled-coil	protein-coding			
chr20-628	6.955185	-0.15733	0.878961	-0.17899	0.857943	0.981636	chr20	62856848	62857955	+	0	NA	exon (NM exon (NM	4421	NM_006602	10732	Hs.126245NM_006602	ENSG000002TCFL5	CHA E2BP-transcrip	protein-coding			
chr22-300	6.955185	-0.15733	0.878961	-0.17899	0.857943	0.981636	chr22	30006631	30008083	+	0	NA	TTS (NR_1TTS (NR_1	308	NR_106876	1.02E+08	NR_106876	ENSG000002MIR6818	hsa-mir-6	microRNA	ncRNA		
chr10-130	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr10	1.33E+08	1.33E+08	+	0	NA	intron (NAluSp SIN	13650	NM_138384	92170	Hs.501575NM_138384	ENSG000002MTG1	GTP GTPBFmitochon	protein-coding			
chr11-106	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr11	10628076	10634116	+	0	NA	intron (NMLTIK LTF	21205	NM_001098	10335	Hs.501895NM_130385	ENSG000002PRRV11	IRAG JAW1murine	reprotein-coding			
chr13-210	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr13	21042470	21043613	+	0	NA	intron (Nintron (N	18545	NM_014572	26524	Hs.78960	NM_014572	ENSG000002CLATS2	KPM	large tun	protein-coding	
chr13-111	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	-18875	NM_001366	1.01E+08	Hs.704267NM_001366	ENSG000002C13orf46	-	chromosom	protein-coding		
chr16-211	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr16	21176049	21176565	+	0	NA	intron (NCharlie1E	-16866	NM_017535	55567	Hs.52650C	NM_017535	ENSG000002DNAH3	DNAH3C-B dynein	protein-coding		
chr16-744	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr16	74494428	74496417	+	0	NA	intron (Nintron (N	-73952	NM_001011	497190	Hs.45467C	NM_001011	ENSG000002CLEC18B	MRLC2	C-type I	protein-coding	
chr19-191	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr19	19283757	19285546	+	0	NA	intron (NTiger2 E	-11350	NM_001001	53345	Hs.531624NM_20351C	ENSG000002TM6SF2	-	transment	protein-coding		
chr2-156	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr2	15617312	15619501	+	0	NA	intron (NMER52D L1	26538	NM_004935	1653	Hs.440595NM_004935	ENSG000002DDX1	DBP-RB UKDEAD-box	protein-coding			
chr2-553	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr2	55300997	55302164	+	0	NA	intron (Nintron (N	19261	NR_027258	344405	Hs.445297NM_00108C	ENSG000002PRORS1P	NCRNA0011	prolyl-tf	pseudo		
chr2-203	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (NMLT1A-int	57342	NM_001114	65065	Hs.648845NM_198945	ENSG000002NBEAL1	A530083C neurobeac	protein-coding			
chr3-273	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr3	27391271	27392057	+	0	NA	intron (Nintron (N	-22204	NM_152534	152110	Hs.506115NM_152534	ENSG000002CNEK10	-	NIMA rel	protein-coding		
chr3-338	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr3	33857253	33858722	+	0	NA	intron (NLM5 LINE	59357	NM_013374	10015	Hs.475895NM_013374	ENSG000002PDC61P	A1P1 AL1 program	protein-coding			
chr3-4931	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr3	49315311	49318711	+	0	NA	intron (Nintron (N	23042	NM_001251	7375	Hs.77500	NM_003363	ENSG000002USP4	UNP Unph	ubiquitin	protein-coding	
chr5-179	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (N2a LINE	4508	NR_110566	1.02E+08	Hs.663255NR_110566	ENSG000002LOC101925	-	uncharact	ncRNA		
chr6-3621	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr6	36217368	36219174	+	0	NA	intron (Nintron (N	21527	NM_015698	27154	Hs.520095NM_015698	ENSG000002BRPF3	-	bromodome	protein-coding		
chr7-644	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr7	6442817	6443552	+	0	NA	intron (NAluYk4 S1	4770	NM_139175	221955	Hs.487495NM_139175	ENSG000002DAGLB	DAGLBETA diacylgly	protein-coding			
chr7-447	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr7	44760403	44761608	+	0	NA	intron (NCharlie4z	4817	NM_174925	83637	Hs.77978	NM_031445	ENSG000002ZMIZ2	NET27 TR3	zinc	finger	protein-coding
chr7-151	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	10658	NM_001308	116988	Hs.647075NM_031945	ENSG000002AGAP3	AGAP-3 CEArFGAP	wiprotein-coding			
chr9-9261	7.408783	-0.15198	0.849383	-0.17893	0.857992	0.981636	chr9	92614793	92616378	+	0	NA	TTS (NM_1TTS (NM_1	-2465	NR_036505	1E+08	Hs.660395NR_036505	LOC100125	-	uncharact	ncRNA		
chr1-316	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr1	31654742	31655619	+	0	NA	intron (Nintron (N	-10304	NR_033688	553115	Hs.470417NM_012392	ENSG000002PEP1	ABP32 PEF	penta-EF-	protein-coding		
chr10-425	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr10	422447	4226377	+	0	NA	intron (Nintron (N	-20502	NR_147612	1.02E+08	Hs.654707NR_147612	ENSG000002LOC10193C	-	uncharact	ncRNA		
chr14-745	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr14	74691942	74693143	+	0	NA	intron (Nintron (N	20538	NM_001035	9870	Hs.497417NM_014821	ENSG000002CAREL1	FIEL1 KI1	apoptosis	protein-coding		
chr14-102	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	11348	NM_030942	81693	Hs.534494NM_030942	ENSG000002AMN	PRO1028 amamion	protein-coding			
chr16-156	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr16	15629702	15630129	+	0	NA	intron (Nintron (N	13239	NM_014647	9665	Hs.173524NM_014647	ENSG000002MARF1	KIAA0430 meiosis	protein-coding			
chr22-315	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr22	31340281	31341201	+	0	NA	TTS (NM_1TTS (NM_1	5392	NR_110542	1.02E+08	Hs.661715NR_110542	ENSG000002PIK3I1P1	-	PIK3I1	ncRNA		
chr5-112	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (NLM1Eg2 L1	22580	NM_001354	324	Hs.158932NM_000035	ENSG000002APC	BTPS2 DP2	APC	regul	protein-coding	
chr5-1725	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (Nintron (N	7174	NM_001317	51121	Hs.546395NM_016095	ENSG000002RPL26L1	RPL26P1	ribosomal	protein-coding		
chr8-388	5.203908	0.179458	1.002982	0.178924	0.857997	0.981636	chr8	38800957	38802210	+	0	NA	intron (NLM1B8 L1N	-3867	NM_001352	6867	Hs.279245NM_006285	ENSG000002TACCI1	Ga55	transfor	protein-coding		
chr2-200	13.10946	-0.11651	0.652007	-0.17879	0.858175	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	intron (NAluSc8 S1	8402	NM_001162	1195	Hs.433732NM_004071	ENSG000002CLK1	CLK CLK SCDC	like	protein-coding		
chr15-101	20.207864	-0.09667	0.540971	-0.17869	0.858179	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (NMIR SINE	6005	NR_003655	374666	Hs.459575NM_199163	WASH3P	FAM39DP	WASP	fam	pseudo	
chr5-6924	7.67714	0.157071	0.879608	0.17857	0.858276	0.981636	chr5	69241036	69241378	+	0	NA	intron (NLM1A3 L1N	6321	NM_001795	1022	Hs.184295NM_001795	ENSG000002CDK7	CAK CAK1	cyclin	de	protein-coding	
chr11-745	7.893814	-0.15555	0.871192	-0.17855	0.858288	0.981636	chr11	74980028	74980340	+	0	NA	Intergeni Intergeni	-8460	NM_001367	10825	Hs.191074NM_006655	ENSG000002NEU3	SIAL3	neuramin	protein-coding		
chr1-226	6.676106	0.161247	0.903303	0.178509	0.858324	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (NMIR SINE	43835	NM_001618	1425	Hs.177766NM_001618	ENSG000002PARP1	ADPRT ADFPoly	(ADP-	protein-coding		
chr3-816	7.87024	-0.14931	0.836546	-0.17848	0.858345	0.981636	chr3	81629550	81629894	+	0	NA	intron (NLM1A4 L1N	131923	NM_000158	2632	Hs.437062NM_000158	ENSG000002GBE1	APBD GBE 1,4-	protein-coding			
chr22-404	7.172694	0.160073	0.89816	0.178223	0.858548	0.981636	chr22	40461763	40462024	+	0	NA	intron (N2a LINE	1547	NM_001282	57591	Hs.654688NM_020831	ENSG000002MRFTA	BSAC MAL	myocardin	protein-coding		
chr1-212	7.196268	0.153368	0.860844	0.178161	0.858597	0.981636	chr1	21232950	21233905	+	0	NA	intron (NMIR SINE	46188	NM_001113	1889	Hs.19508C	NM_001397	ENSG000002ECE1	ECE	endothel	protein-coding	
chr1-363	7.196268																						

chr11-784 7.359786	-0.15284	0.86136	-0.17743	0.859167	0.981636	chr11	78410210	78410568	+	0 NA	intron (NAluSz SIN	7431 NM_080491	9846 Hs. 429434NM_01229c	ENSG00000GAB2	-	GRB2	asc protein-coding	
chr16-566 7.359786	-0.15284	0.86136	-0.17743	0.859167	0.981636	chr16	56368019	56369416	+	0 NA	intron (NMERS5A DN	56272 NM_001322	267 Hs. 295137NM_001144	ENSG00000AMFR	-	GP78 RNFA4	autocrine protein-coding	
chr2-5397 7.359786	-0.15284	0.86136	-0.17743	0.859167	0.981636	chr2	53973479	53974292	+	0 NA	intron (N(TG)n Sin	2772 NM_00132c	98 Hs. 516172NM_13844f	ENSG00000ACYP2	-	ACYM ACVf	acylphosph protein-coding	
chr4-2457 7.359786	-0.15284	0.86136	-0.17743	0.859167	0.981636	chr4	24552945	24554054	+	0 NA	intron (NAluSx1 LI	30879 NM_00135E	1665 Hs. 696074NM_00135f	ENSG00000DHH15	-	DBP1 DDX1	DEAH-box protein-coding	
chr12-456 6.163802	0.16798	0.9476	0.177269	0.859297	0.981636	chr12	45363933	45364189	+	0 NA	intron (NLM1B7 LSI	71371 NM_001142	196527 Hs. 505393NM_00102f	ENSG00000ANO6	-	RNU35B UC	snRNA	
chr2-1711 6.163802	0.16798	0.9476	0.177269	0.859297	0.981636	chr2	1.71E+08	1.71E+08	+	0 NA	intron (NLooper DN	45775 NM_01229c	9874 Hs. 744917NM_01229c	ENSG00000CTLK1	-	PKU-beta	tousled l protein-coding	
chr6-1611 6.163802	0.16798	0.9476	0.177269	0.859297	0.981636	chr6	1.61E+08	1.61E+08	+	0 NA	intron (Nintron (N	50245 NR_024277	79992 Hs. 664873NM_02492c	ENSG00000AGPAT4-1	-	G6orf59 AGPAT4	lncRNA	
chr19-494 12.65587	-0.11795	0.665476	-0.17725	0.859314	0.981636	chr19	49197296	49500258	+	0 NA	TTS (NR_C TTS (NR_C	1058 NR_00128E	44544 Hs. 505393NM_00102f	ENSG00000SNORD35B	-	RNU35B UC	small nuc snoRNA	
chr1-2378 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr1	23783509	23784606	+	0 NA	intron (NMIR SINE	5639 NM_02036E	57095 Hs. 31819 NM_02036E	ENSG00000PITHD1	-	Clorf128 PITH	dom protein-coding	
chr1-6257 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr1	62571686	62573052	+	0 NA	intron (NMIR SINE	-25151 NM_01449E	27329 Hs. 209155NM_01449E	ENSG00000ANGPTL3	-	ANG-5 ANC	angiopoietin protein-coding	
chr10-617 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr10	6108218	6113300	+	0 NA	intron (Nintron (N	21428 NM_00114E	84991 Hs. 498548NM_03290f	ENSG00000RBM17	-	SPF45	RNA bindi protein-coding	
chr10-877 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr10	87075294	87075763	+	0 NA	intron (Nintron (N	18559 NM_00131E	2746 Hs. 500409NM_005271	ENSG00000GLUD1	-	GDH GDH1	glutamate protein-coding	
chr10-996 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr10	99679236	99681550	+	0 NA	intron (Nintron (N	20764 NM_00134E	57089 Hs. 28236 NM_02035f	ENSG00000ENTPD7	-	LALP1	ectonucle protein-coding	
chr10-137 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr10	1.3E+08	1.3E+08	+	0 NA	intron (Nintron (N	30413 NM_001321	10539 Hs. 42644 NM_006541	ENSG00000GLRX3	-	GLRX4 GR	glutared protein-coding	
chr11-368 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr11	3687145	3689490	+	0 NA	intron (NAluY SINE	-16933 NM_00130E	57053 Hs. 732809NM_02040E	ENSG00000CHRNA10	-	-	choliner protein-coding	
chr11-662 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr11	66262350	66263342	+	0 NA	exon (NM exon (NM	5143 NM_00131E	64837 Hs. 280792NM_02282E	ENSG00000KLC2	-	-	kinesin l protein-coding	
chr11-111 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr11	1.11E+08	1.11E+08	+	0 NA	3' UTR (N3' UTR (N	132583 NM_00125E	57569 Hs. 6136 NM_02080f	ENSG00000CARHGAP20	-	RARHOGAP	Rho GTPas protein-coding	
chr11-117 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr11	1.12E+08	1.12E+08	+	0 NA	intron (NLM1E4b LI	13287 NM_03342E	85458 Hs. 655622NM_03342f	ENSG00000DXDC1	-	CCD1	DIX domain protein-coding	
chr11-112 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr11	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	9545 NM_001931	1737 Hs. 335551NM_001931	ENSG00000DLAT	-	DLTA E2F	dihydroli protein-coding	
chr12-567 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr12	56165362	56167571	+	0 NA	intron (Nintron (N	8107 NM_02101E	4637 Hs. 632717NM_02101E	ENSG00000MYL6	-	ESMLC LCL	myosin l protein-coding	
chr12-777 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr12	77042125	77042711	+	0 NA	intron (Nintron (N	23151 NM_203394	144455 Hs. 416377NM_203394	ENSG00000E2F7	-	-	E2F trans protein-coding	
chr12-102 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr12	1.02E+08	1.02E+08	+	0 NA	intron (Nintron (N	13480 NM_024057	79023 Hs. 444276NM_024057	ENSG00000NUP37	-	MCPH24 p	nucleopor protein-coding	
chr12-132 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr12	1.32E+08	1.32E+08	+	0 NA	intron (NLM1E1 LI	25826 NR_00297E	677829 Hs. 742409NR_00297E	ENSG00000SNORA49	-	ACA49	small nuc snoRNA	
chr14-357 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr14	35007136	350010538	+	0 NA	intron (Nintron (N	25845 NM_00313E	6729 Hs. 167535NM_00313E	ENSG00000SRP54	-	-	signal re protein-coding	
chr14-584 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr14	58443408	58444903	+	0 NA	exon (NM exon (NM	4474 NM_00124E	9786 Hs. 232532NM_01474E	ENSG00000KIAA0586	-	JBT523 SF	KIAA0586 protein-coding	
chr15-424 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr15	42445839	42448646	+	0 NA	intron (NFLAM_A SI	10325 NM_02247E	64397 Hs. 511143NM_02247E	ENSG00000ZNF106	-	SH3BP3 Zf	zinc fing protein-coding	
chr15-784 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr15	78499813	78501576	+	0 NA	3' UTR (N3' UTR (N	-6870 NM_00108E	123688 Hs. 307962NM_00108E	ENSG00000HYKK	-	AGPHD1	hydroxyl protein-coding	
chr16-317 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr16	31061437	31064321	+	0 NA	intron (NAluSp SIN	2209 NM_00117E	79759 Hs. 102928NM_02470E	ENSG00000ZNF668	-	-	zinc fing protein-coding	
chr17-752 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr17	75235963	75236969	+	0 NA	TTS (NM_C TTS (NM_C	25140 NR_101400	23166 Hs. 87726 NM_014001	ENSG00000CGA3	-	23663	golgi as protein-coding	
chr17-817 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr17	81558929	81563200	+	0 NA	intron (NAluSx1 SIN	6136 NR_13014C	53163 Hs. 464338NM_017921	ENSG00000NPL0C4	-	NPL4	NPL4 hom protein-coding	
chr18-686 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr18	68675830	68677601	+	0 NA	3' UTR (N3' UTR (N	38393 NM_00135E	54495 Hs. 440534NM_01902E	ENSG00000TMX3	-	PDIA13 T	thioredo protein-coding	
chr19-101 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr19	10151866	10155174	+	0 NA	intron (NAluSx1 SI	-33621 NM_00375E	8666 Hs. 529055NM_00375E	ENSG00000EIF3G	-	EIF3F-P42	euaryot protein-coding	
chr2-5467 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr2	54657856	54663856	+	0 NA	3' UTR (N3' UTR (N	-64156 NM_00103E	400954 Hs. 656692NM_00103E	ENSG00000EML6	-	-	EMAP like protein-coding	
chr2-1137 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr2	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	-7993 NR_03994E	1.01E+08	NR_03994E	ENSG00000MIR4782	-	-	microRNA ncRNA
chr2-2357 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr2	2.35E+08	2.35E+08	+	0 NA	intron (Nintron (N	22068 NM_001371305	6780 Hs. 596704NM_00460E	ENSG00000STAU1	-	PPP1R150	staufen c protein-coding	
chr20-491 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr20	49149678	49153419	+	0 NA	intron (Nintron (N	36822 NM_001322	5116 Hs. 474069NM_006031	ENSG00000PCNT	-	KEN MOPD2	pericentr protein-coding	
chr21-463 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr21	46336822	46339781	+	0 NA	intron (NLM1C3 LI	13634 NM_00131E	84164 Hs. 731754NM_03220f	ENSG00000ASCC2	-	ASC1 p100	activatir protein-coding	
chr22-294 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr22	29830627	29832451	+	0 NA	intron (Nintron (N	6735 NM_00136E	6533 Hs. 529488NM_00304E	ENSG00000SLC6A6	-	TAUT	solute c protein-coding	
chr3-1447 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr3	14417255	14418070	+	0 NA	intron (NAluY SINE	15056 NM_001134	51368 Hs. 517864NM_01592E	ENSG00000TEX264	-	ZSIG11	testis ex protein-coding	
chr3-5163 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr3	51638742	51639674	+	0 NA	intron (Nintron (N	-31967 NM_00112E	25871 Hs. 591288NM_01541E	ENSG00000NEPRO	-	C3orf17 N	nucleolus protein-coding	
chr3-1136 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr3	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	7583 NM_00131E	59343 Hs. 401389NM_02162E	ENSG00000SEN2	-	AXAM2 SM1	SUMO spec protein-coding	
chr3-1856 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr3	1.86E+08	1.86E+08	+	0 NA	intron (NMERS5A DN	26788 NM_02162E	132946 Hs. 444444NM_20691E	ENSG00000CARL9	-	-	ADP ribos protein-coding	
chr4-5645 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr4	56491949	56493870	+	0 NA	intron (NFRAM SINE	-12300 NM_20691E	1767 Hs. 212366NM_00136E	ENSG00000DNAH5	-	CILD3 DN	lysine as protein-coding	
chr5-1376 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr5	13756472	13757540	+	0 NA	intron (NLM1A13 LI	187474 NM_00136E	1E+08 Hs. 608069NR_028474	LOC10030E	-	-	LSM3 hom pseudo	
chr5-6596 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr5	65995150	65995592	+	0 NA	intron (NLM1A8 LI	-49798 NR_028474	51520 Hs. 432674NM_01646E	ENSG00000CLARS	-	HSPC192 I	leucyl-tf protein-coding	
chr5-1461 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr5	1.46E+08	1.46E+08	+	0 NA	intron (Nintron (N	32200 NM_020117	6492 Hs. 520293NM_00506E	ENSG00000SIM1	-	bHLHe14 SIM	bHLH protein-coding	
chr6-1007 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr6	1.01E+08	1.01E+08	+	0 NA	intron (NManRep137	-18862 NM_00506E	10973 Hs. 486031NM_00682E	ENSG00000ASCC3	-	ASC1p200	activatir protein-coding	
chr6-1017 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr6	1.01E+08	1.01E+08	+	0 NA	intron (NMER4B LTF	115674 NM_00682E	383 Hs. 346926NM_00004E	ENSG00000ARG1	-	-	arginase protein-coding	
chr6-1315 7.400925	-0.15013	0.847334	-0.17718	0.859363	0.981636	chr6	1.32E+08	1.32E+08	+	0 NA								



chr22-317.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr22	31709880	31712707	+	0	NA	intron (AluSx SIN	38839	NM_173566	253143	Hs.438906NM_173566	ENSG000000PRR14L	C22orf30	proline	rprotein-coding			
chr3-477.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr3	47756894	47757665	+	0	NA	intron (L1MED LIN	24614	NM_003074	6599	Hs.476175NM_003074	ENSG000000SMARCC1	BAF155 CFSWI SNF	rprotein-coding				
chr3-132f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	21580	NM_001321	79876	Hs.170737NM_024818	ENSG000000CUBA5	EIEE44 SCubiquitin	rprotein-coding				
chr3-130f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr3	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	50150	NM_002958	6259	Hs.654562NM_002958	ENSG000000RYK	D3S3195 Jreceptor	rprotein-coding				
chr4-442f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr4	4437843	4438599	+	0	NA	intron (Nintron (N	23751	NM_001346	53407	Hs.584915NM_016938	ENSG000000STX18	Ufe1	syntaxin	rprotein-coding			
chr5-5694.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr5	56940158	56946137	+	0	NA	intron (AluJr SIN	8983	NM_001297	166968	Hs.657594NM_152622	ENSG000000MIER3		MIER	famiprotein-coding			
chr5-138f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr5	1.39E+08	1.39E+08	+	0	NA	intron (AluSp SIN	-46750	NR_134244	1.05E+08	Hs.445981NR_134244	ENSG000000LOC105379			uncharactericRNA			
chr5-149f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr5	1.49E+08	1.49E+08	+	0	NA	intron (MLT1A0 LI	-53389	NM_001322	134265	Hs.629301NR_152400	ENSG000000AFAP1L1			actin	filprotein-coding		
chr5-175f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr5	1.76E+08	1.76E+08	+	0	NA	3' UTR (N3' UTR (N	48451	NM_022754	94081	Hs.369444NM_022754	ENSG000000SFXM1			SLC56A1 Tsideroflc	rprotein-coding		
chr8-118f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr8	11831256	11833086	+	0	NA	intron (Nintron (N	23027	NM_001287	2222	Hs.593928NM_004462	ENSG000000FDFT1	DGPT ERGC	farnesyl-	rprotein-coding			
chr8-671f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr8	67136301	67138142	+	0	NA	intron (AluS26 SI	53373	NM_001291	79848	Hs.370147NM_024790	ENSG000000CSPF1	CSPF JBTs	centrosom	rprotein-coding			
chr8-140f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (Nintron (N	32212	NR_040712	54108	Hs.279704NM_017444	ENSG000000CHRAC1	CHARC1 CF	chromatin	rprotein-coding			
chr9-340f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr9	34012674	34013793	+	0	NA	intron (Nintron (N	35654	NR_163242	55833	Hs.493735NM_018445	ENSG000000UBAP2	UBAP-2	ubiquitin	rprotein-coding			
chr9-114f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	-22851	NM_000607	5004	Hs.522355NM_000607	ENSG000000CORM1	AGP-A AGF	omomucc	rprotein-coding			
chr9-37f.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr9	3758339	3758852	+	0	NA	intron (Nintron (N	3097	NM_004886	9546	Hs.25527	NM_004886	ENSG000000APBA3	MGC:15815	amyloid t	rprotein-coding		
chr20-584.6.691822	0.156789	0.887536	0.176656	0.859778	0.981636	chr20	58419901	58420414	+	0	NA	intron (AluS2 SIN	30928	NR_036633	9217	Hs.182622NM_004738	ENSG000000VAPB	AL58 VAMF	VAMP	asc	rprotein-coding		
chr11-63f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr11	63652805	63653688	+	0	NA	intron (AluSx SIN	18130	NM_015455	25923	Hs.356715NM_015455	ENSG000000CATL3	HSNF1	atlastin	rprotein-coding			
chr11-68f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr11	68544938	68546082	+	0	NA	intron (LFSLINE_Ve	84758	NM_001352	55291	Hs.503022NM_018312	ENSG000000PPP6R3	C11orf23	protein	rprotein-coding			
chr12-13f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	-2028	NR_002975	677829	Hs.742405NR_002975	ENSG000000SNORA49	ACA49	small	ncsnoRNA			
chr16-48f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr16	4834906	4835831	+	0	NA	intron (Nintron (N	11920	NM_032566	84656	Hs.387255NM_032566	ENSG000000GLYR1	BM045 HIE	glyoxylat	rprotein-coding			
chr19-19f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr19	19201327	19202089	+	0	NA	exon (NM exon (NM	1706	NM_176888	126382	Hs.708155NM_176888	ENSG000000NRC2AP	TRA16	nuclear	rprotein-coding			
chr5-164f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr5	16459317	16460452	+	0	NA	intron (L1ME3A LI	5916	NM_033414	90441	Hs.60300	NM_033414	ENSG000000ZNF622	ZPR9	zinc	fin	rprotein-coding	
chr5-170f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr5	1.71E+08	1.71E+08	+	0	NA	intron (Nintron (N	49196	NM_022897	64901	Hs.410814NM_022897	ENSG000000CRANBP17			RAN	bindi	rprotein-coding	
chr9-129f.6.691822	0.170614	0.966631	0.176504	0.859898	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (AluY SINE	17913	NM_001193	5524	Hs.400742NM_021131	ENSG000000PTPA	PP2A PPP2	protein	rprotein-coding			
chr19-51f.6.691822	0.176413	0.859969	0.176413	0.859969	0.981636	chr19	51874237	51874545	+	0	NA	intron (L2a LINE	13545	NM_001136	84765	Hs.723015NM_032675	ENSG000000ZNF577			zinc	fin	rprotein-coding	
chr17-79f.6.691822	0.187119	0.061211	0.176326	0.860038	0.981636	chr17	7908406	79084570	+	0	NA	intron (N1MB2 LIN	9371	NM_001042	64772	Hs.29288	NM_022755	ENSG000000ENGASE			endo-	fin	rprotein-coding
chr1-180f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr1	1.81E+08	1.81E+08	+	0	NA	exon (NM exon (NM	19198	NR_145481	1.03E+08	Hs.665315NR_145481	ENSG000000K1AA1614			K1AA1614	ncRNA		
chr1-222f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (L1ME1 LIN	-20482	NM_024746	79802	Hs.665666NM_024746	ENSG000000HHIPL2	K1AA1822 HHIP	like	rprotein-coding			
chr1-231f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr1	2.32E+08	2.32E+08	+	0	NA	3' UTR (N3' UTR (N	36315	NM_005999	7257	Hs.13318	NM_005999	ENSG000000TSNAX	C3PO TRAX	translin	rprotein-coding		
chr16-15f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr16	15696212	15700664	+	0	NA	intron (Nintron (N	48193	NM_017668	54820	Hs.655378NM_017668	ENSG000000NDX1	HOM-TES-E	nu	rprotein-coding			
chr16-29f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr16	29400947	29403886	+	0	NA	intron (Nintron (N	2129	NM_001310	728888	Hs.720286NM_001310	ENSG000000NPIP11	NPIP	nuclear	rprotein-coding			
chr17-31f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr17	31217329	31218939	+	0	NA	intron (Nintron (N	79105	NM_002544	4974	Hs.113874NM_002544	ENSG000000OMG	OMGP	oligodenc	rprotein-coding			
chr17-42f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr17	42542623	42543687	+	0	NA	exon (NM exon (NM	6914	NM_000263	4669	Hs.50727	NM_000263	ENSG000000NAGLU	CMT2V MP5N	acetyl-	rprotein-coding		
chr17-81f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr17	81573768	81574692	+	0	NA	intron (Nintron (N	3203	NR_130135	55666	Hs.464335NM_017921	ENSG000000NPLOC4	NPL4	NPL4	homc	rprotein-coding		
chr17-82f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr17	82055204	82056169	+	0	NA	intron (Nintron (N	3723	NM_212492	2873	Hs.268533NM_004127	ENSG000000GPS1	COP51 CSNG	proteir	rprotein-coding			
chr18-27f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr18	27200500	27211631	+	0	NA	intron (HAL LINE	64718	NM_015295	23347	Hs.8118	NM_015295	ENSG000000SMCHD1	BAMS FSH	structure	rprotein-coding		
chr18-86f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr18	8625520	8627473	+	0	NA	intron (Nintron (N	17051	NM_001025	201475	Hs.270074NM_001025	ENSG000000CRAB12			RAB12,	mc	rprotein-coding	
chr2-203f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (AluSx SIN	36652	NR_027671	56886	Hs.743306NM_020120	ENSG000000UGGT1	HUGT1 UGC	UDP-	gluc	rprotein-coding		
chr2-128f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (AluSx SIN	36617	NM_001114	65065	Hs.648846NM_198945	ENSG000000BEAL1	A530083 C1	neurobac	rprotein-coding			
chr20-33f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr20	3323658	3325283	+	0	NA	intron (Nintron (N	83192	NM_001005	25943	Hs.516855NM_001005	ENSG000000C2orf194			chromosom	rprotein-coding		
chr2-42f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr2	42590629	42592392	+	0	NA	intron (Nintron (N	-9499	NR_002184	91695	Hs.534041NR_002184	ENSG000000RR7BP	RR7BP dJ	ribosom	pseudo			
chr4-84f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr4	84735131	84735659	+	0	NA	intron (LTR16A LI	152268	NM_001263	1040	Hs.654896NM_001263	ENSG000000CDS1	CDS1	C1DP-	diac	rprotein-coding		
chr5-113f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	non-codiron-codir	36760	NM_152624	167227	Hs.443875NM_152624	ENSG000000DPC2	NUDT20	decappin	rprotein-coding			
chr5-148f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr5	1.48E+08	1.48E+08	+	0	NA	intron (Nintron (N	56293	NM_030793	81545	Hs.483772NM_030793	ENSG000000FBX038	Fbx38 HBM	F-box	prc	rprotein-coding		
chr6-321f.6.691822	0.151344	0.858697	0.176249	0.860098	0.981636	chr6	32168112	32170195	+	0	NA	TTS (NM_C TTS (NM_C	963	NR_106775	1.02E+08	NR_106775	ENSG000000MIR6721						



chr13-445.6.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr13	44512464	44513592	+	0	NA	intron (NL2c LINE	-38727	NM_001243	8848	Hs.436388	NM_006022	ENSG000002TSC22D1	Ptg-2 TGF	TSC22	don	protein-coding
chr15-492.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr15	49261585	49263848	+	0	NA	intron (NL1PA3 LIN	92469	NM_001298	2585	Hs.122006	NM_002044	ENSG000002GALK2	GK2	galactoki	protein-coding	
chr15-715.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr15	71989761	71990359	+	0	NA	intron (Nintron (N	-124198	NM_001166	123228	Hs.513002	NM_145204	ENSG000002SEN8P	DEN1 NEDF	SUMO	pept	protein-coding
chr16-315.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr16	31909777	31910198	+	0	NA	intron (NL1M1 LINE	36540	NM_003414	10308	Hs.46064E	NM_003414	ENSG000002ZNF267	HZF2	zinc	finger	protein-coding
chr16-686.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr16	68075788	68078649	+	0	NA	intron (NALuSg7 SI	-8152	NM_173163	4775	Hs.43658E	NM_00455E	ENSG000002NFATC3	NF-AT4c	nuclear	f	protein-coding
chr16-705.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr16	70500396	70501179	+	0	NA	intron (NMIR3 SINE	22767	NM_001365	25839	Hs.20868C	NM_01538E	ENSG000002COG4	CDG2J COI	component	protein-coding	
chr19-155.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr19	15388225	15389627	+	0	NA	intron (Nintron (N	-9139	NM_005858	10270	Hs.59449E	NM_00585E	ENSG000002AKAP8	AKAP 95 A-	kinase	protein-coding	
chr20-252.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr20	25271537	25273162	+	0	NA	intron (Nintron (N	24264	NM_002862	58730	Hs.368157	NM_00286E	ENSG000002PYGB	GPBB	glycogen	protein-coding	
chr3-5764.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr3	57640861	57643712	+	0	NA	intron (NALuSx3 SI	44497	NR_132366	1.06E+08	Hs.667207	NR_13236E	ENSG000002ARF4-AS1	-	ARF4	anticrNA	
chr6-358E.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr6	35851123	35852745	+	0	NA	intron (Nintron (N	46582	NM_182548	222662	Hs.367947	NM_18254E	ENSG000002LHFP15	DFNB67 TM	LHFP14	tet	protein-coding
chr6-111C.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (NMIRb SINE	27521	NM_032194	84154	Hs.37226E	NM_032194	ENSG000002RPF2	BXDC1 ba3	ribosome	protein-coding	
chr8-225E.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr8	22591628	22593098	+	0	NA	intron (NALuSx1 SI	-7236	NM_001013	541565	Hs.74350E	NM_17368E	ENSG000002C8orf58	-	chromosom	protein-coding	
chr8-9504.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr8	95046178	95048173	+	0	NA	intron (Nintron (N	22186	NR_148913	137682	Hs.43550C	NM_15241E	ENSG000002DUFAP6	C8orf58 H	NADH:ubiq	protein-coding	
chr9-3238.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chr9	32386612	32388148	+	0	NA	intron (NMER63A DN	2737	NM_001362	48	Hs.56722E	NM_002197	ENSG000002AC01	AC08F3E	3H	NADH:ubiq	protein-coding
chrX-219E.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chrX	21992956	21993533	+	0	NA	intron (Nintron (N	-39081	NM_001282	5251	Hs.495834	NM_000444	ENSG000002PHEX	HPDR HPDF	phosphat	protein-coding	
chrX-685E.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chrX	68523313	68525641	+	0	NA	intron (N(AT)n Sin	25426	NM_173834	286451	Hs.82719	NM_173834	ENSG000002YIPF6	FinGER6	Yip1	dom	protein-coding
chrX-7157.5.675072	0.168104	0.959975	0.175113	0.860991	0.981636	chrX	71379710	71382730	+	0	NA	intron (NLIME3G LI	14863	NR_104387	6872	Hs.15856C	NM_00460E	ENSG000002TAF1	BA2R CCG1	TATA-box	protein-coding	
chr15-734.6.171879	0.144888	0.825562	0.175018	0.861066	0.981636	chr15	75478635	75479142	+	0	NA	intron (Nintron (N	-23073	NM_00114E	25942	Hs.51303E	NM_01547E	ENSG000002SIN3A	WITKOS	SIN3	trarp	protein-coding
chr17-44C.6.171879	0.144888	0.825562	0.175018	0.861066	0.981636	chr17	44082168	44082489	+	0	NA	intron (Nintron (N	11417	NR_028582	92579	Hs.29400E	NM_13838E	ENSG000002G6PC3	SCN4 UGRF	glucose-t	protein-coding	
chr1-244.5.162768	0.176756	1.009944	0.175016	0.861067	0.981636	chr1	24440201	24441019	+	0	NA	intron (Nintron (N	24585	NM_00132E	57185	Hs.52344E	NM_02044E	ENSG000002NPAL3	DJ462023	NIPA	like	protein-coding
chr3-186E.5.162768	0.176756	1.009944	0.175016	0.861067	0.981636	chr3	1.87E+08	1.87E+08	+	0	NA	intron (NMLT1J2 LI	4212	NM_01813E	55171	Hs.51846E	NM_01813E	ENSG000002TBCCD1	-	TBCC	dom	protein-coding
chr2-229E.7.854524	-0.14572	0.832696	-0.175	0.861078	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	3' UTR (N3' UTR (N	87168	NM_00134E	9320	Hs.57264E	NM_00423E	ENSG000002TRIP12	MRD49 TRI	thyroid	protein-coding	
chr17-49E.8.228734	0.142568	0.814704	0.174994	0.861084	0.981636	chr17	49821330	49822681	+	0	NA	intron (Nintron (N	-23905	NM_001247	729220	Hs.43413E	NM_00124791	FLJ45513	-	uncharact	protein-coding	
chr13-951.6.228516	0.163105	0.932368	0.174937	0.861129	0.981636	chr13	95123091	95124394	+	0	NA	intron (Nintron (N	-86602	NR_145733	1.1E+08	NR_145733	SNORD13G	-	small	nucsnRNA		
chr15-49C.6.228516	0.163105	0.932368	0.174937	0.861129	0.981636	chr15	49018926	49019446	+	0	NA	intron (Nintron (N	27260	NM_00119E	9728	Hs.9997	NM_014701	ENSG000002SECSBP2L	SBP2L SLA	SECIS	bir	protein-coding
chr8-480E.6.228516	0.163105	0.932368	0.174937	0.861129	0.981636	chr8	48025108	48025865	+	0	NA	intron (NALuSz SIN	17055	NM_00335E	7336	Hs.49169E	NM_00335E	ENSG000002UBE2V2	DDVIT1 DE	ubiquitin	protein-coding	
chr1-328E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr1	32838488	32839599	+	0	NA	intron (NFLAM_A SI	13729	NR_13510E	64766	Hs.44088C	NM_02275E	ENSG000002S100BP	S100BPBR	S100P	bir	protein-coding
chr1-358E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr1	35824821	35829734	+	0	NA	intron (NALuSx1 SI	19261	NM_01762E	192670	Hs.74485E	NM_01762E	ENSG000002AG04	E1F2C4	argonaut	protein-coding	
chr1-405E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr1	40503039	40503890	+	0	NA	Intergeni Intergeni	-5255	NM_00134E	64789	Hs.59584	NM_02277E	ENSG000002EX05	Clorf176	exonuc	protein-coding	
chr1-776E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr1	77633269	77634024	+	0	NA	intron (NMIR SINE	49012	NM_015534	26009	Hs.48050E	NM_015534	ENSG000002ZZZ3	ATAC1	zinc	finger	protein-coding
chr1-211E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr1	2.11E+08	2.11E+08	+	0	NA	intron (NLIMed LI	26190	NM_018254	55758	Hs.35639E	NM_018254E	ENSG000002RCOR3	-	REST	core	protein-coding
chr10-79E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr10	79200166	79204014	+	0	NA	intron (NFLAM_C SI	133124	NM_02033E	57178	Hs.19311E	NM_02033E	ENSG000002ZM1Z1	MIZ RAI17	zinc	finger	protein-coding
chr10-80E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr10	80517667	80520150	+	0	NA	3' UTR (N3' UTR (N	17034	NR_100661	1.02E+08	Hs.59366E	NR_120661	ENSG000002LOC10192E	-	uncharact	crNA	
chr11-74C.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr11	74089989	74095377	+	0	NA	intron (Nintron (N	78319	NM_015531	26005	Hs.55793E	NM_015531E	ENSG000002C2CD3	OFD14	C2	domair	protein-coding
chr12-10F.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	3' UTR (N3' UTR (N	16424	NM_15231E	121053	Hs.29556E	NM_15231E	ENSG000002C12orf45	-	chromosom	protein-coding	
chr12-11F.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr12	1.17E+08	1.17E+08	+	0	NA	intron (NMER58B DN	17509	NM_01500E	23014	Hs.74037E	NM_01500E	ENSG000002FBX021	FBX21	F-box	prc	protein-coding
chr13-20E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr13	20837019	20839175	+	0	NA	intron (Nintron (N	-64136	NM_00131E	221143	Hs.26674	NM_17492E	ENSG000002EEF1AKMT1	ESP13 N6A	EEF1A	lys	protein-coding
chr13-99E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr13	99559588	99561885	+	0	NA	intron (NALuYk2 SI	-16377	NR_12639E	1.04E+08	Hs.63938E	NR_126390	LINC0103E	-	long	intcrNA	
chr13-102E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr13	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	19671	NM_00101E	196541	Hs.50862E	NM_00101E	ENSG000002METTL21C	C13orf39	methyl	transferase	protein-coding
chr13-114E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (NLIM5 LINE	30505	NM_00132E	22821	Hs.59307E	NM_00736E	ENSG000002CRASA3	GAP11P4B	FRAS	p21	protein-coding
chr15-22E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr15	22902276	22903932	+	0	NA	intron (Nintron (N	14209	NM_00100E	23191	Hs.26704	NM_01460E	ENSG000002CYF1P1	P140SRA	1-cytoplas	protein-coding	
chr16-35E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr16	3507405	3508460	+	0	NA	intron (NLIME4b LI	-1958	NM_02479E	23059	Hs.15599E	NM_015041	ENSG000002CLUAP1	CFAP22 F	cytoplasm	protein-coding	
chr16-43E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr16	4332931	4333686	+	0	NA	intron (Nintron (N	1084	NM_03257E	84662	Hs.59208E	NM_03257E	ENSG000002GLIS2	NKL NPHP7	GLIS	fami	protein-coding
chr16-87E.6.187376	0.160825	0.920072	0.174796	0.86124	0.981636	chr16	87753809	87755987	+	0	NA	intron (Nintron (N	11088	NM_00118E	54758	Hs						



chr16-862	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr16	86272927	86273969	+	0	NA	intron (Nintron (N	12799 NR_104139	1.01E+08	Hs. 640512NR_104139	LINC01081	TCONS0002	long intencRNA
chr17-475	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr17	47944854	47945679	+	0	NA	intron (Nintron (N	3695 NM_018125	55163	Hs. 631742NM_018125	ENSG00000	PNPO	HEL-5-302 pyridoxan protein-coding
chr17-815	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr17	81544672	81550366	+	0	NA	exon (NM_exon (NM	4834 NM_025161	80233	Hs. 31390ENM_025161	ENSG00000	FAAP100	C17orf70 FA core cprotein-coding
chr18-487	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr18	48761606	48763389	+	0	NA	intron (Nintron (N	91897 NR_039897	1.01E+08	NR_039897	ENSG00000	MIR4743	- microRNA ncRNA
chr19-163	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr19	16340305	16417171	+	0	NA	intron (NAluY SINE	14739 NM_001136	69229	Hs. 371282NM_003200	ENSG00000	TCF3	AGM8 E2A transcrip protein-coding
chr19-445	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr19	44981543	44982432	+	0	NA	intron (MER33 DNA	-19477 NM_006509	5971	Hs. 654402NM_006509	ENSG00000	CRELB	I-REL IML RELB protprotein-coding
chr2-8607	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr2	86073963	86075065	+	0	NA	intron (MER117 DN	31372 NM_015424	25885	Hs. 53181ENM_015424	ENSG00000	POLR1A	A190 AFDC RNA polyprotein-coding
chr2-9941	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr2	99411772	99410696	+	0	NA	intron (NAluSx3 SI	74845 NM_015920	9669	Hs. 158688NM_015904	ENSG00000	E1F5B	IF22 eukaryotprotein-coding
chr2-1215	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr2	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	-5330 NR_023343	1E+08	Hs. 68963ENR_023343	ENSG00000	RNU4ATAC	MOPD1 RFWRNA, U4atsnRNA
chr2-1602	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	-1072 NR_103776	1.01E+08	Hs. 726623NR_103776	ENSG00000	LINC02478	- long intencRNA
chr3-5148	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr3	51482768	51483330	+	0	NA	intron (NAluSq2 SI	16954 NM_001171	9730	Hs. 716623NM_014700	ENSG00000	DCAF1	RIP VPRBF DDB1 and protein-coding
chr3-129C	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	3' UTR (N3' UTR (N	29810 NM_000174	2815	Hs. 1144 NM_000174	ENSG00000	GP9	CD42a GPIglycoprotprotein-coding
chr5-660C	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr5	6600887	6602752	+	0	NA	intron (Nintron (N	18543 NR_024424	255167	Hs. 43551ENR_024424	ENSG00000	LINC01018	SRHC long intencRNA
chr6-4224	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr6	42244455	42245810	+	0	NA	intron (N MamTip2 E	-27281 NM_018141	55173	Hs. 380887NM_018141	ENSG00000	MRRP50	MRP-S10 Mitochon protein-coding
chr6-430C	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr6	43031176	43031526	+	0	NA	IntergeniAluY SINE	9728 NM_033112	88745	Hs. 309231NM_033112	ENSG00000	CRP36	C6orf153 ribosomal protein-coding
chr6-1094	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr6	1.09E+08	1.09E+08	+	0	NA	intron (NLa2a LINE	-6902 NM_001286	64780	Hs. 33476 NM_022766	ENSG00000	MICAL1	MICAL MICrotub protein-coding
chr7-848E	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr7	848602	852684	+	0	NA	intron (Nintron (N	9269 NM_001367	23353	Hs. 438072NM_025154	ENSG00000	CCSUN1	UNC4A Sad1 and protein-coding
chr7-2711	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr7	27115573	27117620	+	0	NA	intron (Nintron (N	2999 NM_030661	3200	Hs. 659337NM_030661	ENSG00000	H0XA3	H0X1 H0Xhomeobox protein-coding
chr8-4227	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr8	42274084	42275987	+	0	NA	intron (NAluSx SIN	3733 NR_033818	3551	Hs. 597664NM_001556	ENSG00000	IKBK	IKK-beta inhibitor protein-coding
chr9-982C	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chr9	98234773	98235966	+	0	NA	intron (Nintron (N	-6152 NR_106913	1.02E+08	NR_106913	ENSG00000	MIR6854	hsa-mir-6854 microRNA ncRNA
chrX-535E	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chrX	53582676	53583424	+	0	NA	intron (NLa2a LINE	-25776 NR_029484	406889	NR_029484	ENSG00000	MIRLET7F2	LET7F2 Mi microRNA ncRNA
chrX-129F	6.69968	0.154643	0.887641	0.174218	0.861694	0.981636	chrX	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	16056 NM_001282	6594	Hs. 152292NM_003066	ENSG00000	SMARCA1	TSWI NURF SWI/SNF i protein-coding
chr8-1002	4.650464	0.187149	0.1074392	0.174191	0.861716	0.981636	chr8	1E+08	1E+08	+	0	NA	intron (Nintron (N	28522 NM_001355	25897	Hs. 292882NM_015434	ENSG00000	RNF19A	RNF19 ring fing protein-coding
chr14-1023	13.58849	-0.1117	0.641725	-0.17406	0.861816	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	1572 NR_002964	67811	Hs. 658237NR_002964	ENSG00000	SNORA28	ACA28 small nucsnoRNA
chr5-1511	9.212202	0.134049	0.770689	0.173934	0.861917	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (NMLTIC LTF	-16596 NM_001252	10318	Hs. 355141NM_006056	ENSG00000	TNIP1	ABIN-1 NFNFAIP3 i protein-coding
chrX-159	2.212202	0.134049	0.770689	0.173934	0.861917	0.981636	chrX	1593787	1595080	+	0	NA	intron (Nintron (N	-1022 NM_004043	438	Hs. 522572NM_004043	ENSG00000	ASMT	ASMTY Hicacytiser protein-coding
chr1-217E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr1	21728445	21729228	+	0	NA	intron (Nintron (N	54313 NM_001355	84196	Hs. 467524NM_032236	ENSG00000	USP48	RAP1GAI1 ubiquitir protein-coding
chr1-538E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr1	53881683	53882914	+	0	NA	intron (NLIIP8A LI	7499 NR_03664C	54432	Hs. 11923 NM_018982	ENSG00000	YIPF1	DJ167A19. Yipl dome protein-coding
chr11-71E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr11	71237967	71240631	+	0	NA	IntergeniMIR1_Amm	-14503 NM_012305	22941	Hs. 268722NM_012305	ENSG00000	SHANK2	AUS17 CSH3 and n protein-coding
chr12-651E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr12	6514388	6516009	+	0	NA	intron (NAluJr SIN	4976 NR_004387	692148	NR_004387	ENSG00000	SCARN10	U85 small Ca_ncrNA
chr14-30E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr14	30630632	30632357	+	0	NA	intron (NMER47A DN	9175 NM_016106	23256	Hs. 369166NM_016106	ENSG00000	SCFD1	C14orf16;secl fami protein-coding
chr16-48E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr16	48270079	48270837	+	0	NA	intron (Nintron (N	-22919 NM_001377	85320	Hs. 562267NM_032583	ENSG00000	ABCC11	EHWB MRPE ATP bindi protein-coding
chr2-2627	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr2	26279494	26280688	+	0	NA	exon (NM_exon (NM	31552 NM_001281	3032	Hs. 51584NM_000183	ENSG00000	HADHB	ECCB MSF hydroxycap protein-coding
chr2-276C	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr2	27634643	27636171	+	0	NA	intron (Nintron (N	6357 NM_007266	11321	Hs. 18259 NM_007266	ENSG00000	CPNP1	ATPBD1A GPN-loop protein-coding
chr2-6987	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr2	69870115	69871081	+	0	NA	intron (NLMIB3 LIN	-23358 NR_03786E	11017	Hs. 54649 NM_006857	ENSG00000	SNRNP27	27K RY1 small nuc protein-coding
chr20-627	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr20	62797980	62800088	+	0	NA	exon (NM_exon (NM	2561 NR_136405	55257	Hs. 44326CNR_01827C	ENSG00000	MRGBP	C20orf20 MRG domai protein-coding
chr4-871E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr4	87127322	87127662	+	0	NA	intron (N (CTCCTT) r	92776 NM_001292	57563	Hs. 106601NM_020803	ENSG00000	KLHL8	- kelch lik protein-coding
chr5-104E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr5	10406754	10408825	+	0	NA	intron (NAluJp SIN	5425 NR_162106	1.13E+08	NR_162106	MIR10397	- microRNA ncRNA	
chr5-324C	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr5	32409576	32410715	+	0	NA	intron (NAluJb SIN	-15670 NR_030305	693164	NR_030305	ENSG00000	MIR579	MIRN579 microRNA ncRNA
chr5-770E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr5	77059675	77062699	+	0	NA	intron (NLMIME3A LI	19384 NR_003014	677828	Hs. 69324ENR_003014	ENSG00000	SNORA47	HBI-115 small nucsnoRNA
chr6-411E	8.699898	0.137173	0.788829	0.173895	0.861948	0.981636	chr6	4115389	4117643	+	0	NA	intron (NAluSx1 SI	18952 NM_001166	10455	Hs. 15250 NM_006117	ENSG00000	EC12	ACBD2 DRS enoyl-CoA protein-coding
chr3-107E	9.724506	0.131289	0.755385	0.173805	0.862019	0.981636	chr3	1.08E+08	1.08E+08	+	0	NA	3' UTR (N3' UTR (N	72445 NR_02427E	151658	Hs. 15904ENR_015414	ENSG00000	LINC0063E	- long intencRNA
chr17-37E	7.667433	0.14673	0.844551	0.173738	0.862072	0.981636	chr17	37578812	37579748	+	0	NA	intron (Nintron (N	30138 NM_08055C	11276	Hs. 594647NM_007247	ENSG00000	SYNRG	APIGBP1 Synergim protein-coding
chr2-218E	7.667433	0.14673	0.844551	0.173738	0.862072	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (Nintron (N	-16572 NM_01464C	9654	Hs. 47140ENM_01464C	ENSG00000	TTL4	- tubulin t protein-coding
chr3-502E	7.667433	0.14673	0.844551	0.173738	0.862072	0.981636	chr3	50288527	50288919	+	0	NA	TTS (NM_C TTS (NM_C	3872 NM_006764	7866	Hs. 315177NM_006764	ENSG00000	IFRD2	IFNRP SKM interferc protein-coding
chr1-125E	6.48587	-0.15913	0.916328	-0.17366	0.862132	0.981636	chr1	12574677	12575458	+	0	NA	intron (NAluSx1 SI	3956 NR_106788	1.02E+08	NR_106788	ENSG00000	MIR6730	hsa-mir-6730 microRNA ncRNA
chr10-10C	6.48587	-0.15913	0.916328	-0.17366	0.862132	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (NAluY SINE	-7210 NR_002954	6778				

chr4-1327.7.724288	0.144793	0.838988	0.172581	0.862981	0.981636	chr4	1327765	1329701	+	0	NA	intron (NCpG)	-18475 NM_020894	57654 Hs. 380477ENM_020894	ENSG00000CVSSA	KIAA1530 UV	stimulprotein-coding
chr7-5918.7.724288	0.144793	0.838988	0.172581	0.862981	0.981636	chr7	5918551	5919324	+	0	NA	intron (Nintron (N	20204 NM_015622	51622 Hs. 530000NM_015622	ENSG00000CCZ1	C7orf28A CCZ1	homcprotein-coding
chr1-1506.11.69144	0.119923	0.69517	0.172508	0.863038	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	TTS (NM_2TTS (NM_2	1996 NM_207047	2029 Hs. 632454ENM_004436	ENSG00000CENSA	ARPP-19e	endosulfiprotein-coding
chr1-427.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr1	42706353	42707451	+	0	NA	IntergeniAluSx1 S1	23766 NR_132737	4904 Hs. 473582NM_004455	ENSG00000YBX1	BP-8 CBF-Y-box	birprotein-coding
chr1-1093.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (NAluSq2 S1	40060 NM_00120E	6272 Hs. 485195NM_002955	ENSG00000SORT1	Gp95 LDLc	stortilin protein-coding
chr10-466.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr10	466262	468593	+	0	NA	intron (NLIPA2 LIN	-161137 NR_147612	1.02E+08 Hs. 654707NR_147612	ENSG00000CLOC10193C	-	uncharactncRNA
chr17-166.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr17	16643443	16646141	+	0	NA	intron (NLTR65 LTF	9058 NM_020787	57547 Hs. 128078NM_020787	ENSG00000ZNF624	-	zinc fingprotein-coding
chr17-463.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr17	46356677	46357331	+	0	NA	intron (NAluS2 S1	4783 NM_001366	1.01E+08 Hs. 529555NM_001033	ENSG00000ARL17B	ARL17 ARI	ADP ribosprotein-coding
chr19-493.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr19	49357300	49357748	+	0	NA	intron (Nintron (N	3993 NM_00125E	8463 Hs. 515534NM_00359E	ENSG00000TEAD2	ETF TEAD-TEA	domaiprotein-coding
chr21-327.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr21	32767436	32768203	+	0	NA	intron (NTHE1A LTF	3936 NM_01332E	94104 Hs. 644004NM_01332E	ENSG00000PAXBP1	BMO20 C21PAX3	and protein-coding
chr21-392.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr21	39219113	39221038	+	0	NA	intron (NMIRb SINE	-36561 NM_203433	8624 Hs. 473838NM_00372C	ENSG00000PSMG1	C21LRP DS	proteasoneprotein-coding
chr3-3312.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr3	33121380	33123343	+	0	NA	intron (Nintron (N	8403 NM_006371	10491 Hs. 517888NM_006371	ENSG00000CRTAP	CASP LEPF	cartilageprotein-coding
chr3-1238.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	64477 NM_05302E	4638 Hs. 477377NM_00596E	ENSG00000MYLK	AAT7 KRP myosin	liprotein-coding
chr4-1225.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr4	1.23E+08	1.23E+08	+	0	NA	intron (NHERV32-i	30237 NM_00134E	166378 Hs. 709645NM_145207	ENSG00000SPATA5	AFG2 EHL spermatog	protein-coding
chr4-1766.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr4	1.77E+08	1.77E+08	+	0	NA	intron (NLIPA3 LIN	95792 NM_00542E	7424 Hs. 435215NM_00542E	ENSG00000VEGFC	Flt4-L Ll	vascular protein-coding
chr7-2996.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr7	29966588	29967626	+	0	NA	intron (Nintron (N	22694 NM_01476E	9805 Hs. 52074CNM_01476E	ENSG00000SCRN1	SES1	secernin protein-coding
chr7-931C.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr7	93109642	93110766	+	0	NA	intron (NLIPA5 LIN	7775 NM_017654	54809 Hs. 65641 NM_017654	ENSG00000SAMD9	C7orf5 DF	estriin epsilon protein-coding
chr8-9748.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr8	9748161	9752805	+	0	NA	intron (NMLTIH-int	8811 NR_030327	693182 NR_030327	ENSG00000MIR597	MIRN597 hmicroRNA	ncRNA
chr8-2534.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr8	25347010	25347785	+	0	NA	intron (Nintron (N	1995 NR_10693E	1.02E+08 Hs. 10693E	ENSG00000MIR6876	hsa-mir-6	microRNA ncRNA
chr8-305C.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr8	30509947	30511176	+	0	NA	intron (Nintron (N	-125160 NR_04620E	1E+08 Hs. 126812NR_04620E	ENSG00000RBPMS-AS1	RBPMS	antncRNA
chr8-9002.5.68293	0.165581	0.960008	0.172478	0.863061	0.981636	chr8	90022011	90024171	+	0	NA	intron (Nintron (N	21614 NM_00135E	1666 Hs. 492212NM_00135E	ENSG00000DEC1	DEC1 NADF2	4-dienccprotein-coding
chr1-1102.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr1	11026144	11027503	+	0	NA	3' UTR (N3' UTR (N	14201 NM_00737E	23435 Hs. 300624NM_00737E	ENSG00000TARDBP	ALS10 TDF	TAR DNA tprotein-coding
chr1-5276.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr1	5276027	5279608	+	0	NA	exon (NM exon (NM	-46431 NM_00130E	440590 Hs. 658455NM_001004	ENSG00000CYG11A	ZYG11	zym-11 f2 protein-coding
chr1-202C.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr1	202E+08	2.02E+08	+	0	NA	TTS (NM_2TTS (NM_2	3346 NR_10679E	1.02E+08 Hs. 10679E	ENSG00000MIR6740	hsa-mir-6	microRNA ncRNA
chr11-951.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr11	9513330	9514305	+	0	NA	intron (NAluS2 SIN	52805 NM_00344E	7702 Hs. 523471NM_00344E	ENSG00000ZNF143	SBF STAF zinc	fingprotein-coding
chr11-116.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr11	11925308	11925744	+	0	NA	intron (NLMCa LIN	83114 NM_00101E	27122 Hs. 292155NM_01325E	ENSG00000DKK3	NRIC RIG	dickkopf protein-coding
chr11-478.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr11	47819100	47820019	+	0	NA	intron (Nintron (N	28791 NR_13463E	23279 Hs. 643525NM_015231	ENSG00000NUP160	PHS19	nucleopor protein-coding
chr12-567.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr12	56715843	56716433	+	0	NA	exon (NM exon (NM	9161 NM_005594	4666 Hs. 50573E	ENSG00000NACA	HSD48 NAC	nascent fprotein-coding
chr12-105.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (NLMIEg LIN	26507 NM_00129E	23325 Hs. 12144 NM_01527E	ENSG00000WASHC4	KIAA1033 WASH	comf protein-coding
chr14-582.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr14	58212975	58213863	+	0	NA	intron (Nintron (N	13270 NM_018477	55860 Hs. 509451NM_018477	ENSG00000ACTR10	ACTR11 AR	actin relprotein-coding
chr15-253.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr15	25347501	25348355	+	0	NA	intron (NLMIE2 LIN	69585 NR_00128E	338429 NR_00128E	ENSG00000SNORD109E	HBI1-438E	small nucsnoRNA
chr17-294.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr17	29403694	29405297	+	0	NA	intron (Nintron (N	13570 NM_02514E	57551 Hs. 597434NM_020791	ENSG00000TAOK1	KFC-B MAF	TAO kinasprotein-coding
chr17-454.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr17	45458217	45458626	+	0	NA	exon (NM exon (NM	17014 NR_036271	1E+08 Hs. 036271	ENSG00000MIR4315-2	-	microRNA ncRNA
chr19-525.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr19	52562071	52564352	+	0	NA	IntergeniIntergeni	-7062 NM_01826E	55762 Hs. 235167NM_01826E	ENSG00000ZNF701	-	zinc fingprotein-coding
chr2-2407.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr2	24079188	24080025	+	0	NA	exon (NM exon (NM	2773 NR_11192E	375190 Hs. 710377NM_19855E	ENSG00000FAM228B	-	family wiprotein-coding
chr2-3318.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr2	33180771	33184267	+	0	NA	intron (NAluV SINE	47922 NM_00116E	4052 Hs. 193361NM_000627	ENSG00000LTPB1	-	latent tprotein-coding
chr20-496.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr20	49645339	49647163	+	0	NA	intron (NTiger3 I	67627 NM_00477E	9334 Hs. 370487NM_00477E	ENSG00000CB4GALT5	B4Gal-T5 beta-1,4-	protein-coding
chr22-388.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr22	38504090	38505104	+	0	NA	intron (Nintron (N	1696 NM_00109E	10521 Hs. 52830E	ENSG00000DDX17	P72 RH70	DEAD-box protein-coding
chr3-3705.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr3	37051759	37053561	+	0	NA	TTS (NM_2TTS (NM_2	59310 NM_00125E	4292 Hs. 195364NM_00024E	ENSG00000MLH1	COC42 FCC	mutL homcprotein-coding
chr3-196C.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	3' UTR (N3' UTR (N	30792 NM_00112E	7037 Hs. 529615NM_003234	ENSG00000TFRC	CD71 IMD4	transferr protein-coding
chr6-116.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr6	1.17E+08	1.17E+08	+	0	NA	TTS (NM_2TTS (NM_2	18214 NM_00101E	345895 Hs. 16038NM_00101E	ENSG00000RSPH4A	CILD11 RS	radial sprotein-coding
chr7-1215.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr7	1.21E+08	1.21E+08	+	0	NA	intron (NTiger3a I	8824 NM_01488E	10447 Hs. 434055NM_01488E	ENSG00000FAM3C	GS3786 II	family wiprotein-coding
chr7-1237.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr7	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	41616 NM_003941	8976 Hs. 14372ENM_003941	ENSG00000WASL	N-WASP NWASP	likeprotein-coding
chr8-2305.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr8	23055622	23057194	+	0	NA	intron (NAluS2 SIN	-11621 NR_03887E	286059 Hs. 306677NR_03887E	ENSG00000LOC28605E	-	TNF recep pseudo
chr8-963C.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr8	96305164	96307534	+	0	NA	intron (Nintron (N	44247 NM_014754	9791 Hs. 292575NM_014754	ENSG00000PTDSS1	LMHD PSS	phosphatiprotein-coding
chr8-9852.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr8	98524285	98525218	+	0	NA	intron (NMLTIH LTF	97939 NM_02069E	3788 Hs. 38804E	ENSG00000CKNS2	KV9.2	potassium protein-coding
chr8-1327.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	20006 NM_01601E	51105 Hs. 304362NM_01601E	ENSG00000PHF20L1	CGI-72 IT	PHD fingprotein-coding
chr9-1907.6.931611	-0.15146	0.878592	-0.17239	0.86313	0.981636	chr9	19077394	19080034	+	0	NA	intron (NAluSq2 S1	-14928 NR_00300E	677776 Hs. 68963E	ENSG00000SCARN8	U92	small Ca_ncRNA
chr5-1415.6.931611	-0.151498	0.879374	-0.172279	0.863218	0.981636	chr5	1415E+08	1.42E+08	+	0	NA	intron (NLMIC4 LIN	-				





chr18-137.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr18	13752614	13754840	+	0 NA	intron (AluYm1 S1	27054 NM_001308	8731 Hs. 592347NM_003799	ENSG00000CRNMT	CMT1 CMT1RNA	guanine-protein-coding
chr18-234.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr18	23455203	23456926	+	0 NA	intron (AluSc SIN	2777 NR_145477	8780 Hs. 445511NM_003831	ENSG00000R10K3	SUDD	RIO kinase-protein-coding
chr19-116.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr19	11603899	11604769	+	0 NA	5' UTR (5' UTR (N	6851 NM_145295	199692 Hs. 526665NM_145295	ENSG00000ZNF627		zinc finger-protein-coding
chr2-234.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr2	2.35E+08	2.35E+08	+	0 NA	intron (AluSc8 S1	6943 NM_001371305				
chr2-205.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr2	20566766	20568632	+	0 NA	intron (Nintron (N	59652 NM_001299	51586 Hs. 517421NM_015889	ENSG00000MED15	ARC105 C/mediator	protein-coding
chr3-425.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr3	42560820	42561200	+	0 NA	intron (Nintron (N	-20830 NM_016305	51188 Hs. 534454NM_016305	ENSG00000CSS18L2	KIAA-iso SS18 like	protein-coding
chr3-1207.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr3	1.21E+08	1.21E+08	+	0 NA	intron (NLM2 LIN	-20671 NM_000187	3081 Hs. 368254NM_000187	ENSG00000HGD	UKO HGO	homogentisin-protein-coding
chr3-1605.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr3	1.61E+08	1.61E+08	+	0 NA	TTS (NR_C TTS (NR_C	989 NR_003001	677767 Hs. 675955NR_003001	ENSG00000SCARNA7	A90	small Cajal
chr3-185.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr3	1.86E+08	1.86E+08	+	0 NA	intron (HALIME LI	-48808 NR_126325	646600 Hs. 647949NR_027317	ENSG00000IGF2BP2	3Corf65	IGF2BP2 ncRNA
chr5-129.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr5	1.3E+08	1.3E+08	+	0 NA	intron (Nintron (N	-124844 NM_001257	1E+08 Hs. 529234NM_001257	ENSG00000MINAR2	KIAA1024 membrane	protein-coding
chr6-1497.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr6	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	-123344 NM_001270	9113 Hs. 549084NM_004699	ENSG00000LATS1	WARTS wts large	tumour-protein-coding
chr7-4404.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr7	44046815	44047473	+	0 NA	intron (Nintron (N	2442 NM_001122	28988 Hs. 436500NM_014065	ENSG00000DBNL	ABP1 HIP-1	drebrin 1 protein-coding
chr7-763.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr7	76325811	76326326	+	0 NA	TTS (NM_C TTS (NM_C	23395 NM_001540	3315 Hs. 520975NM_001540	ENSG00000HSPB1	CMT2F HEL heat	shock-protein-coding
chr8-672.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr8	67215580	67218048	+	0 NA	intron (Nintron (N	126967 NM_006421	10565 Hs. 656992NM_006421	ENSG00000ARFGEF1	ARFGEF1 EADP	rhoc-protein-coding
chr8-8654.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr8	86540038	86540237	+	0 NA	intron (Nintron (N	25702 NM_003905	8895 Hs. 191215NM_003905	ENSG00000CPNE3	CPN3 PRO1	copine 3 protein-coding
chr8-1434.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr8	1.43E+08	1.43E+08	+	0 NA	intron (Nintron (N	31030 NR_145785	1.1E+08 NR_145785	SNORD149		small nucleolar
chr9-1367.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chr9	1.37E+08	1.37E+08	+	0 NA	intron (Nintron (N	17099 NR_039821	1.01E+08 NR_039821	ENSG00000MIR4673		microRNA ncRNA
chrX-479.7.170845	0.147342	0.860453	0.171238	0.864037	0.981636	chrX	47977161	47986561	+	0 NA	intron (AluSc8 S1	22128 NM_006962	7569 Hs. 189699NM_006962	ENSG00000ZNF182	HHZ150 KZC	zinc finger-protein-coding
chr14-697.13.12703	-0.11184	0.653312	-0.17119	0.864074	0.981636	chr14	69767939	69776448	+	0 NA	TTS (NM_C TTS (NM_C	-4480 NR_029378	1E+08 Hs. 729252NR_029378	LOC100289		uncharacterized
chr4-386.13.12703	-0.11184	0.653312	-0.17119	0.864074	0.981636	chr4	38688203	38691581	+	0 NA	intron (Nintron (N	-25264 NR_026804	79667 Hs. 29725 NM_024614	ENSG00000KLF3-AS1		KLF3 anticRNA
chr20-46.9.732364	0.129814	0.758492	0.171147	0.864108	0.981636	chr20	46375070	46375486	+	0 NA	exon (NM_exon (NM	-10820 NM_001281	51006 Hs. 593344NM_015945	ENSG00000SLC35C2	BA39402	Isolute c
chr1-111.6.890471	-0.15408	0.900504	-0.1711	0.864145	0.981636	chr1	1.12E+08	1.12E+08	+	0 NA	intron (NLM2c LINE	27399 NM_001370	5906 Hs. 190334NM_002884	ENSG00000CRAP1A	C21KG G-2	RAP1A, me protein-coding
chr11-61.10.20353	0.125783	0.735168	0.171094	0.86415	0.981636	chr11	61364405	61365609	+	0 NA	intron (AluSx SIN	2633 NM_016464	51524 Hs. 406533NM_016464	ENSG00000TMEI138	HSPC196	transmembrane
chr15-41.12.18655	-0.11706	0.684713	-0.17096	0.864256	0.981636	chr15	41093575	41093791	+	0 NA	intron (AluJb SIN	22563 NR_104038	54617 Hs. 292945NM_017555	ENSG00000IN080	IN080A IN	IN080 component-coding
chr3-195.11.16379	-0.12608	0.737546	-0.17094	0.864268	0.981636	chr3	1.96E+08	1.96E+08	+	0 NA	intron (AluJb SIN	30088 NR_003264	255812 Hs. 566872NR_003264	ENSG00000SDHAP1	SDHAL1 SE	succinate pseudo
chr11-77.6.478012	-0.15696	0.918594	-0.17087	0.864326	0.981636	chr11	77701641	77702460	+	0 NA	exon (NM_exon (NM	-64244 NM_001311	1207 Hs. 430733NM_001295	ENSG00000CLNS1A	CLCI CLNS	chloride protein-coding
chr7-77.6.478012	-0.15696	0.918594	-0.17087	0.864326	0.981636	chr7	77160797	77161212	+	0 NA	intron (NLM3 LIN	38389 NM_002087	57639 Hs. 113943NM_002087	ENSG00000CCDC146		coiled-coil
chr1-162.6.650683	0.154691	0.905354	0.170862	0.864332	0.981636	chr1	16252465	16253074	+	0 NA	intron (Nintron (N	-15586 NM_030907	79363 Hs. 546433NM_030907	ENSG00000CPLANE2	C1orf89 F	cilicogene protein-coding
chr10-27.6.650683	0.154691	0.905354	0.170862	0.864332	0.981636	chr10	27218489	27219275	+	0 NA	intron (AluSx1 S1	21604 NM_001301	91452 Hs. 530597NM_145699	ENSG00000ACBD5		acyl-CoA
chr12-89.6.650683	0.154691	0.905354	0.170862	0.864332	0.981636	chr12	89623876	89624789	+	0 NA	exon (NM_exon (NM	84506 NM_001366	490 Hs. 506276NM_001682	ENSG00000ATP2B1	PMCA1 PM	ATPase 1 protein-coding
chr1-669.9.691225	0.12815	0.750488	0.170756	0.864416	0.981636	chr1	66998457	66999062	+	0 NA	TTS (NM_C TTS (NM_C	55389 NM_015135	23169 Hs. 213642NM_015135	ENSG00000SLC35D1	SHNKND UC	solute c
chr12-90.9.691225	0.12815	0.750488	0.170756	0.864416	0.981636	chr12	907310	908569	+	0 NA	exon (NM_exon (NM	25137 NM_001297	5893 Hs. 410355NM_134422	ENSG00000RAD52		RAD52 hom
chr13-41.9.691225	0.12815	0.750488	0.170756	0.864416	0.981636	chr13	41367529	41370749	+	0 NA	exon (NM_exon (NM	-57100 NM_001354	9617 Hs. 382172NM_004294	ENSG00000MTRF1	MRF1 MTF	mitochondrial
chr14-30.9.691225	0.12815	0.750488	0.170756	0.864416	0.981636	chr14	30945098	30948293	+	0 NA	intron (Nintron (N	-56887 NR_038355	1.01E+08 Hs. 729199NR_038355	ENSG00000LOC100505		uncharacterized
chr8-93.9.691225	0.12815	0.750488	0.170756	0.864416	0.981636	chr8	93292084	93292699	+	0 NA	exon (NM_exon (NM	5944 NM_001161	54704 Hs. 22265 NM_018444	ENSG00000PDP1	PDH PDP	pyruvate protein-coding
chr10-12.6.707538	0.152487	0.893027	0.170753	0.864418	0.981636	chr10	1.21E+08	1.21E+08	+	0 NA	exon (NM_exon (NM	51815 NM_081117	55717 Hs. 144447NM_018117	ENSG00000WDR11	BRWD2 DR1	WD repeat
chr14-31.6.707538	0.152487	0.893027	0.170753	0.864418	0.981636	chr14	31305175	31305751	+	0 NA	intron (AluSx SIN	-97670 NM_015382	25831 Hs. 708017NM_015382	ENSG00000HECTD1	EULIR HECT	domain
chr19-49.6.707538	0.152487	0.893027	0.170753	0.864418	0.981636	chr19	49610047	49610472	+	0 NA	intron (AluSq10 S	19077 NM_020715	57479 Hs. 590971NM_020715	ENSG00000PRR12	KIAA1205	proline 1
chr2-148.6.707538	0.152487	0.893027	0.170753	0.864418	0.981636	chr2	1.48E+08	1.48E+08	+	0 NA	intron (NLM3A5 LI	-218611 NM_181742	5000 Hs. 556364NM_002555	ENSG00000CORC4	ORCAL ORC	origin
chr3-575.6.707538	0.152487	0.893027	0.170753	0.864418	0.981636	chr3	57593770	57594277	+	0 NA	intron (AluSq2 S1	3321 NM_001660	378 Hs. 652185NM_001660	ENSG00000ARF4	ARF2	ADP
chr9-816.6.707538	0.152487	0.893027	0.170753	0.864418	0.981636	chr9	81611300	81612176	+	0 NA	intron (Nintron (N	77797 NM_001303	7088 Hs. 197323NM_005077	ENSG00000TLE1	ESG ESG	TLE family
chr9-9207.7.465639	-0.15354	0.899348	-0.17072	0.864445	0.981636	chr9	92079809	92080828	+	0 NA	intron (Nintron (N	35599 NM_006415	10558 Hs. 90458 NM_006415	ENSG00000SPTLC1	HSAH1 HSA	serine
chr10-10.10.66684	0.123663	0.724906	0.170592	0.864545	0.981636	chr10	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	27185 NM_000102	1586 Hs. 438015NM_000102	ENSG00000CYP17A1	CPT7 CYP1	cytochrome
chr15-49.10.66684	0.123663	0.724906	0.170592	0.864545	0.981636	chr15	49260092	49260337	+	0 NA	intron (NLM3A3 LIN	89967 NM_001285	2585 Hs. 122005NM_002044	ENSG00000GALK2	GK2	galactokinase
chr1-100.6.658541	0.152505	0.894734	0.170447	0.864659	0.981636	chr1	1.0E+08	1.0E+08	+	0 NA	intron (Nintron (N	24057 NM_033055	64645 Hs. 124155NM_033055	ENSG00000MFSUD14A	HIAT1	major
chr1-2294.6.658541	0.152505	0.894734	0.170447	0.864659	0.981636	chr1	2.29E+08	2.29E+08	+	0 NA	intron (AluJb SIN	34682 NM_018230	55746 Hs. 12457 NM_018230	ENSG00000NUP133	GAMOS8 N	major nucleolar
chr10-101.6.658541	0.152505	0.894734	0.170447	0.864659	0.981636	chr10	1.01E+08	1.01E+08	+	0 NA	intron (AluSq2 S1	50749 NM_003935	8945 Hs. 643802NM_003935	ENSG00000BTRC	BETA-TRC	beta-tran
chr11-10.6.658541	0.152505	0.894734	0.170447	0.864659	0.981636	chr11	10044805	10045684	+	0 NA	intron (AluSx1 S1	206102 NR_120535	1.02E+08 Hs. 585524NR_120535	ENSG00000LOC101925		uncharacterized
chr11-68.6.658541	0.152505	0.894734	0.170447	0.864659	0.981636	chr11	68564411	68565510	+	0 NA	intron (Nintron (N	104208 NM_001352	55291 Hs. 503022NM_018312	ENSG00000PPP6R3	C11orf23 P	protein
chr12-10.6.658541	0.152505	0.894734	0.170447	0.864659	0.981636	chr12	1.07E+08	1.07E+08	+	0 NA	intron (NLM2c LINE	3124 NM_001033	80298 Hs. 5009 NM_025195	ENSG00000MTERF2	MTERFD3 E	mitochondrial



chr8-4787 7.426349	-0.14394	0.845477	-0.17024	0.864819	0.981636	chr8	47875938	47882148	+	0 NA	intron (Nintron (N	81093 NM_001081	5591 Hs. 491682NM_006904	ENSG000003PRK3D	DNA-PKC I	protein f	protein-coding		
chr8-1447 7.426349	-0.14394	0.845477	-0.17024	0.864819	0.981636	chr8	1.45E+08	1.45E+08	+	0 NA	intron (NAluJr SIN	6351 NM_138367	90987 Hs. 534516NM_138367	ENSG000003ZNF251	-	zinc fing	protein-coding		
chr9-3305 7.426349	-0.14394	0.845477	-0.17024	0.864819	0.981636	chr9	33053106	33059436	+	0 NA	intron (Nintron (N	20403 NM_018225	55234 Hs. 565351NM_018225	ENSG000003CSMU1	BWD SMU-1SMU1	DNA	protein-coding		
chr9-982 7.426349	-0.14394	0.845477	-0.17024	0.864819	0.981636	chr9	98239131	98244347	+	0 NA	intron (Nintron (N	-12522 NR_106911	1.02E+08	NR_106911	ENSG000003MIR6854	hsa-mir-6	miRNA ncRNA		
chr1-2402 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr1	2.4E+08	2.4E+08	+	0 NA	intron (Nintron (N	180656 NM_020066	56776 Hs. 24889	NR_020066	ENSG000003FMN2	-	formin 2	protein-coding	
chr11-703 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr11	70372714	70374345	+	0 NA	intron (Nintron (N	-24977 NM_138566	2017 Hs. 596164NM_005231	ENSG000003CTTN	EMS1	cortactin	protein-coding		
chr15-503 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr15	50307891	50308227	+	0 NA	intron (NLM3B LI	-42333 NM_002112	3067 Hs. 1481	NR_002112	ENSG000003HDC	-	histidine	protein-coding	
chr18-633 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr18	63333558	63335401	+	0 NA	intron (NAluSg SIN	-15099 NM_000657	596 Hs. 150745NM_000633	ENSG000003BCL2	Bcl-2 PPF	BCL2	apopt	protein-coding	
chr20-417 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr20	4177150	4179411	+	0 NA	intron (NAluSg SIN	-14810 NR_033917	728228 Hs. 636379NR_033917	ENSG000003LINC01433	-	long intenc	ncRNA		
chr5-6605 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr5	66055345	66055537	+	0 NA	exon (NM exon (NM	-89759 NM_001322	140890 Hs. 49367	NR_139168	ENSG000003SREK1	SFRS12 SF	splicing	protein-coding	
chr5-1093 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr5	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	-36162 NR_14904C	285638 Hs. 532104NR_14904C	ENSG000003LOC285638	-	uncharacter	ncRNA		
chr5-1604 9.178921	0.130809	0.768558	0.170201	0.864852	0.981636	chr5	1.6E+08	1.6E+08	+	0 NA	exon (NM exon (NM	-6525 NM_001303	63920 Hs. 529464NM_02209C	ENSG000003ZBED8	Buster3 C	zinc fing	protein-coding		
chr19-403 6.642825	0.15697	0.922514	0.170155	0.864888	0.981636	chr19	40328201	40328472	+	0 NA	intron (Nintron (N	20061 NR_046202	126526 Hs. 631557NM_17883C	ENSG000003C19orf47	-	chromosom	protein-coding		
chr5-3478 6.642825	0.15697	0.922514	0.170155	0.864888	0.981636	chr5	34786785	34787228	+	0 NA	intron (NMER9a3 LI	-52158 NM_14472E	153657 Hs. 435742NM_14472E	ENSG000003TTC9C	MC25-1	tetratric	protein-coding		
chr8-767 8.658759	0.135543	0.796767	0.170116	0.864919	0.981636	chr8	76704429	76704949	+	0 NA	exon (NM exon (NM	-21414 NR_02436C	1E+08 Hs. 596423NR_02436C	ENSG000003ZFHX4-AS1	-	ZFHX4	antncRNA		
chr1-2475 8.659091	0.137365	0.807515	0.170108	0.864925	0.981636	chr1	24756971	24757313	+	0 NA	intron (NAluSp SIN	11695 NM_013943	25932 Hs. 440544NM_013943	ENSG000003CLY4	CHLICAL H	chiclike	protein-coding		
chr5-1423 4.66618	0.181067	1.064675	0.170068	0.864957	0.981636	chr5	1.42E+08	1.42E+08	+	0 NA	intron (NAluJb SIN	69716 NR_120664	1.02E+08 Hs. 658949NR_120664	ENSG000003SPRY4-AS1	THLCAF68	SPRY4	antncRNA		
chr18-993 12.17047	0.11579	0.681685	0.169858	0.865122	0.981636	chr18	9936170	9937082	+	0 NA	intron (NAluJb SIN	22610 NM_003574	9218 Hs. 165195NR_003574	ENSG000003VAPA	VAP-33 V	VAMP	assoc	protein-coding	
chr16-577 7.219842	0.147352	0.868214	0.169719	0.865231	0.981636	chr16	57770569	57771304	+	0 NA	intron (Nintron (N	1416 NR_10683C	1.02E+08	NR_10683C	ENSG000003MIR6772	hsa-mir-6	miRNA ncRNA		
chr19-108 7.219842	0.147352	0.868214	0.169719	0.865231	0.981636	chr19	1087716	1089855	+	0 NA	TTS (NM_TTS (NM_C	6590 NM_00269E	5434 Hs. 24301	NR_00269E	ENSG000003POLR2E	RPABC1 R	RNA	protein-coding	
chr3-575 7.219842	0.147352	0.868214	0.169719	0.865231	0.981636	chr3	57558485	57559597	+	0 NA	intron (NLMC5 LI	-30873 NM_001311	7871 Hs. 476432NM_00715E	ENSG000003SLMAP	SLAP	sarcolem	protein-coding		
chr6-9051 7.219842	0.147352	0.868214	0.169719	0.865231	0.981636	chr6	90518309	90519275	+	0 NA	intron (Nintron (N	68280 NM_00318E	6885 Hs. 594838NM_00318E	ENSG000003MAP3K7	CSCF FMD	mitogen-e	protein-coding		
chr6-1345 7.219842	0.147352	0.868214	0.169719	0.865231	0.981636	chr6	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	13530 NR_03743E	1.01E+08	NR_03743E	ENSG000003MIR3662	mir-3662	microRNA	ncRNA	
chr6-3061 18.12813	0.098417	0.580064	0.169665	0.865273	0.981636	chr6	30616390	30617026	+	0 NA	non-codiron-codir	535 NM_002714	5514 Hs. 106015NM_002714	ENSG000003PPR110	CAT53 FBI	protein f	protein-coding		
chr19-344 8.341404	-0.13795	0.813382	-0.1696	0.865327	0.981636	chr19	3441195	3441569	+	0 NA	intron (NLMRc SINE	39143 NM_00113E	284422 Hs. 130714NM_00113E	ENSG000003SMIM24	C19orf77 s	small int	protein-coding		
chr11-294 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr11	2949138	2950440	+	0 NA	intron (Nintron (N	14104 NR_00298E	677833 Hs. 689696NR_00298E	ENSG000003SNORA54	ACA54	small nuc	ncRNA		
chr11-614 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr11	61446507	61449313	+	0 NA	Intergeni Intergeni	17785 NM_011784I	54949 Hs. 313247NM_011784I	ENSG000003SDHAF2	CL10r79 F	succinate	protein-coding		
chr12-965 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr12	96322007	96324205	+	0 NA	intron (NLMEd LI	67608 NM_001303	2004 Hs. 46523	NR_00523C	ENSG000003ELK3	ERP NET S	ETS	trans	protein-coding
chr13-111 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr13	1.11E+08	1.11E+08	+	0 NA	3' UTR (N3' UTR (N	-11543 NM_001303	121793 Hs. 210677NM_152324	ENSG000003TEX29	C19orf16 t	testis e	protein-coding		
chr16-294 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr16	29423129	29426771	+	0 NA	TTS (NR_TTS (NR_1	-20405 NM_00131C	728888 Hs. 270286NR_00131C	ENSG000003NPIP11	NPIP	nuclear f	protein-coding		
chr17-818 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr17	81863440	81863739	+	0 NA	IntergeniAluJb SIN	-3054 NM_00091E	5034 Hs. 464336NM_00091E	ENSG000003P4HB	CLCRP1 D	prolyl 4-	protein-coding		
chr18-956 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr18	9566430	9573885	+	0 NA	exon (NM exon (NM	44402 NR_052003	9989 Hs. 743233NM_005134	ENSG000003PPP4R1	MEG1 PPA	(protein f	protein-coding		
chr20-311 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr20	3154180	3153301	+	0 NA	intron (NHAL LINE	5125 NM_02182E	60493 Hs. 741166NM_02182E	ENSG000003FASTKD5	CL1187M17	FAST	kinase	protein-coding	
chr20-355 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr20	35380496	35384395	+	0 NA	intron (Nintron (N	29528 NM_018244	55245 Hs. 726299NM_018244	ENSG000003UCQC1	FBZF C20	cubiquinol	protein-coding		
chr22-205 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr22	20949196	20953713	+	0 NA	3' UTR (N3' UTR (N	-5638 NR_110537	1.02E+08 Hs. 648264NR_110537	ENSG000003LINC01637	-	long intenc	ncRNA		
chr22-235 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr22	23971221	23971881	+	0 NA	exon (NM exon (NM	2940 NM_001084	1652 Hs. 656723NR_00135E	ENSG000003DDT	D-DT DDC1	D-dopach	protein-coding		
chr4-4262 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr4	426204	426432	+	0 NA	non-codiron-codir	47891 NR_00245I	79963 Hs. 677493NM_02490E	ENSG000003ABCA11P	ABCA11 E	ATP	bindipseudo		
chr5-4352 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr5	43525273	43531320	+	0 NA	intron (Nintron (N	-13148 NM_19856E	375444 Hs. 661641NM_19856E	ENSG000003C5orf34	-	chromosom	protein-coding		
chr5-1592 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr5	1.59E+08	1.59E+08	+	0 NA	intron (NAluJo SIN	7894 NM_14504E	134510 Hs. 591733NM_14504E	ENSG000003UBLCP1	CPUB1	ubiquitin	protein-coding		
chr7-1396 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr7	1.4E+08	1.4E+08	+	0 NA	intron (NLMB5 LI	79781 NM_001113	28996 Hs. 731417NM_02274C	ENSG000003CHIPK2	PRO0593	homeodom	protein-coding		
chr9-3777 7.879948	-0.13974	0.824698	-0.16944	0.86545	0.981636	chr9	37779524	37783393	+	0 NA	intron (Nintron (N	3607 NM_016042	51010 Hs. 602571NM_016042	ENSG000003EXOSC3	NCU1-102 F	exosome	protein-coding		
chr1-1265 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr1	1265898	1268701	+	0 NA	intron (Nintron (N	6555 NM_19445E	118424 Hs. 191587NM_058167	ENSG000003UBEJ2	NCUBE-2 N	ubiquitin	protein-coding		
chr10-733 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr10	73375250	73376093	+	0 NA	3' UTR (N3' UTR (N	-16807 NM_001367	118491 Hs. 591367NM_14517C	ENSG000003CFAP70	TTC18	cilia anc	protein-coding		
chr11-945 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr11	9497258	9498772	+	0 NA	intron (NAluV SINE	37003 NM_003442	7702 Hs. 523471NM_003442	ENSG000003ZNF143	SBF STAR z	inc	protein-coding		
chr12-64 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr12	64481768	64482896	+	0 NA	intron (NAluSx1 SI	30212 NM_013254	29110 Hs. 505874NM_013254	ENSG000003TBK1	FTDLS4 I	TANK	binc	protein-coding	
chr14-102 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr14	1.02E+08	1.02E+08	+	0 NA	intron (NAluSx1 SI	4200 NM_03263C	51550 Hs. 129634NM_03263C	ENSG000003CINP	-	cyclin d	protein-coding		
chr16-375 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr16	3756489	3758838	+	0 NA	intron (Nintron (N	-40139 NM_016292	10131 Hs. 30345	NR_016292	ENSG000003TRAP1	HSP 75 H	TNF	recep	protein-coding
chr16-628 8.666617	0.133802	0.789947	0.169381	0.865497	0.981636	chr16	68315835	68316713	+	0 NA	intron (Nintron (N	5160 NM_00129C	54496 Hs. 640222NM_01902E	ENSG000003PRMT7	SBIDD5	protein e	protein-coding		
chr16-78 8.666617</																			

chr6-2832	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr6	2833645	2834326	+	0	NA	non-codirnon-codir	7878 NR_073112	1992 Hs. 381167NM_030666	ENSG00000SERPINB1	EI ELANH2	serpin fε	protein-coding		
chr6-8412	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr6	8412563	8414256	+	0	NA	non-codirnon-codir	22136 NM_00137C	51000 Hs. 285847NM_015948	ENSG00000SLC35B3	C6orf196	solute cε	protein-coding		
chr6-1437	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	-62142 NM_00132E	84946 Hs. 185677NM_03286C	ENSG00000CLTV1	C6orf93 cLTV1	ribc	protein-coding		
chr7-6596	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr7	65965710	65968532	+	0	NA	intron (Nintron (N	15092 NM_00129E	2990 Hs. 255233NM_000181	ENSG00000GUSB	MBP MS7	glucuronil	protein-coding		
chr7-989C	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr7	98902602	98911868	+	0	NA	intron (NAluSp SIN	25538 NR_00129E	1.07E+08	NR_132754	SCARNA28	ZL1	small Ca <sub>v</sub> ncRNA		
chr7-1023	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	-2224 NR_03166E	1E+08	NR_03166E	ENSG00000MIR5480	MIRN5480	microRNA ncRNA		
chr8-2197	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr8	21974878	21988345	+	0	NA	intron (Nintron (N	-42523 NM_00128E	10361 Hs. 131055NM_18279E	ENSG00000NPM2	-	nucleophc	protein-coding		
chr8-1442	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	intron (NAluSx SIN	6888 NM_00552E	3297 Hs. 530227NM_00552E	ENSG00000HSF1	HSTF1	heat shoc	protein-coding		
chr9-190C	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr9	19062880	19063153	+	0	NA	TTS (NR_C TTS (NR_C	770 NR_00300E	677776 Hs. 689633NR_00300E	ENSG00000SCARNA8	U92	small Ca <sub>v</sub> ncRNA			
chr9-3247	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr9	32478524	32481557	+	0	NA	intron (Nintron (N	46156 NM_01431E	23586 Hs. 190622NM_01431E	ENSG00000DDX58	RIG-I RIC DEXD/H-hc	protein-coding			
chr9-378E	7.691006	0.140981	0.832356	0.169375	0.865501	0.981636	chr9	37890946	37891525	+	0	NA	intron (NAluSx SIN	11092 NM_00341E	92014 Hs. 634122NM_03341E	ENSG00000SLC25A51	CG7943 MC	solute cε	protein-coding		
chr1-119C	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	11961688	11966292	+	0	NA	intron (Nintron (N	-16191 NM_014874	9927 Hs. 376681NM_014874	ENSG00000MFN2	CMT2A CMT1	mitofusir	protein-coding		
chr1-244E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	24453219	24461719	+	0	NA	intron (Nintron (N	41444 NM_00132E	57185 Hs. 523442NM_02044E	ENSG00000NIPAL3	DJ462023	NIPA	like	protein-coding	
chr1-326E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	32696251	32697592	+	0	NA	intron (NAluSz SIN	5849 NM_00116E	81493 Hs. 712631NM_03078E	ENSG00000SYNC	SYNC1 SYN	cooilir	protein-coding		
chr1-3301	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	33018703	33022446	+	0	NA	intron (NAluSz SIN	16309 NM_00119E	204 Hs. 470907NM_00162E	ENSG00000AK2	ADK2	adenylate	protein-coding		
chr1-360C	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	36027077	36030599	+	0	NA	intron (NLIP3 LIN	-55256 NM_01446E	27285 Hs. 127111NM_01446E	ENSG00000TEKT2	TEKTB1 TE	tektin 2	protein-coding		
chr1-3603	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	36039897	36041827	+	0	NA	intron (NAluSz LIN	-43232 NM_01446E	27285 Hs. 127111NM_01446E	ENSG00000TEKT2	TEKTB1 TE	tektin 2	protein-coding		
chr1-437E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	4371549	43771150	+	0	NA	intron (NLT79 LTF	24200 NM_01466E	9682 Hs. 155982NM_01466E	ENSG00000KDMA4	JHDM3A JH	lysine dε	protein-coding		
chr1-446E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	44634452	44638030	+	0	NA	intron (Nintron (N	34815 NR_14581E	1.1E+08	NR_14581E	SNORD145	-	small nucsnRNA		
chr1-922E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	92253388	92256605	+	0	NA	intron (NLIP47 LIN	37081 NM_00101E	388649 Hs. 558822NM_00101E	ENSG00000C1orf146	-	chromoson	protein-coding		
chr1-9311	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	93115099	93116296	+	0	NA	intron (Nintron (N	36414 NM_00735E	22823 Hs. 31016	NR_00735E	ENSG00000MTF2	M96 PCL2	metal res	protein-coding	
chr1-945E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	94508812	94511722	+	0	NA	intron (NLIP3 LIN	31492 NM_00199E	2152 Hs. 62192	NR_00199E	ENSG00000CF3	CD142 TF	coagulatip	protein-coding	
chr1-161E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	intron (NAluSx SIN	2654 NM_00116E	4720 Hs. 173611NM_00455C	ENSG00000NDUFS2	CI-49 MC1	NADH:ubiq	protein-coding		
chr1-172E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	1.73E+08	1.73E+08	+	0	NA	intron (Nintron (N	25317 NM_01428E	51430 Hs. 204559NM_01428E	ENSG00000SUCO	Clorf9 CF	SUN	domaiprotein-coding		
chr1-173E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	1.74E+08	1.74E+08	+	0	NA	intron (Nintron (N	17934 NM_00117E	91687 Hs. 53185E	NR_03331E	ENSG00000CENPL	Clorf155	centromer	protein-coding	
chr1-221E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (NLIME4b LI	3002 NR_02962E	406997	NR_02962E	ENSG00000MIR215	MIRN215	nmicroRNA	ncRNA	
chr10-310	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	314808	3155428	+	0	NA	intron (NAluJb SIN	10142 NR_038284	1.01E+08	Hs. 66536E	NR_038284	ENSG00000PITRM1-AS-	-	PITRM1	arcncRNA
chr10-68E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	68934294	68938531	+	0	NA	intron (NAluY SINE	-19758 NM_00472E	9188 Hs. 223141NM_00472E	ENSG00000DDX21	GUA GURDE	DEXD-box	protein-coding		
chr10-731	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	73161558	73163916	+	0	NA	intron (Nintron (N	5271 NM_00726E	11319 Hs. 631822NM_00726E	ENSG00000ECD	GCR2 HSG1	pedysc	lprotein-coding		
chr10-777	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	77782482	77833412	+	0	NA	Intergeni Intergeni	143808 NM_00474E	9231 Hs. 65269C	NR_00474E	ENSG00000DLG5	LP-DLG P-	discs lar	protein-coding	
chr10-864	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	86464742	86467171	+	0	NA	intron (Nintron (N	55828 NM_00131E	23063 Hs. 20309E	NR_01504E	ENSG00000WAPL	FOE KIAAC	WAPL	cohc	protein-coding
chr10-874	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	87065517	87069328	+	0	NA	intron (NAluJb SIN	26665 NM_00131E	2746 Hs. 50040E	NR_005271E	ENSG00000GLUD1	GDH GDH1	glutamate	protein-coding	
chr10-984	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	98440777	98445251	+	0	NA	intron (Nintron (N	-3307 NR_13445E	1.02E+08	Hs. 43488E	NR_13445E	LOC101927-	-	uncharactncRNA	
chr10-103	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	intron (Nintron (N	61359 NM_00136E	9644 Hs. 678727NM_014631	ENSG00000SH3PXD2A	FISH SH3	SH3	and f	protein-coding	
chr11-89E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr11	8951657	8956780	+	0	NA	intron (NLIMB7 LIN	10224 NM_02064E	56674 Hs. 50185E	NR_02064E	ENSG00000TMEM9B	Clorf10E TMEM9	domin	protein-coding	
chr11-27E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr11	57677608	57678554	+	0	NA	intron (Nintron (N	9967 NM_01545E	25921 Hs. 27239	NR_01545E	ENSG00000ZDHHCS	DHHC5 ZNF	zinc fng	protein-coding	
chr11-68E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr11	68594706	68598916	+	0	NA	intron (Nintron (N	-87733 NM_01597E	51083 Hs. 27895E	NR_01597E	ENSG00000CGAL	ETL8 GAL-	galanin ε	protein-coding	
chr11-83E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr11	83261192	83264822	+	0	NA	intron (NMRB SINE	23400 NM_00128E	60492 Hs. 36886E	NR_02182E	ENSG00000CCDC90B	MDSO11 MC	coiled-c	protein-coding	
chr12-46E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	4655606	4656929	+	0	NA	intron (Nintron (N	9173 NM_00500E	4704 Hs. 75227	NR_00500E	ENSG00000NDUFA9	C6 C1-3E	NADH:ubiq	protein-coding	
chr12-501	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	50115213	50116570	+	0	NA	intron (Nintron (N	3655 NM_00125E	84987 Hs. 38864E	NR_03290E	ENSG00000COX14	C12orf62	cytochron	protein-coding	
chr12-53E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	53252643	53300800	+	0	NA	intron (NAluSx SI	14527 NR_046221	1.01E+08	Hs. 63360E	NR_046221E	ENSG00000LOC10065E	-	uncharactncRNA	
chr12-57E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	57394129	57395476	+	0	NA	intron (Nintron (N	36241 NM_00135E	22864 Hs. 59111E	NR_00135E	ENSG00000R3HDM2	CAG6 PRO1	R3H	domaiprotein-coding	
chr12-88E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	88526616	88528278	+	0	NA	intron (Nintron (N	53024 NM_00089E	4254 Hs. 1048	NR_00089E	ENSG00000KITLG	DCUA DFN	KIT	ligar	protein-coding
chr12-95E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	95234640	95235194	+	0	NA	intron (NSVA_D Ret	17110 NM_01759E	55591 Hs. 24135	NR_01759E	ENSG00000VEZT	VEZATIN	vezatin,	protein-coding	
chr12-11E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	1.18E+08	1.18E+08	+	0	NA	intron (NMRB SINE	35399 NM_02249E	64426 Hs. 41663C	NR_02249E	ENSG00000SUDS3	SAP45 SDS	SZ3	homc	protein-coding
chr12-12E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	9793 NR_03618E	1E+08	NR_03618E	ENSG00000MIR4304	-	microRNA	ncRNA	
chr13-27E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr13	27067864	27071059	+	0	NA	intron (NLIME3 LIN	-56072 NR_04654E	1.01E+08	Hs. 52492E	NR_04654E	USP12-AS1-	-	USP12	antncRNA
chr13-39E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr13	39010602	39011527	+	0	NA	3' UTR (N3' UTR (N	-20205 NM_00114E	161003 Hs. 327794NM_14528E	ENSG00000CSTOML3	Epb7.21 S	tomatoin	protein-coding		
chr14-24E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr14	24210386	24211501	+	0	NA	intron (NAluSx SIN	2545 NM_01416E	29082 Hs. 27976E	NR_01416E	ENSG00000CHMP4A	C14orf12E	charged n	protein-coding	
chr14-63E	7.178702	0.145338	0.858305	0.169332	0.865536	0.981636	chr14	63380371	63382157	+	0										



chr1-2205	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr1	22094597	22095680	+	0	NA	3' UTR (N3' UTR (N	42429	NM_044472	998	Hs.467637NM_001791	ENSG000003CDC42	CDC42Hs Cell divi		
chr11-341	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr11	34108080	34108605	+	0	NA	intron (Nintron (N	2713	NM_001144	55226	Hs.577281NM_024662	ENSG000003NAT10	ALP Kre3N-acetyl		
chr11-765	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr11	76500428	76501533	+	0	NA	intron (NMER2 DNA	55955	NM_020193	56946	Hs.352588NM_020193	ENSG000003EMSY	C11orf30 EMSY		
chr11-765	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr11	76529976	76530390	+	0	NA	intron (NAluSq SIN	85158	NM_020193	56946	Hs.352588NM_020193	ENSG000003EMSY	C11orf30 EMSY		
chr12-206	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr12	26683371	26684650	+	0	NA	intron (Nintron (N	149184	NM_002222	3709	Hs.512233NM_002222	ENSG000003ITPR2	ANHD CFAF inositol		
chr12-987	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr12	98731955	98732762	+	0	NA	intron (Nintron (N	87058	NM_181868	317	Hs.552567NM_00116C	ENSG000003APAF1	APAF-1 Cafapoptotic		
chr12-111	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (NLMJ LINE	-13914	NR_106819	1.02E+08	NR_106819	ENSG000003MIR6761	hsa-mir-6761		
chr12-122	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	17329	NM_00135C	55596	Hs.37706	NM_017612	ENSG000003ZCHC8	zinc fingerprotein-coding	
chr13-495	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr13	49547556	49549504	+	0	NA	intron (NLMB5 LIN	37028	NM_001352	55213	Hs.508021NM_018191	ENSG000003RCBTB1	CLLD7 CLIRCC1		
chr13-671	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr13	77109294	77110619	+	0	NA	intron (NMER11A LI	34442	NR_046711	1.01E+08	Hs.569288NR_046711	ENSG000003MYCBP2-AS	MYCBP2		
chr15-644	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr15	64417054	64422354	+	0	NA	intron (Nintron (N	31868	NM_001321	9325	Hs.50034C	NM_016215	ENSG000003TRIP4	ASC-1 ASC thyroid	
chr15-771	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr15	77112798	77115317	+	0	NA	3' UTR (N3' UTR (N	-42948	NM_198902	10099	Hs.744863NM_005724	ENSG000003SPAN3	TM4-A TM4		
chr15-824	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr15	84791845	84794719	+	0	NA	intron (NAluSx SIN	-23398	NM_020778	57538	Hs.459183NM_020778	ENSG000003ALPK3	CMH27 MAA		
chr16-22C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr16	22085714	22086633	+	0	NA	IntergeniMIR3 SINE	-6517	NM_107376	146177	Hs.10697	NM_173615	ENSG000003VWA3A	Wille	
chr17-536	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr17	5369334	5370557	+	0	NA	intron (NAluSp SIN	-49696	NM_00116C	84268	Hs.462088NM_032308	ENSG000003RPAIN	HRIP RIP		
chr17-161	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr17	16134061	16135078	+	0	NA	intron (Nintron (N	18627	NR_145787	1.1E+08	NR_145787	SNORD163	small nucsnoRNA		
chr17-62C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr17	62666730	62668863	+	0	NA	intron (NLM2c LINE	-38410	NR_147888	1.05E+08	Hs.446268NR_147888	ENSG000003LOC105371	uncharactncRNA		
chr17-62C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr17	62643599	62644331	+	0	NA	intron (Nintron (N	-16887	NM_001252	57674	Hs.195642NM_020914	ENSG000003RNF213	ALO17 C17ring		
chr19-34C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr19	34327562	34331224	+	0	NA	intron (Nintron (N	-35347	NM_001184	2821	Hs.466471NM_000177	ENSG000003GPI	AMF GNP1		
chr2-127C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr2	12736077	12737356	+	0	NA	promoter-promoter-	-561	NR_036072	1E+08	NR_036072	ENSG000003MIR3125	mir-3125		
chr2-456C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr2	45600495	45602164	+	0	NA	intron (NMaamRep60E	9938	NM_018075	55133	Hs.14229	NM_018075	ENSG000003SRBD1	SI RNA	
chr2-208C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr2	2.08E+08	2.08E+08	+	0	NA	intron (NAluSx SIN	-21684	NM_001305	5746	Hs.570296NM_005048	ENSG000003PTH2R	PTH2R		
chr2-230C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (NMLT1C LTF	3590	NM_004500	3431	Hs.14515C	NM_004500	ENSG000003SP110	IF141 IF1SP110	
chr2-241C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr2	2.41E+08	2.41E+08	+	0	NA	intron (Nintron (N	3282	NM_182501	130916	Hs.159556NM_182501	ENSG000003MYERF4	MYERF4		
chr20-35C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr20	35551878	35552785	+	0	NA	intron (NLM2a LINE	10253	NM_015966	51614	Hs.472558NM_015966	ENSG000003ERGIC3	C20orf47 ERGIC		
chr20-367	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr20	36785466	36787366	+	0	NA	3' UTR (N3' UTR (N	-12653	NM_001145	79980	Hs.632268NM_024918	ENSG000003DSN1	C20orf172 DSN1		
chr21-334	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr21	33456612	33457176	+	0	NA	intron (Nintron (N	23808	NM_006134	757	Hs.433666NM_006134	ENSG000003TMEM50B	C21orf47 E		
chr22-205	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr22	20990762	20992782	+	0	NA	exon (NM exon (NM	9475	NM_006767	8216	Hs.78788	NM_006767	ENSG000003LZTR1	BTBD29 LZ	
chr22-314	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr22	31465327	31467998	+	0	NA	intron (NLMIE1 LIN	22894	NM_001164	56478	Hs.517555NM_019843	ENSG000003EIF4ENIF1	EIF4E T		
chr3-4257	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr3	42573578	42576319	+	0	NA	intron (NAluJr SIN	-6892	NM_01630E	51188	Hs.534454NM_01630E	ENSG000003SSL82	KIAA-iso		
chr3-6411	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr3	64119549	64121284	+	0	NA	intron (NMIRc SINE	16946	NR_046701	1.01E+08	Hs.668874NR_046701	PRICKLE2-	PRICKLE2		
chr3-141C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr3	1.41E+08	1.41E+08	+	0	NA	intron (Nintron (N	-10405	NM_00135C	253461	Hs.518301NM_152533	ENSG000003ZBTB38	CIBZ PPP1		
chr4-676C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr4	67654905	67656205	+	0	NA	intron (NLMIP13 LI	45600	NM_018227	55236	Hs.212774NM_018227	ENSG000003UBA6	EI-12 MOF		
chr5-876C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr5	876821	877365	+	0	NA	intron (Nintron (N	15429	NR_13429E	65980	Hs.449278NM_023924	ENSG000003BRD9	LAVS3040 bromodome		
chr5-659C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr5	65929832	65930947	+	0	NA	intron (NAluY SINE	3814	NM_001252	55914	Hs.591774NM_018695	ENSG000003ERBIN	ERBB2 P		
chr5-747	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr5	74777089	74777643	+	0	NA	TTS (NR_CTS (NR_C	-9995	NR_170681	84340	Hs.277154NM_03238C	ENSG000003GFM2	EF-G2nt EG		
chr5-1381	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	exon (NM exon (NM	14888	NM_004661	8697	Hs.73625	NM_004661	ENSG000003CDC23	ANAPC8 AF	
chr5-1507	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (NLMIP3 LIN	10705	NM_001133	51164	Hs.675564NM_016221	ENSG000003DCTN4	DYN1 P62		
chr5-154C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr5	1.55E+08	1.55E+08	+	0	NA	intron (NLMIP3 LIN	36331	NM_015466	25929	Hs.483921NM_015466	ENSG000003GEMIN5	GEMIN-5		
chr6-431C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr6	43192000	43193944	+	0	NA	intron (Nintron (N	10776	NM_01508E	23113	Hs.485434NM_01508E	ENSG000003CUL9	H7AP1 PAF		
chr6-143C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (NLM2a LINE	-24030	NM_001322	84946	Hs.185675NM_03286C	ENSG000003LTV1	C6orf93 LTV1		
chr7-1521	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (NLMJ SINE	109840	NM_001371474	-108238	NM_001200	1.01E+08	Hs.659493NM_001200	ENSG000003SMIM18	small intprotein-coding
chr8-3774	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr8	37744505	37745209	+	0	NA	intron (NMIR3 SINE	2939	NR_003671	728024	Hs.647133NR_003671	LOC728024	chromoson pseudo		
chr8-419C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr8	41931195	41933256	+	0	NA	exon (NM exon (NM	-35848	NR_001142	286	Hs.654433NM_000037	ENSG000003ANK1	ANK SPH1		
chr9-936C	6.666399	0.15036	0.889541	0.169031	0.865772	0.981636	chr9	93636392	93638406	+	0	NA	intron (NLMIB8 LIN	42558	NR_049855	1.01E+08	NR_049855	ENSG000003MIR548AU	microRNA		
chr3-881C	6.92725	-0.14866	0.88004	-0.16893	0.865853	0.981636	chr3	88130217	88130701	+	0	NA	intron (NAluJb SIN	19407	NM_00119E	8545	Hs.444818NM_003663	ENSG000003CGGBP1	CGGBP1 p2CGG		
chr15-101	13.11917	-0.11074	0.65577	-0.16893	0.865854	0.981636	chr15	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	1083	NR_107062	1.02E+08	NR_107062	ENSG000003MIR6859	hsa-mir-6859		
chr10-791	8.715614	0.133854	0.792609	0.168878	0.865892	0.981636	chr10	79120226	79121617	+	0	NA	intron (Nintron (N	51955	NM_020338	57178	Hs.193118NM_020338	ENSG000003ZM121	MIZ RAI17zinc		
chr19-411	8.715614	0.133854	0.792609	0.168878	0.865892	0.981636	chr19	4112368	4114233	+	0	NA	intron (Nintron (N	10829	NM_030662	5605	Hs.465627NM_030662	ENSG000003MAP2K2	CFCA4 MAPK		
chr6-875	8.715614	0.133854	0.792609	0.168878	0.865892	0.981636	chr6	87246587	87247276	+	0	NA	intron (NAluS6 SI	-75657	NM_001287	57150	Hs.70769	NM_020425	ENSG000003SMIM8	C6orf162 small	
chr20-352	10.21139	0.124361	0.736711	0.168806	0.865949	0.981636	chr20	35014850	35016369	+	0	NA	intron (NAluSx1 SI	-25137	NR_039912	1.01E+08	NR_039912	ENSG000003MIR499B	MIR499A microRNA		
chr1-2217	13.61391	-0.1082																			

chr13-772.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr13	77291239	77292058	+	0	NA	intron (AluSp SIN	35446	NM_015057	23077	Hs.591221NM_015057	ENSG000005MYCBP2	Myc-bp2 MYC bindiprotein-coding	
chr13-1118.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (L1P45 LIN	36121	NM_001352	79587	Hs.508722NM_024537	ENSG000005CARS2	COXP27 cysteinyprotein-coding	
chr13-1118.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr13	1.13E+08	1.13E+08	+	0	NA	intron (intron (	13460	NM_005561	3916	Hs.494419NM_005561	ENSG000005LAMP1	CD107a LAMP1 lysosomal protein-coding	
chr13-1118.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	3' UTR (3' UTR (	18667	NM_001366	1.01E+08	Hs.704267NM_001366	ENSG000005C13orf46	chromosom protein-coding	
chr14-358.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr14	35011849	35020209	+	0	NA	intron (L2b LINE	-28878	NM_001075	283635	Hs.446357NM_173607	ENSG000005FAM177A1	C14orf24 family wiprotein-coding	
chr14-498.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr14	49802014	49806478	+	0	NA	intron (AluSg SIN	36093	NM_014315	23588	Hs.509264NM_014315	ENSG000005KLHDC2	HCLP-1 Hckelch don protein-coding	
chr14-678.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr14	67684745	67692622	+	0	NA	intron (FLAM_C SI	7081	NM_001252	51109	Hs.719922NM_016026	ENSG000005RDH11	ARSDR1 Ccr etaloin protein-coding	
chr14-758.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr14	75016530	75020716	+	0	NA	intron (intron (	15702	NM_014235	8892	Hs.409137NM_014235	ENSG000005EIF2B2	EIF-2B2eukaryotiprotein-coding	
chr15-434.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr15	43419765	43423083	+	0	NA	intron (intron (	50323	NM_001286	27229	Hs.584887NM_014444	ENSG000005TUBGCP4	76P GCP-4 tubulin protein-coding	
chr15-636.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr15	63262144	63262937	+	0	NA	intron (intron (	-26903	NR_034088	1E+08	Hs.631162NR_034088	ENSG000005USP3-AS1	USP3 antincRNA	
chr15-762.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr15	76281110	76286202	+	0	NA	intron (intron (	-23504	NR_028510	7302	Hs.684881NR_022721	TYR03P	TYR03P prpseudo	
chr16-116.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr16	11687421	11688020	+	0	NA	intron (intron (	19265	NM_003498	8303	Hs.618522NM_003498	ENSG000005CSNN	stannin protein-coding	
chr16-468.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr16	46955424	46961216	+	0	NA	intron (AluV SINE	15354	NM_005888	10294	Hs.368072NM_005888	ENSG000005DNAJ2	CPR3 DJ3 DnaJ heatprotein-coding	
chr16-588.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr16	58595462	58599324	+	0	NA	intron (AluSx1 SI	32343	NM_206999	23019	Hs.460922NM_016284	ENSG000005CNOT1	AD-005 CCCR4-NOT protein-coding	
chr16-703.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr16	70350702	70360141	+	0	NA	intron (intron (	8518	NM_018332	55308	Hs.656037NM_018332	ENSG000005DDX19A	DDX19-DDXDEAD-box protein-coding	
chr17-406.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr17	4060074	4066605	+	0	NA	intron (FLAM_C SI	79691	NM_015113	23140	Hs.277624NM_015113	ENSG000005ZZEF1	ZZZ4 zinc finger protein-coding	
chr17-658.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr17	6593412	6596166	+	0	NA	intron (NLIME2z LI	-38234	NM_001166	83394	Hs.183983NM_031222	ENSG000005PITPNM3	ACKR6 COF PITPNM3 protein-coding	
chr17-168.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr17	16061115	16067118	+	0	NA	exon (NM exon (NM	64292	NM_011777	54902	Hs.462313NM_011777	ENSG000005TTC19	201020401 tetraetric protein-coding	
chr17-403.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr17	40351909	40352601	+	0	NA	intron (intron (	-9119	NR_110861	1.02E+08	Hs.655717NR_110861	ENSG000005RARA-AS1	RARA antincRNA	
chr18-458.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr18	45897928	45918341	+	0	NA	intron (intron (	59195	NM_020964	57724	Hs.514842NM_020964	ENSG000005CEPG5	HEEWI K1 ectopic I protein-coding	
chr18-2738.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr18	27376943	27377816	+	0	NA	non-codiron-codir	3065	NM_001201	130557	Hs.515872NM_144631	ENSG000005ZNF513	HMF10656 zinc finger protein-coding	
chr20-341.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr20	34109058	34110377	+	0	NA	intron (intron (	2526	NM_001316	8894	Hs.429180NM_003908	ENSG000005EIF2S2	EIF2 EIF2eukaryotiprotein-coding	
chr20-508.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr20	50937951	50954451	+	0	NA	intron (intron (	12363	NM_001317	8813	Hs.654951NM_003858	ENSG000005DPM1	CDG1E MP1 dolichyl protein-coding	
chr21-328.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr21	32663214	32665101	+	0	NA	intron (LTR2 LTR	-51786	NM_001350	56683	Hs.5811	NM_017833	ENSG000005CFAP298	Ar4orf48 cilia antincRNA
chr22-215.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr22	21944617	21946101	+	0	NA	intron (MLTIC SIN	7122	NR_147620	1E+08	Hs.659182NR_147620	LOC100286	uncharactncRNA	
chr22-428.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr22	42834558	42837603	+	0	NA	intron (AluSx SIN	21193	NM_014570	26286	Hs.685222NM_014570	ENSG000005ARFGAP3	ARFGAP1 ADP ribos protein-coding	
chr3-378.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr3	37382812	37384065	+	0	NA	Intergeni L1PRE2C L	-2831	NM_178344	339883	Hs.475942NM_178333	ENSG000005C3orf35	APRGI chromosom protein-coding	
chr4-9907.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr4	99071141	99077947	+	0	NA	intron (intron (	14244	NM_000671	128	Hs.78989	NM_000671	ENSG000005ADH5	ADH-3 ADFA alcohol c protein-coding
chr4-1438.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr4	1.44E+08	1.44E+08	+	0	NA	intron (L2b LINE	-3699	NR_104027	1E+08	Hs.707572NR_104027	ENSG000005SMARCA5-1	SMARCA5 antncRNA	
chr5-1242.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr5	1.28E+08	1.28E+08	+	0	NA	intron (intron (	30355	NM_130805	133619	Hs.483255NM_130805	ENSG000005PRRC1	proline rprotein-coding	
chr6-7382.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr6	73821060	73821634	+	0	NA	intron (L1P1A17 LI	125144	NM_133493	135228	Hs.399891NM_133493	ENSG000005CD109	CPAMD7 pCD109 mol protein-coding	
chr6-8752.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr6	87529665	87530866	+	0	NA	intron (L2a LINE	57291	NM_006416	10559	Hs.423162NM_006416	ENSG000005SLC35A1	CDG2F CMF solute c protein-coding	
chr7-9933.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr7	99333659	99344697	+	0	NA	intron (NLIME3G LI	13280	NM_006405	10552	Hs.124122NM_006405	ENSG000005ARPC1A	Ar40 HEL actin l protein-coding	
chr7-9954.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr7	99546651	99550367	+	0	NA	intron (intron (	3605	NM_145111	221786	Hs.596587NM_145111	ENSG000005FAM200A	C7orf38 family wiprotein-coding	
chr8-1798.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr8	17957378	17969620	+	0	NA	intron (intron (	40511	NM_001352	5108	Hs.491142NM_006197	ENSG000005PCM1	PTCA RET pericent protein-coding	
chr8-9452.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr8	94526544	94531909	+	0	NA	exon (NM exon (NM	24243	NM_015496	25962	Hs.422232NM_015496	ENSG000005VIRMA	KIAA1429 vir like protein-coding	
chr8-1023.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (intron (	54099	NM_001282	51366	Hs.492442NM_015902	ENSG000005CUBR5	DD5 EDD Eubiquitir protein-coding	
chr9-1364.8.674475	0.132112	0.786705	0.167931	0.866638	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (AluJb SIN	4381	NM_015166	23203	Hs.495471NM_015166	ENSG000005PMPCA	Alpha-MPF peptidase protein-coding	
chr1-2142.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr1	21427150	21427728	+	0	NA	Intergeni Intergeni	-12698	NM_001256	84224	Hs.325422NM_032264	ENSG000005NBPF3	AE2 NBPF memb protein-coding	
chr1-2821.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr1	28213999	28214556	+	0	NA	intron (AluSx SIN	18752	NM_014280	22826	Hs.433542NM_014280	ENSG000005DNAJC8	HSPC331 S DnaJ heatprotein-coding	
chr1-1175.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr1	1.18E+08	1.18E+08	+	0	NA	exon (NM exon (NM	22632	NM_006784	10885	Hs.310805NM_006784	ENSG000005WDR3	DIP2 UTP1WD repeat protein-coding	
chr10-132.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr10	32270041	32273045	+	0	NA	intron (intron (	72615	NM_001272	80314	Hs.167802NM_025205	ENSG000005EPC1	Epl1 enhancer protein-coding	
chr10-500.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr10	50075969	50081056	+	0	NA	intron (NLIM5 LINE	10558	NM_001005	387680	Hs.365282NM_018232	ENSG000005WASHC2A	FAM21A F WASH com protein-coding	
chr11-123.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	intron (MLT1A LTF	38719	NM_024766	79827	Hs.591945NM_024766	ENSG000005CLMP	ACAM ASAM CXADR lik protein-coding	
chr12-557.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr12	55781016	55789823	+	0	NA	intron (intron (	32305	NM_033082	84324	Hs.505672NM_033082	ENSG000005SARNP	CIP29 HCCSAP domaiprotein-coding	
chr12-888.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr12	88043628	88051361	+	0	NA	intron (intron (	11958	NM_001005	91298	Hs.591005NM_001005	ENSG000005C12orf29	chromosom protein-coding	
chr12-115.8.418491	-0.1421	0.847236	-0.16773	0.866798	0.981636	chr12	1.2E+08	1.2E+08	+	0	NA	intron (THEID LTF	3367	NM_006255	5564	Hs.741184NM_006255	ENSG000005PRKAB1	AMPK HAMF protein l protein-coding	
chr13-306.8.418491	-0.1421	0.847236	-0.1677																



chr13-491.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr13	49191061	49194949	+	0	NA	intron (Nintron (N	-27333	NM_001507	2862	Hs. 248126	NM_001507	ENSG00000000000	MLNR	GPR38 MTI motilin rprotein-coding
chr14-556.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr14	55641809	55642669	+	0	NA	intron (Nintron (N	62032	NM_001075	3895	Hs. 509414	NM_004986	ENSG00000000000	KTN1	CG1 KNT kineinectin protein-coding
chr14-635.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr14	63536333	63539786	+	0	NA	intron (Nintron (N	-4725	NR_158218	1.12E+08	Hs. 632347	NR_158218		LOC112266	loricrin ncRNA
chr14-100.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	TTS (NR_CTS (NR_C	327	NR_029696	406914		NR_029696	ENSG00000000000	MIR127	MIRN127 nmicroRNA ncRNA
chr15-566.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr15	56699349	56701462	+	0	NA	3' UTR (N3' UTR (N	33681	NM_001288	54816	Hs. 511477	NM_017661	ENSG00000000000	ZNF280D	SUHW4 ZNF zinc finger protein-coding
chr18-270.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr18	2709059	2712757	+	0	NA	intron (Nintron (N	55021	NM_015295	23347	Hs. 8118	NM_015295	ENSG00000000000	CSMCHD1	BAMS FSH structure protein-coding
chr18-566.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr18	56613255	56618135	+	0	NA	intron (Nintron (N	22897	NR_024546	9352	Hs. 114412	NM_004788	ENSG00000000000	TXNL1	HEL-5-114 thioredoxin protein-coding
chr2-2765.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr2	27638633	27640740	+	0	NA	intron (Nintron (N	11321	NR_007266	11321	Hs. 18259	NR_007266	ENSG00000000000	GPN1	ATPBD1A WGNP-loop protein-coding
chr2-3331.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr2	33313225	33315863	+	0	NA	intron (Nintron (N	-103972	NR_039628	1.01E+08		NR_039628	ENSG00000000000	MIR4430	microRNA ncRNA
chr2-612.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr2	61202327	61209659	+	0	NA	intron (Nintron (N	28575	NR_152211	130872	Hs. 655602	NM_152392	ENSG00000000000	AHS2P	AHA1 AHS activator pseudo
chr2-2038.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (Nintron (N	50412	NM_001114	65065	Hs. 648844	NM_198944	ENSG00000000000	NBEAL1	A530083 C neurobeac protein-coding
chr2-2161.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	intron (Nintron (N	46593	NM_021141	7520	Hs. 388733	NM_021141	ENSG00000000000	XRCC5	KARP-1 KAX-ray ref protein-coding
chr20-344.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr20	34424805	34426975	+	0	NA	intron (Nintron (N	-40435	NR_030374	693229		NR_030374	ENSG00000000000	MIR644A	MIR644 MI microRNA ncRNA
chr20-368.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr20	36814918	36816264	+	0	NA	exon (NM exon (NM	-14828	NM_001145	79980	Hs. 632266	NM_024918	ENSG00000000000	CDSN1	C20orf172 DSN1 comp protein-coding
chr3-1543.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr3	15439864	15440640	+	0	NA	3' UTR (N3' UTR (N	12654	NM_033083	85403	Hs. 716733	NM_033083	ENSG00000000000	EAF1	ELL assoc protein-coding
chr3-4777.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr3	47771443	47772896	+	0	NA	intron (Nintron (N	9724	NM_003074	6599	Hs. 476175	NM_003074	ENSG00000000000	SMARCC1	BAF155 CF SWI/SNF rprotein-coding
chr4-139.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	12644	NM_001276	1998	Hs. 634040	NM_006874	ENSG00000000000	CELF2	EU32 NERF E74 like protein-coding
chr4-1398.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	-26183	NM_001184	4717	Hs. 84549	NR_002494	ENSG00000000000	NUFDC1	KFYI1 NADH:ubiquinone protein-coding
chr5-1295.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	-65391	NR_125748	1.04E+08	Hs. 628633	NR_125748	ENSG00000000000	ADAMTS19	ADAMTS19 ncRNA
chr5-1768.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr5	1.79E+08	1.79E+08	+	0	NA	TTS (NM_CTS (NM_C	-9942	NM_030613	80108	Hs. 654533	NM_030613	ENSG00000000000	ZFP2	ZNF751 zfZFP2 zinc protein-coding
chr6-1066.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr6	1.07E+08	1.07E+08	+	0	NA	intron (Nintron (N	-26472	NM_001318	84816	Hs. 155823	NM_032730	ENSG00000000000	RTN4IP1	NIMP OPA1 reticular protein-coding
chr6-1121.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr6	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	31285	NM_001033	619208	Hs. 591340	NM_001033	ENSG00000000000	FAM229B	C6orf225 family wiprotein-coding
chr7-1297.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	52972	NR_029614	406958		NR_029614	ENSG00000000000	MIR182	MIRN182 nmicroRNA ncRNA
chr9-982.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr9	98228553	98231876	+	0	NA	promoter-promoter-	-997	NR_106913	1.02E+08		NR_106913	ENSG00000000000	MIR6854	hsa-mir-6854 microRNA ncRNA
chr9-1104.8.162171	0.135382	0.809898	0.16716	0.867244	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	116726	NM_153366	79987	Hs. 522334	NM_153366	ENSG00000000000	SVPEP1	C9orf13 Cushi, vcp protein-coding
chr1-2084.6.470154	-0.15464	0.925741	-0.16705	0.867335	0.981636	chr1	20848767	20849367	+	0	NA	intron (Nintron (N	-62379	NM_016287	50809	Hs. 142442	NM_016287	ENSG00000000000	HP1BP3	HP1-BP74 thioredoxin protein-coding
chr1-2255.5.641791	0.162952	0.975885	0.166978	0.867387	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	exon (NM exon (NM	23162	NM_000120	2052	Hs. 89649	NR_000120	ENSG00000000000	EPHX1	EPHX EPOxetoxide f protein-coding
chr5-1415.5.641791	0.162952	0.975885	0.166978	0.867387	0.981636	chr5	1.42E+08	1.42E+08	+	0	NA	intron (Nintron (N	2812	NM_004290	9604	Hs. 483611	NM_004290	ENSG00000000000	RNF14	ARA54 HFE ring finger protein-coding
chr1-1825.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr1	1829024	1830060	+	0	NA	intron (Nintron (N	-49511	NM_001355	65220	Hs. 654792	NM_023018	ENSG00000000000	CNADK	dJ283E3.1NAD kinase protein-coding
chr1-1626.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (Nintron (N	16814	NM_001324	6675	Hs. 492856	NM_003111	ENSG00000000000	UAP1	AGX1 UDP-N-acetyl protein-coding
chr10-105.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	5' UTR (N5' UTR (N	407	NM_001351	22978	Hs. 97439	NM_012225	ENSG00000000000	NT5C2	GMP NT5B 5' -nucleo protein-coding
chr10-115.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr10	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	26710	NM_001303	404636	Hs. 434241	NM_207000	ENSG00000000000	DENN10	FAM45A DENN dome protein-coding
chr11-345.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr11	34951257	34952108	+	0	NA	intron (Nintron (N	945	NR_039833	1.01E+08		NR_039833	ENSG00000000000	MIR1343	microRNA ncRNA
chr11-475.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr11	47315615	47316394	+	0	NA	intron (Nintron (N	36698	NM_000256	4607	Hs. 524900	NM_000256	ENSG00000000000	MYBPC3	CMD1M C myosin bi protein-coding
chr11-122.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr11	1.23E+08	1.23E+08	+	0	NA	exon (NM exon (NM	-49286	NM_019604	56253	Hs. 159523	NM_019604	ENSG00000000000	CRTAM	CD355 cytotoxin protein-coding
chr17-324.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr17	32459283	32461248	+	0	NA	intron (Nintron (N	15755	NM_002815	5717	Hs. 443375	NM_002815	ENSG00000000000	PSMD11	Rpn6 59 proteasome protein-coding
chr17-666.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr17	66646130	66646432	+	0	NA	intron (Nintron (N	-140791	NR_030364	693219		NR_030364	ENSG00000000000	MIR634	MIRN634 microRNA ncRNA
chr19-522.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr19	52310653	52311047	+	0	NA	intron (Nintron (N	13681	NM_001297	147657	Hs. 729317	NM_144684	ENSG00000000000	ZNF480	zinc finger protein-coding
chr2-4224.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr2	42246014	42246934	+	0	NA	intron (Nintron (N	-76243	NR_110584	1.03E+08	Hs. 639822	NR_110584		LOC102722	uncharacterncRNA
chr4-2824.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr4	2824045	2824886	+	0	NA	intron (Nintron (N	5651	NM_003023	6452	Hs. 167675	NM_003023	ENSG00000000000	SH3BP2	3BP-2 3BF SH3 doma protein-coding
chr4-4854.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr4	48543563	48544156	+	0	NA	exon (NM exon (NM	53607	NM_175611	326340	Hs. 276457	NM_175611	ENSG00000000000	ZARI	Z3CXXC6 zygote ar protein-coding
chr5-3705.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr5	37025084	37025542	+	0	NA	intron (Nintron (N	148544	NM_015384	25836	Hs. 481927	NM_015384	ENSG00000000000	IPBL	CDLS CDLSNIPBL col protein-coding
chr6-3620.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr6	36202953	36203538	+	0	NA	intron (Nintron (N	6501	NM_015699	27154	Hs. 520099	NM_015699	ENSG00000000000	BRPF3	bromodome protein-coding
chr7-9275.6.964893	-0.14671	0.879916	-0.16673	0.867584	0.981636	chr7	92758510	92759318	+	0	NA	intron (Nintron (N	75045	NM_001255	1021	Hs. 119882	NM_001255	ENSG00000000000	CDK6	MCPH12 PI cyclin d protein-coding
chr13-758.7.87209	-0.13803	0.828044	-0.16673	0.867609	0.981636	chr13	518800774	518801665	+	0	NA	intron (Nintron (N	40558	NM_015842	4008					

chr14-103	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	intron (AluSx SIN	10222	NR_001302	84334	Hs.598441NM_001302	ENSG000002COA8	APOP APOF cytochrome protein-coding	
chr15-70C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr15	70068971	70072134	+	0	NA	intron (AluSx SIN	8916	NR_030714	693214	NR_030714	ENSG000002MIR629	MIRN629 tmicroRNA ncRNA	
chr16-37C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr16	3733773	3738811	+	0	NA	intron (AluSx SIN	-18768	NR_016292	10131	Hs.30345	NR_016292	ENSG000002TRAP1	HSP 75 HSTNF receptor protein-coding
chr16-211	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr16	21164201	21166144	+	0	NA	intron (AluSx SIN	-5732	NR_017533	55567	Hs.52650	NR_017533	ENSG000002DNAH3	DNAH3-3 dyad protein-coding
chr16-314	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr16	31497723	31500662	+	0	NA	intron (AluSx SIN	9199	NR_022744	64755	Hs.9003	NR_022744	ENSG000002C16orf58	RNAC chromosom protein-coding
chr16-564	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr16	56457931	56463980	+	0	NA	intron (AluSx SIN	8871	NR_001324	55239	Hs.23188	NR_018233	ENSG000002COGFD1	TPA1 2-oxoglutarate protein-coding
chr16-666	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr16	66807056	66808758	+	0	NA	intron (AluSx SIN	-6287	NR_001136	283847	Hs.37650	NR_173616	ENSG000002TERB1	CCDC79 telomere protein-coding
chr16-897	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr16	89730226	89732439	+	0	NA	intron (AluSx SIN	9795	NR_001113	92822	Hs.29015	NR_152287	ENSG000002ZNF276	CENP-Z CenZinc finger protein-coding
chr17-60C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr17	60665047	60666833	+	0	NA	3' UTR (AluSx SIN	-1191	NR_001099	54828	Hs.65502	NR_017679	ENSG000002BCAS3	GAOBI MA BCAS3 microprotein-coding
chr17-75C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr17	75231762	75234889	+	0	NA	intron (AluSx SIN	27646	NR_021444	79902	Hs.36281	NR_024844	ENSG000002NUP85	FRONT NF nucleosom protein-coding
chr18-13C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr18	13095003	13098729	+	0	NA	intron (AluSx SIN	105504	NR_032144	55125	Hs.10091	NR_018066	ENSG000002CEP192	PPP1R62 centrosom protein-coding
chr19-30C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr19	3052736	3054077	+	0	NA	3' UTR (AluSx SIN	-5771	NR_001144	7089	Hs.33217	NR_003266	ENSG000002TLE2	ESG ESG2 TLE famil protein-coding
chr19-79C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr19	7935720	7938697	+	0	NA	intron (AluSx SIN	6458	NR_006351	10469	Hs.46578	NR_006351	ENSG000002TIMM44	TIM44 translocase protein-coding
chr19-107	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr19	10772461	10774555	+	0	NA	intron (AluSx SIN	-6746	NR_039903	1.01E+08	NR_039903	ENSG000002MIR4748	mir-4748 microRNA ncRNA	
chr19-17C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr19	17317949	17322727	+	0	NA	3' UTR (AluSx SIN	10775	NR_024056	79016	Hs.46615	NR_024056	ENSG000002CDDA1	C19orf58 DET1 and protein-coding
chr19-19C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr19	19323917	19328756	+	0	NA	intron (AluSx SIN	5507	NR_015325	23383	Hs.65493	NR_015325	ENSG000002MAU2	KIAA0892 MAU2 sistr protein-coding
chr2-3711	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	37116856	37117413	+	0	NA	intron (AluSx SIN	30688	NR_001135	5610	Hs.13143	NR_002755	ENSG000002EIF2AK2	EIF2AK1 Eukaryotic protein-coding
chr2-628C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	62831674	62834392	+	0	NA	intron (AluSx SIN	126136	NR_001354	23301	Hs.21767	NR_015252	ENSG000002HBP1	HPC12 NAC Hich domain protein-coding
chr2-711C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	71109230	71110684	+	0	NA	3' UTR (AluSx SIN	20272	NR_032601	84693	Hs.94949	NR_032601	ENSG000002MCEE	GLOD2 methylmalonate protein-coding
chr2-1121	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	3' UTR (AluSx SIN	-22085	NR_153214	129804	Hs.43769	NR_153214	ENSG000002FBLN7	TM14 fibulin 1 protein-coding
chr2-117C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	1.18E+08	1.18E+08	+	0	NA	intron (AluSx SIN	20841	NR_019044	54520	Hs.10784	NR_019044	ENSG000002CCDC93	- coiled-coil protein-coding
chr2-121C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	1.21E+08	1.21E+08	+	0	NA	intron (AluSx SIN	-11576	NR_014553	29842	Hs.15647	NR_014553	ENSG000002TFCP2L1	CRTR1 LFB transcrip protein-coding
chr2-131C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	1.32E+08	1.32E+08	+	0	NA	intron (AluSx SIN	9665	NR_026922	150776	Hs.53562	NR_026922	ENSG000002LOC150776	- sphingomy pseudo
chr2-201C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	intron (AluSx SIN	8152	NR_001257	4709	Hs.10976	NR_002491	ENSG000002NDFB3	B12 C1-B1NADH:ubiquinone protein-coding
chr2-203C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (AluSx SIN	54754	NR_001114	56065	Hs.64884	NR_19894	ENSG000002NBEAL1	A530083 C1 neurobeac protein-coding
chr21-46C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr21	46502876	46504822	+	0	NA	intron (AluSx SIN	41378	NR_046400	1.01E+08	Hs.73716	NR_046400	ENSG000002DIP2A-IT1	- DIP2A intrncRNA
chr22-201	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr22	20112541	20115358	+	0	NA	TTS (AluSx SIN	802	NR_106874	1.02E+08	NR_106874	ENSG000002MIR6816	hsa-mir-6816 microRNA ncRNA	
chr3-484C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr3	48495811	48496565	+	0	NA	intron (AluSx SIN	8177	NR_001272	51246	Hs.41457	NR_016475	ENSG000002SHISA5	SCOTIN shisa fan protein-coding
chr3-639C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr3	63988662	63991664	+	0	NA	intron (AluSx SIN	-13859	NR_03828E	1.01E+08	Hs.15253	NR_03828E	ENSG000002PSMD6-AS2	PSMD6 antncRNA
chr3-119C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr3	1.19E+08	1.19E+08	+	0	NA	intron (AluSx SIN	-12522	NR_046574	1.01E+08	Hs.72130	NR_046574	ENSG000002B4GALT4-7	B4GALT4 4 ncRNA
chr4-856C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	856604	859474	+	0	NA	intron (AluSx SIN	-31910	NR_006651	10815	Hs.47893	NR_006651	ENSG000002CPLX1	CPX-1 CPX complexin protein-coding
chr4-267C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	2675122	2676886	+	0	NA	intron (AluSx SIN	50572	NR_046333	8603	Hs.65236	NR_003704	ENSG000002FAM193A	C4orf8 RF family w protein-coding
chr4-702C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	7025427	7025871	+	0	NA	exon (AluSx SIN	17752	NR_053376	257236	Hs.65675	NR_153376	ENSG000002CCDC96	- coiled-coil protein-coding
chr4-730C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	73056544	73061795	+	0	NA	intron (AluSx SIN	10547	NR_001297	285521	Hs.35669	NR_173827	ENSG000002COX18	COX18H8 cytochrome protein-coding
chr4-761C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	76120693	76123718	+	0	NA	intron (AluSx SIN	26192	NR_017426	53371	Hs.43043	NR_017426	ENSG000002NUP54	- nucleosom protein-coding
chr4-118C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	intron (AluSx SIN	-11244	NR_103825	729218	Hs.44851	NR_103825	LOC279218	- uncharacter pseudo
chr4-185C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr4	1.85E+08	1.85E+08	+	0	NA	intron (AluSx SIN	8653	NR_018355	55325	Hs.71354	NR_018355	ENSG000002UFSP2	BHD C4orfUM1 spec protein-coding
chr5-2037	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr5	203763	205676	+	0	NA	3' UTR (AluSx SIN	13224	NR_001088	389257	Hs.10314	NR_001088	ENSG000002LRRC14B	- leucine i protein-coding
chr5-3711	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr5	37111211	37115192	+	0	NA	intron (AluSx SIN	-135345	NR_134263	1.05E+08	Hs.17099	NR_134263	ENSG000002LOC105374	- uncharacter pseudo
chr5-177C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr5	1.78E+08	1.78E+08	+	0	NA	intron (AluSx SIN	-17462	NR_016222	51428	Hs.48428	NR_016222	ENSG000002CDDX41	ABS MPLPF DEAD-box protein-coding
chr6-100C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr6	1.01E+08	1.01E+08	+	0	NA	intron (AluSx SIN	-17770	NR_005066	6492	Hs.52029	NR_005066	ENSG000002SIM1	bHLHeL4 SIM bHLH protein-coding
chr6-160C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr6	1.6E+08	1.6E+08	+	0	NA	intron (AluSx SIN	-36177	NR_047511	1E+08	Hs.74216	NR_047511	ENSG000002AIRN	AIR IGF2 antisense ncRNA
chr7-570C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr7	5702133	5703590	+	0	NA	intron (AluSx SIN	9049	NR_106934	1.02E+08	NR_106934	ENSG000002MIR6874	hsa-mir-6874 microRNA ncRNA	
chr7-139C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr7	13930462	13931792	+	0	NA	intron (AluSx SIN	55387	NR_001163	2115	Hs.22634	NR_004956	ENSG000002ETV1	ER81 ETS variat protein-coding
chr7-107C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr7	1.08E+08	1.08E+08	+	0	NA	intron (AluSx SIN	24991	NR_001018	1738	Hs.13171	NR_001018	ENSG000002CCLD	DLDD DLDF dihydrolip protein-coding
chr7-111C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr7	1.12E+08	1.12E+08	+	0	NA	intron (AluSx SIN	35969	NR_103806	1.01E+08	Hs.67751	NR_103806	ENSG000002DOCK4-AS1	- DOCK4 antncRNA
chr7-140C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr7	1.4E+08	1.4E+08	+	0	NA	intron (AluSx SIN	18755	NR_013446	23608	Hs.74488	NR_013446	ENSG000002MKRN1	RNF61 makorin i protein-coding
chr8-224C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr8	22408364	22410475	+	0	NA	intron (AluSx SIN	16583	NR_001351	23516	Hs.49123	NR_015355	ENSG000002SLC39A14	HCIN HMN solute c protein-coding
chr8-335C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr8	33501212	33509236	+	0	NA	intron (AluSx SIN	7911	NR_001333	80185	Hs.77135	NR_025111	ENSG000002TT12	C8orf41 VTELO2 intr protein-coding
chr8-864C	7.18656	0.143327	0.86071	0.166522	0.867747	0.981636	chr8	86433546	86436219	+	0	NA	intron (AluSx SIN	73804	NR					



chr2-7395	8.374686	-0.13389	0.805915	-0.16613	0.868054	0.981636	chr2	73950495	73952046	+	0	NA	intron (intron (N	24390 NR_13489E	1716 Hs. 469022NM_00192E	ENSG00000CDGUOK	MTDPS3 NC deoxyguar protein-coding	
chr7-106	8.374686	-0.13389	0.805915	-0.16613	0.868054	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	3' UTR (3' UTR (N	20738 NM_18271E	6856 Hs. 80919 NM_006754	ENSG00000SYPL1	H-SP1 SYF synaptopl protein-coding	
chr12-131	9.706941	0.12516	0.75378	0.166043	0.868123	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (THE1B-int	32673 NM_00459E	6433 Hs. 308171NM_00459E	ENSG00000SFSWAP	SFRS8 SW splicing protein-coding	
chr4-8677	9.706941	0.12516	0.75378	0.166043	0.868123	0.981636	chr4	86771553	86773204	+	0	NA	intron (AluSx SIN	77006 NM_19796E	345274 Hs. 452996NM_19796E	ENSG00000SLC10A6	SOAT solute c protein-coding	
chr1-1562	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr1	1.56E+08	1.56E+08	+	0	NA	intron (AluJo SIN	4173 NM_015327	23381 Hs. 516837NM_015327	ENSG00000SMG5	EST1B LPI5MG5 nonprotein-coding	
chr15-642	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr15	64201997	64205006	+	0	NA	intron (AluSp SIN	-40346 NM_00094E	5479 Hs. 434937NM_00094E	ENSG00000PPIB	B CYP-S1 peptidyl protein-coding	
chr16-145	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr16	14879138	14882305	+	0	NA	intron (AluSq2 SI	-20922 NR_03614E	1E+08	NR_03614E	ENSG00000MIR3179	microRNA ncRNA
chr16-505	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr16	50363128	50363402	+	0	NA	intron (intron (N	5723 NM_00117E	29117 Hs. 437894NM_01326E	ENSG00000BRD7	BP75 CEL1 bromodome protein-coding	
chr2-6524	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr2	65242317	65243425	+	0	NA	intron (intron (N	15176 NM_00100E	10097 Hs. 643727NM_00572E	ENSG00000ACTR2	ARP2 actin rel protein-coding	
chr2-9936	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr2	99367744	99370194	+	0	NA	intron (intron (N	31569 NM_015904	9669 Hs. 158688NM_015904	ENSG00000EIF5B	IF2 eukaryot protein-coding	
chr3-197	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (intron (N	-21269 NM_03331E	4241 Hs. 184727NM_00592E	ENSG00000MELTF	CD228 MAF melanot protein-coding	
chr5-6962	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr5	69639081	69639993	+	0	NA	TTS (NR_C TTS (NR_C	8392 NR_157804	1.02E+08 Hs. 63401E	NR_157804	LOC10192E	putative pseudo uncharactericRNA
chr6-176	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr6	17660223	17662475	+	0	NA	intron (intron (N	-44781 NR_13461E	1.05E+08 Hs. 71870E	NR_13461E	ENSG00000LOC105374	uncharactericRNA
chr8-942	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr8	94256034	94258812	+	0	NA	intron (AluSq2 SI	4896 NM_18170E	2669 Hs. 65446E	NR_005261	ENSG00000CGEM	KIR GTP bindi protein-coding
chr9-128	7.649867	0.139084	0.83764	0.166042	0.868124	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (AluJb SIN	-16637 NM_00119E	6709 Hs. 372331NM_00312E	ENSG00000SPTAN1	EIEE5 NE spectrin protein-coding	
chr1-1801	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (intron (N	3381 NM_00282E	5768 Hs. 71917E	NR_00282E	ENSG00000QSOX1	Q6 QSCN6 quiescin protein-coding
chr1-1205	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr1	1.81E+08	1.81E+08	+	0	NA	3' UTR (3' UTR (N	-21374 NR_145481	1.03E+08 Hs. 66531E	NR_145481	ENSG00000KIAA1614	KIAA1614 ncRNA
chr10-124	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr10	1.24E+08	1.24E+08	+	0	NA	intron (intron (N	17716 NM_00132E	4942 Hs. 52333E	NR_000274	ENSG00000OAT	GACR HOG ornithine protein-coding
chr11-947	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr11	94797989	9480184	+	0	NA	intron (intron (N	18074 NM_00344E	7702 Hs. 523471NM_00344E	ENSG00000ZNF143	SBF STAF zinc fing protein-coding	
chr11-364	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr11	36489991	36490631	+	0	NA	exon (NM exon (NM	19961 NM_14580E	7189 Hs. 44417E	NR_00462E	ENSG00000TRAF6	MGC:3310 TNF rece protein-coding
chr14-594	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr14	59473922	59476096	+	0	NA	non-codiron-codir	8566 NM_001331	112849 Hs. 729061NM_144581	ENSG00000L3HPDH	C14orf14E trans-L-c protein-coding	
chr16-224	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr16	224075	227541	+	0	NA	intron (N (AAAAG)n	3641 NM_01803E	55692 Hs. 16803 NM_01803E	ENSG00000LUC7L	LUC7B1 LUC7 like protein-coding	
chr16-86	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr16	86504529	86508278	+	0	NA	intron (intron (N	2457 NR_03392E	400550 Hs. 44882E	NR_03392E	ENSG00000FENDRR	FOXF1-AS1 FOXF1 ad ncRNA
chr2-2411	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr2	2.41E+08	2.41E+08	+	0	NA	intron (intron (N	-17926 NM_001001	50636 Hs. 16390E	NR_001001	ENSG00000AN07	D-TMPP DI anoctami protein-coding
chr22-298	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr22	29822396	29825847	+	0	NA	intron (AluJr SIN	14153 NM_00136E	84164 Hs. 731754NM_032204	ENSG00000ASCC2	ASC1p100 activati protein-coding	
chr3-1837	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (intron (N	9106 NR_046727	1.01E+08 NR_046727	YEATS2-AS	YEATS2 arcncRNA	
chr5-6604	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr5	66042901	66045173	+	0	NA	intron (intron (N	-98464 NR_028474	1E+08 Hs. 60806E	NR_028474	LOC10030E	LSM3 homc pseudo
chr5-1491	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr5	1.49E+08	1.49E+08	+	0	NA	intron (intron (N	43349 NM_00137E	22885 Hs. 49688 NM_01494E	ENSG00000ABLIM3	HMFN1661 actin bir protein-coding	
chr6-108	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr6	1.09E+08	1.09E+08	+	0	NA	intron (intron (N	8737 NM_00145E	2309 Hs. 22095E	NR_00145E	ENSG00000FOX03	AF6q21 FK forkhead protein-coding
chr7-6451	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr7	64519654	64522994	+	0	NA	exon (NM exon (NM	4174 NM_17855E	340252 Hs. 52088E	NR_17855E	ENSG00000ZNF680	zinc fing protein-coding
chr7-668	9.194637	0.127643	0.768934	0.166	0.868157	0.981636	chr7	66806727	66809997	+	0	NA	3' UTR (3' UTR (N	36464 NR_003934	729156 Hs. 70987E	NR_003934	ENSG00000GTF2IRD1E	GTF2I ref pseudo
chr1-114	8.211168	0.135419	0.816574	0.165838	0.868284	0.981636	chr1	1.15E+08	1.15E+08	+	0	NA	3' UTR (3' UTR (N	13757 NM_00587E	10286 Hs. 22960 NM_00587E	ENSG00000BCAS2	DAMI SPF2 BCAS2 pr protein-coding	
chr17-496	8.211168	0.135419	0.816574	0.165838	0.868284	0.981636	chr17	49609877	49611072	+	0	NA	intron (AluSx SIN	16115 NM_00137E	8045 Hs. 46338E	NR_00356E	ENSG00000SPOF	BTBD32 TE speckle protein-coding
chr22-41	8.211168	0.135419	0.816574	0.165838	0.868284	0.981636	chr22	41339181	41341945	+	0	NA	intron (L2c LINE	-26770 NM_00114E	7008 Hs. 18115E	NR_00321E	ENSG00000CTEF	TEF trans protein-coding
chr1-9387	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr1	93876440	93877605	+	0	NA	exon (NM exon (NM	2184 NM_014597	30836 Hs. 85769 NM_014597	ENSG00000DNTTIP2	ERBP FCF2 deoxynul protein-coding	
chr1-2132	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr1	2.13E+08	2.13E+08	+	0	NA	intron (L1PA4 LIN	163227 NM_012424	26750 Hs. 59141E	NR_012424	ENSG00000RPS6K1C	RPK118 RS ribosome protein-coding
chr10-737	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr10	73746322	73756701	+	0	NA	intron (AluSx SIN	7139 NM_00492E	9632 Hs. 81964 NM_00492E	ENSG00000SEC24C	SEC24 hom protein-coding	
chr11-117	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (THE1A LTF	69845 NM_01495E	22897 Hs. 50400E	NR_01495E	ENSG00000CEP164	PPH15 centroson protein-coding
chr12-107	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr12	1.08E+08	1.08E+08	+	0	NA	exon (NM exon (NM	7046 NM_01240E	11108 Hs. 50665E	NR_01240E	ENSG00000PRD4M	PFM1 PR/SET c protein-coding
chr14-572	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr14	57228306	57229018	+	0	NA	intron (L1PA7 LIN	40243 NM_006544	10640 Hs. 74398E	NR_006544	ENSG00000EXOC5	HSEC10 PF exocyst c protein-coding
chr16-58	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr16	58543265	58547358	+	0	NA	intron (intron (N	3322 NR_00297E	67727 Hs. 68859E	NR_00297E	ENSG00000SNORA46	ACA46 small nucsnRNA
chr19-534	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr19	53488826	53492017	+	0	NA	exon (NM exon (NM	22688 NM_001004	126017 Hs. 71078E	NR_001004	ENSG00000ZNF813	zinc fing protein-coding
chr3-1192	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr3	1.19E+08	1.19E+08	+	0	NA	exon (NM exon (NM	3368 NR_046574	1.01E+08 Hs. 721307E	NR_046574	ENSG00000B4GALT4	B4GALT4 ncRNA
chr7-2281	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr7	22816315	22818274	+	0	NA	intron (intron (N	5555 NM_01905E	54543 Hs. 11231E	NR_01905E	ENSG00000TOMM7	TOM7 transloc c protein-coding
chr7-561	10.1781	0.121393	0.732022	0.165832	0.868289	0.981636	chr7	56100198	56104249	+	0	NA	intron (intron (N	4253 NM_01613E	5142 Hs. 38999E	NR_01613E	ENSG00000CHCHD2	C7orf17 C coiled-c protein-coding
chr1-1252	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr1	1.252113	1.2527236	+	0	NA	3' UTR (3' UTR (N	-7952 NM_001014	388581 Hs. 19761E	NR_001014	ENSG00000C1QTNF12	C1QDC2 C1C1 and I protein-coding
chr1-1651	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr1	1651837	1657720	+	0	NA	intron (AluV SINE	4226 NM_03349C	984 Hs. 65122E	NR_00178E	ENSG00000CDK11B	CDC2L1 C cyclin d protein-coding
chr1-228	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr1	22864907	22868803	+	0	NA	intron (AluSq2 SI	-3629 NR_036214	1E+08 NR_036214	ENSG00000MIR4253	microRNA ncRNA	
chr1-5281	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr1	52813736	52814458	+	0	NA	intron (AluX1 SI	-28663 NM_001307	440590 Hs. 65845E	NR_001004	ENSG00000ZYG11A	ZYG11 yig-11 f protein-coding
chr1-1795	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr1	1.8E+08	1.8E+08	+	0	NA	intron (intron (N	31812 NM_01560E	26092 Hs. 49645E	NR_01560E	ENSG00000TOR1AIP1	LAP1 LAP1 torsin 1 protein-coding
chr10-50	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr10	50082441	50087578	+	0	NA	intron (L1MC4 LIN	17055 NM_00100E	387680 Hs. 36528E	NR_01823E	ENSG00000WASHC2A	FAM21A F WASH com protein-coding
chr11-44	8.682333	0.130446	0.786882	0.165775	0.868334	0.981636	chr11	44582493	44583423	+	0	NA	intron (intron (N	17295 NM_002231	3732 Hs. 52777E	NR_002231	ENSG00000CD82	4F9 C33 CD82 mole protein-coding
chr12-962	8.682333	0.130446	0.786882															

chr14-92c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr14	92030509	92032792	+	0	NA	intron (NLoop)DN	8409 NM_004235	9321 Hs. 63233cNM_004235	ENSG000003TRIP11	ACG1A CEV thyroid f protein-coding
chr15-43c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr15	43054253	43060609	+	0	NA	intron (Nintron (N	48607 NM_17491f	197131 Hs. 591121NM_17491f	ENSG000003UBR1	JBS ubiquitin protein-coding
chr15-63c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr15	63301809	63302675	+	0	NA	intron (Nintron (N	24637 NM_031301	83464 Hs. 51170cNM_031301	ENSG000003APH1B	APH-1B PFaph-1 hom protein-coding
chr15-64c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr15	64398305	64404554	+	0	NA	intron (NAluSc8 S1	13593 NM_001321	9325 Hs. 50034cNM_01621f	ENSG000003TRIP4	ASC-1 ASC thyroid f protein-coding
chr15-65c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr15	65453189	65453942	+	0	NA	intron (NAluSx S1	30618 NM_001032	57722 Hs. 458607NM_02096f	ENSG000003IGDCc4	DDM36 NOF immunogl protein-coding
chr16-48c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr16	4820639	4827078	+	0	NA	exon (NM_exon (NM	-20908 NM_02458f	79641 Hs. 45979cNM_02458f	ENSG000003ROGDI	KTZS rogdi atyp protein-coding
chr16-90c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr16	9092694	9098360	+	0	NA	intron (Nintron (N	3883 NM_014117	29035 Hs. 221497NM_014117	ENSG000003C16orf72	PRO0149 chromosom protein-coding
chr16-115c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr16	11887150	11892531	+	0	NA	intron (NAluSx S1	26116 NM_002094	2935 Hs. 52878cNM_002094	ENSG000003GSP1	55169.2 EG1 to S f protein-coding
chr16-466c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr16	46659729	46664689	+	0	NA	intron (Nintron (N	26969 NM_01820f	55737 Hs. 45452cNM_01820f	ENSG000003VPS35	MEM3 PARF VPS35 ret protein-coding
chr16-694c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr16	69426524	69433695	+	0	NA	intron (Nintron (N	5514 NM_03057f	80777 Hs. 461131NM_03057f	ENSG000003CYB5B	CYB5-B C cytochrom protein-coding
chr17-247c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr17	2476327	2476769	+	0	NA	intron (N L2 LINE L	35340 NM_02408f	79066 Hs. 632237NM_02408f	ENSG000003METTL16	METTL10D methyl tr protein-coding
chr17-29f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr17	29509461	29512915	+	0	NA	intron (Nintron (N	55849 NM_198147	116236 Hs. 10651cNM_198147	ENSG000003ABHD15	abhydrolase protein-coding
chr17-29c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr17	29668354	29672283	+	0	NA	intron (N LTR89 LTF	-48895 NM_032854	84940 Hs. 14304cNM_032854	ENSG000003COR06	coronin f protein-coding
chr17-31c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr17	31887681	31896337	+	0	NA	intron (NAluSg LTF	9703 NM_01842f	55813 Hs. 58986cNM_01842f	ENSG000003UTP6	C17orf40 UTP6 smal protein-coding
chr17-61c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr17	61965712	61966744	+	0	NA	intron (Nintron (N	-38246 NM_00133c	57508 Hs. 27964cNM_02074f	ENSG000003INTS2	INT2 KIAA integratc protein-coding
chr17-82c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr17	82943566	82945459	+	0	NA	3' UTR (N3' UTR (N	62436 NR_13546f	146712 Hs. 607824NM_00100f	ENSG000003B3GNTL1	3-Gn-78 EUDP-GlcNA protein-coding
chr18-63c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr18	63348132	63362600	+	0	NA	intron (Nintron (N	11840 NM_00203f	2531 Hs. 74050 NM_00203f	ENSG000003KDSR	DHSR EKV3 f-ketoid protein-coding
chr19-18c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr19	18931989	18936479	+	0	NA	intron (Nintron (N	4815 NM_00114f	9454 Hs. 72020cNM_00483f	ENSG000003HOMER3	HOMER-3 hommer sca protein-coding
chr19-467c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr19	46720401	46730513	+	0	NA	intron (Nintron (N	-8330 NM_016457	25865 Hs. 466987NM_016457	ENSG000003PRKD2	HSPC187 F protein f protein-coding
chr19-49c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr19	49615817	49619224	+	0	NA	intron (NAluJo SIN	22623 NM_00627c	6237 Hs. 51553cNM_00627c	ENSG000003RRAS	R-Ras RAS relat protein-coding
chr19-52c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr19	52633752	52634893	+	0	NA	intron (Nintron (N	4069 NM_00110f	55769 Hs. 46721cNM_01830c	ENSG000003ZNF83	HPF1 ZNF8 zinc fing protein-coding
chr2-393f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	39358403	39361300	+	0	NA	intron (N THE1C-int	77434 NM_00361f	8491 Hs. 65575cNM_00361f	ENSG000003MAP4K3	GLK MAPKK mitogen-e protein-coding
chr2-442c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	44209245	44210398	+	0	NA	intron (Nintron (N	40946 NM_00270f	5495 Hs. 41676cNM_00270f	ENSG000003PPM1B	PP2C-beta protein f protein-coding
chr2-950f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	95099703	95101690	+	0	NA	intron (Nintron (N	18611 NM_001321	64969 Hs. 65525cNM_03190c	ENSG000003MRP55	MRP-55 SE mitochochr protein-coding
chr2-109f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	1.1E+08	1.1E+08	+	0	NA	intron (NAluSc SIN	-48963 NR_03809f	1E+08 Hs. 53561cNM_00120f	ENSG000003LIMS4	LIMS3L LIM zinc protein-coding
chr2-1914c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	exon (NM_exon (NM	178446 NM_001161	4430 Hs. 43962cNM_01222f	ENSG000003MYO1B	MMI-alpha myosin I f protein-coding
chr2-1974c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	1.97E+08	1.97E+08	+	0	NA	intron (Nintron (N	12696 NM_00132c	8219 Hs. 60659cNM_025147	ENSG000003COQ10B	- coenzyme protein-coding
chr2-223f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr2	2.24E+08	2.24E+08	+	0	NA	intron (NAluSx SIN	45647 NM_02083c	57590 Hs. 36835cNM_02083c	ENSG000003WDFY1	FENS-1 FEWD repeat protein-coding
chr20-321c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr20	32156474	32159420	+	0	NA	exon (NM_exon (NM	32413 NR_002781	128854 Hs. 647447NR_002781	ENSG000003TSPY26P	TSPYL3 beta testis sp pseudo
chr20-32f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr20	32833782	32834708	+	0	NA	intron (NAluJo SIN	14291 NM_01232f	22919 Hs. 472437NR_01232f	ENSG000003MAPRE1	EB1 microtubul protein-coding
chr20-351c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr20	35125392	35127704	+	0	NA	intron (N MR SINE	20788 NM_00114f	55741 Hs. 720177NM_01821f	ENSG000003CEDEM2	C20orf31 ER degradc protein-coding
chr20-37c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr20	38517636	38518835	+	0	NA	intron (Nintron (N	1672 NR_03960f	1.01E+08 Hs. 03960f	ENSG000003MIR54802	- microRNA ncRNA
chr21-38f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr21	37952921	37989998	+	0	NA	intron (Nintron (N	14197 NR_00331f	7267 Hs. 368214NM_00331f	ENSG000003TTC3	DCRR1 RNf tetraatric protein-coding
chr22-29f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr22	29545795	29548932	+	0	NA	intron (N THE1A-int	6292 NM_00100f	8563 Hs. 75361 NM_00367f	ENSG000003THOC5	C22orf19 THO compl protein-coding
chr3-125f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr3	12588819	12592567	+	0	NA	intron (Nintron (N	33606 NM_01416f	23609 Hs. 59166cNM_01416f	ENSG000003MKRN2	HSPC070 Fmakorin i protein-coding
chr3-490f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr3	49067280	49075573	+	0	NA	intron (NAluSx3 S1	21206 NM_00132c	54870 Hs. 29738cNM_01773c	ENSG000003QRICH1	AB-DIP Fglutamine protein-coding
chr3-493c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr3	49333287	49337131	+	0	NA	intron (Nintron (N	4844 NM_001251	7375 Hs. 77500 NM_00336f	ENSG000003CUSP4	UNP Umph ubiquitir protein-coding
chr3-1294c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	5454 NM_00127f	8930 Hs. 35947 NM_00392f	ENSG000003MBD4	MED1 methyl-Cp protein-coding
chr3-180f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr3	1.81E+08	1.81E+08	+	0	NA	intron (Nintron (N	36235 NM_00136f	8087 Hs. 478407NM_00508f	ENSG000003FXR1	FXR1P FMRI atyp protein-coding
chr4-1691c.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr4	1691653	1696359	+	0	NA	intron (Nintron (N	-9693 NM_001174	152877 Hs. 143314NM_00101f	ENSG000003FAM53A	DNTNP family wiprotein-coding
chr4-150f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr4	15061188	15064664	+	0	NA	intron (Nintron (N	60445 NM_001177	132864 Hs. 656937NM_18248f	ENSG000003CPEB2	CPE-BP2 cytoplasm protein-coding
chr4-253f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr4	25388816	25398970	+	0	NA	intron (Nintron (N	16530 NM_013367	29945 Hs. 15217cNM_013367	ENSG000003ANAPC4	APC4 anaphase protein-coding
chr4-397f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr4	39769536	39770699	+	0	NA	intron (N CpG	71981 NM_001111	3093 Hs. 50308 NM_00533f	ENSG000003UBE2K	E2-25K H ubiquitir protein-coding
chr4-569f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr4	56965898	56970191	+	0	NA	intron (NAluSx SIN	9562 NM_03231f	84273 Hs. 8715 NM_03231f	ENSG000003NOA1	C4orf14 N trich o protein-coding
chr4-183f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr4	1.84E+08	1.84E+08	+	0	NA	intron (N MR SINE	36968 NM_02194f	60684 Hs. 44324cNM_02194f	ENSG000003TRAPP11	C4orf41 F trafficir protein-coding
chr5-104f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr5	10409698	10414478	+	0	NA	intron (Nintron (N	9724 NR_16210f	1.13E+08 Hs. NR_16210f	MIR10397	- microRNA ncRNA
chr5-1291f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr5	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	9540 NR_03977f	1.01E+08 Hs. NR_03977f	ENSG000003MIR4633	- microRNA ncRNA
chr5-150f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	44698 NM_00154f	3340 Hs. 22205cNM_00154f	ENSG000003NDST1	HSST MRT4N-deacetyl protein-coding
chr6-110f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	exon (NM_exon (NM	15525 NM_001287	262 Hs. 15911cNM_001634	ENSG000003AMD1	ADOMETDC adenosyln protein-coding
chr6-126f.170029	0.133615	0.8082	0.165325	0.868689	0.981636	chr6	1.26E+08	1.26E+08	+	0	NA	intron (Nintron (N	24999 NM_001031	60487 Hs. 40418cNM_02182c	ENSG000	



chr7-5336 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr7	5336088	5338152	+	0	NA	intron (N)IMEf LIN	54177 NM_00104C	222962 Hs. 4302	NM_153247	ENSG00000SLC29A4	ENT4 PMA1	solute cε protein-coding	
chr7-4442 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr7	4422534	4422639	+	0	NA	intron (N)intron (N)	64692 NM_015332	23386 Hs. 488171	NM_015332	ENSG00000NUCD3	NudCL	Nudc domε protein-coding	
chr7-474 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr7	47407228	47415149	+	0	NA	intron (N)intron (N)	53615 NR_145813	1.1E+08	NR_145813	SNORD151	-	small nucsnoRNA	
chr7-7452 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr7	47523670	47530587	+	0	NA	intron (N)Alu SINE	51183 NM_002274F	64759 Hs. 520814	NM_002274	ENSG00000TNS3	TEM6 TENS	tensin 3 protein-coding	
chr7-747 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr7	74400222	74405354	+	0	NA	intron (N)intron (N)	-51118 NM_00568E	9569 Hs. 64705E	NM_00568E	ENSG00000GTF2IRD1	BEN CREAM	GTF2I reprotein-coding	
chr7-139 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (N)intron (N)	8267 NM_08066C	92092 Hs. 51283E	NM_08066C	ENSG00000CZ3HAV1L	C7orf39	zinc fing protein-coding	
chr8-832 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr8	8325191	8329601	+	0	NA	intron (N)AluSx SIN	58848 NM_00136E	157285 Hs. 58386E	NM_00108C	ENSG00000PRAG1	NACK PEAK	PEAK1 relprotein-coding	
chr8-2805 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr8	28098055	28099899	+	0	NA	intron (N)intron (N)	5838 NM_001284	55140 Hs. 49133E	NM_018091	ENSG00000ELP3	KAT9	elongator protein-coding	
chr8-585 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr8	58566400	58570089	+	0	NA	intron (N)Tiger3b	14983 NM_00562E	6386 Hs. 200804	NM_00562E	ENSG00000SDCBP	MDA-9 MDA	syndecan protein-coding	
chr8-9771 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr8	97717900	97725618	+	0	NA	intron (N)intron (N)	-54029 NM_018407	55353 Hs. 492314	NM_018407	ENSG00000LAPTM4B	LAPTM4bet	lysosomal protein-coding	
chr9-324 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chr9	32483688	32488522	+	0	NA	intron (N)intron (N)	40091 NM_014314	23586 Hs. 190622	NM_014314	ENSG00000DDX58	RIG-I RIC	DEXD/Hε protein-coding	
chrX-240 7.913229	-0.13562	0.821213	-0.16514	0.868834	0.981636	chrX	24056436	24078803	+	0	NA	intron (N)AluSx SIN	12663 NM_00141E	1968 Hs. 539684	NM_00141E	ENSG00000EIF2S3	EIF2 EIF2	eukaryoti protein-coding	
chr1-2114 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr1	21148198	21149099	+	0	NA	intron (N)Alu SINE	19391 NM_00119E	8672 Hs. 467084	NM_00376C	ENSG00000EIF4G3	eIF-4G 3 ε	eukaryoti protein-coding	
chr10-27 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr10	27210285	27210681	+	0	NA	intron (N)AluSx SIN	30003 NM_001301	91452 Hs. 530597	NM_14569E	ENSG00000ACBD5	-	acyl-CoA protein-coding	
chr11-614 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr11	61408031	61422395	+	0	NA	intron (N)AluSx SIN	14698 NM_024811	79869 Hs. 718984	NM_024811	ENSG00000CPSPF7	CFIm59	cleavage protein-coding	
chr11-627 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr11	62733239	62735793	+	0	NA	intron (N)AluSx SIN	6030 NM_17381C	283237 Hs. 31704	NM_17381C	ENSG00000TTC9C	-	tetractin protein-coding	
chr11-11 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (N)intron (N)	-35432 NM_00003E	335 Hs. 93194	NM_00003E	ENSG00000CAPOA1	apo(a)	apolipoprotein-coding	
chr11-12 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr11	1.26E+08	1.26E+08	+	0	NA	intron (N)L2c LINE	5363 NM_00133C	9538 Hs. 643514	NM_00487E	ENSG00000E124	EPG4 PIGE	E124 autc protein-coding	
chr12-69 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr12	69573685	69574902	+	0	NA	exon (NM)exon (NM)	-10430 NR_03747E	1.01E+08	NR_03747E	ENSG00000MIR3913	2-mir-3913	microRNA ncRNA	
chr13-33 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr13	33161157	33167586	+	0	NA	intron (N)intron (N)	21720 NM_00124E	90627 Hs. 156551	NM_052851	ENSG00000CSTARD13	ARHGAP37 STAR	relε protein-coding	
chr17-21 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr17	21314609	21314976	+	0	NA	3' UTR (N)3' UTR (N)	26756 NM_00275E	5606 Hs. 51401E	NM_00275E	ENSG00000MAP2K3	MAPK3 MEI	mitogen-ε protein-coding	
chr2-3644 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr2	36447653	36448176	+	0	NA	intron (N)intron (N)	92136 NM_016441	51232 Hs. 699247	NM_016441	ENSG00000CRIM1	CRIM-1 SE	cysteine protein-coding	
chr2-100 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr2	1E+08	1E+08	+	0	NA	exon (NM)exon (NM)	98386 NM_00102E	3899 Hs. 444414	NM_00228E	ENSG00000CAFF3	LAF4 MLL1	AFA/FMR2 protein-coding	
chr2-101 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr2	1.02E+08	1.02E+08	+	0	NA	intron (N)MIRb SINE	137827 NM_145687	9448 Hs. 70101E	NM_004834	ENSG00000MAP4K4	FLH21957 mi	togen-ε protein-coding	
chr20-38 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr20	38539825	38541622	+	0	NA	intron (N)intron (N)	24160 NR_03960E	1.01E+08	NR_03960E	ENSG00000MIR54802	-	microRNA ncRNA	
chr22-38 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr22	38214357	38214793	+	0	NA	exon (NM)exon (NM)	10145 NR_132774	1.07E+08	NR_132774	SNORA92	-	small nucsnoRNA	
chr22-41 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr22	41489601	41655997	+	0	NA	intron (N)Alu Jo SIN	31184 NM_00128E	2547 Hs. 29249E	NM_00146E	ENSG00000XRCC6	CTC75 CTC	X-ray reprotein-coding	
chr3-179 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr3	1.8E+08	1.8E+08	+	0	NA	intron (N)LIPA4 LIN	14928 NM_00249E	4711 Hs. 730674	NM_00249E	ENSG00000NDUF5	CISGDH SC	NADH:ubiq protein-coding	
chr4-44 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr4	445726	427931	+	0	NA	intron (N)LIPA7 LIN	14081 NR_002451	79963 Hs. 67749E	NM_02490E	ENSG00000ABCA11P	ABCA11 ES	ATP bindipseudo	
chr6-132 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr6	1.32E+08	1.32E+08	+	0	NA	intron (N)Tiger12	50019 NM_00132E	8417 Hs. 59314E	NM_00356E	ENSG00000STX7	-	syntxin protein-coding	
chr7-77 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr7	77596545	77599590	+	0	NA	intron (N)Alu Jb SIN	60024 NM_001131	5782 Hs. 61812	NM_00283E	ENSG00000PTPN12	PTP-PEST	protein tprotein-coding	
chr7-10 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	Intergeni Intergeni	-57878 NR_024394	154822 Hs. 54478E	NM_19834E	ENSG00000LINC0068E	-	long intncRNA	
chr8-10 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (N)intron (N)	72504 NR_12541E	1.02E+08	Hs. 49244E	NR_12541E	ENSG00000UBR5-AS1	-	UBR5 antncRNA
chr9-57 9.665801	0.123576	0.748535	0.16509	0.868873	0.981636	chr9	5772314	5774914	+	0	NA	intron (N)MIR3 SINE	59503 NM_02489E	79956 Hs. 59107E	NM_02489E	ENSG00000CERMP1	FXNA KIA	endoplasm protein-coding	
chr6-1611 7.46789	-0.14131	0.856148	-0.16506	0.868898	0.981636	chr6	1611727	1612641	+	0	NA	3' UTR (N)3' UTR (N)	2269 NM_00145E	2296 Hs. 34888E	NM_00145E	ENSG00000FOX1C	ARL ASGE	forkhead protein-coding	
chr15-514 12.66682	0.109579	0.664567	0.164887	0.869033	0.981636	chr15	51484595	51486318	+	0	NA	intron (N)intron (N)	108210 NM_00133C	342035 Hs. 526441	NM_18178E	ENSG00000GLDN	CROM COL	gliomedir protein-coding	
chr1-20 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	20852739	20855651	+	0	NA	intron (N)intron (N)	-67507 NM_016287	50809 Hs. 14244E	NM_016287	ENSG00000CHP1BP3	HP1-BP74	heterochr protein-coding	
chr1-2444 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	24444535	24448429	+	0	NA	intron (N)LIPA11 LI	30367 NM_00132E	57185 Hs. 52344E	NM_02044E	ENSG00000NIPAL3	DJ462023.	NIPA like protein-coding	
chr1-2861 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	28614626	28615733	+	0	NA	intron (N)intron (N)	22684 NM_00119E	115273 Hs. 652321	NM_152304	ENSG00000RAB42	-	RAB42, mε protein-coding	
chr1-5184 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	51846635	51847313	+	0	NA	intron (N)LTR12C LI	-10572 NR_03158C	1E+08	NR_03158C	ENSG00000MIR761	hsa-mir-7	microRNA ncRNA	
chr1-6694 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	66948535	66948822	+	0	NA	TTS (NM_C)TTS (NM_C)	18422 NM_001077	57708 Hs. 60543E	NM_02094E	ENSG00000MIR1E1	ER1 MI	-EFMIR1 trε protein-coding	
chr1-15 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	1.1783	NM_002122	+	0	NA	intron (N)intron (N)	11783 NM_002122	54856 Hs. 656361	NM_03229E	ENSG00000GON4L	GON-4 GON	-E2F1 trε protein-coding	
chr1-2444 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr1	2.44E+08	2.44E+08	+	0	NA	intron (N)intron (N)	28694 NM_00112E	159 Hs. 49831E	NM_00112E	ENSG00000ADSS	ADEH ADS	adenylost protein-coding	
chr10-73 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr10	73801608	73804552	+	0	NA	exon (NM)exon (NM)	-1681 NR_038357	1.01E+08	Hs. 63182E	NR_038357	ENSG00000ZSWIM8-AS	-	ZSWIM8 arncRNA
chr10-91 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr10	91813053	91815051	+	0	NA	intron (N)Tiger3b	15626 NM_02523E	80351 Hs. 329327	NM_02523E	ENSG00000TNSK5	ARTD6 PAF	tankyrase protein-coding	
chr10-97 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr10	97476771	97479170	+	0	NA	intron (N)intron (N)	20452 NM_02236E	64210 Hs. 500721	NM_02236E	ENSG00000MMS19	CIA04 MET	MMS19 hon protein-coding	
chr11-6 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr11	68921654	68923644	+	0	NA	intron (N)AluSx4 SI	18798 NM_00218C	3508 Hs. 50304E	NM_00218C	ENSG00000IGHMBP2	CATF1 CMI	immunoglε protein-coding	
chr12-651 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr12	6519967	6524356	+	0	NA	intron (N)AluJr4 SI	11939 NR_004387	692148	NR_004387	ENSG00000SCARNA10	U85	small Ca_ncRNA	
chr12-49 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr12	49034133	49036283	+	0	NA	intron (N)MIRc SINE	-16432 NM_00120E	5571 Hs. 53086E	NM_00273E	ENSG00000PRKAG1	AMPKG	protein tε protein-coding	
chr13-11 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (N)(GGA)n Si	79657 NR_148221	1.05E+08	Hs. 13472E	NR_148221	LOC10537C	-	uncharactncRNA
chr14-9 7.657725	0.137209	0.833649	0.164588	0.869268	0.981636	chr14	92803260	92803780	+	0	NA	intron (N)LIM5 LINE	9215 NM_00511E	9950 Hs. 10432C	NM_00511E	ENSG00000GOLGA5	GOLIM5 RF	golgin Aε protein-coding	
chr15-28 7.657725	0.137209	0.833649	0.164588																

chr16-502.7.459631	-0.13952	0.85019	-0.16411	0.869646	0.981636	chr16	50228775	50229648	+	0	NA	exon (NM exon (NM	-37340	NR_001114	113	Hs. 513575	ENSG000003ADCY7	AC7	adenylateprotein-coding
chr4-1254.7.459631	-0.13952	0.85019	-0.16411	0.869646	0.981636	chr4	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	-90199	NR_031746	1E+08	NR_031746	ENSG000003MIR2054	hsa-mir-2microRNA	ncRNA
chr11-949.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr11	94963327	94972024	+	0	NA	intron (Nintron (N	5881	NR_016403	51503	Hs. 503597	ENSG000003CWC15	AD002 C11CWC15	splprotein-coding
chr13-111.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	21589	NR_017664	55608	Hs. 525163	ENSG000003ANKRD10	-	ankyrin 1protein-coding
chr14-103.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	60011	NR_001822	1152	Hs. 173724	ENSG000003CKB	B-CK BCK	creatine protein-coding
chr16-148.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr16	14853998	14856721	+	0	NA	intron (Nintron (N	21638	NR_014287	23420	Hs. 743963	ENSG000003NOMO1	Nomo PM5	NODAL mocprotein-coding
chr16-533.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr16	53314371	53317092	+	0	NA	intron (NAluS2 SIN	55481	NR_001347	643802	Hs. 451333	ENSG000003LOC643802	-	u3 small protein-coding
chr16-693.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr16	69333491	69336473	+	0	NA	exon (NM exon (NM	-4394	NR_022341	64146	Hs. 130845	ENSG000003PDF	-	peptide cprotein-coding
chr17-287.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr17	28746547	28751185	+	0	NA	intron (Nintron (N	4855	NR_004295	9618	Hs. 8375	ENSG000003TRAF4	CART1 MLN	TNF receprprotein-coding
chr17-312.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr17	31226353	31228557	+	0	NA	intron (Nintron (N	69784	NR_002544	4974	Hs. 113874	ENSG000003OMG	OMGP	oligodencprotein-coding
chr19-137.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr19	13777810	13779460	+	0	NA	3' UTR (N3' UTR (N	4179	NR_014047	28974	Hs. 231616	ENSG000003C19orf53	OMG PCO23	chromosonprotein-coding
chr2-1053.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr2	1.05E+08	1.05E+08	+	0	NA	intron (NAluS2 SIN	4467	NR_001288	79074	Hs. 549577	ENSG000003C2orf49	asw	chromosonprotein-coding
chr2-1087.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr2	1.09E+08	1.09E+08	+	0	NA	exon (NM exon (NM	-31733	NR_001351	165055	Hs. 362702	ENSG000003CCDC138	-	coiled-cprotein-coding
chr2-1332.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	-53216	NR_110294	1.02E+08	Hs. 661917	ENSG000003NCKAP5-AS-	-	NCKAP5 arncRNA
chr2-1825.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr2	1.83E+08	1.83E+08	+	0	NA	intron (Nintron (N	37788	NR_013436	10787	Hs. 603732	ENSG000003NCKAP1	HEM2 NAP1	NCK assocprotein-coding
chr20-372.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr20	37204307	37206027	+	0	NA	intron (Nintron (N	-25619	NR_021362	140699	Hs. 349122	ENSG000003MROH8	C20orf131	maestro tprotein-coding
chr4-1697.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr4	1697446	16995627	+	0	NA	intron (NAluSc8 SIN	13812	NR_001306	7884	Hs. 298342	ENSG000003SLBP	HBP	stem-loopprotein-coding
chr6-7243.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr6	7248722	7249782	+	0	NA	3' UTR (N3' UTR (N	63947	NR_001292	6745	Hs. 114033	ENSG000003SSR1	TRAPA	signal seprotein-coding
chr6-4354.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr6	43549073	43551644	+	0	NA	intron (Nintron (N	25680	NR_020755	57510	Hs. 203206	ENSG000003XPO5	exp5	exportin protein-coding
chr7-6672.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr7	66723109	66725981	+	0	NA	intron (NAluSc SIN	-16188	NR_001367	27342	Hs. 530055	ENSG000003RABGEF1	RABEX5 RA	RAB guaniprotein-coding
chr7-1003.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr7	1E+08	1E+08	+	0	NA	intron (NLM13D L1	-3515	NR_003613	5379	Hs. 634244	ENSG000003PMS2P1	PMS2L1 PW	PMS1 homcpseudo
chr7-1378.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr7	1.38E+08	1.38E+08	+	0	NA	intron (Nintron (N	-33788	NR_004717	9162	Hs. 242947	ENSG000003DGM1	DGK-IOTA	diacylglyprotein-coding
chr8-3044.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr8	30442358	30443954	+	0	NA	intron (Nintron (N	-57755	NR_046205	1E+08	Hs. 126812	ENSG000003RBPMS-AS1	-	RBPMS antncRNA
chr9-8631.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr9	86317560	86319678	+	0	NA	intron (Nintron (N	35791	NR_024617	79670	Hs. 597057	ENSG000003TUT7	PAPD6 TEM	terminal protein-coding
chr9-1213.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	26574	NR_198194	2040	Hs. 253903	ENSG000003STOM	BNDF EPB7	stomatin protein-coding
chr9-1292.9.153497	0.126014	0.767985	0.164085	0.869665	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	2880	NR_003071	692206	Hs. 693255	ENSG000003SNORD90	HBII1-295	small nucsnRNA
chr1-3902.11.16943	0.114962	0.701764	0.163819	0.869874	0.981636	chr1	39028618	39032204	+	0	NA	intron (NAluSx1 SIN	4061	NR_004552	4725	Hs. 632388	ENSG000003NDUFS5	CI-15K CINADP	ubiqu protein-coding
chr1-1485.11.16943	0.114962	0.701764	0.163819	0.869874	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	intron (Nintron (N	7922	NR_015383	25832	Hs. 534676	ENSG000003NBPF14	DJ328E19	NBPF memtprotein-coding
chr18-352.11.16943	0.114962	0.701764	0.163819	0.869874	0.981636	chr18	35293279	35308359	+	0	NA	intron (NLM1E LIN	10547	NR_024566	10778	Hs. 314242	ENSG000003ZNF271P	CT-ZFP48	zinc fingpseudo
chr19-585.11.16943	0.114962	0.701764	0.163819	0.869874	0.981636	chr19	58282596	58296667	+	0	NA	intron (NMLT1D L1	10665	NR_144447	1.09E+08	Hs. 715293	ENSG000003ZNF8-ERVK-	ZNF8-ERVK	ncRNA
chr5-1634.11.16943	0.114962	0.701764	0.163819	0.869874	0.981636	chr5	1.63E+08	1.63E+08	+	0	NA	3' UTR (N3' UTR (N	6428	NR_199246	900	Hs. 79101	ENSG000003CCNG1	CCNG	cyclin G1protein-coding
chr10-925.1.126129	0.173539	1.059458	-0.1638	0.869889	0.981636	chr10	92218998	92319407	+	0	NA	intron (NTiger3 B	28035	NR_017824	54708	Hs. 573493	ENSG0000035-Mar	MARCH-V V	membrane protein-coding
chr12-652.6.957035	-0.14466	0.884047	-0.16363	0.870022	0.981636	chr12	65220624	65221585	+	0	NA	intron (NLM1B1 L1	51521	NR_014315	23592	Hs. 744152	ENSG000003LEMDD3	MAN1	LEM domainprotein-coding
chr15-636.6.957035	-0.14466	0.884047	-0.16363	0.870022	0.981636	chr15	63682214	63682539	+	0	NA	intron (NMER68-int	-81549	NR_03408C	1E+08	Hs. 631163	ENSG000003CASP3-AS1	-	USP3 antncRNA
chr9-1291.6.957035	-0.14466	0.884047	-0.16363	0.870022	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	25115	NR_163192	56904	Hs. 460233	ENSG000003SH3GLB2	PP6569 PF	SH3 domainprotein-coding
chr1-1461.10.18596	0.119968	0.733562	0.163542	0.870092	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	intron (NMLT2A1 L1	-17804	NR_001035	1E+08	Hs. 714127	ENSG000003NBPF10	AB6 AG1 NBPF	memtprotein-coding
chr19-236.10.18596	0.119968	0.733562	0.163542	0.870092	0.981636	chr19	23660024	23663206	+	0	NA	intron (NAluSx SIN	25597	NR_13833C	171392	Hs. 264343	ENSG000003ZNF675	TBZF TIZ	zinc fingprotein-coding
chr22-428.10.18596	0.119968	0.733562	0.163542	0.870092	0.981636	chr22	42845270	42849640	+	0	NA	intron (Nintron (N	11163	NR_014573	26286	Hs. 685222	ENSG000003ARFGAP3	ARFGAP1	ADP ribosprotein-coding
chr4-5700.10.18596	0.119968	0.733562	0.163542	0.870092	0.981636	chr4	572004792	57207410	+	0	NA	intron (Nintron (N	27205	NR_000938	5431	Hs. 602757	ENSG000003POLR2B	POLR2B RF	RNA polynprotein-coding
chr6-1703.10.18596	0.119968	0.733562	0.163542	0.870092	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	18906	NR_039787	1.01E+08	NR_039787	ENSG000003MIR4644	-	microRNA ncRNA
chr8-7065.10.18596	0.119968	0.733562	0.163542	0.870092	0.981636	chr8	70655678	70657591	+	0	NA	intron (NLM1P1 LIN	12551	NR_016027	51110	Hs. 118554	ENSG000003LACTB2	CGI-83	lactamaseprotein-coding
chr11-778.6.633335	0.130432	0.797828	0.163484	0.870137	0.981636	chr11	77824385	77825310	+	0	NA	intron (Nintron (N	12947	NR_001311	1207	Hs. 430733	ENSG000003CLNS1A	CLC1 CLNS	chloride protein-coding
chr18-577.8.633335	0.130432	0.797828	0.163484	0.870137	0.981636	chr18	57724493	57727253	+	0	NA	intron (NLM1I LINE	77442	NR_005603	5205	Hs. 216622	ENSG000003ATP8B1	ATPIC BRIAT	phase p1protein-coding
chr1-1025.7.145421	0.141293	0.864278	0.163481	0.87014	0.981636	chr1	10256040	10257271	+	0	NA	intron (Nintron (N	25891	NR_001362	23095	Hs. 97858	ENSG000003KIF1B	CMT2 CMT2	kinesin fprotein-coding
chr14-451.7.145421	0.141293	0.864278	0.163481	0.87014	0.981636	chr14	45095707	45097672	+	0	NA	intron (Nintron (N	12573	NR_017922	55015	Hs. 274337	ENSG000003PRPF39	-	pre-mRNA protein-coding
chr14-761.7.145421	0.141293	0.864278	0.163481	0.87014	0.981636	chr14	76172612	76173617	+	0	NA	3' UTR (N3' UTR (N	18760	NR_110314	55668	Hs. 410231	ENSG000003GPATCH2L	C14orf11E	G-patch cprotein-coding
chr15-635.7.145421	0.141293	0.864278	0.163481	0.87014	0.981636	chr15	63567095	63568006	+	0	NA	intron (NAluV SINE	-29837	NR_001367	238307	Hs. 631163	ENSG000003FBXL22	FBXL22	F-box ancpprotein-coding
chr16-146.7.145421	0.141293	0.864278	0.163481	0.87014	0.981636	chr16													





chr22-237.7.194418	0.141266	0.867822	0.162783	0.87069	0.981636	chr22	23799506	23802461	+	0	NA	exon (NM exon (NM	14017 NM_003073	6598 Hs. 534353	ENSG000003SMARCB1	BAF47 CSS SWI/SNF	rprotein-coding		
chr22-382.7.194418	0.141266	0.867822	0.162783	0.87069	0.981636	chr22	38232596	38235174	+	0	NA	intron (NAIuSx SIN	-9165 NR_132774	1.07E+08	NR_132774	SNORA92	small nucsnoRNA		
chr4-121.7.194418	0.141266	0.867822	0.162783	0.87069	0.981636	chr4	1215964	1216453	+	0	NA	non-codir non-codir	6088 NR_104331	285463 Hs. 707614	NR_104331 ENSG00000CTBP1-AS	PCAT10	CTBP1 antncRNA		
chr6-166.7.194418	0.141266	0.867822	0.162783	0.87069	0.981636	chr6	1.67E+08	1.67E+08	+	0	NA	promoter-promoter-	-188 NR_031734	1E+08	NR_031734 ENSG00000MIR1913	MIRN1913 microRNA	ncRNA		
chr17-78.14.64786	0.101399	0.622923	0.162779	0.870693	0.981636	chr17	78357152	78358880	+	0	NA	3' UTR (3' UTR (N	2063 NM_003955	9021 Hs. 527975	NR_003955 ENSG00000S0CS3	ATOD4 CIS suppress	protein-coding		
chr1-375.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr1	37508058	37509368	+	0	NA	intron (Nintron (N	6053 NR_073091	64769 Hs. 17118	NR_022756 ENSG00000MEAF6	C1orf149 MYST Esa1	protein-coding		
chr1-229.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr1	2.29E+08	2.29E+08	+	0	NA	exon (NM exon (NM	-30568 NM_001100	58 Hs. 1288	NR_001100 ENSG00000ACTA1	ACTA1 ASMP actin a	protein-coding		
chr11-102.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr11	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	94428 NM_001195	10413 Hs. 503692	NR_006106 ENSG00000YAP1	YAP1 YAP Yes	assocprotein-coding		
chr12-647.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr12	64736516	64737054	+	0	NA	intron (Nintron (N	22621 NM_002076	2799 Hs. 334534	NR_002076 ENSG00000CGNS	G6S	glucosami	protein-coding	
chr14-31.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr14	91939492	91940148	+	0	NA	intron (MLTIE2 L1	7882 NM_006325	10516 Hs. 332708	NR_006325 ENSG00000FBLN5	ADCL2 ARC fibulin 1	protein-coding		
chr15-32.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr15	32531045	32533468	+	0	NA	intron (MIRc SINE	1485 NR_036650	1E+08 Hs. 562622	NR_036650	WHAMMP1	WHDc1P1	Was	protseuso
chr3-457.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr3	45722289	45724694	+	0	NA	exon (NM exon (NM	34095 NM_001315	22908 Hs. 156509	NR_014016 ENSG00000SACM1L	SAC1	SAC1 like	protein-coding	
chr4-3997.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr4	39973243	39974344	+	0	NA	intron (Nintron (N	4118 NM_001100	23244 Hs. 331431	NR_015200 ENSG00000PDS5A	PDS5A	SCCSD5	coha	protein-coding
chr9-3307.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr9	33070120	33073777	+	0	NA	intron (Nintron (N	4726 NM_018225	55234 Hs. 565351	NR_018225 ENSG00000SMU1	BWD SMU-1	SMU1	cone	protein-coding
chr9-1104.8.641193	0.12874	0.790996	0.162757	0.87071	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	-87308 NM_001288	255220 Hs. 147064	NR_001006 ENSG00000TXNDC8	SPTRX-3 S	thioredo	protein-coding	
chr1-1561.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr1	1561541	15651267	+	0	NA	intron (NAIuSg7 SI	11529 NM_014188	29101 Hs. 30026	NR_014188 ENSG00000SSU72	HSPC182 FSSU72	hon	protein-coding	
chr1-157.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr1	15782247	15782663	+	0	NA	intron (Nintron (N	-17586 NM_001024	54751 Hs. 530101	NR_017556 ENSG00000FBLIM1	CAL FBLP	filam	protein-coding	
chr1-254.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr1	25488500	25490099	+	0	NA	intron (Nintron (N	-45286 NM_015627	26119 Hs. 590911	NR_015627 ENSG00000LDLRAP1	ARH ARH1	low	densiprotein-coding	
chr1-527.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr1	52772389	52773036	+	0	NA	intron (NAIu SINE	46259 NM_024646	79699 Hs. 47628	NR_024646 ENSG00000ZYG11B	ZYG11	zyl-1	protein-coding	
chr1-116.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr1	1.16E+08	1.16E+08	+	0	NA	intron (Nintron (N	14496 NM_001160	476 Hs. 371889	NR_000701 ENSG00000ATP1A1	CMT2DD HCAT	Pase	protein-coding	
chr1-236.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (Nintron (N	-21324 NR_034040	1E+08 Hs. 67737	NR_034040 ENSG00000LGAL58-AS	-	LGAL58	arncRNA	
chr10-427.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr10	42790319	42795301	+	0	NA	intron (Nintron (N	10015 NM_014753	9790 Hs. 10848	NR_014753 ENSG00000BMS1	ACC BMS1 BMS1	ribc	protein-coding	
chr11-122.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr11	12258836	12261785	+	0	NA	3' UTR (3' UTR (N	-26590 NM_032867	84953 Hs. 60371	NR_032867 ENSG00000MICALCL	Ebitein MICAL	C-t	protein-coding	
chr11-471.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr11	47164713	47172622	+	0	NA	intron (NAIuS6 SI	8212 NM_032388	84364 Hs. 436204	NR_032388 ENSG00000ARFGAP2	IRZ NBLA1 ADP	ribp	protein-coding	
chr11-94.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr11	94829438	94830743	+	0	NA	exon (NM exon (NM	61734 NM_001301	154810 Hs. 503594	NR_130847 ENSG00000AMOTL1	JEAP	angiomot	protein-coding	
chr11-31.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr11	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	105379 NM_001258	57569 Hs. 6136	NR_020809 ENSG00000ARHGAP20	RARHOGAP	Rho	GTPas	protein-coding
chr12-34.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr12	341708	343825	+	0	NA	intron (Nintron (N	46554 NM_001042	5927 Hs. 76272	NR_005056 ENSG00000KDM5A	RBBP-2 RE	lysine	deprotein-coding	
chr12-80.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr12	8089382	8093408	+	0	NA	intron (MERIA DNA	9121 NM_015505	25977 Hs. 555927	NR_015505 ENSG00000NECAP1	EIEEF21	NECAP	enc	protein-coding
chr12-111.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (NAIuSc8 SI	28237 NM_006768	8315 Hs. 53094	NR_006768 ENSG00000BRAP	BRAP2 IMF	BRCA1	ass	protein-coding
chr13-24.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr13	24465547	24466737	+	0	NA	intron (MERS3 DNA	46686 NM_006437	143 Hs. 744855	NR_006437 ENSG00000PARP4	ADPRTL1 Apol	(ADP-	protein-coding	
chr14-73.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	73217159	73220880	+	0	NA	intron (Nintron (N	-18487 NR_158677	89932 Hs. 509909	NR_173462 ENSG00000CAPLN	PPN	papilin,	protein-coding	
chr14-74.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	74811993	74813827	+	0	NA	intron (Nintron (N	49594 NR_019588	56250 Hs. 53111	NR_019588 ENSG00000YLPMP1	C14orf17 C14	YLP	motif	protein-coding
chr14-94.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	94048746	94056898	+	0	NA	intron (Nintron (N	26482 NM_023112	78990 Hs. 27881	NR_023112 ENSG00000OTUB2	C14orf137 OTU	deub	protein-coding	
chr14-102.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	-45980 NM_030943	81693 Hs. 534494	NR_030943 ENSG00000AMN	PRO1028 e	amion	as	protein-coding
chr14-102.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	30340 NM_030944	81693 Hs. 534494	NR_030944 ENSG00000AMN	PRO1028 e	amion	as	protein-coding
chr14-102.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	1.03E+08	1.03E+08	+	0	NA	intron (NAIuSx1 SI	56790 NM_030944	81693 Hs. 534494	NR_030944 ENSG00000AMN	PRO1028 e	amion	as	protein-coding
chr14-104.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr14	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	-11383 NM_152328	122622 Hs. 592327	NR_152328 ENSG00000ADSSL1	Adssl MP	adenylo	protein-coding	
chr15-25.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr15	22908306	22913084	+	0	NA	exon (NM exon (NM	6753 NM_001033	23191 Hs. 26704	NR_014608 ENSG00000CYF1P1	P140SRA	cytoplasm	protein-coding	
chr16-22.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr16	2580815	2584448	+	0	NA	intron (Nintron (N	-20753 NR_105441	652276 Hs. 72044	NR_105441 ENSG00000LOC652276	-	potassium	pseudo	
chr17-44.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr17	44090875	44093157	+	0	NA	intron (Nintron (N	21105 NR_028582	92579 Hs. 29400	NR_138387 ENSG00000G6PC3	SCN4 UGRF	glucose-t	protein-coding	
chr18-99.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr18	9938026	9940581	+	0	NA	intron (NAIuSx1 SI	25287 NM_003574	9218 Hs. 11518	NR_003574 ENSG00000VAPA	VAP-33 V	VAMP	ass	protein-coding
chr18-231.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr18	2194932	2319828	+	0	NA	intron (L3 LINE C	40755 NM_138375	91768 Hs. 11108	NR_138375 ENSG00000CABLES1	CABL1 CAE	Cdk5	and	protein-coding
chr19-104.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr19	10487335	10497546	+	0	NA	intron (NAIuSx4 SI	10331 NM_012288	9817 Hs. 46587	NR_012288 ENSG00000KEAP1	INrf2 KLF	kelch	lik	protein-coding
chr19-13.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr19	13809224	13811587	+	0	NA	intron (NAIuSg SIN	14962 NM_023072	65249 Hs. 46601	NR_023072 ENSG00000ZSLIM4	-	zinc	fin	protein-coding
chr19-31.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr19	31276489	31279311	+	0	NA	exon (NM exon (NM	71536 NR_138036	57616 Hs. 27843	NR_020856 ENSG00000TSHZ3	TSH3 ZNF	teashirt	protein-coding	
chr19-34.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr19	34376133	34387158	+	0	NA	intron (Nintron (N	16449 NM_001325	2821 Hs. 46647	NR_000177 ENSG00000GPI	AMF GNP1	(G	protein-coding	
chr19-44.8.177887	0.131844	0.810225	0.162725	0.870735	0.981636	chr19	44870698	44879791	+	0	NA	intron (Nintron (N	-15976 NM_001128	10452 Hs. 65590	NR_006114 ENSG00000TOMM40	C19orf11 T	transloc	protein-coding	
chr19-49.8.1778																			



chr21-334 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr21 33431335 33434534 + 0 NA intron (NAluSz6|SI 30038 NM\_001325 3460 Hs. 634632NM\_005534ENSG000001FNGR2 AF-1|IFGF interfe protein-coding

chr3-4704 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr3 47040038 47043692 + 0 NA intron (Nintron (N 30323 NR\_024046 1E+08 Hs. 201522NR\_024046 NRAADD neurotrop pseudo

chr3-6905 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr3 69058203 69062117 + 0 NA intron (NML3|LINE|C -7827 NM\_007114 7110 Hs. 267632NM\_007114ENSG000002TMF1 ARA160|TATA elem protein-coding

chr3-128 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr3 1.29E+08 1.29E+08 0 NA intron (NMLT1A|LTF -36110 NR\_162138 1.13E+08 NR\_162138 MIR12124 microRNA ncRNA

chr3-132 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr3 1.33E+08 1.33E+08 0 NA intron (Nintron (N 24198 NR\_002811 348808 Hs. 586111NR\_002811ENSG000002NHP3-AS1 INCRNA0011NHP3 antncRNA

chr3-143 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr3 1.43E+08 1.43E+08 0 NA intron (NTiger1|I 28076 NM\_00132C 23350 Hs. 596572NM\_00108CENSG000002SURP SR140|fsA2 snRNP protein-coding

chr3-185 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr3 1.86E+08 1.86E+08 0 NA intron (NLa2|LINE| 41225 NR\_12632C 646600 Hs. 647949NR\_027317ENSG000002IGF2BP2-3 C3orf65 IGF2BP2 antncRNA

chr4-427 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr4 427633 438897 + 0 NA intron (NMER50-int 40944 NR\_002451 79963 Hs. 677493NM\_02490CENSG000002ABCA11P ABCA11|ES-ATP bind pseudo

chr4-707 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr4 70768649 70771778 + 0 NA intron (NTiger1|I 35803 NM\_00134E 22902 Hs. 740904NM\_014961ENSG000002RUFY3 RIPX|SINCRUN and I protein-coding

chr4-988 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr4 98883721 98887225 + 0 NA intron (NAluJb|SIN 43660 NM\_00113C 1977 Hs. 13211 NM\_001968ENSG000002EIF4E AUTS19|CEukaryot protein-coding

chr5-104 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 10402172 10406653 + 0 NA intron (Nintron (N 2048 NR\_16210E 1.13E+08 NR\_16210E MIR10397 microRNA ncRNA

chr5-346 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 34665934 34668516 + 0 NA intron (Nintron (N 10734 NM\_00114E 26064 Hs. 43140CNM\_015577ENSG000002CRAI14 NORPEG|R|retinoic protein-coding

chr5-804 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 80460169 80463434 + 0 NA intron (NAluSx1|SI -26299 NM\_20554E 167555 Hs. 338182NM\_20554EENSG000002FAM151B UNQ9217 family wiprotein-coding

chr5-132 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 1.1094 NM\_052971 116842 Hs. 337588NM\_052971ENSG000002LEAP2 LEAP-2 liver en protein-coding

chr5-141 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 1.42E+08 1.42E+08 0 NA intron (NAluJb|SIN 12727 NM\_00429C 9604 Hs. 483616NM\_00429CENSG000002RN14 ARA54|HFE ring fing protein-coding

chr5-150 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 1.5E+08 1.5E+08 0 NA intron (NCR1\_Mam|I 6144 NM\_00136E 22993 Hs. 719189NM\_01498CENSG000002HMGXB3 HMGX3|SMF HMG-box c protein-coding

chr5-17 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr5 1.77E+08 1.77E+08 0 NA intron (NAluSz|SIN 28720 NM\_00103E 53917 Hs. 16258 NM\_130781ENSG000002RAB22 RAB24, me protein-coding

chr6-246 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr6 24662370 24664383 + 0 NA intron (NMIR|SINE| 3523 NM\_016614 51567 Hs. 40301CNCM\_016614ENSG000002DP2 ADO22|EAF tyrosyl-I protein-coding

chr6-364 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr6 36495091 36498169 + 0 NA intron (Nintron (N 50849 NM\_007271 11329 Hs. 409578NM\_007271ENSG000002STK38 NDR|NDR1 serine/t protein-coding

chr7-248 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr7 24814351 24815669 + 0 NA intron (Nintron (N -5701 NM\_001127 1687 Hs. 520708NM\_00440CENSG000002GSDME DFNA5|ICF gasderm protein-coding

chr7-449 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr7 44052421 44057898 + 0 NA intron (NLM44|LIN 3393 NR\_10689E 1.02E+08 NR\_10689EENSG000002MIR6837 hsa-mir-6837 microRNA ncRNA

chr7-442 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr7 44203922 44212979 + 0 NA intron (Nintron (N 7472 NM\_00136E 10652 Hs. 520794NM\_00655EENSG000002YKT6 YKT6 v-S protein-coding

chr7-734 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr7 73440644 73448273 + 0 NA intron (Nintron (N 10680 NM\_00350E 8326 Hs. 647029NM\_00350EENSG000002FZD9 CD349|FZ1 frizzled protein-coding

chr7-100 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr7 10106800 10108208 + 0 NA intron (Nintron (N 7170 NM\_00101E 402682 Hs. 53484EENSG000002UFSF1 UFSF1 spec protein-coding

chr7-101 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr7 1.01E+08 1.01E+08 0 NA intron (NAluSz6|SI 9307 NM\_00060E 5054 Hs. 41479EENSG000002SERPINE1 PAI-1|PAI-1serpin f protein-coding

chr8-305 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr8 30544479 30550964 + 0 NA TTS (NM\_CTS (NM\_C -90859 NM\_00120E 1.01E+08 Hs. 65949EENSG000002SMIM18 -small int protein-coding

chr8-865 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr8 86503860 86506957 + 0 NA intron (Nintron (N 3278 NM\_01603E 51115 Hs. 14538EENSG000002RMDN1 CGI-90|fregulator protein-coding

chr8-123 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr8 1.24E+08 1.24E+08 0 NA intron (NLM8B|LIN 32068 NM\_14496E 157769 Hs. 459174NM\_14496EENSG000002FAM91A1 family wiprotein-coding

chr9-362 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr9 36218139 36224575 + 0 NA intron (NMIRB|SINE 30436 NM\_001184 1211 Hs. 522114NM\_00183EENSG000002CLTA LCA clathrin protein-coding

chr9-112 9.161355 0.124433 0.766611 0.162315 0.871057 0.981636 chr9 1.12E+08 1.12E+08 0 NA intron (NTHEID-int 40818 NM\_001244 9991 Hs. 26998EENSG000002PTBP3 ROD1 polypr protein-coding

chr1-917 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr1 9176875 9180290 + 0 NA intron (Nintron (N -3622 NR\_13273E 1.03E+08 Hs. 59929EENSG000002LNCTAM34 GUARDIN|I long non ncRNA

chr1-363 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr1 36392545 36394441 + 0 NA TTS (NM\_CTS (NM\_C 4415 NM\_032881 84967 Hs. 603131NM\_032881ENSG000002LSM10 MSTO704|MSLSM10, U7 protein-coding

chr1-17 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr1 1.18E+08 1.18E+08 0 NA intron (Nintron (N 13530 NM\_006784 10885 Hs. 13108EENSG000002WDR3 DIP2|UTP1WD reuprotein-coding

chr1-178 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr1 1.79E+08 1.79E+08 0 NA intron (Nintron (N -9786 NM\_00467E 9068 Hs. 591474NM\_00467EENSG000002CANGPTL1 ANG3|ANGF angiopoie protein-coding

chr1-186 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr1 1.86E+08 1.86E+08 0 NA intron (Nintron (N -12004 NM\_00237E 10896 Hs. 67923EENSG000002OCLM TISR oculomed protein-coding

chr1-246 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr1 2.47E+08 2.47E+08 0 NA intron (NTiger4|I 2589 NM\_00236E 64216 Hs. 7395 NM\_02236EENSG000002TFB2M Hkpl|mtTF transcrip protein-coding

chr10-701 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr10 70110867 70115816 + 0 NA 3' UTR (3' UTR (N 19484 NM\_032797 84883 Hs. 65068CNCM\_032797ENSG000002ATFM2 AMID|PRG:apoptosis protein-coding

chr12-56 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr12 56540028 56541089 + 0 NA intron (NAluJr|SIN 18738 NM\_00289E 5939 Hs. 50572EENSG000002RBM52 SCR3 RNA bindi protein-coding

chr12-98 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr12 98662355 98668432 + 0 NA intron (NLM4Ea|LI 20093 NM\_18186E 317 Hs. 55265EENSG000002APAF1 APAF-1|CE apoptotic protein-coding

chr12-10 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr12 1.1E+08 1.1E+08 0 NA exon (NM\_exon (NM\_ 34736 NM\_05716E 9815 Hs. 43499EENSG000002GIT2 CAT-2|CAT1G ArfG| protein-coding

chr12-12 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr12 1.21E+08 1.21E+08 0 NA intron (NAluSx1|SIN 13615 NM\_00127E 10645 Hs. 29734EENSG000002CAMKK2 CAMKK|CAM calcium/c protein-coding

chr12-121 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr12 1.21E+08 1.21E+08 0 NA exon (NM\_exon (NM\_ 21815 NM\_00133C 51433 Hs. 7101 NM\_01623EENSG000002ANAPC5 ANPC5 anaphase protein-coding

chr13-32 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr13 32264861 32269451 + 0 NA intron (Nintron (N 44798 NM\_00113E 646799 Hs. 569254NM\_00113EENSG000002ZARIL Z3CXXC7|zygote ar protein-coding

chr13-49 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr13 49254353 49257971 + 0 NA intron (Nintron (N 8237 NM\_030911 81602 Hs. 38822CNCM\_030911ENSG000002CDADC1 NYD-SP15|cytidine protein-coding

chr13-75 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr13 75573057 75574083 + 0 NA intron (NMLT1B|LTF 23820 NM\_00600E 7347 Hs. 162241NM\_00600EENSG000002UCHL3 UCH-L3 ubiqutin protein-coding

chr14-75 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr14 75431953 75436095 + 0 NA intron (Nintron (N 1890 NM\_00113E 122953 Hs. 19648EENSG000002JDP2 JUNDM2 Jun dimer protein-coding

chr15-75 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr15 75386509 75387367 + 0 NA intron (NAluJb|SIN -18311 NM\_00125E 4123 Hs. 26232 NM\_00671EENSG000002MAN2C1 MANG68|ABC mannose di protein-coding

chr16-16 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr16 16032986 16034371 + 0 NA intron (NAluSx|SIN 84062 NM\_00499E 4363 Hs. 391464NM\_00499EENSG000002ABCC1 ABC29|ABC ATP bindi protein-coding

chr16-24 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr16 24928729 24935270 + 0 NA intron (NAluJb|SIN 83370 NM\_00100E 55114 Hs. 37379EENSG000002ARHGAP17 MSTO706|MS Rho GTPas protein-coding

chr16-25 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr16 25140031 25140230 + 0 NA TTS (NR\_CTS (NR\_C 8902 NR\_03999E 1.01E+08 Hs. 65757EENSG000002LCMT1-AS2 LCMT1 antncRNA

chr16-67 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr16 67233393 67239339 + 0 NA intron (Nintron (N 9236 NR\_134524 29100 Hs. 43320EENSG000002TMEM208 HSPC171 transmemt protein-coding

chr17-39 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 39436049 39439955 + 0 NA intron (NAluS2|SI 13261 NM\_004774 5469 Hs. 643754NM\_004774ENSG000002MED1 CRSP1|CRS mediator protein-coding

chr17-48 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 48069652 48071148 + 0 NA 3' UTR (3' UTR (N 22041 NM\_003204 4779 Hs. 514284NM\_003204ENSG000002NFE2L1 LCR-F1|NF nuclear f protein-coding

chr17-75 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 75051805 75054773 + 0 NA intron (Nintron (N 6064 NM\_01535E 23510 Hs. 51446EENSG000002KCTD2 -potassium protein-coding

chr17-75 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 75263588 75266719 + 0 NA intron (NAluSx1|SI -2790 NM\_00117E 23163 Hs. 87726 NM\_014001ENSG000002GGA3 -golgi ass protein-coding

chr17-75 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 75662034 75663191 + 0 NA exon (NM\_exon (NM\_ -4504 NM\_001301 29115 Hs. 65508EENSG000002SAP30BP HCNPG|HTF SAP30 bir protein-coding

chr17-80 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 80207634 80216994 + 0 NA intron (Nintron (N 8919 NM\_00135E 6448 Hs. 31074 NM\_00019EENSG000002SGSH HSS|MPS3|N-sulfolig protein-coding

chr17-80 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr17 80265550 80269954 + 0 NA intron (NTiger1|I 57674 Hs. 19564EENSG000002RNFP213 ALO17|C17ring fing protein-coding

chr18-41 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr18 41999313 42000964 + 0 NA intron (NAluS2|SI 44904 NM\_002647 5289 Hs. 464971NM\_002647ENSG000002PIK3C3 VPS34|Vps phosphat i protein-coding

chr19-20 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr19 2704695 2709321 + 0 NA exon (NM\_exon (NM\_ 19318 NM\_130807 126308 Hs. 74493EENSG000002MOB3A MOB-LAK|MOB kinase protein-coding

chr19-16 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr19 16839631 16843676 + 0 NA intron (Nintron (N 12255 NM\_001297 23309 Hs. 13999 NM\_01526EENSG000002SIN3B SIN3 trar protein-coding

chr19-46 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr19 46732884 46736156 + 0 NA intron (Nintron (N -11537 NM\_00103E 79147 Hs. 51549EENSG000002CFKP LGM2D2|LC fukutin i protein-coding

chr19-47 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr19 47143768 47146531 + 0 NA intron (NAluSp|SIN 14314 NM\_00114E 10055 Hs. 51550EENSG000002SAE1 AOS1|HSPC5001 act protein-coding

chr2-55 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr2 55262083 55265020 + 0 NA intron (NAluSg4|SI 5628 NM\_00100E 4528 Hs. 149894NM\_00245EENSG000002MTIF2 -mitochon protein-coding

chr2-69 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr2 69412112 69415178 + 0 NA intron (NAluSz6|SI 23790 NR\_04563E 27247 Hs. 43043EENSG000002CNFU1 CGI-33|HINFU1 iror protein-coding

chr2-69 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr2 69935279 69938099 + 0 NA intron (Nintron (N 21805 NM\_002357 4084 Hs. 46890EENSG000002MXD1 BHLH58|WMAX dimer protein-coding

chr2-22 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr2 2.3E+08 2.3E+08 0 NA intron (Nintron (N -5335 NM\_13907E 92737 Hs. 234074NM\_13907EENSG000002DNER UNQ26|beta/delta/notr protein-coding

chr20-58 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr20 58356786 58357323 + 0 NA intron (NLM3Ea|LI -32065 NM\_00473E 9217 Hs. 18262EENSG000002VAPB ALS8|VAMF VAMP assc protein-coding

chr21-1 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr21 17603594 17604878 + 0 NA exon (NM\_exon (NM\_ -7450 NR\_14907E 1.11E+08 Hs. 60713EENSG000002BTG3-AS1 ASBEL BTG3 antncRNA

chr21-32 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr21 32356257 32358780 + 0 NA intron (Nintron (N 677846 Hs. 71229EENSG000002SNORA80 ACA67|SNC small nucsRNA

chr21-36 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr21 36345823 36346196 + 0 NA intron (NAluSx|SIN 25812 NM\_01535E 23515 Hs. 42115CNCM\_01535EENSG000002MORC3 NXP2|ZWE MORC fami protein-coding

chr22-20 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr22 20508633 20587904 + 0 NA 3' UTR (3' UTR (N 79096 NM\_00129E 51586 Hs. 517421NM\_01588EENSG000002MED15 ARC105|CA mediator protein-coding

chr22-38 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr22 38244128 38245856 + 0 NA intron (Nintron (N -20272 NR\_132774 1.07E+08 NR\_132774 SNORA92 -small nucsRNA

chr3-50 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr3 50066344 50072068 + 0 NA intron (Nintron (N -19713 NM\_00577E 10181 Hs. 43948CNCM\_00577EENSG000002RBM5 G15|H37|RNA bindi protein-coding

chr3-56 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr3 56567275 56570040 + 0 NA intron (Nintron (N 11482 NM\_001141 285331 Hs. 47639EENSG000002CCDC66 -coiled-cc protein-coding

chr3-56 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr3 56664300 56666527 + 0 NA intron (NAluSx|SIN -1367 NM\_015224 23272 Hs. 116877NM\_015224ENSG000002TASOR C3orf63|F transcrip protein-coding

chr3-12 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr3 1.24E+08 1.24E+08 0 NA intron (NLM3Ei|LI 42198 NM\_05302E 4638 Hs. 47737EENSG000002MYLK AAT7|KRP|myosin I protein-coding

chr4-76 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr4 75652592 75658634 + 0 NA intron (Nintron (N 17546 NM\_012297 9908 Hs. 30367EENSG000002G3BP2 -G3BP stre protein-coding

chr5-44 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr5 45247 460441 + 0 NA intron (Nintron (N 14168 NM\_007277 11336 Hs. 481464NM\_007277ENSG000002EXOC3 SEC6|SEC6 exocyst c protein-coding

chr5-34 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr5 34701194 34702848 + 0 NA intron (NAluS2|SI 14462 NM\_00114E 26064 Hs. 43140CNCM\_015577ENSG000002CRAI14 NORPEG|R|retinoic protein-coding

chr5-34 7.665583 0.135328 0.833797 0.162304 0.871067 0.981636 chr5

chr2-2195 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr2	2.2E+08	2.2E+08	+	0 NA	intron (Nintron (N	2270 NM_00119E	79586 Hs. 516711NM_02453E	ENSG00000CHPF	CHSY2 CSS chondroitinprotein-coding	
chr21-466 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr21	46538904	46540315	+	0 NA	intron (Nintron (N	65473 NM_006272	6285 Hs. 422181NM_006272	ENSG00000S100B	NEF S100 S100 calcprotein-coding	
chr4-8305 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr4	83057107	83060083	+	0 NA	intron (Nintron (N	23412 NM_00133C	51138 Hs. 190384NM_01612E	ENSG00000COPS4	CSN4 SGN4COP9 sigrprotein-coding	
chr4-8804 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr4	88041151	88044309	+	0 NA	intron (Nintron (N	35095 NR_156488	5311 Hs. 181272NM_000297	ENSG00000PKD2	APPD2 PC2 polycystinprotein-coding	
chr5-1347 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr5	135E+08	1.35E+08	+	0 NA	intron (Nintron (N	17110 NM_01482E	9879 Hs. 406549NM_01482E	ENSG00000DDX46	PRPF5 Prp DEAD-box protein-coding	
chr5-1771 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (Nintron (N	35433 NM_00136E	64324 Hs. 106861NM_02245E	ENSG00000CNSD1	ARA267 Kv nuclear rprotein-coding	
chr5-1775 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr5	1.78E+08	1.78E+08	+	0 NA	exon (NM exon (NM	-2602 NM_00130E	79930 Hs. 720849NM_02487E	ENSG00000DOK3	DOKL docking rprotein-coding	
chr7-2484 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr7	24848924	24851299	+	0 NA	intron (Nintron (N	42510 NR_104111	26031 Hs. 52025E	ENSG00000OSBPL3	ORP-3 ORF oxysterolprotein-coding	
chr7-7457 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr7	74532813	74533570	+	0 NA	intron (Nintron (N	-62777 NR_16211E	1.13E+08	NR_162116	MIR10525	- microRNA ncRNA
chr9-1333 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chr9	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	3795 NM_00136E	6837 Hs. 78354 NM_00675E	ENSG00000MED22	MED24 SRE mediator protein-coding	
chrX-2721 7.153279	0.139296	0.862118	0.161574	0.871641	0.981636	chrX	2721597	2725016	+	0 NA	intron (Nintron (N	-28746 NM_001141	7499 Hs. 17967E	ENSG00000CXG	PBDX Xg glycof protein-coding	
chr20-277 30.07905	0.075375	0.466776	0.161479	0.871716	0.981636	chr20	27790199	27790448	+	0 NA	IntergeniALR/Alpha	812342 NR_13231E	1E+08	Hs. 529357NR_13231E	ENSG00000FRG1CP	- FSHD regipseudo
chr15-566 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr15	56698504	56698904	+	0 NA	3' UTR (N3' UTR (N	35382 NM_00128E	54816 Hs. 511477NM_01766E	ENSG00000ZNF280D	SUHW4 ZNF zinc fingprotein-coding	
chr15-812 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr15	81286184	81286888	+	0 NA	intron (Nintron (N	-10434 NM_00451E	3603 Hs. 45909E	ENSG00000LL16	LHF NLL1E interleukprotein-coding	
chr16-821 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr16	82155144	82155843	+	0 NA	intron (Nintron (N	14731 NM_00579E	10200 Hs. 34440C	ENSG00000MPHOSPH6	MPP MPP-epsilon-phase rprotein-coding	
chr17-345 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr17	34989457	34990385	+	0 NA	intron (Nintron (N	9409 NM_01397E	3980 Hs. 10029E	ENSG00000LIG3	LIG2 LIG2 DNA ligasprotein-coding	
chr2-739 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr2	73947071	73948941	+	0 NA	intron (Nintron (N	21126 NR_13489E	1716 Hs. 469022NM_00192E	ENSG00000CDGUOK	MTDPS3 NC deoxyguarprotein-coding	
chr2-2034 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr2	2.03E+08	2.03E+08	+	0 NA	intron (Nintron (N	70421 NM_001114	65065 Hs. 64884E	ENSG00000NEAL1	A530083 C neurobeacprotein-coding	
chr21-29C 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr21	29030845	29032544	+	0 NA	intron (Nintron (N	7026 NM_006447	10600 Hs. 99819	ENSG00000USP16	UBP-M UBF ubiquitir protein-coding	
chr7-9892 8.407968	-0.12999	0.805783	-0.16133	0.871836	0.981636	chr7	98926812	98932894	+	0 NA	intron (Nintron (N	48156 NR_132754	1.07E+08	NR_132754	SCARNA28	ZL1 small Ca_ncRNA
chr1-2442 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	24421525	24422325	+	0 NA	intron (Nintron (N	5900 NM_00132E	57185 Hs. 52344E	ENSG00000NIPAL3	DJ462023. NIPA likeprotein-coding	
chr1-2865 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	28697420	28698263	+	0 NA	intron (Nintron (N	29057 NM_00658E	10691 Hs. 63237E	ENSG00000GMEB1	P96P P Pligluocortprotein-coding	
chr1-2876 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	28769245	28770516	+	0 NA	TTS (NM_C TTS (NM_C	32940 NM_00117E	51441 Hs. 53228E	ENSG00000YTHDF2	CAHL HGRC YTH N6-meprotein-coding	
chr1-5505 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	55093207	55098984	+	0 NA	intron (Nintron (N	55873 NR_110451	255738 Hs. 18844	ENSG00000CPSK9	FH3 HCHO propteiprotein-coding	
chr1-1087 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	13833 NM_00726E	6814 Hs. 53043E	ENSG00000STXP3	MUNC18-3 syntaxin protein-coding	
chr1-1126 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	-25384 NM_00128E	4343 Hs. 514941NM_02096E	ENSG00000MOV10	fSAP113 gMov10 R1Cprotein-coding	
chr1-1128 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	6771 NR_103744	1.01E+08	Hs. 41828E	ENSG00000SLC16A1	- SLC16A1 encRNA
chr1-2241 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr1	2.24E+08	2.24E+08	+	0 NA	TTS (NM_C TTS (NM_C	10195 NM_001321	8560 Hs. 29987E	ENSG00000DEGS1	DEGS DEGS delta 4-cprotein-coding	
chr10-69C 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr10	69015668	69017497	+	0 NA	3' UTR (N3' UTR (N	27779 NM_015634	26128 Hs. 27958C	ENSG00000KIF1BP	KBPI KIAA1K1F1 bicnprotein-coding	
chr11-467 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr11	46785522	46792168	+	0 NA	intron (Nintron (N	-26346 NR_00305E	692108 Hs. 69325E	ENSG00000SNORD67	HBB1 HBB1 small nucsnRNA	
chr11-118 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr11	1.19E+08	1.19E+08	+	0 NA	exon (NM exon (NM	-23731 NM_00134E	143941 Hs. 65344E	ENSG00000TTC36	HBP21 tetratricprotein-coding	
chr12-275 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr12	2798444	2800479	+	0 NA	intron (Nintron (N	4491 NM_002014	2288 Hs. 52418E	ENSG00000PKBP4	FKBP51 FKBP proprotein-coding	
chr12-962 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr12	96296609	96297482	+	0 NA	intron (Nintron (N	41547 NM_00130E	2004 Hs. 46523	ENSG00000ELK3	ERP NET SETS transprotein-coding	
chr14-965 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr14	96556014	96559310	+	0 NA	intron (Nintron (N	54797 NM_00129E	10914 Hs. 25372E	ENSG00000PAPOLA	PAP PAP-epsilon (A) rprotein-coding	
chr2-2767 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr2	27675563	27679504	+	0 NA	intron (Nintron (N	-13693 NR_00128E	9913 Hs. 6232	ENSG00000SUTP7L	SPT7L STA7 SPT7 likeprotein-coding	
chr22-494 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr22	49819671	49824001	+	0 NA	intron (Nintron (N	2495 NR_146334	23774 Hs. 12795C	ENSG00000BRD1	BRL BRPF1 bromodome protein-coding	
chr3-172 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr3	1.72E+08	1.72E+08	+	0 NA	intron (Nintron (N	123242 NM_00412E	2693 Hs. 13021E	ENSG00000GHSR	GHPD growth hcprotein-coding	
chr4-8674 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr4	86769885	86770695	+	0 NA	intron (Nintron (N	79139 NM_19796E	345274 Hs. 45299E	ENSG00000SLC10A6	SOAT solute cprotein-coding	
chr5-2734 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr5	273410	273410	+	0 NA	intron (Nintron (N	2656 NM_00126E	10016 Hs. 50823	ENSG00000PDCD6	ALG-2 ALC programme protein-coding	
chr5-134 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr5	1.34E+08	1.34E+08	+	0 NA	IntergeniAluJb SIN	18326 NM_08065E	91368 Hs. 15650E	ENSG00000CDKN2A1P	C2A1L CDKN2A irprotein-coding	
chr7-7458 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr7	74589793	74593175	+	0 NA	intron (Nintron (N	-4484 NR_16211E	1.13E+08	NR_162116	MIR10525	- microRNA ncRNA
chr8-2215 8.649051	0.127073	0.787748	0.161312	0.871848	0.981636	chr8	22194937	22195922	+	0 NA	intron (Nintron (N	30057 NR_03340E	649 Hs. 1274	ENSG00000BMP1	O113 PCOI bone morrprotein-coding	
chr12-575 8.121031	0.133575	0.828097	0.161303	0.871855	0.981636	chr12	57539571	57539770	+	0 NA	intron (Nintron (N	7189 NM_00134E	10540 Hs. 28912E	ENSG00000DCTN2	DCTN50 Dydyactin protein-coding	
chr20-344 8.121031	0.133575	0.828097	0.161303	0.871855	0.981636	chr20	34473226	34473649	+	0 NA	intron (Nintron (N	7112 NR_030374	693229	NR_030374	ENSG00000MIR644A	MIR644 MimicroRNA ncRNA
chr20-35C 8.121031	0.133575	0.828097	0.161303	0.871855	0.981636	chr20	35088910	35089897	+	0 NA	intron (Nintron (N	3568 NM_01563E	26133 Hs. 16807E	ENSG00000TRPC4P	C20orf18E transientprotein-coding	
chr1-5206 12.63192	0.107188	0.664663	0.161267	0.871883	0.981636	chr1	52060313	52061564	+	0 NA	intron (Nintron (N	4643 NM_15226E	91408 Hs. 42983E	ENSG00000BTF3L4	- basic trprotein-coding	
chr1-1542 12.63192	0.107188	0.664663	0.161267	0.871883	0.981636	chr1	1.54E+08	1.54E+08	+	0 NA	intron (Nintron (N	-2145 NM_001127	9898 Hs. 490551NM_01484E	ENSG00000UBAP2L	NICE-4 N ubiquitir protein-coding	
chr1-1815 11.64845	0.11087	0.68771	0.161216	0.871923	0.981636	chr1	185212	187667	+	0 NA	IntergeniIntergeni	1519 NR_10706E	1.02E+08	NR_10706E	ENSG00000MIR6859	- hsa-mir-epsilon microRNA ncRNA
chr1-1951 11.64845	0.11087	0.68771	0.161216	0.871923	0.981636	chr1	19195674	19201301	+	0 NA	intron (Nintron (N	11779 NM_02076E	23352 Hs. 14807E	ENSG00000UBR4	RBAF600 u ubiquitir protein-coding	
chr15-758 8.861566	-0.12723	0.789898	-0.16107	0.87204	0.981636	chr15	75869515	75870109	+	0 NA	intron (Nintron (N	25768 NM_00114E	92912 Hs. 23033	ENSG00000UBE2Q2	- ubiquitir protein-coding	
chr15-795 8.128889	0.131789	0.818415	0.16103	0.87207	0.981636	chr15	79316180	79316826	+	0 NA	intron (Nintron (N	5391 NM_001301	23423 Hs. 71608	ENSG00000TMED3	C15orf22 transment protein-coding	
chr16-46C 8.128889	0.131789	0.818415	0.16103	0.87207	0.981636	chr16	46970382	46971333	+	0 NA	intron (Nintron (N	2817 NM_00588C	10294 Hs. 3			



chr4-1435	8.40011	-0.12831	0.800769	-0.16023	0.872697	0.981636	chr4	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	-9299 NR_003675	441046 Hs. 135705NM_001011	ENSG000004GUSBP5	GYPELOC44GUSB	pseudogene	
chr5-373C	8.40011	-0.12831	0.800769	-0.16023	0.872697	0.981636	chr5	37304932	37305796	+	0	NA	intron (NAluJo SIN	-55936 NM_023073	65250 Hs. 586199NM_023073	ENSG000004CLANE1	C5orf42 Fci	lignone protein-coding	
chr5-7147	8.40011	-0.12831	0.800769	-0.16023	0.872697	0.981636	chr5	71470368	71472725	+	0	NA	intron (Nintron (N	15895 NM_018425	55814 Hs. 258272NM_018425	ENSG000004BDP1	DFNB112 FB	double protein-coding	
chr5-1384	8.40011	-0.12831	0.800769	-0.16023	0.872697	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (NAluSg4 SI	-5910 NR_073445	51308 Hs. 416099NM_016605	ENSG000004REEP2	C5orf19 Sreceptor	protein-coding	
chr9-980C	8.40011	-0.12831	0.800769	-0.16023	0.872697	0.981636	chr9	98005090	98006059	+	0	NA	intron (Nintron (N	22233 NM_006401	51401 Hs. 730654NM_006401	ENSG000004ANP32B	A5orf11 PHA	acidic protein-coding	
chr1-1662	12.16862	0.108381	0.676628	0.160178	0.872741	0.981636	chr1	16626214	16626792	+	0	NA	intron (Nintron (N	4403 NR_026752	84809 Hs. 631865NR_026752	ENSG000004CROCCP2	CROCC1	CROCC	pseudogene
chr9-1266	8.812569	-0.128	0.799703	-0.16006	0.872833	0.981636	chr9	1.27E+08	1.27E+08	+	0	NA	intron (NMIRb SINE	3582 NM_001099	403341 Hs. 177633NM_023482	ENSG000004ZBTB34	ZNF178	zinc finger protein-coding	
chr1-3895	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr1	38998558	39007620	+	0	NA	intron (Nintron (N	11813 NM_024595	79647 Hs. 293565NM_024595	ENSG000004AKIRIN1	C9orf108 akirin	1 protein-coding	
chr1-4025	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr1	40259801	40263425	+	0	NA	intron (Nl2c LINE	3377 NM_005857	10269 Hs. 132642NM_005857	ENSG000004ZMPSTE24	FACE-1 FA	zinc metal protein-coding	
chr1-1095	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (Nl1MA9 LIN	-25811 NM_001266	343263 Hs. 443402NM_001010	ENSG000004MYBPHL	-	myosin b protein-coding	
chr10-286	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr10	28614790	28620176	+	0	NA	intron (Nintron (N	-60038 NM_012342	25805 Hs. 533336NM_012342	ENSG000004BAMBI	NMA	BMP and epsilon protein-coding	
chr10-101	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	exon (NM exon (NM	-15566 NM_006993	10360 Hs. 90691 NM_006993	ENSG000004NPM3	PORMIN T	nucleoph protein-coding	
chr11-344	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr11	34460752	34470103	+	0	NA	intron (Nintron (N	26493 NM_001752	847 Hs. 502302NM_001752	ENSG000004CAT	-	catalase protein-coding	
chr11-105	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr11	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	5091 NM_001223	834 Hs. 2490 NM_001223	ENSG000004CASP1	ICE IL1B	caspase 1 protein-coding	
chr14-497	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr14	49778296	49786646	+	0	NA	3' UTR (N3' UTR (N	14318 NM_014315	23588 Hs. 509264NM_014315	ENSG000004KLHDC2	HCLP1 H	cellular protein-coding	
chr14-885	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr14	88571558	88580249	+	0	NA	exon (NM exon (NM	12556 NM_001322	79882 Hs. 684046NM_024824	ENSG000004ZC3H14	MRT56 MSU	zinc finger protein-coding	
chr14-105	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	intron (Nintron (N	39246 NM_001100	7517 Hs. 592322NM_005432	ENSG000004XRCC3	CM66	X-ray receptor protein-coding	
chr16-275	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr16	27523952	27529105	+	0	NA	intron (NHAL LINE	23385 NM_001520	2975 Hs. 371718NM_001520	ENSG000004GTF3C1	TF111C TF	general protein-coding	
chr17-161	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr17	16069288	16072419	+	0	NA	intron (NAluSg2 SI	71029 NM_017775	54902 Hs. 462316NM_017775	ENSG000004TTC19	201020401	tetralytic protein-coding	
chr17-425	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr17	42959428	42962149	+	0	NA	intron (Nl2a LINE	3666 NM_001261	80755 Hs. 317403NM_001261	ENSG000004AARSD1	-	alanine-t protein-coding	
chr17-554	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr17	55406022	55414359	+	0	NA	intron (NMIRa SINE	11645 NM_012325	23531 Hs. 463483NM_012325	ENSG000004MMD	MMA MMD1	monocyte protein-coding	
chr17-805	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr17	80341345	80346157	+	0	NA	intron (Nintron (N	-71416 NR_148041	284131 Hs. 389678NM_173627	ENSG000004ENDOV	-	endonucle protein-coding	
chr17-805	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr17	80385161	80391050	+	0	NA	intron (NAluY SINE	-27062 NR_148041	284131 Hs. 389678NM_173627	ENSG000004ENDOV	-	endonucle protein-coding	
chr19-443	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr19	44327957	44339645	+	0	NA	intron (NMSTA LTR	22879 NM_001083	7771 Hs. 48589 NM_013380	ENSG000004ZNF112	ZFP112 Z	zinc finger protein-coding	
chr2-6933	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr2	69333549	69340006	+	0	NA	intron (NAluJo SIN	50450 NM_002056	2673 Hs. 580300NM_002056	ENSG000004GFP1	CMS12 CMS	glutamine protein-coding	
chr2-1602	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr2	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	-4399 NR_103775	1.01E+08 Hs. 729532NR_103775	ENSG000004LINC02478	-	long intencRNA	
chr3-584C	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr3	58405023	58412083	+	0	NA	intron (Nintron (N	24994 NM_000925	5162 Hs. 511357NM_000925	ENSG000004PDHB	PDHBD PD	pyruvate protein-coding	
chr5-5528	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr5	55285275	55298948	+	0	NA	intron (Nl1MB3 LIN	15583 NM_001345	54505 Hs. 593266NM_019030	ENSG000004DHX29	DDX29	DEXH-box protein-coding	
chr5-1341	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr5	1.34E+08	1.34E+08	+	0	NA	intron (NFLAM_C SI	-21973 NM_006930	6500 Hs. 171625NM_006930	ENSG000004SKP1	EMC19 OC	S-phase h protein-coding	
chr6-3284	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr6	32846555	32851612	+	0	NA	exon (NM exon (NM	3678 NM_001292	6890 Hs. 352018NM_000593	ENSG000004TAP1	ABC17 ABC	transport protein-coding	
chr7-7547	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr7	75471896	75475614	+	0	NA	intron (NAluYa5 SI	12544 NR_160303	1E+08 Hs. 712563NM_001095	ENSG000004POM121C	POM121-2	POM121	protein-coding
chr8-1411	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (Nl1MB5 LIN	9657 NR_148197	22898 Hs. 18166 NM_014957	ENSG000004DENND3	-	DENN domain protein-coding	
chr9-1215	10.15268	0.117046	0.731398	0.160031	0.872857	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	17851 NM_000177	2934 Hs. 522373NM_000177	ENSG000004CSN	ADF AGEL	gelsoin protein-coding	
chr2-628C	7.954369	-0.13323	0.832618	-0.16001	0.872873	0.981636	chr2	62806492	62807137	+	0	NA	intron (Nl1MCa LIN	99917 NM_001354	23301 Hs. 271667NM_015252	ENSG000004EHPB1	HPC12 NAC	EH domain protein-coding	
chr1-9238	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr1	92388296	92389257	+	0	NA	3' UTR (N3' UTR (N	89701 NM_024813	79871 Hs. 444421NM_024813	ENSG000004RPAP2	Clorf82 F	RNA polymerase protein-coding	
chr10-454	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr10	45926808	45927461	+	0	NA	intron (Nl1ME2z LI	45240 NR_160518	1.14E+08 NR_160518	ENSG000004PARGP1-AC	PARGP1-AC	pseudogene	
chr12-112	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	-36599 NR_106921	1.02E+08 NR_106921	ENSG000004MIR6861	hsa-mir-6	microRNA ncRNA	
chr13-951	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr13	95156753	95160693	+	0	NA	intron (Nintron (N	-51726 NR_145733	1.1E+08 NR_145733	SNORD13G	-	small nucleosRNA	
chr15-598	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr15	59065847	59069811	+	0	NA	intron (Nintron (N	-37267 NR_004701	9133 Hs. 194698NM_004701	ENSG000004CCN2B	Hst17299	cyclin B protein-coding	
chr17-365	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr17	36995683	36998143	+	0	NA	intron (Nintron (N	-36832 NR_036055	1E+08 NR_036055	ENSG000004MIR2909	-	microRNA ncRNA	
chr18-241	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr18	24166496	24167480	+	0	NA	intron (Nintron (N	27504 NM_138644	26256 Hs. 511983NM_012188	ENSG000004CABYR	CABYRa C	calcium h protein-coding	
chr19-395	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr19	39385716	39386567	+	0	NA	exon (NM exon (NM	4965 NM_001256	54623 Hs. 667414NM_019088	ENSG000004PAF1	F23149_1 PAF1	hom protein-coding	
chr2-1696	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr2	1.7E+08	1.7E+08	+	0	NA	intron (NAluSx1 SI	21389 NM_004792	9360 Hs. 470544NM_004792	ENSG000004PPIG	CARS-Cyp	peptidyl protein-coding	
chr21-255	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr21	25591966	25592693	+	0	NA	intron (Nl1MD1 LIN	-9105 NR_024092	282566 Hs. 384588NM_024092	ENSG000004LINC00515	C2orf71	long intencRNA	
chr3-172	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (NTHE1B LTF	201146 NM_001135	64778 Hs. 744888NM_022763	ENSG000004FNDC3B	FAD104 F	fibronectin protein-coding	
chr3-172	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (NmamRTE1 I	159898 NM_004122	2693 Hs. 130212NM_004122	ENSG000004GHSR	GHD1	growth h protein-coding	
chr7-882C	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr7	88207243	88210487	+	0	NA	intron (Nintron (N	-7795 NR_120517	1.03E+08 NR_120517	LOC1027225	-	uncharactercRNA	
chr8-937C	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr8	93703571	93707034	+	0	NA	intron (Nintron (N	4752 NR_156452	137392 Hs. 125033NM_145265	ENSG000004FAM92A	FAM92A1 F	family w protein-coding	
chr8-9988	8.136747	0.130031	0.812875	0.159964	0.872909	0.981636	chr8	99881219	99883222	+	0	NA	intron (Nl1MB2 LIN	11487 NM_004374	1345 Hs. 351875NM_004374	ENSG000004COX6C	-	cytochrome protein-coding	
chr10-285	11.13615	0.112286	0.702051	0.15994	0.872928	0.981636	chr10	28524061	28526025	+	0	NA	intron (Nl1M4 LINE	7311 NR_033805	220906 Hs. 403255NR_033805	WAC-AS1	-	WAC antisenseRNA	
chr16-224	11.13615	0.112286	0.702051	0.15994	0.872928	0.981636	chr16	22472136	22474050	+	0	NA	intron (NAluY SINE	-31356 NR_024455	1E+08 Hs. 648435NR_024455	LOC100190	-	uncharactercRNA	
chr6-1341	12.63978	0.106610	0.662959	0.159911	0.872951														

chr17-602.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr17	60221059	60223493	+	0	NA	intron (Nintron (N	9369 NR_002999	677681	NR_002999	ENSG000003SCARNA20	ACA66	small Ca <sub>v</sub> ncRNA
chr17-695.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr17	69964871	69965801	+	0	NA	intron (NMLT1J1-ir	3629 NR_110875	1.03E+08	Hs.451405NR_110874	ENSG000003LINC01497-		long intencRNA
chr2-2414.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr2	2.41E+08	2.41E+08	+	0	NA	intron (NAluXs1 SI	57519 NM_014805	9855	Hs.726315NM_014805	ENSG000003FARP2	FIR FRG FFERM, ARI	protein-coding
chr6-296.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr6	29609248	29609650	+	0	NA	intron (Nintron (N	18779 NM_021903	2550	Hs.167017NM_001470	ENSG000003GABR1	GABABR1 [Gamma-aminoprotein-coding	
chr6-3744.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr6	37448958	37450808	+	0	NA	intron (N2c LINE	66622 NM_021903	23070	Hs.520102NM_015050	ENSG000003CMTR1	FTSJD2 KI cap methylprotein-coding	
chr8-384.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr8	38427476	38429832	+	0	NA	intron (Nintron (N	39070 NM_001174	2260	Hs.264887NM_015850	ENSG000003FGFR1	BFGFR CD3 fibroblas protein-coding	
chr9-124.8.185745	0.130037	0.816073	0.159344	0.873398	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	exon (NM exon (NM	12879 NM_030978	81873	Hs.132499NM_030978	ENSG000003ARPC5L	ARPC16-2 actin relprotein-coding	
chr1-291.7.946511	-0.13151	0.825324	-0.15934	0.8734	0.981636	chr1	29165810	29166877	+	0	NA	intron (Nintron (N	15557 NM_005626	6429	Hs.469977NM_005626	ENSG000003SRSA4	SFRS4 SRF serine arprotein-coding	
chr12-57.7.946511	-0.13151	0.825324	-0.15934	0.8734	0.981636	chr12	57099277	57100459	+	0	NA	exon (NM exon (NM	10421 NM_001178	6778	Hs.524515NM_003150	ENSG000003STAT6	D12S1644 signal trprotein-coding	
chr14-91.7.946511	-0.13151	0.825324	-0.15934	0.8734	0.981636	chr14	91987099	91988170	+	0	NA	intron (Nintron (N	-39932 NM_006326	10516	Hs.332708NM_006326	ENSG000003FBLN5	ADML2 ARC fibulin 5 protein-coding	
chr4-887.7.946511	-0.13151	0.825324	-0.15934	0.8734	0.981636	chr4	88730831	88731671	+	0	NA	intron (Nintron (N	21462 NR_002806	285512	Hs.744957NR_002806	ENSG000003FAM13A-AS	FAM13A10S FAM13A arncRNA	
chr6-157.7.946511	-0.13151	0.825324	-0.15934	0.8734	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	-53520 NM_003898	8871	Hs.434494NM_003898	ENSG000003SYNJ2	INPP5H synaptoje protein-coding	
chr16-28.11.65631	0.109615	0.687929	0.159341	0.8734	0.981636	chr16	28825487	28836099	+	0	NA	intron (Nintron (N	7745 NM_145714	11273	Hs.460499NM_007245	ENSG000003ATXN2L	A2D AZL2 ataxin 2 protein-coding	
chr19-388.11.65631	0.109615	0.687929	0.159341	0.8734	0.981636	chr19	38835788	38847435	+	0	NA	intron (Nintron (N	8366 NM_001533	3191	Hs.644909NM_001533	ENSG000003HNRNPL	HNRNPL P/Chateroger protein-coding	
chr19-574.11.65631	0.109615	0.687929	0.159341	0.8734	0.981636	chr19	57490485	57494763	+	0	NA	intron (Nintron (N	4874 NM_001098	79744	Hs.744333NM_024691	ENSG000003ZNF419	ZAPHIR Zn zinc fingprotein-coding	
chr3-129.11.65631	0.109615	0.687929	0.159341	0.8734	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (NAluSc SINE	-6094 NR_106884	1.02E+08	NR_106884	ENSG000003MIR6826	hsa-mir-618 microRNA ncRNA	
chr6-107.11.65631	0.109615	0.687929	0.159341	0.8734	0.981636	chr6	1.08E+08	1.08E+08	+	0	NA	intron (NTrigger I	39868 NM_007214	11231	Hs.26904 NM_007214	ENSG000003SEC63	DNAJC23 ESEC63 honprotein-coding	
chr1-5507.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr1	55075781	55075986	+	0	NA	intron (NAluJr SINE	35661 NR_110451	255738	Hs.18844 NM_174930	ENSG000003PCCS9	PH3 HCHOI propteiprotein-coding	
chr13-44.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr13	44999454	45000700	+	0	NA	intron (Nintron (N	10539 NM_018555	55425	Hs.731811NM_018555	ENSG000003GALP1P1	ADQ29 K1A GALP1P mcprotein-coding	
chr16-2.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr16	28377277	28380122	+	0	NA	TTS (NM_C TTS (NM_C	12352 NR_107058	1.02E+08	NR_107058	ENSG000003MIR6862-2	hsa-mir-618 microRNA ncRNA	
chr19-221.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr19	2210283	2211123	+	0	NA	exon (NM exon (NM	23446 NR_031596	1E+08	NR_031596	ENSG000003MIR1227	MIRN1227 microRNA ncRNA	
chr2-6394.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr2	63941205	63942405	+	0	NA	intron (NAluS2 SINE	77623 NM_016516	51542	Hs.48499 NM_016516	ENSG000003VPS54	HCC8 PPP1VPS54 sut protein-coding	
chr4-178.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr4	17802606	17804503	+	0	NA	exon (NM exon (NM	7203 NR_144303	54876	Hs.614787NM_017741	ENSG000003DCAF16	C4orf30 DDB1 and protein-coding	
chr8-569.8.698049	0.127074	0.797655	0.159309	0.873425	0.981636	chr8	56963405	56964266	+	0	NA	exon (NM exon (NM	30032 NM_017812	54928	Hs.438689NM_017812	ENSG000003IMPAD1	GPAPP IMF inositol protein-coding	
chr1-777.8.351112	-0.129	0.81027	-0.1592	0.873511	0.981636	chr1	7778296	7779743	+	0	NA	intron (NAluV SINE	-5168 NM_001288	8863	Hs.162200NM_016831	ENSG000003PER3	FASPS3 G1period ciprotein-coding	
chr16-67.8.351112	-0.129	0.81027	-0.1592	0.873511	0.981636	chr16	67067740	67067975	+	0	NA	intron (NLM4a1 LI	38708 NM_001368	865	Hs.460988NM_001750	ENSG000003CBFB	PEBP2B core-binc protein-coding	
chr16-302.16.1672	0.095729	0.601344	0.159188	0.873521	0.981636	chr16	30252496	30252926	+	0	NA	IntergeniAluXs1 SINE	-4298 NM_001321	613037	Hs.585733NM_001321	ENSG000003NIPB13	- nuclear lprotein-coding	
chr1-218.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr1	21863688	21865505	+	0	NA	intron (NMIRb SINE	52331 NM_001013	401944	Hs.745155NM_001013	ENSG000003LDLRAD2	- low densiprotein-coding	
chr1-316.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr1	31653119	31653500	+	0	NA	intron (NMIRb SINE	-8439 NR_033688	553115	Hs.470417NM_012392	ENSG000003PEP1	ABP32 PEF penta-EF- protein-coding	
chr1-4344.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr1	43443422	43444466	+	0	NA	intron (Nintron (N	-4595 NR_106799	1.02E+08	NR_106799	ENSG000003MIR6735	hsa-mir-618 microRNA ncRNA	
chr1-202.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr1	2.03E+08	2.03E+08	+	0	NA	intron (NFLAM_A SI	-8946 NM_002871	5877	Hs.90875 NM_002871	ENSG000003CRAB1F	MSS4 RASCAB interprotein-coding	
chr10-10.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (Nintron (N	11379 NM_017902	55662	Hs.500788NM_017902	ENSG000003HIF1AN	FIH1 hypoxia iprotein-coding	
chr11-104.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr11	10498194	10500952	+	0	NA	intron (NMIR SINE	8753 NR_039706	1.01E+08	NR_039706	ENSG000003MIR4485	miR-4485 microRNA ncRNA	
chr12-12.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	exon (NM exon (NM	24876 NM_012463	23545	Hs.25786 NM_012463	ENSG000003ATP6VOA2	A2 ARCL ATPase H+protein-coding	
chr16-36.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr16	3685596	3686494	+	0	NA	exon (NM exon (NM	31341 NM_001351	1773	Hs.629638NM_005222	ENSG000003DNASE1	DNL1 DN1 deoxyribc protein-coding	
chr16-48.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr16	4853143	4859661	+	0	NA	intron (Nintron (N	8022 NM_001288	29855	Hs.442061NM_016930	ENSG000003UBN1	UT1 UT4 ubiquitc protein-coding	
chr19-44.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr19	44895357	44898114	+	0	NA	intron (N2b LINE	5481 NM_006114	10452	Hs.655909NM_006114	ENSG000003TOMM40	C19orf1 I transloc protein-coding	
chr2-3831.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr2	38312186	38312798	+	0	NA	intron (NAluXs3 SI	64038 NM_001330	64225	Hs.594959NM_022374	ENSG000003ATL2	ARL3IP2 ATlastin protein-coding	
chr21-39.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr21	39239585	39240433	+	0	NA	intron (NLM1C1 LI	-56495 NM_203433	8624	Hs.473838NM_003720	ENSG000003PSMG1	C21LRP DS proteason protein-coding	
chr22-467.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr22	46793741	46794094	+	0	NA	intron (Nintron (N	19990 NM_001284	25771	Hs.435044NM_014340	ENSG000003TBC1D22A	C22orf4 E TBC1 dom protein-coding	
chr3-123.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (N3 LINE	66183 NM_053026	4638	Hs.473772NM_005960	ENSG000003MYLK	AAD7 KR myosin l protein-coding	
chr3-17.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (NMLT1D LTF	181614 NM_004122	2693	Hs.130212NM_004122	ENSG000003GHSR	GHTP growth hprotein-coding	
chr4-315.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr4	3153871	3154944	+	0	NA	exon (NM exon (NM	79726 NM_002111	3064	Hs.518455NM_002111	ENSG000003HHT	HD IT15 I huntingtiprotein-coding	
chr5-149.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr5	1.48E+08	1.48E+08	+	0	NA	intron (Nintron (N	41392 NM_030799	81545	Hs.483775NM_030799	ENSG000003FBX038	Fbx38 HMM F-box prcprotein-coding	
chr7-147.7.673441	0.133407	0.838084	0.159181	0.873526	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	intron (N2a LINE	6529 NM_003575	8427	Hs.729056NM_003575	ENSG000003ZNF282	HUB1 zinc fing protein-coding	
chr1-264.8.656909	0.125402	0.787925	0.159155	0.873547	0.981636	chr1	26435737	26448380	+	0	NA	intron (NLM2E2 LI	9737 NM_0205861	79947	Hs.369385NM_024887	ENSG000003DHD5	CIT CPT I dehydrat protein-coding	
chr1-3754.8.656909	0.125402	0.787925	0.159155	0.873547	0.981636	chr1	37546208	37548961	+	0	NA	intron (NAluS2 SINE	6709 NM_024700	79753	Hs.47232 NM_024700	ENSG000003SNIP1	AB1 PMRE Smad nucl protein-coding	
chr1-144.8.656909	0.125402	0.787925	0.159155	0.873547	0.981636	chr1	1.44E+08	1.44E+08	+	0	NA	in						



chr16-466 9.640377	0.119022	0.749286	0.158848	0.873789	0.981636	chr16	46670489	46672534	+	0 NA	intron (AluSx3 SI	17667 NM_01820E	55737 Hs. 45452ENM_01820E	ENSG000000VPS35	MEM3 PARFVPS35	retprotein-coding	
chr2-8502 9.640377	0.119022	0.749286	0.158848	0.873789	0.981636	chr2	85022937	85031154	+	0 NA	intron (AluJb SIN	37802 NR_14645E	1.01E+08 Hs. 43439ENR_14645E	ENSG000000LINC01964-		long intencRNA	
chr5-1775 9.640377	0.119022	0.749286	0.158848	0.873789	0.981636	chr5	1.78E+08	1.78E+08	+	0 NA	exon (NM_exon (NM	3196 NM_01751C	54732 Hs. 27992ENM_01751C	ENSG000000TMED9	GMP25 HSC	transmem protein-coding	
chr7-9889 9.640377	0.119022	0.749286	0.158848	0.873789	0.981636	chr7	98891083	98894750	+	0 NA	intron (intron (N	11219 NR_132754	1.07E+08	NR_132754	SCARNA28	ZL1	small Ca <sup>2+</sup> cRNA
chr7-9892 9.640377	0.119022	0.749286	0.158848	0.873789	0.981636	chr7	98924902	98926513	+	0 NA	intron (intron (N	44010 NR_132754	1.07E+08	NR_132754	SCARNA28	ZL1	small Ca <sup>2+</sup> cRNA
chr7-1569 9.640377	0.119022	0.749286	0.158848	0.873789	0.981636	chr7	1.57E+08	1.57E+08	+	0 NA	intron (intron (N	4592 NM_13840C	64434 Hs. 15825 NM_13840C	ENSG000000CNOM1	C7orf3 PF	nucleolar protein-coding	
chr10-757 7.616585	0.135201	0.851423	0.158794	0.873831	0.981636	chr10	75026536	75027552	+	0 NA	intron (AluSx SIN	5311 NR_14581E	1.1E+08	NR_14581E	SNORD172		small nucleolar RNA
chr3-5031 7.616585	0.135201	0.851423	0.158794	0.873831	0.981636	chr3	50319410	50319611	+	0 NA	intron (intron (N	3235 NM_00377E	8692 Hs. 76873 NM_00377E	ENSG000000CHVAL2	LUC2A	hyaluronin protein-coding	
chr5-7467 7.616585	0.135201	0.851423	0.158794	0.873831	0.981636	chr5	74634272	74634982	+	0 NA	intron (intron (N	-5396 NM_00129E	3074 Hs. 69293 NM_000521	ENSG000000CHEXB	ENC-1AS F	hexosamin protein-coding	
chr11-183 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr11	18305617	18307031	+	0 NA	exon (NM_exon (NM	15816 NM_00721E	11234 Hs. 43759ENM_00721E	ENSG000000HPS5	A1BP63 BLHPS5	biogprotein-coding	
chr11-837 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr11	83073869	83074710	+	0 NA	TTS (NR_C TTS (NR_C	-2223 NR_03890E	1.01E+08 Hs. 50342ENR_03890E	ENSG000000RAB30-DT	RAB30-AS1 RAB30	divncRNA	
chr12-118 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr12	1.18E+08	1.18E+08	+	0 NA	intron (intron (N	3439 NM_02249I	64426 Hs. 41663CNM_02249I	ENSG000000SUDS3	SAP45 SDS	SDS3 homc protein-coding	
chr13-727 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr13	72791352	72793679	+	0 NA	exon (NM_exon (NM	10382 NR_14620E	10464 Hs. 44192ENM_00634E	ENSG000000PIBF1	C13orf24	progester protein-coding	
chr14-697 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr14	69778417	69779067	+	0 NA	intron (intron (N	-11029 NR_02937E	89932 Hs. 50990ENM_17346E	ENSG000000PAPLN	PPN	papilin, protein-coding	
chr14-731 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr14	73199873	73201748	+	0 NA	intron (AluSx SIN	-36696 NR_15867E	124446 Hs. 460574NM_19428E	ENSG000000TMEM219	IGFBP-3R	transmem protein-coding	
chr16-296 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr16	29663951	29666124	+	0 NA	intron (intron (N	2958 NR_16146E	786 Hs. 14798ENM_000727	ENSG000000CACNG1	CACNG1	calcium v protein-coding	
chr17-671 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr17	67121594	67124005	+	0 NA	intron (intron (N	78245 NM_000727	91768 Hs. 11108 NM_13837E	ENSG000000CABLES1	CABL CAF	Cdk5 and protein-coding	
chr18-231 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr18	23189150	23191414	+	0 NA	intron (intron (N	34457 NM_13837E	51341 Hs. 591384NM_01589E	ENSG000000ZBTB7A	FBI-1 FBI	zinc fing protein-coding	
chr19-408 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr19	4089269	4092037	+	0 NA	exon (NM_exon (NM	-23754 NM_01589E	5300 Hs. 46584ENM_006221	ENSG000000CPIN1	DOD UBL5	peptidyl r protein-coding	
chr19-987 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr19	9838289	9844267	+	0 NA	intron (intron (N	5960 NR_03883C	5746 Hs. 57029ENM_00504E	ENSG000000PTH2R	PTH2R	parathyrc protein-coding	
chr2-2087 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr2	2.08E+08	2.08E+08	+	0 NA	intron (intron (N	-12580 NR_00130E	1841 Hs. 47187ENM_01214E	ENSG000000DTYMK	CDC8 PP37	deoxythyn protein-coding	
chr2-2416 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr2	2.42E+08	2.42E+08	+	0 NA	intron (intron (N	16923 NR_03325E	257203 Hs. 50515ENM_14867E	ENSG000000DSCR9	NCRNA000E Down	syncncRNA	
chr21-372 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr21	37236774	37237762	+	0 NA	intron (intron (N	28765 NR_02671E	55254 Hs. 594171NM_01826E	ENSG000000TMEM39A		transmem protein-coding	
chr3-1194 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr3	1.19E+08	1.19E+08	+	0 NA	intron (Tigger1 I	20379 NR_07350E	84162 Hs. 408142NM_01531E	ENSG000000K1AA1109	ALKKUCS FK1AA1109	protein-coding	
chr4-1222 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (intron (N	49602 NM_01531E	-18094 NM_00100E	387082 Hs. 65716ENM_00100E	ENSG000000SUMO4	IDDM5 SM1	small ubi protein-coding
chr6-1452 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr6	1.49E+08	1.49E+08	+	0 NA	intron (NL2 LINE I	24807 NM_01602C	51106 Hs. 27990ENM_01602C	ENSG000000TFB1M	CG1-75 C1	transri protein-coding	
chr6-1557 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr6	1.58E+08	1.58E+08	+	0 NA	intron (intron (N	-59379 NM_00389E	8871 Hs. 434494NM_00389E	ENSG000000SVN12	INPP5H	synaptoe protein-coding	
chr7-1027 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr7	1.03E+08	1.03E+08	+	0 NA	5' UTR (N5' UTR (N	678 NM_00136E	1.08E+08	NM_00136E	ENSG000000UPK3BL2		uroplakin protein-coding
chr9-9547 7.161137	0.137252	0.864534	0.158759	0.873859	0.981636	chr9	95471693	95474025	+	0 NA	intron (intron (N	9250 NR_03898E	1.01E+08 Hs. 661847NR_03898E	LOC100507-		uncharactercRNA	
chr9-1518 5.153061	0.162555	1.024678	0.158664	0.873953	0.981636	chr9	15187063	15187390	+	0 NA	intron (intron (N	62992 NM_00116E	158219 Hs. 56363CNM_152574	ENSG000000TTC39B	C9orf52	tetratric protein-coding	
chr14-361 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr14	36115059	36116435	+	0 NA	exon (NM_exon (NM	17756 NM_00119E	23405 Hs. 87889 NM_030621	ENSG000000DICER1	DCR1 Dicer	dicer 1, protein-coding	
chr16-956 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr16	9561629	95616303	+	0 NA	intron (intron (N	7642 NM_001351	1773 Hs. 62963ENM_00522E	ENSG000000DNASE1	DNL1 DRNI	deoxyribc protein-coding	
chr16-745 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr16	74923056	74924029	+	0 NA	intron (AluSx SIN	61581 NM_030581	79726 Hs. 280951NM_030581	ENSG000000WDR59	CDW12 FP	WD repeat protein-coding	
chr2-2508 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr2	95089418	95091312	+	0 NA	intron (intron (N	31192 NM_001321	64969 Hs. 65525ENM_03190E	ENSG000000MRP55	MRP-55 SM	mitochonc protein-coding	
chr5-1297 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr5	1.3E+08	1.3E+08	+	0 NA	intron (LTR9D LTF	-23216 NM_001257	1E+08 Hs. 582534NM_001257	ENSG000000MINAR2	K1AA1024I	membrane protein-coding	
chr7-743 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr7	74339037	74340295	+	0 NA	intron (MIR SINE	50191 NM_00338E	7461 Hs. 64701ENM_00338E	ENSG000000CLIP2	CLIP CLIF	CAP-Gly c protein-coding	
chr7-100 6.689972	0.143678	0.905869	0.158608	0.873978	0.981636	chr7	1E+08	1E+08	+	0 NA	promoter-promoter-	-336 NR_10689E	1.02E+08	NR_10689E	ENSG000000MIR6840	hsa-mir-6	microRNA ncRNA
chr15-784 12.1248	0.107107	0.6755	0.15856	0.874015	0.981636	chr15	78488341	78489227	+	0 NA	intron (intron (N	-18780 NM_00108E	123688 Hs. 307962NM_00101E	ENSG000000CHVKK	AGPHD1	hydroxyl protein-coding	
chr1-6596 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr1	6596885	6599362	+	0 NA	intron (intron (N	4746 NM_001324	9903 Hs. 7764 NM_014851	ENSG000000KHLH21		kelch lik protein-coding	
chr1-6666 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr1	66663457	66667811	+	0 NA	intron (L1P6 LIN	37644 NR_03606E	1E+08	NR_03606E	ENSG000000MIR3117	mir-3117	microRNA ncRNA
chr1-1097 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr1	1.1E+08	1.1E+08	+	0 NA	intron (intron (N	-6626 NR_02958E	406974	NR_02958E	ENSG000000MIR197	MIRN197	microRNA ncRNA
chr10-151 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr10	15102180	15106098	+	0 NA	exon (NM_exon (NM	6784 NM_006414	10557 Hs. 94986 NM_006414	ENSG000000CRPP38		ribonucle protein-coding	
chr10-688 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr10	68944456	68945836	+	0 NA	intron (L1M5 LINE	-10980 NM_00472E	9188 Hs. 223141NM_00472E	ENSG000000DDX21	GUA GDF	DEXd-box protein-coding	
chr11-115 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr11	1.19E+08	1.19E+08	+	0 NA	intron (intron (N	2977 NM_001311	7070 Hs. 644697NM_00628E	ENSG000000ETHY1	CD90 CDw	Thy-1 cel protein-coding	
chr11-128 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr11	1.29E+08	1.29E+08	+	0 NA	intron (intron (N	9339 NM_00523E	2113 Hs. 36943ENM_00523E	ENSG000000ETS1	ETS-1 EWS	ETS protc protein-coding	
chr12-144 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr12	14433953	14438785	+	0 NA	intron (intron (N	52088 NM_18135E	55729 Hs. 50485ENM_01817E	ENSG000000ATF7IP	AM ATF	-1	inactivatir protein-coding
chr13-514 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr13	51455702	51456214	+	0 NA	IntergenimER52A LI	2613 NR_10381E	1.01E+08 Hs. 594897NR_10381E	ENSG000000INTS6-AS1-	INTS6	antncRNA	
chr13-112 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr13	1.13E+08	1.13E+08	+	0 NA	intron (intron (N	-103363 NR_046661E	1.01E+08 Hs. 65869ENR_046661	ENSG000000ATP11A-AC-	ATP11A	arcncRNA	
chr14-311 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr14	31139166	31141782	+	0 NA	intron (in FAM SINE	67319 NM_01538E	25831 Hs. 708017NM_01538E	ENSG000000HECTD1	EULIR	HECT domc protein-coding	
chr14-677 8.392252	-0.12667	0.799004	-0.15853	0.874037	0.981636	chr14</											

chr9-3395	8.144605	0.12827	0.81117	0.158129	0.874355	0.981636	chr9	33932202	33934306	+	0	NA	intron (intron (N	1110	NM_001282	55833	Hs.49373c	NM_01844c	ENSG00000CUBAP2	UBAP-2	ubiquitin protein-coding
chr16-892	12.64764	0.104854	0.663184	0.158106	0.874373	0.981636	chr16	89220449	89234898	+	0	NA	exon (NM exon (NM	9970	NM_182531	197320	Hs.64738f	NM_182531	ENSG00000ZNF778	-	zinc finger protein-coding
chr21-466	12.64764	0.104854	0.663184	0.158106	0.874373	0.981636	chr21	46652315	46656139	+	0	NA	3' UTR (3' UTR (N	18553	NM_206962	3275	Hs.15416e	NM_00153c	ENSG00000PRMT2	HRMT1L1	protein epsilon protein-coding
chr11-618	7.202276	0.139114	0.880144	0.158058	0.874411	0.981636	chr11	61886621	61887273	+	0	NA	intron (intron (N	4598	NM_021727	3995	Hs.21765	NM_021727	ENSG00000FADS3	CYB5RF1	l fatty acyl protein-coding
chr16-265	7.202276	0.139114	0.880144	0.158058	0.874411	0.981636	chr16	2696189	26983221	+	0	NA	intron (intron (N	14732	NM_018992	54442	Hs.61960	NM_01899c	ENSG00000KCTD5	-	potassium protein-coding
chr15-228	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr15	22862911	22863532	+	0	NA	intron (AluS6 SI	24580	NM_001008	81614	Hs.59100e	NM_03092c	ENSG00000CNP2A	SLC57A2	NIPA magr protein-coding
chr15-587	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr15	58716613	58718331	+	0	NA	intron (intron (N	-23865	NR_07341c	664618	Hs.670224	NR_002927	HSP90AB4	HSP90B4	heat shock pseudo
chr15-785	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr15	78920866	78923366	+	0	NA	3' UTR (3' UTR (N	22982	NM_001319	1512	Hs.148641	NM_00439c	ENSG00000CTSH	ACC-4	ACC theatsir protein-coding
chr16-234	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr16	23480885	23481269	+	0	NA	intron (intron (N	-27888	NM_15360c	91949	Hs.185807	NM_15360c	ENSG00000COG7	CDG2E	component protein-coding
chr19-541	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr19	54186014	54186719	+	0	NA	intron (NL2 LINE L	3214	NM_001146	79143	Hs.46277c	NM_02429c	ENSG00000MBOAT7	BB1	LENG4 membrane protein-coding
chr20-44	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr20	44056632	44058549	+	0	NA	intron (intron (N	111694	NM_001098	84969	Hs.26608	NM_03288c	ENSG00000TOX2	C20orf10C	TOX high protein-coding
chr3-1505	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr3	1.51E+08	1.51E+08	+	0	NA	intron (AluY SINE	15462	NM_03202c	83939	Hs.65578c	NM_03202c	ENSG00000EIF2A	CDA02	EIF eukaryoti protein-coding
chr4-3135	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr4	3135155	3136171	+	0	NA	intron (intron (N	60982	NM_002211	3064	Hs.51845c	NM_002211	ENSG00000HHT	HD IT15	l huntingt protein-coding
chr5-1375	6.648833	0.141651	0.896593	0.157989	0.874466	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (intron (N	-35048	NR_03790c	1E+08	Hs.61662c	NR_03790c	LOC100103c	-	uncharactericnRNA
chr1-8415	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr1	84196623	84198232	+	0	NA	intron (TTTTAT)r	15795	NM_001242	5567	Hs.48732c	NM_002731	ENSG00000PRKACB	PKA C-beta	protein-coding
chr1-159	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr1	1.59E+08	1.59E+08	+	0	NA	intron (intron (N	27488	NM_001206	3428	Hs.38025c	NM_005531	ENSG00000IFI16	IFNGIP1	l interferc protein-coding
chr10-95	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr10	95617793	95623657	+	0	NA	intron (ALIPA6 LIN	35986	NM_00132c	5828	Hs.50064c	NM_00286c	ENSG00000ALDH18A1	ADL3	ALC aldehyde protein-coding
chr10-996	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr10	99610225	99611465	+	0	NA	3' UTR (3' UTR (N	9594	NM_031212	81894	Hs.40379c	NM_031212	ENSG00000SLC25A28	MFRN2	MRS solute epsilon protein-coding
chr10-103	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	exon (NM exon (NM	9940	NM_01591c	51063	Hs.24154c	NM_01591c	ENSG00000CALHM2	FAM26B	calcium I protein-coding
chr11-434	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr11	43460731	43461288	+	0	NA	intron (intron (N	-98647	NR_031577	1E+08	NR_031577	ENSG00000MIR670	hsa-mir-6	microRNA ncRNA	
chr11-636	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr11	63655284	63657586	+	0	NA	intron (NLIMEc LIN	14941	NM_01545c	25923	Hs.35671c	NM_01545c	ENSG00000ATL3	HSN1F	atlastin protein-coding
chr11-111	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (NLIMDa LIN	3655	NM_001352	79796	Hs.74515c	NM_02474c	ENSG00000ALG9	CDGL1	DLIE ALG9 alpl protein-coding
chr12-12	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	exon (NM exon (NM	30391	NR_103517	10198	Hs.577404	NM_02278c	ENSG00000MPHOSPH9	MPP-9	MPPM f protein-coding
chr13-236	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr13	23629216	23629851	+	0	NA	intron (intron (N	50173	NM_018647	55504	Hs.14916c	NM_01864c	ENSG00000TNFRSF19	TAJ1	TAJ-g-TNF receptor protein-coding
chr15-562	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr15	56222984	56223936	+	0	NA	intron (NLIMEF LIN	20419	NM_001368	64864	Hs.74508c	NM_02284c	ENSG00000RFX7	RFXDC2	regulator protein-coding
chr19-417	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr19	41288256	41290481	+	0	NA	intron (intron (N	-20804	NM_05284c	90324	Hs.437497	NM_05284c	ENSG00000CCDC97	-	coiled-co protein-coding
chr2-4328	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr2	43283638	43285041	+	0	NA	intron (NMSTA-int	57128	NR_027251	1E+08	Hs.19448c	NM_17852c	ENSG00000LINC012c	-	long intcncRNA
chr2-714	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr2	71425722	71429229	+	0	NA	intron (intron (N	-26086	NM_00113c	8291	Hs.25218c	NM_00349c	ENSG00000DYSF	FER1L1	lC dysferlin protein-coding
chr2-157	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr2	1.57E+08	1.57E+08	+	0	NA	intron (intron (N	29085	NM_00130c	57471	Hs.443894	NM_020711	ENSG00000ERMN	JN KIAA1	l ermin protein-coding
chr20-564	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr20	56447441	56447766	+	0	NA	intron (NLTR78 LTF	-20982	NM_016407	51507	Hs.517134	NM_016407	ENSG00000RTF2	C20orf43	l replicat protein-coding
chr3-373	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr3	37301345	37303168	+	0	NA	exon (NM exon (NM	-58061	NR_14902c	152048	Hs.59617c	NM_15253c	ENSG00000CLOC15204c	-	uncharactericnRNA
chr3-129	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (AluY SINE	12462	NM_001204	339122	Hs.38113c	NM_19849c	ENSG00000RAB43	RAB11B	l RAB43, mc protein-coding
chr5-138	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr5	13805782	13809076	+	0	NA	intron (intron (N	137051	NM_00136c	1767	Hs.21236c	NM_00136c	ENSG00000DNAH5	CILD3	DNB dynein alpha protein-coding
chr5-709	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr5	70953451	70957507	+	0	NA	Intergeni Intergeni	30538	NM_001297	6606	Hs.53578c	NM_000344	ENSG00000CSMN1	BCD541	lG survival protein-coding
chr6-419	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr6	41912338	41917283	+	0	NA	intron (intron (N	6133	NM_00130c	9477	Hs.278434	NM_00427c	ENSG00000MED20	PRO0213	l mediator protein-coding
chr7-659	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr7	6593595	6596557	+	0	NA	intron (AluJb SIN	5153	NM_00130c	79034	Hs.48751c	NM_024067	ENSG00000C7orf26	-	chromosom protein-coding
chr7-743	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr7	74394024	74397370	+	0	NA	intron (intron (N	-58209	NM_00568c	9569	Hs.64705c	NM_00568c	ENSG00000GTF2IRD1	BEN CREAM	GTF2I ref protein-coding
chr7-989	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr7	98915195	98918150	+	0	NA	intron (intron (N	34975	NR_132754	1.07E+08	NR_132754	SCARNA28	ZL1	small Ca ncRNA	
chr7-140	7.938653	-0.1298	0.821675	-0.15797	0.874478	0.981636	chr7	1.41E+08	1.41E+08	+	0	NA	3' UTR (3' UTR (N	58152	NR_134477	27147	Hs.6385	NM_01568c	ENSG00000DENND2A	FAM31D	l KIDENN dome protein-coding
chr1-1627	10.16054	0.115612	0.732938	0.157738	0.874663	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (intron (N	-30300	NM_001304	51478	Hs.49292c	NM_016371	ENSG00000HSD17B7	PRAP SDR	l hydroxyst protein-coding
chr1-1791	10.16054	0.115612	0.732938	0.157738	0.874663	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	intron (AluX1 SI	29903	NM_0022371	64222	Hs.58495c	NM_022371	ENSG00000TOR3A	ADIR ADIF	l torsin epsilon protein-coding
chr1-2312	10.16054	0.115612	0.732938	0.157738	0.874663	0.981636	chr1	2313	2313E+08	+	0	NA	intron (FLAM_A SI	27313	NM_00131c	8443	Hs.49802c	NM_01423c	ENSG00000GNP47	DAP-AT	lD galacton protein-coding
chr1-2448	10.16054	0.115612	0.732938	0.157738	0.874663	0.981636	chr1	2.45E+08	2.45E+08	+	0	NA	non-codiron-codir	8967	NM_19807c	116228	Hs.41149c	NM_19807c	ENSG00000COX20	FAM36A	cytochron protein-coding
chr10-73	10.16054	0.115612	0.732938	0.157738	0.874663	0.981636	chr10	73386345	73388686	+	0	NA	intron (AluS2 SIN	26543	NM_00115c	310	Hs.63182c	NM_00115c	ENSG00000ANXA7	ANX7 SNX	l amexin I protein-coding
chr10-79	10.16054	0.115612	0.732938	0.157738	0.874663	0.981636	chr10	79349149	79354860	+	0	NA	intron (intron (N	4535	NM_00115c	10105	Hs.38107c	NM_00572c	ENSG00000PPIF	CYP3	CyP-terminal dyll protein-coding
chr11-62	10.16054	0.115612	0.																		



chr16-885.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr16	8895914	8898289	+	0 NA	intron (Nintron (N	-28089 NM_00127E	23589 Hs. 632184NM_01431E	ENSG000002CARHSP1	CRHSP-24 calcium i protein-coding	
chr17-584.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr17	58490546	58495036	+	0 NA	intron (Nintron (N	-4383 NM_00108C	124535 Hs. 380061NM_00108C	ENSG000002HSF5	HSF 5 HSTheat shocprotein-coding	
chr17-671.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr17	67199179	67201436	+	0 NA	intron (Nintron (N	-44469 NR_13639E	1.02E+08 Hs. 569824NR_13639E	LOC10192E-	uncharactncRNA	
chr19-309.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr19	309354685	309369000	+	0 NA	intron (Nintron (N	15333 NM_00130C	55095 Hs. 612332NM_01802E	ENSG000002SAMD4B	SMGB Smausterial e protein-coding	
chr19-505.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr19	50578307	50793568	+	0 NA	intron (Nintron (N	2480 NM_00712C	7376 Hs. 432977NM_00712E	ENSG000002NRIH2	LXR-β LX nuclear i protein-coding	
chr2-227.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr2	2.27E+08	2.27E+08	+	0 NA	intron (Nintron (N	4072 NM_00127E	56947 Hs. 47152E	ENSG000002CMFF	C2orf33 Emi tohnc protein-coding	
chr9-132E.9.177071	0.121237	0.773298	0.156779	0.875419	0.981636	chr9	1.33E+08	1.33E+08	+	0 NA	intron (Nintron (N	21785 NM_00131E	11092 Hs. 62595 NM_01895E	ENSG000002SPACA9	C9orf9 Mesper acir protein-coding	
chr3-985E.6.136529	0.146699	0.935964	0.156735	0.875453	0.981636	chr3	98589778	98590585	+	0 NA	intron (NAluSx SIN	3430 NM_00009E	1371 Hs. 476982NM_00009E	ENSG000002CPOX	COX CPOpropr protein-coding	
chr1-935E.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr1	9356024	9357523	+	0 NA	intron (Nintron (N	63879 NM_02510E	80176 Hs. 8261 NM_02510E	ENSG000002SPSB1	SSB-1 SSE splA/ryar protein-coding	
chr1-201.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (Nintron (N	27522 NR_03170E	1E+08 NR_03170E	ENSG000002MIR664A	MIR664 MI microRNA ncRNA	
chr10-102.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr10	1.03E+08	1.03E+08	+	0 NA	intron (Nintron (N	8434 NM_00117E	51684 Hs. 40408E	ENSG000002SUFU	JBT532 PF/SUFU nege protein-coding	
chr12-57E.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr12	57696328	57697346	+	0 NA	intron (NAlu SINE	2705 NM_00681E	10956 Hs. 527861NM_00681E	ENSG000002COS9	ERLEC2 OSOS9 endor protein-coding	
chr12-131.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr12	1.32E+08	1.32E+08	+	0 NA	exon (NM exon (NM	36729 NM_01540E	57634 Hs. 72347E	ENSG000002EP400	CAGH32 P4E1A bindi protein-coding	
chr15-494.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr15	49429475	49430713	+	0 NA	intron (Nintron (N	6852 NM_02000E	2252 Hs. 56726E	ENSG000002FGF7	HBF7-7 KC fibrob protein-coding	
chr17-53E.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr17	533824	534403	+	0 NA	intron (NAluS6 S1	-88173 NM_18270E	359845 Hs. 34558E	ENSG000002RFLNB	CFM1 FAMIrefilin E protein-coding	
chr18-577.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr18	57741212	57742172	+	0 NA	intron (NMLT1F2 L1	61623 NM_00560E	5205 Hs. 21662E	ENSG000002ATP8B1	ATP1C BR1ATPase p protein-coding	
chr2-206E.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr2	2.06E+08	2.06E+08	+	0 NA	intron (Nintron (N	7464 NM_00119E	4719 Hs. 471207NM_00500E	ENSG000002NDUFS1	CT-75kd CNADH: X protein-coding	
chr5-168E.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr5	16859461	16860256	+	0 NA	intron (Nintron (N	76430 NM_01233A	4651 Hs. 48172E	ENSG000002MYO10	- myosin X protein-coding	
chr5-154E.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr5	1.55E+08	1.55E+08	+	0 NA	intron (Nintron (N	6900 NM_01546E	25929 Hs. 483921NM_01546E	ENSG000002GEMIN5	GEMIN-5 gem nucle protein-coding	
chr7-9951.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr7	99511775	99513625	+	0 NA	intron (Nintron (N	6695 NM_00131E	23660 Hs. 11083E	ENSG000002ZKSCAN5	ZFP-95 Zf zinc fing protein-coding	
chr7-1041.7.632301	0.13149	0.838974	0.156727	0.87546	0.981636	chr7	91489452	91489756	+	0 NA	intron (NLP1A8 LIN	29720 NM_00255E	5001 Hs. 43294E	ENSG000002ORC5	ORC5L ORC origin r protein-coding	
chr15-39E.14.11013	0.098936	0.631322	0.156712	0.875472	0.981636	chr15	39581184	39594452	+	0 NA	intron (NMR SINE	6739 NM_00324E	7057 Hs. 16422E	ENSG000002THBS1	THBS THBS thrombos protein-coding	
chr9-723E.14.11013	0.098936	0.631322	0.156712	0.875472	0.981636	chr9	72354268	72364308	+	0 NA	intron (Nintron (N	5268 NM_00127E	7763 Hs. 40609E	ENSG000002ZFAND5	ZA20D2 Zf zinc fing protein-coding	
chr14-914.8.309973	-0.13163	0.840001	-0.15671	0.875475	0.981636	chr14	91489452	91489756	+	0 NA	intron (Nintron (N	20100 NM_00136E	55671 Hs. 53388E	ENSG000002PPP4R3A	FLFL1 K1 protein i protein-coding	
chr12-194.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr12	1940371	1941743	+	0 NA	TTS (NR TTS (NR_1	-4481 NR_03654E	1E+08 Hs. 737031NR_03654E	ENSG000002LINC0094C-	long intencRNA	
chr12-71E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr12	71859382	78160161	+	0 NA	intron (Nintron (N	199775 NR_135021	1.05E+08 Hs. 15689E	NR_135021	ENSG000002LINC0242A-	long intencRNA
chr12-118.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr12	1.81E+08	1.81E+08	+	0 NA	intron (NLC2 LINE	21905 NM_00256E	5037 Hs. 43386E	ENSG000002PEBP1	HCNP HCNF phosphat i protein-coding	
chr17-64E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr17	64514006	64514689	+	0 NA	non-codir non-codir	7370 NR_13364A	90799 Hs. 56971E	ENSG000002CEP95	CCDC45 centroson protein-coding	
chr18-18E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr18	186200	186465	+	0 NA	intron (NAluJr SIN	27775 NM_005151	9097 Hs. 46441E	ENSG000002USP14	TGT ubiquitir protein-coding	
chr21-46E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr21	46241200	46241874	+	0 NA	non-codir non-codir	12006 NR_11056E	114044 Hs. 65509E	NR_00277E	ENSG000002MCM3AP-AS	TCORF85 MCM3AP arncRNA
chr5-1284.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr5	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	116722 NM_00199E	2201 Hs. 51929E	ENSG000002FBN2	CCA DA9 E fibrillir protein-coding	
chr7-724E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr7	74341883	74342112	+	0 NA	intron (Nintron (N	52522 NM_00338E	7461 Hs. 64701E	ENSG000002CLIP2	CLIP CLIF CAP-Gly c protein-coding	
chr7-129E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr7	1.3E+08	1.3E+08	+	0 NA	intron (NLM1Eg LIN	28000 NM_00104C	4899 Hs. 65436E	ENSG000002NRF1	ALPHA-PAL nuclear i protein-coding	
chr7-140E.7.436057	-0.13392	0.855576	-0.15653	0.875614	0.981636	chr7	1.41E+08	1.41E+08	+	0 NA	intron (Nintron (N	56504 NR_13447E	27147 Hs. 6385 NM_01568E	ENSG000002DENND2A	FAM31D KIDENN dom e protein-coding	
chr8-666E.10.11154	0.115547	0.738289	0.156506	0.875634	0.981636	chr8	66634272	66635294	+	0 NA	exon (NM exon (NM	-21565 NM_00129A	4603 Hs. 44589E	ENSG000002MYBL1	A-MYB AMY MYB prot protein-coding	
chr15-281.8.894848	-0.12352	0.789663	-0.15642	0.8757	0.981636	chr15	28160045	28160330	+	0 NA	intron (NLP1A5 LIN	-60872 NM_00027E	4948 Hs. 654411NM_00027E	ENSG000002OCA2	BEY BEY1 OCA2 mele protein-coding	
chr5-373E.8.894848	-0.12352	0.789663	-0.15642	0.8757	0.981636	chr5	37392087	37392802	+	0 NA	intron (NAluSx SIN	13126 NM_00134E	55100 Hs. 21369E	ENSG000002WDR70	- WD repeat protein-coding	
chr11-34E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr11	34913352	34913894	+	0 NA	intron (NLR12_ L1	-2507 NM_00116E	8050 Hs. 50231E	ENSG000002PDHX	DDBP E3E pyruvate protein-coding	
chr11-68E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr11	68915268	68916220	+	0 NA	intron (NAluS2 SIN	11893 NM_00218E	3508 Hs. 50343E	ENSG000002IGHMBP2	CATF1 CMI immunogl protein-coding	
chr15-43E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr15	43003545	43003978	+	0 NA	intron (Nintron (N	-82983 NM_17350C	146057 Hs. 646511NM_17350E	ENSG000002TTBK2	SCA11 TTE tau tubul protein-coding	
chr15-434.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr15	43454445	43456344	+	0 NA	intron (Nintron (N	37762 NM_001141	7158 Hs. 44096E	ENSG000002TP53BP1	53BP1 TDF tumor pr protein-coding	
chr16-23E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr16	23548403	23552439	+	0 NA	intron (Nintron (N	6929 NM_00118E	124454 Hs. 620541NM_00108E	ENSG000002EARS2	COXP12 W glutamyl protein-coding	
chr16-89E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr16	89267037	89268344	+	0 NA	TTS (NM TTS (NM_C	-28438 NR_13633E	1.05E+08 Hs. 657381NR_13633E	ENSG000002LOC105371-	uncharactncRNA	
chr17-75E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr17	75320678	75322590	+	0 NA	intron (Nintron (N	-32185 NM_02173A	60386 Hs. 51447E	ENSG000002SLC25A19	DNC MCPH4 THO ce protein-coding	
chr18-21E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr18	213683	216864	+	0 NA	TTS (NM TTS (NM_C	52774 NM_005131	9984 Hs. 71254E	ENSG000002DHCX	HPR1 P84 THO ce protein-coding	
chr19-18E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr19	18925106	18926111	+	0 NA	intron (NAluSx3 S1	5848 NM_01907C	54555 Hs. 143181NM_01907E	ENSG000002DX49	Ddbp8 R27 DEAD-box protein-coding	
chr19-44E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr19	44756267	44760760	+	0 NA	promoter-promoter-	-144 NR_10705E	1.02E+08 NR_10705E	ENSG000002MIR8085	hsa-mir-5 microRNA ncRNA	
chr2-372E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr2	37240236	37244478	+	0 NA	non-codir non-codir	10699 NR_14640E	55471 Hs. 43346E	ENSG000002NDUFAF7	C2orf56 NADH: ubic protein-coding	
chr2-234E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr2	2.35E+08	2.35E+08	+	0 NA	intron (Nintron (N	4557 NM_001371305	128854 Hs. 647447NR_002781	ENSG000002TSPY26P	TSPYL3 b testis sr pseudo	
chr20-321.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr20	32160707	32163168	+	0 NA	intron (Nintron (N	28423 NR_002781	128854 Hs. 647447NR_002781	ENSG000002TSPY26P	TSPYL3 b testis sr pseudo	
chr20-36E.8.664767	0.123701	0.791527	0.156282	0.875811	0.981636	chr20	36523675	36525746	+	0 NA	intron (NAluSp SIN	-16809 NM_18152E	10398 Hs. 50468E	ENSG000002MYL9	LC20 MLC-myosin l i protein-coding	
chr21-43E.8.664767	0.123701	0.791527	0.156282													

chr4-1866 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr4	1.87E+08	1.87E+08	0	NA	intron (NMIRb SINE	56049 NM_00524E	2195 Hs. 481371NM_00524E	ENSG0000CFAT1	CDHF7 CDF FAT atypicprotein-coding
chr5-3716 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr5	37168080	37171409	0	NA	intron (NAluSx SIN	-79302 NR_13426E	1.05E+08 Hs. 17099E NR_13426E	ENSG0000CLOC105374	- uncharactericRNA
chr5-1266 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr5	1.27E+08	1.27E+08	0	NA	intron (NAluSx SIN	10053 NM_032177	51808 Hs. 555731NM_032177	ENSG0000CFHAX	RNUXA phosphoryprotein-coding
chr5-1346 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr5	1.35E+08	1.35E+08	0	NA	exon (NM exon (NM	9218 NM_00113E	134553 Hs. 70853E NM_15240E	ENSG0000C5orf24	- chromosonprotein-coding
chr5-1775 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr5	1.77E+08	1.77E+08	0	NA	TTS (NM_CTS (NM_C	3271 NM_001271	27166 Hs. 744904NM_013237	ENSG0000CPRELID1	CGI-106 FPRELI donprotein-coding
chr6-1396 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr6	1390508	1396209	0	NA	intron (NCpG	-2947 NR_10677E	1.02E+08 NR_10677E	ENSG0000CMIR6720	hsa-mir-εmicroRNA ncRNA
chr6-4266 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr6	42662797	42666413	0	NA	intron (Nintron (N	57992 NM_000322	5961 Hs. 65448E NM_000322	ENSG0000CPRH2	AOFMD AVP peripherprotein-coding
chr6-1371 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr6	1.37E+08	1.37E+08	0	NA	exon (NM exon (NM	20827 NM_00136E	3459 Hs. 520414NM_00041E	ENSG0000CFNGR1	CD119 IFN interfeerprotein-coding
chr8-3896 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr8	38989714	38995100	0	NA	intron (NAluJo SIN	4102 NM_03194C	83877 Hs. 7471 NM_03194C	ENSG0000CTM2D2	BLP1 TM2 domaiprotein-coding
chr8-3907 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr8	39071246	39073183	0	NA	intron (Nintron (N	-35315 NM_00131E	203102 Hs. 52154E NM_145004	ENSG0000CADAM32	- ADAM metae protein-coding
chr8-7686 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr8	76850478	76851202	0	NA	intron (Nintron (N	116010 NR_13046C	1E+08 NR_13046C	ENSG0000CMIR3149	- microRNA ncRNA
chr9-1296 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr9	1.3E+08	1.3E+08	0	NA	intron (NCharlie4z	65264 NM_01503E	23048 Hs. 18940E NM_01503E	ENSG0000CFNBP1	FBP17 formin biprotein-coding
chrX-2012 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chrX	20133608	20138530	0	NA	TTS (NR_CTS (NR_C	344 NR_02335E	1E+08 NR_02335E	SCARNA9L	- small Ca ncRNA
chr1-3208 7.930795	-0.12808	0.821515	-0.15591	0.876103	0.981636	chr1	32083370	32084121	0	NA	intron (NAluSx SIN	-3014 NR_04985E	1.01E+08 NR_04985E	ENSG0000CMIR5585	- microRNA ncRNA
chr1-1181 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr1	11815589	11818278	0	NA	intron (Nintron (N	10742 NM_00128E	1185 Hs. 19304E NM_00128E	ENSG0000CCLCN6	CLC-6 chloride protein-coding
chr1-6700 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr1	67002836	67004065	0	NA	3' UTR (N3' UTR (N	50698 NM_01513E	23169 Hs. 21364E NM_01513E	ENSG0000CSLC35D1	SHNKND SOLUTE cεprotein-coding
chr1-151 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr1	1.52E+08	1.52E+08	0	NA	intron (NLTRI2C LI	2236 NM_05305E	117145 Hs. 16407E NM_05305E	ENSG0000CTHEM4	CTMP thioesterprotein-coding
chr12-12 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr12	1.2E+08	1.2E+08	0	NA	intron (NMIRb SINE	17621 NR_038924	1.01E+08 Hs. 56920E NR_038924	ENSG0000CPXN-AS1	EyeLinc4 PXN anticncRNA
chr14-547 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr14	54778191	54780162	0	NA	intron (Nintron (N	24343 NM_001161	23034 Hs. 98259 NM_01558E	ENSG0000CSAMD4A	SAMD4 SMA sterile εprotein-coding
chr15-904 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr15	90434712	90434911	0	NA	intron (NTigger4a	46569 NM_00387E	8826 Hs. 430551NM_00387E	ENSG0000CIQAP1	HUMORFAM01IQ motif protein-coding
chr15-925 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr15	92973345	92975298	0	NA	intron (Nintron (N	69622 NR_03613E	1E+08 NR_03613E	ENSG0000CMIR3175	mir-3175 microRNA ncRNA
chr16-162 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr16	16252223	16256679	0	NA	intron (Nintron (N	21856 NM_173614	283820 Hs. 460141NM_173614	ENSG0000CNOMO2	Nomo PM5 NODAL mocprotein-coding
chr17-72 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr17	7321288	7324271	0	NA	exon (NM exon (NM	6331 NM_03244E	84461 Hs. 654794NM_03244E	ENSG0000CNEURL4	- neuronalε protein-coding
chr17-432 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr17	42774912	42777912	0	NA	intron (NAluSx3 SI	2963 NM_03235E	50016E NM_03235E	ENSG0000CVPS25	DERP9 EAF vacuolar protein-coding
chr17-501 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr17	50134661	50136391	0	NA	intron (Nintron (N	-5366 NM_001257	201191 Hs. 56776E NM_17492E	ENSG0000CSAMD14	- sterile εprotein-coding
chr17-81 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr17	81913836	81915939	0	NA	intron (Nintron (N	3289 NM_01653E	51547 Hs. 51463E NM_01653E	ENSG0000CSIRT7	SIRT7 sirtuin 7protein-coding
chr2-151 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr2	1.51E+08	1.51E+08	0	NA	3' UTR (N3' UTR (N	12486 NM_198557	375287 Hs. 30244E NM_198557	ENSG0000CBM43	C2orf38 RNA bindiprotein-coding
chr21-392 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr21	39204546	39205662	0	NA	intron (Nintron (N	-21590 NM_20343E	8624 Hs. 47383E NM_00372E	ENSG0000CPMG1	C21LRP DS proteasoneprotein-coding
chr3-4787 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr3	47870520	47872217	0	NA	intron (NL2b LINE	21813 NR_03159E	ENSG0000CMIR1226	MIRN1226 microRNA ncRNA	
chr4-5546 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr4	55465915	55466432	0	NA	intron (NTHEIC LTF	70216 NM_01847E	55858 Hs. 47976E NM_01847E	ENSG0000CTMEM165	CDG2K T2E transmentprotein-coding
chr8-9812 9.135931	0.119634	0.768969	0.155578	0.876366	0.981636	chr8	98128024	98132711	0	NA	intron (Nintron (N	12527 NM_01502E	10940 Hs. 25282E NM_01502E	ENSG0000CPOP1	ANXD2 POP1 homcprotein-coding
chr1-3945 11.62303	0.107043	0.688069	0.155571	0.876371	0.981636	chr1	39453948	39461395	0	NA	intron (NL2c LINE	-33965 NM_18180E	353500 Hs. 472497NM_18180E	ENSG0000CBMP8A	- bone morph protein-coding
chr20-367 11.62303	0.107043	0.688069	0.155571	0.876371	0.981636	chr20	36796400	36796632	0	NA	intron (Nintron (N	-22753 NM_00114E	79980 Hs. 63226E NM_02491E	ENSG0000CSLR2	C20orf172 DSN1 com protein-coding
chr1-229E 8.88699	-0.12187	0.783465	-0.15555	0.876384	0.981636	chr1	2.3E+08	2.3E+08	0	NA	intron (NMIRb SINE	19255 NM_01440E	27097 Hs. 270621NM_01440E	ENSG0000CTAF5L	PAF65B TATA-box protein-coding
chr15-56E 8.88699	-0.12187	0.783465	-0.15555	0.876384	0.981636	chr15	56676142	56676479	0	NA	intron (Nintron (N	57776 NM_00128E	54816 Hs. 511477NM_017661	ENSG0000CZNF280D	SUHW4 ZNF zinc fingprotein-coding
chr16-68E 8.88699	-0.12187	0.783465	-0.15555	0.876384	0.981636	chr16	68337791	68337990	0	NA	intron (NL2c LINE	26776 NM_00129C	54496 Hs. 64022E NM_01902E	ENSG0000CPRMT7	SIBDSS protein εprotein-coding
chr2-614E 8.88699	-0.12187	0.783465	-0.15555	0.876384	0.981636	chr2	61488040	61488395	0	NA	exon (NM exon (NM	-17130 NM_01470E	9736 Hs. 64470E NM_01470E	ENSG0000CUSP34	- ubiquitin protein-coding
chr3-1261 8.88699	-0.12187	0.783465	-0.15555	0.876384	0.981636	chr3	12611174	12612336	0	NA	intron (Nintron (N	51753 NM_001354	5894 Hs. 15913E NM_00288E	ENSG0000CRAF1	CMD1NN CFRAF1 prcprotein-coding
chr6-100E 8.88699	-0.12187	0.783465	-0.15555	0.876384	0.981636	chr6	1.01E+08	1.01E+08	0	NA	intron (NAluYc SIN	-46179 NM_00506E	6492 Hs. 52029E NM_00506E	ENSG0000CSIM1	bHLHeL4 SIM bHLHeL protein-coding
chr1-1611 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr1	1.61E+08	1.61E+08	0	NA	intron (Nintron (N	4398 NM_00103E	9191 Hs. 74409E NM_00421E	ENSG0000CDEDD	CASP8IP1 death effprotein-coding
chr1-1657 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr1	1.66E+08	1.66E+08	0	NA	intron (NL2a LINE	3011 NM_00136E	54499 Hs. 31498 NM_01902E	ENSG0000CTMCO1	HP10122 Ftransmentprotein-coding
chr1-193 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr1	1.93E+08	1.93E+08	0	NA	intron (NAluX1 SI	5248 NM_19796E	51022 Hs. 4828E NM_01606E	ENSG0000CLRXC2	IG1-133 GLutaredc protein-coding
chr1-246E 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr1	2.47E+08	2.47E+08	0	NA	intron (NAluS6 SI	10432 NM_02236E	64216 Hs. 7395 NM_02236E	ENSG0000CTFBZM	Hkp1 mtTF transcrip protein-coding
chr10-934 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr10	93412403	93412692	0	NA	intron (Nintron (N	69787 NM_013451	26509 Hs. 60208E NM_013451	ENSG0000CVMYOF	FERL13 myoferlin protein-coding
chr10-102 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr10	1.03E+08	1.03E+08	0	NA	intron (Nintron (N	25043 NM_00010E	1586 Hs. 43801E NM_00010E	ENSG0000CYP17A1	CP17 CYP1 cytochroprotein-coding
chr12-193 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr12	19360781	19362460	0	NA	exon (NM exon (NM	-77872 NM_001114	121536 Hs. 126497NM_15320E	ENSG0000CAEBP2	- AE bindir protein-coding
chr12-644 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr12	64470734	64472511	0	NA	intron (NAluSx SIN	19502 NM_013254	29110 Hs. 505874NM_013254	ENSG0000CTBK1	FTDALS4 ITANK bincprotein-coding
chr12-111 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr12	1.11E+08	1.11E+08	0	NA	intron (NAluJo SIN	13232 NM_00547E	10019 Hs. 506784NM_00547E	ENSG0000CSH2B3	IDDM20 LNSH2B adaf protein-coding
chr12-12 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr12	1.24E+08	1.24E+08	0	NA	intron (NAluJ SINE	3976 NM_001414	1967 Hs. 74127E NM_001414	ENSG0000EIF2B1	EIF2B EIF eukaryoti protein-coding
chr15-61E 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr15	61944631	61945844	0	NA	intron (NTHEIC LTF	115210 NM_017684	54832 Hs. 51166E NM_017684	ENSG0000CVPS13C	PARK23 vacuolar protein-coding
chr16-144 8.152463	0.126473	0.813202	0.155525	0.876407	0.981636	chr16	14988754	14991010	0	NA	intron (NCpG	14856 NM_00128E	23042 Hs. 370781NM_01502E	ENSG0000CPDXDC1	LP8165 pyridoxal protein-coding
chr16-71E 8.152463	0.126473	0.813202	0.155525</												



chr14-694 7.640159	0.129593	0.839121	0.154439	0.877264	0.981636	chr14	69456503	69457619	+	0 NA	intron (Nintron (N	-27667 NM_001161	400224 Hs. 509799	ENSG00000PLEKHD1	UPF0639	pleckstriprotein-coding		
chr15-526 7.640159	0.129593	0.839121	0.154439	0.877264	0.981636	chr15	52624329	52624797	+	0 NA	intron (Nintron (N	27477 NM_001288	56204 Hs. 152388	ENSG00000FAM214A	KIAA1370	family wiprotein-coding		
chr17-625 7.640159	0.129593	0.839121	0.154439	0.877264	0.981636	chr17	62575550	62577920	+	0 NA	exon (NM_exon (NM	-50935 NM_006035	9902 Hs. 7835	ENSG00000MRC2	CD280	CLFmannose rprotein-coding		
chr2-2034 7.640159	0.129593	0.839121	0.154439	0.877264	0.981636	chr2	2.03E+08	2.03E+08	+	0 NA	3' UTR (N3' UTR (N	72428 NM_001282	10152 Hs. 471156	ENSG00000AB12	hba-2	ABIabl interprotein-coding		
chr6-1586 7.640159	0.129593	0.839121	0.154439	0.877264	0.981636	chr6	1.59E+08	1.59E+08	+	0 NA	intron (Nintron (N	17109 NR_106981	1.02E+08	NR_106981	ENSG00000MIR1761	hsa-mir-7	microRNA ncRNA	
chr9-9652 7.640159	0.129593	0.839121	0.154439	0.877264	0.981636	chr9	96526249	96526467	+	0 NA	intron (NAluY SINE	40473 NM_001351	8555 Hs. 40582	ENSG00000CDC14B	CDC14B3	Cell diviprotein-coding		
chr1-1934 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr1	19354234	19357400	+	0 NA	intron (Nintron (N	43491 NM_00104C	54896 Hs. 64762C	ENSG00000SLC66A1	LAAT-1	l L solute cprotein-coding		
chr1-2094 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr1	20941489	20942271	+	0 NA	exon (NM_exon (NM	46552 NR_031657	1E+08	NR_031657	ENSG00000MIR1256	MIRN1256	microRNA ncRNA	
chr14-528 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr14	52890053	52893936	+	0 NA	intron (N L2b LINE	59056 NM_006832	10979 Hs. 509342	ENSG00000FERMT2	KIND2	MICfermitin protein-coding		
chr17-456 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr17	45601885	45607504	+	0 NA	intron (N FLAM_C SI	23377 NM_0021075	4836 Hs. 53279C	ENSG00000NMT1	NMT	-Myrist protein-coding		
chr21-366 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr21	36052584	36056915	+	0 NA	intron (Nintron (N	5615 NM_001007	54093 Hs. 60620C	ENSG00000SETD4	C2lorf18	SET domainprotein-coding		
chr21-372 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr21	37223155	37225040	+	0 NA	3' UTR (N3' UTR (N	15594 NR_02671E	257203 Hs. 50515E	ENSG00000DSCR9	NCRNA0002	Down syncncRNA		
chr22-411 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr22	41160433	41166148	+	0 NA	intron (NAluYa5 SI	34211 NR_110514	1.02E+08	Hs. 517517	NR_110514	EP300-AS1	EP300 antncRNA	
chr5-1548 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr5	1.55E+08	1.55E+08	+	0 NA	TTS (NM_C TTS (NM_C	28751 NM_001301	9337 Hs. 26703	NR_00477E	ENSG00000CNOT8	CAF1	CAL CCR4-NOT protein-coding	
chr6-1106 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr6	1.11E+08	1.11E+08	+	0 NA	intron (N L2c LINE	4123 NM_032194	84154 Hs. 37226E	ENSG00000RPF7	BXDC1	ba2:ribosome protein-coding		
chr6-1597 8.879132	-0.12028	0.780327	-0.15414	0.877497	0.981636	chr6	1.6E+08	1.6E+08	+	0 NA	intron (NAluJb SIN	-10040 NM_005891	39 Hs. 571037	NR_005891	ENSG00000ACAT2	-	acetyl-Ccprotein-coding	
chr1-235 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr1	2.35E+08	2.35E+08	+	0 NA	intron (NAluY SINE	14031 NM_001287	6905 Hs. 74499E	ENSG00000CTBCE	HRD	KCS K tubulin rprotein-coding		
chr11-106 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr11	10622612	10623664	+	0 NA	intron (Nintron (N	29163 NM_001098	10335 Hs. 50189E	ENSG00000MRV11	IRAG	JAW murine rprotein-coding		
chr16-366 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr16	3658277	36587260	+	0 NA	TTS (NM_C TTS (NM_C	3794 NM_001351	1773 Hs. 62963E	ENSG00000DNASE1	DNL1	DRNI deoxyribcprotein-coding		
chr17-462 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr17	42564553	42566466	+	0 NA	exon (NM_exon (NM	-1551 NM_170607	6945 Hs. 38301E	ENSG00000CMLX	MAD7	MXD7MAX dimerprotein-coding		
chr17-465 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr17	46548070	46549226	+	0 NA	exon (NM_exon (NM	31064 NM_00133C	1.01E+08	Hs. 55925E	ENSG00000ARL17B	ARL17	ARI ADP ribosprotein-coding	
chr19-194 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr19	19465568	19469345	+	0 NA	intron (N LIME3A LI	32393 NR_03037C	693225	NR_03037C	ENSG00000MIR640	MIRN640	l microRNA ncRNA	
chr19-196 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr19	36182207	36183741	+	0 NA	exon (NM_exon (NM	-30527 NM_001864	1346 Hs. 421621	NR_001864	ENSG00000COX7A1	COX7A	COX cytochroprotein-coding	
chr4-1161 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (Nintron (N	-2388 NR_10382E	729218 Hs. 44851E	NR_10382E	LOC72921E	-	uncharactpseudo	
chr5-1136 9.656093	0.115991	0.752577	0.154124	0.877512	0.981636	chr5	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	50720 NM_00134E	64848 Hs. 231942	NR_02282E	ENSG00000YTHDC2	CAHL	h YTH YTH domainprotein-coding	
chr1-193 8.623627	0.121981	0.792023	0.154012	0.8776	0.981636	chr1	19339349	19339860	+	0 NA	exon (NM_exon (NM	27278 NM_00104C	54896 Hs. 64762C	ENSG00000SLC66A1	LAAT-1	l L solute cprotein-coding		
chr17-383 8.623627	0.121981	0.792023	0.154012	0.8776	0.981636	chr17	3839470	3840235	+	0 NA	intron (N MR SINE	6394 NM_001114	55421 Hs. 12096E	ENSG00000NCBP3	C17orf85	nuclear cprotein-coding		
chr3-1838 8.623627	0.121981	0.792023	0.154012	0.8776	0.981636	chr3	1.84E+08	1.84E+08	+	0 NA	intron (Nintron (N	25180 NM_001037	55486 Hs. 47846E	ENSG00000PARL	PRO2207	Fpreseniliprotein-coding		
chr7-1396 8.623627	0.121981	0.792023	0.154012	0.8776	0.981636	chr7	1.39E+08	1.39E+08	+	0 NA	intron (NAluSx SIN	19920 NM_01601E	51631 Hs. 73148E	ENSG00000LUC7L2	CGI-59	CC LUC7 likeprotein-coding		
chr19-522 13.13452	0.10047	0.65257	0.15396	0.877641	0.981636	chr19	52611986	52620547	+	0 NA	intron (Nintron (N	19582 NR_023311	7696 Hs. 37364E	NR_003438	ZNF137P	-	zinc fingpseudo	
chr9-839 13.60568	0.098559	0.641157	0.153721	0.87783	0.981636	chr9	83968996	83978160	+	0 NA	intron (Nintron (N	-3721 NR_02960E	407043	NR_02960E	ENSG00000MIR7-1	MIRN7-1	l microRNA ncRNA	
chr16-482 11.63089	0.105786	0.688288	0.153695	0.877851	0.981636	chr16	48290218	48290832	+	0 NA	intron (N MER21B LI	-42986 NM_00137C	85320 Hs. 652267	NR_03258E	ENSG00000ABCC11	EWWD	MRP&ATP bindiprotein-coding	
chr12-104 11.63089	0.105786	0.688288	0.153695	0.877851	0.981636	chr12	1.04E+08	1.04E+08	+	0 NA	intron (Nintron (N	41976 NM_00100E	493861 Hs. 65985E	NR_00100E	ENSG00000EID3	NS4EB	NSEP300 intrprotein-coding	
chr16-482 11.63089	0.105786	0.688288	0.153695	0.877851	0.981636	chr16	48285852	48287784	+	0 NA	intron (N LIM4 LINE	-39279 NM_00137C	85320 Hs. 652267	NR_03258E	ENSG00000ABCC11	EWWD	MRP&ATP bindiprotein-coding	
chr2-6187 11.63089	0.105786	0.688288	0.153695	0.877851	0.981636	chr2	61874274	61884932	+	0 NA	intron (Nintron (N	9053 NM_00643C	10575 Hs. 42150E	NR_00643C	ENSG00000CCT4	CCT-DEL7	chaperon rprotein-coding	
chr5-3888 11.63089	0.105786	0.688288	0.153695	0.877851	0.981636	chr5	38881476	38888013	+	0 NA	intron (Nintron (N	38732 NM_00132E	9180 Hs. 12065E	NR_00399E	ENSG00000COSMR	IL-31R	be-oncostatiprotein-coding	
chr13-952 10.12726	0.11269	0.733296	0.153675	0.877866	0.981636	chr13	95262218	95266784	+	0 NA	intron (N LIMC4 LIN	36945 NM_00584E	10257 Hs. 50842E	NR_00584E	ENSG00000ABCC4	MOAT-B	MCATP bindiprotein-coding	
chr15-424 10.12726	0.11269	0.733296	0.153675	0.877866	0.981636	chr15	42414412	42418784	+	0 NA	3' UTR (N3' UTR (N	11819 NM_17308E	825 Hs. 143261	NR_00007C	ENSG00000CAPN3	CANP3	CAN calpain cprotein-coding	
chr2-3236 10.12726	0.11269	0.733296	0.153675	0.877866	0.981636	chr2	32383407	32384070	+	0 NA	intron (NAluSg SIN	26185 NM_01625E	57448 Hs. 150207	NR_01625E	ENSG00000BLRC6	APOLLON	Ebaculoviriprotein-coding	
chr20-27 27.53325	0.073562	0.478734	0.153659	0.877879	0.981636	chr20	27091973	27092179	+	0 NA	IntergeniALR/Alpha	-882843 NR_04009E	284801 Hs. 37069E	NR_04009E	ENSG00000MIR663AHC	-	MIR663A lncRNA	
chr10-777 6.144387	0.144263	0.938965	0.15364	0.877894	0.981636	chr10	77780703	77781113	+	0 NA	IntergeniIntergeni	-143100 NM_00132E	3778 Hs. 14479E	NR_00224E	ENSG00000KCNMA1	BKTM	CADFe potassiumprotein-coding	
chr1-6186 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr1	6188903	6197265	+	0 NA	intron (Nintron (N	6511 NM_00098E	6146 Hs. 51532E	NR_00098E	ENSG00000RPL22	EAP	HBP1 rribosomalprotein-coding	
chr1-212 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr1	2.12E+08	2.12E+08	+	0 NA	intron (Nintron (N	6629 NR_00438E	692157 Hs. 70795E	NR_00438E	ENSG00000SNORA16B	U98b	small nucsnRNA	
chr10-118 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr10	1.18E+08	1.18E+08	+	0 NA	intron (Nintron (N	7048 NM_02206E	63877 Hs. 10557E	NR_02206E	ENSG00000FAM204A	C10orf84	family wiprotein-coding	
chr11-662 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr11	66270025	66275142	+	0 NA	intron (Nintron (N	3944 NM_030981	81876 Hs. 30081E	NR_030981	ENSG00000RAB1B	-	RAB1B, meprotein-coding	
chr12-215 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr12	21515900	21517033	+	0 NA	3' UTR (N3' UTR (N	-9830 NM_03057E	80763 Hs. 13069E	NR_03057E	ENSG00000SPX	C12orf39	spexin hprotein-coding	
chr13-205 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr13	20985709	20991246	+	0 NA	exon (NM_exon (NM	-39049 NR_10405E	1.02E+08	Hs. 63763E	NR_10405E	ENSG00000LINC00367	-	long intncRNA
chr14-648 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr14	65076570	65079011	+	0 NA	intron (Nintron (N	-12128 NR_04512E	1.01E+08	Hs. 711267	NR_04512E	ENSG00000LOC10050E	-	uncharactncRNA
chr14-757 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr14	74732659	74733976	+	0 NA	intron (N LTR104 Me	20173 NM_00131E	51077 Hs. 57982E	NR_01596E	ENSG00000PCF1	Bka	C14orf1 rRN rprotein-coding	
chr14-776 8.425533	-0.12282	0.799426	-0.15363	0.877898	0.981636	chr1												

chr19-435	12.62221	0.101304	0.663408	0.152703	0.878632	0.981636	chr19	43912720	43927370	+	0	NA	intron (Nintron (N	15237	NM_00342E	7596	Hs.38128E	NM_00342E	ENSG000002ZNF45	KOX5 ZNF1	zinc finger protein-coding
chr2-8537	12.62221	0.101304	0.663408	0.152703	0.878632	0.981636	chr2	85378543	85381432	+	0	NA	intron (NMER4-int)	25218	NM_001113E	84173	Hs.269999C	NM_03221E	ENSG000002ELMOD3	DFNB88 LS	ELMO domain protein-coding
chr10-997	8.672625	0.121943	0.798714	0.152674	0.878656	0.981636	chr10	99755719	99757116	+	0	NA	TTS (NM_TTS (NM_C	-23751	NM_00132C	1355	Hs.28326	NM_00437E	ENSG000002COX15	CEMCOX2	cytochrome protein-coding
chr19-368	8.672625	0.121943	0.798714	0.152674	0.878656	0.981636	chr19	36859922	36860583	+	0	NA	intron (NAluY SINE	8601	NM_001242	25850	Hs.362324N	NM_00341E	ENSG000002ZNF345	HZF10	zinc finger protein-coding
chr5-6571	8.672625	0.121943	0.798714	0.152674	0.878656	0.981636	chr5	65711530	65712650	+	0	NA	intron (NAluJo SINE	8601	NM_001242	54557	Hs.482301N	NM_01907E	ENSG000002SGTB	SGT2	small gtp protein-coding
chr1-777	7.881798	-0.12859	0.842342	-0.15265	0.878672	0.981636	chr1	77708314	77709388	+	0	NA	intron (NLMC4 LIN	-25424	NM_00130E	26009	Hs.48050E	NM_01553E	ENSG000002ZZ3	ATAC1	zinc finger protein-coding
chr15-671	7.881798	-0.12859	0.842342	-0.15265	0.878672	0.981636	chr15	67111169	67111661	+	0	NA	intron (NLM1B7 LIN	-14301	NM_001114E	4088	Hs.72798E	NM_00590E	ENSG000002SMAD3	HSPC193 FS	MAD fami protein-coding
chr20-366	7.881798	-0.12859	0.842342	-0.15265	0.878672	0.981636	chr20	36838792	36839247	+	0	NA	intron (NMIRc SINE	20854	NM_001918E	140710	Hs.460807E	NM_08062E	ENSG000002SOGA1	C20orf117	suppressor protein-coding
chr5-1771	7.881798	-0.12859	0.842342	-0.15265	0.878672	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (NAluSx SIN	9721	NM_00136E	64324	Hs.106861N	NM_02245E	ENSG000002CNSD1	ARA267 K	nuclear r protein-coding
chr1-378	10.64742	0.109717	0.71939	0.152514	0.878781	0.981636	chr1	37803080	37806822	+	0	NA	intron (NMIRb SINE	-2839	NM_19844E	127687	Hs.53274E	NM_19844E	ENSG000002Clorf122	ALAESM	chromosome protein-coding
chr12-927	10.64742	0.109717	0.71939	0.152514	0.878781	0.981636	chr12	92776803	92779582	+	0	NA	intron (Nintron (N	41703	NM_001004	440107	Hs.59101E	NM_001004	ENSG000002PLEKHG7	-	pleckstrin protein-coding
chr14-214	10.64742	0.109717	0.71939	0.152514	0.878781	0.981636	chr14	21421564	21431672	+	0	NA	intron (NMIRc SINE	10657	NM_02092C	57680	Hs.53069E	NM_02092C	ENSG000002CHD8	AUTS18 H	chromosome protein-coding
chr19-583	10.64742	0.109717	0.71939	0.152514	0.878781	0.981636	chr19	58337505	58340297	+	0	NA	exon (NM exon (NM	4213	NR_106864E	1.02E+08	NR_106864E	ENSG000002MIR6806	hsa-mir-6	microRNA ncRNA	
chr6-994C	10.64742	0.109717	0.71939	0.152514	0.878781	0.981636	chr6	99404034	99407233	+	0	NA	intron (Nintron (N	-11688	NM_017421	51805	Hs.17362E	NM_017421	ENSG000002COQ3	DHBM2 E	coenzyme protein-coding
chr9-1223	10.64742	0.109717	0.71939	0.152514	0.878781	0.981636	chr9	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	4839	NM_001271	5742	Hs.20197E	NM_00096E	ENSG000002PTGS1	COX1 COX	prostaglandin protein-coding
chr21-44C	7.428199	-0.13188	0.865468	-0.15238	0.878886	0.981636	chr21	44075715	44075914	+	0	NA	intron (NAluSp SIN	1490	NM_00135E	7109	Hs.126221N	NM_00327E	ENSG000002TRAPP10	EHOC-1 E	trafficking protein-coding
chr4-1451	6.607693	0.139174	0.913778	0.152306	0.878946	0.981636	chr4	1.45E+08	1.45E+08	+	0	NA	intron (Nintron (N	16938	NM_01749E	54726	Hs.270851N	NM_01749E	ENSG000002TUD4	DUBA6 H	OTU deubiquitin protein-coding
chr5-728	11.11858	0.106983	0.702649	0.152257	0.878984	0.981636	chr5	72861085	72863634	+	0	NA	intron (NAluJo SIN	14220	NM_001364	3842	Hs.482497N	NM_00227E	ENSG000002CNTP01	IPO2 K	PNP transport protein-coding
chr9-992E	11.11858	0.106983	0.702649	0.152257	0.878984	0.981636	chr9	99227830	99231578	+	0	NA	intron (NLM1A2 LIN	7422	NM_00680E	10952	Hs.191887N	NM_00680E	ENSG000002SEC61B	-	SEC61 trans protein-coding
chr12-494	7.210134	0.136823	0.898752	0.152236	0.879001	0.981636	chr12	49462448	49462871	+	0	NA	intron (NLTRID LTF	73485	NR_03326E	1E+08	Hs.687044N	NR_03326E	LOC10033E	-	FGFR1 oncogene
chr1-231E	7.811274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr1	2.31E+08	2.31E+08	+	0	NA	exon (NM exon (NM	29735	NM_00131E	8443	Hs.49802E	NM_01423E	ENSG000002GNP4T	DAP-AT D	glycylserine protein-coding
chr11-74E	8.871274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr11	74935319	74936824	+	0	NA	intron (Nintron (N	13020	NM_00127C	143570	Hs.37014E	NM_18296E	ENSG000002XRRA1	-	X-ray crystal protein-coding
chr14-24E	8.871274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr14	24149535	24153843	+	0	NA	intron (Nintron (N	4191	NM_01799E	55072	Hs.375217N	NM_01799E	ENSG000002RNF31	HOIP P	ubiquitin protein-coding
chr16-69E	8.871274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr16	69993155	69997259	+	0	NA	intron (Nintron (N	-35139	NR_03626E	1E+08	NR_03626E	ENSG000002MIR1972-2	-	microRNA ncRNA	
chr20-347	8.871274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr20	34748737	34749805	+	0	NA	intron (NLM1C5 LIN	33133	NM_00124E	23054	Hs.368971N	NM_01407E	ENSG000002NCOA6	AIB3 A	ASC nuclear r protein-coding
chr3-154E	8.871274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr3	1.54E+08	1.54E+08	+	0	NA	intron (Nintron (N	10073	NM_02086E	170506	Hs.44627C	NM_02086E	ENSG000002DHX36	DDX36 G	4FDEAH-box protein-coding
chr3-180E	8.871274	-0.11873	0.780144	-0.15219	0.879037	0.981636	chr3	1.81E+08	1.81E+08	+	0	NA	intron (NLM1P2 LIN	31175	NM_00119C	131118	Hs.230601N	NM_14526E	ENSG000002DNAJ19	PAM18 T	M DnaJ heat protein-coding
chr1-222E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (NAluSx SIN	-6885	NR_11061E	1.01E+08	Hs.553851N	NR_11061E	ENSG000002TAF1A-AS1	-	TAF1A ant ncRNA
chr12-89E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr12	894906	896549	+	0	NA	intron (NAluSx SIN	37349	NM_001297	5893	Hs.41035E	NM_13442E	ENSG000002RAD52	-	RAD52 hom protein-coding
chr12-27E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr12	27578951	27579684	+	0	NA	intron (NLM1E3A LIN	55111	NM_00119E	8496	Hs.17244E	NM_00362E	ENSG000002PPF1BP1	L2 SGT2	PI3FIIA protein-coding
chr15-42E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr15	42530561	42531434	+	0	NA	intron (Nintron (N	17796	NM_15326C	255252	Hs.234681N	NM_15326C	ENSG000002LRR57	-	leucine r protein-coding
chr21-37E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr21	37236045	37231974	+	0	NA	intron (Nintron (N	22806	NR_02671E	257203	Hs.50515E	NM_14867E	ENSG000002DSCR9	NCRNA000E	Down syndrome ncRNA
chr3-170E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	exon (NM exon (NM	-64320	NM_005414	6498	Hs.53665E	NM_005414	ENSG000002SKIL	SNOA1 S	KI like protein-coding
chr7-328E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr7	32870095	32871060	+	0	NA	exon (NM exon (NM	21183	NM_01548E	25948	Hs.372541N	NM_01548E	ENSG000002KBTBD2	BKLHD1	kelch repeat protein-coding
chr7-760E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr7	76018587	76018801	+	0	NA	intron (NLM1B7 LIN	11830	NM_001317	51657	Hs.11615	NM_01608E	ENSG000002STYXL1	DUSP24	M serine/thr protein-coding
chr8-193E	8.160321	0.124612	0.81907	0.152138	0.879078	0.981636	chr8	19365391	19365781	+	0	NA	intron (Nintron (N	51610	NM_001174	63898	Hs.30320E	NM_02207E	ENSG000002SH2D4A	PPP1R38	S2H2 domain protein-coding
chr19-35E	8.111323	0.12458	0.819491	0.152022	0.87917	0.981636	chr19	35998248	35998458	+	0	NA	IntergeniAluSq2 SI	3165	NM_00104E	644096	Hs.35646C	NM_00104E	ENSG000002SDHAF1	LYR8M	succinate protein-coding
chr7-766E	8.111323	0.12458	0.819491	0.152022	0.87917	0.981636	chr7	76611083	76612030	+	0	NA	exon (NM exon (NM	15747	NM_15299E	22932	Hs.488877N	NM_01223C	ENSG000002POMZP3	POM-2P3	F20M121 ar protein-coding
chr2-324E	9.614954	0.14443	0.752785	0.152008	0.87918	0.981636	chr2	32431315	32432538	+	0	NA	intron (NLa2 LINE	74898	NM_01625E	57448	Hs.150107N	NM_01625E	ENSG000002BIRC6	POLLON E	ubiquitin protein-coding
chr20-23E	9.614954	0.14443	0.752785	0.152008	0.87918	0.981636	chr20	23374489	23376522	+	0	NA	non-coding non-coding	11142	NM_001317	64412	Hs.70946E	NM_02248E	ENSG000002GZF1	JLSM Z	BTE GDNF ind protein-coding
chr3-125E	9.614954	0.14443	0.752785	0.152008	0.87918	0.981636	chr3	1.26E+08	1.26E+08	+	0	NA	intron (NAluSp SIN	32716	NM_02277E	114885	Hs.47744C	NM_02277E	ENSG000002OSBPL11	ORF-110	Oxysterol protein-coding
chr1-191E	13.09338	0.099283	0.653153	0.152006	0.879182	0.981636	chr1	19190807	19194739	+	0	NA	intron (NLa2 LINE	17493	NM_02076E	23352	Hs.14807E	NM_02076E	ENSG000002UBR4	BRAF600	Zubiquitin protein-coding
chr17-501	13.61354	0.097477	0.641386	0.151978	0.879204	0.981636	chr17	50187779	50201460	+	0	NA	exon (NM exon (NM	7020	NM_00008E	1277	Hs.17292E	NM_00008E	ENSG000002COL1A1	EDSARTH1	collagen protein-coding
chr1-375E	8.417675	-0.1212	0.797664	-0.15194	0.879235	0.981636	chr1	37565574	37570181	+	0	NA	intron (Nintron (N	10937	NM_00346E	7802	Hs.40605E	NM_00346E	ENSG000002DNAL11	P28 dJ	2E dynein a protein-coding
chr1-3941E	8.417675	-0.1212	0.797664	-0.15194	0.879235	0.981636	chr1	39419313	39424819</												



chr17-63:8.631485	0.120298	0.792199	0.151853	0.879303	0.981636	chr17	63376843	63377650	+	0 NA	intron (THE1D-int	63021 NM_00133C	1534 Hs. 355264NM_00191E	ENSG00000CYB561	CYB561A1	cytochromprotein-coding
chr22-287:8.631485	0.120298	0.792199	0.151853	0.879303	0.981636	chr22	28780953	28783645	+	0 NA	intron (AluSx1 SI	9162 NM_001284	150275 Hs. 406466NM_17351	ENSG00000CCDC117	dJ3661A.1	coiled-cpprotein-coding
chr3-978:8.631485	0.120298	0.792199	0.151853	0.879303	0.981636	chr3	9783689	9786029	+	0 NA	intron (AluSq2 SI	-7636 NM_001024	10093 Hs. 323342NM_00571E	ENSG00000CARPC4	ARC20 P2C	actin relprotein-coding
chr3-640:8.631485	0.120298	0.792199	0.151853	0.879303	0.981636	chr3	64098905	64100693	+	0 NA	exon (NM exon (NM	-3671 NR_046701.1	01E+08 Hs. 668874NR_046701	PRICKLE2--	PRICKLE2	ncRNA
chr5-179:8.631485	0.120298	0.792199	0.151853	0.879303	0.981636	chr5	1.8E+08	1.8E+08	+	0 NA	intron (L1M5 LINE	10253 NM_198866	23061 Hs. 155829NM_01504E	ENSG00000TBC1D9B	GRAMD9B	TBC1 domprotein-coding
chr9-3391:8.631485	0.120298	0.792199	0.151853	0.879303	0.981636	chr9	33912458	33914028	+	0 NA	intron (AluSx1 SI	21121 NM_00128E	55833 Hs. 493739NM_01844E	ENSG00000CUBAP2	UBAP-2	ubiquitin protein-coding
chr6-150:9.086934	0.139442	0.788376	0.151504	0.879578	0.981636	chr6	1.51E+08	1.51E+08	+	0 NA	intron (MLT1J LTF	-12676 NM_00135C	25902 Hs. 59134E NM_01544E	ENSG00000MTHFD1L	FTFHSFDC1	methyleneprotein-coding
chr11-125:7.722438	0.133053	0.878345	0.151481	0.879596	0.981636	chr11	1.3E+08	1.3E+08	+	0 NA	intron (intron (N	-6979 NM_001144	4798 Hs. 530539NM_00616E	ENSG00000NFRKB	IN080G	nuclear fprotein-coding
chr2-2011:10.13512	0.11124	0.734839	0.15138	0.879676	0.981636	chr2	2.01E+08	2.01E+08	+	0 NA	non-codiron-codir	-7059 NR_04003C	65072 Hs. 66461E NR_04003C	ENSG00000CFLAR-AS1	ALS2CR10	CFLAR antncRNA
chr11-124:10.17626	0.112662	0.744307	0.151365	0.879688	0.981636	chr11	1.24E+08	1.24E+08	+	0 NA	exon (NM exon (NM	29905 NM_00113C	4013 Hs. 152944NM_01462E	ENSG00000VWA5A	BCSC-1 Bc	von Wille protein-coding
chr3-978:8.079892	0.131617	0.869634	0.151348	0.879701	0.981636	chr3	97887249	97887467	+	0 NA	intron (intron (N	65347 NM_15360E	131544 Hs. 73337E NM_15360E	ENSG00000CRYBG3	DKFZp667C	crystallinprotein-coding
chr1-205:11.63875	0.104514	0.69069	0.151319	0.879724	0.981636	chr1	2.06E+08	2.06E+08	+	0 NA	3' UTR (3' UTR (N	16681 NM_00197E	2005 Hs. 49752E NM_00197E	ENSG00000CELK4	SAP1	ETS transprotein-coding
chr2-216:11.63875	0.104514	0.69069	0.151319	0.879724	0.981636	chr2	2.16E+08	2.16E+08	+	0 NA	exon (NM exon (NM	2243 NM_001127	50485 Hs. 516674NM_01414E	ENSG00000SMARCAL1	HARP HHA5 SWI	rprotein-coding
chr1-258:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr1	25808606	25810399	+	0 NA	intron (L2b LINE	9309 NM_020451	57190 Hs. 32339E NM_020451	ENSG00000SELENON	CFTD MHFAS	selenoprprotein-coding
chr1-155:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr1	1.55E+08	1.55E+08	+	0 NA	intron (intron (N	-27970 NR_03028E	693140 NR_03028E	ENSG00000MIR555	MIRN555	lncRNA ncRNA
chr11-94:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr11	94839185	94839732	+	0 NA	intron (MIRb SINE	71102 NM_001301	154810 Hs. 503594NM_13084E	ENSG00000AMOTL1	JEAP	angiomotiprotein-coding
chr12-12:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr12	1.2E+08	1.2E+08	+	0 NA	intron (AluY SINE	9426 NR_033684	283459 Hs. 70688E NM_17681E	ENSG00000CGATC	15E1.2	glutamyl protein-coding
chr13-95:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr13	95118562	95119223	+	0 NA	intron (L3 LINE C	-91452 NR_145733	1.1E+08 NR_145733	SNORD13G	-	small nucsnRNA
chr15-90:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr15	90230461	90231454	+	0 NA	exon (NM exon (NM	2984 NM_006384	10519 Hs. 71555E NM_006384	ENSG00000CIB1	CIB1 CIBP	calcium protein-coding
chr18-107:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr18	10726406	10726646	+	0 NA	intron (CpG	33123 NR_10684E	1.02E+08 NR_10684E	ENSG00000MIR6788	hsa-mir-6	microRNA ncRNA
chr2-165:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr2	1658436	1659227	+	0 NA	intron (intron (N	85684 NM_01229E	7837 Hs. 332197NM_01229E	ENSG00000PXDN	ASG7 COF	peroxidasprotein-coding
chr2-148:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr2	1.48E+08	1.48E+08	+	0 NA	intron (AluY SINE	-157484 NM_18174E	5000 Hs. 558364NM_00255E	ENSG00000CORC4	ORCAL ORC	origin rprotein-coding
chr6-181:7.648017	0.127621	0.843434	0.151311	0.87973	0.981636	chr6	18168255	18168776	+	0 NA	intron (L1MB5 LIN	13093 NM_001364	221656 Hs. 70933E NM_15304E	ENSG00000KDM1B	AOF1 C6or	lysine deprotein-coding
chr12-76:21.80955	-0.07945	0.525195	-0.15127	0.879763	0.981636	chr12	76027992	76031108	+	0 NA	3' UTR (3' UTR (N	2226 NM_00735C	22822 Hs. 60208E NM_00735C	ENSG00000PHLDA1	DT1P1B11	pleckstriprotein-coding
chr13-95:9.37387	-0.11618	0.76878	-0.15112	0.879882	0.981636	chr13	95305901	95306789	+	0 NA	IntergeniL1PA4 LIN	-4894 NM_00110E	10257 Hs. 50842E NM_00584E	ENSG00000ABCCA	MOAT-B MC	ATP bindi protein-coding
chr14-54:9.094792	0.117889	0.780358	0.15107	0.87992	0.981636	chr14	54822287	54483637	+	0 NA	intron (intron (N	6018 NM_004124	2764 Hs. 15141E NM_004124	ENSG00000GMFB	GMF	glia mat protein-coding
chr21-62:9.094792	0.117889	0.780358	0.15107	0.87992	0.981636	chr21	61682848	6262986	+	0 NA	intron (intron (N	4719 NM_001322	1.03E+08 Hs. 743984NM_001322	LOC102724	-	uncharactprotein-coding
chr18-99:7.469339	-0.12945	0.857254	-0.151	0.879974	0.981636	chr18	9931896	9934228	+	0 NA	intron (AluSg7 SI	19046 NM_003574	9218 Hs. 16519E NM_003574	ENSG00000VAPA	VAP-33 VAV	VAMP asscprotein-coding
chr1-648:9.663951	0.114418	0.75868	0.150812	0.880124	0.981636	chr1	64833507	64834344	+	0 NA	TTS (NM_C	88850 NM_018211	55225 Hs. 59144E NM_018211	ENSG00000RAVER2	-	ribonucle protein-coding
chr16-51:9.663951	0.114418	0.75868	0.150812	0.880124	0.981636	chr16	51139946	51140458	+	0 NA	exon (NM exon (NM	10395 NM_001127	6299 Hs. 135787NM_00296E	ENSG00000SALL1	HEL-S-89	spalt likprotein-coding
chr9-137:9.663951	0.114418	0.75868	0.150812	0.880124	0.981636	chr9	1.34E+08	1.34E+08	+	0 NA	intron (intron (N	-27923 NM_007101	1757 Hs. 19800E NM_007101	ENSG00000SARDH	BPR-2 DMC	sarcosine protein-coding
chr10-89:10.60628	0.129287	0.71938	0.150528	0.880348	0.981636	chr10	89013957	89014865	+	0 NA	non-codiron-codir	-21434 NR_028371	1E+08 Hs. 24413E NR_028371	FAS-AS1	FAS-AS1	antisncRNA
chr15-76:7.689157	0.108296	0.860377	0.150278	0.880545	0.981636	chr15	76211513	76212671	+	0 NA	IntergeniIntergeni	12036E NR_12036E	1.02E+08 Hs. 631721NR_12036E	ENSG00000LOC10192E	-	uncharactncRNA
chr19-48:7.689157	0.129296	0.860377	0.150278	0.880545	0.981636	chr19	48860747	48861269	+	0 NA	intron (AluSx SIN	7609 NM_001161	57664 Hs. 9469 NM_020904	ENSG00000PLEKHA4	PEPPI	pleckstriprotein-coding
chr19-18:9.920271	-0.11823	0.786781	-0.15027	0.880551	0.981636	chr19	18936902	18938817	+	0 NA	intron (intron (N	1190 NM_00114E	9454 Hs. 72020E NM_00483E	ENSG00000HOMER3	HOMER-3 V	homer scprotein-coding
chr3-188:8.920271	-0.11823	0.786781	-0.15027	0.880551	0.981636	chr3	1.89E+08	1.89E+08	+	0 NA	3' UTR (3' UTR (N	72744 NR_04687E	1.01E+08 Hs. 616287NR_04687E	ENSG00000TPRG1-AS1	TPRG1	antncRNA
chr4-540:8.920271	-0.11823	0.786781	-0.15027	0.880551	0.981636	chr4	54043743	54044201	+	0 NA	intron (L1PA4 LIN	20633 NM_01211C	26511 Hs. 33539E NM_01211C	ENSG00000CHIC2	BTL	cysteine protein-coding
chr7-147:8.935987	-0.1216	0.809313	-0.15025	0.880567	0.981636	chr7	1472925	1473362	+	0 NA	exon (NM exon (NM	-13673 NM_182924	79778 Hs. 376617NM_02472E	ENSG00000MICALL2	JRAB MICA	MICAL likprotein-coding
chr19-26:21.11413	0.081104	0.539943	0.150209	0.8806	0.981636	chr19	26924459	26925713	+	0 NA	IntergeniALR Alpha	-868345 NR_14673E	1.02E+08 Hs. 567934NR_14673E	ENSG00000LOC10192E	-	uncharactncRNA
chr1-155:8.119181	0.122814	0.817772	0.150182	0.880621	0.981636	chr1	1.56E+08	1.56E+08	+	0 NA	intron (AluJr SIN	-23073 NR_132767	0.07E+08 NR_132767	SCARNA26E	-	small Ca_ncRNA
chr11-647:8.119181	0.122814	0.817772	0.150182	0.880621	0.981636	chr11	6476732	6478426	+	0 NA	intron (intron (N	-3120 NM_00124E	10612 Hs. 59199E NM_00645E	ENSG00000TRIM3	BERP HACI	tripartitprotein-coding
chr2-117:8.119181	0.122814	0.817772	0.150182	0.880621	0.981636	chr2	1.18E+08	1.18E+08	+	0 NA	intron (intron (N	3243 NM_00677E	8886 Hs. 744922NM_00677E	ENSG00000DDX18	Has1 MrDE	DEAD-box protein-coding
chr5-1771:8.119181	0.122814	0.817772	0.150182	0.880621	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (intron (N	15668 NM_00136E	64324 Hs. 106861NM_02245E	ENSG00000CNSD1	ARA26 Kb	nuclear rprotein-coding
chr18-21:7.591162	0.129265	0.86107	0.150122	0.880668	0.981636	chr18	21629171	21630289	+	0 NA	3' UTR (3' UTR (N	17416 NM_00693E	6632 Hs. 464734NM_00693E	ENSG00000SNRPD1	HsT2456 S	small nucprotein-coding
chr10-35:7.135713	0.131017	0.872827	0.150107	0.880681	0.981636	chr10	35026857	35027352	+	0 NA	intron (intron (N	47179 NM_00119E	8453 Hs. 82919 NM_003591	ENSG00000CUL2	-	cullin 2 protein-coding
chr11-74:7.135713	0.131017	0.872827	0.150107	0.880681	0.981636	chr11	74099412	74099936	+	0 NA	intron (intron (N	39417 NM_00127C	143570 Hs. 37014E NM_18296E	ENSG00000XRR1	-	X-ray racprotein-coding
chr11-75:7.135713	0.131017	0.872827	0.150107	0.880681	0.981636	chr11	75410494	75410987	+	0 NA	intron (SVA_E Ret	6319 NR_00002E	114599 Hs. 68908E NR_00002E	ENSG00000SNORD15B	RNU15B U1	small nucsnRNA
chr22-214:7.135713	0.131017	0.872827	0.150107	0.880681	0.981636	chr22	21471164	21471846	+	0 NA	IntergeniAluJb SIN	4335 NM_001207	645426 Hs. 376511NM_001207	ENSG00000TMEM191C	-	transmem protein-coding
chr7-447:7.135713	0.131017	0.872827	0.150107	0.880681	0.981636	chr7	44757221	44757957	+	0 NA	intron (intron (N	1401 NM_17492E	83637 Hs. 77978 NM_03144E	ENSG00000ZM1Z	NET27 TR	zinc fingprotein-coding
chr7-133:7.135713	0.131017	0.872827	0.150107	0.880681	0.981636	chr7	1.33E+08	1.33E+08	+	0 NA	intron (intron (N	15178 NM_01781E	54927 Hs. 65501E NM_01781E	ENSG00000CHCHD3	MICOS19	coiled-cpprotein-coding

chr15-425.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr15	42974489	42977041	+	0 NA	intron (Alu)Jr SIN	-54987 NM_17350C	146057 Hs. 646511NM_17350C	ENSG000002TBK2	SCA11 TTE tau tubulprotein-coding
chr17-21C.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr17	21024863	21028581	+	0 NA	intron (Alu)Jo SIN	16289 NM_01527E	23326 Hs. 462492NM_01527E	ENSG000002USP22	USP3L ubiquitin protein-coding
chr17-37E.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr17	37535177	37535935	+	0 NA	intron (intron) (N	45665 NM_00702E	11072 Hs. 91448 NM_00702E	ENSG000002DUSP14	MKP-L MKF dual specprotein-coding
chr18-26C.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr18	26028713	26030381	+	0 NA	intron (NL2a) LINE	61066 NM_001007	6760 Hs. 129261NM_005637	ENSG000002SS18	SSXT SYT SS18 subtprotein-coding
chr2-318E.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr2	31898449	31900186	+	0 NA	intron (L1P47) LIN	-95337 NR_146994	1.05E+08 Hs. 580386NR_146994	ENSG000002LINC0194E	long intencRNA
chr22-237.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr22	23793588	23795363	+	0 NA	intron (Alu)Jr SIN	7509 NM_00307E	6598 Hs. 534355NM_00307E	ENSG000002SMARCB1	BAF47 CSS SWI/SNF 1protein-coding
chr5-347E.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr5	34763493	34769037	+	0 NA	intron (THE1A-int	-72899 NM_14472E	153657 Hs. 435742NM_14472E	ENSG000002TTC23L	MC25-1 tetraatricprotein-coding
chr9-1302.8.912414	-0.11664	0.780602	-0.14942	0.881222	0.981636	chr9	1.3E+08	1.3E+08	+	0 NA	intron (L1M5) LINE	-13898 NR_16214E	1.13E+08 Hs. 162140	MIR12126	microRNA ncRNA
chr1-3627.6.152245	-0.14165	0.94809	-0.149406	0.881233	0.981636	chr1	3627142	3627799	+	0 NA	intron (intron) (N	2455 NM_18275E	127262 Hs. 20529 NM_18275E	ENSG000002TPRGL	FAM79A h-tumor prcprotein-coding
chr22-205.6.152245	-0.14165	0.94809	-0.149406	0.881233	0.981636	chr22	20985347	20986123	+	0 NA	intron (intron) (N	3438 NM_006767	8216 Hs. 78788 NM_006767	ENSG000002LZTR1	BTBD29 L2 leucine zprotein-coding
chr13-27C.8.639343	-0.118558	0.795818	-0.148977	0.881572	0.981636	chr13	27075098	27075297	+	0 NA	exon (NM exon) (NM	-50336 NR_046547	1.01E+08 Hs. 52492E NR_046547	USP12-AS1	USP12 antncRNA
chr14-37E.8.639343	-0.118558	0.795818	-0.148977	0.881572	0.981636	chr14	37293158	37293963	+	0 NA	intron (L1P4A) LIN	95623 NM_00119E	145282 Hs. 66039E NM_138731	ENSG000002MIPOL1	CCDC193 mirror-inprotein-coding
chr16-691.8.639343	-0.118558	0.795818	-0.148977	0.881572	0.981636	chr16	69119609	69121698	+	0 NA	intron (intron) (N	11306 NM_00136E	1.13E+08 Hs. 85962 NM_001002847	DERPC	CHTF8 DERPC prcprotein-coding
chr13-207C.8.639343	-0.118558	0.795818	-0.148977	0.881572	0.981636	chr13	27075098	27075297	+	0 NA	exon (NM exon) (NM	95623 NM_00119E	145282 Hs. 66039E NM_138731	ENSG000002MIPOL1	CCDC193 mirror-inprotein-coding
chr6-4367.8.639343	-0.118558	0.795818	-0.148977	0.881572	0.981636	chr6	43677576	43678420	+	0 NA	TTS (NR_C TTS (NR_C	95623 NM_00119E	145282 Hs. 66039E NM_138731	ENSG000002MIPOL1	CCDC193 mirror-inprotein-coding
chr11-67E.10.61414	-0.10691	0.71959	-0.148571	0.881892	0.981636	chr11	67224919	67225888	+	0 NA	intron (intron) (N	9814 NM_01813E	55168 Hs. 52014E NM_01813E	ENSG000002MRPS18A	HumanS18E mitochondonprotein-coding
chr13-10E.10.61414	-0.10691	0.71959	-0.148571	0.881892	0.981636	chr13	1.03E+08	1.03E+08	+	0 NA	intron (Alu)Sj SIN	-14611 NM_00125E	22992 Hs. 124147NM_01230E	ENSG000002KDM2A	CXHC8 FBI lysine deprotein-coding
chr4-293E.10.61414	-0.10691	0.71959	-0.148571	0.881892	0.981636	chr4	2938082	2940556	+	0 NA	intron (NLIMB8) LIN	36029 NM_00101C	196541 Hs. 50862E NM_00101C	ENSG000002METTL21C	C13orf39 methyl trcprotein-coding
chr6-436E.10.61414	-0.10691	0.71959	-0.148571	0.881892	0.981636	chr6	43600773	43602283	+	0 NA	exon (NM exon) (NM	3773 NR_01545E	317648 Hs. 39817E NR_01545E	ENSG000002NOP14-AS1	C4orf10 FNOP14 antncRNA
chrX-240E.10.61414	-0.10691	0.71959	-0.148571	0.881892	0.981636	chrX	24209467	24212295	+	0 NA	intron (Alu)Sq2 SI	25343 NM_001291	5429 Hs. 655467NM_00650E	ENSG000002POLH	RAD30 RAL DNA polynprotein-coding
chr2-610E.10.14297	-0.10975	0.739105	-0.148491	0.881955	0.981636	chr2	61031214	61033008	+	0 NA	exon (NM exon) (NM	61152 NM_00117E	7543 Hs. 336681NM_00341C	ENSG000002ZFX	ZNF296 zinc fing protein-coding
chr6-313E.10.14297	-0.10975	0.739105	-0.148491	0.881955	0.981636	chr6	31353732	31355592	+	0 NA	exon (NM exon) (NM	-13852 NM_00132E	150962 Hs. 36834E NM_14470E	ENSG000002PUS10	CCDC139 Pseudoprotein-coding
chr17-557.9.192787	-0.11737	0.793716	-0.148462	0.881978	0.981636	chr17	55773544	55774410	+	0 NA	TTS (NR_C TTS (NR_C	654 NR_106951	1.02E+08 Hs. 106951	ENSG000002MIR6891	hsa-mir-6microRNA ncRNA
chr16-69E.13.10909	-0.097033	0.653608	-0.148458	0.881981	0.981636	chr16	69370016	69371033	+	0 NA	intron (intron) (N	22872 NM_00110E	58488 Hs. 28521E NM_02121E	ENSG000002CPTP	PC-TP ST phosphatiprotein-coding
chr1-153E.11.6466	-0.103213	0.695331	-0.148438	0.881997	0.981636	chr1	1.54E+08	1.54E+08	+	0 NA	exon (NM exon) (NM	15483 NM_00565E	7014 Hs. 63335 NM_00565E	ENSG000002TERF2	TRBF2 TRF telomericprotein-coding
chr14-321.8.680483	-0.120098	0.809833	-0.148310	0.882106	0.981636	chr14	32136559	32137004	+	0 NA	Intergeni Intergeni	-1528 NM_006694	10899 Hs. 6396 NM_006694	ENSG000002JTB	HJTB HSPC jumping tprotein-coding
chr12-327.9.358154	-0.11312	0.762894	-0.14828	0.882125	0.981636	chr12	327516	328998	+	0 NA	intron (intron) (N	59477 NM_00117E	394 Hs. 59231E NM_00117E	ENSG000002ARHGAP5	GF12 RhoC GTPas protein-coding
chr13-99E.9.358154	-0.11312	0.762894	-0.14828	0.882125	0.981636	chr13	99550292	99550683	+	0 NA	intron (intron) (N	61063 NM_00104E	5927 Hs. 76272 NM_00505E	ENSG000002KDM5A	RBBP-2 RF2 lysine deprotein-coding
chr15-50E.9.358154	-0.11312	0.762894	-0.14828	0.882125	0.981636	chr15	50588875	50589769	+	0 NA	intron (NL2) LINE I	-26625 NR_12639C	1.04E+08 Hs. 639387NR_126390	LINC0103E	long intencRNA
chr3-880E.9.358154	-0.11312	0.762894	-0.14828	0.882125	0.981636	chr3	88055172	88056370	+	0 NA	intron (Alu)Sj SIN	-42656 NM_20349A	373509 Hs. 67775E NM_20349A	ENSG000002USP50	ubiquitin protein-coding
chr4-756E.9.358154	-0.11312	0.762894	-0.14828	0.882125	0.981636	chr4	75644692	75644956	+	0 NA	exon (NM exon) (NM	3225 NM_00366E	8545 Hs. 44481E NM_00366E	ENSG000002CGGBP1	CGGBP1 p2CGG triplprotein-coding
chr5-143E.9.358154	-0.11312	0.762894	-0.14828	0.882125	0.981636	chr5	14320171	14322782	+	0 NA	3' UTR (3' UTR (N	-14296 NM_00133C	8999 Hs. 59169E NM_00394E	ENSG000002CDKL2	KKIAMRE F cyclin deprotein-coding
chr1-329E.8.904556	-0.12003	0.809945	-0.148195	0.882189	0.981636	chr1	32936891	32937090	+	0 NA	intron (intron) (N	-142506 NR_14581E	1.1E+08 Hs. 14581E	SNORD170	small nucsnRNA
chr22-411.7.606877	-0.125599	0.848497	-0.148026	0.882323	0.981636	chr22	41117920	41118994	+	0 NA	exon (NM exon) (NM	27819 NM_001127	127544 Hs. 591504NM_153341	ENSG000002RNF19B	IBRD3 NR ring fingprotein-coding
chr1-244E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	24449405	24452171	+	0 NA	intron (intron) (N	25865 NM_00136E	2033 Hs. 517517NM_00142E	ENSG000002CEP300	KAT3B MKI E1A bindiprotein-coding
chr1-314E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	31423435	31431963	+	0 NA	intron (intron) (N	34763 NM_00132E	57185 Hs. 52344E NM_02044E	ENSG000002NIPAL3	DJ462023. NIPA likeprotein-coding
chr1-1114.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	1.11E+08	1.11E+08	+	0 NA	intron (Alu)Sx1 SI	14341 NM_01856E	347735 Hs. 27065E NM_01856E	ENSG000002SERINC2	FKSG84 PF serine ir protein-coding
chr1-1457.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	1.46E+08	1.46E+08	+	0 NA	intron (intron) (N	9581 NM_00168E	515 Hs. 51487E NM_00168E	ENSG000002ATP5PB	ATP5F1 PIATP syntt protein-coding
chr1-1831.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	1.83E+08	1.83E+08	+	0 NA	intron (NL2a) LINE	40637 NR_10384E	11126 Hs. 488237NM_00705E	ENSG000002CD160	Byc5 NK1 CD160 molprotein-coding
chr1-220C.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	3' UTR (3' UTR (N	-1929 NR_14904E	1.11E+08 Hs. 60406E NR_14904E	ENSG000002LAMC1-AS1	IN-LAMC2 LAMC1 antncRNA
chr1-223E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	2.24E+08	2.24E+08	+	0 NA	intron (intron) (N	41681 NM_00444E	2058 Hs. 49778E NM_00444E	ENSG000002EPRS	EARS GLUF glutamyl- protein-coding
chr1-231E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr1	2.24E+08	2.24E+08	+	0 NA	intron (NLIM5) LINE	37973 NM_001013E	7159 Hs. 52396E NM_00542E	ENSG000002TP53BP2	53BP2 ASF tumor prcprotein-coding
chr10-63E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr10	38095878	38096833	+	0 NA	intron (intron) (N	4022 NM_00101C	83932 Hs. 55489E NM_03201E	ENSG000002SPRIN	C1orf124 SprT prcprotein-coding
chr10-40E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr10	43387165	43395178	+	0 NA	intron (intron) (N	2018 NM_001324	7587 Hs. 29257E NM_003421	ENSG000002ZNF37A	KOX21 ZNF zinc fingprotein-coding
chr10-63E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr10	43387165	43395178	+	0 NA	intron (Alu)Sx1 SI	5660 NM_00109E	3185 Hs. 808 NM_00496E	ENSG000002HNRNPF	HNRPF OK/heterogeprotein-coding
chr10-93E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr10	93331415	93345055	+	0 NA	intron (THE1B) LTF	37000 NM_00135C	9886 Hs. 737374NM_01483E	ENSG000002RHOBTB1	RHOBTB1 Rho relatprotein-coding
chr11-86E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr11	8690766	8700902	+	0 NA	intron (intron) (N	144099 NM_013451	26509 Hs. 60208E NM_013451	ENSG000002MYOF	FERL3 myoferlir protein-coding
chr11-114.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr11	1.14E+08	1.14E+08	+	0 NA	intron (intron) (N	10395 NR_002977	677826 Hs. 74555E NR_002977	ENSG000002SNORA3B	ACA3-2 SN small nucsnRNA
chr12-57E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr12	57494051	57506738	+	0 NA	TTS (NM_C TTS (NM_C	10958 NM_01552E	25996 Hs. 67719E NM_01552E	ENSG000002CREX02	CGI-114 RNA exon protein-coding
chr13-23E.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr13	23356555	23359052	+	0 NA	exon (NM exon) (NM	-11570 NM_00131E	64333 Hs. 43712E NM_03249E	ENSG000002ARHGAP9	OCI RGL1 Rho GTPas protein-coding
chr14-241.8.904556	-0.11508	0.777475	-0.14802	0.882327	0.981636	chr14	24162647</								



chr6-1286 8.401959	-0.1179	0.803742	-0.14669	0.883379	0.981636	chr6	56613596	56614542	+	0	NA	TTS (NM_C	28820	NM_01554E	667	Hs. 60491E	00172	ENSG00000	CDS	BP240	BP240	dystonin protein-coding		
chr8-4307 8.401959	-0.1179	0.803742	-0.14669	0.883379	0.981636	chr8	43074003	43075127	+	0	NA	intron (NLIM2 LINE	18242	NM_002027	2339	Hs. 37031E	002027	ENSG00000	FNTA	FPTA	PGGT	farnesyl protein-coding		
chr9-7025 8.401959	-0.1179	0.803742	-0.14669	0.883379	0.981636	chr9	70290245	70292992	+	0	NA	intron (NLIM4 LINE	32640	NM_01511C	23137	Hs. 53418E	01511C	ENSG00000	SMC5	SMC5L1		structure protein-coding		
chr9-9206 8.401959	-0.1179	0.803742	-0.14669	0.883379	0.981636	chr9	92060974	92063980	+	0	NA	intron (NLIM1 LINE	52936	NM_00641E	10558	Hs. 90458	NM_00641E	ENSG00000	SPTLC1	HSAN1	HSA	serine p protein-coding		
chr12-10C 8.855558	-0.11566	0.78875	-0.14664	0.883415	0.981636	chr12	1E+08	1E+08	+	0	NA	intron (NALuSx3 SI	12091	NR_04856E	64431	Hs. 11508E	02249E	ENSG00000	ACTR6	HPG1	CDAL	actin re protein-coding		
chr5-149E 8.855558	-0.11566	0.78875	-0.14664	0.883415	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	exon (NM_exon (NM	5268	NM_03095E	81789	Hs. 16933E	03095E	ENSG00000	CTIGD6			tigger tr protein-coding		
chr11-111 12.07663	0.099691	0.680017	0.146601	0.883447	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (NALuJb SIN	27297	NR_106814	1.02E+08	NR_106814	ENSG00000	MIR6756		hsa-mir-ε	microRNA	ncRNA		
chr19-381 12.12563	0.099748	0.680525	0.146575	0.883467	0.981636	chr19	38162033	38163367	+	0	NA	promoter-promoter-	-396	NR_145800	1.1E+08	NR_145800	SNORD152					small ncnRNA		
chr2-131F 6.193384	0.143349	0.978101	0.146559	0.88348	0.981636	chr2	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	16641	NR_026922	150776	Hs. 53562E	NR_026922	ENSG00000	LLOC15077E				sphingomy pseudo	
chr1-180E 11.17544	0.10557	0.721205	0.146361	0.883621	0.981636	chr1	1.81E+08	1.81E+08	+	0	NA	intron (NLIP4 LINE	51581	NM_00473E	9213	Hs. 22765E	NM_00473E	ENSG00000	XPR1	IBGC6	SLC	xenotropin protein-coding		
chr14-351 7.143571	0.128802	0.880032	0.146361	0.883637	0.981636	chr14	35105978	35106289	+	0	NA	intron (NALuY SINE	16409	NM_00130E	55012	Hs. 53071E	NM_00130E	ENSG00000	PPP2R3C	C14orf10		protein i protein-coding		
chr17-427 7.143571	0.128802	0.880032	0.146361	0.883637	0.981636	chr17	42713235	42713637	+	0	NA	intron (Nintron (N	-5285	NR_10683E	1.02E+08	NR_10683E	ENSG00000	MIR6780A		hsa-mir-ε	microRNA	ncRNA		
chr2-217 7.143571	0.128802	0.880032	0.146361	0.883637	0.981636	chr2	21777118	21777455	+	0	NA	intron (NL2 LINE L	-41492	NM_01331E	29799	Hs. 51743E	NM_01331E	ENSG00000	YPEL1	FKSG3		yippee lip protein-coding		
chr7-186E 8.450957	-0.11732	0.801792	-0.14632	0.883671	0.981636	chr7	1.86E+08	1.86E+08	+	0	NA	TTS (NR_C	-10514	NM_00112E	346653	Hs. 44523E	NM_00112E	ENSG00000	FAM71F2	FAM137B		family wiprotein-coding		
chr15-73E 8.450957	-0.11732	0.801792	-0.14632	0.883671	0.981636	chr15	73947002	73948030	+	0	NA	intron (Nintron (N	29613	NM_001127	10216	Hs. 64772E	NM_005807	ENSG00000	PRG4	CACP	HAPC	proteogly protein-coding		
chr6-314I 8.450957	-0.11732	0.801792	-0.14632	0.883671	0.981636	chr6	3141120	3141945	+	0	NA	intron (NALuSx3 SI	-19268	NR_04006E	1E+08	Hs. 59978E	NR_04006E	ENSG00000	LOXL1-AS1	LOXL1		antncRNA		
chr7-982E 8.450957	-0.11732	0.801792	-0.14632	0.883671	0.981636	chr7	98290860	98294617	+	0	NA	intron (NALuSx3 SI	16012	NM_00131C	7280	Hs. 65454E	NM_00106E	ENSG00000	TUBB2A	CDCBM5	TU	tubulin t protein-coding		
chr5-109E 9.159505	0.114648	0.784024	0.14623	0.88374	0.981636	chr5	1.1E+08	1.1E+08	+	0	NA	3' UTR (N3' UTR (N	11052	NM_01537E	25798	Hs. 56743E	NM_01537E	ENSG00000	BRI3	I3		brain pr protein-coding		
chr2-239E 9.350296	-0.11165	0.764066	-0.14613	0.883819	0.981636	chr2	2.4E+08	2.4E+08	+	0	NA	intron (Nintron (N	-42564	NR_03317E	1E+08	Hs. 36840E	NR_03317E	LINC0184E				long intncRNA		
chr5-131I 9.350296	-0.11165	0.764066	-0.14613	0.883819	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (NLIMC4 LIN	38824	NR_136157	4705	Hs. 27767E	NM_00454E	ENSG00000	NDUFA10	CI-42KD	C	ubiquitin protein-coding		
chr1-145E 10.26535	-0.10666	0.75737	-0.14611	0.883837	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	intron (Nintron (N	4136	NM_00534C	3094	Hs. 48330E	NM_00534C	ENSG00000	HINT1	HINT	NMAH	histidine protein-coding		
chr1-326E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr1	32656939	32677527	+	0	NA	non-codirnon-codir	34372	NR_104217	1.02E+08	Hs. 53467E	NR_104217	ENSG00000	CNBP25P	WI2-925H4	NBP	ment pseudo		
chr1-393E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr1	39385520	39386741	+	0	NA	intron (NLTR13A LI	15875	NM_00113E	5928	Hs. 16003	NM_00561C	ENSG00000	RBBP4	NURF55	IRF	REB	bindir protein-coding	
chr1-923E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr1	92303928	92305976	+	0	NA	intron (Nintron (N	-22943	NM_01503E	643314	Hs. 65876E	NM_01503E	ENSG00000	KIAA0754				KIAA0754 protein-coding	
chr1-673E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr1	67306836	67307929	+	0	NA	intron (NALuSx6 SI	5893	NM_02481E	79871	Hs. 44442E	NM_02481E	ENSG00000	RPAP2	C1orf82	F	RNA polyn protein-coding		
chr10-243I 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr10	243E+08	2.43E+08	+	0	NA	intron (Nintron (N	-33322	NR_02940I	731275	Hs. 72235E	NR_02940I	ENSG00000	LINC01347-				long intncRNA	
chr10-678E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr10	67806836	67910792	+	0	NA	intron (NALuSx2 SIN	17412	NM_001314	23211	Hs. 36977E	NM_01223E	ENSG00000	SIRT1	SIR2	SIR2	sirtuin protein-coding		
chr10-92E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr10	92554119	92556074	+	0	NA	intron (NLIM1 LINE	18410	NM_001322	3416	Hs. 50054E	NM_00496E	ENSG00000	IDE	INSULYSIN		insulin c protein-coding		
chr10-93E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr10	93969624	93969866	+	0	NA	intron (Nintron (N	4507	NM_001347	118924	Hs. 58665E	NM_14524E	ENSG00000	FRA10AC1	C1orf4	F	FR1A0A	asp protein-coding	
chr10-11E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr10	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	18612	NM_00124E	22876	Hs. 36975E	NM_014937	ENSG00000	INPP5F	MSTP007			inositol protein-coding	
chr11-64E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr11	64871182	64875153	+	0	NA	intron (Nintron (N	5442	NR_162101	1.13E+08	NR_162101	MIR10392						microRNA	ncRNA
chr11-77E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr11	77682359	77686179	+	0	NA	intron (Nintron (N	-46463	NM_001311	1207	Hs. 43073E	NM_00129E	ENSG00000	CLNS1A	CLC1	CLNS	chloride protein-coding		
chr11-12E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr11	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	-8126	NM_001114	1111	Hs. 24523E	NM_001274	ENSG00000	CHEK1	CHK1			checkpoir protein-coding	
chr12-10E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (NTHEIC LTF	43200	NM_00129E	23325	Hs. 12144	NM_01527E	ENSG00000	WASHC4	KIAA1033		WASH comp protein-coding		
chr13-11E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (NMTR SINE	10079	NR_04658E	1.01E+08	Hs. 50871E	NR_04658E	ENSG00000	COL4A2-AS-	COL4A2		arncRNA		
chr14-73E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr14	73206150	73209433	+	0	NA	intron (NMERS2A LI	-29715	NR_15867E	89932	Hs. 50990E	NM_17346E	ENSG00000	PAPLN	PPN	paplin, protein-coding			
chr14-921E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr14	92157201	92159649	+	0	NA	intron (Nintron (N	36456	NM_001322	53981	Hs. 65763E	NM_017437	ENSG00000	CPSF2	CPSF100		cleavage protein-coding		
chr15-77E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr15	77206152	77209002	+	0	NA	intron (NLIMC2 LIN	17827	NR_02681E	81698	Hs. 65693E	NM_030944	LINC00597E	C15orf5				long intncRNA	
chr15-85E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr15	85664330	85665823	+	0	NA	intron (NALuJc SIN	45126	NM_00127C	11214	Hs. 45921E	NM_00667E	ENSG00000	AKAP13	AKAP-13			A-kinase protein-coding	
chr16-117E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	11748720	11757863	+	0	NA	intron (Nintron (N	-10434	NR_13667E	51061	Hs. 31384E	NM_015914	ENSG00000	TXNDC11	EFP1			thioredox protein-coding	
chr16-15E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	15059693	15069865	+	0	NA	intron (Nintron (N	-8700	NM_00127E	123803	Hs. 59204E	NM_173474	ENSG00000	NTANI	PNAAL	PNAAL	-	termin protein-coding	
chr16-214E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	21466467	21469322	+	0	NA	intron (Nintron (N	-33439	NR_02445E	1E+08	Hs. 64843E	NR_02445E	LOC10019C-					uncharactncRNA	
chr16-30E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	30350552	30353734	+	0	NA	3' UTR (N3' UTR (N	2791	NM_00124E	10421	Hs. 20267E	NM_00611C	ENSG00000	CD2BP2	FWP010	L	ICD2	cyto protein-coding	
chr16-53E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	53306207	53308044	+	0	NA	intron (Nintron (N	64087	NM_001347	643802	Hs. 45133E	NM_001207030	LOC64380E-					u3 small protein-coding	
chr16-68E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	68301469	68304334	+	0	NA	intron (Nintron (N	8045	NM_03217E	84138	Hs. 72952E	NM_03217E	ENSG00000	SLC7A60S	-				solute c protein-coding
chr16-74E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	74642107	74644823	+	0	NA	intron (Nintron (N	23412	NM_018124	55159	Hs. 56752E	NM_018124	ENSG00000	RFPWD3	FANCW	RNF	ring fing protein-coding		
chr16-89E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr16	89733268	89738301	+	0	NA	intron (NALuSx1 SI	14247	NM_00111E	92822	Hs. 290154E	NM_15228E	ENSG00000	ZNF276	CENP-2			C zinc fing protein-coding	
chr18-27E 8.896698	-0.11354	0.777291	-0.14607	0.883866	0.981636	chr18	2769651	2773645	+	0	NA	intron (Nintron (N	-75358	NM_03204E	84034	Hs. 53281E	NM_03204E	ENSG00000	CEMLIN2	EMILIN-2				

chr7-6492	8.134897	-0.11906	0.825725	0.144188	0.885352	0.981636	chr7	64921750	649222347	+	0	NA	intron (NLM3 LINE	18806 NM_021144	10793 Hs. 520888NM_021144	ENSG000002ZNF273	HZF9	zinc finger protein-coding	
chr2-9721	11.14216	0.1029	0.713956	0.144127	0.8854	0.981636	chr2	97214747	97216011	+	0	NA	intron (Nintron (N	-63338 NR_103732	1.01E+08 Hs. 732616NR_103732	LOC100506	-	uncharactericRNA	
chr8-430C	8.721622	0.121501	0.845626	0.143682	0.885752	0.981636	chr8	43008911	43009390	+	0	NA	intron (NAluSx SI	-47149 NR_03369E	2339 Hs. 370312NM_020272	ENSG00000CFNTA	FPTA PGGT	farnesyl protein-coding	
chr1-316F	7.50262	-0.12468	0.867987	-0.14364	0.885786	0.981636	chr1	31658672	31658871	+	0	NA	intron (Nintron (N	-13895 NR_03368E	553115 Hs. 470417NM_01239E	ENSG00000PEF1	ABP33 PEF	pena-EP- protein-coding	
chr10-12E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (NMLT1F2 LI	-9179 NR_039704	1.01E+08	NR_039704	ENSG00000MIR4484	MBP-4484	microRNA ncRNA
chr13-331	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr13	33103673	33106780	+	0	NA	3' UTR (N3' UTR (N	80865 NM_00124E	90627 Hs. 156551NM_052851	ENSG00000CSTARD13	ARHGAP37 STAR	relaxin protein-coding	
chr13-44E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr13	44977226	44980533	+	0	NA	intron (Nintron (N	10592 NM_01234E	22747 Hs. 525006NM_01234E	ENSG00000NUF1P1	NUF1P baE	nuclear f protein-coding	
chr14-51E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr14	51692930	51694837	+	0	NA	intron (Nintron (N	-23400 NM_001267	122786 Hs. 434914NM_15233C	ENSG00000FRMD6	C14orf31 FERM	domain protein-coding	
chr19-12E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr19	12656789	12658277	+	0	NA	exon (NM exon (NM	9209 NM_00052E	4125 Hs. 356769NM_00052E	ENSG00000MAN2B1	LAMAN MAN	mannosidase protein-coding	
chr2-392E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr2	39290590	39294638	+	0	NA	intron (NMLT1B LTF	-48631 NR_144521	344387 Hs. 403201NM_01000E	ENSG00000CDKL4	-	cyclin D protein-coding	
chr2-203I	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (NLa2a LINE	-45054 NM_17753E	57404 Hs. 446066NM_020674	ENSG00000CYP20A1	CYP-M	cytochrome protein-coding	
chr3-2747	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr3	27477394	27478347	+	0	NA	intron (NAluSx SIN	6514 NM_001321	9497 Hs. 250072NM_00361E	ENSG00000SLC4A7	NBC2 NBC2	solute carrier protein-coding	
chr5-959C	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr5	95903808	95908544	+	0	NA	intron (Nintron (N	53944 NR_02693E	202299 Hs. 8373	17561E	ENSG00000LINC01554	C5orf27 DF	long intencRNA
chr6-993E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr6	99399979	99403559	+	0	NA	intron (NMER33 DNA	-7574 NM_017421	51805 Hs. 173622NM_017421	ENSG00000COQ3	DHBM2 DF	coenzyme protein-coding	
chr6-100E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr6	1.01E+08	1.01E+08	+	0	NA	intron (NMLT2A2 LI	61900 NM_00682E	10973 Hs. 486031NM_00682E	ENSG00000ASCC3	ASC1p200 activatir	protein-coding	
chr6-111E	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	3' UTR (N3' UTR (N	7788 NM_15336E	91749 Hs. 400572NM_15336E	ENSG00000MFSDB4B	KIAA1919 major	fac protein-coding	
chr9-130I	8.88884	-0.11199	0.780052	-0.14357	0.885843	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	39922 NR_135124	401554 Hs. 522437NR_135124	ENSG00000GPRACR	LncGPR107 GPR107	acncRNA	
chr15-42E	7.453623	-0.1253	0.872916	-0.14354	0.885864	0.981636	chr15	42520166	42520555	+	0	NA	intron (Nintron (N	24726 NM_00382E	8773 Hs. 511145NM_00382E	ENSG00000SNAP23	Hst17016 synapto	s protein-coding	
chr9-363A	8.945695	-0.11298	0.787333	-0.1435	0.885897	0.981636	chr9	36343450	36344675	+	0	NA	intron (NAluSx SI	56207 NM_19432E	152006 Hs. 333503NM_022781	ENSG00000RNF38	-	ring finger protein-coding	
chr9-111E	8.945695	-0.11298	0.787333	-0.1435	0.885897	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	exon (NM exon (NM	-63957 NM_20585E	26248 Hs. 381312NM_20585E	ENSG00000COR2K2	HSHTPCRHC olfactory	protein-coding	
chr12-1119	2.006645	0.115998	0.810095	0.143191	0.88614	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (NSVA_F Ret	36750 NM_025247	80724 Hs. 331141NM_025247	ENSG00000ACAD10	-	acyl-CoA protein-coding	
chr6-111E	8.394102	-0.11618	0.811849	-0.1431	0.886211	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (NLM3A3 LIN	-98793 NR_03410E	643749 Hs. 486222NR_03410E	ENSG00000TRAF3IP2	C6UAS C6c	TRAF3IP2 ncRNA	
chr9-9597	8.394102	-0.11618	0.811849	-0.1431	0.886211	0.981636	chr9	95972068	95972723	+	0	NA	exon (NM exon (NM	49416 NR_02412E	1E+08 Hs. 43431CNR_02412E	ENSG00000LINC0009E	NCRNA000E	long intencRNA	
chr11-114	8.8477	-0.1141	0.797875	-0.14301	0.886282	0.981636	chr11	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	6234 NM_00616E	4837 Hs. 503911NM_00616E	ENSG00000NMMT	-	nicotinan protein-coding	
chr14-71I	8.8477	-0.1141	0.797875	-0.14301	0.886282	0.981636	chr14	71102312	71102824	+	0	NA	intron (Nintron (N	195109 NM_00130E	22994 Hs. 446655NM_01498E	ENSG00000PCNX1	PCNX PCNX	pecanase I protein-coding	
chr22-507	10.62985	0.104032	0.727602	0.142979	0.886307	0.981636	chr22	50789438	50790263	+	0	NA	intron (Nintron (N	6121 NR_02698E	284942 Hs. 406135NM_203302	RPL23AP8E	RPL23A_4E	ribosomal pseudo	
chr16-24E	8.937837	-0.11144	0.781154	-0.14266	0.886559	0.981636	chr16	24973152	24974131	+	0	NA	intron (NLa2c LINE	41728 NM_00100E	55114 Hs. 373793NR_018054	ENSG00000ARHGAP17	MST066 MS	Rho GTPase protein-coding	
chr17-53E	8.937837	-0.11144	0.781154	-0.14266	0.886559	0.981636	chr17	5360816	5362548	+	0	NA	intron (Nintron (N	-57959 NM_00116C	84268 Hs. 462086NM_03230E	ENSG00000CPAIN	HRIP RIP	RPA interprotein-coding	
chr18-45E	8.937837	-0.11144	0.781154	-0.14266	0.886559	0.981636	chr18	45884009	45885274	+	0	NA	exon (NM exon (NM	58966 NM_21360E	284266 Hs. 287692NM_21360E	ENSG00000SIGLEC15	CD33L3 Hs	sialic acid protein-coding	
chr20-17E	8.937837	-0.11144	0.781154	-0.14266	0.886559	0.981636	chr20	17624871	17636204	+	0	NA	intron (Nintron (N	51655 NM_00136E	6238 Hs. 47221E	004587	ENSG00000RRBP1	ES 130	E3 ribosome protein-coding
chr4-150I	8.937837	-0.11144	0.781154	-0.14266	0.886559	0.981636	chr4	15015203	15016522	+	0	NA	intron (NMER44A DN	13381 NM_001177	132864 Hs. 656937NM_18248E	ENSG00000CPEB2	CPE-BP2 C	cytoplasm protein-coding	
chr9-125E	8.937837	-0.11144	0.781154	-0.14266	0.886559	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (NAluSx SIN	12808 NM_005347	3309 Hs. 743241NM_005347	ENSG00000HSPA5	BTP GRP7E	heat shock protein-coding	
chr1-2057	8.937177	-0.1067	0.747981	-0.14265	0.886567	0.981636	chr1	2.06E+08	2.06E+08	+	0	NA	intron (Nintron (N	23247 NM_002731	64710 Hs. 213061NM_022731	ENSG00000NUCKS1	JC7 NUCKS	nuclear protein-coding	
chr5-151E	8.937177	-0.1067	0.747981	-0.14265	0.886567	0.981636	chr5	1.52E+08	1.52E+08	+	0	NA	intron (NAluSq2 SI	4672 NR_10987E	1.02E+08 Hs. 57102E	NR_10987E	ENSG00000CLMAT3	CTB-113P1	colorectal ncRNA
chr1-1127	9.126223	0.111419	0.781108	0.142642	0.886573	0.981636	chr1	11233870	11234354	+	0	NA	intron (Nintron (N	28439 NM_00495E	2475 Hs. 338207NM_00495E	ENSG00000MTOR	FRAP FRAF	mechanism protein-coding	
chr1-267E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr1	26760615	26768047	+	0	NA	intron (Nintron (N	-23632 NM_017837	55650 Hs. 25960E	NR_017837	ENSG00000PIGV	FND MTF-1	phosphatidyl protein-coding
chr1-110C	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	exon (NM exon (NM	16999 NM_00649E	257 Hs. 66995E	NM_00649E	ENSG00000CALX3	FND FND1	ALX homeo protein-coding
chr1-112E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (NLM3A6 LIN	4823 NR_103744	1.01E+08 Hs. 41828E	NR_10374E	ENSG00000SLC16A1	-	SLC16A1 ncRNA
chr1-222E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (Nintron (N	11614 NM_022831	64853 Hs. 15662E	NM_022831	ENSG00000AIDA	-	ACLIN1 intc protein-coding
chr1-243I	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr1	2.43E+08	2.43E+08	+	0	NA	intron (Nintron (N	55491 NM_01481E	9859 Hs. 53363E	NM_01481E	ENSG00000CEP170	FAM68A K	centrosome protein-coding
chr10-11E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr10	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	18744 NR_13666E	7073 Hs. 50120E	NM_00325E	ENSG00000TIAL1	TCPB TIAF	TIAI1 cytc protein-coding
chr11-11E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	TTS (NR TTS (NR_C	2368 NR_16040C	26521 Hs. 27991E	NM_01245E	ENSG00000TIMM8B	DDP2 TIMM	translocase protein-coding
chr12-57E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr12	57511339	57518789	+	0	NA	intron (Nintron (N	2376 NR_10681E	1.02E+08	NR_10681E	ENSG00000MIR6758	hsa-mir-6	microRNA ncRNA
chr16-67E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr16	67830468	67832216	+	0	NA	exon (NM exon (NM	-10978 NM_020457	57215 Hs. 63220C	NM_020457	ENSG00000THAP11	CTG-B43a THAP	domain protein-coding
chr17-36E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr17	69674851	69684958	+	0	NA	intron (NAluY SINE	28771 NR_14575E	57215 Hs. 63220C	NR_14575E	SNORD13H	-	small nuc snoRNA
chr17-36E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr17	36577699	36588780	+	0	NA	intron (NAluSc SIN	-8640 NM_02430E	79154 Hs. 46285E	NM_02430E	ENSG00000DHR511	ARPG836 S	dehydroge protein-coding
chr17-57E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr17	57973659	57974864	+	0	NA	3' UTR (N3' UTR (N	13993 NM_00714E	7716 Hs. 46356E	NM_00714E	ENSG00000VEZF1	DB1 ZNF1E	vascular protein-coding
chr17-75I	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr17	75143000	75144849	+	0	NA	intron (NHY1 scRNA	7549 NM_00128E	51155 Hs. 53280E	NM_01618E	ENSG00000JPT1	ARM2 HNI	Jupiter n protein-coding
chr18-26I	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr18	26031566	26036054	+	0	NA	intron (Nintron (N	56803 NM_001007	6760 Hs. 129261NM_005637	ENSG00000SS18	SSXT SVT	SS18 sub protein-coding	
chr19-21E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr19	2122665	2123761	+	0	NA	intron (Nintron (N	26298 NM_00103E	113177 Hs. 42404E	NM_05287E	ENSG00000IZUM04	C19orf36 IZUM	fan protein-coding
chr19-16E	9.383578	-0.10816	0.758752	-0.14255	0.886646	0.981636	chr19	16552905	16555174	+	0	NA	intron (NAluSz6 SI	-11604 NM_006387	10523 Hs. 740364NM_006387	ENSG00000CCHERP	DAN16 SC	calcium I protein-coding	
chr19-40E	9.383578	-0.1																	



chr3-1848	8.880982	-0.11041	0.785866	-0.1405	0.888267	0.981636	chr3	1.85E+08	1.85E+08	+	0	NA	intron (Nintron (N	43176 NM_00134E	23355 Hs. 269262	1.01530	ENSG000000VPSS8	KIAA0804	VPSS8	subt protein-coding
chr6-5648	8.880982	-0.11041	0.785866	-0.1405	0.888267	0.981636	chr6	56490963	56493654	+	0	NA	exon (NM exon (NM	-98180 NM_00131E	81578 Hs. 47629	1.03082	ENSG000000COL21A1	COL1A1	FF collagen	protein-coding
chr1-1614	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr1	16146830	16149568	+	0	NA	intron (Nintron (N	7870 NM_00132E	1969 Hs. 17159	1.00443	ENSG000000CEPHA2	ARCC2	CTFEPH recep	protein-coding
chr10-100	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr10	1.01E+08	1.01E+08	+	0	NA	intron (Nintron (N	-22586 NM_01789E	57715 Hs. 59192	1.01789	ENSG000000SEMA4G		semaphorin	protein-coding
chr11-433	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr11	43328637	4332613	+	0	NA	intron (Nintron (N	18629 NM_00114E	8539 Hs. 43577	1.00659	ENSG000000AP15	AAC-11	AA apoptotic	protein-coding
chr11-627	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr11	62710786	62712343	+	0	NA	intron (Nintron (N	-1945 NR_03794E	26580 Hs. 53370	1.03266	ENSG000000BCL2L1	GNG3LG	HM BCL2L1 li	protein-coding
chr12-462	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr12	46202780	46204529	+	0	NA	intron (Nintron (N	62862 NM_00127E	81539 Hs. 53377	1.03067	ENSG000000SLC38A1	ATA1	NET3 solute c	protein-coding
chr12-962	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr12	96298436	96300752	+	0	NA	intron (Nintron (N	44966 NM_00130E	2004 Hs. 46523	1.00523	ENSG000000ELK3	ERP	NET3 SETS	trans protein-coding
chr13-331	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr13	33115181	33120198	+	0	NA	3' UTR (N3' UTR (N	68402 NM_00124E	90627 Hs. 15655	1.05285	ENSG000000STARD13	ARHGAP37	STAR rel	protein-coding
chr14-306	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr14	30633084	30635460	+	0	NA	intron (Nintron (N	31538 NM_01610E	23256 Hs. 36916	1.01610	ENSG000000SCFD1	C14orf163	secl1 fami	protein-coding
chr15-762	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr15	76230912	76231548	+	0	NA	intron (Nintron (N	28922 NR_02851E	7302 Hs. 68488	1.02272	ENSG000000TYR03P		TYR03P pr	pseudo
chr17-321	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr17	32174953	32180480	+	0	NA	intron (Nintron (N	-26145 NR_00222E	503640 Hs. 63175	1.02222	ENSG000000ARGFXP2		arginine-p	pseudo
chr2-235C	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr2	2.35E+08	2.35E+08	+	0	NA	intron (Nintron (N	9373 NM_001371306						
chr20-367	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr20	36793205	36793659	+	0	NA	exon (NM exon (NM	-19669 NM_00114E	79980 Hs. 63226	1.02491	ENSG000000CDSN1	C20orf172	DSN1 comp	protein-coding
chr20-495	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr20	49951542	49954515	+	0	NA	3' UTR (N3' UTR (N	16631 NM_01868E	55905 Hs. 14494	1.01868	ENSG000000RNFI14	PSORS12	zring fing	protein-coding
chr3-4792	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr3	47926092	47928184	+	0	NA	intron (Nintron (N	77583 NR_03159E	1E+08	1.03159	ENSG000000MIR1226	MIRN1226	microRNA	ncRNA
chr5-7534	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr5	75344579	75349001	+	0	NA	intron (Nintron (N	9570 NM_00085E	3156 Hs. 62809	1.00085	ENSG000000HMGR	LDLCLQ3	3-hydroxy	protein-coding
chr6-752C	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr6	75237156	75241056	+	0	NA	intron (Nintron (N	4695 NR_15878E	1347 Hs. 70312	1.00186	ENSG000000COX7A2	COX7AL	CC cytochrome	protein-coding
chr9-269C	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr9	26905202	26906004	+	0	NA	exon (NM exon (NM	-12775 NM_00116E	79886 Hs. 17835	1.02482	ENSG000000CAAP1	C9orf82	Caspase	protein-coding
chr9-976E	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr9	97651831	97659489	+	0	NA	intron (Nintron (N	21839 NM_00248E	4686 Hs. 59566	1.00248	ENSG000000NCBP1	CBP80	NCE nuclear	protein-coding
chr9-1101	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	31558 NM_00113E	445815 Hs. 59190	1.00720	ENSG000000PALM2-AK7	AKAP-2	AK PALM2-AK7	protein-coding
chr9-110E	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	76988 NM_15336E	79987 Hs. 52233	1.01536	ENSG000000SVEP1	C9orf13	Cushi,	protein-coding
chr9-132Z	9.37572	-0.10669	0.759918	-0.1404	0.888343	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	3' UTR (N3' UTR (N	90911 NM_00135E	23064 Hs. 46031	1.01504	ENSG000000SETX	ALS4	AOA2 senatax	protein-coding
chr2-203C	9.829319	-0.10531	0.750333	-0.14036	0.888379	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (Nintron (N	63953 NM_00111E	65065 Hs. 64884	1.01984	ENSG000000NBEAL1	A530083	Cneurobeac	protein-coding
chr14-58E	8.427383	-0.11234	0.806117	-0.13936	0.889166	0.981636	chr14	58232444	58233211	+	0	NA	intron (Nintron (N	-11978 NR_03812E	5684 Hs. 55879	1.00278	ENSG000000PSMA3	HCB	PSC3 proteaso	protein-coding
chr2-985E	8.427383	-0.11234	0.806117	-0.13936	0.889166	0.981636	chr2	98599595	98600094	+	0	NA	3' UTR (N3' UTR (N	8668 NM_00100E	493753 Hs. 59653	1.00100	ENSG000000COA5	6330578E1	cytochrome	protein-coding
chr2-201C	8.427383	-0.11234	0.806117	-0.13936	0.889166	0.981636	chr2	20119360	20122544	+	0	NA	intron (Nintron (N	3205 NM_00127E	5902 Hs. 24763	1.00288	ENSG000000RANBP1	HTF9A	RAN bindi	protein-coding
chr7-128E	8.427383	-0.11234	0.806117	-0.13936	0.889166	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	IntergeniL2a LINE	-58728 NR_02436E	402483 Hs. 72235	1.00103	ENSG000000LINC0100C		long intenc	ncRNA
chr1-928E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr1	92849583	92850588	+	0	NA	intron (Nintron (N	9366 NR_00244E	26782 Hs. 18094	1.00244	ENSG000000SNORA66	LIGU-2	U6c small	nucsnRNA
chr1-113C	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	26367 NM_00131E	9860 Hs. 44897	1.01481	ENSG000000LRIG2	RNG-6	L1C leucine	protein-coding
chr1-1147	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr1	1.15E+08	1.15E+08	+	0	NA	exon (NM exon (NM	-9449 NM_00252E	4893 Hs. 48650	1.00252	ENSG000000CNRAS	ALPS4	CMNRRAS	prot protein-coding
chr10-11E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr10	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	-4643 NM_21364E	119559 Hs. 65516	1.01788	ENSG000000SFAX4	BCRM1	COX siderofl	protein-coding
chr12-15E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr12	15898043	15905240	+	0	NA	intron (Nintron (N	-6991 NM_00130E	51071 Hs. 39429	1.01594	ENSG000000DERA	CG1-26	DF deoxyrib	protein-coding
chr12-10E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr12	1.07E+08	1.07E+08	+	0	NA	intron (Nintron (N	3133 NM_00131E	90488 Hs. 25766	1.01526	ENSG000000TMEM263	C12orf23	transmemt	protein-coding
chr13-30E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr13	30279474	30280130	+	0	NA	intron (Nintron (N	27209 NM_00101E	84056 Hs. 24359	1.00321	ENSG000000KATNAL1		katanin	protein-coding
chr14-30E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr14	30602070	30603404	+	0	NA	intron (Nintron (N	-19517 NM_00128E	23256 Hs. 36916	1.01610	ENSG000000SCFD1	C14orf163	secl1 fami	protein-coding
chr16-64E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr16	64970725	64973098	+	0	NA	intron (Nintron (N	150152 NM_00179E	1009 Hs. 11647	1.00179	ENSG000000CDH11	CAD11	CDf cadherin	protein-coding
chr17-324	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr17	32446790	32450113	+	0	NA	intron (Nintron (N	4026 NM_00281E	5717 Hs. 44337	1.00281	ENSG000000PSMD11	Rpn6	S9 proteaso	protein-coding
chr19-101	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr19	10107851	10111293	+	0	NA	promoter-promoter	-177 NR_00368E	1E+08	1.00368	ENSG000000SNORD105E		small nucsnRNA	
chr2-8504	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr2	85047911	85050885	+	0	NA	exon (NM exon (NM	17949 NR_14645E	1.01E+08	1.43439	ENSG000000LINC01964		long intenc	ncRNA
chr2-174E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr2	1.74E+08	1.74E+08	+	0	NA	3' UTR (N3' UTR (N	13374 NM_00114E	1E+08	1.00114	ENSG000000SP9	ZNF990	Sp9 trans	protein-coding
chr2-216E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr2	2.16E+08	2.16E+08	+	0	NA	3' UTR (N3' UTR (N	-11076 NR_00371E	150967 Hs. 56876	1.00119	ENSG000000LINC0196C	PK155	long intenc	ncRNA
chr4-264E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr4	26429086	26431134	+	0	NA	intron (Nintron (N	60374 NM_00073E	886 Hs. 129	1.00073	ENSG000000CCKAR	CCK-A	CCk cholect	protein-coding
chr4-388E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr4	38894336	38900775	+	0	NA	intron (Nintron (N	29523 NR_03030E	693159 Hs. 44972	1.00303	ENSG000000MIR574	MIR574-3	microRNA	ncRNA
chr4-420E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr4	42021229	42024281	+	0	NA	intron (Nintron (N	32225 NM_00634E	10463 Hs. 47963	1.00634	ENSG000000SLC30A9	BILAPES	Csolute c	protein-coding
chr4-118E	8.922121	-0.10837	0.777842	-0.13932	0.889201	0.981636	chr4	1.19E+08	1.19E+08	+	0	NA	non-codirnon-codir	656 NR_10382E	729218 Hs. 44851	1.01382	ENSG000000LOC72921E		uncharact	pseudo
chr8-193E	8.922121																			

chr22-24c7.973785	-0.11424	0.838389	-0.13627	0.891611	0.981636	chr22	24083208	24083424	+	0	NA	exon (NM exon (NM	71946	NM_001199	23523	Hs.51747ENM_01229f	ENSG00000CABIN1	CAIN KB-ε calcineurin protein-coding	
chr1-427f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr1	42700161	42704576	+	0	NA	non-codir non-codir	19232	NR_132737	4904	Hs.473583NM_004455f	ENSG00000YBX1	BP-8 CBF-Y-box bir protein-coding	
chr1-1131f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	44262	NM_001312	9860	Hs.448972NM_01481f	ENSG00000CLRIG2	LIG-2 LIG leucine r protein-coding	
chr1-101f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr1	2.02E+08	2.02E+08	+	0	NA	intron (NAluSx1 S1	9887	NR_106797	1.02E+08	NR_106797f	ENSG00000MIR6739	hsa-mir-ε microRNA ncRNA	
chr10-20f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	intron (NAluG4 S1	6663	NM_004471	9221	Hs.52323f	ENSG00000NOLC1	NOPP130 nucleolar protein-coding	
chr11-107f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr11	10771897	10776850	+	0	NA	intron (Nintron (N	23127	NM_00134f	9646	Hs.725151NM_01463f	ENSG00000CCTR9	SH2BP1 TSCTR9 homc protein-coding	
chr11-111f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	13951	NM_00271f	5519	Hs.26912f	ENSG00000PPP2R1B	PP2A-Abet protein r protein-coding	
chr12-107f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr12	10750939	10710720	+	0	NA	intron (Nintron (N	14994	NM_003651	8531	Hs.22188f	ENSG00000YBX3	CSDA CSDA-Y-box bir protein-coding	
chr12-64c9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr12	64047984	64050375	+	0	NA	intron (N LIMA3 LIN	173117	NM_00130c	144577	Hs.444671NM_15244f	ENSG00000C12orf66	- chromoson protein-coding	
chr12-12f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NAluSq2 S1	7063	NM_00133c	55596	Hs.37706	NM_01761f	ENSG00000ZCHC8	- zinc fing protein-coding
chr13-41f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr13	41361722	41363185	+	0	NA	intron (Nintron (N	-50415	NM_001354	9617	Hs.38217f	ENSG00000MTRF1	MRF1 MTTF mitochon protein-coding	
chr13-11c9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	25219	NM_001267	1E+08	Hs.64003f	ENSG000001267044	COL4A2-AS-	COL4A2 ar protein-coding
chr14-21f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr14	21258801	21266232	+	0	NA	intron (Nintron (N	3183	Hs.50884f	ENSG00000HNRNPC	C1 C2 HNF hetero protein-coding			
chr16-118f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr16	11836994	11842707	+	0	NA	exon (NM exon (NM	-11018	NR_02405c	400500	Hs.24611	NR_02404f	ENSG00000BCAR4	- breast cncRNA
chr17-307f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr17	30790810	30792610	+	0	NA	non-codir non-codir	32982	NM_01598f	51379	Hs.64937f	ENSG00000CRLF3	CREME-9 cytokine protein-coding	
chr17-45f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr17	45093879	45100747	+	0	NA	intron (Nintron (N	17120	NR_106842	1.02E+08	NR_106842f	ENSG00000MIR6784	hsa-mir-ε microRNA ncRNA	
chr17-624f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr17	62446591	62446942	+	0	NA	intron (Nintron (N	22881	NM_18172f	339175	Hs.381204NM_18172f	ENSG00000METTL2	METTL2 methyltrc protein-coding	
chr17-81f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr17	81563955	81566264	+	0	NA	intron (Nintron (N	1493	NR_13014c	55666	Hs.46433f	ENSG00000NPLC2A	NPL4 nly trc protein-coding	
chr18-51f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr18	51078216	51079335	+	0	NA	3' UTR (N3' UTR (N	48562	NM_00535f	4089	Hs.75862	NM_00535f	ENSG00000SMAD4	DPc4 JIP SMAD fami protein-coding
chr2-3387f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr2	3387666	3390132	+	0	NA	intron (Nintron (N	9205	NM_01603c	51112	Hs.25271f	ENSG00000TRAPP12	CGI-87 PE trafficki protein-coding	
chr2-3544f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr2	3544482	3552164	+	0	NA	intron (N L2b LINE	10010	NM_00128f	246243	Hs.56800f	ENSG00000C293f	ENSG00000C293f	H1RNA H1 nucleol protein-coding
chr2-199f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr2	2E+08	2E+08	+	0	NA	intron (Nintron (N	-5643	NM_00103f	129450	Hs.20461f	ENSG00000TYW5	C2orf60 tRNA-yw s protein-coding	
chr2-2381f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	intron (NAluY SINE	14407	NM_03076f	80895	Hs.92033	NM_03076f	ENSG00000ILKAP	ILKAP2 II ILK assoc protein-coding
chr20-34f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr20	34529206	34531032	+	0	NA	5' UTR (N5' UTR (N	13735	NM_01418f	83658	Hs.52932f	ENSG00000DYNLRB1	B1TH BLP dynein l protein-coding	
chr20-57f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr20	57353971	57357736	+	0	NA	intron (Nintron (N	3645	NM_00119c	1E+08	NM_00119f	ENSG00000MTRNR2L3	HN3 MT-RNR2 l protein-coding	
chr3-274f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr3	27432618	27442763	+	0	NA	intron (Nintron (N	19088	NM_00125f	9497	Hs.25007f	ENSG00000SLC4A7	NBC2 NBC3 solute ε protein-coding	
chr3-1324f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr3	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	76492	NM_00132f	23317	Hs.12707	NM_01526f	ENSG00000DNACJ13	PARK21 RN DnaJ heat protein-coding
chr4-880f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr4	88065566	88066376	+	0	NA	intron (Nintron (N	58336	NR_15648f	5311	Hs.18127f	ENSG00000PKD2	APKD2 PC2 polycysti protein-coding	
chr4-168f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (NAluSx4 S1	81296	NM_00136f	23022	Hs.15122f	ENSG00000PALLD	CGI-151 C palladin, protein-coding	
chr5-349f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr5	34909198	34912431	+	0	NA	intron (Nintron (N	4690	NR_026591	5810	Hs.38114	NM_00285f	ENSG00000RAD1	HRA1 REC RAD1 chec protein-coding
chr5-552f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr5	55261730	55263376	+	0	NA	non-codir non-codir	-28836	NR_125347	10309	Hs.3041	NM_02114f	ENSG00000CCNO	CCNU CILL cyclin 0 protein-coding
chr5-137f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (Nintron (N	52406	NM_01438f	27039	Hs.71688f	ENSG00000PKD2L2	TRPP5 polycysti protein-coding	
chr5-149f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	intron (N LIMA4 LIN	26643	NM_001271	1452	Hs.52982f	ENSG00000CSNK1A1	CK1 CK1a trc ki protein-coding	
chr6-729f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr6	7293270	7310025	+	0	NA	intron (N MER117 DN	11552	NM_00129f	6745	Hs.11403f	ENSG00000CSSR1	TRAPA signal sε protein-coding	
chr6-283f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr6	28389287	28393767	+	0	NA	non-codir non-codir	7239	NM_00136f	9753	Hs.13481f	ENSG00000ZSCAN12	ZFP96 ZNF zinc fing protein-coding	
chr7-640f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr7	6406448	6417645	+	0	NA	intron (NAluSx1 S1	35908	NM_13917f	221955	Hs.48749f	ENSG00000DAGLB	DAGLBETA diacylgly protein-coding	
chr7-103f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (N Charlie7ε	4921	NM_00427f	9512	Hs.18421f	ENSG00000PMPCB	Beta-MPP peptidase protein-coding	
chr7-105f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	intron (NAluSq2 S1	5628	NM_02193c	60561	Hs.53138f	ENSG00000RINT1	RINT-1 RBD50 intr protein-coding	
chr8-670f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr8	67080516	67081072	+	0	NA	intron (N MER21C L1	-3054	NM_001291	79848	Hs.370147f	ENSG00000CSP1	CSP1 JBT5 centroson protein-coding	
chr9-127f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	57400	NM_00100f	90678	Hs.49518f	ENSG00000CLRSAM1	CMT2P RIF leucine r protein-coding	
chr9-127f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (Nintron (N	40885	NM_002283f	64855	Hs.52240f	ENSG00000NIBAN2	C9orf88 Fniban apc protein-coding	
chr9-137f9.409002	-0.10326	0.757781	-0.13626	0.891614	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	7836	NM_00127f	6835	Hs.15944f	ENSG00000SURF2	SURF-2 surfeit ζ protein-coding	
chr12-694f10.35734	-0.09904	0.729365	-0.13579	0.891989	0.981636	chr12	69487023	69488279	+	0	NA	intron (N Tigger1 I	17263	NM_00127f	10818	Hs.59344f	ENSG00000FRS2	FRS1A FRS fibrobls protein-coding	
chr13-237f10.35734	-0.123788	0.912556	-0.13565	0.892098	0.981636	chr13	23780309	23780596	+	0	NA	intron (N LIPA5 LIN	-108416	NM_001014	542767	Hs.642624f	ENSG00000PCOTH	C1QTNF9B-Pro-X-Gly protein-coding	
chr4-166f9.911598	-0.10151	0.748712	-0.13558	0.89215	0.981636	chr4	56930521	56931949	+	0	NA	exon (NM exon (NM	22322	NM_00119f	5978	Hs.30783f	ENSG00000CREST	DFNA27 GIRE1 siler protein-coding	
chr4-186f9.911598	-0.10151	0.748712	-0.13558	0.89215	0.981636	chr4	1.87E+08	1.87E+08	+	0	NA	intron (Nintron (N	40781	NM_00524f	2195	Hs.48137f	ENSG00000PAT1	CDHP7 CDF FAT1 atyp protein-coding	
chr1-4357f9.963261	-0.10619	0.785121	-0.13525	0.892414	0.981636	chr1	43579031	43579564	+	0	NA	intron (Nintron (N	48414	NM_00284c	5792	Hs.27206f	ENSG00000PTPRF	BNAH2 LAF intrafla protein-coding	
chr12-11c8.150613	0.114802	0.850508	-0.13498	0.892628	0.981636	chr12	1.1E+08	1.1E+08	+	0	NA	intron (NAluS6 S1	17959	NM_001347	28981	Hs.52382f	ENSG00000IFT81	CDV-1 CDV intrafla protein-coding	
chr1-277f9.854742	-0.10055	0.745056	-0.13496	0.892647	0.981636	chr1	27793977	27795020	+	0	NA	intron (Nintron (N	21279	NM_177424	23673	Hs.52385f	ENSG00000STX12	STX13 STX syntaxin protein-coding	
chr10-864f9.854742	-0.10055	0.745056	-0.13496	0.892647	0.981636	chr10	86499061	86500302	+	0	NA	intron (N MER44A DN	22103	NM_00131f	23063	Hs.20309f	ENSG00000WAPL	FOE KIAAC WAPL cohe protein-coding	
chr16-69f9.854742	-0.10055	0.745056	-0.13496	0.892647	0.981636	chr16	69382057	69384481	+	0	NA	intron (N Tigger4ε	2738	NM_00565f	7014	Hs.63335	NM_00565f	ENSG00000TERF2	TRBF2 TRF telomeri protein-coding
chr17-57f9.854742	-0.10055	0.745056	-0.13496	0.892647	0.981636	chr17	57846423	57846746	+	0	NA	intron (N SVA B Ret	3460	NM_01607c	51649	Hs.5836	NM_01607f	ENSG00000MRP53	CG1-138 Fmitchonc protein-coding
chr8-383f9.854742	-0.10055	0.745056	-0.13496	0.892647	0.981636	chr8	38304768	38305956	+	0	NA	exon (NM exon (NM	-36130	NM_00					



chr6-7351	17.55379	-0.07545	0.573519	-0.13156	0.895331	0.981636	chr6	73515430	73520912	+	0 NA	TTS (NR_TTS (NR_1	267 NR_132981	1.07E+08	NR_132981	SNORD141E	small ncusnoRNA	
chr7-1078	8.411667	-0.10864	0.826178	-0.13149	0.895385	0.981636	chr7	1.08E+08	1.08E+08	+	0 NA	intron (NMERS8A DN	-9758 NM_00127C	110662	Hs. 97627	NR_181581	ENSG00000DUS4L	DUS4 PP3E dihydrour protein-coding
chr1-5178	9.393286	-0.10028	0.762865	-0.13146	0.895414	0.981636	chr1	51786953	51792341	+	0 NA	TTS (NM_TTS (NM_C	46755 NR_03158C	1E+08	NR_03158C	ENSG00000CMIR761	hsa-mir-7 microRNA ncRNA	
chr11-83C	9.393286	-0.10028	0.762865	-0.13146	0.895414	0.981636	chr11	86024213	86026111	+	0 NA	intron (NAIUs SIN	43922 NM_007166	8301	Hs. 16389	NR_007166	ENSG00000PICALM	CALM CLTF phosphatid protein-coding
chr15-26C	9.393286	-0.10028	0.762865	-0.13146	0.895414	0.981636	chr15	23008021	23008281	+	0 NA	intron (NFIAM_C SI	-27253 NM_001324	23191	Hs. 26704	NR_01460F	ENSG00000CYFIP1	P140SRA cytoplasm protein-coding
chr17-59C	9.393286	-0.10028	0.762865	-0.13146	0.895414	0.981636	chr17	59669187	59669994	+	0 NA	intron (Nintron (N	38008 NM_016077	51651	Hs. 12677	NR_016077	ENSG00000CPTRH2	BIT1 CFAP peptidyl protein-coding
chr2-2327	9.393286	-0.10028	0.762865	-0.13146	0.895414	0.981636	chr2	2.33E+08	2.33E+08	+	0 NA	exon (NM exon (NM	5356 NM_002242	3769	Hs. 46733	NR_002242	ENSG00000KCNJ13	KTR1.4 K1 potassium protein-coding
chr5-176C	9.393286	-0.10028	0.762865	-0.13146	0.895414	0.981636	chr5	1.76E+08	1.76E+08	+	0 NA	intron (NAIuY SINE	2682 NM_020444	57179	Hs. 74325	NR_020444	ENSG00000KIAA1191	p33MONOX KIAA1191 protein-coding
chr1-2431	11.56247	0.092623	0.70465	0.131445	0.895423	0.981636	chr1	2.43E+08	2.43E+08	+	0 NA	intron (NAIuY SINE	65943 NM_014812	9859	Hs. 53363	NR_014812	ENSG00000CCEP170	FAM68A KAP centrosome protein-coding
chr10-10C	10.39062	-0.09591	0.729729	-0.13143	0.895435	0.981636	chr10	1E+08	1E+08	+	0 NA	intron (NLIMB3 LIN	4789 NM_001278	1147	Hs. 18999	NR_001278	ENSG00000CHUK	IKBK1 IKF component protein-coding
chr11-12C	10.39062	-0.09591	0.729729	-0.13143	0.895435	0.981636	chr11	1.23E+08	1.23E+08	+	0 NA	intron (NAIuSx1 SI	5361 NM_02476E	79827	Hs. 59194	NR_02476E	ENSG00000CLMP	ACAM ASAM CXADR l1k protein-coding
chr18-21C	10.39062	-0.09591	0.729729	-0.13143	0.895435	0.981636	chr18	21623138	21624702	+	0 NA	exon (NM exon (NM	11606 NM_00693E	6632	Hs. 46473	NR_00693E	ENSG00000SNRPD1	Hst2456 S small nuc protein-coding
chr20-384	10.39062	-0.09591	0.729729	-0.13143	0.895435	0.981636	chr20	38420444	38422381	+	0 NA	intron (Nintron (N	3918 NR_00291C	26776	Hs. 44047	NR_00291C	ENSG00000SNORAT1B	RNU71B U7 small ncusnoRNA
chr1-207C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr1	20759247	20777024	+	0 NA	intron (Nintron (N	18553 NM_016287	50809	Hs. 14282	NR_016287	ENSG00000HP1BP3	HP1-BP74 heteroch protein-coding
chr1-6741	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr1	67416879	67426208	+	0 NA	intron (Nintron (N	8859 NM_00101E	26135	Hs. 53041	NR_01564C	ENSG00000SERBP1	CGI-55 CF SERPINE1 protein-coding
chr1-952A	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr1	95241547	95242670	+	0 NA	intron (NLTR2B2 LI	7898 NM_01548E	25950	Hs. 48351	NR_01548E	ENSG00000RWDD3	RSUME RWD domain protein-coding
chr1-100C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr1	1E+08	1E+08	+	0 NA	intron (Nintron (N	-3504 NR_11043E	1.01E+08	Hs. 19226	NR_11043A	RTCA-AS1	RTCA anticRNA
chr1-182C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr1	1.83E+08	1.83E+08	+	0 NA	intron (Nintron (N	-4663 NR_14893E	647070	Hs. 19151	NR_14893E	LOC64707C	uncharactncRNA
chr10-687	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr10	68746331	68763686	+	0 NA	promoter-promoter-	-164 NR_00307E	692211	NR_00307E	ENSG00000SNORD98	HBII-419 small ncusnoRNA	
chr10-10C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr10	1E+08	1E+08	+	0 NA	intron (Nintron (N	7497 NM_005871	10285	Hs. 63209	NR_005871	ENSG00000SMNDC1	SMNR SPF survival protein-coding
chr12-507	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr12	50796271	50800915	+	0 NA	intron (NAIuY SINE	34492 NM_005171	466	Hs. 64856	NR_005171	ENSG00000ATF1	EWS-ATF1 activator protein-coding
chr12-71C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr12	71605921	71637180	+	0 NA	intron (NAIuSz SIN	42298 NM_14498E	196441	Hs. 24579	NR_14498E	ENSG00000ZFC3H1	CCDC131 zinc fing protein-coding
chr12-71C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr12	71909665	71911479	+	0 NA	intron (NLIPA3 LIN	-28273 NR_17335E	121278	Hs. 73657	NR_17335E	ENSG00000TPH2	ADHD7 NTF tryptophan protein-coding
chr13-11C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr13	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	87277 NR_148221	1.05E+08	Hs. 13472	NR_148221	LOC10537C	uncharactncRNA
chr13-114	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	intron (NMLT1A LTF	7817 NR_04983E	1.01E+08	NR_04983E	ENSG00000MIR548AR	microRNA ncRNA	
chr14-23C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr14	23097045	23099683	+	0 NA	TTS (NM_TTS (NM_C	-2750 NM_00116A	22985	Hs. 12449	NR_00116A	ENSG00000ACIN1	ACINUS ACapoptosis protein-coding
chr14-504	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr14	50478067	50484563	+	0 NA	intron (N(AT)n Sin	51254 NM_198794	11183	Hs. 13049	NR_00657E	ENSG00000MAP4K5	GCKR KHS miptogen protein-coding
chr15-484	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr15	48463664	48474734	+	0 NA	intron (Nintron (N	137002 NM_00194E	1854	Hs. 52798	NR_00194E	ENSG00000CDDUT	dUTPase deoxyuric protein-coding
chr15-491	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr15	49132272	49135297	+	0 NA	exon (NM exon (NM	21815 NM_00114E	9318	Hs. 36961	NR_00423E	ENSG00000COPS2	ALIEN CSN COP9 sig protein-coding
chr15-784	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr15	78482878	78486333	+	0 NA	intron (N(Tigger L2	-22959 NM_00108E	123688	Hs. 30796	NR_00101E	ENSG00000HYKK	AGPHD1 hydroxyl protein-coding
chr17-557	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr17	5577881	5581523	+	0 NA	intron (NLIPA15 LI	4807 NM_033004	22861	Hs. 65227	NR_01492E	ENSG00000NLRP1	AIADK CAF/NLR famil protein-coding
chr17-161	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr17	16001330	16010006	+	0 NA	intron (Nintron (N	5844 NM_01777E	54902	Hs. 46231	NR_01777E	ENSG00000TTC19	20102040 tetraatric protein-coding
chr17-47C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr17	47133744	47147117	+	0 NA	intron (Nintron (N	48865 NM_00125E	996	Hs. 46329	NR_00125E	ENSG00000CDDC27	ANAP3 AF cell divi protein-coding
chr17-471	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr17	47148688	47158355	+	0 NA	intron (Nintron (N	35774 NM_00125E	996	Hs. 46329	NR_00125E	ENSG00000CDDC27	ANAP3 AF cell divi protein-coding
chr2-166C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr2	1668563	1680588	+	0 NA	intron (Nintron (N	69940 NM_01229E	7837	Hs. 33219	NR_01229E	ENSG00000PXD	ASGD7 COF peroxidas protein-coding
chr2-614C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr2	61489281	61501808	+	0 NA	exon (NM exon (NM	-24457 NR_01470E	9736	Hs. 64470	NR_01470E	ENSG00000USP34	ubiquitin protein-coding
chr2-169C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr2	1.7E+08	1.7E+08	+	0 NA	TTS (NM_TTS (NM_C	-4901 NR_14575A	1.1E+08	NR_14575A	SNORD3K	small ncusnoRNA	
chr2-190C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr2	1.91E+08	1.91E+08	+	0 NA	intron (N(Tigger L1	36355 NM_01490E	2744	Hs. 11644	NR_01490E	ENSG00000GLS	AAD20 CAS glutamine protein-coding
chr2-202C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr2	2.02E+08	2.02E+08	+	0 NA	exon (NM exon (NM	6265 NR_14577A	1.1E+08	NR_14577A	ENSG00000SNORD70B	small ncusnoRNA	
chr2-208C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr2	2.08E+08	2.08E+08	+	0 NA	intron (NL2a LINE	22922 NM_00117E	200576	Hs. 74499	NR_01504C	ENSG00000PIKFYVE	CFD FAB1 phosphoir protein-coding
chr21-29C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr21	29055514	29071002	+	0 NA	intron (NL2c LINE	10440 NM_00658E	10694	Hs. 12511	NR_00658E	ENSG00000CCT8	C2lorf112 chaperon protein-coding
chr21-34F	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr21	34825573	34835285	+	0 NA	intron (Nintron (N	58270 NM_001001	861	Hs. 14926	NR_001175A	ENSG00000CNRX1	AML1 AML1RUNX fami protein-coding
chr21-391	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr21	39199447	39200322	+	0 NA	intron (NAIuS2 SI	-16370 NM_20343E	8624	Hs. 47383	NR_00372C	ENSG00000PSMG1	C21LRP DC proteasome protein-coding
chr3-6904	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr3	69046176	69048319	+	0 NA	intron (Nintron (N	1788 NR_036087	1E+08	NR_036087	ENSG00000MIR3136	mir-3136 microRNA ncRNA	
chr3-1337	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	86347 NR_05302E	4638	Hs. 47737	NR_00596E	ENSG00000MYLK	AAT7 KRP myosin l1 protein-coding
chr3-123C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr3	1.34E+08	1.34E+08	+	0 NA	intron (NAIuSx SIN	9157 NM_00128E	55573	Hs. 51826	NR_01754E	ENSG00000CDV3	H41 CDV3 homc protein-coding
chr3-141C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr3	1.41E+08	1.41E+08	+	0 NA	exon (NM exon (NM	42254 NM_00135C	253461	Hs. 51830	NR_15253E	ENSG00000ZBTB38	CIBZ PPP1zinc fing protein-coding
chr4-102C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr4	1.03E+08	1.03E+08	+	0 NA	intron (NFIAM_A SI	111006 NM_00590E	4126	Hs. 48041	NR_00590E	ENSG00000MANBA	MANB1 mannosid e protein-coding
chr4-118C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (NAIuJo SIN	29257 NM_014822	9871	Hs. 18964	NR_01482E	ENSG00000SEC24C	CLCRP2 SEC24 hon protein-coding
chr4-186C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr4	1.87E+08	1.87E+08	+	0 NA	intron (NAIuJo SIN	32185 NM_00524E	2195	Hs. 48137	NR_00524E	ENSG00000FAT1	CDHF7 CDF FAT1 atyp protein-coding
chr5-323C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr5	32395992	32404196	+	0 NA	non-codiron-codir	-5619 NR_03030E	693164	NR_03030E	ENSG00000MIR579	MIRN579 microRNA ncRNA	
chr6-301C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr6	3010089	3012888	+	0 NA	intron (NLIM3F LIN	11330 NM_00131E	4835	Hs. 53305	NR_00090A	ENSG00000NQ02	DHQP DIAE-riboseyl protein-coding
chr8-202C	9.888024	-0.09727	0.740444	-0.13136	0.89549	0.981636	chr8	20208892	20210776	+	0 NA	intron (Nintron (N	12453 NM_00169E					

chr22-507.9.921306	-0.094	0.741254	-0.12681	0.89909	0.981636	chr22	50792061	50792260	+	0	NA	intron (NMER4A1 LI	8431	NR_026982	284942	Hs.406135NM_0203302	RPL23AP82	RPL23A_4c	ribosomal pseudo	
chr9-123.9.921306	-0.094	0.741254	-0.12681	0.89909	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (intron (N	32807	NM_005294	2844	Hs.722035NM_005294	ENSG00000GPR21	-	G protein-coding	
chr9-132f.9.921306	-0.094	0.741254	-0.12681	0.89909	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	intron (intron (N	33167	NM_001322	64794	Hs.660767NM_022779	ENSG00000CDDX31	PPP1R25	DEAD-box protein-coding	
chr10-127.10.36705	-0.09185	0.725547	-0.12659	0.899263	0.981636	chr10	1.27E+08	1.27E+08	+	0	NA	intron (intron (N	126950	NM_00129C	1793	Hs.159195NM_00138C	ENSG00000CDOCK1	DOCK180	cardiac protein-coding	
chr14-517.10.36705	-0.09185	0.725547	-0.12659	0.899263	0.981636	chr14	51702451	51709356	+	0	NA	intron (intron (N	-11380	NM_001267	122786	Hs.434914NM_15233C	ENSG00000CFRMD6	C14orf31	FERM domain protein-coding	
chr17-724.10.36705	-0.09185	0.725547	-0.12659	0.899263	0.981636	chr17	7240465	7241263	+	0	NA	exon (NM_exon (NM	-1407	NM_024297	79142	Hs.644724NM_024297	ENSG00000CPHF23	hJUNE-1b	PHD finger protein-coding	
chr17-81f.10.36705	-0.09185	0.725547	-0.12659	0.899263	0.981636	chr17	81886832	81889984	+	0	NA	non-codirnon-codir	-2382	NM_001288	51529	Hs.534455NM_01647C	ENSG00000CANAPC11	APC11	Apcanaphase protein-coding	
chr4-5427.10.36705	-0.09185	0.725547	-0.12659	0.899263	0.981636	chr4	54272110	54277426	+	0	NA	intron (intron (N	40808	NM_001347	5156	Hs.74615	NM_00620C	ENSG00000PDGFR1	CD140A	PII platelet protein-coding
chr8-117f.10.36705	-0.09185	0.725547	-0.12659	0.899263	0.981636	chr8	1.18E+08	1.18E+08	+	0	NA	intron (intron (N	100703	NR_145799	1.1E+08	NR_145799	SNORD168	-	small nucleolar RNA	
chr2-171f.9.872308	-0.09443	0.747713	-0.12629	0.899502	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	intron (ALuJr SIN	-35385	NM_002477C	79828	Hs.135145NM_02477C	ENSG00000CMTTL8	TIP	methyltransferase protein-coding	
chr12-58f.10.86178	-0.0895	0.710932	-0.1259	0.899815	0.981636	chr12	58874396	58876562	+	0	NA	intron (intron (N	44067	NM_001136	121227	Hs.253735NM_153377	ENSG00000CLRIG3	LIG3	leucine protein-coding	
chr15-671.10.86178	-0.0895	0.710932	-0.1259	0.899815	0.981636	chr15	67184122	67193610	+	0	NA	intron (intron (N	22711	NM_001145	4088	Hs.727985NM_005905	ENSG00000CSMAD3	HSPC193	SMAD family protein-coding	
chr14-88f.10.41604	-0.09142	0.729026	-0.1254	0.900205	0.981636	chr14	88602464	88603753	+	0	NA	intron (intron (N	8688	NM_207662	79882	Hs.684045NM_024824	ENSG00000CZC3H14	MRT56	MSU zinc finger protein-coding	
chr19-19C.10.41604	-0.09142	0.729026	-0.1254	0.900205	0.981636	chr19	19016592	19019211	+	0	NA	intron (intron (N	15616	NR_147913	10147	Hs.77876	NM_014884	ENSG00000CSUGP2	SFRS14	5FSURP and protein-coding
chr14-814.8.486088	-0.10255	0.817906	-0.12538	0.900226	0.981636	chr14	81493263	81493540	+	0	NA	intron (ALuSz SIN	40452	NM_005065	6400	Hs.18130C	NM_005065	ENSG00000CSEL1L	Hrd3	PRO1SEL1L adp protein-coding
chr5-813f.9.831168	-0.09628	0.768487	-0.12529	0.900294	0.981636	chr5	81304806	81305548	+	0	NA	intron (intron (N	3590	NM_001131	84240	Hs.15536	NM_03228C	ENSG00000CZCHC9	PPP1R41	zinc finger protein-coding
chr1-230f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr1	23092143	23094833	+	0	NA	exon (NM_exon (NM	49183	NR_036057	5E+08	NR_036057	ENSG00000CMIR3115	mir-3115	microRNA ncRNA	
chr10-68f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr10	68371448	68375538	+	0	NA	intron (ALuJr SIN	33696	NM_017987	55680	Hs.653144NM_017987	ENSG00000CRUFY2	RAB1P4RZ	ZRUN and Fprotein-coding	
chr11-12f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr11	1.26E+08	1.26E+08	+	0	NA	intron (intron (N	4064	NM_003135	6734	Hs.368375NM_003135	ENSG00000CSRPR4	DP SRPR SRPR	receptor protein-coding	
chr12-98f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr12	98648646	98650992	+	0	NA	intron (ML2c LINE	4519	NM_181868	317	Hs.552567NM_00116C	ENSG00000CAPAF1	APAF-1	Ceapoptotic protein-coding	
chr12-101f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	11489	NM_001177	400	Hs.372615NM_001177	ENSG00000CARL1	ARFL1	ADP ribosyl protein-coding	
chr13-32f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr13	32235185	32238916	+	0	NA	intron (intron (N	74904	NM_001136	646799	Hs.569254NM_001136	ENSG00000CZAR1L	Z3CXXC7	Zzygote ar protein-coding	
chr15-82f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr15	82813147	82820600	+	0	NA	intron (intron (N	7245	NM_00108C	123720	Hs.37736C	NM_00108C	ENSG00000CWHAMM	WHAMM1	WASP hom protein-coding
chr15-101f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr15	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	17134	NM_01491E	22856	Hs.110485NM_01491E	ENSG00000CHSY1	CHSY1	CSS1 chondroitin protein-coding	
chr16-53f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr16	53273813	53276781	+	0	NA	intron (ALuSx1 SI	66846	NM_001352	80205	Hs.59159	NM_015287	ENSG00000CHD9	ADD13	CHL chromodon protein-coding
chr17-46f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr17	46049186	46050715	+	0	NA	intron (ALuSx SIN	50700	NM_001007	26474	Hs.661831NM_001007	ENSG00000CSTH	MAPTIT	saitohin protein-coding	
chr19-12C.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr19	12097933	12098836	+	0	NA	intron (MERR9A LI	6087	NM_00134E	38850	Hs.127475NM_001004314	ZNF788P	ZNF788	zinc finger protein-coding	
chr2-741f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr2	74162336	74172296	+	0	NA	intron (ALuSx3 SI	10998	NM_001317	55233	Hs.602092NM_018221	ENSG00000CMOB1A	C2orf6	MAPMOB kinase protein-coding	
chr20-44f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr20	44480717	44480954	+	0	NA	intron (MLT10 LTF	4961	NM_001261	79183	Hs.283865NM_024331	ENSG00000CTTPAL	C2orf121	alpha top protein-coding	
chr3-690f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr3	69024389	69027384	+	0	NA	intron (intron (N	-12202	NM_001278	285203	Hs.518055NM_173654	ENSG00000EOGT	AR61	AOSBGF domain protein-coding	
chr4-183f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr4	1.83E+08	1.83E+08	+	0	NA	intron (MLMB8 LI	-33283	NR_126477	1.02E+08	Hs.570715NR_126477	ENSG00000CWWC2-AS1	-	WWC2 anticRNA	
chr7-776f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr7	77626796	77629174	+	0	NA	intron (intron (N	68280	NR_134254	1.01E+08	Hs.72451	NR_038361	ENSG00000CAPTR	RSBN1L-AS	Alu-mediated ncRNA
chr9-703f.9.913448	-0.0926	0.741054	-0.12496	0.900558	0.981636	chr9	70305303	70308057	+	0	NA	intron (intron (N	47702	NM_01511C	23137	Hs.534185NM_01511C	ENSG00000CSC5	SMC5L1	structure protein-coding	
chr15-70f.9.913448	-0.09531	0.765012	-0.12459	0.900852	0.981636	chr15	70662639	70665916	+	0	NA	intron (intron (N	29028	NR_126482	1.05E+08	NR_126482	ENSG00000CSALRNA2	SAL-RNA2	senescence ncRNA	
chr19-84f.9.913448	-0.09531	0.765012	-0.12459	0.900852	0.981636	chr19	8463599	8465884	+	0	NA	intron (intron (N	19766	NM_03120C	4670	Hs.465805NM_005965	ENSG00000CHNRPMP	CEAR	HNRP heterologous protein-coding	
chr7-128f.9.913448	-0.09531	0.765012	-0.12459	0.900852	0.981636	chr7	1.28E+08	1.28E+08	+	0	NA	exon (NM_exon (NM	13033	NM_018077	55131	Hs.274265NM_018077	ENSG00000CRBM28	ANES	RNA bindi protein-coding	
chr12-124.11.35652	-0.08747	0.702543	-0.1245	0.900921	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (intron (N	102048	NM_00120C	9612	Hs.13751C	NM_006312	ENSG00000CNCOR2	CTG26	N-C nuclear protein-coding
chr10-11f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr10	1.2E+08	1.2E+08	+	0	NA	intron (intron (N	6487	NM_00719C	11196	Hs.435004NM_00719C	ENSG00000CSEC23P	MSTP053	FSEC23 intron protein-coding	
chr12-49f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr12	49054481	49055316	+	0	NA	intron (intron (N	246	NM_00348C	8085	Hs.731384NM_00348C	ENSG00000CKMT2D	ADD10	ALF lysine protein-coding	
chr12-105f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (MIR3 SINE	22434	NR_13389E	83892	Hs.524731NM_031954	ENSG00000CKCTD10	BTBD28	MS potassium protein-coding	
chr12-114f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr12	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	11503	NM_18148E	6910	Hs.381715NM_000192	ENSG00000CBX5	HOS	T-box protein-coding	
chr14-23f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr14	23029207	23033594	+	0	NA	intron (intron (N	3500	NM_002797	5693	Hs.42299C	NM_002797	ENSG00000CPSMB5	LMPX	MB1 proteasome protein-coding
chr17-29f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr17	29262560	29264941	+	0	NA	3' UTR (3' UTR (N	16893	NM_00520E	1411	Hs.46275	NM_00520E	ENSG00000CRYBA1	CRYB1	CTF crystallin protein-coding
chr17-38f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr17	38495366	38507511	+	0	NA	intron (ALuJ SINE	72974	NM_001195	57636	Hs.374445NM_02087C	ENSG00000CARHGAP23	-	Rho GTPase protein-coding	
chr19-241.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr19	24124587	24130530	+	0	NA	exon (NM_exon (NM	35889	NR_003603	1E+08	Hs.149312NR_003603	ENSG00000CAVCRIP1	-	hepatitis pseudo	
chr20-441.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr20	44197326	44200630	+	0	NA	intron (MERR44C DN	-11400	NM_02043C	57158	Hs.441737NM_02043C	ENSG00000CJPH2	CMH17	JP-junctophin protein-coding	
chr5-167f.10.40819	-0.09008	0.72526	-0.1242	0.901157	0.981636	chr5	16709056	16711525	+	0	NA	intron (intron (N	-93232	NM_001034	54463	Hs.481704NM_01900C	ENSG00000CRETREG1			



chr3-1944 10.87935	-0.08396	0.708886	-0.11843	0.905723	0.981636	chr3	1.94E+08	1.94E+08	+	0 NA	intron (Nintron (N	19002 NM_024524	79572 Hs. 529609	ENSG000004ATP13A3	AFURS1	ATPase 1;protein-coding
chr4-5338 10.87935	-0.08396	0.708886	-0.11843	0.905723	0.981636	chr4	53389760	53392556	+	0 NA	intron (Nintron (N	13505 NM_001134	81608 Hs. 555109	ENSG000004FIP1L1	FIP1 Rhe factor irprotein-coding	
chr5-1385 10.87935	-0.08396	0.708886	-0.11843	0.905723	0.981636	chr5	1.39E+08	1.39E+08	+	0 NA	exon (NM_exon (NM	6390 NM_004134	3313 Hs. 184233	ENSG000004HSPA9	CRP40 CS heat shocprotein-coding	
chr5-1681 10.87935	-0.08396	0.708886	-0.11843	0.905723	0.981636	chr5	1.69E+08	1.69E+08	+	0 NA	intron (NMLT2A LI	-16413 NM_001355	345630 Hs. 166262	ENSG000004FBLL1	- fibrillarprotein-coding	
chr6-1121 10.87935	-0.08396	0.708886	-0.11843	0.905723	0.981636	chr6	1.12E+08	1.12E+08	+	0 NA	intron (NLIPA7 LI	-35845 NR_121199	1.02E+08 Hs. 510007	NR_121193	LOC101927	- uncharacterncRNA
chr7-1934 10.87935	-0.08396	0.708886	-0.11843	0.905723	0.981636	chr7	193499	202604	+	0 NA	intron (Nintron (N	5480 NM_020222	56975 Hs. 134742	ENSG000004FAM20C	DMP-4 DMF FAM20C gcprotein-coding	
chr8-131C 10.38461	-0.08603	0.72282	-0.11814	0.905954	0.981636	chr8	13108854	13114847	+	0 NA	intron (Nintron (N	4394 NM_001164	10395 Hs. 134299	ENSG000004DLC1	ARHGAP7 F DLC1 Rho protein-coding	
chr6-1354 9.938871	-0.08788	0.744551	-0.11803	0.906047	0.981636	chr6	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	14395 NM_001134	54806 Hs. 386684	ENSG000004AHI1	AHI-1 JBT Abelson tpotein-coding	
chr16-303 11.37409	-0.08206	0.696355	-0.11784	0.906192	0.981636	chr16	30300077	30301090	+	0 NA	intron (NAluSq2 SI	34791 NR_002452	595101 Hs. 654656	ENSG000004SMG1P5	- SMG1 pset pseudo	
chr3-149C 11.37409	-0.08206	0.696355	-0.11784	0.906192	0.981636	chr3	1.49E+08	1.49E+08	+	0 NA	intron (Nintron (N	33418 NM_004534	2992 Hs. 134299	ENSG000004GYG1	GD515 GYC glycogeninprotein-coding	
chr6-5661 10.43361	-0.08561	0.727226	-0.11772	0.906292	0.981636	chr6	56615801	56617334	+	0 NA	exon (NM_exon (NM	667 Hs. 604919	ENSG000004CST	BP240 BP dyostonin protein-coding		
chr1-1681 11.86883	-0.08042	0.689534	-0.11663	0.907155	0.981636	chr1	1.68E+08	1.68E+08	+	0 NA	intron (NAluJb SIN	18080 NM_001031	261726 Hs. 209431	ENSG000004TIPRL	TIP TIP41TOR signcprotein-coding	
chr4-121C 10.87149	-0.08267	0.710882	-0.11629	0.907423	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (Nintron (N	16235 NM_001154	308 Hs. 480652	ENSG000004ANXA5	ANX5 ENX2 amexin fprotein-coding	
chr6-1362 10.87149	-0.08267	0.710882	-0.11629	0.907423	0.981636	chr6	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	19733 NM_001107	9774 Hs. 486542	ENSG000004BCLAF1	BTF bk21 BCL2 assocprotein-coding	
chr19-211 11.36623	-0.08082	0.695105	-0.11627	0.907436	0.981636	chr19	21180772	21184651	+	0 NA	exon (NM_exon (NM	40671 NM_133472	170959 Hs. 156256	ENSG000004ZNF431	- zinc fingprotein-coding	
chr7-9941 11.36623	-0.08082	0.695105	-0.11627	0.907436	0.981636	chr7	99410678	99413910	+	0 NA	intron (NKanga2_a	3122 NR_162133	1.13E+08	NR_162133	MIR12119	- microRNA ncRNA
chr7-152 10.42575	-0.08428	0.725841	-0.11611	0.907565	0.981636	chr7	1.52E+08	1.52E+08	+	0 NA	exon (NM_exon (NM	101983 NM_001371474				
chr18-79E 8.024632	-0.10088	0.872078	-0.11568	0.907903	0.981636	chr18	79918936	79919431	+	0 NA	intron (Nintron (N	32470 NM_001146	80148 Hs. 288284	ENSG000004SLC66A2	PQLC1 solute cprotein-coding	
chr7-597E 11.86097	-0.07918	0.685366	-0.11553	0.908027	0.981636	chr7	5976031	5978705	+	0 NA	intron (Nintron (N	-6685 NM_173565	222967 Hs. 442339	ENSG000004RSPH10B	- radial fsprotein-coding	
chr19-53C 10.92049	-0.08226	0.712169	-0.11551	0.908043	0.981636	chr19	53090596	53092047	+	0 NA	intron (Nintron (N	-4284 NM_001322	90338 Hs. 655967	ENSG000004ZNF160	F11 HKR1 zinc fingprotein-coding	
chr6-1494 12.30671	-0.07806	0.676274	-0.11543	0.908103	0.981636	chr6	1.49E+08	1.49E+08	+	0 NA	3' UTR (N3' UTR (N	9601 NM_001002	387082 Hs. 657168	ENSG000004SUM04	IDDM5 SMI small ubiprotein-coding	
chr3-172E 8.949395	-0.09248	0.807101	-0.11458	0.90878	0.981636	chr3	1.73E+08	1.73E+08	+	0 NA	3' UTR (N3' UTR (N	69666 NM_001345	1894 Hs. 518299	ENSG000004CCT2	ARHGEF31 epithelicprotein-coding	
chr12-69F 11.35837	-0.07959	0.695923	-0.11437	0.908946	0.981636	chr12	69587021	69595655	+	0 NA	intron (Nintron (N	5449 NM_001194	10576 Hs. 189772	ENSG000004CCT2	99D8.1 CC chaperoniprotein-coding	
chr16-30C 11.35837	-0.07959	0.695923	-0.11437	0.908946	0.981636	chr16	30066441	30074246	+	0 NA	TTS (NM_TTS (NM_C	4583 NM_184041	226 Hs. 513499	ENSG000004ALDOA	ALDA ALD aldolase, protein-coding	
chr4-8281 11.35837	-0.07959	0.695923	-0.11437	0.908946	0.981636	chr4	82817750	82831481	+	0 NA	exon (NM_exon (NM	-25758 NR_024906	79966 Hs. 379191	ENSG000004SCD5	ACOD4 FAI stearoyl-protein-coding	
chr1-2201 11.41523	-0.08047	0.704703	-0.11419	0.909086	0.981636	chr1	2.2E+08	2.2E+08	+	0 NA	intron (NLIPIA7 LI	30526 NR_031705	1E+08	NR_031705	ENSG000004MIR664A	MIR664 MimicroRNA ncRNA
chr8-1447 11.85311	-0.07797	0.683192	-0.11413	0.909138	0.981636	chr8	1.45E+08	1.45E+08	+	0 NA	intron (Nintron (N	1798 NR_106909	1.02E+08	NR_106909	ENSG000004MIR6850	hsa-mir-6microRNA ncRNA
chr1-193C 10.91263	-0.08099	0.709748	-0.11411	0.909154	0.981636	chr1	1.93E+08	1.93E+08	+	0 NA	intron (NAluSx SIN	8128 NR_135611	1.07E+08	NR_135611	ENSG000004SCARNA18E	- small Ca_ncRNA
chr10-151 10.91263	-0.08099	0.709748	-0.11411	0.909154	0.981636	chr10	15131848	15135415	+	0 NA	intron (NAluJ SIN	21716 NR_036506	1E+08 Hs. 714691	NR_036506	ENSG000004PPIAP30	- peptidy pseudo
chr2-985E 10.91263	-0.08099	0.709748	-0.11411	0.909154	0.981636	chr2	9856345	9858845	+	0 NA	intron (NTHEID LITR	14121 NM_005688	9014 Hs. 584833	ENSG000004TAF1B	MGC:9349 TATA-box protein-coding	
chr21-452 10.91263	-0.08099	0.709748	-0.11411	0.909154	0.981636	chr21	45271562	45272799	+	0 NA	intron (NLIPIB1 LI	15715 NM_015227	23275 Hs. 592164	ENSG000004POFUT2	C2orf80 protein (protein-coding	
chr11-95E 10.41789	-0.08292	0.726813	-0.11409	0.909166	0.981636	chr11	95979208	95979460	+	0 NA	exon (NM_exon (NM	-55127 NM_016155	8898 Hs. 181322	ENSG000004MTMR2	CMT4B myotubule protein-coding	
chr14-102 10.41789	-0.08292	0.726813	-0.11409	0.909166	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (NAluSq2 SI	42273 NR_030942	81693 Hs. 534494	ENSG000004AMN	PRO1028 eamion asprotein-coding	
chr5-401E 9.436275	-0.08856	0.777202	-0.11395	0.909281	0.981636	chr5	401660	402235	+	0 NA	intron (NLM3 LINE	41213 NR_126522	116349 Hs. 446702	ENSG000004EXOC3-AS1	5orf55 EXOC3 antncRNA	
chr11-117 3.718028	-0.13431	1.179496	-0.11387	0.909338	0.981636	chr11	1.19E+08	1.19E+08	+	0 NA	intron (NLM7 LIN	33425 NM_005188	867 Hs. 504099	ENSG000004CBL	C-CBL CBL cl protcprotein-coding	
chr22-402 3.718028	-0.13431	1.179496	-0.11387	0.909338	0.981636	chr22	40792592	40793237	+	0 NA	intron (Nintron (N	21044 NR_039922	1.01E+08	NR_039922	ENSG000004MIR4766	mir-4766 microRNA ncRNA
chr16-58E 9.395136	-0.09021	0.795384	-0.11342	0.909699	0.981636	chr16	58584992	58585194	+	0 NA	intron (Nintron (N	-25162 NR_00298C	677830 Hs. 677519	ENSG000004SNORA50A	ACA50 SNC small nucsnoRNA	
chr10-792 4.220625	-0.12603	1.114212	-0.11306	0.909983	0.981636	chr10	79252107	79252909	+	0 NA	intron (Nintron (N	-94961 NM_005725	10105 Hs. 381072	ENSG000004PPIF	CYP3 Cyp-peptidy protein-coding	
chr20-441 9.923155	-0.08491	0.751841	-0.11294	0.910081	0.981636	chr20	44196654	44196928	+	0 NA	3' UTR (N3' UTR (N	-9213 NM_020433	57158 Hs. 441737	ENSG000004JPH2	CMH17 JP-junctophiprotein-coding	
chr11-126 10.90477	-0.0797	0.709537	-0.11233	0.91056	0.981636	chr11	1.26E+08	1.26E+08	+	0 NA	intron (NAluSz SIN	26447 NM_024555	79607 Hs. 276319	ENSG000004FAM118B	- family wiprotein-coding	
chr16-302 10.90477	-0.0797	0.709537	-0.11233	0.91056	0.981636	chr16	30252888	30259772	+	0 NA	IntergeniLIPIA5 LI	-10617 NM_001321	613037 Hs. 585732	ENSG000004NIP1B3	- nuclear fprotein-coding	
chr4-8681 10.90477	-0.0797	0.709537	-0.11233	0.91056	0.981636	chr4	86813173	86816218	+	0 NA	3' UTR (N3' UTR (N	36489 NM_197962	345274 Hs. 452999	ENSG000004SLC10A6	SOAT solute cprotein-coding	
chr6-1334 10.90477	-0.0797	0.709537	-0.11233	0.91056	0.981636	chr6	1.33E+08	1.33E+08	+	0 NA	intron (NLM5 LIN	228162 NM_001301	2070 Hs. 596688	ENSG000004EYAA	CMDJ1 DF EYAA transprotein-coding	
chr2-994C 11.39951	-0.07798	0.695864	-0.11207	0.910771	0.981636	chr2	99438630	99439028	+	0 NA	exon (NM_exon (NM	51188 NM_016316	51455 Hs. 443077	ENSG000004REV1	AIBP80 RF RETV1 DNA protein-coding	
chr21-371 11.39951	-0.07798	0.695864	-0.11207	0.910771	0.981636	chr21	37108102	37110293	+	0 NA	intron (NLIPIA4 LI	26250 NM_003316	7267 Hs. 368214	ENSG000004TTC3	DCRR1 RNF tetraictrprotein-coding	
chr22-292 11.39951	-0.07798	0.695864	-0.11207	0.910771	0.981636	chr22	29281215	29290405	+	0 NA	intron (Nintron (N	17542 NM_005243	2130 Hs. 374477	ENSG000004EWSR1	EWS EWS-F EWS RNA tpotein-coding	
chr9-7401 11.39951	-0.07798	0.695864	-0.11207	0.910771	0.981636	chr9	740158	743079	+	0 NA	intron (NAlu SINE	34941 NM_001354	23189 Hs. 306764	ENSG000004KANK1	ANKRD15 CKN motif protein-coding	
chr18-164 10.41004	-0.08153	0.730171	-0.11165	0.911097	0.981636	chr18	16433391	16433909	+	0 NA	IntergeniALR Alpha	-1107831 NR_027417	644669 Hs. 579474	ENSG000004LOC64466E	- ankyrin tpseudo	
chr21-25E 10.41004	-0.08153	0.730171	-0.11165	0.911097	0.981636	chr21	25891439	25891742	+	0 NA	intron (Nintron (N	-155936 NM_001003	522 Hs. 246319	ENSG000004ATP5PF	ATP5 ATP ATP syntpprotein-coding	
chr12-111 4.666365	-0.11774	1.058096	-0.11127	0.911402	0.981636	chr12	1.12E+08	1.12E+08	+	0 NA	intron (NAluSc SIN	-16877 NM_00069C	217 Hs. 604551	ENSG000004ALDH2	ALDH-E2 aldehyde protein-coding	
chr2-175 4.212767	-0.12283	1.105401	-0.11112	0.91152	0.981636	chr2	1.75E+08	1.75E+08	+	0 NA	IntergeniTiger2 b	-6650 NM_001255	1386 Hs. 592519	ENSG000004ATF2	CRE-BP1 C activatir protein-coding	
chr20-35E 4.212767	-0.12283	1.105401	-0.11112	0.91152	0.981636	chr20	3596769	3597426	+	0 NA	intron (NLM1 LINE	66302 NM_022133	64096 Hs. 302022	ENSG000004GFRA4	- GDNF famiprotein-coding	
chr12-497 10.85578	-0.08002	0.721782	-0.11086													

chr10-735	11.88824	-0.06776	0.683889	-0.09908	0.921077	0.981636	chr10	73912172	73917750	+	0	NA	intron (Nintron (N	3829 NM_002658	5328 Hs. 77274 NM_002658	ENSG000001PLAU	ATF1 BDPL1 plasminogen protein-coding
chr6-7285	10.41974	-0.07384	0.749242	-0.09855	0.921493	0.981636	chr6	7289723	7290442	+	0	NA	intron (Nintron (N	23117 NM_001292	6745 Hs. 114033 NM_003144	ENSG000001SSR1	TRAPA signal protein-coding
chr12-455	5.178669	-0.09875	1.003486	-0.09841	0.921607	0.981636	chr12	45383090	45385050	+	0	NA	intron (Nintron (N	91380 NM_001142	196527 Hs. 505333 NM_001022	ENSG000001CAN06	BDPL17 SCANoctamin protein-coding
chr15-655	5.178669	-0.09875	1.003486	-0.09841	0.921607	0.981636	chr15	65397275	65398082	+	0	NA	intron (Nintron (N	-19676 NM_004884	9543 Hs. 128292 NM_004884	ENSG000001IGDC3	HsT18880 immunoglobulin protein-coding
chr2-201C	5.178669	-0.09875	1.003486	-0.09841	0.921607	0.981636	chr2	210196	2.01E+08	+	0	NA	intron (Nintron (N	27906 NM_001321	285172 Hs. 24701 NM_173822	ENSG000001FAMI26B	HYCC2 family wiprotein-coding
chr22-264	5.178669	-0.09875	1.003486	-0.09841	0.921607	0.981636	chr22	26480589	26481437	+	0	NA	intron (Nintron (N	-1332 NM_152841	89781 Hs. 474433 NM_022081	ENSG000001CHPS4	BLOC3S2 LHPS4 biogen protein-coding
chr6-1112	5.178669	-0.09875	1.003486	-0.09841	0.921607	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	3' UTR (N3' UTR (N	11238 NM_153366	91749 Hs. 400572 NM_153366	ENSG000001MPSD4B	KIAA1919 major facprotein-coding
chr6-1571	5.178669	-0.09875	1.003486	-0.09841	0.921607	0.981636	chr6	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	138087 NM_018452	729515 Hs. 157212 NM_018452	ENSG000001MEM242	BMO33 C6c transmem protein-coding
chr1-1535	12.86986	-0.06459	0.657624	-0.09822	0.921759	0.981636	chr1	1.54E+08	1.54E+08	+	0	NA	intron (Nintron (N	2894 NM_00103C	6232 Hs. 546291 NM_00103C	ENSG000001CRPS27	DBA17 MP5 ribosomal protein-coding
chr11-582	12.86986	-0.06459	0.657624	-0.09822	0.921759	0.981636	chr11	582054	585960	+	0	NA	intron (Nintron (N	7537 NM_00128E	57661 Hs. 325833 NM_020901	ENSG000001PHRF1	PPP1R125 PHD and i protein-coding
chr20-621	12.86986	-0.06459	0.657624	-0.09822	0.921759	0.981636	chr20	62137414	62140667	+	0	NA	intron (Nintron (N	4354 NM_00279E	5688 Hs. 233952 NM_00279E	ENSG000001PSMA7	C6 HEL-5 proteasome protein-coding
chr5-1093	12.86986	-0.06459	0.657624	-0.09822	0.921759	0.981636	chr5	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	41091 NM_01481E	9867 Hs. 483033 NM_01481E	ENSG000001CPJA2	Neurodapl praja rir protein-coding
chr8-431C	12.86986	-0.06459	0.657624	-0.09822	0.921759	0.981636	chr8	43102241	43112873	+	0	NA	intron (Nintron (N	14042 NM_032237	84197 Hs. 491644 NM_032237	ENSG000001POMK	MDDG12 N protein (protein-coding
chr11-104	12.86986	-0.06459	1.11037	-0.09811	0.921844	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	Intergeni MERR46C DN	33936 NM_00001E	38 Hs. 232375 NM_00001E	ENSG000001ACAT1	ACAT MAT acetyl-C protein-coding
chr19-115	4.230332	-0.10894	1.11037	-0.09811	0.921844	0.981636	chr19	11933587	11934364	+	0	NA	intron (Nintron (N	8868 NM_14456E	90592 Hs. 528488 NM_14456E	ENSG000001ZNF700	- zinc fing protein-coding
chr7-943C	12.37512	-0.06554	0.669733	-0.09786	0.922041	0.981636	chr7	94395708	94431041	+	0	NA	intron (Nintron (N	18813 NM_000008E	1278 Hs. 489142 NM_000008E	ENSG000001COL1A2	EDSAR2B2 collagen protein-coding
chr11-754	12.862	-0.06349	0.657399	-0.09658	0.923062	0.981636	chr11	75400672	75406711	+	0	NA	promoter-promoter-exon (NM exon (NM	-705 NR_00002E	114599 Hs. 689088 NR_00002E	ENSG000001SNORD15B	RNU15B U1small nucsnoRNA
chr3-1975	12.862	-0.06349	0.657399	-0.09658	0.923062	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (Nintron (N	3917 NM_000099E	6165 Hs. 529631 NM_000099E	ENSG000001RPL35A	DBA5 L35 ribosomal protein-coding
chr4-119E	12.862	-0.06349	0.657399	-0.09658	0.923062	0.981636	chr4	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	4279 NM_03343C	8654 Hs. 647971 NM_001083	ENSG000001PDE5A	CGB-PDE C phosphodi protein-coding
chr10-59E	5.129672	-0.09997	1.037441	-0.09637	0.923231	0.981636	chr10	59807808	59808213	+	0	NA	intron (Nintron (N	-54555 NM_001304	1.01E+08 Hs. 648799 NM_001304	ENSG000001MRLN	LINC00948 myoregulin protein-coding
chr19-202	4.725071	-0.10139	1.05214	-0.09637	0.923231	0.981636	chr19	2098400	2099938	+	0	NA	intron (Nintron (N	2254 NM_001033E	113177 Hs. 424045 NM_05287E	ENSG000001TZUM04	C19orf36 IZUM04 fan protein-coding
chr1-456E	4.676073	-0.10231	1.06496	-0.09607	0.923466	0.981636	chr1	45609749	45610524	+	0	NA	intron (Nintron (N	13918 NM_00119C	149483 Hs. 18912 NM_15250C	ENSG000001CCDC17	- coiled-c protein-coding
chr13-952	4.676073	-0.10231	1.06496	-0.09607	0.923466	0.981636	chr13	95249722	95250884	+	0	NA	intron (Nintron (N	39959 NR_145733	1.1E+08 NR_145733	SNORD13G	- small nucsnoRNA
chr17-82	4.676073	-0.10231	1.06496	-0.09607	0.923466	0.981636	chr17	82941812	82942519	+	0	NA	TTS (NM_C TTS (NM_C	64823 NR_13546E	146712 Hs. 607824 NM_00100E	ENSG000001BGNLTL1	3-Gn-T8 EUDP-GlcN protein-coding
chr19-525	4.676073	-0.10231	1.06496	-0.09607	0.923466	0.981636	chr19	52927346	52928777	+	0	NA	non-codiron-codir	-10130 NM_00131C	388559 NM_00131C	ENSG000001ZNF888	- zinc fing protein-coding
chr5-657	4.676073	-0.10231	1.06496	-0.09607	0.923466	0.981636	chr5	65705704	65706819	+	0	NA	intron (Nintron (N	15848 NM_01907E	54557 Hs. 482301 NM_01907E	ENSG000001SGTB	SGT2 small glt protein-coding
chr11-117	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr11	59802 NM_01495E	22897 Hs. 50400E	ENSG000001CEP164	64214 NM_001984	2098 Hs. 432491 NM_001984	ENSG000001CESD	51573 Hs. 512607 NM_016641	ENSG000001GDE1	NPHP15 centrosome protein-coding	
chr13-467	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr13	46732101	46733794	+	0	NA	intron (Nintron (N	19505727	19506558	ENSG000001GDE1	FGH esterase protein-coding
chr16-19E	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr16	67635376	67637100	+	0	NA	intron (Nintron (N	-8906 NM_00101E	146206 Hs. 611432 NM_00101E	ENSG000001CARMIL2	363E6.2 N glycerol p protein-coding
chr17-735	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr17	73218288	73220548	+	0	NA	intron (Nintron (N	8299 NM_00128E	84923 Hs. 74127E NM_032837	ENSG000001FAM104A	CARMIL2B capping f protein-coding
chr2-612E	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr2	61267655	61269212	+	0	NA	intron (Nintron (N	91015 NR_152211	130872 Hs. 655602 NM_15239E	ENSG000001AHS2P	AHA1 AHS activator pseudo
chr22-314	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr22	31448041	31450110	+	0	NA	intron (Nintron (N	40481 NM_001164	56478 Hs. 51755E NM_01984E	ENSG000001EIF4ENIF1	EIF4E-T Clas eukaryot protein-coding
chr7-923E	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr7	92354293	92355223	+	0	NA	intron (Nintron (N	82556 NR_14599E	1.05E+08 NM_001317	ENSG000001TMBIM7P	- transmem pseudo
chr8-506E	5.170811	-0.09614	1.00349	-0.09581	0.923674	0.981636	chr8	54089401	54091006	+	0	NA	intron (Nintron (N	11801 NM_00127E	10434 Hs. 74404E NM_00633C	ENSG000001LYPLA1	APT-1 API lysophosph protein-coding
chr6-104E	6.119448	-0.09038	0.947764	-0.09536	0.924025	0.981636	chr6	1.07E+08	1.07E+08	+	0	NA	intron (Nintron (N	-23518 NM_00131E	84816 Hs. 15583E NM_03273C	ENSG000001RTN4IP1	NIMP OPA reticular protein-coding
chr1-122E	29.75365	0.044698	0.46934	0.095236	0.924127	0.981636	chr1	1.23E+08	1.23E+08	+	0	NA	Intergeni ALR Alphe	1163975 NR_00395E	647121 Hs. 69768E NR_00395E	ENSG000001EMBPI1	- embigin f pseudo
chr1-9261	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr1	92619272	92619886	+	0	NA	intron (Nintron (N	-132654 NM_00526E	2672 Hs. 73172 NM_00526E	ENSG000001GFT1	GFT-1 GFI growth f protein-coding
chr11-117	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	8419 NM_01495E	22897 Hs. 50400E NM_01495E	ENSG000001CEP164	NPHP15 centrosome protein-coding
chr15-61E	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr15	61913259	61914248	+	0	NA	intron (Nintron (N	146694 NM_017684	54832 Hs. 51166E NM_017684	ENSG000001VPS13C	PARK23 vacuolar protein-coding
chr19-351	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr19	3518955	3519745	+	0	NA	intron (Nintron (N	-3606 NM_00113E	51343 Hs. 413133 NM_01626E	ENSG000001FZRI	CDC20C C fizzy an protein-coding
chr19-454	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr19	45420805	45422262	+	0	NA	intron (Nintron (N	1995 NM_00136E	2067 Hs. 435981 NM_00198E	ENSG000001ERCC1	CORF54 RAI ERCC exciprotein-coding
chr2-183C	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr2	1.83E+08	1.83E+08	+	0	NA	intron (Nintron (N	16409 NM_01343E	10787 Hs. 60373E NM_01343E	ENSG000001CNCKAP1	HEM2 NAP NCK assoc protein-coding
chr21-32E	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr21	32635897	32636736	+	0	NA	intron (Nintron (N	-23445 NM_00135E	56683 Hs. 5811 NM_01783E	ENSG000001CFAP298	C21orf48 cilia an protein-coding
chr7-1021	5.665549	-0.09117	0.967091	-0.09427	0.924896	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	-169166 NM_02097E	10603 Hs. 48944E NM_02097E	ENSG000001SH2B2	APS SH2B adaf protein-coding
chr16-651	4.222474	-0.10555	1.120036	-0.09424	0.924917	0.981636	chr16	65116697	65117340	+	0	NA	intron (Nintron (N	5045 NM_001797	1009 Hs. 116471 NM_001797	ENSG000001CDH11	CAD11 CDF cadherin protein-coding
chr2-232E	4.222474	-0.10555	1.120036	-0.09424	0.924917	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (Nintron (N	10410 NM_00133C	9470 Hs. 29202E NM_00484E	ENSG000001EIF4E2	4E-1P 4E eukaryot protein-coding
chr7-158E	4.222474	-0.10555	1.120036	-0.09424	0.924917	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	intron (Nintron (N	28897 NM_00135E	55112 Hs. 38994E NM_018051	ENSG000001WDR60	FAP163 SFWD repeat protein-coding
chr17-28E	4.712123	-0.09856	1.048283	-0.09402	0.925096	0.981636	chr17	28829475	28830620	+	0	NA	intron (Nintron (N	12743 NM_00128E	55731 Hs. 56453E NM_01818E	ENSG000001FAM222B	FAP163 family wiprotein-coding
chr2-9661	4.712123	-0.09856	1.048283	-0.09402	0.925096	0.981636	chr2	96619709	96620473	+	0	NA	intron (Nintron (N	17900 NR_04765E	55683 Hs. 516341 NM_017991	ENSG000001KANSL3	KIAA1310 KAT8 regu protein-coding
chr3-1411	4.712123	-0.09856	1.048283	-0.09402	0.925096	0.981636	chr3	14113875	14115088	+	0	NA	intron (Nintron (N	10389 NM_00109E	131474 Hs. 51781E NM_14463E	ENSG000001CHCHD4	MIA40 TIV coiled-c protein-coding
chr12-10E	8.984341	0.079684	0.847628	0.094008	0.925102	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	12780 NM_01470E	9733 Hs. 58484E NM_01470E	ENSG000001SART3	DSAP1 PIC spliced protein-coding
chr16-197	12.46877	0.063842	0.685084	0.093188	0.925754	0.981636	chr16	19714375	19714619	+	0	NA	exon (NM exon (NM	-1959 NM_00130E	124152 Hs. 460217 NM_15320E	ENSG000001IQCK	- IQ motif protein-coding
chr1-100E	5.162953	-0.09356	1.010361	-0.0926	0.926222	0.981636	chr1	1									



chr8-4802	4.701497	-0.0926	1.064636	-0.08697	0.930691	0.981636	chr8	48026234	48027457	+	0	NA	intron (N)LM8B LIN	18414	NM_00335C	7336	Hs.49169	ENM_00335C	ENSG000003	UBE2V2	DDVIT1 DL	ubiquitin protein-coding		
chr5-4951	19.36322	0.048185	0.555038	0.086814	0.93082	0.981636	chr5	49555906	49557483	+	0	NA	IntergeniALR Alpha	884594	NM_198445	133418	Hs.561411	NM_198445	ENSG000003	EMB	GP70	emigin protein-coding		
chr5-1727	15.40762	0.052903	0.610999	0.086584	0.931002	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (N)intron (N)	2007	NM_004417	1843	Hs.17169	ENM_004417	ENSG000003	DUSP1	CL100 HVF	dual spec protein-coding		
chr12-124	5.690973	-0.08316	0.960457	-0.08658	0.931005	0.981636	chr12	1.25E+08	1.25E+08	+	0	NA	intron (N)Tiger18a	32967	NM_03265E	57647	Hs.10738	ENM_03265E	ENSG000003	DHX37	DDX37 Dhr	DEAH-box protein-coding		
chr13-325	5.690973	-0.08316	0.960457	-0.08658	0.931005	0.981636	chr13	32773291	32773931	+	0	NA	intron (N)intron (N)	138041	NR_047022	1.01E+08	Hs.40629	CNR_047020	LINC00425			long intencRNA		
chr16-475	5.690973	-0.08316	0.960457	-0.08658	0.931005	0.981636	chr16	47546387	47547237	+	0	NA	intron (N)LIPA6 LIN	85481	NM_001031	5257	Hs.78060	NM_00029	ENSG000003	PHKB	-		phosphory protein-coding	
chr3-966	5.690973	-0.08316	0.960457	-0.08658	0.931005	0.981636	chr3	9666275	9667798	+	0	NA	intron (N)intron (N)	17531	NM_02248E	64619	Hs.47538	ENM_02248E	ENSG000003	MTRM14	C3orf29	myotubul protein-coding		
chr1-2201	9.023631	0.069682	0.804919	0.08657	0.931013	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (N)L2a LINE	-34464	NR_029711	406969	NR_029711	ENSG000003	MIR194-1	MIRN194-1	lincRNA	ncRNA		
chr6-3477	11.45202	0.060851	0.704963	0.086318	0.931213	0.981636	chr6	34773458	34774411	+	0	NA	TTS (NM_C)TTS (NM_C)	16429	NM_00309	6631	Hs.1063	NM_00309	ENSG000003	CNRPC	U1C Yhc1	small nuc protein-coding		
chr3-1217	6.136714	-0.08033	0.932021	-0.08619	0.931316	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (N)AluSg SIN	-21788	NM_00125E	2804	Hs.21338	ENM_004487	ENSG000003	GOLGB1	GCP GCP37	soluble B1 protein-coding		
chr10-792	5.641976	-0.08399	0.976306	-0.08602	0.931447	0.981636	chr10	79204586	79206505	+	0	NA	intron (N)intron (N)	136579	NM_02033E	57178	Hs.19311	ENM_02033E	ENSG000003	ZMIZ1	MIZ RAI1	7zinc fing protein-coding		
chr11-674	5.641976	-0.08399	0.976306	-0.08602	0.931447	0.981636	chr11	67440274	67440638	+	0	NA	intron (N)intron (N)	-2774	NM_00560E	5790	Hs.15597	ENM_00560E	ENSG000003	PTPRCAP	CD45-AP I	protein t protein-coding		
chr2-2706	5.641976	-0.08399	0.976306	-0.08602	0.931447	0.981636	chr2	27064866	27065756	+	0	NA	intron (N)intron (N)	6343	NM_001134	1E+08	Hs.50294	ENM_001134	ENSG000003	COST4	-		oligosacc protein-coding	
chr2-1215	5.641976	-0.08399	0.976306	-0.08602	0.931447	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	intron (N)intron (N)	30171	NM_004807	9394	Hs.51284	ENM_004807	ENSG000003	HS6ST1	HH15 HS6	heparan s protein-coding		
chr4-4757	5.641976	-0.08399	0.976306	-0.08602	0.931447	0.981636	chr4	47576925	47577910	+	0	NA	intron (N)intron (N)	-75252	NR_10702C	1.02E+08	NR_10702C	ENSG000003	MIR8053	hsa-mir-ε	microRNA	ncRNA		
chr6-1395	17.84387	0.048883	0.569906	0.085774	0.931646	0.981636	chr6	1.39E+08	1.39E+08	+	0	NA	intron (N)intron (N)	1047	NM_00116E	10370	Hs.82071	NM_00607	ENSG000003	CITFED2	ASDB MRG-Cbp	p300 protein-coding		
chr20-345	8.503469	0.070669	0.82434	0.085728	0.931682	0.981636	chr20	34929802	34930001	+	0	NA	intron (N)L2c LINE	25734	NM_00132E	2937	Hs.82327	NM_00017	ENSG000003	CSSG	GSHS HEL	-glutathion protein-coding		
chr19-344	6.631452	-0.07746	0.905605	-0.08554	0.931836	0.981636	chr19	34523997	34544711	+	0	NA	3' UTR (N)3' UTR (N)	-10886	NM_001184	2821	Hs.46647	NM_00017	ENSG000003	GPI	AMF GNP1	glucose t protein-coding		
chr9-1335	13.84547	-0.05442	0.637375	-0.08538	0.931959	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	promoter-promoter-	44	NR_00001E	26813	NR_00001E	ENSG000003	SNORD36C	RNU36C U	small nuc snoRNA			
chr17-78	9.981676	0.064199	0.755025	0.085029	0.932238	0.981636	chr17	78807227	78807924	+	0	NA	exon (NM)exon (NM)	-25233	NM_00476E	9267	Hs.19121	ENM_00476E	ENSG000003	CYTH1	B2-1 CYC	cytohesin protein-coding		
chr9-9921	9.453656	0.066778	0.785681	0.084994	0.932266	0.981636	chr9	99218133	99218503	+	0	NA	exon (NM)exon (NM)	3624	NR_02453Z	85365	Hs.40919	NM_033087	ENSG000003	ALG2	CDG1I CDC	ALG2 alpl protein-coding		
chr20-206	6.185711	-0.0798	0.939732	-0.08492	0.932327	0.981636	chr20	20026435	20027004	+	0	NA	intron (N)intron (N)	8924	NM_181527	51126	Hs.36878	ENM_01610C	ENSG000003	NAA20	NAT3 NAT3N	(alpha)-protein-coding		
chr20-284	6.185711	-0.0798	0.939732	-0.08492	0.932327	0.981636	chr20	28402081	28402763	+	0	NA	IntergeniALR Alpha	200243	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG000003	FRG1CP	-		FSHD repseudo	
chr4-1382	6.185711	-0.0798	0.939732	-0.08492	0.932327	0.981636	chr4	1.38E+08	1.38E+08	+	0	NA	intron (N)intron (N)	2190	NM_014331	23657	Hs.390594	NM_014331	ENSG000003	SLCTA11	CCBR1 xCT	soluble c protein-coding		
chr2-1018	12.41007	0.057396	0.677483	0.084719	0.932485	0.981636	chr2	1.02E+08	1.02E+08	+	0	NA	intron (N)intron (N)	134173	NM_145687	9448	Hs.70101	ENM_004834	ENSG000003	MAP4K4	FLH2 1957	mitogen-ε protein-coding		
chr1-225	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr1	22508177	22509858	+	0	NA	intron (N)intron (N)	-54472	NM_00100E	2046	Hs.28361	ENM_02052E	ENSG000003	EPH8A	EEL EK3 E	EPH receptor protein-coding		
chr12-102	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr12	1020949	1030428	+	0	NA	intron (N)intron (N)	1990	NM_001301	23085	Hs.60121	ENM_17803E	ENSG000003	ERC1	Cast2 ELF	ELKS/RAB	ε protein-coding	
chr13-252	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr13	25272046	25272849	+	0	NA	intron (N)LM5 LINE	15041	NM_00468E	9107	Hs.64370	ENM_00468E	ENSG000003	MTR6	-		myotubul protein-coding	
chr13-421	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr13	42162042	42162378	+	0	NA	intron (N)intron (N)	24152	NM_001204	160851	Hs.63038	ENM_15291C	ENSG000003	DGKH	DGKTA	diacylglycerol protein-coding		
chr16-465	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr16	4695496	4696267	+	0	NA	TTS (NM_C)TTS (NM_C)	2163	NM_00137C	84309	Hs.51331	ENM_03234E	ENSG000003	NUDT16L1	SDDG5 TIRF	nucleic hyc protein-coding		
chr16-685	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr16	68933261	68933891	+	0	NA	intron (N)MLT1H LTF	90045	NM_02456E	79613	Hs.13526	NM_02456E	ENSG000003	TANGO6	TMCO7	transport protein-coding		
chr17-371	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr17	37128257	37129302	+	0	NA	intron (N)intron (N)	95034	NR_03605E	1E+08	NR_03605E	ENSG000003	MIR2909	-		microRNA	ncRNA	
chr18-355	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr18	35310094	35310551	+	0	NA	non-codiron-codir	20050	NM_02456E	10778	Hs.31424	ENM_00662E	ENSG000003	ZNF2719	CT-ZFP48	zinc fing pseudo		
chr19-12	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr19	1209221	1213566	+	0	NA	intron (N)intron (N)	5594	NM_00045E	6794	Hs.51500	ENM_00045E	ENSG000003	CSTK11	LKB1 PJS	serine/t protein-coding		
chr19-157	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr19	1578787	1580481	+	0	NA	intron (N)intron (N)	-11309	NM_001174	399664	Hs.43649	ENM_20330A	ENSG000003	MEX3D	MEX-3D MF	mex-3 RNr protein-coding		
chr2-235	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr2	69476143	69476852	+	0	NA	intron (N)intron (N)	-38869	NM_001072	27247	Hs.43043	ENM_01570C	ENSG000003	NFU1	CG3-33 HNFU1	RNAr protein-coding		
chr2-1331	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr2	1.33E+08	1.33E+08	+	0	NA	intron (N)LIPA5 LIN	-75736	NR_110294	1.02E+08	Hs.661917	NR_110294	ENSG000003	CNKAP5-AS	-		NCKAP5 arncRNA	
chr2-210	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr2	2.1E+08	2.1E+08	+	0	NA	intron (N)AluJo SIN	9272	NM_00131E	6120	Hs.28226	ENM_00691E	ENSG000003	RPE	RPE2-1	ribulose- protein-coding		
chr2-235	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr2	2.35E+08	2.35E+08	+	0	NA	intron (N)intron (N)	-22127	NM_001371306									
chr20-941	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr20	9410749	9412362	+	0	NA	intron (N)intron (N)	-102803	NM_00119E	24141	Hs.22920	NM_012261	ENSG000003	LAMP5	BAD-LAMP L	lysosomal protein-coding		
chr5-435	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr5	43538833	43539525	+	0	NA	intron (N)intron (N)	17898	NM_006451	10605	Hs.48202	ENM_006451	ENSG000003	PAIP1	-		poly (A) t protein-coding	
chr5-185	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (N)AluSq2 SI	32026	NM_016604	51780	Hs.48348	ENM_016604	ENSG000003	KDM3B	5qNCA C5c	lysine de protein-coding		
chr5-177	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (N)AluJb SIN	29204	NM_00130E	23567	Hs.48425	ENM_01227E	ENSG000003	ZNF346	JAZ Zfp34	zinc fing protein-coding		
chr6-1552	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr6	15522128	15522992	+	0	NA	TTS (NM_C)TTS (NM_C)	140468	NR_03644E	84062	Hs.57114	ENM_03212E	ENSG000003	DTNBP1	BLOC1S8 L	dystrobre protein-coding		
chr7-474	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr7	47490555	47490960	+	0	NA	intron (N)MLT1G3 LI	-25954	NR_145813	1.1E+08	NR_145813	SNORD151	-		small nuc snoRNA			
chr9-324	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr9	32459374	32460102	+	0	NA	intron (N)intron (N)	66458	NM_014314	23586	Hs.19062	ENM_014314	ENSG000003	DDX58	RIG-I RIC	B5x/H-bc protein-coding		
chr9-1347	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (N)intron (N)	-64148	NR_138045	414316	Hs.57156	NR_138045	ENSG000003	COL5A1-AS	C9orf104 COL5A1	arncRNA		
chr11-331	5.683115	-0.08075	0.957471	-0.08434	0.932786	0.981636	chr11	33149815	33152281	+	0	NA	intron (N)LM8B LIN	10432	NM_00132E	1479	Hs.44402	ENM_00132E	ENSG000003	CSTF3	CSTF-77	cle		

chr7-7431 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chr7	74319915	74323421	+ 0 NA	intron (AluSg7 SI	32193 NM_003388	7461 Hs. 64701ENM_003388	ENSG000004CLIP2	CLIP CLIFCAP-Gly cprotein-coding
chr7-7537 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chr7	75371400	75372876	+ 0 NA	IntergeniAluJr SIN	12938 NR_040588	54441 Hs. 63231CNM_018991	STAG3L1	STAG3L1 stromal pseudo
chr7-1507 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chr7	1.51E+08	1.51E+08	+ 0 NA	IntergeniMER31-int	28522 NM_018384	55340 Hs. 64707ENM_018384	ENSG000004GIMAP5	HIMAP3 ATGase, lprotein-coding
chr8-6724 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chr8	67242038	67243599	+ 0 NA	intron (NLIM1 LINE	100963 NM_006421	10565 Hs. 656902NM_006421	ENSG000004ARFGEF1	ARFGEF1 EADP ribosprotein-coding
chr9-7514 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chr9	75143879	75144552	+ 0 NA	intron (Nintron (N	55701 NM_012388	26578 Hs. 494192NM_012388	ENSG000004OSTF1	OSTF SH3P2osteoclastprotein-coding
chr9-1297 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chr9	1.3E+08	1.3E+08	+ 0 NA	3' UTR (N3' UTR (N	-3788 NR_132102	1.02E+08 Hs. 11259ENR_132102	ENSG000004PRRX2-AS1	PRRX2 antncRNA
chrX-7157 6.169995	-0.07513	0.923222	-0.08138	0.935142	0.981636	chrX	71573662	71574711	+ 0 NA	3' UTR (N3' UTR (N	-3838 NM_052957	93953 Hs. 135167NM_052957	ENSG000004GCNA	ACR4 NAAF germ cellprotein-coding
chr14-761 5.229517	-0.08144	1.003301	-0.08117	0.935304	0.981636	chr14	76195170	76196004	+ 0 NA	intron (Nintron (N	41233 NR_110314	55668 Hs. 410231NM_01792f	ENSG000004GPATCH2L	140rf118G-patch cprotein-coding
chr7-158 14.36563	-0.05072	0.626309	-0.08098	0.935457	0.981636	chr7	1.59E+08	1.59E+08	+ 0 NA	intron (Nintron (N	59331 NM_001350	55112 Hs. 38994ENM_018051	ENSG000004WDR60	FAP163 SFWD repeatprotein-coding
chr10-18 4.734778	-0.08587	1.061179	-0.08092	0.935506	0.981636	chr10	18577798	18578804	+ 0 NA	intron (AluSx SIN	73282 NM_001351	221078 Hs. 396177NM_18254f	ENSG000004NSUN6	4933414ECNOP2/Sun protein-coding
chr10-92 6.615736	-0.07325	0.905392	-0.08091	0.935516	0.981636	chr10	92008475	92009230	+ 0 NA	exon (NM exon (NM	85088 NM_003972	9044 Hs. 50052fNM_003972	ENSG000004BTAF1	MOT1 TAF-4B-TP12 lprotein-coding
chr12-15 6.615736	-0.07325	0.905392	-0.08091	0.935516	0.981636	chr12	15884270	15885290	+ 0 NA	intron (Nintron (N	2393 NM_007178	11171 Hs. 743971NM_007178	ENSG000004STRAP	MAWD PT-Wserine/tlprotein-coding
chr15-84 6.615736	-0.07325	0.905392	-0.08091	0.935516	0.981636	chr15	84769342	84770072	+ 0 NA	intron (NL2a LINE	21115 NM_014630	9640 Hs. 79347 NM_014630	ENSG000004ZNF592	CAMOS SC2zinc fingerprotein-coding
chr3-186 6.615736	-0.07325	0.905392	-0.08091	0.935516	0.981636	chr3	1.87E+08	1.87E+08	+ 0 NA	intron (NLIME3F LI	7609 NM_016306	51726 Hs. 317192NM_016306	ENSG000004DNABJ11	ABBP-2 AE DnaJ heatprotein-coding
chr4-113 6.615736	-0.07325	0.905392	-0.08091	0.935516	0.981636	chr4	1.14E+08	1.14E+08	+ 0 NA	intron (Nintron (N	216060 NM_001354	287 Hs. 620557NM_00114f	ENSG000004ANK2	ANK-2 LQ1ankyrin 2protein-coding
chr13-114 7.110474	-0.07108	0.879185	-0.08085	0.935556	0.981636	chr13	1.14E+08	1.14E+08	+ 0 NA	intron (NMIRc SINE	35105 NM_001327	22821 Hs. 59307fNM_00736f	ENSG000004RASAS4	GAP1P4BFRAS p21 fprotein-coding
chr5-777 7.110474	-0.07108	0.879185	-0.08085	0.935556	0.981636	chr5	77770837	77771203	+ 0 NA	intron (AluSx1 SI	5319 NM_001297	6902 Hs. 291212NM_004607	ENSG000004CTBCA	- tubulin fprotein-coding
chr5-1771 7.471003	-0.071584	0.885447	-0.08085	0.935556	0.981636	chr5	17770808	1.77E+08	+ 0 NA	intron (AluJb SIN	17630 NM_001366	64324 Hs. 106861NM_02245f	ENSG000004NSD1	ARA267 kub nuclear lprotein-coding
chr20-27 15.34725	-0.04923	0.611416	-0.08051	0.935829	0.981636	chr20	27758540	27758824	+ 0 NA	IntergeniALR/Alpha	843983 NR_13231f	1E+08 Hs. 529357NR_13231f	ENSG000004FRG1CP	- FSHD regipseudo
chr1-137 6.664734	-0.07262	0.902412	-0.08047	0.935861	0.981636	chr1	1372724	1373638	+ 0 NA	TTS (NM_C TTS (NM_C	2026 NM_001127	54998 Hs. 63251fNM_01790f	ENSG000004AURKAIPI1	AIP AKTIP aurora lprotein-coding
chr17-15 6.664734	-0.07262	0.902412	-0.08047	0.935861	0.981636	chr17	15505979	15506499	+ 0 NA	intron (NLTR12C LI	-35403 NR_146601	94145 Hs. 69733fNR_146601	CDRT3	- CMT1A dupncRNA
chr2-6111 6.664734	-0.07262	0.902412	-0.08047	0.935861	0.981636	chr2	61119807	61120441	+ 0 NA	intron (NLIME1 LI	24851 NR_03649f	339803 Hs. 25243fNR_03649f	ENSG000004LOC33980f	- uncharactncRNA
chr20-134 6.664734	-0.07262	0.902412	-0.08047	0.935861	0.981636	chr20	1347015	1347542	+ 0 NA	exon (NM exon (NM	12587 NM_02182f	60493 Hs. 74116fNM_02182f	ENSG000004FASTKDS5	dJ1187M17FAST kinaseprotein-coding
chr6-16 6.664734	-0.07262	0.902412	-0.08047	0.935861	0.981636	chr6	1.66E+08	1.66E+08	+ 0 NA	intron (Nintron (N	-13405 NM_17592f	285800 Hs. 731862NM_17592f	ENSG000004PRR18	- proline lprotein-coding
chr9-1207 6.664734	-0.07262	0.902412	-0.08047	0.935861	0.981636	chr9	1.21E+08	1.21E+08	+ 0 NA	3' UTR (N3' UTR (N	29434 NM_012164	26190 Hs. 49498fNM_012164	ENSG000004FBXW2	FBW2 FwdZf-box ancprotein-coding
chr17-29 10.89858	-0.05859	0.728616	-0.08043	0.935909	0.981636	chr17	29632603	29636530	+ 0 NA	exon (NM exon (NM	-14943 NM_032854	84940 Hs. 14304fNM_032854	ENSG000004CORO6	- coronin fprotein-coding
chr11-75 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr11	75973728	75974055	+ 0 NA	intron (NLIP16 LI	158681 NM_003366	7405 Hs. 20247fNM_003366	ENSG000004UVRAG	DHTX VPSfUV radiatprotein-coding
chr13-30 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr13	30639202	30641522	+ 0 NA	intron (Nintron (N	6147 NM_001321	10208 Hs. 533831NM_00580f	ENSG000004USPL1	C13orf22 ubiquitin rprotein-coding
chr13-11 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr13	1.11E+08	1.11E+08	+ 0 NA	intron (AluSp SIN	26604 NM_01821C	55739 Hs. 408324NM_01821C	ENSG000004NAXD	CARKD LP2NAD(P)HX protein-coding
chr14-10 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr14	1.01E+08	1.01E+08	+ 0 NA	promoter-promoter-	-198 NR_030172	574450 Hs. NR_030172	ENSG000004MIR493	MIRN493 miR miRNA ncRNA
chr14-10 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr14	1.04E+08	1.04E+08	+ 0 NA	intron (AluS2 SIN	25363 NM_001100	7517 Hs. 59232fNM_00543f	ENSG000004XRC33	CMM6 X-ray repprotein-coding
chr17-36 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr17	3638811	3639439	+ 0 NA	intron (Nintron (N	2365 NM_004937	1497 Hs. 187667NM_004937	ENSG000004CTNS	CTNS-LSB cystinosis lprotein-coding
chr2-135 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr2	1.35E+08	1.35E+08	+ 0 NA	intron (N Tigger17a	-22021 NR_14572f	1.1E+08 NR_14572f	ENSG000004SNORA40B	- small nucsnRNA
chr8-387 5.180519	-0.08208	1.021037	-0.08039	0.935929	0.981636	chr8	38789328	38790027	+ 0 NA	intron (NL2a LINE	1571 NM_001352	6867 Hs. 27924fNM_00628f	ENSG000004TACCI1	Ga55 transformprotein-coding
chr12-43 9.44921	-0.06409	0.797744	-0.08035	0.935958	0.981636	chr12	43751437	43752137	+ 0 NA	intron (NLIP15 LI	7003 NM_001098	83448 Hs. 23554 NM_03129f	ENSG000004PUSL7	- pseudouricprotein-coding
chr4-139 4.77223	0.061591	0.76815	0.080259	0.936031	0.981636	chr4	1.39E+08	1.39E+08	+ 0 NA	3' UTR (N3' UTR (N	19093 NR_03129f	83452 Hs. 59167fNM_03129f	ENSG000004RAB33B	SMC2 RAB33B, nprotein-coding
chr1-162 6.120998	-0.07601	0.948234	-0.08016	0.936108	0.981636	chr1	16255642	16256156	+ 0 NA	intron (Nintron (N	-18716 NM_030907	79363 Hs. 54643fNM_030907	ENSG000004CLANE2	C1orf89 Fciliogeneprotein-coding
chr3-115 6.120998	-0.07601	0.948234	-0.08016	0.936108	0.981636	chr3	11594681	11595478	+ 0 NA	intron (AluSp SIN	9502 NM_001284	9686 Hs. 74038fNM_01466f	ENSG000004VGLL4	VGL-4 vestigial lprotein-coding
chr4-70 10.95544	0.057165	0.714319	0.080028	0.936215	0.981636	chr4	7013195	7013447	+ 0 NA	intron (NMER20 DNA	25813 NM_00128f	57533 Hs. 518611NM_02077f	ENSG000004TBC1D14	- TBC1 domeprotein-coding
chr18-29 8.478046	-0.064899	0.812788	-0.079847	0.936359	0.981636	chr18	2925954	2926429	+ 0 NA	intron (Nintron (N	20432 NR_02665f	727896 Hs. 67312fNR_02665f	LOC72789f	- cysteine pseudo
chr4-10 9.576522	-0.065429	0.747454	-0.079508	0.936629	0.981636	chr4	1.06E+08	1.06E+08	+ 0 NA	intron (NSVA_A Ret	-4644 NM_00116f	93627 Hs. 15149fNM_03311f	ENSG000004TBCK	HSPC302 TBC1 domeprotein-coding
chr14-10 9.748861	-0.069189	0.871855	-0.079358	0.936748	0.981636	chr14	1.01E+08	1.01E+08	+ 0 NA	IntergeniIntergeni	-2829 NR_030172	574450 Hs. NR_030172	ENSG000004MIR493	MIRN493 microRNA ncRNA
chr1-113 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr1	1.13E+08	1.13E+08	+ 0 NA	3' UTR (N3' UTR (N	53794 NM_001312	9860 Hs. 44897fNM_01481f	ENSG000004LRIG2	LIG-2 LILc leucine lprotein-coding
chr1-145 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr1	1.46E+08	1.46E+08	+ 0 NA	intron (AluS6 SI	36888 NR_10384f	11126 Hs. 48823fNM_00705f	ENSG000004CD160	BY55 NK1 CD160 molprotein-coding
chr10-27 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr10	27083971	27085742	+ 0 NA	intron (AluS2 SI	15642 NM_00125f	22852 Hs. 361041NM_01491f	ENSG000004ANKRD26	THC2 bA14ankyrin lprotein-coding
chr12-46 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr12	4661985	4662941	+ 0 NA	intron (Nintron (N	13349 NM_005002	4704 Hs. 75227 NM_005002	ENSG000004NDUFA9	CC6 C1-3cNADH:ubiq protein-coding
chr12-10 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr12	1.05E+08	1.05E+08	+ 0 NA	intron (Nintron (N	10075 NM_00125f	55198 Hs. 50660fNM_01817f	ENSG000004APPL2	DIP13B adaptor fprotein-coding
chr13-11 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr13	1.14E+08	1.14E+08	+ 0 NA	intron (AluJb SIN	12085 NM_001351	65110 Hs. 53385fNM_02301f	ENSG000004UPF3A	HUPF3A REUPF3A regprotein-coding
chr14-104 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr14	1.05E+08	1.05E+08	+ 0 NA	intron (Nintron (N	12487 NM_00516f	207 Hs. 52562fNM_00516f	ENSG000004AKT1	AKT CWS6 AKT serirprotein-coding
chr15-63 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr15	63297318	63298584	+ 0 NA	intron (Nintron (N	20346 NM_031301	83464 Hs. 51170fNM_031301	ENSG000004APH1B	APH-1B PFaph-1 honprotein-coding
chr16-71 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr16	71689566	71691039	+ 0 NA	intron (NMLT1N2 LI	8399 NR_033337	1E+08 Hs. 72511fNR_033337	ENSG000004SNORA70D	U70D small nucsnRNA
chr16-84 6.162138	-0.07291	0.923142	-0.07899	0.937044	0.981636	chr16	84096876	84097336	+ 0 NA	intron (NCR1-3_Crc	19836 NM_003379f	8720 Hs. 75890 NM_003791	ENSG00000	



chr11-866	7.143756	-0.06646	0.871712	-0.07624	0.939226	0.981636	chr11	86827177	86827609	+	0	NA	intron (NLIPA3 LIN	26851	NM_001293	11098	Hs.25338	NM_00717	ENSG00000	CRSS23	SIG13 SPL	serine p1protein-coding			
chr16-156	7.143756	-0.06646	0.871712	-0.07624	0.939226	0.981636	chr16	15619063	15620080	+	0	NA	intron (Nintron (N	-8476	NR_106761	1.02E+08	NR_106761	ENSG00000	MIR6506	hsa-mir-ε	microRNA ncRNA				
chr17-322	7.143756	-0.06646	0.871712	-0.07624	0.939226	0.981636	chr17	32200464	32201292	+	0	NA	intron (Nintron (N	-49307	NR_002222	503640	Hs.631752	NR_002222	ARGFXP2	-	arginine-pseudo				
chr13-756	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr13	75699106	75700737	+	0	NA	intron (NMER1 BL L	-60399	NM_001366	4008	Hs.207631	NM_005358	ENSG00000	LM07	FBX LIM	domaiprotein-coding			
chr13-958	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr13	95849512	95851327	+	0	NA	intron (NERV3-16A3	17380	NM_006260	5611	Hs.59214	NM_006260	ENSG00000	CNAJ3C	ACBDH ERC	DnaJ	domaiprotein-coding		
chr16-187	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr16	18797385	18799039	+	0	NA	intron (NCharlie	3158	NM_001313	23204	Hs.634882	NM_015161	ENSG00000	CARL6P1	ATP1 ARL	ADP	ribosprotein-coding		
chr17-187	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr17	18736487	18736897	+	0	NA	TTS (NM_CTS (NM_C	-7362	NR_051988	10517	Hs.59212E	NM_031456	ENSG00000	FBXW10	10517 HRE	F-box	anprotein-coding		
chr17-302	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr17	30248221	30249261	+	0	NA	3' UTR (N3' UTR (N	-13044	NR_00104E	6532	Hs.29792	NM_00104E	ENSG00000	SLC6A4	5-FHT 5-F	solute c	protein-coding		
chr17-788	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr17	78863403	78864044	+	0	NA	intron (Nintron (N	-23196	NM_001321	57602	Hs.464242	NM_02509C	ENSG00000	CUSP36	DUB1	ubiquitin	protein-coding		
chr19-196	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr19	19519758	19521740	+	0	NA	intron (NLMIB8 LIN	4524	NM_015966	51079	Hs.534452	NM_015966	ENSG00000	NDUFA13	B16.6 CD	NADH:ubiq	protein-coding		
chr19-370	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr19	37097986	37099362	+	0	NA	non-codiron-codir	20241	NM_001325	147923	Hs.444952	NM_14468E	ENSG00000	ZNF420	APAK	zinc fing	protein-coding		
chr2-3064	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr2	30640309	30641013	+	0	NA	3' UTR (N3' UTR (N	166785	NM_14457E	92291	Hs.660911	NM_14457E	ENSG00000	CAPN13	-	calpain I	protein-coding		
chr22-205	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr22	20521160	20522224	+	0	NA	intron (NALu SINE	13645	NM_001293	51586	Hs.517421	NM_01588E	ENSG00000	MED15	ARC105 C	mediator	protein-coding		
chr3-4371	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr3	43718463	43721047	+	0	NA	non-codiron-codir	-28161	NM_00134E	55129	Hs.656657	NM_01807E	ENSG00000	CNA10	SCAR10 C	antiamir	protein-coding		
chr4-4194	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr4	41948705	41951030	+	0	NA	intron (Nintron (N	14438	NM_01812E	55161	Hs.31082	NM_01812E	ENSG00000	TMEM33	1600019D1	transmemt	protein-coding		
chr4-139C	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr4	1.39E+08	1.39E+08	+	0	NA	intron (N(TA)n Sin	28215	NM_01211E	25819	Hs.639842	NM_01211E	ENSG00000	NOCT	CCR4L CC	nocturnin	protein-coding		
chr6-244C	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr6	24409395	24410078	+	0	NA	intron (Nintron (N	6800	NR_10442E	57380	Hs.658612	NM_02066E	ENSG00000	CMS2	HPT MR	S21	magnesium	protein-coding	
chr6-965C	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr6	96535892	96539450	+	0	NA	intron (Nintron (N	15865	NM_01532E	23376	Hs.149367	NM_01532E	ENSG00000	UFL1	K1AA0776 U	FMI1	spec	protein-coding	
chr6-1114	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	-12152	NR_03410E	643749	Hs.48622E	NR_03410E	ENSG00000	TRAF3IP2	-	C6UAS C6	TRAF3IP2	ncRNA	
chr7-1587	6.15428	-0.07072	0.928325	-0.07618	0.939278	0.981636	chr7	1.59E+08	1.59E+08	+	0	NA	intron (Nintron (N	-40424	NR_104054	54892	Hs.18616	NM_01776C	ENSG00000	CNAPG2	3KS CAP	-Cnc-SMC	protein-coding		
chr10-431	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr10	43179612	43180310	+	0	NA	intron (NLMIB7 LIN	25064	NM_00131E	55454	Hs.65756E	NM_01859C	ENSG00000	CSGALNACT1	CHGN2 C	chondroit	protein-coding		
chr12-625	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr12	62504432	62504467	+	0	NA	intron (NL2a LINE	37123	NM_01502E	23041	Hs.38937E	NM_01502E	ENSG00000	MON2	-	MON2	hmc	protein-coding	
chr2-1117	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr2	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	-16789	NR_03992E	1.01E+08	NR_03992E	ENSG00000	MIR4771-1	-2-	-	microRNA	ncRNA		
chr2-1175	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr2	1.18E+08	1.18E+08	+	0	NA	intron (NMIRb SINE	36699	NM_019044	54520	Hs.10784E	NM_019044	ENSG00000	CCDC93	-	coiled-c	protein-coding		
chr20-335	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr20	3326484	3327282	+	0	NA	intron (Nintron (N	80779	NM_00100E	25943	Hs.51685E	NM_00100E	ENSG00000	C20orf194	-	chromoson	protein-coding		
chr20-49C	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr20	4901079	4901807	+	0	NA	intron (Nintron (N	-77835	NM_014737	9770	Hs.631504	NM_014737	ENSG00000	CRASSF7	CENP-34 F	ras	assoc	protein-coding	
chr20-49C	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr20	49063834	49064547	+	0	NA	intron (NMER20 DN	17878	NM_00131E	1434	Hs.90073	NM_00131E	ENSG00000	SEIL	CAS CSE1	chromoson	protein-coding		
chr3-485E	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr3	48525979	48527319	+	0	NA	intron (NMLTIC LTF	-21823	NM_00127E	51246	Hs.41457E	NM_01647E	ENSG00000	SHISA5	SCOTIN	shisa	fan	protein-coding	
chr4-788E	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr4	78830478	78831105	+	0	NA	intron (NTigger1 I	54413	NM_19889E	55589	Hs.146551	NM_01759E	ENSG00000	BMP2K	BIKE HRIF	BMP2	indt	protein-coding	
chr5-436E	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr5	43695948	43696731	+	0	NA	intron (NTHE1B-int	-93109	NR_07311E	1.01E+08	Hs.48204E	NR_07311E	NNT-AS1	-	NNT	antisRNA			
chr6-143E	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr6	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	14150	NM_001317	5325	Hs.74322E	NM_00265E	ENSG00000	PLAGL1	LOT1 ZAC	PLAG1	lik	protein-coding	
chr6-152E	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr6	1.52E+08	1.52E+08	+	0	NA	intron (NALuSz SIN	-36871	NR_120501	1.01E+08	Hs.57120E	NR_120501	SYNE1-AS1	-	SYNE1	antncRNA			
chr7-7521	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr7	75219844	75220378	+	0	NA	intron (Nintron (N	-17076	NR_14607E	643862	NR_14607E	SPDYE10P	-	speedy/R1	pseudo				
chr7-152E	5.708539	-0.07288	0.957543	-0.07612	0.939327	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	146631	NM_001371474	146631	NM_001371474								
chr11-18E	4.493761	0.061386	0.809656	0.075817	0.939565	0.981636	chr11	18546333	18546595	+	0	NA	intron (Nintron (N	-19522	NM_00629E	7251	Hs.52351E	NM_00629E	ENSG00000	TSGL101	TSG10 VPS	tumor sus	protein-coding		
chr3-5247	8.493761	0.061386	0.809656	0.075817	0.939565	0.981636	chr3	52478451	52479276	+	0	NA	intron (Nintron (N	-16475	NM_01513E	23166	Hs.30198E	NM_01513E	ENSG00000	STAB1	CLEVER-1	stabilin	protein-coding		
chr4-137E	14.83661	0.046755	0.617352	0.075735	0.93963	0.981636	chr4	1.38E+08	1.38E+08	+	0	NA	intron (Nintron (N	6513	NM_01903E	54510	Hs.591691	NM_01903E	ENSG00000	PCDH18	PCDH68L	protocadl	protein-coding		
chr3-123C	6.966557	0.068426	0.903553	0.07573	0.939634	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	intron (NLMIB7 LIN	26983	NM_01243C	26984	Hs.477361	NM_01243C	ENSG00000	SEC22A	SEC22L2	SEC22	hon	protein-coding	
chr17-605	6.203277	-0.07007	0.925858	-0.07569	0.93967	0.981636	chr17	60520391	60521378	+	0	NA	intron (Nintron (N	5356	NM_00128E	10513	Hs.84084	NM_00638C	ENSG00000	APPPB2	APP-BP2	Amyloid t	protein-coding		
chr19-466	6.203277	-0.07007	0.925858	-0.07569	0.93967	0.981636	chr19	46675177	46676793	+	0	NA	intron (NALuJb SIN	14507	NR_040041	1.01E+08	Hs.434327	NR_040041	ENSG00000	DACT3-AS1	-	DACT3	antncRNA		
chr2-693E	6.203277	-0.07007	0.925858	-0.07569	0.93967	0.981636	chr2	69382190	69383007	+	0	NA	intron (Nintron (N	4632	NM_00205E	2673	Hs.58030C	NM_00205E	ENSG00000	GFTH1	CMS12 C	ms glutamine	protein-coding		
chr20-344	6.203277	-0.07007	0.925858	-0.07569	0.93967	0.981636	chr20	34412228	34413153	+	0	NA	intron (Nintron (N	49417	NM_001324	83737	Hs.63227E	NM_03148E	ENSG00000	GPTT1	ADMFD A	ifitichy E3	protein-coding		
chr5-774E	6.203277	-0.07007	0.925858	-0.07569	0.93967	0.981636	chr5	77435815	77436401	+	0	NA	intron (Nintron (N	56208	NM_01826E	55255	Hs.48257E	NM_01826E	ENSG00000	WDR41	MSTP048	WD	repeat	protein-coding	
chr11-17E	11.40118	0.05272	0.696979	0.075641	0.939705	0.981636	chr11	17073426	17076595	+	0	NA	promoter-promoter-	-266	NR_00002E	26822	NR_00002E	ENSG00000	SNORD14A	RNU14	RNU	snoRNA			
chr5-172E	7.494577	0.064937	0.859243	0.075574	0.939758	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (NALuSz6 SI	5458	NM_001317	51121	Hs.54639C	NM_01609E	ENSG00000	RPL26L1	RPL26P1	ribosomal	protein-coding		
chr16-821	9.92297	0.056307	0.746633	0.075414	0.939885	0.981636	chr16	82161604	82164796	+	0	NA	intron (Nintron (N	7024	NM_00579E	10200	Hs.34440C	NM_00579E	ENSG00000	MPHOSPH6	MPP MPP	-E	m-phase	protein-coding	
chr2-555E	9.92297	0.056307	0.746633	0.075414	0.939885	0.981636	chr2	55557309	55557552	+	0	NA	intron (NALuJb SIN	37835	NM_080667	112942	Hs.26420E	NM_080667	ENSG00000	CFAP36	BARTL1 C	cilia	nc	protein-coding	
chr1-1164	8.444764	0.061217	0.812088	0.075382	0.939911																				

chr18-13c.7.00681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr18	13049887	13050920	+	0	NA	intron (Nintron (N	59041 NM_032142	55125 Hs. 100914NM_018066	ENSG00000CEP192	PPP1R62	centrosomprotein-coding		
chr19-16c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr19	16632624	16633164	+	0	NA	Intergeni Intergeni	-4690 NM_004831	9441 Hs. 71504CNM_004831	ENSG00000MED26	CRSP7 CRS	mediator protein-coding		
chr19-21c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr19	21039052	21039458	+	0	NA	intron (Nintron (N	18598 NM_001172	80264 Hs. 729202NM_025189	ENSG00000ZNF430	-	zinc fingprotein-coding		
chr2-36c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr2	36492781	36493750	+	0	NA	intron (Nintron (N	104923 NM_001042	9637 Hs. 258566CNM_005102	ENSG00000PE22	Hum3CL	fasciculεprotein-coding		
chr2-60c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr2	60894482	60895409	+	0	NA	intron (Nintron (N	13392 NM_002908	5966 Hs. 631886CNM_002908	ENSG00000REL	C-Hel	REL protprotein-coding		
chr21-25c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr21	25587825	25589759	+	0	NA	intron (Nintron (N	-5568 NR_024092	282566 Hs. 384589NR_024092	ENSG00000LINC00515	C21orf71	long intencRNA		
chr21-44c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr21	44776638	44778601	+	0	NA	intron (Nintron (N	24201 NM_182688	7327 Hs. 529422CNM_003344	ENSG00000UBE2G2	UBC7	ubiquitinprotein-coding		
chr3-172c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	170735 NM_004122	2693 Hs. 130212NM_004122	ENSG00000GHSR	GHDP	growth hprotein-coding		
chr4-151c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr4	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	23959 NM_004564	5188 Hs. 119316NM_004564	ENSG00000GATB	HSPC199 F	glutamyl-protein-coding		
chr5-1341c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr5	1.47E+08	1.34E+08	+	0	NA	intron (Nintron (N	21004 NM_001366	6932 Hs. 573156NM_003202	ENSG00000TCF7	TCF-1	transcripprotein-coding		
chr7-254c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr7	2545790	2547354	+	0	NA	intron (Nintron (N	8952 NM_00135C	221927 Hs. 520622NM_152744	ENSG00000BRAT1	BAAT1 C7c	BRCA1 nucprotein-coding		
chr7-650c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr7	65066163	65068115	+	0	NA	intron (Nintron (N	1140 NR_145725	1.1E+08	NR_145725	ENSG00000SNORA22C	-	small nucsnoRNA	
chr8-2237c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr8	22378872	22379590	+	0	NA	intron (Nintron (N	11693 NM_00113E	23516 Hs. 491232NM_015356	ENSG00000SLC39A14	HCIN HMNI	solute cprotein-coding		
chr9-8367c.5.700681	-0.07046	0.960441	-0.07337	0.941514	0.981636	chr9	83672455	83673023	+	0	NA	intron (Nintron (N	-35096 NR_135833	1.05E+08	Hs. 9589 NR_135833	ENSG00000LOC105376	-	uncharactncRNA	
chr3-172c.7.086901	-0.06538	0.891924	-0.07337	0.941566	0.981636	chr3	1.72E+08	1.72E+08	+	0	NA	intron (Nintron (N	186290 NM_004122	2693 Hs. 130212NM_004122	ENSG00000GHSR	GHDP	growth hprotein-coding		
chr15-49c.6.690157	-0.06572	0.897505	-0.07323	0.941624	0.981636	chr15	49264958	49265467	+	0	NA	intron (Nintron (N	94965 NM_00128E	2585 Hs. 122006NM_002044	ENSG00000GALK2	GK2	galactokiprotein-coding		
chr17-40c.6.690157	-0.06572	0.897505	-0.07323	0.941624	0.981636	chr17	4092901	4094112	+	0	NA	intron (Nintron (N	49524 NM_01511E	23140 Hs. 277624NM_01511E	ENSG00000ZZEF1	ZZZ4	zinc fingprotein-coding		
chr9-134c.6.690157	-0.06572	0.897505	-0.07323	0.941624	0.981636	chr9	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	3350 NM_001291	6256 Hs. 590886NM_002957	ENSG00000XRRA	NR2B1	retinoid protein-coding		
chr7-7474c.10.40985	0.053061	0.726549	0.073032	0.941781	0.981636	chr7	74744046	74745980	+	0	NA	intron (Nintron (N	-16095 NR_110044	1.02E+08	Hs. 654772NR_110044	ENSG00000LOC101926	-	uncharactncRNA	
chr8-1167c.10.40985	0.053061	0.726549	0.073032	0.941781	0.981636	chr8	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	34440 NM_00375E	8667 Hs. 492599NM_00375E	ENSG00000EIF33	EIF3S3 e	eukaryotiprotein-coding		
chr17-665c.6.146422	-0.06849	0.939346	-0.07291	0.941878	0.981636	chr17	65043602	65044836	+	0	NA	intron (Nintron (N	11555 NM_00128E	10672 Hs. 515018NM_006572	ENSG00000GNA13	G13	G proteinprotein-coding		
chr5-730c.7.453438	0.062829	0.862675	0.072824	0.941946	0.981636	chr5	73069031	73069654	+	0	NA	intron (Nintron (N	-51233 NM_001161	134285 Hs. 162246NM_17349C	ENSG00000TMEM171	PRP2	transmemprotein-coding		
chr8-2544c.7.453438	0.062829	0.862675	0.072824	0.941946	0.981636	chr8	25445152	25445530	+	0	NA	intron (Nintron (N	13092 NM_017634	54793 Hs. 72071 NM_017634	ENSG00000KCTD9	BTBD27	potassiumprotein-coding		
chr1-149c.12.41608	0.048917	0.671823	0.072812	0.941956	0.981636	chr1	1.49E+08	1.49E+08	+	0	NA	Intergeni Intergeni	-7401 NM_001037	400818 Hs. 44508CNM_001037	ENSG00000NBPF9	AE01	NBPF memprotein-coding		
chr14-30c.8.931644	0.057096	0.784329	0.072796	0.941969	0.981636	chr14	30684181	30684392	+	0	NA	intron (Nintron (N	61967 NM_01610E	23256 Hs. 369166NM_01610E	ENSG00000SCFD1	C14orf163	secl famprotein-coding		
chr17-17c.8.931644	0.057096	0.784329	0.072796	0.941969	0.981636	chr17	17898243	17898758	+	0	NA	intron (Nintron (N	-61489 NM_00417E	6720 Hs. 592122NM_00417E	ENSG00000SREBF1	SREBF1 bf	solut rprotein-coding		
chr22-24c.8.931644	0.057096	0.784329	0.072796	0.941969	0.981636	chr22	24321568	24322179	+	0	NA	exon (NM exon (NM	-20235 NM_001254	23384 Hs. 474384NM_01533C	ENSG00000SPECC1L	CLYTA GBE	sperm protein-coding		
chr7-1521c.8.931644	0.057096	0.784329	0.072796	0.941969	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	exon (NM exon (NM	79288 NM_001371474	7011 Hs. 508833NM_00711C	ENSG00000TEP1	TLPT1 TP1	telomerasprotein-coding		
chr14-20c.7.981457	0.061006	0.828113	0.072582	0.942138	0.981636	chr14	20390064	20391034	+	0	NA	intron (Nintron (N	22952 NM_00711C	400550 Hs. 448822NR_03392E	ENSG00000FENDRR	FOXF1-AS1	FOXF1 adncRNA		
chr16-86c.12.8951	0.04771	0.658254	0.072479	0.94222	0.981636	chr16	86488362	86491123	+	0	NA	intron (Nintron (N	19118 NR_03392E	-66117 NR_146904	1.05E+08	Hs. 210837NR_146904	ENSG00000LINC01926	-	long intencRNA
chr18-587c.12.8951	0.04771	0.658254	0.072479	0.94222	0.981636	chr18	58745197	58750329	+	0	NA	exon (NM exon (NM	7659 NM_00342C	7584 Hs. 288658NM_00342C	ENSG00000ZNF35	H10.10 HF1	zinc fingprotein-coding		
chr3-446c.12.8951	0.04771	0.658254	0.072479	0.94222	0.981636	chr3	44650988	44661795	+	0	NA	intron (Nintron (N	-13761 NM_001367	10825 Hs. 191074NM_00665E	ENSG00000NEU3	SIAL3	neuraminprotein-coding		
chr11-74c.9.459664	0.055208	0.761813	0.07247	0.942228	0.981636	chr11	74974592	74975174	+	0	NA	intron (Nintron (N	41559 NM_003291	7174 Hs. 432424NM_003291	ENSG00000TPP2	TPP-2 TPF	tripepticprotein-coding		
chr13-10c.9.459664	0.055208	0.761813	0.07247	0.942228	0.981636	chr13	1.03E+08	1.03E+08	+	0	NA	intron (Nintron (N	41559 NM_003291	7174 Hs. 432424NM_003291	ENSG00000TPP2	TPP-2 TPF	tripepticprotein-coding		
chr6-822c.9.459664	0.055208	0.761813	0.07247	0.942228	0.981636	chr6	82238899	82239439	+	0	NA	intron (Nintron (N	8575 NM_00130C	25998 Hs. 306422NM_01552E	ENSG00000IBTK	BTBD26 BI	inhibiti protein-coding		
chr8-981c.9.459664	0.055208	0.761813	0.07247	0.942228	0.981636	chr8	98135910	98139258	+	0	NA	intron (Nintron (N	19744 NM_01502E	10940 Hs. 46161CNM_01774C	ENSG00000POPI	ANXD2	POPI homprotein-coding		
chr19-534c.7.184896	-0.06423	0.887663	-0.07235	0.942319	0.981636	chr19	53436887	53438307	+	0	NA	intron (Nintron (N	5613 NM_00100E	388561 Hs. 433292NM_00100E	ENSG00000ZNF761	ZNF468	zinc fingprotein-coding		
chr7-149c.7.184896	-0.06423	0.887663	-0.07235	0.942319	0.981636	chr7	1490106	1490401	+	0	NA	intron (Nintron (N	14136 NM_00108C	26173 Hs. 532188NM_00108C	ENSG00000INTS1	INT1 NET2	integrat protein-coding		
chr10-68c.7.622778	-0.06114	0.846135	-0.07226	0.942397	0.981636	chr10	68395572	68396330	+	0	NA	intron (Nintron (N	11238 NM_017987	55680 Hs. 653144NM_017987	ENSG00000RUFY2	RAB1P4R ZRUN	and fprotein-coding		
chr5-1194c.7.622778	-0.06114	0.846135	-0.07226	0.942397	0.981636	chr5	1.19E+08	1.19E+08	+	0	NA	intron (Nintron (N	25411 NM_000414	3295 Hs. 406861NM_000414	ENSG00000HSD17B4	DBP MFE-2	hydroxystprotein-coding		
chr9-124c.10.88887	0.051843	0.712583	0.072249	0.942404	0.981636	chr9	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	1819 NM_00279E	5695 Hs. 213477NM_00279E	ENSG00000PSMB7	Z	proteasomprotein-coding		
chr16-84c.11.41689	0.05017	0.695222	0.072164	0.942471	0.981636	chr16	84974105	84976718	+	0	NA	3' UTR (N3' UTR (N	36124 NM_00114E	55625 Hs. 46161CNM_01774C	ENSG00000ZNF761	DHHC7 SEF	zinc fingprotein-coding		
chr22-30c.11.41689	0.05017	0.695222	0.072164	0.942471	0.981636	chr22	30971566	30974278	+	0	NA	non-codirnon-codir	3711 NR_152867	55000 Hs. 554822NR_00232E	ENSG00000TUG1	LINC0008C	taurine tncRNA		
chr3-405c.11.41689	0.05017	0.695222	0.072164	0.942471	0.981636	chr3	40529691	40535740	+	0	NA	exon (NM exon (NM	7755 NM_198484	285268 Hs. 19977 NM_198484	ENSG00000ZNF621	-	zinc fingprotein-coding		
chr5-954c.11.41689	0.05017	0.695222	0.072164	0.942471	0.981636	chr5	95487449	95492359	+	0	NA	intron (Nintron (N	65101 NM_01463E	9652 Hs. 482866NM_01463E	ENSG00000TTC37	KIAA0372	tetratricprotein-coding		
chr4-5187c.8.117516	-0.0603	0.835704	-0.07215	0.942482	0.981636	chr4	51874419	51874916	+	0	NA	intron (Nintron (N	31088 NM_001287	23142 Hs. 605388NM_01511E	ENSG00000DCUN1D4	-	defectiveprotein-coding		
chr2-238c.6.982273	0.063761	0.884295	0.072104	0.942519	0.981636	chr2	2.38E+08	2.38E+08	+	0	NA	intron (Nintron (N	12977 NM_01651C	55552 Hs. 731906NM_01651C	ENSG00000SCLY	SCL hSCL	selenocysprotein-coding		
chr19-117c.13.37412	0.046594	0.646373	0.072085	0.942534	0.981636	chr19	11720568	11725792	+	0	NA	exon (NM exon (NM	15766 NM_00108C	55552 Hs. 142167NM_017507	ENSG00000ZNF823	HSZF36	zinc fingprotein-coding		
chr1-120c.7.12804	-0.06249	0.867209	-0.07206	0.942557	0.981636	chr1	1.21												



chr2-5532 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr2	55326214	55327692 +	0 NA	intron (Nintron (N	44634 NR_02725E	344405 Hs. 445292NR_00108C	ENSG00000PRORSD1P	NCRNA0011	prolyl-tf pseudo
chr2-6132 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr2	61320918	61322514 +	0 NA	intron (Nintron (N	95661 NR_003707	1E+08 Hs. 67582E NR_003707	ENSG00000SNORA70B	-	small nucsnoRNA
chr2-6935 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr2	69394395	69395311 +	0 NA	TTS (NM_C	-7599 NM_001244	2673 Hs. 58030C	ENSG00000GFPT1	CMS12 CMS	glutamine protein-coding
chr2-1875 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr2	1.88E+08	1.88E+08 +	0 NA	intron (N	20968 NM_00132E	7035 Hs. 51657E NR_006287	ENSG00000TFP1	EPI LAC1	tissue f protein-coding
chr2-2247 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr2	2.25E+08	2.25E+08 +	0 NA	intron (N	180441 NM_00129E	55619 Hs. 46578 NR_01468E	ENSG00000DOCK10	DRIP2	dedicator protein-coding
chr20-327 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr20	3277051	3277801 +	0 NA	intron (N	-38236 NM_001174	83959 Hs. 105607NR_032034	ENSG00000SLC4A11	BTR1 CDPE	solute c protein-coding
chr21-43C 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr21	43099519	43100891 +	0 NA	intron (N	7365 NM_00132C	1.03E+08 Hs. 36511E	ENSG00000U2AF15	-	U2 small protein-coding
chr21-437 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr21	43759002	43759908 +	0 NA	3' UTR (N	16920 NM_00010C	1476 Hs. 695 NR_00010C	ENSG00000CSTB	CPI-B CST	cytstatin protein-coding
chr22-24C 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr22	24396839	24397131 +	0 NA	intron (N	-26612 NM_00127E	135 Hs. 19702E	ENSG00000ADORA2A	A2AR ADOF	adenosine protein-coding
chr22-404 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr22	40428370	40430690 +	0 NA	exon (NM	33760 NM_00112E	57591 Hs. 65468E	ENSG00000MRFTA	BSAC MAL	myocardin protein-coding
chr4-397E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr4	39759274	39762439 +	0 NA	intron (N	62720 NM_00111E	3093 Hs. 50308 NR_00533E	ENSG00000UBE2K	E2-25K H	ubiquitin protein-coding
chr4-1187 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr4	1.19E+08	1.19E+08 +	0 NA	intron (N	24138 NM_020961	57721 Hs. 59687E	ENSG00000METTL14	hMETTL14	methyltransferase protein-coding
chr5-431E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr5	43162399	43162869 +	0 NA	intron (N	-29591 NM_153361	167359 Hs. 25845 NM_153361	ENSG00000N1M1K	N1M1	seriprotein-coding
chr5-554E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr5	55400334	55401583 +	0 NA	intron (N	92969 NM_01536C	23517 Hs. 274531NR_01536C	ENSG00000MTREX	Dobl KIAA	Mtr4 exos protein-coding
chr5-970E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr5	97028971	97029509 +	0 NA	3' UTR (N	70807 NM_17592C	4012 Hs. 52719E	ENSG00000LNPEP	CAP IRAP	leucyl ar protein-coding
chr6-326E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr6	3263453	3265424 +	0 NA	3' UTR (N	5491 NM_00112E	389362 Hs. 20706E	ENSG00000PSMG4	C6orf86 F	proteasome protein-coding
chr6-130E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr6	1.31E+08	1.31E+08 +	0 NA	intron (N	49112 NM_00119E	1.01E+08 Hs. 38871E	ENSG00000CSMLR1	-	small let protein-coding
chr7-446A 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr7	44648082	44648891 +	0 NA	intron (N	41859 NM_00100C	4967 Hs. 488181NR_002541	ENSG00000OGDH	AKGDH E1k	oxoglutarate protein-coding
chr7-151E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr7	1.51E+08	1.51E+08 +	0 NA	TTS (NM_C	3816 NM_00671E	10922 Hs. 647094NR_00671E	ENSG00000FASTK	FAST	Fas activ protein-coding
chr8-541E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr8	54142942	54148989 +	0 NA	intron (N	10724 NM_01417E	29088 Hs. 18349 NR_01417E	ENSG00000MRPL15	HSPC145 L	mitochondr protein-coding
chr8-125E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr8	1.25E+08	1.25E+08 +	0 NA	intron (N	12753 NM_00312E	6713 Hs. 71465 NR_00312E	ENSG00000SQLE	-	squalene protein-coding
chr8-140E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr8	1.41E+08	1.41E+08 +	0 NA	intron (N	-36061 NM_012154	27161 Hs. 66018E	ENSG00000AGO2	CASC7 E1F	argon aut protein-coding
chr9-566E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr9	5665671	5666360 +	0 NA	intron (N	36896 NM_00120E	57589 Hs. 21152C	ENSG00000CRIC1	CIP150 K1R1C1	homc protein-coding
chr9-928E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr9	92867098	92868957 +	0 NA	intron (N	9941 NM_001354	83744 Hs. 66837E	ENSG00000ZNF484	BA526D8.4	zinc finger protein-coding
chr9-123E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr9	1.23E+08	1.23E+08 +	0 NA	intron (N	-19456 NM_005294	2844 Hs. 72203E	ENSG00000GPR21	-	G protein protein-coding
chr9-124E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chr9	1.25E+08	1.25E+08 +	0 NA	intron (N	35057 NM_002077	2800 Hs. 59504 NM_002077	ENSG00000GOLGA1	golgin-97	golgin Al protein-coding
chrX-123E 6.187561	-0.06565	0.920454	-0.07133	0.943138	0.981636	chrX	1.24E+08	1.24E+08 +	0 NA	intron (N	34045 NM_001167	331 Hs. 35607E	ENSG00000XIAP	AP13 BIRC	X-linked protein-coding
chr15-40C 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr15	40030079	40037953 +	0 NA	intron (N	5165 NM_003134	6727 Hs. 53373E	ENSG00000SRP14	ALURBP	signal r protein-coding
chr2-333E 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr2	33363931	33365797 +	0 NA	intron (N	-53652 NR_03962E	1.01E+08 NR_03962E	ENSG00000MIR4430	-	microRNA ncRNA
chr21-62E 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr21	6234323	6234575 +	0 NA	intron (N	17321 NM_00132E	1.03E+08 Hs. 743984NR_00132E	ENSG00000LOC10272E	-	uncharacter protein-coding
chr21-64E 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr21	6486281	6487203 +	0 NA	intron (N	12506 NM_00132C	1.03E+08 Hs. 36511E	ENSG00000U2AF15	-	U2 small protein-coding
chr3-143E 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr3	1.43E+08	1.43E+08 +	0 NA	intron (N	19391 NM_00132C	23350 Hs. 59657E	ENSG00000U2SURP	SR140 fS2	snRNP protein-coding
chr3-179E 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr3	1.8E+08	1.8E+08 +	0 NA	intron (N	3629 NM_00120E	57129 Hs. 287334NR_02040E	ENSG00000MRPL47	CGI-204 L	trictulc protein-coding
chr7-740E 10.41771	0.051658	0.724248	0.071327	0.943138	0.981636	chr7	74099016	74101595 +	0 NA	intron (N	7088 NM_001204	3984 Hs. 64703E	ENSG00000LIMK1	LIMK LIM	LIM domain protein-coding
chr11-11E 6.633302	-0.06424	0.901983	-0.07122	0.943219	0.981636	chr11	1.17E+08	1.17E+08 +	0 NA	intron (N	-116483 NR_00003E	335 Hs. 93194 NR_00003E	ENSG00000APOA1	apo(a)	apolipoprotein-coding
chr5-167E 6.633302	-0.06424	0.901983	-0.07122	0.943219	0.981636	chr5	16742708	16743239 +	0 NA	intron (N	-125915 NM_001034	54463 Hs. 481704NR_01900C	ENSG00000RETREG1	FAMI34B J	reticuloprotein-coding
chr9-982E 6.633302	-0.06424	0.901983	-0.07122	0.943219	0.981636	chr9	98250451	98251273 +	0 NA	intron (N	4787 NM_001267	55357 Hs. 37101E	ENSG00000TBC1D2	PARIS-1 F	TBC1 domain protein-coding
chr16-224 15.3491	-0.04334	0.608669	-0.07121	0.943234	0.981636	chr16	22485076	22486536 +	0 NA	intron (N	-18643 NR_02445E	1E+08 Hs. 64843E	ENSG00000LOC10019C	-	uncharacter protein-coding
chr1-2464 12.37494	0.04778E	0.668749	0.071155	0.943274	0.981636	chr1	24645534	24665943 +	0 NA	non-codir	8903 NM_00136E	10250 Hs. 18192 NR_00583E	ENSG00000SRRM1	160-KD P	serine ar protein-coding
chr13-77C 8.939502	0.05542	0.779728	0.071076	0.943338	0.981636	chr13	77057786	77058922 +	0 NA	exon (NM	-17160 NR_04671E	1.01E+08 Hs. 56928E	ENSG00000MYCBP2-AS	-	MYCBP2 arncRNA
chr15-41C 8.939502	0.05542	0.779728	0.071076	0.943338	0.981636	chr15	41053634	41057545 +	0 NA	intron (N	60657 NR_10403E	54617 Hs. 29294E	ENSG00000IN080	IN080A IN	IN080 con protein-coding
chr4-564E 8.939502	0.05542	0.779728	0.071076	0.943338	0.981636	chr4	56490141	56490907 +	0 NA	intron (N	-14685 NR_20691E	132946 Hs. 44444E	ENSG00000ARL9	-	ADP ribos protein-coding
chr5-967E 8.939502	0.05542	0.779728	0.071076	0.943338	0.981636	chr5	96765402	96769795 +	0 NA	intron (N	23996 NR_10428E	831 Hs. 43618E	ENSG00000CAST	BS-17 P	calpastat protein-coding
chr10-961 7.461296	0.060716	0.854274	0.071073	0.94334	0.981636	chr10	96133784	96134437 +	0 NA	intron (N	3488 NM_00133C	9849 Hs. 60082E	ENSG00000ZNF518A	ZNF518	zinc finger protein-coding
chr19-44E 7.461296	0.060716	0.854274	0.071073	0.94334	0.981636	chr19	44900539	44900947 +	0 NA	intron (N	6088 NM_00481E	9404 Hs. 125474NR_00481E	ENSG00000CLPXN	LDPL	leupaxin protein-coding
chr20-37E 7.461296	0.060716	0.854274	0.071073	0.94334	0.981636	chr20	37518689	37519195 +	0 NA	exon (NM	-5053 NM_000041	348 Hs. 65443E	ENSG00000APOE	AD2 APO	E-apolipoprotein-coding
chr5-7077 7.461296	0.060716	0.854274	0.071073	0.94334	0.981636	chr5	70771816	70772886 +	0 NA	intron (N	1361 NM_001317	10904 Hs. 472651NR_00669E	ENSG00000BLCAP	BC10	BLCAP ap protein-coding
chr7-5991 7.461296	0.060716	0.854274	0.071073	0.94334	0.981636	chr7	5991002	59929284 +	0 NA	intron (N	4285 NR_16065E	1.03E+08 Hs. 71115E	ENSG00000LOC10272A	-	POM121 trp pseudo
chr8-123E 7.461296	0.060716	0.854274	0.071073	0.94334	0.981636	chr8	1.24E+08	1.24E+08 +	0 NA	3' UTR (N	1695 NM_00132E	5395 Hs. 632637NR_00053E	ENSG00000PMS2	HNPC4 M	PMS1 homc protein-coding
chr1-1204 7.177038	-0.06206	0.873856	-0.07102	0.943384	0.981636	chr1	1.2E+08	1.2E+08 +	0 NA	promoter	-95 NR_00324E	76784 Hs. 65718E	ENSG00000PFN1P2	C1orf152 P	profilin pseudo
chr1-150E 7.177038	-0.06206	0.873856	-0.07102	0.943384	0.981636	chr1	1.5E+08	1.5E+08 +	0 NA	intron (N	12167 NR_018997	54460 Hs. 40588C	ENSG00000MRP52	MDSO16 M	mitochondr protein-coding
chr18-12E 7.177038	-0.06206	0.873856	-0.07102	0.943384	0.981636	chr18	12361259	12361508 +	0 NA	intron (N	15893 NM_00679E	10939 Hs. 72635E	ENSG00000AFG3L2	SCA28 SFA	AFG3 like protein-coding
chr18-21E 7.177038	-0.06206	0.873856	-0.07102	0.943384	0.981636	chr18	21858873	21859332 +	0 NA	intron (N	-27696				

chr16-696	12.3828	-0.046416	0.668972	0.069384	0.944684	0.981636	chr16	69634290	69638200	+	0 NA	intron (THE1A-int	70279	NR_138713	10725	Hs.371987NM_006599	ENSG000002CNFAT5	NF-AT5	NF nuclear f protein-coding	
chr1-279C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr1	27908701	27909747	+	0 NA	intron (Tigger12	5351	NR_002946	6118	Hs.79411	NR_002946	ENSG000002RPA2	REP24	RP-replicatiprotein-coding
chr1-109C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr1	1.09E+08	1.09E+08	+	0 NA	intron (AluSq2 SI	-30273	NR_001266	343263	Hs.443402NM_001010	ENSG000002MYBPHL		myosin bi-protein-coding	
chr11-196C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr11	963190	965110	+	0 NA	intron (intron (	38280	NR_012306	161	Hs.19121	NR_012306	ENSG000002AP2A2	ADTAP	CLF adaptor i-protein-coding
chr15-25C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr15	25091548	25093015	+	0 NA	TTS (NR_1TTS (NR_C	496	NR_003337	1E+08	NR_003337	ENSG000002SNORD116	HBB1	-85-2 small nucsnRNA	
chr15-59C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr15	59073183	59074279	+	0 NA	intron (Tigger1 I	-31415	NR_004701	9133	Hs.194699NM_004701	ENSG000002CCNB2	HsT17299	cyclin B2 protein-coding	
chr20-44C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr20	44614823	44617731	+	0 NA	intron (NL2c LINE	33698	NR_001281	11142	Hs.472831NM_007066	ENSG000002PKIG	PK1-gamma	cAMP-depe protein-coding	
chr3-115C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr3	11564724	11567298	+	0 NA	intron (intron (	2787	NR_001128	9686	Hs.740389NM_014667	ENSG000002VGLL4	VGL-4	vestigial protein-coding	
chr3-524C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr3	52485712	52488465	+	0 NA	intron (intron (	-8250	NR_015136	23166	Hs.301989NM_015136	ENSG000002STAB1	CLEVER-1	stabilin protein-coding	
chr3-183C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr3	183E+08	1.83E+08	+	0 NA	intron (NLJMC1 LIN	48156	NR_12064C	56922	Hs.47469	NR_020166	ENSG000002MCCC1	MCC-B	MCC methylcr protein-coding
chr4-776C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr4	7762023	7763900	+	0 NA	3' UTR (3' UTR (	8871	NR_026892	84740	Hs.663029NM_032654	ENSG000002AFAP1-AS1	AFAP1-AS1	AFAP1 antncRNA	
chr5-529C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr5	52992797	52993208	+	0 NA	intron (intron (	3650	NR_073104	3673	Hs.482077NM_002203	ENSG000002ITGA2	BR CD49B	integrin protein-coding	
chr5-707C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr5	70793668	70794496	+	0 NA	intron (AluSg4 SI	-14996	NR_157804	1.02E+08	Hs.634012	NR_157804	LOC101922		putative pseudo
chr8-2217	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr8	22179924	22180747	+	0 NA	intron (intron (	14963	NR_033403	649	Hs.1274	NR_001199	ENSG000002BMP1	O113	PCOL bone morp protein-coding
chr8-265C	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr8	26589412	26592487	+	0 NA	intron (intron (	12544	NR_001244	1808	Hs.593187NM_001386	ENSG000002DPYSL2	CRMP-2	CF dihydropy protein-coding	
chr9-1212	7.16918	-0.06001	0.865059	-0.06937	0.944697	0.981636	chr9	1.21E+08	1.21E+08	+	0 NA	intron (NMIRb SINE	-4208	NR_001356	2934	Hs.522373	NR_000177	ENSG000002GSN	ADF AGEL	gelsolin protein-coding
chr1-1184	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	11841261	11843923	+	0 NA	non-codiron-codir	2273	NR_037806	1E+08	Hs.710019	NR_037806	NPPA-AS1	NPPA-AS1 NPPA	antncRNA
chr1-170	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	17030987	17033770	+	0 NA	intron (AluSx1 SI	-20450	NR_001141	23400	Hs.128866NM_022088	ENSG000002ATP13A2	CLN12	HSA ATPase	protein-coding
chr1-279C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	27986628	27991360	+	0 NA	intron (intron (	29532	NR_018056	55113	Hs.55024	NR_018056	ENSG000002XKR8	XRG8	HxKX relate protein-coding
chr1-578	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	52782913	52788115	+	0 NA	intron (AluSc SIN	-57246	NR_001307	440590	Hs.658459NM_001004	ENSG000002ZYG11A	ZYG11	zyg-11 f2 protein-coding	
chr1-169C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	77866939	77867138	+	0 NA	intron (intron (	-21477	NR_144573	91624	Hs.612389NM_144573	ENSG000002NEXN	CMH20	NEI nexlin f protein-coding	
chr1-1081	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	1.08E+08	1.08E+08	+	0 NA	intron (AluSx1 SI	10072	NR_213651	29957	Hs.656877NM_013386	ENSG000002SLC25A24	APC1	SCAM solute protein-coding	
chr1-1457	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	1.46E+08	1.46E+08	+	0 NA	intron (NLIMB2 LIN	26230	NR_014456	27246	Hs.523556NM_014456	ENSG000002RNFI15	BCA2	ZNF ring fing protein-coding	
chr1-169C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	1.7E+08	1.7E+08	+	0 NA	intron (intron (	17747	NR_020423	57147	Hs.435566NM_020423	ENSG000002SCYL3	PACE-1	PA SCYL1	like protein-coding
chr1-2118	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	2.12E+08	2.12E+08	+	0 NA	intron (NLIPA17 LI	-23036	NR_135818	1.03E+08	Hs.147656	NR_135818	ENSG000002LPGAT1-AS-	LPGAT1	arncRNA
chr1-244	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr1	2.45E+08	2.45E+08	+	0 NA	intron (AluSp SIN	40582	NR_016076	51028	Hs.498317NM_016076	ENSG000002DEST12	Clorf121	desumoylase protein-coding	
chr10-146	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr10	14940903	14942532	+	0 NA	intron (NLIM3 LINE	12379	NR_001356	64221	Hs.659319NM_022487	ENSG000002DCLRE1C	A-SCID	DCDNA cross protein-coding	
chr10-177	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr10	17712635	17719238	+	0 NA	3' UTR (3' UTR (	-36265	NR_001098	653567	Hs.564135NM_001010	ENSG000002TMEM236	FAM23A	F2 transmem protein-coding	
chr10-49C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr10	49954191	49955587	+	0 NA	TTS (NR_1TTS (NR_1	677	NR_145778	1.1E+08	NR_145778	SNORA74C-		small nucsnRNA	
chr10-87C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr10	87902485	87905121	+	0 NA	intron (NLIPA6 LIN	40178	NR_000314	5728	Hs.500466NM_000314	ENSG000002PTEN	10q23del1	phosphatase protein-coding	
chr11-128	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr11	12879899	12880933	+	0 NA	intron (NMIRb SINE	109132	NR_038904	1.01E+08	Hs.153409	NR_038904	ENSG000002LINC0095E	BLACAT2	long intncRNA
chr11-18C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr11	18543837	18545648	+	0 NA	exon (NM exon (NM	-17800	NR_006292	7251	Hs.523512NM_006292	ENSG000002TSG101	TSG101	VPS tumor sup protein-coding	
chr11-63C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr11	63987865	63989867	+	0 NA	intron (intron (	3013	NR_003098	55611	Hs.473788NM_017677	ENSG000002OTUB1	TSC2	OTUB1 protein-coding	
chr11-70C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr11	70328250	70331236	+	0 NA	intron (AluJb SIN	45788	NR_031624	1E+08	NR_031624	ENSG000002MIR548K	MIRN548K	microRNA ncRNA	
chr11-118	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr11	1.18E+08	1.18E+08	+	0 NA	exon (NM exon (NM	15495	NR_004788	9354	Hs.75275	NR_004788	ENSG000002UBE4A	E4 UBOX2	ubiquitin protein-coding
chr12-76C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr12	76357086	76358886	+	0 NA	intron (intron (	-9571	NR_024688	79738	Hs.96322	NR_024688	ENSG000002BBS10	C12orf58	Bardet-Bi protein-coding
chr12-111	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr12	1.11E+08	1.12E+08	+	0 NA	intron (intron (	66043	NR_001291	10019	Hs.506784NM_005477	ENSG000002SH2B3	IDDM20	LN SH2B	adaf protein-coding
chr12-116	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr12	1.18E+08	1.18E+08	+	0 NA	intron (intron (	8361	NR_002567	5037	Hs.433866NM_002567	ENSG000002PEBP1	HSP6 HCNF	phosphatid protein-coding	
chr14-50C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr14	50934032	50936821	+	0 NA	intron (NMIR SINE	9057	NR_002863	5836	Hs.282417NM_002863	ENSG000002PYGL	CSND	glyogen protein-coding	
chr14-73C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr14	73932037	73935675	+	0 NA	3' UTR (3' UTR (	-16078	NR_18248C	51004	Hs.131555NM_182477	ENSG000002COQ6	CGI-10	CCoenzyme protein-coding	
chr15-44C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr15	44649985	44651944	+	0 NA	intron (AluSx1 SI	12698	NR_001166	80208	Hs.656271NM_025137	ENSG000002SPG11	ALM5	CMT2 SPG11	ves protein-coding
chr15-74C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr15	74684941	74686430	+	0 NA	intron (AluJo SIN	10389	NR_001142	80153	Hs.96852	NR_025083	ENSG000002EDC3	LSM16	MRI enhancer protein-coding
chr15-75C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr15	75492087	75493693	+	0 NA	intron (AluJo SIN	-37075	NR_001142	25942	Hs.513039NM_015477	ENSG000002SIN3A	WTKOS	SIN3	trarp protein-coding
chr15-83C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr15	83048172	83050420	+	0 NA	intron (NMER6 DNA	17956	NR_001011	53339	Hs.459145NM_025238	ENSG000002BTBD1	C15orf1	NBTB	doma protein-coding
chr15-90C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr15	88463166	88463984	+	0 NA	intron (NL2c LINE	3813	NR_022163	26589	Hs.534261NM_022163	ENSG000002MRPL46	C15orf4	Lmi tochoan protein-coding	
chr15-98C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr15	90638756	90643467	+	0 NA	non-codiron-codir	-19123	NR_120371	1.02E+08	Hs.615349	NR_120371	ENSG000002LINC0158E		long intncRNA
chr16-24C	6.674441	-0.06154	0.887718	-0.06933	0.944728	0.981636	chr16	2436040	2437556	+	0 NA</									



chr1-1505	8.596539	-0.05597	0.813355	-0.06882	0.945136	0.981636	chr1	15059877	15060494	+	0	NA	exon (NM exon (NM	92279 NR_027136	200197 Hs. 531424NM_182534	ENSG000002MEM51-AS1	C1orf126	TMEM51	arncRNA	
chr16-295	10.37657	0.050137	0.730799	0.068606	0.945303	0.981636	chr16	29550314	29551580	+	0	NA	intron (N intron (N	44145 NR_135305	440354 Hs. 55270CNR_002473	SMG1P2	-	SMG1	pseudogene	
chr14-358	8.101801	-0.05651	0.824645	-0.06853	0.945367	0.981636	chr14	35026487	35027251	+	0	NA	intron (N AluSc SIN	-18038 NM_001075	283635 Hs. 446357NM_173607	ENSG000002FAM177A1	C14orf24	family wiprotein-coding	uncharacterized	
chr3-3728	8.101801	-0.05651	0.824645	-0.06853	0.945367	0.981636	chr3	37251669	37254113	+	0	NA	intron (N L1ME3B L1	-8696 NR_149022	152048 Hs. 596176NM_152532	ENSG000002LOC152042E	-	-	-	
chr1-5385	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr1	53856264	53857308	+	0	NA	intron (N intron (N	-18490 NR_001166	55706 Hs. 476522NM_018087	ENSG000002NDC1	NET3 TMEB	NDC1	trar protein-coding	putative protein-coding
chr10-314	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr10	31472687	31473669	+	0	NA	intron (N LIPA3 LIN	-73423 NM_001368	1.01E+08 Hs. 730227NM_001368169	LOC100505E	-	-	-	
chr10-111	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr10	1.11E+08	1.11E+08	+	0	NA	intron (N intron (N	21507 NR_031614	1E+08 Hs. NR_031614	ENSG000002MIR548E	MIRN548E	microRNA ncRNA	-	
chr12-456	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr12	45940862	45941726	+	0	NA	intron (N L1MA9 LIN	49280 NM_004715	9169 Hs. 210367NM_004715	ENSG000002SCAF11	CASP11	SR-relate protein-coding	-	
chr13-524	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr13	52445104	52446067	+	0	NA	intron (N AluY SINE	4659 NM_001282	51028 Hs. 109522NM_016075	ENSG000002VPS36	C13orf9	vacuolar protein-coding	long intncRNA	
chr13-956	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr13	95058356	95059170	+	0	NA	intron (N MIRb SINE	97822 NR_047487	1.01E+08 Hs. 48706 NR_047487	ENSG000002LINC00557	-	-	-	
chr13-984	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr13	98473623	98475261	+	0	NA	intron (N intron (N	46823 NM_003576	8428 Hs. 508514NM_003576	ENSG000002STK24	HEL-S-95	serine/t protein-coding	-	
chr14-507	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr14	50737884	50738947	+	0	NA	intron (N intron (N	-70109 NM_021818	60485 Hs. 642842NM_021818	ENSG000002SAV1	SAV WW45	salvador protein-coding	uncharacterized	
chr15-327	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr15	32778630	32779013	+	0	NA	intron (N L1MB7 LIN	-59956 NR_109767	1E+08 Hs. 610544NR_109767	ENSG000002LOC100131	-	-	-	
chr15-325	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr15	32900202	32901056	+	0	NA	intron (N intron (N	167545 NM_001103	342184 Hs. 657645NM_198502	ENSG000002FMM1	FMM LD	formin 1 protein-coding	-	
chr16-162	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr16	1622804	1623328	+	0	NA	intron (N AluJb SIN	8426 NM_020825	57585 Hs. 603676NM_020825	ENSG000002CRAMP1	CRAMP1 L	cramped protein-coding	-	
chr17-285	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr17	28562492	28563356	+	0	NA	intron (N AluJb SIN	8600 NM_033198	94005 Hs. 462556NM_033198	ENSG000002PIGS	GP1BD18	phosphatid protein-coding	-	
chr17-306	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr17	30610522	30612445	+	0	NA	intron (N intron (N	-12835 NR_03342C	6459 Hs. 684866NR_033420	SH3GLIP2	CNSA-P2 SSH3	domaipseudo	-	
chr17-685	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr17	68533938	68535799	+	0	NA	TTS (NM_C TTS (NM_C	19474 NM_001276	5573 Hs. 280342NM_002734	ENSG000002PKRARI1	ACRDYS1	protein f protein-coding	-	
chr19-875	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr19	875340	875840	+	0	NA	intron (N intron (N	15926 NM_001928	1675 Hs. 155597NM_001928	ENSG000002CFD	ADIPSLIN	complemer protein-coding	-	
chr19-176	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr19	17237989	17240351	+	0	NA	intron (N AluSc5 SI	6172 NM_005234	2063 Hs. 466148NM_005234	ENSG000002NR2F6	EAR-2 EAF	nuclear r protein-coding	-	
chr19-1062	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr19	10650887	10651861	+	0	NA	intron (N MER33 DNA	38601 NM_022489	79954 Hs. 222494NM_024894	ENSG000002NOL10	PQBP5	nuclear r protein-coding	-	
chr2-2875	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr2	28759029	28761462	+	0	NA	intron (N Tigger3b	8415 NM_002705	5500 Hs. 702907NM_002705	ENSG000002PPP1CB	HEL-S-80r	protein f protein-coding	-	
chr2-1572	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr2	1.57E+08	1.57E+08	+	0	NA	intron (N LIPA6 LIN	16709 NM_001325	11227 Hs. 269027NM_014568	ENSG000002GALNT5	GALNAC-T5	polypeptide protein-coding	-	
chr2-2005	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	intron (N AluJb SIN	20746 NM_001142	60491 Hs. 145284NM_021824	ENSG000002NIF3L1	ALS2CR1	CNGG1	te protein-coding	-
chr2-2017	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (N (GAGAA) n	-7815 NM_033066	58538 Hs. 63085 NM_033066	ENSG000002MPP4	ALS2CR5	membrane protein-coding	-	
chr2-2031	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (N AluJr SIN	-91744 NM_177538	57404 Hs. 446065NM_020674	ENSG000002CYP20A1	CYP-M	cytochron protein-coding	-	
chr20-213	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr20	21382200	21384754	+	0	NA	intron (N MIR3 SINE	10449 NM_033176	644524 Hs. NR_033176	ENSG000002NKX2-4	NKX2.4	homeoprotein-coding	-	
chr3-967	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr3	9670694	9671478	+	0	NA	exon (NM exon (NM	21581 NM_02248E	64419 Hs. 475382NM_02248E	ENSG000002MTMR14	C3orf29	myotubule protein-coding	-	
chr3-457	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr3	45709705	45711543	+	0	NA	intron (N intron (N	21228 NM_001315	22908 Hs. 156505NM_014015	ENSG000002SACM1L	SAC1	SAC1	like protein-coding	-
chr3-1413	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr3	1.41E+08	1.41E+08	+	0	NA	intron (N intron (N	-6374 NM_00135C	25346 Hs. 518301NM_152535	ENSG000002ZBTB38	SIBZ PPP1	zinc finger protein-coding	-	
chr4-207	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr4	20704648	20707601	+	0	NA	intron (N intron (N	5666 NM_00133C	133015 Hs. 479292NM_145045	ENSG000002PACRGL	C4orf28	parkin cc protein-coding	-	
chr4-478	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr4	47895667	47899518	+	0	NA	exon (NM exon (NM	-15185 NR_125875	1.02E+08 Hs. 13419CNR_125879	LOC101927-	-	-	-	
chr5-1705	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr5	1.71E+08	1.71E+08	+	0	NA	intron (N THE1B-int	119052 NM_022897	64901 Hs. 41081CNM_022897	ENSG000002RANBP17	-	-	-	
chr6-734	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr6	73492861	73493991	+	0	NA	intron (N AluSq2 SI	25012 NR_132981	1.07E+08 Hs. NR_132981	SNORD141E	-	-	-	
chr8-1334	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr8	1.33E+08	1.33E+08	+	0	NA	intron (N intron (N	83859 NM_003033	6482 Hs. 374257NM_003033	ENSG000002ST3GAL1	Gal-Nac6S	ST3 beta-protein-coding	-	
chr9-1377	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	intron (N intron (N	44140 NR_147508	651337 Hs. 603195NR_147508	ENSG000002LOC651337	-	-	-	
chrX-1581	6.179703	-0.06341	0.925617	-0.06851	0.945383	0.981636	chrX	15818390	15819634	+	0	NA	intron (N AluSq2 SI	28561 NM_00508E	8233 Hs. 171905NM_00508E	ENSG000002ZRSR2	U2AF1-RS2	zinc finger protein-coding	-	
chr1-7384	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr1	7384442	740754	+	0	NA	Intergeni Intergeni	-9247 NR_028327	1E+08 Hs. 728864NR_028327	LOC100133E	-	-	-	
chr10-10	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr10	58389636	58390008	+	0	NA	intron (N intron (N	4412 NM_003201	7019 Hs. 594252NM_003201	ENSG000002CYP20A1	MDPFS15	transcrip protein-coding	-	
chr10-918	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr10	91830399	91832029	+	0	NA	intron (N intron (N	32788 NM_02523E	80351 Hs. 329327NM_02523E	ENSG000002TNKS2	ARTD6	PAF tankyrase protein-coding	-	
chr16-68	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr16	68307581	68308925	+	0	NA	intron (N intron (N	2743 NM_03217E	84138 Hs. 729522NM_03217E	ENSG000002SLC7A60S	-	-	-	
chr2-461	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr2	46104140	46106494	+	0	NA	intron (N Tigger2 E	-192090 NM_00143C	2034 Hs. 46841CNM_00143C	ENSG000002EPAS1	ECYT4	HIF endotheliprotein-coding	-	
chr2-2031	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr2	2.03E+08	2.03E+08	+	0	NA	intron (N intron (N	-70618 NM_177538	57404 Hs. 446065NM_020674	ENSG000002CYP20A1	CYP-M	cytochron protein-coding	-	
chr2-146	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr2	46509201	46512283	+	0	NA	intron (N AluY SINE	48271 NR_04640C	1.01E+08 Hs. 737161NR_04640C	ENSG000002DIP2A-IT1	DIP2A	intncRNA	-	
chr3-730	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr3	73005481	73006745	+	0	NA	intron (N L1ME1 LIN	9302 NM_174907	151987 Hs. 431092NM_174907	ENSG000002PPP4R2	PP4R2	protein f protein-coding	-	
chr4-1501	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr4	15016804	15017841	+	0	NA	intron (N intron (N	14841 NM_001177	132864 Hs. 656937NM_18248E	ENSG000002CPEB2	CPE-BP2	cytoplasm protein-coding	-	
chr5-714	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr5	71458623	71462541	+	0	NA	intron (N intron (N	4931 NM_01842E	55814 Hs. 258272NM_01842E	ENSG000002BDP1	DFNB112	EB double protein-coding	-	
chr5-1379	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr5	1.38E+08	1.38E+08	+	0	NA	intron (N intron (N	63593 NM_01438E	27039 Hs. 716884NM_01438E	ENSG000002PKD2L2	TRPP5	polycystiprotein-coding	-	
chr7-4291	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr7	42919509	42923919	+	0	NA	intron (N intron (N	-9624 NM_001099	79020 Hs. 698122NM_024054	ENSG000002C7orf25	-	-	-	
chr7-129	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr7	1.3E+08	1.3E+08	+	0	NA	intron (N THE1B-int	30607 NM_00104C	4899 Hs. 654365NM_005011	ENSG000002NRF1	ALPHA-PAL	nuclear r protein-coding	-	
chr9-113	9.426382	0.05193	0.758115	0.068499	0.945388	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	3							



chr22-467.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr22	46715734	46720521	+	0 NA	intron (Nintron (N	20125 NM_022766	64781 Hs. 200668NM_022766	ENSG000002CERK	LK4 dA59F ceramide protein-coding										
chr3-1612.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr3	1.61E+08	1.61E+08	+	0 NA	intron (Nintron (N	17993 NM_015938	51068 Hs. 598836NM_015938	ENSG000002NMD3	CGI-07 NMD3 ribcprotein-coding										
chr5-7145.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr5	71494144	71498226	+	0 NA	intron (NAluY SINE	40534 NM_018425	55814 Hs. 258272NM_018425	ENSG000002BDP1	DFNB112 FB double protein-coding										
chr5-7221.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr5	72219119	72221097	+	0 NA	3' UTR (N3' UTR (N	40321 NM_001324	4131 Hs. 335075NM_005909	ENSG000002MAP1B	FUTSCH Pm microtubule protein-coding										
chr5-1484.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr5	1.48E+08	1.48E+08	+	0 NA	intron (NTiger1 L	50798 NM_030793	81545 Hs. 483772NM_030793	ENSG000002FBX038	Fbx38 HMM-F box prcprotein-coding										
chr5-1544.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr5	1.54E+08	1.54E+08	+	0 NA	intron (NCharlie E	9524 NR_037897	386627 Hs. 652021NR_037897	SAP30L-AS	GALNT10-?SAP30L arncRNA										
chr5-1765.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr5	1.77E+08	1.77E+08	+	0 NA	intron (Nintron (N	51583 NM_016296	51720 Hs. 232721NM_016296	ENSG000002UTMC1	RAP80 X2f ubiquitin protein-coding										
chr6-3655.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr6	36535310	36541071	+	0 NA	intron (NAluY SINE	9289 NM_007271	11329 Hs. 409578NM_007271	ENSG000002STK38	NDR NDR1 serine/t protein-coding										
chr6-8987.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr6	89856504	89860023	+	0 NA	intron (NAluSx1 SI	28363 NM_012115	9994 Hs. 558218NM_012115	ENSG000002CASP8AP2	CED-4 FLA caspase 8 protein-coding										
chr6-1496.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr6	1.5E+08	1.5E+08	+	0 NA	intron (NAluYf1 SI	27382 NM_007044	11104 Hs. 450175NM_007044	ENSG000002KATNA1	28969 Hs. 487636NM_014038	ENSG000002BZW2	HSPC028 N basic leu protein-coding								
chr7-1677.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr7	16704273	16707126	+	0 NA	intron (NAluY SINE	44485 NM_001362	6566 NR_104007	695009NR_104007	LOC100101	FKBP prolpseudo									
chr7-7297.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr7	72975673	72976823	+	0 NA	IntergeniCpG	6260 NM_001301	7978 Hs. 532218NM_006988	ENSG000002MTERF1	MTERF mitochondon protein-coding										
chr7-9187.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr7	91874028	91874856	+	0 NA	exon (NM exon (NM	2917 NM_001317	23471 Hs. 491988NM_014294	ENSG000002TRAM1	PNAS8 TR transloc protein-coding										
chr8-7067.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr8	706202089	70670416	+	0 NA	intron (Nintron (N	5023026	5024690	+	0 NA	intron (Nintron (N	11451 NM_001282	55833 Hs. 493736NM_018445	ENSG000002UBAP2	UBAP-2 ubiquitin protein-coding					
chr9-5025.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr9	5023026	5024690	+	0 NA	intron (Nintron (N	33920191	33925635	+	0 NA	intron (Nintron (N	16749431	16750959	+	0 NA	intron (N3 LINE C	30583 NM_032796	94056 Hs. 744258NM_032796	ENSG000002SYAP1	BSTA PRO3 synapse 8 protein-coding
chr9-3392.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chr9	33920191	33925635	+	0 NA	intron (Nintron (N	47640121	47641314	+	0 NA	intron (Nintron (N	9887 NM_005225	2002 Hs. 181128NM_005225	ENSG000002ELK1	ETS trans protein-coding					
chrX-1674.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chrX	49032950	49035174	+	0 NA	intron (Nintron (N	74279749	74281418	+	0 NA	intron (Nintron (N	6626 NR_030258	66414 NR_030258	ENSG000002MIR545	MIRN545 microRNA ncRNA					
chrX-4767.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chrX	1.04E+08	1.04E+08	+	0 NA	intron (Nintron (N	2931 NM_012288	9643 Hs. 326387NM_012288	ENSG000002MORF4L2	MORFL2 MF mortality protein-coding										
chrX-4902.7.161322	-0.05804	0.860718	-0.06743	0.946241	0.981636	chrX	2.2E+08	2.2E+08	+	0 NA	non-codirnon-codir	122 NR_001587	6791 Hs. 654845NR_001587	AURKAP1	AURKAP1 aurora kipseudo										
chr1-2202.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr1	11734649	11736070	+	0 NA	intron (NMER20B DN	7498 NM_001303	51061 Hs. 313847NM_015914	ENSG000002TXNDC11	EFP1 thioredox protein-coding										
chr16-117.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr16	69356586	69357152	+	0 NA	3' UTR (N3' UTR (N	-5083 NM_144676	146456 Hs. 729118NM_144676	ENSG000002TMED6	PRO34237 transmem protein-coding										
chr16-693.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr16	49661922	49663023	+	0 NA	exon (NM exon (NM	-2670 NM_138635	83596 Hs. 289052NM_138635	ENSG000002BCL2L12	BCL2 like protein-coding										
chr19-496.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr19	58245359	58246103	+	0 NA	intron (Nintron (N	-17078 NM_001304	140731 Hs. 266571NM_080674	ENSG000002ANKRD60	C20orf86 ankyrin r protein-coding										
chr20-582.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr20	530558084	58261041	+	0 NA	intron (Nintron (N	49645 NM_176806	4338 Hs. 163646NM_004531	ENSG000002MOC52	MCPBE MC mylben protein-coding										
chr5-5305.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr5	1.28E+08	1.28E+08	+	0 NA	intron (Nintron (N	84388 NM_001995	2201 Hs. 519294NM_001995	ENSG000002FBN2	CCA DA9 F fibrillir protein-coding										
chr5-1284.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr5	25977972	25979294	+	0 NA	intron (NAluJb SIN	15831 NM_006355	10475 Hs. 584851NM_006355	ENSG000002TRIM38	RNF15 ROF tripartit protein-coding										
chr6-2597.8.427198	0.05399	0.801208	0.067386	0.946274	0.981636	chr6	1.25E+08	1.25E+08	+	0 NA	intron (Nintron (N	42860 NM_014846	9897 Hs. 270045NM_014846	ENSG000002WASHIC5	KIAA0196 WASH com protein-coding										
chr16-287.8.427198	0.05426	0.805707	0.067345	0.946307	0.981636	chr16	28735212	28737078	+	0 NA	TTS (NM_TTS (NM_C	11893 NR_106922	1.02E+08	NR_106922	ENSG000002MIR6862	hsa-mir-6 microRNA ncRNA									
chr19-931.8.427198	0.05426	0.805707	0.067345	0.946307	0.981636	chr19	9303853	9304980	+	0 NA	intron (Nintron (N	5422 NM_198535	374879 Hs. 633842NM_198535	ENSG000002ZNF699	hang zinc fing protein-coding										
chr15-655.7.733963	-0.06488	0.964456	-0.06727	0.946366	0.981636	chr15	65113145	65114024	+	0 NA	IntergeniAluS6 SI	-7225 NM_001163	390595 Hs. 659255NM_001163	ENSG000002UBAP1L	UBAP-1L ubiquitin protein-coding										
chr19-105.7.733963	-0.06488	0.964456	-0.06727	0.946366	0.981636	chr19	10362008	10362495	+	0 NA	intron (Nintron (N	18321 NM_003331	7297 Hs. 75516 NM_003331	ENSG000002CTYK2	IMD35 JTK tyrosine protein-coding										
chr2-3392.7.733963	-0.06488	0.964456	-0.06727	0.946366	0.981636	chr2	3392327	3393043	+	0 NA	intron (Nintron (N	12991 NM_01603C	51112 Hs. 252713NM_01603C	ENSG000002TRAPP12	CGI-87 PF trafficki protein-coding										
chr2-8576.7.733963	-0.06488	0.964456	-0.06727	0.946366	0.981636	chr2	85767882	85770287	+	0 NA	intron (Nintron (N	14593 NR_106715	1.02E+08	NR_106715	ENSG000002MIR6071	hsa-mir-6 microRNA ncRNA									
chr7-1031.5.733963	-0.06488	0.964456	-0.06727	0.946366	0.981636	chr7	1.03E+08	1.03E+08	+	0 NA	3' UTR (N3' UTR (N	27949 NM_001161	83787 Hs. 287412NM_031905	ENSG000002CARM10	PNAS-112 armadill protein-coding										
chr1-3127.6.948992	0.059365	0.883816	0.067169	0.946447	0.981636	chr1	31275238	31275770	+	0 NA	intron (NAluS6 SI	21284 NM_004814	9410 Hs. 33962 NM_004814	ENSG000002SNRP40	40K HPRF small nuc protein-coding										
chr1-114.6.948992	0.059365	0.883816	0.067169	0.946447	0.981636	chr1	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	90088 NM_003302C	51592 Hs. 28637 NM_015905	ENSG000002TRIM33	CTC7 tripartit protein-coding										
chr17-186.6.948992	0.059365	0.883816	0.067169	0.946447	0.981636	chr17	18908325	18908934	+	0 NA	intron (Nintron (N	-42047 NM_001282	125206 Hs. 462418NM_152351	ENSG000002SLC5A10	SGLT-5 Solute c protein-coding										
chr17-58.6.948992	0.059365	0.883816	0.067169	0.946447	0.981636	chr17	58091186	58091911	+	0 NA	3' UTR (N3' UTR (N	8129 NM_080677	140735 Hs. 720595NM_080677	ENSG000002DYLL2	DNCL1B Dynein l protein-coding										
chr14-231.10.38443	0.048727	0.725915	0.067125	0.946482	0.981636	chr14	23232425	23232655	+	0 NA	3' UTR (N3' UTR (N	2534 NM_00136C	8106 Hs. 391464NM_004995	ENSG000002PABPN1	OPMD PAB2 poly (A) t protein-coding										
chr16-155.10.38443	0.048727	0.725915	0.067125	0.946482	0.981636	chr16	15980877	15982539	+	0 NA	intron (Nintron (N	32092 NM_004995	4363 Hs. 391464NM_004995	ENSG000002ABCC1	ABC29 ABCATP bindi protein-coding										
chr13-755.5.998805	0.063727	0.949569	0.067112	0.946493	0.981636	chr13	75575615	75576369	+	0 NA	intron (NAluSx SIN	26242 NM_006002	7347 Hs. 162241NM_006002	ENSG000002UCHL3	UCH-13 ubiquitin protein-coding										
chr2-2175.5.998805	0.063727	0.949569	0.067112	0.946493	0.981636	chr2	2.18E+08	2.18E+08	+	0 NA	exon (NM exon (NM	9602 NR_106867	1.02E+08	NR_106867	ENSG000002MIR6809	hsa-mir-6 microRNA ncRNA									
chr3-195.8.588681	-0.05416	0.808276	-0.06701	0.946573	0.981636	chr3	1.95E+08	1.95E+08	+	0 NA	intron (Nintron (N	-55688 NM_152531	152002 Hs. 478741NM_152531	ENSG000002XXYL1T	C3orf21 xyloside protein-coding										
chr1-2261.8.955218	0.052218	0.780095	0.066938	0.946631	0.981636	chr1	2.26E+08	2.26E+08	+	0 NA	intron (Nintron (N	2451 NM_002735	64746 Hs. 520207NM_002735	ENSG000002ACBD3	CGP60 GOC acyl-CoA protein-coding										
chr16-857.8.955218	0.052218	0.780095	0.066938	0.946631	0.981636	chr16	85787391	85788937	+	0 NA	intron (Nintron (N	-4251 NR_135193	1.02E+08	Hs. 662217NR_135193	ENSG000002LOC1010192	uncharactncRNA									
chr6-7347.8.955218	0.052218	0.780095	0.066938	0.946631	0.981636	chr6	73470144	73472081	+	0 NA	intron (Nintron (N	9375 NM_001122	25821 Hs. 347614NM_012122	ENSG000002MT01	CGI-02 Cm microRNA ncRNA										
chr8-2384.8.955218	0.052218	0.780095	0.066938	0.946631	0.981636	chr8	23848414	23852192	+	0 NA	intron (Nintron (N	4639 NM_003155	6781 Hs. 25590 NM_003155	ENSG000002STC1	STC stannioce protein-coding										
chr1-2688.10.91245	0.047497	0.709691	0.066927	0.94664	0.981636	chr1	26880060	26887856	+	0 NA	exon (NM exon (NM	6025 NM_018066	54707 Hs. 14333 NM_018066	ENSG000002GPN2	ATPBD1B GPN-loop protein-coding										
chr12-562.10.91245	0.047497	0.709691	0.066927	0.94664	0.981636	chr12	56204818	56217489	+	0 NA	intron (NAluSg SIN	10548 NM_001242	10193 Hs. 524502NM_005785	ENSG000002RNF41	FLRP NRDF fing protein-coding										
chr13-205.10.91245	0.047497	0.70																							



chr16-295	11.39147	0.046209	0.694555	0.06653	0.946956	0.981636	chr16	29559662	1.9561670	+	0	NA	intron (Nintron (N	34426 NR_13530E	440354 Hs. 55270CR_002473	SMG1P2	-	SMG1 pset pseudo
chr3-4712	11.39147	0.046209	0.694555	0.06653	0.946956	0.981636	chr3	47122869	47124351	+	0	NA	exon (NM exon (NM	40367 NM_01415E	29072 Hs. 517941NM_012271	ENSG00000SETD2	HBP231 H1SET	domaiprotein-coding
chr3-1976	11.39147	0.046209	0.694555	0.06653	0.946956	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	intron (NMER4-int	11246 NR_00326E	220729 Hs. 478854NR_00326E	ENSG00000CLOC220729	-	succinate pseudo
chr8-1448	11.39147	0.046209	0.694555	0.06653	0.946956	0.981636	chr8	1.45E+08	1.45E+08	+	0	NA	intron (NLM1E3D LI	16065 NM_00136E	58500 Hs. 532277NM_001061	ENSG00000ZNF250	MZF647 ZNF	zinc fingerprotein-coding
chr1-1592	8.90622	0.052028	0.782189	0.066516	0.946967	0.981636	chr1	15928065	15930571	+	0	NA	exon (NM exon (NM	46814 NM_001324	7709 Hs. 433764NM_00344E	ENSG00000ZBTB17	ZIF-1 ZNF	zinc fingerprotein-coding
chr1-6656	8.90622	0.052028	0.782189	0.066516	0.946967	0.981636	chr1	66566343	66567617	+	0	NA	intron (NLMER4 LIN	32827 NM_032291	84251 Hs. 132121NM_032291	ENSG00000CSGIP1	-	SH3 domainprotein-coding
chr10-73C	8.90622	0.052028	0.782189	0.066516	0.946967	0.981636	chr10	73013189	73016940	+	0	NA	intron (NAluSz SIN	-60258 NM_03256E	84647 Hs. 33317E_NM_03256E	ENSG00000PLA2G12B	FKSG71 G	phospholiprotein-coding
chr12-51C	8.90622	0.052028	0.782189	0.066516	0.946967	0.981636	chr12	51052473	51052713	+	0	NA	intron (NAluSg SIN	4266 NR_04502C	25875 Hs. 65527E_NM_01541E	ENSG00000LETMD1	111001901LETMD1	donorprotein-coding
chr15-636	8.90622	0.052028	0.782189	0.066516	0.946967	0.981636	chr15	63625374	63625631	+	0	NA	intron (NAluSz SIN	-24675 NR_03408C	1E+08 Hs. 63116E_NR_03408C	ENSG00000CASP3-AS1	-	USP3 anticrRNA
chr3-149E	8.90622	0.052028	0.782189	0.066516	0.946967	0.981636	chr3	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	3928 NM_00262E	5217 Hs. 91747 NM_00262E	ENSG00000PFN2	D3S1319E	profilin protein-coding
chr1-2741	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr1	27410813	27416007	+	0	NA	intron (Nintron (N	20788 NM_005281	2827 Hs. 66542 NM_005281	ENSG00000GPR3	ACCA	G protein-coding
chr11-613	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr11	61394902	61395366	+	0	NA	intron (NAluJr SIN	2547 NM_00117E	51259 Hs. 26745 NM_01649E	ENSG00000TMEM216	HSPC244	transmembraneprotein-coding
chr12-68E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr12	68649919	68660765	+	0	NA	intron (Nintron (N	-27967 NR_03333E	1E+08 Hs. 72453E_NR_03333E	ENSG00000SNORA70G	U70G	small nucleosRNA
chr12-112	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr12	1.13E+08	1.13E+08	+	0	NA	intron (NMIR1 Am	19637 NM_00103E	4939 Hs. 41433E_NM_00253E	ENSG00000OAS2	-	2'-5'-oligoprotein-coding
chr14-884	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr14	88478479	88480336	+	0	NA	exon (NM exon (NM	75600 NM_00703E	11099 Hs. 43704C_NM_00703E	ENSG00000PTPN21	PTPDI PTF	protein tyrosine kinase
chr16-58E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr16	58569367	58578780	+	0	NA	intron (NAluJo SIN	-14142 NR_00298C	677830 Hs. 67751E_NR_00298C	ENSG00000SNORA50A	ACA50 SNC	small nucleosRNA
chr17-67E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr17	67217573	67218606	+	0	NA	intron (NAluSg SIN	-26687 NR_13639E	1.02E+08 Hs. 569824NR_13639E	LOC10192E	-	uncharacterizedncRNA
chr18-54E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr18	54287374	54290627	+	0	NA	intron (NLM14a LI	19426 NM_001351	11201 Hs. 43853E_NM_00719E	ENSG00000POL1	RAD30B RAD	DNA polymerase
chr18-63E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr18	63392112	63404188	+	0	NA	intron (N(TA)n Sin	24326 NM_00486E	9525 Hs. 12655E_NM_00486E	ENSG00000VPS4B	MIG1 SKD1	vacuolar protein-coding
chr19-114	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr19	1142737	1144715	+	0	NA	intron (NMLTIC LTF	-11505 NM_00110E	22904 Hs. 40870E_NM_01496E	ENSG00000CBNO2	KIAA0963	strawberry protein-coding
chr2-3251	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr2	32515168	32520604	+	0	NA	intron (Nintron (N	-14267 NR_03028E	693143 NR_03028E	ENSG00000MIR558	MIR558	microRNA ncRNA
chr2-462E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr2	46297964	46299493	+	0	NA	intron (NCPG	1321 NM_00143C	2034 Hs. 46841E_NM_00143C	ENSG00000EPAS1	ECYT4 HIF	endothelin protein-coding
chr2-732A	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr2	73243061	73246430	+	0	NA	intron (Nintron (N	10437 NM_00642E	10574 Hs. 36814E_NM_00642E	ENSG00000CCT7	CCTETA C	chaperonin protein-coding
chr2-1021	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr2	1.02E+08	1.02E+08	+	0	NA	intron (N(L2c LINE	-13800 NM_001351	8808 Hs. 65986E_NM_00385E	ENSG00000L1RL2	IL-1Rrp2	interleukin protein-coding
chr2-1974	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr2	1.97E+08	1.97E+08	+	0	NA	3' UTR (N3' UTR (N	12176 NR_13278E	1.07E+08 NR_13278E	SNORA105E	-	small nucleosRNA
chr20-34C	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr20	34087663	34090024	+	0	NA	3' UTR (N3' UTR (N	23400 NM_00131E	8894 Hs. 42918C_NM_00390E	ENSG00000EIF2S2	EIF2 EIF2	eukaryotic protein-coding
chr4-1684	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (NLM1E2z LI	12824 NM_001291	91351 Hs. 535011NM_00101E	ENSG00000DDX60L	-	DexH/Hc protein-coding
chr6-359C	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr6	35909143	35911281	+	0	NA	intron (NAluSp SIN	10886 NM_003137	6732 Hs. 443861NM_003137	ENSG00000SRPK1	SFRSK1 SRSF	protprotein-coding
chr8-670A	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr8	67047599	67052975	+	0	NA	intron (NAluYe6 SI	11846 NM_006837	10987 Hs. 49191E_NM_006837	ENSG00000COPS5	CSN5 JAB1	COP9 sig protein-coding
chr9-575E	9.43424	0.050415	0.758308	0.066484	0.946992	0.981636	chr9	5756183	57581142	+	0	NA	intron (Nintron (N	75955 NM_02489E	79956 Hs. 59107E_NM_02489E	ENSG00000ERMP1	FXNA KIAA	endoplasmic protein-coding
chr13-72E	5.684965	-0.06524	0.98579	-0.06618	0.947231	0.981636	chr13	72843470	72844245	+	0	NA	intron (Nintron (N	61724 NR_14620E	10464 Hs. 44192E_NM_00634E	ENSG00000PIBF1	C13orf24	progesterone protein-coding
chr2-340E	5.684965	-0.06524	0.98579	-0.06618	0.947231	0.981636	chr2	3406328	3406527	+	0	NA	intron (Nintron (N	26733 NM_01603C	51112 Hs. 25271E_NM_01603C	ENSG00000TRAPP12	CG1-87 PF	trickrack protein-coding
chr14-88E	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr14	88872039	88872588	+	0	NA	intron (Nintron (N	47662 NM_00136E	123016 Hs. 30305E_NM_14459E	ENSG00000TTCS	BBS8 RP51	tetratric protein-coding
chr2-117E	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr2	11791124	11793357	+	0	NA	intron (NMIR3 SINE	24796 NR_036071	1E+08 NR_036071	ENSG00000MIR548S	-	microRNA ncRNA
chr20-52E	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr20	526281	528471	+	0	NA	intron (Nintron (N	16414 NM_00136E	1457 Hs. 64405E_NM_00189E	ENSG00000CSNK2A1	CK2A1 CKI	casein kinase protein-coding
chr3-1587	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr3	1.58E+08	1.58E+08	+	0	NA	intron (Nintron (N	13643 NM_001271	51319 Hs. 59128E_NM_01662E	ENSG00000RSRC1	BM-011 MF	arginine protein-coding
chr3-1841	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	7595 NM_003907	8893 Hs. 283551NM_003907	ENSG00000EIF2B5	CACH CLE	eukaryotic protein-coding
chr5-172E	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr5	1.72E+08	1.72E+08	+	0	NA	intron (NLMC LINE	-68930 NM_03364E	23291 Hs. 48413E_NM_01230C	ENSG00000FBXW11	BTRC2 BTF	beta ancrprotein-coding
chr6-170E	7.956034	0.054385	0.821907	0.06617	0.947243	0.981636	chr6	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	3736 NR_039787	1.01E+08 NR_039787	ENSG00000MIR4644	-	microRNA ncRNA
chr1-1124	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr1	11245818	11246736	+	0	NA	intron (Nintron (N	16274 NM_00495E	2475 Hs. 338207NM_00495E	ENSG00000MTOR	FRAP FRAF	mechanism protein-coding
chr1-2051	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr1	2.05E+08	2.05E+08	+	0	NA	intron (N(L2b LINE	10172 NM_00119E	5929 Hs. 51923E_NM_00505E	ENSG00000RBBP5	RBQ3 SWD18	bindin protein-coding
chr11-60E	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr11	60920207	60921937	+	0	NA	intron (Nintron (N	-3388 NR_178031	54972 Hs. 11855E_NM_01787C	ENSG00000TMEM132A	GBP HSPA	transmembraneprotein-coding
chr13-39E	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr13	39680527	39681157	+	0	NA	intron (NMLT1E2 LI	-16707 NR_03619C	1E+08 NR_03619C	ENSG00000MIR4305	-	microRNA ncRNA
chr13-77E	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr13	77065332	77067847	+	0	NA	intron (NLMC5 LIN	-8925 NR_04671E	1.01E+08 Hs. 56928E_NR_04671E	ENSG00000MYCBP2-AS	-	MYCBP2 arncRNA
chr15-42E	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr15	42545288	42546118	+	0	NA	intron (Nintron (N	3090 NM_15326E	255252 Hs. 234681NM_15326E	ENSG00000LRRCS7	-	leucine rich protein-coding
chr2-257A	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr2	25748662	25749334	+	0	NA	intron (Nintron (N	45693 NM_00136E	55252 Hs. 11981E_NM_01826E	ENSG00000ASXL2	ASXH2 SH	ASXL trarprotein-coding
chr5-154E	6.477827	0.060183	0.909622	0.066163	0.947248	0.981636	chr5	1.54E+08	1.54E+08	+	0	NA	intron (Nintron (N	64629 NM_198321	55568 Hs. 631797NM_01754C	ENSG00000GALNT10	GALNACT1C	polypeptide protein-coding
chr5-150C	11.87049	0.045023	0.681417	0.066072	0.94732	0.981636	chr5	1.5E+08	1.5E+08	+	0	NA	intron (NLM1Ec LIN	12613 NM_00136E	22993 Hs. 71918E_NM_01498E	ENSG00000HMGXB3	HMGX3 SMF	HMG-box protein-coding
chr2-201E	7.428014	0.056674	0.858107	0.066046	0.947341	0.981636	chr2	2.01E+08	2.01E+08	+	0	NA	exon (NM exon (NM	24570 NM_03335E	841 Hs. 59976E_NM_00122E	ENSG00000CASP8	ALPS2B C	caseinase epsilon protein-coding
chr9-121E	7.428014	0.056674	0.858107	0.066046	0.947341	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	8216 NM_198194	2040 Hs. 25390E_NM_00409E	ENSG00000STOM	BND7 EPB7	stomatol protein-coding
chr1-172E	9.913263	0.048803	0.739655	0.06598	0.947394	0.981636	chr1	17426819	17428997	+	0	NA	intron (Nintron (N	10628 NM_00113E	55920 Hs. 380857NM_01871E	ENSG00000RCC2	TD-60	regulator protein-coding
chr1-114E	9.913263	0.048803	0.739655	0.06598	0.947394	0.9816												

chr11-673.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr11	67308079	67308607	+	0	NA	intron (Nintron (N	4813	NR_017857	54961	Hs.29173	NR_017857	ENSG000003SSH3	SSH3L	slingshotprotein-coding	
chr15-505.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr15	50957358	50962159	+	0	NA	intron (N1MA4A LI	15629	NR_027642	1E+08	Hs.73049	NR_027642	DCAF13P3	-	DDBI and pseudo	
chr16-532.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr16	53298594	53300953	+	0	NA	intron (Nintron (N	71439	NR_001347	643802	Hs.45133	NR_001207030	LOC643802	-	u3 small protein-coding	
chr17-324.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr17	32469192	32471186	+	0	NA	intron (NAluJb SIN	-16804	NR_003888	8851	Hs.50001	NR_003888	ENSG000003CDK5R1	CDK5P35	Cyclin dependent protein-coding	
chr19-467.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr19	4677520	4680239	+	0	NA	promoter-promoter-	-403	NR_001242	1E+08	Hs.67813	NR_001242901	PPP9-AS1	-	PPP9 antipeptide-coding	
chr2-1272.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr2	12723472	12725046	+	0	NA	intron (N12c LINE	7323	NR_027303	28951	Hs.467751	NR_021643	ENSG000003TRIB2	C5WF GS3	tribbles protein-coding	
chr2-2272.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr2	2.28E+08	2.28E+08	+	0	NA	intron (Nintron (N	63366	NR_001133	3267	Hs.352962	NR_004504	ENSG000003AGFG1	HRB RAB FAR GAP	wiprotein-coding	
chr20-385.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr20	38524806	38527222	+	0	NA	exon (NM exon (NM	9451	NR_039605	1.01E+08	NR_039605	ENSG000003MIR54802	-	microRNA ncRNA		
chr21-466.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr21	46650579	46652033	+	0	NA	intron (Nintron (N	15632	NR_206962	3275	Hs.15416	NR_001533	ENSG000003PRMT2	HRMT1L1	protein-coding	
chr22-205.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr22	20565130	20566753	+	0	NA	intron (Nintron (N	57894	NR_001293	51586	Hs.51742	NR_015883	ENSG000003MED15	ARC105 C	mediator protein-coding	
chr3-4048.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr3	40485088	40489470	+	0	NA	exon (NM exon (NM	10157	NR_173655	285267	Hs.40715	NR_173655	ENSG000003ZNF619	-	zinc finger protein-coding	
chr4-1254.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr4	1.25E+08	1.25E+08	+	0	NA	exon (NM exon (NM	-38441	NR_031746	1E+08	NR_031746	ENSG000003MIR2054	hsa-mir-2	microRNA ncRNA		
chr5-9576.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr5	95789968	95794074	+	0	NA	intron (NHALI LINE	30705	NR_002064	2745	Hs.28988	NR_002064	ENSG000003GLRX	GRX GRX1	glutaredc protein-coding	
chr7-7662.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr7	76623868	76625941	+	0	NA	intron (NAluYml SI	2399	NR_152992	22932	Hs.48867	NR_012233	ENSG000003POMZP3	POM-ZP3 POM121	arprotein-coding	
chr9-8932.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr9	89329287	89330963	+	0	NA	intron (NMER6B DNA	11274	NR_001282	79048	Hs.59804	NR_024077	ENSG000003SECSBP2	SBP2	SECS1 birprotein-coding	
chr9-9233.8.435056	0.052268	0.797935	0.065505	0.947772	0.981636	chr9	92300763	92308619	+	0	NA	intron (N1M03 LIN	-10935	NR_073446	3376	Hs.44540	NR_002161	ENSG000003IARS	GRIDH1 I	isoleucylprotein-coding	
chr4-8929.5.478643	0.064916	0.991762	0.065455	0.947811	0.981636	chr4	89229898	89230662	+	0	NA	intron (Nintron (N	-29364	NR_034077	1E+08	Hs.72891	NR_034077	ENSG000003THAP9-AS1	-	THAP9 antncRNA	
chr1-1124.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr1	1.12E+08	1.12E+08	+	0	NA	intron (N1Tiger14a	6055	NR_03621C	1E+08	NR_03621C	ENSG000003MIR4256	-	microRNA ncRNA		
chr1-1147.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr1	1.15E+08	1.15E+08	+	0	NA	intron (Nintron (N	-16953	NR_002524	4893	Hs.48650	NR_002524	ENSG000003NRAS	ALPS4 CMNRAS	protprotein-coding	
chr13-727.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr13	72775201	72777815	+	0	NA	intron (Nintron (N	5392	NR_001322	22894	Hs.74410	NR_014953	ENSG000003DIS3	2810028NC	DIS3 homc protein-coding	
chr15-925.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr15	92975781	92987851	+	0	NA	intron (Nintron (N	77417	NR_036133	1E+08	NR_036133	ENSG000003MIR3175	mir-3175	microRNA ncRNA		
chr17-665.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr17	6632211	6635299	+	0	NA	intron (N1LME2z LI	6956	NR_001351	9851	Hs.28070	NR_014804	ENSG000003KIAA0753	MNR OFIP	KIAA0753 protein-coding	
chr17-401.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr17	40125973	40137469	+	0	NA	intron (Nintron (N	-8816	NR_007355	22794	Hs.74328	NR_007355	ENSG000003CASC3	BTZ MLN51	CASC3 exc protein-coding	
chr17-481.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr17	48915283	48929144	+	0	NA	intron (NAluSg SIN	-13230	NR_135674	1.05E+08	Hs.65524	NR_135674	ENSG000003LOC105371	-	uncharactncRNA	
chr19-162.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr19	16216238	16224599	+	0	NA	intron (NAluSz SIN	22507	NR_032493	8907	Hs.71040	NR_032493	ENSG000003AP1M1	AP47 CLAF	adaptor protein-coding	
chr20-384.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr20	38427364	38433560	+	0	NA	promoter-promoter-	-658	NR_003017	677839	Hs.71151	NR_003017	ENSG000003SNORA71C	U71c	small nucsnoRNA	
chr3-9425.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr3	9425984	94380160	+	0	NA	intron (Nintron (N	34300	NR_00108C	55209	Hs.28816	NR_018187	ENSG000003SETD5	-	SET domain protein-coding	
chr3-5225.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr3	52255774	52263759	+	0	NA	exon (NM exon (NM	8595	NR_02966C	406890	NR_02966C	ENSG000003MIRLET7G	LET7G MI7	microRNA ncRNA		
chr5-1233.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr5	1.23E+08	1.23E+08	+	0	NA	intron (N1LIPA4 LIN	67452	NR_001166	153241	Hs.48320	NR_15322	ENSG000003CEP120	CCDC100 J	centrosome protein-coding	
chr8-3038.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chr8	30385895	30387539	+	0	NA	intron (Nintron (N	-1366	NR_04620E	1E+08	Hs.12681	NR_04620E	ENSG000003RBPMS-AS1	-	RBPMS antncRNA	
chrX-4576.10.39228	0.047342	0.723614	0.065425	0.947836	0.981636	chrX	45769034	45769841	+	0	NA	IntergeniIntergeni	-22313	NR_02963E	407007	NR_02963E	ENSG000003MIR222	MIRN222	microRNA ncRNA		
chr10-115.6.95685	0.057203	0.876876	0.065235	0.947987	0.981636	chr10	11930164	11931467	+	0	NA	intron (Nintron (N	-36105	NR_038222	219731	Hs.57678	NR_038222	ENSG000003PROSER2-1	-	PROSER2 ncRNA	
chr10-495.6.95685	0.057203	0.876876	0.065235	0.947987	0.981636	chr10	49973623	49974748	+	0	NA	non-codiron-codir	-14133	NR_00136E	414189	Hs.53615	NR_001077	ENSG000003AGAP6	AGAP-6 C	ArfGAP wiprotein-coding	
chr19-171.6.95685	0.057203	0.876876	0.065235	0.947987	0.981636	chr19	17151200	17151778	+	0	NA	intron (N1LIM4 LINE	59254	NR_145784	1.1E+08	NR_145784	SNORA118	-	small nucsnoRNA		
chr2-175.6.95685	0.057203	0.876876	0.065235	0.947987	0.981636	chr2	1.75E+08	1.75E+08	+	0	NA	non-codiron-codir	-69023	NR_038133	1123	Hs.38013	NR_001822	ENSG000003CHN1	ARHGAP2 C	chimerin protein-coding	
chr22-502.6.95685	0.057203	0.876876	0.065235	0.947987	0.981636	chr22	19627	1931454	+	0	NA	exon (NM exon (NM	83642	Hs.36540	NR_031454	83642	Hs.36540	NR_031454	ENSG000003SELENOO	SELO	selenopr protein-coding
chr1-4485.6.171845	-0.06108	0.9366	-0.06521	0.948005	0.981636	chr1	44857304	44857739	+	0	NA	intron (NAluSp SIN	-14268	NR_00373E	8643	Hs.59149	NR_00373E	ENSG000003PTCH2	PTC2	patched 2 protein-coding	
chr2-3721.6.171845	-0.06108	0.9366	-0.06521	0.948005	0.981636	chr2	37215589	37217423	+	0	NA	TTS (NR_1TTS (NR_1	15090	NR_00576C	10153	Hs.13540	NR_00576C	ENSG000003CEBPZ	CBF CBF2 C	CAAT en protein-coding	
chr2-2261.6.171845	-0.06108	0.9366	-0.06521	0.948005	0.981636	chr2	2.26E+08	2.26E+08	+	0	NA	TTS (NR_1TTS (NR_1	38141	NR_046102	646736	Hs.71283	NR_046102	LOC646736	-	uncharactncRNA	
chr20-601.6.171845	-0.06108	0.9366	-0.06521	0.948005	0.981636	chr20	6015184	6016640	+	0	NA	intron (Nintron (N	8663	NR_001322	54675	Hs.74395	NR_01909E	ENSG000003CRLS1	C20orf15	cardiolin protein-coding	
chr4-675.6.171845	-0.06108	0.9366	-0.06521	0.948005	0.981636	chr4	67506264	67507528	+	0	NA	exon (NM exon (NM	38607	NR_001812	1060	Hs.47986	NR_001812	ENSG000003CENPF	CENP-C C	centrosome protein-coding	
chr6-145.6.171845	-0.06108	0.9366	-0.06521	0.948005	0.981636	chr6	1.46E+08	1.46E+08	+	0	NA	intron (N1MSTD LTR	25672	NR_17308E	257218	Hs.72397	NR_17308E	ENSG000003SHPRH	ba54515.2	SNF2 hist protein-coding	
chr1-1593.7.153464	-0.05611	0.860586	-0.06521	0.948014	0.981636	chr1	15937514	15938028	+	0	NA	intron (Nintron (N	38361	NR_001324	7709	Hs.43376	NR_003444	ENSG000003ZBTB17	MIZ-1 ZNF	zinc finger protein-coding	
chr1-2074.7.153464	-0.05611	0.860586	-0.06521	0.948014	0.981636	chr1	20741631	20743015	+	0	NA	TTS (NM_1TTS (NM_1	-9620	NR_001103	400745	Hs.59152	NR_001103	ENSG000003SH2D5	-	SH2 domain protein-coding	
chr1-1124.7.153464	-0.05611	0.860586	-0.06521	0.948014	0.981636	chr1	21241785	21248075	+	0	NA	intron (N1L2b LINE	34685	NR_001113	1889	Hs.19508	NR_001397	ENSG000003ECE1	ECE	endothelin protein-coding	
chr11-212.7.153464	-0.05611	0.860586	-0.06521	0.948014	0.981636	chr11	12930239	12935918	+	0	NA	intron (N1Tiger3c	56470	NR_038904	1.01E+08	Hs.15340	NR_038904	ENSG000003LINC			



chr16-50c	6.42883	0.060381	0.937279	0.064422	0.948634	0.981636	chr16	50351459	50352457	+	0	NA	intron (N) LIMA6 LIN	17030	NM_001173	29117	Hs.437894NM_01326c	ENSG000000CBRD7	BP75 CELI1bromodome protein-coding	
chr1-1377	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr1	13778019	13779606	+	0	NA	exon (NM) exon (NM)	29397	NM_001007	7799	Hs.37182c	ENSG000000PRDM2	HUMHOXY1 PR/SET dc protein-coding	
chr1-5137	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr1	51372022	51372505	+	0	NA	intron (N) intron (N)	-27147	NM_001144	22996	Hs.11294c	ENSG000000TTC39A	C1orf34 Tetratric protein-coding	
chr1-145f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	exon (NM) exon (NM)	10370	NM_001097	653519	Hs.50432c	ENSG000000GPR89A	GPHR GPR6G protei protein-coding	
chr1-1514	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr1	1.51E+08	1.51E+08	+	0	NA	intron (N) AluJr SIN	17140	NM_00279c	5692	Hs.89545	ENSG000000PSMB84	HN3 HN33 protease protein-coding	
chr10-102	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr10	1.02E+08	1.02E+08	+	0	NA	3' UTR (N) 3' UTR (N)	18308	NM_02478c	79847	Hs.30906c	ENSG000000MFSD13A	C10orf77 major fac protein-coding	
chr10-104	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	intron (N) AluJr4 S1	28763	NR_03076c	64068	ENSG000000MIR936	MIRN936 miRNA ncRNA		
chr13-79f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr13	79335429	79336903	+	0	NA	intron (N) intron (N)	70055	NM_00128c	51467	Hs.55852c	ENSG000000RBM26	ARRS2 C13RNA bindi protein-coding	
chr14-99f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr14	99914042	99915879	+	0	NA	intron (N) intron (N)	-56462	NM_00133c	51466	Hs.125867	ENSG000000EVL	RNB6 Enah/Vasf protein-coding	
chr15-34f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr15	34873862	34875290	+	0	NA	intron (N) intron (N)	-79027	NM_00515c	70	Hs.118127	ENSG000000ACTC1	ACT ASDFactin al protein-coding	
chr17-42f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr17	4258830	4261394	+	0	NA	intron (N) L2a LINE	3735	NM_001257	51479	Hs.696087	ENSG000000ANKFY1	ANKHZN Tlankyrin 1 protein-coding	
chr19-49f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr19	49342953	49343682	+	0	NA	exon (NM) exon (NM)	7911	NM_00104c	951	Hs.16655c	ENSG000000CD37	GP52-40 ICD37 molc protein-coding	
chr21-28f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr21	28875947	28876586	+	0	NA	3' UTR (N) 3' UTR (N)	9101	NM_01324c	29104	Hs.16384c	ENSG000000N6MT1	C21orf127N-6 adeniprotein-coding	
chr3-469f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr3	46923712	46925115	+	0	NA	intron (N) intron (N)	42164	NM_001184	5745	Hs.1019	NM_00031c	ENSG000000PTHIR	EKNS PFE parathy protein-coding
chr3-1964	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr3	1.96E+08	1.96E+08	+	0	NA	intron (N) intron (N)	30653	NM_152617	165918	Hs.25064c	ENSG000000RN168	hRNF168 ring fing protein-coding	
chr5-1414	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr5	14146329	14149955	+	0	NA	intron (N) (A)A(TTAA)	4800	NM_00711c	7204	Hs.130031	ENSG000000TRIO	ARGHF23 trio Rho protein-coding	
chr6-131f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr6	1.32E+08	1.32E+08	+	0	NA	intron (N) intron (N)	18747	NM_00483c	9439	Hs.29679	ENSG000000MED23	ARC130 CFmediator protein-coding	
chr6-149f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr6	1.5E+08	1.5E+08	+	0	NA	intron (N) AluJo SIN	3300	NR_077247	645958	Hs.632614	NR_077247	RPS18P9	RPS18_6_7ribosomal pseudo
chr9-361f	7.435872	0.054644	0.849664	0.064313	0.948721	0.981636	chr9	36107668	36112574	+	0	NA	intron (N) intron (N)	-26415	NR_104637	152007	Hs.49381c	ENSG000000GLIPR2	C9orf19 CGLI pathc protein-coding	
chr8-125c	8.62982	-0.05217	0.811374	-0.06429	0.948737	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	intron (N) intron (N)	30106	NM_10484c	9897	Hs.27004c	ENSG000000WASHC5	KIAA0196 WASH com protein-coding	
chr1-1457	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	3' UTR (N) 3' UTR (N)	26870	NR_10384c	11126	Hs.488237	ENSG000000CD160	BY55 NK1 CD160 molc protein-coding	
chr10-105	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	exon (NM) exon (NM)	6638	NM_01497c	22984	Hs.23949c	ENSG000000PDCD11	ALG-4 ALC programme protein-coding	
chr11-57f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr11	57556426	57558608	+	0	NA	intron (N) AluSp SIN	10155	NM_00422c	9246	Hs.425777	ENSG000000UBE2L6	RIG-B UB ubiquitir protein-coding	
chr15-99f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr15	99674469	99676884	+	0	NA	intron (N) intron (N)	42698	NM_00113c	4205	Hs.26867c	ENSG000000MEF2A	ADCAD1 RS myocyte c protein-coding	
chr16-15f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr16	15038091	15037829	+	0	NA	exon (NM) exon (NM)	21714	NM_17347c	123803	Hs.59204c	ENSG000000NTAN1	PNAAL PNAI-N-termin protein-coding	
chr22-38c	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr22	38686723	38689421	+	0	NA	intron (N) intron (N)	6115	NM_02024c	56993	Hs.59507c	ENSG000000TOMM22	IC9-2 MS1 transloc protein-coding	
chr3-581f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr3	58156773	58157127	+	0	NA	intron (N) AluSx SIN	13685	NR_135534	1.05E+08	Hs.613914	NR_135534	ENSG000000FLNB-AS1	FLNB anticnRNA
chr7-728f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr7	72897859	72901707	+	0	NA	intron (N) AluY SINE	9156	NM_17202c	9883	Hs.655217	ENSG000000POM121	P145 POM1POM121 t protein-coding	
chr9-324f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr9	32417814	32419570	+	0	NA	intron (N) L2a LINE	18409	NM_001362	48	Hs.56722c	ENSG000000AC01	ACONS HEI acitase protein-coding	
chr9-132f	9.442098	0.04891	0.761414	0.064235	0.948783	0.981636	chr9	1.33E+08	1.33E+08	+	0	NA	intron (N) intron (N)	18264	NM_001362	7248	Hs.370854	ENSG000000TSC1	LAM1 TSC TSC compl protein-coding	
chr1-1204	11.87835	0.043801	0.682663	0.064162	0.948841	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (N) LIP2 LINE	-22149	NR_00324c	767846	Hs.65718c	ENSG000000PFN1P2	C1orf152 profilin pseudo	
chr12-69f	11.87835	0.043801	0.682663	0.064162	0.948841	0.981636	chr12	69571297	69572497	+	0	NA	intron (N) intron (N)	-12826	NR_03747c	1.01E+08	NR_03747c	ENSG000000MIR3913	mir-3913-microRNA ncRNA	
chr6-306f	11.87835	0.043801	0.682663	0.064162	0.948841	0.981636	chr6	30601401	30609908	+	0	NA	intron (N) AluY SINE	11559	NM_002714	5514	Hs.10601c	ENSG000000PPP1R10	CAT53 FBI protein protein-coding	
chr15-687	5.957665	0.061081	0.952226	0.064146	0.948854	0.981636	chr15	68782098	68782324	+	0	NA	intron (N) intron (N)	19714	NR_036197	1E+08	NR_036197	ENSG000000MIR4312	microRNA ncRNA	
chr3-1344	5.957665	0.061081	0.952226	0.064146	0.948854	0.981636	chr3	1.34E+08	1.34E+08	+	0	NA	3' UTR (N) 3' UTR (N)	-7861	NM_00135c	80254	Hs.443301	ENSG000000CEP63	SKCL6 centroson protein-coding	
chr2-324c	8.086085	-0.05309	0.827843	-0.06413	0.948887	0.981636	chr2	32401264	32401947	+	0	NA	exon (NM) exon (NM)	44577	NM_01625c	57448	Hs.150107	ENSG000000BTRC6	APOLLON Ebaculovir protein-coding	
chr1-779f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr1	77951981	77953419	+	0	NA	intron (N) intron (N)	26372	NR_13015c	8880	Hs.56738c	ENSG000000FUBP1	FBP FUBP far upstr protein-coding	
chr1-200f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (N) AluSq SIN	-56585	NM_00529c	2848	Hs.53431c	ENSG000000GPR25	G protein protein-coding	
chr1-248f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr1	2.49E+08	2.49E+08	+	0	NA	exon (NM) exon (NM)	11975	NM_001017	267002	Hs.602037	ENSG000000PGBD2	giggyBac protein-coding	
chr10-974	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr10	97459355	97463639	+	0	NA	exon (NM) exon (NM)	15322	NM_19804c	84287	Hs.76662	ENSG000000ZDHH16	APH2 DHH zinc fing protein-coding	
chr12-87f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr12	871230	871846	+	0	NA	intron (N) intron (N)	61538	NM_001297	5893	Hs.41035c	ENSG000000RAD52	RAD52 hon protein-coding	
chr18-57f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr18	57660245	57660935	+	0	NA	intron (N) AluSg SIN	30259	NM_001242	1.01E+08	Hs.6064c	ENSG000000LOC100505	uncharact protein-coding	
chr2-993c	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr2	99363373	99365273	+	0	NA	exon (NM) exon (NM)	26934	NM_015904	9669	Hs.15868c	ENSG000000EIF5B	IF2 eukaryoti protein-coding	
chr2-378	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr2	37888154	37890774	+	0	NA	TTS (NM) TTS (NM) C	-16833	NM_03338c	85377	Hs.51761c	ENSG000000MICALL1	MICAL-L1 MICAL lik protein-coding	
chr3-1324	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr3	1.32E+08	1.32E+08	+	0	NA	intron (N) intron (N)	66534	NM_00132c	23317	Hs.12707	ENSG000000DNAJC13	PARK21 RN DNAJ heat protein-coding	
chr4-265f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr4	2.657911	2.658417	+	0	NA	intron (N) MIR SINE	32732	NR_04633c	8603	Hs.652364	ENSG000000FAM193A	C9orf8 RF family w protein-coding	
chr5-315f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636	chr5	31534314	31537165	+	0	NA	intron (N) intron (N)	3438	NM_01835c	55322	Hs.51924c	ENSG000000C5orf22	chromoson protein-coding	
chr5-346f	9.393101	0.048709	0.760248	0.064069	0.948915	0.981636														



chr3-4912.7.640344	-0.0532	0.835983	-0.06364	0.949255	0.981636	chr3	49129399	49131571	+	0	NA	intron (Nintron (N	2565 NM_002292	3913 Hs. 439726NM_002292	ENSG000003LAMB2	LAMS NPHS laminin sprotein-coding
chr3-1794.7.640344	-0.0532	0.835983	-0.06364	0.949255	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (NAluS2 SI	33122 NM_021625	59345 Hs. 173032NM_021625	ENSG000003GNB4	CMTD1F G proteirprotein-coding
chr4-6833.7.640344	-0.0532	0.835983	-0.06364	0.949255	0.981636	chr4	68334583	68337430	+	0	NA	intron (Nintron (N	14084 NM_001330	91746 Hs. 175955NM_133370	ENSG000003YTHDC1	YT521 YTFYTH domainprotein-coding
chr6-1384.7.640344	-0.0532	0.835983	-0.06364	0.949255	0.981636	chr6	1.38E+08	1.38E+08	+	0	NA	intron (NMLT1A LI	2325 NM_014320	23593 Hs. 486589NM_014320	ENSG000003HEBP2	G6HF34B heme bincprotein-coding
chr6-1666.7.640344	-0.0532	0.835983	-0.06364	0.949255	0.981636	chr6	1.67E+08	1.67E+08	+	0	NA	intron (Nintron (N	8893 NM_021135	6196 Hs. 655277NM_021135	ENSG000003RPS6KA2	HU-2 MBF ribosomalprotein-coding
chr1-1905.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr1	19092410	19109025	+	0	NA	intron (Nintron (N	109549 NM_020765	23352 Hs. 148075NM_020765	ENSG000003CUBR4	RBAF600 Zubiquitin protein-coding
chr1-5652.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr1	56521900	56525997	+	0	NA	intron (NLa2 LINE	55615 NM_003711	8613 Hs. 405155NM_003711	ENSG000003PLPP3	Dr142 LPF phospholiprotein-coding
chr1-1512.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr1	51512100	5151E+08	+	0	NA	intron (Nintron (N	8064 NM_020832	57592 Hs. 146755NM_020832	ENSG000003ZNF687	PDB6 zinc fingprotein-coding
chr11-704.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr11	70404342	70423938	+	0	NA	intron (NAluY SINE	15611 NM_001184	2017 Hs. 596164NM_005231	ENSG000003CTTN	EMS1 cortactin protein-coding
chr12-656.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr12	6569517	6602856	+	0	NA	intron (NAluY SINE	-4577 NR_003012	677780 Hs. 689692NR_003012	ENSG000003SCARNA11	ACA57 small ncRNA
chr14-102.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	exon (NM exon (NM	53885 NM_005345	3320 Hs. 525600NM_005345	ENSG000003HSP90AA1	EL52 HEL-heat shockprotein-coding
chr15-590.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr15	59080645	59082671	+	0	NA	intron (NAluJo SIN	-23488 NM_004701	9133 Hs. 194695NM_004701	ENSG000003CCNB2	Hs1T7299 cyclin B2protein-coding
chr16-1346.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr16	30703381	30725534	+	0	NA	intron (NAluY SINE	3920 NR_002966	677813 Hs. 689715NR_002966	ENSG000003SNORA30	ACA30 SNC small nucsnoRNA
chr19-207.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr19	22298881	22305553	+	0	NA	exon (NM exon (NM	3932 NR_031596	1E+08 NR_031596	ENSG000003MIR1227	MIRN1227 microRNA ncRNA
chr19-361.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr19	36142153	36149565	+	0	NA	exon (NM exon (NM	4869 NM_001302	826 Hs. 515371NM_001302	ENSG000003CAPNS1	CALPALIN1 calpain sprotein-coding
chr19-515.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr19	51580335	51588161	+	0	NA	intron (Nintron (N	10132 NR_034159	729975 Hs. 171678NR_034159	LINC01530	long intncRNA
chr19-573.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr19	53342275	53354311	+	0	NA	intron (Nintron (N	14544 NM_138374	91664 Hs. 720672NM_138374	ENSG000003ZNF845	zinc fingprotein-coding
chr19-554.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr19	57412277	57422109	+	0	NA	exon (NM exon (NM	8542 NM_006959	7565 Hs. 729402NM_006959	ENSG000003CNF17	HPF3 KOX1zinc fingprotein-coding
chr19-575.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr19	57501271	57509210	+	0	NA	intron (Nintron (N	5527 NR_130705	374928 Hs. 579575NR_198542	ENSG000003ZNF773	ZNF419B zinc fingprotein-coding
chr20-2182.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr20	2.18E+08	2.18E+08	+	0	NA	intron (Nintron (N	-16130 NM_001321	151306 Hs. 160954NM_170695	ENSG000003GPBAR1	BG37 GPCF proteinprotein-coding
chr20-390.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr20	3908079	3915753	+	0	NA	intron (Nintron (N	-5578 NR_029515	406896 NR_029515	ENSG000003MIR103A2	MIR103-2 microRNA ncRNA
chr22-416.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr22	41622819	41632263	+	0	NA	intron (NAluX1 SI	6246 NM_001285	2547 Hs. 292493NM_001465	ENSG000003XRC6	CTC75 CTCX-ray repprotein-coding
chr3-1415.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr3	14155098	14173485	+	0	NA	intron (Nintron (N	14310 NR_148951	7508 Hs. 475535NM_004625	ENSG000003XPC	RAD4 XP3 XPC complprotein-coding
chr3-4906.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr3	49062831	49066238	+	0	NA	intron (NAluX1 SI	29098 NM_001320	54870 Hs. 274987NM_017730	ENSG000003TRICH1	AB-DIP VEFglutaminprotein-coding
chr3-5005.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr3	50090640	50121009	+	0	NA	intron (Nintron (N	-4836 NR_045388	1.01E+08 Hs. 439482NR_045388	ENSG000003RBM5-AS1	LUST RBM5 antncRNA
chr4-3890.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr4	38905489	38919635	+	0	NA	intron (NAluSx3 SI	44530 NR_030300	693159 NR_030300	ENSG000003MIR574	MIR574-3f microRNA ncRNA
chr5-1346.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	23180 NM_021982	10802 Hs. 595542NM_021982	ENSG000003SEC24A	SEC24 honprotein-coding
chr7-2331.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr7	23317088	23319094	+	0	NA	intron (NMRB SINE	18752 NM_138445	115416 Hs. 87385 NM_138445	ENSG000003MALSU1	C7orf30 nmitochonprotein-coding
chr8-3046.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr8	30469935	30471759	+	0	NA	intron (Nintron (N	-8544 NR_046205	1E+08 Hs. 126815NR_046205	ENSG000003RBPMS-AS1	RBPMS antncRNA
chr9-1215.10.40014	0.045964	0.723821	0.063502	0.949366	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (NMRB3 DNA	28450 NM_000177	2934 Hs. 522375NM_000177	ENSG000003GSN	ADF AGEL gelsolin protein-coding
chr17-424.11.82935	0.043617	0.68754	0.063439	0.949417	0.981636	chr17	42466981	42467180	+	0	NA	intron (NAluY SINE	8202 NM_005177	535 Hs. 463074NM_005177	ENSG000003ATP6VOA1	ATP6N1 ATATPase H+protein-coding
chr10-875.7.697199	-0.05489	0.865171	-0.06344	0.949417	0.981636	chr10	87518038	87518204	+	0	NA	intron (Nintron (N	10538 NM_001175	9562 Hs. 121260NM_004897	ENSG000003MNP1	HIPER1 Mimultipe protein-coding
chr1-1985.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr1	19897506	19900374	+	0	NA	intron (NAluJb SIN	16520 NM_015207	23252 Hs. 374987NM_015207	ENSG000003OTUD3	DUBA4 TUO deubiquitinprotein-coding
chr13-454.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr13	45489916	45492704	+	0	NA	intron (Nintron (N	26371 NM_031431	83548 Hs. 507945NM_031431	ENSG000003COG3	SEC34 componentprotein-coding
chr3-1217.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (NLa2c LINE	-41019 NM_005335	3059 Hs. 14601 NM_005335	ENSG000003HCLS1	CTTNL HS1hematopoieprotein-coding
chr4-7882.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr4	78826154	78828131	+	0	NA	intron (NMRER2 int	55589 NM_199892	55589 Hs. 146551NM_017595	ENSG000003BMP2K	BKE HRIF BMP2 indprotein-coding
chr5-9552.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr5	95521425	95523077	+	0	NA	exon (NM exon (NM	32754 NM_014635	9652 Hs. 482865NM_014635	ENSG000003TTC37	KIAA0372 tetratricprotein-coding
chr5-1464.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (NMR SINE	16949 NM_006705	10915 Hs. 443465NM_006705	ENSG000003TCERG1	CAL50 TAF transcripprotein-coding
chr9-4701.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr9	4701995	4704593	+	0	NA	intron (NLA_C_Mam	22933 NM_001195	50808 Hs. 146551NM_016282	ENSG000003AK3	AK3L1 AK6adenylateprotein-coding
chr9-1300.7.914894	0.052407	0.826837	0.063382	0.949462	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	29702 NM_020960	57720 Hs. 512461NM_020960	ENSG000003GPR107	GCDRP LUSG proteirprotein-coding
chr1-3207.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr1	32076676	32080174	+	0	NA	intron (NAluJb SIN	5452 NM_001315	55116 Hs. 25544 NM_018055	ENSG000003TMEM39B	transment protein-coding
chr10-777.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr10	7774825	7776451	+	0	NA	intron (Nintron (N	12355 NM_012311	22944 Hs. 397915NM_012311	ENSG000003KIN	BTCD KIN1Kin17 DNprotein-coding
chr10-475.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr10	47549106	47550654	+	0	NA	intron (NAluJb SIN	3620 NR_160414	1.14E+08 Hs. 463017NR_160414	BMS1P2-AC	BMS1P2-ACpseudo
chr10-734.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr10	73465451	73466221	+	0	NA	intron (NCR1-3_Crc	-29916 NR_132103	1.02E+08 Hs. 434502NR_132103	ENSG000003PPP3CB-AS1	USP54-AS1 PPP3CB arncRNA
chr10-137.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr10	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	26007 NM_001321	10539 Hs. 42644 NM_006541	ENSG000003GLRX3	GLRX4 GR3glutaredprotein-coding
chr13-190.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr13	19754819	19755767	+	0	NA	intron (Nintron (N	27652 NM_001354	55269 Hs. 213195NM_001042	ENSG000003PSPC1	PSP1 paratredprotein-coding
chr13-115.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (Nintron (N	22039 NM_000705	496 Hs. 434202NM_000705	ENSG000003ATP4B	ATP6B ATPase H+protein-coding
chr15-638.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr15	63658414	63660357	+	0	NA	intron (NAluJr4 SI	-58558 NR_034080	1E+08 Hs. 631165NR_034080	ENSG000003USP3-AS1	USP3 antncRNA
chr15-985.8.442914	0.050584	0.798107	0.06338	0.949464	0.981636	chr15	98921570	98926798	+	0	NA	intron (Nintron (N	81472 NM_001102	145814 Hs. 592021NM_001102	ENSG000003PGPEP1L	pyroglut protein-coding
chr15-101.8.442914	0.050584	0.798107	0.06338	0.												



chr19-498.6.436688.0.057858.0.919972.0.062891.0.949854.0.981636	chr19	49836861	49837728	+	0	NA	TTS (NM_C TTS (NM_C	5276	NR_10685E	1.02E+08	NR_10685E	ENSG00000MIR6800	hsa-mir-ε microRNA	ncRNA		
chr20-636.6.436688.0.057858.0.919972.0.062891.0.949854.0.981636	chr20	63927008	63927242	+	0	NA	intron (N LIMD LINE	7257	NR_03063E	1E+08	NR_03063E	ENSG00000MIR941-3	MIRN941-ε microRNA	ncRNA		
chr3-3734.6.436688.0.057858.0.919972.0.062891.0.949854.0.981636	chr3	37349554	37350408	+	0	NA	intron (N intron (N	-36288	NM_178344	339883	Hs. 47594E	ENSG00000C3orf35	APRG1	chromosom protein-coding		
chr3-1192.6.436688.0.057858.0.919972.0.062891.0.949854.0.981636	chr3	1.19E+08	1.19E+08	+	0	NA	intron (N intron (N	-212	NR_046574	1.01E+08	Hs. 721307	ENSG00000B4GALT4-1	B4GALT4	ε ncRNA		
chr9-3435.4.958481.0.066878.1.063638.0.062876.0.949865.0.981636	chr9	34397145	34397541	+	0	NA	TTS (NM_C TTS (NM_C	467	NR_03259E	84688	Hs. 503334	NR_03259E	ENSG00000C9orf24	CBE1 NYD	chromosom protein-coding	
chr9-1377.8.191938.0.054666.0.869566.0.062866.0.949874.0.981636	chr9	1.38E+08	1.38E+08	+	0	NA	exon (NM_exon (NM	-2485	NR_14750E	651337	Hs. 60319E	NR_14750E	ENSG00000CLOC651337-	uncharactncRNA		
chr1-532C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr1	53200002	53207116	+	0	NA	intron (N HAL LINE	7135	NR_00009E	1376	Hs. 71353E	NR_00009E	ENSG00000CPT2	CPT1 CPT2	carnitine protein-coding	
chr1-1002.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr1	1E+08	1E+08	+	0	NA	intron (N intron (N	-4318	NR_03027E	693138	NR_03027E	ENSG00000MIR553	MIRN553 ε microRNA	ncRNA		
chr10-811.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr10	811956	817491	+	0	NA	exon (NM_exon (NM	116982	NM_001351	23185	Hs. 15906E	NR_01515E	ENSG00000CLARP4B	KIAA0217 La	ribom protein-coding	
chr10-105.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr10	1.1E+08	1.1E+08	+	0	NA	intron (N AG N Sin	41676	NM_001324	7511	Hs. 39062E	NR_02038E	ENSG00000CXPPEP1	APP1 SAMF	X-prolyl protein-coding	
chr10-11E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr10	1.2E+08	1.2E+08	+	0	NA	intron (N LIMC4 LIN	25737	NM_024834	79892	Hs. 12462E	NR_024834	ENSG00000CMCBP	C10orf15 minichron	protein-coding	
chr11-60C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr11	600797	604240	+	0	NA	intron (N AluSq2 SI	13432	NM_00402E	3665	Hs. 16612C	NR_00157E	ENSG00000CIRF7	IMD39 IRF	interferc protein-coding	
chr11-467.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr11	46745679	46755690	+	0	NA	intron (N intron (N	2508	NR_04984E	1.01E+08	NR_04984E	ENSG00000MIR5582	-	microRNA	ncRNA	
chr11-64C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr11	64360601	64364468	+	0	NA	intron (N intron (N	3372	NM_00100E	8986	Hs. 105584	NR_00394E	ENSG00000CRPS6KA4	MSK2 RSK	ribosomal protein-coding	
chr12-101.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr12	1.01E+08	1.01E+08	+	0	NA	Intergeni LIPA3 LIN	17613	NM_001177	400	Hs. 37261E	NR_001177	ENSG00000CARL1	ARFL1	ADP ribos protein-coding	
chr12-105.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr12	1.05E+08	1.05E+08	+	0	NA	intron (N intron (N	14692	NM_001034	160428	Hs. 42572	NR_001034	ENSG00000CALDH1L2	mtFHD	aldehyde protein-coding	
chr12-122.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (N intron (N	5091	NM_00367E	8562	Hs. 22293	NR_00367E	ENSG00000CENR	DRP DRP1	aldensity r protein-coding	
chr13-23C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr13	23822045	23828059	+	0	NA	intron (N intron (N	-63816	NM_001014	542767	Hs. 642624	NR_001014442	PCOTH	C1QTNF9B	Pro-X-Gly protein-coding	
chr13-454.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr13	45493396	45499494	+	0	NA	intron (N AluJb SIN	31506	NM_031431	83548	Hs. 50794E	NR_031431	ENSG00000COCG3	SEC3A	component protein-coding	
chr13-491.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr13	49186042	49189454	+	0	NA	intron (N TTTT n S	-32590	NM_001507	2862	Hs. 24812E	NR_001507	ENSG00000CMLNR	GPR38 MTL	motilin r protein-coding	
chr13-111.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (N intron (N	34667	NM_001354	8874	Hs. 50873E	NR_00389E	ENSG00000CARHGEF7	BETA	PiX Rho	guani protein-coding
chr14-962.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr14	96236258	96245371	+	0	NA	exon (NM_exon (NM	-15396	NM_00071C	623	Hs. 52557E	NR_00071C	ENSG00000CBDKRB1	BIBKR B1F	bradykinin protein-coding	
chr15-39E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr15	39800941	39801915	+	0	NA	exon (NM_exon (NM	18522	NR_13566E	1.05E+08	Hs. 58784E	NR_13566E	ENSG00000CLOC10537C	-	uncharactncRNA	
chr15-59E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr15	59668032	59682520	+	0	NA	intron (N intron (N	13650	NM_00132C	663	Hs. 59251E	NR_00433C	ENSG00000CBNIP2	BNIP-2 N1ECL2	inte protein-coding	
chr15-651.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr15	65149156	65155899	+	0	NA	non-codirnon-codir	-18719	NM_005707	10081	Hs. 45859E	NR_005707	ENSG00000CPDCD7	ES18 HES1	programa protein-coding	
chr16-11E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr16	11843843	11849933	+	0	NA	intron (N intron (N	4654	NM_01565E	26156	Hs. 40184E	NR_01565E	ENSG00000CRSL1D1	CSIG L12	ribosomal protein-coding	
chr16-23C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr16	23658390	23662692	+	0	NA	intron (N La2 LINE	-18348	NM_00503C	5347	Hs. 59204E	NR_00503C	ENSG00000CPLK1	PLK1 STK1	polo like protein-coding	
chr16-69C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr16	69314681	69327119	+	0	NA	intron (N intron (N	9550	NM_01324E	27183	Hs. 12842C	NR_01324E	ENSG00000CVPS4A	SKD1 SKD1	vacuolar protein-coding	
chr17-47E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	4797483	4799112	+	0	NA	exon (NM_exon (NM	2133	NM_00279E	5694	Hs. 77060	NR_00279E	ENSG00000CPSMB6	DELTA	LMF proteasom protein-coding	
chr17-65E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	6582570	6589943	+	0	NA	intron (N MS A LTR	-29701	NM_00116E	83394	Hs. 18398E	NR_03122C	ENSG00000CPTPNM3	ACKR6 COF	PITPNM3	ε protein-coding
chr17-31E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	31988519	31999543	+	0	NA	intron (N intron (N	-13352	NM_001321	114659	Hs. 514071	NR_05288E	ENSG00000CLRRC37B	LRRC37	leucine r protein-coding	
chr17-39E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	39509036	39512481	+	0	NA	intron (N AluSp SIN	49272	NM_01508E	51755	Hs. 34502E	NR_01508E	ENSG00000CCKD12	CRK7 CRKf	cyclin d protein-coding	
chr17-42E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	42954211	42958745	+	0	NA	exon (NM_exon (NM	7976	NM_001261	80755	Hs. 31740C	NR_001261	ENSG00000CAARSD1	-	alanyl-t	protein-coding
chr17-48E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	48929578	48939669	+	0	NA	intron (N AluJr SIN	10219	NM_001317	11267	Hs. 12724E	NR_00724E	ENSG00000CSNF8	Dot3 EAP	SNF8	subt protein-coding
chr17-60C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	60051265	60059788	+	0	NA	exon (NM_exon (NM	-12421	NR_03989E	1.01E+08	NR_03989E	ENSG00000MIR4737	-	microRNA	ncRNA	
chr17-60C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	60455903	60465752	+	0	NA	intron (N AluSx SIN	38748	NM_181707	124773	Hs. 12931E	NR_181707	ENSG00000C17orf64	-	chromosom protein-coding	
chr17-62C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr17	62027813	62033677	+	0	NA	intron (N intron (N	34533	NM_005121	9969	Hs. 28267E	NR_005121	ENSG00000CMED13	ARC250 DF	mediator protein-coding	
chr2-3974.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	39748633	39751962	+	0	NA	intron (N LIPA1 LI	28961	NM_02526E	80745	Hs. 59204E	NR_02526E	ENSG00000CTHUMPD2	C2orf8	THUMP	don protein-coding
chr2-546E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	54625867	54633574	+	0	NA	exon (NM_exon (NM	71326	NM_17831E	6711	Hs. 50317E	NR_00312E	ENSG00000CSPTBN1	ELF1 HELL3	spectrin protein-coding	
chr2-558E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	55869828	55875812	+	0	NA	intron (N intron (N	50962	NM_00103E	2202	Hs. 76224	NR_00410E	ENSG00000CFEMP1	DHRD DRAL	EGF cont	ε protein-coding
chr2-6507.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	65079803	65085216	+	0	NA	intron (N intron (N	26093	NM_00131E	23177	Hs. 70925E	NR_01514E	ENSG00000CEP68	KIAA0582	centrosom protein-coding	
chr2-711E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	71134038	71140567	+	0	NA	intron (N LIM5 LINE	6668	NM_005791	10199	Hs. 65620E	NR_005791	ENSG00000CMPHOSPHL1C	CT90 MPP1	M-phase	ε protein-coding
chr2-101E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	1.02E+08	1.02E+08	+	0	NA	intron (N intron (N	-107910	NR_103791	1.01E+08	Hs. 51624E	NR_103791	LINC01127-	-	long intencRNA	
chr2-1897.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (N intron (N	8441	NM_001371388	1841	Hs. 47187E	NR_01214E	ENSG00000CDTYMK	CDC8 PP37	deoxythym protein-coding	
chr2-241E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	2.42E+08	2.42E+08	+	0	NA	intron (N CpG	19823	NR_03325E	10043	Hs. 47470E	NR_00548E	ENSG00000CTOM1	-	target of	protein-coding
chr2-251E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	35284454	35291604	+	0	NA	intron (N MER58C DN	-1246	NM_00113E	51386	Hs. 44685E	NR_016091	ENSG00000CEIF3L	EIF3E1P E	eukaryoti protein-coding	
chr2-37E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	37850662	37857900	+	0	NA	intron (N La2 LINE	4862	NM_00136C	26286	Hs. 68522E	NR_01457C	ENSG00000CARFGAP3	ARFGAP1	ADP ribos protein-coding	
chr2-42E.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	42821384	42834228	+	0	NA	intron (N AluJo SIN	29467	NM_01457C	1499	Hs. 47601E	NR_001904	ENSG00000CTNNB1	CTNNB1 EVF	catenin t protein-coding	
chr2-412C.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr2	41223899	41228298	+	0	NA	intron (N MER1B DNA	26593	NM_00109E	-40657	NM_017577	ENSG00000GRAMD1C	-	GRAM dom	protein-coding	
chr3-1137.8.921936.0.048791.0.776207.0.062859.0.949879.0.981636	chr3	1.14E+08	1.14E+08	+	0	NA	intron (N AluSx SIN	-40657	NM_01757							

chr7-128f	7.44373	0.052699	0.845638	0.062318	0.950309	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	IntergeniLIMEg LIN	-55593 NR_02436f	402483 Hs. 72235CNCM_001039682	LINC0100C-	long intencRNA	
chr9-472C	7.44373	0.052699	0.845638	0.062318	0.950309	0.981636	chr9	4720619	4723136	+	0	NA	intron (Nintron (N	4350 NM_001199	50808 Hs. 732022NM_01628f	ENSG00000AK3	AK3L1 AKfadenylateprotein-coding	
chr9-3391	7.44373	0.052699	0.845638	0.062318	0.950309	0.981636	chr9	33916058	33919642	+	0	NA	3' UTR (N3' UTR (N	16514 NM_00128f	55833 Hs. 49373fNCM_01844f	ENSG00000UBAP2	UBAP-2 ubiquitin protein-coding	
chr9-128f	7.44373	0.052699	0.845638	0.062318	0.950309	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	exon (NM exon (NM	2954 NM_01603f	51117 Hs. 98541 NM_01603f	ENSG00000COQ4	CGI-92 CC coenzyme protein-coding	
chr1-7023	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr1	70230750	70235313	+	0	NA	intron (Nintron (N	11651 NM_00135f	9295 Hs. 47969fNCM_00476f	ENSG00000SRSF11	NET2 SFRS serine ar protein-coding	
chr1-7023	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr1	70238651	70247901	+	0	NA	intron (NMER8 DNA	21896 NM_00135f	9295 Hs. 47969fNCM_00476f	ENSG00000SRSF11	NET2 SFRS serine ar protein-coding	
chr1-112f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	-9941 NM_00128f	4343 Hs. 514941NM_02096f	ENSG00000MOV10	fSAP113 gMov10 RfS protein-coding	
chr1-162f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (Nintron (N	21770 NM_01586f	127933 Hs. 12731CNCM_14462f	ENSG00000UHMK1	KIS KIST U2AF homc protein-coding	
chr1-1791	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr1	1.79E+08	1.79E+08	+	0	NA	exon (NM exon (NM	24357 NM_00515f	27 Hs. 15947fNCM_00515f	ENSG00000CABL2	ABLL ARG ABL protc protein-coding	
chr10-121	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr10	12136117	12140040	+	0	NA	intron (Nintron (N	-7412 NR_03969f	1.01E+08	NR_03969f	ENSG00000MIR548AK	- microRNA ncRNA
chr10-121	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr10	27110362	27118292	+	0	NA	intron (Nintron (N	-13829 NM_01491f	22852 Hs. 361041NM_01491f	ENSG00000ANKRD26	THC2 ba14ankyrin r protein-coding	
chr10-46f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr10	46007262	46017191	+	0	NA	intron (NIME4c LI	7311 NM_00114f	8031 Hs. 64365fNCM_00543f	ENSG00000NCOA4	ARA70 ELF nuclear r protein-coding	
chr10-97f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr10	97644025	97645440	+	0	NA	intron (NMLT1J LTF	4046 NM_01842f	55361 Hs. 25300 NM_01842f	ENSG00000PI4K2A	PI4KII PI phosphatid protein-coding	
chr11-107	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr11	10752037	10760997	+	0	NA	intron (Nintron (N	5721 NM_00134f	9646 Hs. 725151NM_01463f	ENSG00000CTR9	SH2BP1 TSCTR9 homc protein-coding	
chr11-107	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr11	10762262	10770638	+	0	NA	exon (NM exon (NM	15204 NM_00134f	9646 Hs. 725151NM_01463f	ENSG00000CTR9	SH2BP1 TSCTR9 homc protein-coding	
chr11-11f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr11	11995959	12002893	+	0	NA	intron (NLA_C_Mam	7393 NM_00101f	27122 Hs. 29215fNCM_01325f	ENSG00000DKK3	REIC RIG dickkopf protein-coding	
chr11-32f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr11	32588896	32596630	+	0	NA	intron (Nintron (N	8932 NM_00636f	1048 Hs. 502244NM_00636f	ENSG00000EIF3M	B5 GA17 Eukaryoti protein-coding	
chr12-50f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr12	50472794	50477105	+	0	NA	intron (Nintron (N	18378 NR_13275f	1.07E+08	NR_13275f	SNORD133	ZL142 ZL4small nucsnRNA
chr14-67f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr14	67376247	67378963	+	0	NA	intron (N2b LINE	17277 NM_00409f	1965 Hs. 151777NM_00409f	ENSG00000EIF2S1	EIF-2 EIF eukaryoti protein-coding	
chr15-39f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr15	39949214	39958054	+	0	NA	intron (NLTR79 LTF	19519 NM_00101f	440275 Hs. 65667fNCM_00101f	ENSG00000EIF2AK4	GCN2 PVOE eukaryoti protein-coding	
chr15-48f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr15	48509660	48515637	+	0	NA	intron (NLIPIA13 LI	133140 NM_00013f	2200 Hs. 59113fNCM_00101f	ENSG00000FBN1	ACM1CD EC fibrilli r protein-coding	
chr15-491	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr15	49139114	49144264	+	0	NA	intron (Nintron (N	13910 NM_00114f	9318 Hs. 369614NM_00423f	ENSG00000COPS2	ALIEN CSN COP9 sigr protein-coding	
chr17-23f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr17	2320716	2334972	+	0	NA	intron (Nintron (N	1366 NR_00307f	692208	NR_00307f	ENSG00000SNORD91B	HBII-296f small nucsnRNA
chr17-46f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr17	46222048	46223537	+	0	NA	intron (Nintron (N	2582 NM_00119f	284058 Hs. 648744NM_01544f	ENSG00000KANSL1	CENP-36 KAT8 regu protein-coding	
chr19-19f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr19	19023271	19031796	+	0	NA	intron (N2a LINE	5984 NR_14791f	10147 Hs. 77876 NM_01488f	ENSG00000SUGP2	SFRS14 SF SURP and protein-coding	
chr2-364f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	36442279	36447651	+	0	NA	intron (N2c LINE	89187 NM_01644f	51232 Hs. 699247NM_01644f	ENSG00000CRIM1	CRIM-1 Sf cysteine protein-coding	
chr2-861f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	86110899	86112565	+	0	NA	intron (NALuSp SIN	5497 NM_01795f	55037 Hs. 32348fNCM_01795f	ENSG00000PTCD3	MRP-539f pentatric protein-coding	
chr2-885f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	88574117	88575336	+	0	NA	exon (NM exon (NM	36006 NR_11023f	1.02E+08	NR_11023f	ENSG00000LOC10192f	- uncharactncRNA
chr2-1351	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (NSVA_C Ret	-30830 NR_14572f	1.1E+08	NR_14572f	ENSG00000SNORA40B	- small nucsnRNA
chr2-169f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	1.7E+08	1.7E+08	+	0	NA	intron (NLIIM8 LIN	31421 NM_00479f	9360 Hs. 470544NM_00479f	ENSG00000PP1G	CARS-Cyp peptidyl r protein-coding	
chr2-191f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (NMLT1A0 LI	32709 NM_00116f	4430 Hs. 43962CNCM_01222f	ENSG00000MYO1B	MMI-alpha myosin II f protein-coding	
chr2-221	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr2	41168589	41172709	+	0	NA	intron (Nintron (N	26852 NR_11051f	1.02E+08	NR_11051f	EP300-AS1-	EP300 antncRNA
chr3-451	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr3	15216988	15221872	+	0	NA	intron (N2c LINE	13184 NM_01429f	23473 Hs. 595234NM_01429f	ENSG00000CAPN7	CALPAINT calpain f protein-coding	
chr3-988	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr3	98806730	98808205	+	0	NA	intron (NMLT1A0 LI	44160 NM_00132f	10402 Hs. 14871fNCM_00610f	ENSG00000CT3GAL6	SIAT10 ST13 beta protein-coding	
chr3-125f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr3	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	29768 NM_02073f	57493 Hs. 47742CNCM_02073f	ENSG00000HEG1	HEG MS11 heart dev protein-coding	
chr3-156f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr3	1.57E+08	1.57E+08	+	0	NA	intron (NALuJb SIN	944 NM_00130f	6747 Hs. 51834fNCM_00710f	ENSG00000SSR3	TRAPG signal s protein-coding	
chr4-699f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr4	6995013	6997646	+	0	NA	exon (NM exon (NM	8821 NM_00128f	57533 Hs. 518611NM_02077f	ENSG00000TBC1D14	- TBC1 domc protein-coding	
chr4-887f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr4	88747530	88750757	+	0	NA	intron (Nintron (N	39326 NR_00280f	28512 Hs. 74495fNCM_00280f	ENSG00000FAM13A-AS	FAM13A10 FAM13A arncRNA	
chr5-138f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr5	13828112	13830599	+	0	NA	intron (Nintron (N	11525 NM_00136f	1767 Hs. 21236CNCM_00136f	ENSG00000DNAH5	CILD3 DNA dynein ar protein-coding	
chr5-394f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr5	39416867	39418470	+	0	NA	intron (Nintron (N	7312 NM_00134f	1601 Hs. 696631NM_00134f	ENSG00000DAB2	DOC-2 DOC DAB adapt protein-coding	
chr5-656f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr5	65637408	65638846	+	0	NA	intron (NALuSx SIN	13100 NM_02494f	80006 Hs. 59176CNCM_02494f	ENSG00000TRAPP13	C5orf44 S trafficki protein-coding	
chr5-138f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr5	1.39E+08	1.39E+08	+	0	NA	intron (NALuJb SIN	27369 NM_00129f	2107 Hs. 36916fNCM_00473f	ENSG00000ETF1	D5S1995 Eukaryoti protein-coding	
chr6-435f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr6	43519386	43525304	+	0	NA	TTS (NM_TTS (NM_C	5256 NM_00136f	9533 Hs. 74350fNCM_00487f	ENSG00000POLR1C	AC40 HLD1RNA polyn protein-coding	
chr6-111f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (NX6A LINE	7151 NM_15336f	91749 Hs. 40057fNCM_15336f	ENSG00000MFS4B	KIAA1919 major fac protein-coding	
chr7-926f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr7	92615219	92618146	+	0	NA	intron (Nintron (N	-26292 NM_00104f	257145 Hs. 18564 NM_15278f	ENSG00000FAM133B	- family wi protein-coding	
chr8-390f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr8	39082587	39083701	+	0	NA	intron (N2c LINE	-24385 NM_00131f	203102 Hs. 52154fNCM_14500f	ENSG00000ADAM32	- ADAM metc protein-coding	
chr8-102f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	41080 NR_12541f	1.02E+08	NR_12541f	ENSG00000UBR5-AS1	- UBR5 antncRNA
chr8-102f	9.400959	0.047186	0.757528	0.062289	0.950333	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	56878 NR_12541f	1.02E+08	NR_12541f	ENSG00000UBR5-AS1	- UBR5 antncRNA
chr9-122f	9.400959	0.047186	0.757528	0.062289	0													



chr11-295	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr11	2955911	2960562	+	0	NA	intron (Nintron (N	5657	NR_002982	677833	Hs.689696	NR_002982	ENSG000003NORA54	ACA54	small	nucsnRNA	
chr11-936	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr11	93683187	93685283	+	0	NA	intron (Nintron (N	22553	NM_033395	85459	Hs.458418	NM_033395	ENSG000003CEP295	KIAA1731	centrosom	protein-coding	
chr12-645	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr12	6496697	6497162	+	0	NA	intron (Nintron (N	2827	NM_014866	9918	Hs.5719	NM_014866	ENSG000003NCAPD2	CAP-D2	CNnon-SMC	protein-coding	
chr12-121	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr12	12148638	12151297	+	0	NA	intron (Nintron (N	38015	NR_036052	1E+08	NR_036052	ENSG000003MIR1244	MIR1244	lmi	ncRNA		
chr12-121	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr12	21645344	21646941	+	0	NA	intron (Nintron (N	11652	NM_0011174	3945	Hs.446145	NM_002300	ENSG000003LDHB	HEL-S-281	lactate	protein-coding	
chr12-928	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr12	92887796	92890100	+	0	NA	intron (NAluSz SIN	40347	NM_003566	8411	Hs.567367	NM_003566	ENSG000003CEEA1	MST105	MSearly enc	protein-coding	
chr12-131	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	-40304	NM_016155	4326	Hs.709245	NM_016155	ENSG000003MMP17	MMP-17	MTmatrix	protein-coding	
chr13-207	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr13	20061352	20063531	+	0	NA	intron (Nintron (N	-40260	NR_126388	1.04E+08	Hs.578016	NR_126388	ENSG000003LINC01072		long intencr	RNA	
chr13-95	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr13	95092008	95093185	+	0	NA	intron (Nintron (N	-117748	NR_145733	1.1E+08	NR_145733	SNORD13G		small	nucsnRNA		
chr14-311	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr14	31162943	31163428	+	0	NA	intron (NAluJo SIN	44608	NM_015382	25831	Hs.708017	NM_015382	ENSG000003HECTD1	EULLR	HECT dom	protein-coding	
chr14-691	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr14	69114478	69116660	+	0	NA	intron (Nintron (N	37030	NM_001284	8816	Hs.509780	NM_003861	ENSG000003DCAF5	BCRG2	BCF	protein-coding	
chr14-967	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr14	96552107	96554879	+	0	NA	intron (NAluJb SIN	50628	NM_001293	10914	Hs.253722	NM_032632	ENSG000003PAPOLA	PAP	PAP- $\alpha$ poly(A)	protein-coding	
chr14-103	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	intron (Nintron (N	5786	NM_001130	3831	Hs.20107	NM_005552	ENSG000003KLC1	KLC	KNS2	protein-coding	
chr15-140	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr15	43024699	43027825	+	0	NA	intron (Nintron (N	79776	NM_174911	197131	Hs.591121	NM_174911	ENSG000003UBR1	JBS	ubiquitin	protein-coding	
chr15-551	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr15	55188413	55191488	+	0	NA	intron (Nintron (N	6991	NM_016304	51187	Hs.274772	NM_016304	ENSG000003RSL24D1	C15orf15	ribosomal	protein-coding	
chr15-64	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr15	64087387	64089433	+	0	NA	intron (Nintron (N	5428	NM_032231	84191	Hs.439545	NM_032231	ENSG000003CIA02A	CIA2A	FAM	cytosolic	
chr15-75	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr15	75933223	75936877	+	0	NA	non-codirnon-codir	31172	NM_147188	26263	Hs.591111	NM_012170	ENSG000003FBX022	FBX22	FISF-box	protein-coding	
chr16-293	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr16	29368805	29368925	+	0	NA	intron (Nintron (N	16680	NM_001310	72888	Hs.720288	NM_001310	ENSG000003NIP1B11	NPIP1	nuclear	protein-coding	
chr17-202	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr17	20245443	20250545	+	0	NA	intron (Nintron (N	-73180	NR_023388	348254	Hs.462475	NR_023388	CCDC144C	CCDC144C	coiled-c	pseudo	
chr17-607	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr17	60207407	60208533	+	0	NA	intron (Nintron (N	23675	NR_002996	677681	NR_002996	ENSG000003SCARNA20	ACA66	small	ncRNA		
chr18-497	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr18	49790016	49793047	+	0	NA	exon (NM exon (NM	22002	NM_006111	10449	Hs.200133	NM_006111	ENSG000003ACAA2	DSAEAC	acetyl-C	protein-coding	
chr19-115	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr19	11935957	11936201	+	0	NA	intron (Nintron (N	10972	NM_144566	90592	Hs.528488	NM_144566	ENSG000003ZNF700		zinc	protein-coding	
chr19-58	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr19	58516288	58517213	+	0	NA	exon (NM exon (NM	2852	NM_001316	84878	Hs.515662	NM_032792	ENSG000003ZBTB45	ZNF499	zinc	protein-coding	
chr2-6941	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr2	69418064	69421180	+	0	NA	intron (Nintron (N	17813	NR_045632	27247	Hs.430432	NM_015700	ENSG000003NFU1	CGI-33	HINFU1	iror	protein-coding
chr2-8605	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr2	86096816	86098989	+	0	NA	intron (Nintron (N	7984	NM_015425	25885	Hs.531818	NM_015425	ENSG000003POLR1A	A190	AFC	protein-coding	
chr2-2234	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr2	2.02E+08	2.02E+08	+	0	NA	intron (Nintron (N	92663	NM_001204	659	Hs.471111	NM_001204	ENSG000003BMPR2	BMPR-II	Ebone	protein-coding	
chr2-2238	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr2	2.24E+08	2.24E+08	+	0	NA	IntergeniMLT11 LTF	-36575	NR_110906	130340	Hs.632555	NM_178814	ENSG000003AP153	PSORS15	adaptor	protein-coding	
chr20-176	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr20	17602718	17603640	+	0	NA	intron (Nintron (N	33104	NM_006878	11034	Hs.304192	NM_006878	ENSG000003DSTN	ACTDP1	ADF	protein-coding	
chr3-333	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr3	33395821	33402918	+	0	NA	intron (Nintron (N	41009	NM_001128	7342	Hs.729122	NM_014517	ENSG000003UBP1	LBP-1B	LF	protein-coding	
chr4-1997	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr4	1997439	1999410	+	0	NA	intron (Nintron (N	10550	NM_005662	7469	Hs.21771	NM_005662	ENSG000003NELFA	NELF-A	PF	protein-coding	
chr4-391	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr4	39102529	39107050	+	0	NA	intron (NAluSc SIN	42557	NM_199035	51088	Hs.272251	NM_015990	ENSG000003KLHL5		kelch	protein-coding	
chr7-3257	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr7	32572528	32577640	+	0	NA	intron (Nintron (N	79595	NM_015066	23080	Hs.128055	NM_015066	ENSG000003AVL9	KIAA0241	AVL9	cell	protein-coding
chr7-474	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr7	47433206	47453119	+	0	NA	intron (Nintron (N	30641	NR_145811	1.1E+08	NR_145811	SNORD151		small	nucsnRNA		
chr7-730	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr7	73068878	73069399	+	0	NA	IntergeniIntergeni	-11231	NR_003664	728524	Hs.571272	NM_001023562	SPDYEBP		speedy	protein-coding	
chr7-137	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr7	1.38E+08	1.38E+08	+	0	NA	TTS (NM_CTS (NM_C	20780	NM_001318	64764	Hs.490273	NM_194071	ENSG000003CREB3L2	BBF2H7	cAMP	protein-coding	
chr7-157	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr7	1.57E+08	1.57E+08	+	0	NA	TTS (NM_CTS (NM_C	-82373	NM_005494	10049	Hs.490745	NM_005494	ENSG000003DNABJ6	DJ4	DnaJ	protein-coding	
chr9-100	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr9	1E+08	1E+08	+	0	NA	TTS (NM_CTS (NM_C	50953	NM_001161	54881	Hs.494645	NM_017744	ENSG000003TEX10	Ipi1	ba2C	protein-coding	
chr9-125	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	3' UTR (N3' UTR (N	46122	NM_001330	26130	Hs.42376	NM_015632	ENSG000003GAPVD1	GAPX5	GATTPase	protein-coding	
chr9-1341	7.922752	0.050572	0.821272	0.061578	0.950899	0.981636	chr9	1.34E+08	1.34E+08	+	0	NA	intron (Nintron (N	2385	NM_052821	11091	Hs.397638	NM_017588	ENSG000003WDR5	BIG-3	CFAD	protein-coding	
chr8-4797	7.386874	0.054828	0.890473	0.061572	0.950904	0.981636	chr8	47977328	47977641	+	0	NA	3' UTR (N3' UTR (N	16543	NM_182744	4173	Hs.460184	NM_005914	ENSG000003MCM4	CDC21	CD	protein-coding	
chr21-28	6.678818	0.050617	0.855887	-0.061535	0.950935	0.981636	chr21	28984843	28985229	+	0	NA	intron (Nintron (N	7841	NM_001320	26046	Hs.288773	NM_015562	ENSG000003LTN1	C21orf10	listerin	protein-coding	
chr16-29	12.84425	0.040619	0.66053	0.061495	0.950965	0.981636	chr16	29501957	29505807	+	0	NA	intron (Nintron (N	1992	NM_001355	440353	NR_001355	NP1PB12		nuclear	protein-coding		
chr4-247	12.84425	0.040619	0.66053	0.061495	0.950965	0.981636	chr4	2470899	2473553	+	0	NA	intron (Nintron (N	2773	NM_001188	6047	Hs.66394	NR_002938	ENSG000003CRNF4	RES4-26	Spring	protein-coding	
chr10-495	7.632486	-0.05141	0.837732	-0.06136	0.951071	0.981636	chr10	49925452	49932244	+	0	NA	intron (Nintron (N	11179	NR_136755	8505	Hs.535298	NM_003631	ENSG000003PARG	PARG99	poly(ADP-	protein-coding	
chr13-405	7.632486	-0.05141	0.837732	-0.06136	0.951071	0.981636	chr13	40950070	40951075	+	0	NA	intron (Nintron (N	-28798	NR_003365	283507	Hs.442781	NR_003365	ENSG000003SUGT1P3	SUGT1L1	SUGT1	pseud	
chr14-391	7.632486	-0.05141	0.837732	-0.06136	0.951071	0.981636	chr14	39152337	39155075	+	0	NA	intron (Nintron (N	16627	NM_001075	122553	Hs.13303	NM_177452	ENSG000003TRAPP6B	NEDMEBA1	trafficki	protein-coding	
chr14-10	7.632486	-0.05141	0.837732	-0.06136	0.951071	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	TTS (NR_CTS (NR_C	252	NR_003236	767568	NR_003236	SNORD113-14q	(I-8)	small	nucsnRNA		
chr16-88	7.632486	-0.05141	0.837732	-0.06136	0.951071	0.981636	chr16	88588341	88591126	+	0	NA	intron (Nintron (N	19330	NM_144604	102425	Hs.93670	NM_144604	ENSG000003ZC3H18	NHNI	zinc	protein-coding	
chr17-671	7.632486	-0.05141	0.837732	-0.06136	0.95107																		

chr17-381 8.176222	-0.05051	0.832258	-0.0607	0.951601	0.981636	chr17	3812870	3813346	+ 0 NA	exon (NM_exon (NM_192000))	11920 NM_002208	3682 Hs. 513867NM_002208	ENSG000001TGAE	CD103 HUM integrin protein-coding
chr3-1895 8.176222	-0.05051	0.832258	-0.0607	0.951601	0.981636	chr3	1.9E+08	1.9E+08	+ 0 NA	intron (NLIP47 LIN	138895 NR_030642	1E+08 NR_030642	ENSG000001MIR944	MIRN944 hmicroRNA ncRNA
chr16-214 11.36605	0.042239	0.696082	0.060682	0.951613	0.981636	chr16	21407833	21412128	+ 0 NA	intron (NAluSx4 SI	15398 NM_130464	23117 Hs. 611072NM_130464	NPIP3B	KIAA02201 nuclear protein-coding
chr17-161 11.36605	0.042239	0.696082	0.060682	0.951613	0.981636	chr17	16101270	16101842	+ 0 NA	exon (NM_exon (NM_151640))	NR_145787	1.1E+08 NR_145787	SNORD163	small nucleolar RNA
chr6-2837 11.36605	0.042239	0.696082	0.060682	0.951613	0.981636	chr6	2837321	2838177	+ 0 NA	intron (Nintron (N_4114))	NR_073112	1992 Hs. 381167NM_030666	ENSG000001SERPINB1	EI ELANHE serpin protein-coding
chr1-2187 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr1	21871805	21882164	+ 0 NA	intron (NAluSx SIN	60326 NM_001291	3339 Hs. 562227NM_005529	ENSG000001HSPG2	HSPG PLC heparan protein-coding
chr1-3294 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr1	32941653	32942354	+ 0 NA	intron (NAluV SINE	22806 NM_001127	127544 Hs. 591504NM_153341	ENSG000001RNF19B	ITBRDC3 NKR ing protein-coding
chr1-3935 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr1	39336132	39342763	+ 0 NA	intron (NL2 LINE L	-69266 NM_015038	643314 Hs. 658766NM_015038	ENSG000001KIAA0754	KIAA0754 protein-coding
chr1-1793 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr1	1.79E+08	1.79E+08	+ 0 NA	intron (Nintron (N_8662))	NR_030642	126859 Hs. 658505NM_144696	ENSG000001AXDND1	C1orf125 axonemal protein-coding
chr10-856 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr10	86621908	86624586	+ 0 NA	intron (Nintron (N_32512))	NR_001333	6623 Hs. 349477NM_003087	ENSG000001SNCG	BCLG1 SR synuclein protein-coding
chr10-956 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr10	95613169	95616686	+ 0 NA	intron (NLIME3 LIN	41784 NM_001323	5832 Hs. 500645NM_002866	ENSG000001ALDH18A1	ADCSL3 AR aldehyde protein-coding
chr10-103 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr10	1.03E+08	1.03E+08	+ 0 NA	intron (Nintron (N_49299))	NR_001351	22978 Hs. 97439 NM_012225	ENSG000001CNT5C2	GMP NT5B 5' nucleol protein-coding
chr10-115 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr10	1.19E+08	1.19E+08	+ 0 NA	intron (Nintron (N_5390))	NR_001303	404636 Hs. 434241NM_207005	ENSG000001DENND10	FAM45A DENN domain protein-coding
chr10-118 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr10	1.2E+08	1.2E+08	+ 0 NA	non-coding-non-coding	-16349 NR_039833	1.01E+08 NR_039833	ENSG000001MIR4682	microRNA ncRNA
chr11-595 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr11	59584034	59589173	+ 0 NA	intron (NLIMB2 LIN	8555 NR_036120	1E+08 NR_036120	ENSG000001MIR3162	mir-3162 microRNA ncRNA
chr11-116 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr11	1.17E+08	1.17E+08	+ 0 NA	exon (NM_exon (NM_5937))	NR_001155	84811 Hs. 437341NM_032722	ENSG000001BUD13	Cwc26 f5 BUD13 hom protein-coding
chr11-118 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr11	1.19E+08	1.19E+08	+ 0 NA	intron (Nintron (N_17019))	NR_106773	1.02E+08 NR_106773	ENSG000001MIR6716	hsa-mir-6716 microRNA ncRNA
chr11-118 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr11	1.19E+08	1.19E+08	+ 0 NA	intron (NL2 LINE L	8346 NR_106773	1.02E+08 NR_106773	ENSG000001MIR6716	hsa-mir-6716 microRNA ncRNA
chr13-236 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr13	23626542	23629160	+ 0 NA	intron (Nintron (N_48491))	NR_018647	55504 Hs. 149166NM_018647	ENSG000001TNFRSF19	TAJ TAJ-α TNF receptor protein-coding
chr15-434 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr15	43456790	43459215	+ 0 NA	intron (NAluSx SIN	35154 NM_001141	7158 Hs. 440965NM_005657	ENSG000001TP53BP1	53BP1 TDF tumor protein-coding
chr16-27 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr16	27344678	27356684	+ 0 NA	intron (Nintron (N_36707))	NR_001257	3566 Hs. 513457NM_000418	ENSG000001ILR	CD124 IL-1 interleukin protein-coding
chr16-532 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr16	53245455	53248717	+ 0 NA	intron (NL2c LINE L	38635 NM_001352	80205 Hs. 59159 NM_015287	ENSG000001CHD9	AD013 CHE chromodon protein-coding
chr17-324 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr17	32463018	32466955	+ 0 NA	intron (Nintron (N_20476))	NR_002815	5717 Hs. 443379NM_002815	ENSG000001PSMD11	Rpn6 S9 proteasome protein-coding
chr17-426 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr17	42668476	42673486	+ 0 NA	intron (NCPg-1116	5030 NR_073574	79990 Hs. 632251NM_024927	ENSG000001PLEKH3	pleckstrin protein-coding
chr19-165 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr19	16559628	16567695	+ 0 NA	intron (NAluSz SIN	8754 NM_024881	79939 Hs. 620596NM_024881	ENSG000001SLC35E1	solute carrier protein-coding
chr19-358 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr19	35888058	35890578	+ 0 NA	intron (NAluJr SIN	10419 NM_001321	84807 Hs. 446653NM_032721	ENSG000001NFKBID	IkbNS Ike NFKB inhibitor protein-coding
chr2-2031 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr2	2.03E+08	2.03E+08	+ 0 NA	exon (NM_exon (NM_20337))	NR_177538	57404 Hs. 466631NM_020674	ENSG000001CYP20A1	CYP-m cytochrome protein-coding
chr2-2186 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr2	2.19E+08	2.19E+08	+ 0 NA	intron (Nintron (N_20337))	NR_001366	7701 Hs. 657966NM_001105	ENSG000001ZNF142	HAF454 NE zinc finger protein-coding
chr2-2298 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr2	2.3E+08	2.3E+08	+ 0 NA	intron (Nintron (N_42751))	NR_001348	9320 Hs. 572642NM_004235	ENSG000001TRIP12	MRD49 TRI thyroid l protein-coding
chr2-2325 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr2	2.33E+08	2.33E+08	+ 0 NA	intron (NAluSx4 SI	15138 NM_001330	9470 Hs. 529202NM_004845	ENSG000001EIF4E	4E-LP 4E eukaryotic protein-coding
chr2-2413 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr2	2.41E+08	2.41E+08	+ 0 NA	exon (NM_exon (NM_19843))	NR_001321	4735 Hs. 721234NM_004404	ENSG000001SEPTIN2	DIFF6 NEI septin 2 protein-coding
chr21-335 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr21	33905774	33913276	+ 0 NA	intron (NAluSz SIN	6279 NM_001697	539 Hs. 409144NM_001697	ENSG000001ATP5P0	ATP5P0 ATF ATP synthet protein-coding
chr22-245 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr22	24557795	24557772	+ 0 NA	intron (NLTR16B1 L	2784 NM_004175	6634 Hs. 356545NM_004175	ENSG000001SNRPD3	SMD3 Sm-1 small nucleol protein-coding
chr22-413 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr22	41342674	41358666	+ 0 NA	intron (NL2a LINE L	-16663 NM_001148	7008 Hs. 181155NM_003215	ENSG000001CTEF	TEF trans protein-coding
chr3-1447 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr3	14477070	14480172	+ 0 NA	intron (Nintron (N_61721))	NR_001088	80852 Hs. 517815NM_001088	ENSG000001GRIP2	glutamate protein-coding
chr4-1758 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr4	17581534	17586367	+ 0 NA	intron (Nintron (N_6646))	NR_015907	51056 Hs. 570791NM_015907	ENSG000001LAP3	HEL-5-10ε leucine protein-coding
chr7-6433 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr7	64333629	6435432	+ 0 NA	intron (Nintron (N_98988317))	NR_98993137	221955 Hs. 487495NM_139179	ENSG000001DAGLB	DAGLBETA diacylglycerol protein-coding
chr7-9808 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr7	98988317	98993137	+ 0 NA	intron (Nintron (N_22438))	NR_110102	1.02E+08 Hs. 636663NR_110102	LOC101927	uncharacterized ncRNA
chr7-1008 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr7	1.01E+08	1.01E+08	+ 0 NA	intron (NAluV SINE	-5266 NM_001363	56996 Hs. 521087NM_020245	ENSG000001SLC12A9	CCG6 CIP1 solute carrier protein-coding
chr7-1395 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr7	1.4E+08	1.4E+08	+ 0 NA	intron (NLTR65 LTF	51014 NM_001088	154790 Hs. 57806 NM_001088	ENSG000001CLEC2L	C-type lectin protein-coding
chr8-1411 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr8	1.41E+08	1.41E+08	+ 0 NA	3' UTR (N3' UTR (N_13892))	NR_148197	22898 Hs. 18166 NM_014957	ENSG000001DENND3	DENN domain protein-coding
chr9-1133 8.929794	0.047199	0.777962	0.06067	0.951622	0.981636	chr9	1.13E+08	1.13E+08	+ 0 NA	intron (Nintron (N_41928))	NR_001198	22887 Hs. 26023 NM_014947	ENSG000001FOXJ3	forkhead protein-coding
chr1-4225 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr1	42292770	42293285	+ 0 NA	intron (NAluJb SIN	7264 NM_024102	79084 Hs. 204777NM_024102	ENSG000001WDR77	HKMT1069 WD repeat protein-coding
chr1-1114 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr1	1.11E+08	1.11E+08	+ 0 NA	3' UTR (N3' UTR (N_59792135))	NR_59793608	59792135	ENSG000001MIR3608	LINC00946 myoregulin protein-coding
chr16-587 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr16	48299436	48300052	+ 0 NA	exon (NM_exon (NM_62835504))	NR_62836612	23301 Hs. 271667NM_015252	ENSG000001EHPB1	MRP2 MRPE1 bindin protein-coding
chr2-6283 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr2	62835504	62836612	+ 0 NA	intron (NLIP2 LIN	129161 NM_001354	23301 Hs. 271667NM_015252	ENSG000001EHPB1	HPC12 NACH domain protein-coding
chr2-1341 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr2	1.34E+08	1.34E+08	+ 0 NA	intron (NLTR12C LI	3849 NR_037455	1.01E+08 NR_037455	ENSG000001MIR3679	mir-3679 microRNA ncRNA
chr5-1751 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr5	1.76E+08	1.76E+08	+ 0 NA	intron (Nintron (N_31540))	NR_022754	94081 Hs. 369444NM_022754	ENSG000001SFXN1	SLC56A1 sideroflexin protein-coding
chr7-1507 7.681484	-0.05096	0.840244	-0.06064	0.951642	0.981636	chr7	1.51E+08	1.51E+08	+ 0 NA	Intergenic AluSc SIN	29682 NM_001101	28959 Hs. 647099NM_014020	ENSG000001TMEM176B	LRS MS4E2 transmembrane protein-coding
chr15-700 6.972565	0.053127	0.877117	0.06057	0.951702	0.981636	chr15	70051127	70053012	+ 0 NA	intron (NMIRb SINE	27399 NR_030714	693214 NR_030714	ENSG000001MIR629	MIRN629 hmicroRNA ncRNA
chr17-596 6.972565	0.053127	0.877117	0.06057	0.951702	0.981636	chr17	59599006	59600164	+ 0 NA	intron (Nintron (N_20104))	NR_001288	1213 Hs. 491351NM_004855	ENSG000001CLTC	CHC CHC1 clathrin protein-coding
chr19-405 6.494359	0.059596	0.984832	0.060514	0.951747	0.981636	chr19</								



chr1-3232	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr1	32324139	32328856	+	0	NA	intron (NMER112 DN	9736	NM_023000	65108	Hs.75061	NM_023000	ENSG000003MARCKSL1	F52 MACM	MARCKS	liprotein-coding	
chr1-4367	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr1	43679493	43680817	+	0	NA	intron (Nintron (N	27186	NR_033827	1E+08	Hs.65556	NR_033827	KDMA4-AS1-		KDMA4	antncRNA	
chr1-4671	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr1	46714762	46716712	+	0	NA	intron (Nintron (N	3377	NM_014774	9813	Hs.70768	ENM_014774	ENSG000003EFCAB14	KIAA0494	EF-hand	cprotein-coding	
chr1-6665	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr1	66654132	66657121	+	0	NA	intron (Nintron (N	27186	NR_036066	1E+08	NR_036066	ENSG000003MIR3117	mir-3117	microRNA	ncRNA		
chr1-8455	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr1	84509201	84510036	+	0	NA	intron (Nintron (N	17706	NM_007266	2787	Hs.64542	NR_005274	ENSG000003CNG5		G	protein-coding	
chr1-1087	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (Nintron (N	17706	NM_007266	6814	Hs.53043	ENM_007266	ENSG000003STXPB3	MUNC18-3	syntaxin	protein-coding	
chr10-152	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr10	45886618	45888237	+	0	NA	intron (Nintron (N	33550	NM_001291	119016	Hs.31443	NR_13344	ENSG000003AGAP4	AGAP-4 AC	ArFGAP	wiprotein-coding	
chr10-126	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr10	1.21E+08	1.21E+08	+	0	NA	3' UTR (N3' UTR (N	57839	NM_018117	55717	Hs.14444	NR_018117	ENSG000003WDR11	BRWD2 DRWD	repeatprotein-coding		
chr10-132	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr10	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	9117	NM_001012	503542	Hs.64968	NM_001012	ENSG000003SPRN	SHAD00 SF	shadow of	protein-coding	
chr12-49	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr12	49643828	49644338	+	0	NA	3' UTR (N3' UTR (N	13539	NM_001362	25766	Hs.70682	NM_012272	ENSG000003PRPF40B	HYPX	pre-mRNA	protein-coding	
chr13-111	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr13	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	41746	NM_001352	79587	Hs.50872	NM_002453	ENSG000003CARS2	COCPD27 C	cysteiny	protein-coding	
chr15-64	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr15	64678368	64679143	+	0	NA	intron (Nintron (N	24526	NM_001301	4947	Hs.74492	NR_002537	ENSG000003OAZ2	AZ2	ornithine	protein-coding	
chr15-94	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr15	94457656	94458806	+	0	NA	exon (NM exon (NM	102301	NM_001155	55784	Hs.33368	NM_01834	ENSG000003MCTP2		luciferase	protein-coding	
chr17-507	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr17	50737503	50738304	+	0	NA	intron (NMER105 DN	18300	NM_001330	51747	Hs.13029	NR_006107	ENSG000003LUC7L3	CRA CREAF	LUC7 like	protein-coding	
chr19-373	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr19	37355298	37356852	+	0	NA	intron (Nintron (N	15024	NM_032452	84503	Hs.59094	NR_032452	ENSG000003ZNF527		zinc fing	protein-coding	
chr2-1098	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr2	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	40813	NM_005054	84220	Hs.46963	NR_005054	ENSG000003RGPD5	BS-63 BS	RANBP2	lprotein-coding	
chr2-1127	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	intron (Nintron (N	26783	NM_001137	84172	Hs.74512	NR_019014	ENSG000003POLR1B	RPA135 RF	RNA poly	protein-coding	
chr2-237	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr2	1.28E+08	1.28E+08	+	0	NA	3' UTR (N3' UTR (N	51232	NM_004807	9394	Hs.51284	NR_004807	ENSG000003HSG6ST1	HH15 HSG	heparan s	protein-coding	
chr2-186	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr2	1.87E+08	1.87E+08	+	0	NA	exon (NM exon (NM	17174	NM_177454	165215	Hs.28872	NM_177454	ENSG000003FAM171B	KIAA1946	family wiprotein-coding		
chr2-218	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (Nintron (N	14126	NM_001366	7701	Hs.65796	NR_001105	ENSG000003ZNF142	HA4654 NE	zinc fing	protein-coding	
chr2-237	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr2	2.37E+08	2.37E+08	+	0	NA	intron (NMIR SINE	14708	NM_005716	1293	Hs.23324	NR_00436	ENSG000003COL6A3	BTHLM1 Dy	collagen	protein-coding	
chr20-63	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr20	63942375	63944593	+	0	NA	promoter-promoter-	758	NR_030377	693232	NR_030377	ENSG000003MIR647	MIRN647 mi	microRNA	ncRNA		
chr21-42	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr21	42006969	42008240	+	0	NA	intron (N2c LINE	1590	NR_119384	150142	Hs.14383	NR_19807	ENSG000003ZNF295-AS	C21orf12 ZNF	295	arncRNA	
chr3-710	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr3	71042380	71044795	+	0	NA	intron (Nintron (N	20337	NM_001346	27086	Hs.59368	NM_032682	ENSG000003POXP1	I2CC4 HSF	forkhead	protein-coding	
chr3-122	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	exon (NM exon (NM	19941	NM_017554	54625	Hs.51820	NR_017554	ENSG000003PARP14	ARTD8 BAL	poly (ADP-	protein-coding	
chr3-124	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr3	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	33534	NR_036088	1E+08	NR_036088	ENSG000003MIR544B		microRNA	ncRNA		
chr3-147	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr3	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	26126	NM_002628	5217	Hs.91747	NM_002628	ENSG000003PFN2	D3S1319 P	profilin	protein-coding	
chr4-186	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr4	1.87E+08	1.87E+08	+	0	NA	intron (Nintron (N	49144	NM_00524E	2195	Hs.48137	NR_00524E	ENSG000003FAT1	CDHF7 CDF	FAT atyp	protein-coding	
chr5-373	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr5	37316548	37317326	+	0	NA	intron (Nintron (N	54169	NM_15348E	9631	Hs.54769	NR_00429E	ENSG000003CNP155	ATFB15 N1	nucleoporin	protein-coding	
chr5-658	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr5	65882242	65887756	+	0	NA	intron (Nintron (N	21703	NM_015342	23398	Hs.12143	NR_015342	ENSG000003PPWD1		peptidyl	protein-coding	
chr5-129	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (N2b LINE	97131	NM_001257	1E+08	Hs.58253	NR_001257	ENSG000003CMINAR2	KIAA1024 M	membrane	protein-coding	
chr5-129	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	67360	NM_001257	1E+08	Hs.58253	NR_001257	ENSG000003CMINAR2	KIAA1024 M	membrane	protein-coding	
chr5-140	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr5	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N	42051	NM_017978	54882	Hs.59408	NR_017978	ENSG000003ANKHD1	MASK MSK	ankyrin	lprotein-coding	
chr5-150	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr5	1.51E+08	1.51E+08	+	0	NA	intron (NMIR SINE	14118	NM_00154E	3340	Hs.22205	NR_00154E	ENSG000003NDST1	HSST MRT	4N-deacety	protein-coding	
chr6-107	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr6	10702123	10706239	+	0	NA	intron (Nintron (N	9209	NM_01790E	55003	Hs.31023	NR_01790E	ENSG000003PAK11P1	MAK11 PTF	PAK1 inte	protein-coding	
chr6-332	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr6	33266573	33268042	+	0	NA	exon (NM exon (NM	4569	NM_02255E	6293	Hs.48035	NR_02255E	ENSG000003VPS52	ARE1 SAC2	VPS52	su	protein-coding
chr7-149	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr7	1.49E+08	1.49E+08	+	0	NA	non-codirnon-codir	16065	NR_130107	1.03E+08	Hs.62198	NR_130107	ENSG000003GHET1		lncRNA-GF	gastric	ncRNA
chr7-157	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr7	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	51170	NM_014671	9690	Hs.11835	NR_014671	ENSG000003UBE3C	HECTH2	ubiquitin	protein-coding	
chr9-763	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr9	76387597	76388622	+	0	NA	intron (Nintron (N	6317	NR_01833E	55312	Hs.37558	NM_01833E	ENSG000003RFK	RIFK	riboflav	protein-coding	
chr9-981	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr9	98106489	98107990	+	0	NA	intron (Nintron (N	11983	NM_01478E	9830	Hs.57563	NR_01478E	ENSG000003TRIM14		tripartit	protein-coding	
chr9-114	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr9	1.14E+08	1.14E+08	+	0	NA	intron (NMER102c I	48711	NM_00163E	259	Hs.43691	NR_00163E	ENSG000003AMPB	A1M EDC1	alpha-1-n	protein-coding	
chr9-137	7.186745	-0.05176	0.858814	-0.06026	0.951945	0.981636	chr9	1.37E+08	1.37E+08	+	0	NA	intron (Nintron (N	10225	NM_01772E	54863	Hs.49554	NR_01772E	ENSG000003TOR4A	C9orf167	torsin	lprotein-coding	
chr15-44	8.119366	-0.04899	0.815142	-0.0601	0.952077	0.981636	chr15	44603351	44606071	+	0	NA	intron (Nintron (N	58951	NM_00116E	80208	Hs.65627	NR_025137	ENSG000003SPG11	ALS5 CMT	2SPG11	ves	protein-coding
chr15-65	8.119366	-0.04899	0.815142	-0.0601	0.952077	0.981636	chr15	65499902	65500640	+	0	NA	intron (Nintron (N	17003	NM_19796E	54878	Hs.45860	NR_01774E	ENSG000003DPP8	DP8 DPRP-	dipeptid	protein-coding	
chr15-80	8.119366	-0.04899	0.815142	-0.0601	0.952077	0.981636	chr15	80515600	80516559	+	0	NA	intron (Nintron (N	46865	NR_12036E	1.02E+08	Hs.56942	NR_12036E	ENSG000003LOC10192E		uncharact	ncRNA	
chr18-51	8.119366	-0.04899	0.815142	-0.0601	0.952077	0.981636	chr18	51176386	51177883	+	0	NA	exon (NM exon (NM	21097	NM_01662E	51320	Hs.46514	NR_01662E	ENSG000003MEX3C	BM-013 MF	mex-3	RN	protein-coding
chr20-34	8.119366	-0.04899	0.815142	-0.0601	0.952077	0.981636	chr20	34456786	34458412	+	0	NA	intron (Nintron (N	8726	NR_030374	693229	NR_030374	ENSG000003MIR644A	MIR644 MI	microRNA	ncRNA		
chr20-47	8.119366	-0.04899	0.815142	-0.0601	0.952077	0.981636	chr20	47224558	47224752	+	0	NA	intron (Nintron (N	5769	NR_03741E	5740	Hs.30208	NR_000961	ENSG000003PTG15	CYP8 CYP	prostagl	protein-coding	
chr20-49	8.119366	-0.04899	0.815142	-0.0601	0.952																		

chr1-1554	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr1	1.55E+08	1.55E+08	+	0	NA	intron (AluY SINE	16411	NR_03418C	645682	Hs.632482	NR_03418C	ENSG000005P05F1P4	OC3 OC4	POU class pseudo
chr11-775	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr11	77937402	77938012	+	0	NA	intron (AluJo SIN	56961	NR_033547	92105	Hs.533722	NR_033547	ENSG00000INTS4	INT4	MSTC integratc protein-coding
chr16-744	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr16	74475041	74475973	+	0	NA	intron (intron (	-54037	NR_001011	497190	Hs.45467	CNM_001011	ENSG00000CLEC18B	MRLC2	C-type Ie protein-coding
chr17-795	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr17	7934438	7935044	+	0	NA	intron (intron (	2535	NR_001352	116840	Hs.348012	NR_001352	ENSG00000CNTROB	LIP8 PP12	centrobrin protein-coding
chr17-667	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr17	66736616	66737537	+	0	NA	intron (AluY SINE	-49996	NR_030364	693219	NR_030364	ENSG00000MIR634	MIRN634	lmiicroRNA ncRNA	
chr2-1995	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr2	1.99E+08	1.99E+08	+	0	NA	intron (intron (	77100	NR_134967	23314	Hs.516617	NR_01526E	ENSG00000SATB2	GLSS	SATB home protein-coding
chr20-376	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr20	37237605	37238362	+	0	NA	intron (AluJb SIN	18925	NR_021081	2691	Hs.37023	NR_021081	ENSG00000GHRH	GHRF GRF	growth hc protein-coding
chr4-1406	5.973381	0.05614	0.940251	0.059708	0.952388	0.981636	chr4	1.41E+08	1.41E+08	+	0	NA	intron (intron (	-17762	NR_07721E	644962	Hs.67650C	NR_07721E	TNRC18P1	-	trinuclec pseudo
chr2-1444	9.100985	-0.04674	0.783079	-0.05969	0.9524	0.981636	chr2	1.44E+08	1.44E+08	+	0	NA	intron (intron (	-28614	NR_04024E	1E+08	Hs.56078E	NR_04024E	ENSG00000ZEB2-AS1	ZEB2-AS1 ZEB2	antincRNA
chr9-5742	9.100985	-0.04674	0.783079	-0.05969	0.9524	0.981636	chr9	5742966	5744129	+	0	NA	intron (intron (	89570	NR_02489E	79956	Hs.59107E	NR_02489E	ENSG00000ERMP1	FXNA KIAF	endoplasm protein-coding
chr19-144	5.445361	0.059489	0.999196	0.059536	0.952525	0.981636	chr19	14466199	14466165	+	0	NA	intron (AluJb SIN	9022	NR_00095E	5731	Hs.15936C	NR_00095E	ENSG00000PTGER1	EP1	prostagl protein-coding
chr20-114	5.445361	0.059489	0.999196	0.059536	0.952525	0.981636	chr20	1140753	1141671	+	0	NA	intron (LIMB8 LIN	22610	NR_00132E	9491	Hs.471917	NR_006814	ENSG00000PSPMF1	PI31	proteasom protein-coding
chr1-1922	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	19222572	19231993	+	0	NA	intron (MIRb SINE	16896	NR_13511E	1.02E+08	Hs.660534	NR_135114	ENSG00000EMC1-AS1	-	EMC1 antincRNA
chr1-328C	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	32802241	32804937	+	0	NA	intron (Tigger E	-13853	NR_00125E	64766	Hs.44088C	NR_02275E	ENSG00000S100PBP	S100PBP	S100P protein-coding
chr1-3591	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	35918917	35920529	+	0	NA	3' UTR (3' UTR (	-11382	NR_177422	192669	Hs.65765E	NR_02485E	ENSG00000AGO3	EIF2C3	argonautc protein-coding
chr1-518C	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	51802175	51804405	+	0	NA	intron (AluS2 SIN	33112	NR_03158C	1E+08	NR_03158C	ENSG00000MIR761	hsa-mir-7	microRNA ncRNA	
chr1-681E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	68158111	68159266	+	0	NA	intron (MER30 DNA	24922	NR_03166C	1E+08	NR_03166C	ENSG00000MIR1262	MIRN1262	microRNA ncRNA	
chr1-777E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	77783546	77788890	+	0	NA	intron (THE1B-int	6413	NR_00136E	374986	Hs.43775E	NR_19854E	ENSG00000MIG1A	FAM73	mitoguarc protein-coding
chr1-1002	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	1E+08	1E+08	+	0	NA	intron (LIP47 LIN	-27627	NR_00125E	127495	Hs.44277	NR_14462C	ENSG00000LRR39	-	leucine r protein-coding
chr1-162E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	1.63E+08	1.63E+08	+	0	NA	intron (intron (	31227	NR_00132A	6675	Hs.49285E	NR_00311E	ENSG00000UAP1	AGX AGX1	UDP-N-acc protein-coding
chr1-226E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	2.26E+08	2.26E+08	+	0	NA	intron (intron (	40340	NR_00161E	142	Hs.17776C	NR_00161E	ENSG00000PARP1	ADPRT ADF	poly (ADP- protein-coding
chr1-236E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	TTS (NM_C TTS (NM_C	-24304	NR_03404C	1E+08	Hs.67737E	NR_03404C	ENSG00000LGALS8-AS-	-	LGALS8 arncRNA
chr1-240E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (LIMEc LIN	23296	NR_02246E	64388	Hs.98206	NR_02246E	ENSG00000GREM2	CKTSF1B2	gremlin 2 protein-coding
chr10-10E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	intron (intron (	13429	NR_01591E	51063	Hs.24154E	NR_01591E	ENSG00000CALHM2	FAM26B	calcium f protein-coding
chr11-47E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr11	47573391	47575433	+	0	NA	TTS (NM_C TTS (NM_C	4359	NR_00131E	55709	Hs.71848E	NR_01650E	ENSG00000KBTBD4	BKLDHD4	HS kelch r protein-coding
chr11-737	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr11	73704206	73705229	+	0	NA	intron (AluY SINE	55376	NR_00124E	5870	Hs.50322E	NR_00286E	ENSG00000RAB6A	RAB6	RAB6, m protein-coding
chr11-11E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr11	1.19E+08	1.19E+08	+	0	NA	intron (intron (	-3579	NR_00304C	649946	Hs.64721E	NR_003040	RPL23AP64	RPL23A_2E	ribosomal pseudo
chr12-487	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr12	48701798	48706258	+	0	NA	intron (intron (	12679	NR_00124C	904	Hs.92308	NR_00124C	ENSG00000CCNT1	CCNT CYC	cyclin T1 protein-coding
chr12-95E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr12	95252548	95253789	+	0	NA	intron (intron (	35361	NR_01759E	55591	Hs.24135	NR_01759E	ENSG00000VEZT	VEZATIN	vezatin, protein-coding
chr12-111	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr12	1.12E+08	1.12E+08	+	0	NA	intron (intron (	-8756	NR_03663E	8759	Hs.66170E	NR_03663E	ADAM1A	ADAM1 ADAM	metc pseudo
chr13-11C	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr13	1.1E+08	1.1E+08	+	0	NA	intron (AluY SINE	-9034	NR_001267	1E+08	Hs.64003E	NR_001267044	COL4A2-AS-	-	COL4A2 ar protein-coding
chr14-55E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr14	55677926	55680650	+	0	NA	intron (intron (	-87002	NR_004844	645683	Hs.663461	NR_004844	ENSG00000RPL13AP3	RPL13A	11 ribosomal pseudo
chr14-601	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr14	60144038	60146250	+	0	NA	3' UTR (3' UTR (	-27054	NR_01602E	51635	Hs.59179	NR_01602E	ENSG00000DHR57	CI-8E	5E dehydrog protein-coding
chr14-81E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr14	81502528	81504877	+	0	NA	intron (intron (	30151	NR_00506E	6400	Hs.18130C	NR_00506E	ENSG00000SEL1L	Hrd3 PRO1	SEL1L adc protein-coding
chr15-407	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr15	40733905	40736631	+	0	NA	TTS (NM_C TTS (NM_C	19986	NR_01814E	55177	Hs.511067	NR_01814E	ENSG00000RMDN3	FAM82A2	F regulator protein-coding
chr15-75E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr15	75388100	75390180	+	0	NA	intron (intron (	-20513	NR_00125E	4123	Hs.26232	NR_00671E	ENSG00000MAN2C1	MAN6A8 MA	mannosidc protein-coding
chr15-784	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr15	78476697	78479144	+	0	NA	intron (AluJr SIN	-29644	NR_00108E	123688	Hs.30796E	NR_00101E	ENSG00000CHYK	AGPHD1	hydroxyl protein-coding
chr16-48E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr16	48822385	48833266	+	0	NA	intron (intron (	16508	NR_03256E	84656	Hs.38725E	NR_03256E	ENSG00000GLYR1	BMO45	HEF glyoxylat protein-coding
chr16-18E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr16	18879093	18872407	+	0	NA	intron (intron (	54709	NR_01509E	23049	Hs.46017E	NR_01509E	ENSG00000SMG1	61E3.4 ATSMG1	non protein-coding
chr16-71E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr16	71285037	71286062	+	0	NA	exon (NM_exon (NM	3853	NR_01834E	55783	Hs.72782	NR_01834E	ENSG00000CMTR2	AFT FTS	J1 cap methy protein-coding
chr17-411	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr17	4115001	4117472	+	0	NA	intron (AluS2 SI	26794	NR_01511E	23140	Hs.277624	NR_01511E	ENSG00000ZZEF1	ZZZ4	zinc fing protein-coding
chr17-46E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr17	4689131	4690988	+	0	NA	intron (LIPB1 LIN	14078	NR_01438E	27043	Hs.74489E	NR_01438E	ENSG00000PEL1P	MNAR P16C	proline, protein-coding
chr17-17E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr17	17254849	17261777	+	0	NA	intron (AluSx SIN	-21145	NR_14460E	201163	Hs.31652	NR_14460E	ENSG00000FLCN	BHD DENNE	folliculiprotein-coding
chr17-46E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr17	46336863	46337226	+	0	NA	3' UTR (3' UTR (	24743	NR_00136E	1.01E+08	Hs.55925E	NR_00103E	ENSG00000ARL17B	ARL17 ARL	ADP ribos protein-coding
chr17-50E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr17	50365687	50370727	+	0	NA	exon (NM_exon (NM	4977	NR_016504	51264	Hs.7736	NR_016504	ENSG00000MRPL27	L27mt	mitochon protein-coding
chr17-64E	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr17	64641971	64647551	+	0	NA	intron (AluSx SIN	17546	NR_02273E	64750	Hs.515011	NR_02273E	ENSG00000SMURF2	SMAD	spec protein-coding
chr19-50C	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr19	50036869	50042178	+	0	NA	intron (MER20 DNA	-11066	NR_027257	400710	Hs.62896E	NR_027257	ENSG00000LOC40071C	-	uncharactcRNA
chr19-521	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr19	52166030	52168329	+	0	NA	intron (intron (	4442	NR_00110E	162962	Hs.631584	NR_00110E	ENSG00000ZNF836	-	zinc fing protein-coding
chr2-9627	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr2	96274321	96276061	+	0	NA	intron (intron (	8966	NR_004804	9391	Hs.12109	NR_004804	ENSG00000CIA01	CIA1 WDR	cytosolic protein-coding
chr2-2031	7.93061	0.04878	0.819554	0.05952	0.952538	0.981636	chr2														



chr3-1968	9.936836	0.044429	0.752614	0.059033	0.952926	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (NAIuY SINE	-52790 NM_001308	205564 Hs. 240777CNM_152699	ENSG000003ENP5	-	SUMO specprotein-coding
chr18-795	7.40259	0.050621	0.857692	0.05902	0.952936	0.981636	chr18	79975848	79976566	+	0	NA	intron (NFRAM SINE	11564 NM_001136	440498 Hs. 191582NM_001136	ENSG000003HSP1L1	-	heat shocprotein-coding
chr3-179	7.40259	0.050621	0.857692	0.05902	0.952936	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	3' UTR (N3' UTR (N	-10754 NM_03354C	55669 Hs. 478388NM_017927	ENSG000003CFN1	hfz01 hfz	mitofusir protein-coding
chr11-66	10.41586	0.043162	0.731835	0.058977	0.95297	0.981636	chr11	66340153	66341014	+	0	NA	intron (Nintron (N	-3807 NM_001363	9610 Hs. 1030 NM_004292	ENSG000003RIN1	-	Ras and Fprotein-coding
chr11-70	10.41586	0.043162	0.731835	0.058977	0.95297	0.981636	chr11	70378577	70379090	+	0	NA	TTS (NM_TTS (NM_L	-19671 NM_13856E	2017 Hs. 596164NM_005231	ENSG000003CTN	EMS1	cortactir protein-coding
chr18-458	10.41586	0.043162	0.731835	0.058977	0.95297	0.981636	chr18	45858262	45860704	+	0	NA	intron (Nintron (N	33808 NM_21360E	284266 Hs. 287692NM_21360E	ENSG000003IGLEC15	CD33L3 Hs	sialic acprotein-coding
chr1-2305	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr1	23056928	23056946	+	0	NA	intron (NAIuJb SIN	13891 NR_036057	1E+08 NR_036057	ENSG000003MIR3115	mir-3115	microRNA ncRNA
chr1-9232	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr1	92323551	92323734	+	0	NA	intron (Nintron (N	26389 NM_02481E	79871 Hs. 444422NM_02481E	ENSG000003RPAP2	Clorf82 F RNA	polynprotein-coding
chr1-1204	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	-10503 NR_00324E	767846 Hs. 657188NR_00324E	ENSG000003PFNIP2	Clorf152 profilin	pseudo
chr10-21	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr10	21537533	21545288	+	0	NA	intron (NAIuSx SIN	7238 NM_00119E	8028 Hs. 30385 NM_004641	ENSG000003MLL10	AF10	MLLT10 hiprotein-coding
chr10-734	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr10	73436779	73438170	+	0	NA	3' UTR (N3' UTR (N	-3913 NM_00102E	118490 Hs. 631822NM_00102E	ENSG000003MSS51	ZMYND17	MSS51 mitprotein-coding
chr11-167	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr11	16744532	16756339	+	0	NA	intron (NCharlie3	11788 NM_014267	10944 Hs. 368222NM_014267	ENSG000003C11orf58	IMAGE145C	chromosom protein-coding
chr11-337	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr11	33712328	33722606	+	0	NA	exon (NM exon (NM	5260 NM_001127	966 Hs. 278572NM_000611	ENSG000003CD59	16.3A5 FD	C59 moleprotein-coding
chr11-118	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr11	1.08E+08	1.19E+08	+	0	NA	TTS (NR_TTS (NR_C	1532 NR_00304C	649946 Hs. 647212NR_00304C	RPL23A P6	25ribosomalspseudo	
chr12-107	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr12	1.08E+08	1.08E+08	+	0	NA	non-codiron-codir	3038 NR_120474	1.02E+08 Hs. 667022NR_120474	ENSG000003LOC10192E	-	uncharactncRNA
chr12-12	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr12	1.23E+08	1.23E+08	+	0	NA	intron (Nintron (N	11225 NR_103517	10198 Hs. 577404NM_02278E	ENSG000003MPHOSPH9	MPP-9 MPM	phase fprotein-coding
chr12-13	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (NAIuSx4 SI	1418 NR_00297E	677829 Hs. 742402NR_00297E	ENSG000003NOR49	ACA49	ACA49 small ncsnoRNA
chr12-132	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	3' UTR (N3' UTR (N	16011 NM_00117C	192111 Hs. 102558NM_13857E	ENSG000003PGAM4	BXLBV68	PGAM facprotein-coding
chr13-306	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr13	30658774	30659160	+	0	NA	exon (NM exon (NM	24752 NM_001321	10208 Hs. 533831NM_00580C	ENSG000003USPL1	C13orf22 ubiquitin	protein-coding
chr13-10	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr13	51373465	51376970	+	0	NA	intron (NAIuS6 SI	-26578 NR_04987E	1.01E+08 NR_04987E	ENSG000003MIR5693	-	microRNA ncRNA
chr13-51	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr13	1E+08	1E+08	+	0	NA	intron (NLIJM4 LINE	32906 NM_00135E	5095 Hs. 80741 NM_00028E	ENSG000003PCCA	-	propionyl protein-coding
chr14-58	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr14	58207279	58210973	+	0	NA	intron (Nintron (N	8977 NM_018477	55860 Hs. 509451NM_018477	ENSG000003ACTR10	ACTR11 Ar	actin relprotein-coding
chr14-594	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr14	59487664	59491426	+	0	NA	intron (NMSTB-int	5028 NM_01647E	51528 Hs. 44685CNM_01647E	ENSG000003JKAMP	C14orf10C JNK1	MAPK fprotein-coding
chr14-65	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr14	65085786	65091979	+	0	NA	intron (Nintron (N	-1036 NR_045122	1.01E+08 Hs. 711267NR_045122	ENSG000003LOC10050E	-	uncharactncRNA
chr15-41	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr15	41048760	41050776	+	0	NA	intron (NAIuSx1 SI	66478 NR_10403E	54617 Hs. 292942NM_01755E	ENSG000003IN080	IN080A IN	IN080 conprotein-coding
chr15-48	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr15	48531888	48533373	+	0	NA	intron (Nintron (N	113158 NM_00013E	2200 Hs. 591133NM_00013E	ENSG000003FBN1	ACMDC EC	fibrillir protein-coding
chr15-731	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr15	73165687	73167384	+	0	NA	intron (NLTFR39 LTF	114051 NM_00117E	4756 Hs. 38861E NM_00249E	ENSG000003NEO1	IGDC2C NC	neogenin protein-coding
chr15-774	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr15	77470873	77472699	+	0	NA	exon (NM exon (NM	50898 NM_001304	10363 Hs. 69594 NM_01820C	ENSG000003HMG20A	HMGX1 HMC	high mobiprotein-coding
chr16-14	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr16	14644394	14650178	+	0	NA	intron (NAIuS6 SI	14605 NM_016561	51283 Hs. 435555NM_016561	ENSG000003BFAR	BAR RN	F47bifunctin protein-coding
chr16-28	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr16	28110378	28111898	+	0	NA	intron (Nintron (N	-47424 NM_00110E	146395 Hs. 91910 NM_14467E	ENSG000003GSL1	PRO19651 GSG1	likeprotein-coding
chr16-58	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr16	58586599	58589436	+	0	NA	intron (Nintron (N	-28086 NR_00298C	677830 Hs. 67751E NR_00298C	ENSG000003SNORA50A	ACA50 SNC	small ncsnoRNA
chr16-62	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr16	69299482	69302059	+	0	NA	intron (Nintron (N	-10580 NM_01324E	27183 Hs. 12842CNM_01324E	ENSG000003VPS4A	ELP2 SKD1	vacular protein-coding
chr17-76	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr17	761985	763464	+	0	NA	intron (Nintron (N	10391 NR_02412C	1E+08 Hs. 662289NR_02412C	ENSG000003DBIL5P	SKDP2	diazepam pseudo
chr17-15	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr17	1537881	1541989	+	0	NA	intron (NAIuS7 SIN	22857 NM_006224	5306 Hs. 42981E NM_006224	ENSG000003PITPNA	HEL-S-36 phosphat	protein-coding
chr17-35	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr17	35594069	35602838	+	0	NA	intron (Nintron (N	11131 NM_00103C	163 Hs. 51481E NM_00128E	ENSG000003AP2B1	ADTB2 AP	adaptor rprotein-coding
chr17-35	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr17	35627096	35629808	+	0	NA	intron (NAIuJb SIN	41130 NM_00103C	163 Hs. 51481E NM_00128E	ENSG000003AP2B1	ADTB2 AP	adaptor rprotein-coding
chr17-637	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr17	63757284	63761436	+	0	NA	intron (NAIuSx1 SI	14237 NM_02019E	57003 Hs. 202011NM_02019E	ENSG000003CCDC47	GK001 MS1	coiled-cprotein-coding
chr17-64	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr17	64521419	64527476	+	0	NA	intron (NAIuSx3 SI	17470 NR_133644	90799 Hs. 56971E NM_13836E	ENSG000003CEP95	CCDC45	centrosom protein-coding
chr19-88	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr19	889434	890442	+	0	NA	intron (Nintron (N	3249 NM_005481	10025 Hs. 365207NM_005481	ENSG000003MD16	DRIP92 TI	mediator protein-coding
chr19-92	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr19	928719	932695	+	0	NA	intron (NAIuY SINE	4672 NM_005224	1820 Hs. 50129E NM_005224	ENSG000003ARID3A	BRIGHT DFAT	-rich iprotein-coding
chr19-15	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr19	15360375	15362490	+	0	NA	intron (NAIuY SINE	18355 NM_00585E	10270 Hs. 51449E NM_00585E	ENSG000003AKAP8	AKAP 95 A	-kinase protein-coding
chr19-47	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr19	47149947	47152251	+	0	NA	intron (Nintron (N	20264 NM_00114E	10055 Hs. 59500C NM_00550C	ENSG000003SAE1	AOS1 HSP	SUMO1 actprotein-coding
chr19-49	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr19	49087287	49089001	+	0	NA	intron (NAIuSx SIN	2693 NM_001301	6625 Hs. 467097NM_00308E	ENSG000003SNRNP70	RNPUIZ RF	small nucprotein-coding
chr2-392	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	39271329	39274081	+	0	NA	intron (Nintron (N	-28722 NR_144521	344387 Hs. 403201NM_00100E	ENSG000003CDKL4	-	cyclin deprotein-coding
chr2-54	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	54651993	54655412	+	0	NA	exon (NM exon (NM	-17130 NM_00103E	400954 Hs. 656692NM_00103E	ENSG000003EML6	-	EMAP likeprotein-coding
chr2-61	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	61033906	61036080	+	0	NA	intron (NLIPA6 LIN	-16734 NM_00132E	150962 Hs. 36834E NM_14470E	ENSG000003PUS10	CCDC139 I	pseudouriprotein-coding
chr2-61	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	61513840	61522247	+	0	NA	intron (NAIuSx SIN	20313 NM_00340C	7514 Hs. 370777NM_00340C	ENSG000003XPO1	CRM-1 CRM	expotin protein-coding
chr2-96	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	96183655	96187206	+	0	NA	3' UTR (N3' UTR (N	-22986 NR_04632E	285033 Hs. 58648 NM_001037228	STARTD7-AS-	STARTD7	arncRNA
chr2-131	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	-35869 NR_16347E	1.08E+08 Hs. 591242NM_001365239	LOC10798E	-	uncharactncRNA
chr2-230	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	2.3E+08	2.3E+08	+	0	NA	intron (NMLT1D LTF	-44090 NM_00120E	6672 Hs. 36905E NM_00311E	ENSG000003SP100	lysp100b	SP100 nucprotein-coding
chr2-237	8.409632	0.046995	0.797416	0.058934	0.953005	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (Nintron (N	17919 NM_00035E	80210 Hs. 162411NM_02513E	ENSG000003ARMC9	ARM JBT5E	armadillcprotein-coding
chr2-231	8.409																	

chr12-108.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	3' UTR (N3' UTR (N	40253 NM_001161	54434 Hs.199762NM_018984	ENSG000003SSH1	SSH1L	slingshotprotein-coding
chr12-115.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr12	1.2E+08	1.2E+08	+	0 NA	intron (Nintron (N	11456 NM_006255	5564 Hs.741184NM_006255	ENSG000003PRKAB1	AMPK HAMF	protein-coding
chr14-951.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr14	95102539	95106166	+	0 NA	intron (Nintron (N	29151 NM_001195	23405 Hs.87889 NM_030621	ENSG000003DICER1	DCR1 Dicer	Dicer 1, protein-coding
chr15-28.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr15	28252876	28256126	+	0 NA	exon (NM exon (NM	67651 NM_004667	8924 Hs.43489NM_004667	ENSG000003HERC2	D15F37S1 HECT	and protein-coding
chr16-18.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	18840995	18842958	+	0 NA	intron (Nintron (N	-40427 NM_015161	23204 Hs.634882NM_015161	ENSG000003ARL6IP1	AIP1 ARL6	ADP ribos protein-coding
chr16-23.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	23687218	23690226	+	0 NA	exon (NM exon (NM	9833 NM_00503C	5347 Hs.59204NM_00503C	ENSG000003PLK1	PLK STPK1	polo like protein-coding
chr16-27.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	27356979	27357631	+	0 NA	intron (NAluJr SIN	43331 NM_001257	3566 Hs.513457NM_000418	ENSG000003ILAR	CD124 IL	interleukin protein-coding
chr16-28.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	28869444	28871436	+	0 NA	intron (Nintron (N	6447 NM_015503	25970 Hs.15744 NM_015503	ENSG000003SH2B1	PSM SH2B	adap protein-coding
chr16-31.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	31733508	31735088	+	0 NA	intron (NAluJr4 SI	21069 NM_00113C	12441 Hs.52882NM_001004	ENSG000003ZNF720		zinc fing protein-coding
chr16-84.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	84574015	84574410	+	0 NA	intron (NMIR3 SINE	43866 NM_021145	23406 Hs.289092NM_021145	ENSG000003COTL1	CLP	coactosin protein-coding
chr16-89.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr16	89272270	89275993	+	0 NA	intron (Nintron (N	-21997 NR_136335	1.05E+08 Hs.657381NR_136335	ENSG000003LOC105371		uncharactncRNA
chr17-40.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr17	40031234	40031926	+	0 NA	exon (NM exon (NM	-3935 NR_10236E	1.01E+08 NR_10236E	ENSG000003SNORD124		small nuc snoRNA
chr18-45.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr18	45874053	45879518	+	0 NA	intron (Nintron (N	51110 NM_213602	284266 Hs.287692NM_213602	ENSG000003SIGLEC15	CD33L3 Hs	sialic ac protein-coding
chr19-59.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr19	59979787	5941545	+	0 NA	intron (Nintron (N	26412 NM_00405E	828 Hs.584744NM_00405E	ENSG000003CAPS	CAP51	calcyp protein-coding
chr19-171.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr19	17174262	17179021	+	0 NA	intron (Nintron (N	-38716 NM_018467	55850 Hs.16187 NM_018467	ENSG000003USE1	D12 MDSO5	unconvent protein-coding
chr19-45.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr19	45353820	45357677	+	0 NA	intron (Nintron (N	14839 NM_00113C	2068 Hs.487294NM_00040C	ENSG000003ERC2C	COFS2 EMC	ERCC exciprotein-coding
chr2-950.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr2	9504045	9505095	+	0 NA	intron (NAluSx3 SI	29515 NM_00132C	285148 Hs.66722NM_00103E	ENSG000003IAH1		isoamyl ε protein-coding
chr2-854.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr2	48459798	48461749	+	0 NA	intron (Nintron (N	20004 NM_001193	129285 Hs.65461E	ENSG000003PP1R21	CCDC128	kyosmylin protein-coding
chr21-43.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr21	43752572	43757799	+	0 NA	intron (Nintron (N	13699 NM_001331	8566 Hs.284491NM_003681	ENSG000003PDXK	C21orf124	pyridoxal protein-coding
chr22-45.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr22	45195427	45200456	+	0 NA	exon (NM exon (NM	3078 NR_031651	1E+08 NR_031651	ENSG000003MIR1249	MIRN1249	microRNA ncRNA
chr22-46.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr22	46097502	46103936	+	0 NA	intron (Nintron (N	9675 NR_03741E	1.01E+08 NR_03741E	ENSG000003MIR3619		microRNA ncRNA
chr3-25.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr3	25610433	25613091	+	0 NA	intron (Nintron (N	52610 NM_00106E	7155 Hs.475733NM_00106E	ENSG000003TOP2B	TOP1IB tDNA	topo protein-coding
chr3-57.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr3	57588830	57590407	+	0 NA	intron (NAluSg SIN	7726 NM_00166C	378 Hs.652183NM_00166C	ENSG000003ARF4	ARF2	ADP ribos protein-coding
chr3-179.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr3	1.79E+08	1.79E+08	+	0 NA	intron (Nintron (N	18944 NM_03354C	55669 Hs.478383NM_017927	ENSG000003MPN1	hfz01 hfz	m1tofusir protein-coding
chr3-185.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr3	1.86E+08	1.86E+08	+	0 NA	intron (NAluSg SIN	41244 NM_021627	59343 Hs.401383NM_021627	ENSG000003SEN2P	AXAM2 SM1	SUMO spec protein-coding
chr4-19.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr4	1974677	1975657	+	0 NA	TTS (NR_CTTs (NR_C	531 NR_003004	677770 Hs.676951NR_003004	ENSG000003SCARNA22	ACA11	small ncRNA
chr4-26.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr4	26772218	26775164	+	0 NA	Intergeni (LIPA11 LI	86553 NR_13467E	1.05E+08 Hs.548853NR_13467E	ENSG000003STIM2-AS1	STIM2	antncRNA
chr4-71.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr4	71560002	71562274	+	0 NA	intron (Nintron (N	222085 NM_00375E	8671 Hs.5462 NM_00375E	ENSG000003SLC44A	HNBC1 KNE	solute c protein-coding
chr4-151.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr4	1.51E+08	1.51E+08	+	0 NA	exon (NM exon (NM	210 NM_00112E	152503 Hs.744982NM_00100E	ENSG000003SH3D19	EBP EVE1 SH3	doma protein-coding
chr6-17.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr6	17832135	17832504	+	0 NA	intron (Nintron (N	125276 NR_13461E	1.05E+08 Hs.718703NR_13461E	ENSG000003LOC105374		uncharactncRNA
chr7-13.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr7	1.39E+08	1.39E+08	+	0 NA	intron (NMLT1J LTF	21400 NM_02011E	56829 Hs.133512NM_02011E	ENSG000003ZC3HAV1	ARTD13 FL	zinc fing protein-coding
chr7-15.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr7	1.57E+08	1.57E+08	+	0 NA	intron (Nintron (N	45651 NM_05824A	10049 Hs.490745NM_005494	ENSG000003DNAJB6	DJ4 DnaJ DnaJ	heat protein-coding
chr8-14.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	exon (NM exon (NM	27452 NR_04071E	54108 Hs.279704NM_017444	ENSG000003CHRAC1	CHARC1 CF	chromatir protein-coding
chr9-12.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr9	1.22E+08	1.22E+08	+	0 NA	TTS (NM_CTTs (NM_C	16413 NM_01422E	4702 Hs.495035NM_01422E	ENSG000003NDUF48	CI-19KD CNADH	ubiq protein-coding
chr9-12.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr9	1.23E+08	1.23E+08	+	0 NA	intron (Nintron (N	18640 NR_030331	693185 NR_030331	ENSG000003MIR600	MIRN600	microRNA ncRNA
chr9-13.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr9	1.34E+08	1.34E+08	+	0 NA	intron (NAluSz SIN	8096 NM_052821	11091 Hs.397633NR_052821	ENSG000003WDR5	BIG-3 CFAD	repeat protein-coding
chr9-13.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr9	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	33286 NR_039691	1.01E+08 NR_039691	ENSG000003MIR3689C		microRNA ncRNA
chrX-73.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chrX	73999211	74003295	+	0 NA	intron (NLM3de LI	55444 NR_02458E	554203 Hs.64831E	ENSG000003JPX	DCBALD06 JPX	transncRNA
chr17-11.7.673626	-0.04911	0.834326	-0.05886	0.953064	0.981636	chr17	7190355	7191296	+	0 NA	intron (Nintron (N	-11261 NM_001197	432 Hs.12056 NM_001671	ENSG000003ASGR1	ASGRP1	Asialogly protein-coding
chr10-12.7.673626	-0.04962	0.843375	-0.05883	0.953087	0.981636	chr10	1.25E+08	1.25E+08	+	0 NA	intron (Nintron (N	25637 NM_01758C	54764 Hs.595155NM_01758C	ENSG000003ZRANB1	TRABID	zinc fing protein-coding
chr5-12.7.673626	-0.04962	0.843375	-0.05883	0.953087	0.981636	chr5	1.3E+08	1.3E+08	+	0 NA	intron (Nintron (N	-59834 NR_125744E	1.04E+08 Hs.628633NR_125744E	ENSG000003ADAMTS19-	ADAMTS19	ncRNA
chr8-14.7.673626	-0.04962	0.843375	-0.05883	0.953087	0.981636	chr8	1.41E+08	1.41E+08	+	0 NA	intron (NAluJb SIN	-13587 NR_02989E	442893 NR_02989E	ENSG000003MIR151A	MIR151 Mi	microRNA ncRNA
chr1-36.2.4.974197	0.060427	1.028977	0.058725	0.953171	0.981636	chr1	36226687	36227556	+	0 NA	intron (N2a LINE	2678 NM_001321	9967 Hs.744057NM_00511E	ENSG000003THR4P3	BCLAF2 TF	thyroid l protein-coding
chr10-11.4.974197	0.060427	1.028977	0.058725	0.953171	0.981636	chr10	11937054	11937549	+	0 NA	intron (N2c LINE	-42591 NR_03822E	219731 Hs.576787NR_03822E	ENSG000003PROSER2-1	PROSER2	ncRNA
chr15-55.10.84588	0.041846	0.712669	0.058718	0.953177	0.981636	chr15	55847541	55848624	+	0 NA	intron (NTrigger19E	69049 NM_001284	4734 Hs.1565 NM_006154	ENSG000003NEDD4	NEDD4-1 FN	NEDD4 E3 protein-coding
chr1-10.11.3739	0.040948	0.698494	0.058623	0.953252	0.981636	chr1	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	17168 NM_00651E	6301 Hs.53117E	ENSG000003SARS	NEDMAS SE	eryl-tR3 protein-coding
chr5-14.11.3739	0.040948	0.698494	0.058623	0.953252	0.981636	chr5	1.41E+08	1.41E+08	+	0 NA	intron (Nintron (N	4244 NM_00373E	8637 Hs.594084NM_00373E	ENSG000003EIF4EBP3	4E-BP3 4E	eukaryotir protein-coding
chr10-61.7.243601	-0.05317	0.908234	-0.05854	0.95332	0.981636	chr10	61956183	61956529	+	0 NA	intron (NMERIB DNA	54657 NM_03219E	84159 Hs.535297NM_03219E	ENSG000003CARID5B1	DESRT MR	FAT-rich iprotein-coding
chr12-12.8.45863	0.047221	0.808945	0.058373	0.953451	0.981636	chr12	1.21E+08	1.21E+08	+	0 NA	intron (NMIR SINE	14098 NM_001037	8655 Hs.5120 NM_00374E	ENSG000003DYNL5	DLCL1 CLAF	dynein l iprotein-coding
chr14-21.4.8.45863	0.047221	0.808945	0.058373	0.953451	0.981636	chr14	21419717	21420978	+	0 NA	intron (Nintron (N	16928 NM_02092C	57680 Hs.53069E	ENSG000003CHDR	AHTS13 HE	chromodon protein-coding
chr1-31.8.888655	0.045393	0.														



chr7-9311.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chr7	93112699	93114608	+	0	NA	intron (NLIPA5 LIN	4326	NM_017654	54809	Hs.65641	NM_017654	ENSG000003SAMD9	C7orf5 DFsterile ε protein-coding
chr7-1285.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	15560	NM_001364	3663	Hs.521181	NM_032645	ENSG000001IRF5	SLEB10 interfercprotein-coding
chr8-1022.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	50526	NR_125415	1.02E+08	Hs.492445	NR_125415	ENSG000001UBR5-AS1	UBR5 antincRNA
chr8-1436.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chr8	1.44E+08	1.44E+08	+	0	NA	intron (Nintron (N	5951	NM_001082	9831	Hs.43133	NM_014788	ENSG000001ZNF623	zinc fingerprotein-coding
chr9-1285.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chr9	1.29E+08	1.29E+08	+	0	NA	exon (NM_exon (NM	11371	NM_014908	22845	Hs.531563	NM_014908	ENSG000001DOLK	CDG1M DK dolichol protein-coding
chr9-1325.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chr9	1.32E+08	1.32E+08	+	0	NA	intron (NLIMC4 LIN	50587	NM_001351	23064	Hs.460317	NM_015045	ENSG000001SETX	ALS4 AOA2 senataxir protein-coding
chrX-2012.6.931426	0.050806	0.874221	0.058115	0.953657	0.981636	chrX	20128669	20131277	+	0	NA	intron (Nintron (N	6440	NR_023358	1E+08	NR_023358	SCARNA9L	small Ca <sub>v</sub> ncRNA	
chr15-5262.6.501401	0.053747	0.925982	0.058044	0.953714	0.981636	chr15	52664724	52665656	+	0	NA	intron (NLIPA16 LI	-13150	NM_001288	56204	Hs.152388	NM_019600	ENSG000001FAM214A	KIAA1370 family wiprotein-coding
chr1-2845.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr1	28496625	28497892	+	0	NA	3' UTR (N3' UTR (N	-8685	NM_001048	1104	Hs.469722	NM_001265	ENSG000001RCC1	CHC1 RCC1 regulator protein-coding
chr1-3517.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr1	35101040	35101985	+	0	NA	intron (Nintron (N	22127	NM_024772	79830	Hs.471245	NM_024772	ENSG000001ZMYM1	MYM zinc fingerprotein-coding
chr1-5147.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr1	51478924	51479528	+	0	NA	intron (NLIPA5 LIN	40040	NM_001981	2060	Hs.83722	NM_001981	ENSG000001EPRS15	AF-1P AF1 epidermalprotein-coding
chr1-6813.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr1	68131649	68132755	+	0	NA	intron (Nintron (N	51408	NR_031664	1E+08	NR_031664	ENSG000001MIR1262	MIRN1262 microRNA ncRNA	
chr1-2202.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (Nintron (N	3837	NR_001587	6791	Hs.654845	NR_001587	AURKAP1	AURKAP1 aurora kipsudo
chr10-115.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr10	11942059	11944041	+	0	NA	intron (Nintron (N	-48340	NR_038222	219731	Hs.576787	NR_038222	ENSG000001PROSER2-1	PROSER2 εncRNA
chr10-1217.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr10	12165709	12169230	+	0	NA	3' UTR (N3' UTR (N	28422	NM_014142	11164	Hs.555955	NM_014142	ENSG000001NUDT5	YSA1 YSA1 nudix hycprotein-coding
chr10-927.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr10	92024664	92025496	+	0	NA	intron (Nintron (N	101310	NM_003972	9044	Hs.500525	NM_003972	ENSG000001BTAF1	MOT1 TAF(B-TFIID) protein-coding
chr10-100.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr10	2E+08	2E+08	+	0	NA	intron (NMER68 LTF	10822	NM_001347	10613	Hs.150087	NM_006455	ENSG000001CERLIN1	C10orf69 ER lipid protein-coding
chr11-337.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr11	33767046	33769720	+	0	NA	intron (Nintron (N	6137	NM_033400	26273	Hs.406787	NM_012175	ENSG000001FBX03	FBA FBX3 E-box prcprotein-coding
chr11-745.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr11	74915059	74917200	+	0	NA	intron (NLIM4c LIN	32962	NM_001277	143570	Hs.370145	NM_182965	ENSG000001XRR1A	X-ray racprotein-coding
chr11-704.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr11	74971451	74973297	+	0	NA	intron (Nintron (N	-16270	NM_001367	10825	Hs.191074	NM_006655	ENSG000001CNEU3	SIAL3 neuramin protein-coding
chr11-105.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	intron (NALuS6 SI	-24265	NM_000019	38	Hs.232375	NM_000019	ENSG000001ACAT1	ACAT MAT acetyl-Cp protein-coding
chr12-165.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	16360152	16365481	+	0	NA	intron (NALuJo SIN	9399	NM_145764	4257	Hs.389700	NM_020300	ENSG000001MGST1	GST12 MGs microsome protein-coding
chr12-214.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	21495914	21496345	+	0	NA	intron (NERVL-E ir	5506	NM_002907	5965	Hs.235055	NM_002907	ENSG000001RECQL	RECQL1 RecQ like protein-coding
chr12-227.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	22056629	22058458	+	0	NA	intron (Nintron (N	11325	NM_018686	55907	Hs.311345	NM_018686	ENSG000001CMAS	RCSL cytidine protein-coding
chr12-306.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	30672740	30675599	+	0	NA	intron (Nintron (N	3075	NM_001190	10526	Hs.505135	NM_006390	ENSG000001IPO8	RANBP8 importin protein-coding
chr12-527.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	52073380	52077123	+	0	NA	intron (Nintron (N	-4453	NM_001365	1.14E+08	Hs.524431	NM_001369216	SMIM41	small intprotein-coding
chr12-57.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	57095601	57097709	+	0	NA	exon (NM_exon (NM	7541	NM_001330	4665	Hs.159225	NM_005967	ENSG000001MRPL2	MADER NGLF-A biprotein-coding
chr12-577.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	57795669	57800517	+	0	NA	TTS (NM_TTS (NM_C	15306	NM_001172	10102	Hs.632704	NM_005725	ENSG000001TSFM	EFTS EFTS Ts translprotein-coding
chr12-896.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	89626432	89630958	+	0	NA	intron (NL3 LINE C	80203	NM_001366	490	Hs.506275	NM_001685	ENSG000001ATP2B1	PMCA1 PMCA tase h protein-coding
chr12-934.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	93484430	93489867	+	0	NA	intron (NALuJb SIN	19634	NR_038160	28977	Hs.199575	NM_014050	ENSG000001MRPL42	HSPC204 L mitochondrion protein-coding
chr12-122.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NALuSx3 SI	-21824	NM_001351	65082	Hs.487885	NM_022915	ENSG000001VPS33A	MPSPS VPS33A ccprotein-coding
chr13-202.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr13	20072367	20075513	+	0	NA	intron (NLIMB3 LI	-28761	NR_126388	1.04E+08	Hs.578015	NR_126388	ENSG000001LINC01072	long intncRNA
chr13-952.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr13	95252089	95253348	+	0	NA	intron (NMER44D DN	42374	NR_145733	1.1E+08	NR_145733	SNORD130	small nucsnRNA	
chr14-705.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr14	70583712	70585098	+	0	NA	3' UTR (N3' UTR (N	16285	NM_001284	10001	Hs.497355	NM_005465	ENSG000001MED6	ARC33 NY-mediator protein-coding
chr14-737.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr14	73203407	73204293	+	0	NA	intron (Nintron (N	-33656	NR_158677	89932	Hs.509905	NM_173465	ENSG000001PAPLN	PPN papilin, protein-coding
chr14-732.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr14	73729094	73731298	+	0	NA	intron (NMIR SINE	-16062	NM_006025	9240	Hs.194705	NM_006025	ENSG000001PNMA1	MA1 PNMA famprotein-coding
chr15-506.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr15	50610912	50612105	+	0	NA	intron (Nintron (N	-64842	NM_203494	373509	Hs.677755	NM_203494	ENSG000001CASP50	ubiquitin protein-coding
chr15-857.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr15	85731098	85734988	+	0	NA	intron (NHAL1M8 LI	25682	NR_120366	1.02E+08	Hs.513112	NR_120366	LOC101925	uncharactcrRNA
chr15-885.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr15	88909781	88911488	+	0	NA	intron (NL2c LINE	2534	NM_001310	4240	Hs.3745	NM_005925	ENSG000001MFGF8	BA46 EDL1 milik fat protein-coding
chr16-800.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr16	80067	81771	+	0	NA	intron (Nintron (N	2694	NM_001015	4350	Hs.459595	NM_002434	ENSG000001MCPG	AAG ADPG N-methyl protein-coding
chr16-691.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr16	69163164	69165070	+	0	NA	intron (NALuYm1 SI	-23005	NM_006755	6645	Hs.461117	NM_006755	ENSG000001SNTB2	D16S2531E synthrophin protein-coding
chr17-182.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr17	1827022	1827756	+	0	NA	intron (NL2b LINE	2513	NM_052925	114826	Hs.514602	NM_052925	ENSG000001SMYD4	ZMYND21 SET and h protein-coding
chr18-210.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr18	21011567	21018222	+	0	NA	intron (Nintron (N	96919	NM_005405	6093	Hs.306307	NM_005405	ENSG000001ROCK1	P16OROCK Rho assoc protein-coding
chr18-494.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr18	49480528	49484847	+	0	NA	intron (NALuS5 SI	4547	NM_001195	497661	Hs.603040	NM_001035	ENSG000001C18orf32	chromosn protein-coding
chr18-622.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr18	62258243	62263407	+	0	NA	intron (NLIM4A LI	-64462	NM_001270	8792	Hs.204044	NM_003835	ENSG000001TNFRSF11	CD265 FEC TN recep protein-coding
chr19-106.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr19	10690437	10691641	+	0	NA	3' UTR (N3' UTR (N	-10400	NM_031205	81890	Hs.631635	NM_031205	ENSG000001QTRT1	FP3235 T queuine t protein-coding
chr2-3261.7.178887	-0.04984	0.858682	-0.05804	0.953718	0.981636	chr2	32610160	32613712	+	0	NA	intron (NALuJo SIN</							

chr7-6731	9.895697	0.042833	0.741931	0.057732	0.953962	0.981636	chr7	6731856	6738896	+	0	NA	promoter-promoter-	71 NR_002217	441194	Hs. 71559CNR_002217	ENSG00000PMS2CL	PMS2P13	PMS2	C-terminus	pseudo	
chr1-110	9.367677	0.043937	0.762587	0.057616	0.954054	0.981636	chr1	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	17344	NR_033088	85369	Hs. 58499ENR_033088	ENSG00000STRIP1	FAM40A	FRS3	striatin protein-coding	
chr15-658	9.367677	0.043937	0.762587	0.057616	0.954054	0.981636	chr15	65886910	65890537	+	0	NA	3' UTR (N3' UTR (N	19232	NR_001206	8766	Hs. 321541NM_004663	ENSG00000CRAB11A	YL8	RAB11A	nprotein-coding	
chr2-120	9.367677	0.043937	0.762587	0.057616	0.954054	0.981636	chr2	1.2E+08	1.2E+08	+	0	NA	intron (NArthur B	27242	NR_002281	5899	Hs. 46982CNR_002281	ENSG00000RALB		RAM	like protein-coding	
chr12-124	6.741005	-0.05203	0.903303	-0.0576	0.954069	0.981636	chr12	1.24E+08	1.24E+08	+	0	NA	intron (Nintron (N	-60871	NR_10694C	1.02E+08	NR_10694C	ENSG00000MIR6880		hsa-mir-6	microRNA ncRNA	
chr1-1124	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr1	1.12E+08	1.12E+08	+	0	NA	intron (NAluSx3 SI	23970	NR_018704	55917	Hs. 74410CNR_018704	ENSG00000CTTNP2		CTTNP2	protein-coding	
chr11-86	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr11	8634135	8635092	+	0	NA	intron (Nintron (N	24223	NR_01481E	9866	Hs. 13083ENR_01481E	ENSG00000TRIM66		Clorf29	tripartite protein-coding	
chr14-915	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr14	91972187	91974182	+	0	NA	intron (NAluSg SIN	-25482	NR_00632E	10516	Hs. 33270ENR_00632E	ENSG00000FBLN5		AD1orf21	ARCFibulin 1 protein-coding	
chr17-357	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr17	35718007	35719187	+	0	NA	intron (NFLAM_A SI	-13042	NR_03331E	91608	Hs. 744994NM_03331E	ENSG00000CRASL10B		RRP17	VTSRAS like protein-coding	
chr19-362	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr19	36239001	36240300	+	0	NA	intron (Nintron (N	6028	NR_00136E	147929	Hs. 59633ENR_152477	ENSG00000ZNF565			zinc finger protein-coding	
chr19-365	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr19	36926605	36927252	+	0	NA	intron (NMIR SINE	10596	NR_001204	374900	Hs. 40422CNR_19853E	ENSG00000ZNF568		ZFP568	zinc finger protein-coding	
chr2-8814	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr2	8814806	8815751	+	0	NA	intron (NAluJb SIN	22335	NR_00134E	57498	Hs. 9873	NR_02073E	ENSG00000KIDINS22C		ARMS SIN	kinase D protein-coding
chr20-233	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr20	23387303	23388297	+	0	NA	intron (NLMIB7 LIN	23437	NR_001317	64412	Hs. 709462CNR_02248E	ENSG00000GZF1		JLSM ZBT	GFND ind protein-coding	
chr5-905	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr5	9053578	9054244	+	0	NA	promoter-promoter-	-16	NR_03977E	1.01E+08	NR_03977E	ENSG00000MIR4636		mir-4636	microRNA ncRNA	
chr7-129	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (NLMIB2 LIN	21674	NR_03405E	23534	Hs. 19361ENR_01247E	ENSG00000TNPO3		IP012 LGM	transport protein-coding	
chr8-786	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr8	78697260	78698691	+	0	NA	intron (Nintron (N	26399	NR_07723E	1.01E+08	Hs. 388511NR_07723E		LOC101241-		chromosome pseudo	
chr8-104	5.453219	0.056679	0.984766	0.057556	0.954102	0.981636	chr8	1.05E+08	1.05E+08	+	0	NA	intron (NLMIB LIN	-1754	NR_03033C	693127	NR_03033C	ENSG00000MIR5483		MIRN5483	microRNA ncRNA	
chr1-208	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr1	20861282	20863160	+	0	NA	intron (Nintron (N	-57533	NR_016287	50809	Hs. 142442CNR_016287	ENSG00000HIP1BP3		HP1-BP74	heteroch protein-coding	
chr1-218	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr1	21868232	21868693	+	0	NA	intron (NATAATG T	56197	NR_00101E	401944	Hs. 74515ENR_00101E	ENSG00000LDLRAD2			low density protein-coding	
chr10-294	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr10	29463594	29464644	+	0	NA	intron (Nintron (N	53876	NR_11092E	1.03E+08	Hs. 49920ENR_00393C	ENSG00000CVIL-AS1			SVIL anticRNA	
chr11-434	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr11	43408647	43409116	+	0	NA	intron (NAluJb SIN	49961	NR_01825E	55761	Hs. 19118ENR_01825E	ENSG00000TTC17			tetratric protein-coding	
chr16-66	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr16	66610857	66614558	+	0	NA	non-codnon-codir	7976	NR_03761E	123920	Hs. 29819ENR_144601	ENSG00000CMTM3		BNAS2 CKI	CKLF like protein-coding	
chr19-24	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr19	24046701	24047094	+	0	NA	intron (NAluSz6 SI	13448	NR_00127E	9534	Hs. 43440ENR_00487E	ENSG00000ZNF254		BMZF-5	HE zinc finger protein-coding	
chr4-150	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr4	15065500	15067900	+	0	NA	3' UTR (N3' UTR (N	64219	NR_001177	132864	Hs. 656937NM_18248E	ENSG00000CPEB2		CPE-BP2	cytoplasm protein-coding	
chr5-148	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr5	1.48E+08	1.48E+08	+	0	NA	intron (Nintron (N	21539	NR_03079E	81545	Hs. 483772CNR_03079E	ENSG00000FBX038		Fbx38	HMMF-box prc protein-coding	
chr7-1024	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (NTrigger4 I	-12367	NR_001271	80228	Hs. 36330ENR_032831	ENSG00000CORAI2		C7orf19	CORAI calc protein-coding	
chr7-139	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	3' UTR (N3' UTR (N	-3341	NR_16210E	1.13E+08	NR_16210E		MIR10399		microRNA ncRNA	
chr8-9902	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr8	99023305	99024383	+	0	NA	intron (NLMIA5 LIN	10578	NR_01789C	157680	Hs. 19154CNR_01524E	ENSG00000VPS13B		CHS1 COH	vacuolar protein-coding	
chr9-349	6.160506	-0.04683	0.813745	-0.05755	0.954108	0.981636	chr9	34996570	34997963	+	0	NA	3' UTR (N3' UTR (N	6976	NR_00113E	25822	Hs. 23750ENR_01226E	ENSG00000DNAJB5		Hsc40	DnaJ heat protein-coding	
chr1-361	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr1	36167585	36168565	+	0	NA	intron (NAluSc SIN	11915	NR_00128E	55700	Hs. 35609ENR_018067	ENSG00000MAP7D1		PARCC1 RF	MAP7 dom protein-coding	
chr14-362	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr14	36297036	36299962	+	0	NA	TTS (NM_C TTS (NM_C	22138	NR_00130E	51562	Hs. 368647NM_01658E	ENSG00000CMBIP			MAP3K12 t protein-coding	
chr16-87	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr16	87835452	87839927	+	0	NA	intron (Nintron (N	-3029	NR_10683E	1.02E+08	NR_10683E	ENSG00000MIR6775		hsa-mir-6	microRNA ncRNA	
chr19-15	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr19	15270300	15272400	+	0	NA	intron (Nintron (N	8886	NR_05824C	23476	Hs. 18776ENR_01429E	ENSG00000BRD4		CAP HUNK	1 bromodomain protein-coding	
chr19-37	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr19	37328859	37329870	+	0	NA	non-codnon-codir	-5260	NR_13812E	284459	Hs. 64024ENR_18178E	ENSG00000ZNF875		HKR1	zinc finger protein-coding	
chr19-51	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr19	51939781	53191978	+	0	NA	intron (NMER21B LI	2129	NR_00135E	79788	Hs. 74523CNR_02473E	ENSG00000ZNF665		ZFP160L	zinc finger protein-coding	
chr3-966	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr3	96625100	96626909	+	0	NA	intron (NMIR SINE	13204	NR_00224E	64419	Hs. 47538ENR_02248E	ENSG00000MTMR14		C3orf29	myotubule protein-coding	
chr7-1514	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	TTS (NM_C TTS (NM_C	-24802	NR_13177E	155051	Hs. 647104NM_144727	ENSG00000CRYGN			crystallin protein-coding	
chr7-156	7.459446	0.048915	0.850088	0.057541	0.954114	0.981636	chr7	1.57E+08	1.57E+08	+	0	NA	intron (Nintron (N	13558	NR_13840C	64434	Hs. 15825	NR_13840C	ENSG00000NOM1		C7orf3	PF nucleolar protein-coding
chr11-474	10.37472	0.041636	0.725698	0.057373	0.954248	0.981636	chr11	47421842	47425139	+	0	NA	intron (NMIR3 SINE	2983	NR_002804	5702	Hs. 20575ENR_002804	ENSG00000PSCM3		TBP1	proteasome protein-coding	
chr12-48	10.37472	0.041636	0.725698	0.057373	0.954248	0.981636	chr12	48694304	48696135	+	0	NA	intron (Nintron (N	-12981	NR_01782E	54934	Hs. 50541ENR_01782E	ENSG00000KANSL2		C12orf41 KAT8	regt protein-coding	
chr16-104	10.37472	0.041636	0.725698	0.057373	0.954248	0.981636	chr16	16467	16761	+	0	NA	TTS (NR_C TTS (NR_C	505	NR_10706E	1.02E+08	NR_10706E	ENSG00000MIR6859		hsa-mir-6	microRNA ncRNA	
chr3-160	10.37472	0.041636	0.725698	0.057373	0.954248	0.981636	chr3	1E+08	1E+08	+	0	NA	intron (Nintron (N	28967	NR_01482C	9868	Hs. 22725ENR_01482C	ENSG00000TOM70		TOMM70A	translocase protein-coding	
chr7-6114	10.37472	0.041636	0.725698	0.057373	0.954248	0.981636	chr7	6114896	6117641	+	0	NA	intron (Nintron (N	11319	NR_03217E	84132	Hs. 31856	NR_03217E	ENSG00000CASP42			ubiquitin protein-coding
chr9-1911	10.37472	0.041636	0.725698	0.057373	0.954248	0.981636	chr9	19115284	19123901	+	0	NA	intron (Nintron (N	7900	NR_00112E	123	Hs. 3416	NR_00112E	ENSG00000PLIN2		ADFP ADRF	perilipin protein-coding
chr7-9327	5.710389	-0.0569	0.992711	-0.05731	0.954295	0.981636	chr7	93276505	93277344	+	0	NA	TTS (NM_C TTS (NM_C	44458	NR_01766E	55610	Hs. 202424NM_01766E	ENSG00000V				



chr1-3095 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	30935059	30937777	+	0	NA	promoter-promoter-	-642 NR_033295	692235	NR_033295	SNORD103E	U103B	small	nucsnRNA			
chr1-3634 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	36344647	36348616	+	0	NA	intron (NMIRb SINE	-23397 NM_018166	55194 Hs. 87016	NR_018166	ENSG00000EVA1B	Clorf78	[Eva-1 hon	protein-coding			
chr1-3757 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	37579397	37593634	+	0	NA	intron (Nintron (N	9422 NM_013285	29889 Hs. 75528	NR_013285	ENSG00000C	GNL2	HUMAUA	NTIG	protein-coding		
chr1-3801 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	38016317	38026257	+	0	NA	intron (Nintron (N	8553 NM_016037	51118 Hs. 472038	NR_016037	ENSG00000C	UTP11	CG1-94	[CUTP11 sm	protein-coding		
chr1-8565 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	85637579	85664048	+	0	NA	Intergeni	LIM4 LINE	58272 NM_001554	3491 Hs. 8867	NR_001554	ENSG00000CC	NI	CYR61	[G] cellular	protein-coding	
chr1-1178 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	1.18E+08	1.18E+08	+	0	NA	intron (NMIR SINE	49983 NM_017686	54834 Hs. 310805	NR_017686	ENSG00000C	GDAP2	MACROD3	[S] gangliosid	protein-coding		
chr1-1204 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr1	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N	5255 NR_102405	728841 Hs. 44508	NR_01037501	NBPF8	NBPF8	memt	protein-coding			
chr10-104 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	3' UTR (N3' UTR (N	-9105 NR_120622	1.02E+08 Hs. 670333	NR_120622	ITPR1P-AS-	ITPR1P	ancRNA				
chr10-12 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr10	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	8476 NM_018117	55717 Hs. 144447	NR_018117	ENSG00000C	WDR11	BRWD2	[DR]WD	repeat	protein-coding	
chr11-302 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr11	3022447	3030873	+	0	NA	exon (NM exon (NM	-2634 NR_04658	1.01E+08 Hs. 27487	NR_04658	ENSG00000C	CARS-AS1	CARS	antncRNA			
chr11-374 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr11	3749120	3752927	+	0	NA	intron (NMER1 DN	46523 NR_157591	4928 Hs. 52475	NR_005387	ENSG00000C	NUP98	ADIR2	[N]F nucleop	protein-coding		
chr11-276 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr11	27686507	27689036	+	0	NA	intron (NLIPA7 LIN	11896 NM_170734	627 Hs. 50218	NR_001705	ENSG00000C	BDNF	ANON2	[BU] brain der	protein-coding		
chr11-936 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr11	93679012	93680050	+	0	NA	exon (NM exon (NM	17849 NM_033395	85459 Hs. 45841	NR_033395	ENSG00000C	CEP295	KIAA1731	centrosom	protein-coding		
chr11-108 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr11	1.08E+08	1.08E+08	+	0	NA	non-codir non-codir	111493 NM_00133C	160140 Hs. 65318	NR_152587	ENSG00000C	C11orf65		chromoson	protein-coding		
chr12-88C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr12	88059345	88060315	+	0	NA	intron (Nintron (N	24294 NM_001005	91298 Hs. 59100	NR_001005	ENSG00000C	C12orf29		chromoson	protein-coding		
chr12-108 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr12	1.09E+08	1.09E+08	+	0	NA	intron (NLIMC4 LIN	14275 NM_007076	11153 Hs. 66189	NR_007076	ENSG00000C	FICD	HIP13	[HY] FIC	doma	protein-coding	
chr12-121 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr12	1.22E+08	1.22E+08	+	0	NA	intron (NALuY SINE	2737 NR_048555	5715 Hs. 13115	NR_002813	ENSG00000C	PMSD9	Rpn4	[p27	proteasom	protein-coding	
chr13-197 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr13	19749218	19753070	+	0	NA	intron (Nintron (N	31801 NM_001354	55269 Hs. 21319	NR_001042	ENSG00000C	PSPC1	PSP1	paraspecl	protein-coding		
chr13-46C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr13	46016664	46017391	+	0	NA	intron (NL2 LINE L	35719 NM_00133C	23091 Hs. 13610	NR_01507C	ENSG00000C	ZC3H13	KIAA0853	[z]inc	fin	protein-coding	
chr13-52 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr13	52023789	52025374	+	0	NA	promoter-promoter-	-110 NM_021645	9724 Hs. 51296	NR_021645	ENSG00000C	UTP14C	2700066	[J2]UTP14C	sn	protein-coding	
chr13-951 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr13	95103582	95111063	+	0	NA	intron (Nintron (N	-10322 NR_145733	1.1E+08	NR_145733	SNORD13G		small	nucsnRNA			
chr14-24C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr14	24237309	24241415	+	0	NA	TTS (NM_C	3261 NM_001095	26277 Hs. 49619	NR_012461	ENSG00000C	TINF2	DKCA3	[TIM	TERF1	intr	protein-coding
chr14-617 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr14	61771933	61785397	+	0	NA	intron (Nintron (N	16245 NM_003082	6617 Hs. 17931	NR_003082	ENSG00000C	SNAPC1	PTFgamma	[small	nuc	protein-coding	
chr14-774 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr14	77702650	77703332	+	0	NA	intron (Nintron (N	5332 NM_00602C	8846 Hs. 94542	NR_00602C	ENSG00000C	ALKBH1	ABH	[ABH] alkB	huc	protein-coding	
chr14-954 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr14	95435457	95436607	+	0	NA	intron (NL2 LINE L	39803 NM_001363	161176 Hs. 41502	NR_024633	ENSG00000C	SYNE3	C14orf135	spectrin	protein-coding		
chr14-10 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr14	1.04E+08	1.04E+08	+	0	NA	intron (Nintron (N	21657 NM_00110C	7517 Hs. 59232	NR_005433	ENSG00000C	XRCC3	MM6	X-ray	ref	protein-coding	
chr15-44C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr15	44586281	44587397	+	0	NA	intron (Nintron (N	49692 NM_00375E	8669 Hs. 40405	NR_00375E	ENSG00000C	E1F3J	E1F3S1	[e]ukaryot	protein-coding		
chr15-504 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr15	50466089	50466932	+	0	NA	intron (NALuSzl SIN	42105 NM_00112E	9101 Hs. 44373	NR_005154	ENSG00000C	USP8	HumORF8	[F]ubiquit	protein-coding		
chr15-92C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr15	92988517	92999031	+	0	NA	intron (NLIM4 LINE	83432 NM_00116E	56963 Hs. 27127	NR_020211	ENSG00000C	RGMA	RGM	repulsive	protein-coding		
chr16-58C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr16	58621135	58623764	+	0	NA	intron (NLIMC1 LIN	7377 NM_026099	23019 Hs. 46092	NR_016284	ENSG00000C	CNOT1	AD-005	[CE]CCR4-NOT	protein-coding		
chr16-72C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr16	72958926	72959649	+	0	NA	exon (NM exon (NM	88841 NM_00688E	463 Hs. 59829	NR_00688E	ENSG00000C	ZFXH3	ATBF1	[AT]E	zinc	fin	protein-coding
chr16-74 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr16	74467735	74474551	+	0	NA	intron (Nintron (N	-49673 NM_001011	497190 Hs. 45467	NR_001011	ENSG00000C	CLEC18B	MRLC2	C-type	lc	protein-coding	
chr17-724 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr17	7244030	7244765	+	0	NA	intron (NALuJo SIN	-2948 NM_00272E	11337 Hs. 64742	NR_00272E	ENSG00000C	GABARAP	ATG8A	[GAE]GABA	tp	protein-coding	
chr17-16C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr17	16072569	16077198	+	0	NA	intron (NALuY SINE	75059 NM_01777E	54902 Hs. 46231	NR_01777E	ENSG00000C	TTC19	201020401	tetratric	protein-coding		
chr17-18C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr17	18093825	18098646	+	0	NA	intron (Nintron (N	7387 NM_00133C	1819 Hs. 78582	NR_00138E	ENSG00000C	DRG2		developm	protein-coding		
chr17-304 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr17	30445075	30446382	+	0	NA	exon (NM exon (NM	-31680 NR_004871	9527 Hs. 46268	NR_004871	ENSG00000C	GOSR1	GOLIM2	[GC] golgi	SN	protein-coding	
chr17-47C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr17	47978603	47979529	+	0	NA	intron (Nintron (N	7953 NM_00127E	80279 Hs. 20157	NR_025197	ENSG00000C	CDK5RAP3	C53	[HSF-2	CDK5	regt	protein-coding
chr17-51C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr17	51077227	51077991	+	0	NA	intron (Nintron (N	-30731 NM_001251	9043 Hs. 46343	NR_003971	ENSG00000C	SPAG9	CT89	[HLC-] sperm	ass	protein-coding	
chr18-86C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr18	8633275	8639642	+	0	NA	intron (Nintron (N	27013 NM_00102E	201475 Hs. 27007	NR_00102E	ENSG00000C	RAB12		RAB12,	m	protein-coding	
chr19-331 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr19	33102446	33103617	+	0	NA	intron (Nintron (N	21850 NM_01802E	55094 Hs. 46643	NR_01802E	ENSG00000C	GPATCH1	ECGP	[GPA]G-patch	c	protein-coding	
chr19-37 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr19	37196151	37200909	+	0	NA	intron (NALuSp SIN	12006 NM_15227E	92285 Hs. 39056	NR_15227E	ENSG00000C	ZNF585B	SZFP41	zinc	fin	protein-coding	
chr19-40C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr19	40586697	40589020	+	0	NA	intron (NALuJr SIN	-5308 NM_00357E	8425 Hs. 40676	NR_00357E	ENSG00000C	LTBP4	ARCL1C	[L] latent	tp	protein-coding	
chr19-49C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr19	49645264	49649242	+	0	NA	intron (Nintron (N	5044 NM_02122E	58506 Hs. 10352	NR_02122E	ENSG00000C	SCAF1	SRA1	SR-relate	protein-coding		
chr2-168C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr2	1683675	1685196	+	0	NA	intron (Nintron (N	60080 NM_01229E	7837 Hs. 33219	NR_01229E	ENSG00000C	PXDN	ASGD7	[CO] peroxidas	protein-coding		
chr2-875C 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr2	8756399	8758265	+	0	NA	3' UTR (N3' UTR (N	75276 NM_00216E	3398 Hs. 18091	NR_00216E	ENSG00000C	ID2	IGT8	[ID2] inhibitor	protein-coding		
chr2-941 7.665768	-0.0473	0.832285	-0.05683	0.954682	0.981636	chr2	9410869															



chr11-112	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr11	1.12E+08	1.12E+08	0	NA	intron (AluX4 SI	5011 NR_07706C	6392 Hs. 35627CNM_003002	ENSG000000CDHD	CBT1 CII-	succinate protein-coding
chr12-163	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr12	16353215	16359137	0	NA	intron (MLT1A0 LI	2759 NM_145764	4257 Hs. 38970CNM_02030C	ENSG000000MGST1	GST12 MG5	microsome protein-coding
chr12-193	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr12	19365996	19368482	0	NA	intron (intron (N	-72253 NM_001114	121536 Hs. 126497NM_153207	ENSG000000CAEBP2	AE	bindir protein-coding
chr13-363	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr13	36324689	36326594	0	NA	intron (intron (N	20753 NM_015087	23111 Hs. 440414NM_015087	ENSG000000SPART	SPG20 TAF	spartin protein-coding
chr13-454	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr13	45404015	45408517	0	NA	intron (AluXs1 SI	-11896 NR_047031	0.01E+08 Hs. 658036NR_047031	ENSG000000SLC25A30-	SLC25A30	ncRNA
chr13-11C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr13	1.1E+08	1.1E+08	0	NA	intron (intron (N	-21398 NM_001267	1E+08 Hs. 640035NM_001267044	COL4A2-AS-	COL4A2	ar protein-coding
chr13-112	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr13	1.13E+08	1.13E+08	0	NA	intron (NL2b LINE	32561 NM_006322	10426 Hs. 224152NM_006322	ENSG000000TUBGCP3	104p ALP	tubulin g protein-coding
chr13-115	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr13	1.14E+08	1.14E+08	0	NA	intron (intron (N	-6028 NM_001365	0.01E+08 Hs. 704267NM_001365	ENSG000000C13orf46	104p	chromosom protein-coding
chr13-114	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr13	1.14E+08	1.14E+08	0	NA	intron (intron (N	-36193 NM_001365	0.01E+08 Hs. 704267NM_001365	ENSG000000C13orf46	-	chromosom protein-coding
chr14-645	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr14	64629386	64927614	0	NA	intron (intron (N	11368 NM_001202	0.01E+08 Hs. 325531NM_001202	ENSG000000CHURC1-F	FNTB FTa	CHURC1-F protein-coding
chr14-73C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr14	73085671	73087698	0	NA	intron (NLIMC5 LIN	28150 NM_021235	58517 Hs. 531106NM_021235	ENSG000000RBM25	NET52 REI	RNA bindi protein-coding
chr14-777	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr14	77714510	77717870	0	NA	intron (AluYe5 SI	8087 NR_052025	81892 Hs. 655105NM_03121C	ENSG000000SLIRP	C14orf155	SRA stem protein-coding
chr15-404	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr15	40407693	40412053	0	NA	intron (AluV SINE	4076 NR_148925	3712 Hs. 513642NM_002222	ENSG000000IVD	ACAD2	isovalery protein-coding
chr15-421	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr15	42186470	42190883	0	NA	intron (intron (N	10990 NR_030357	693212 NR_030357	ENSG000000MIR627	MIRN627	microRNA ncRNA
chr15-43C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr15	43013664	43017302	0	NA	intron (NSVA_D Ret	90555 NM_174916	197131 Hs. 591121NM_174916	ENSG000000CUBR1	JBS	ubiquitin protein-coding
chr15-75E	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr15	75686620	75693251	0	NA	exon (NM exon (NM	22913 NM_001897	1464 Hs. 513044NM_001897	ENSG000000CSPG4	HMW-MAA	chondroitin protein-coding
chr15-771	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr15	77154865	77158328	0	NA	intron (NLIP4 LIN	68808 NR_026813	81698 Hs. 656935NM_030944	LINC00597	C15orf5	long intncRNA
chr15-78C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr15	78010944	78012877	0	NA	intron (AluXs SIN	-17685 NR_026998	91450 Hs. 406766NR_026998	LOC91450	-	uncharactericncRNA
chr16-213	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	213745	223852	0	NA	intron (intron (N	10651 NM_018032	55692 Hs. 16803 NM_018032	ENSG000000LUC7L	LUC7B L	LUC7 like protein-coding
chr16-351	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	3517551	3517904	0	NA	intron (NLIMC4 LIN	7833 NM_024793	23059 Hs. 155995NM_015041	ENSG000000CLUA1P	CFAP22 F	clusterin protein-coding
chr16-16C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	16009408	16013986	0	NA	intron (AluXs SIN	62081 NM_004996	4363 Hs. 391464NM_004996	ENSG000000ABCC1	ABC29 ABC	ATP bindi protein-coding
chr16-185	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	18319663	18320494	0	NA	intron (intron (N	12584 NM_001282	0.01E+08 Hs. 634612NM_001282	ENSG000000NIP1A7	NIP1A8	nuclear protein-coding
chr16-574	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	57452234	57455059	0	NA	intron (MamRep137	-6118 NM_001308	57019 Hs. 4900 NM_02031	ENSG000000CIAPIN1	Anamorsircytoc	protein-coding
chr16-683	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	68305026	68306692	0	NA	intron (AluJb SIN	5087 NM_032178	84138 Hs. 72952CNM_032178	ENSG000000SLC7A60S	-	solute c protein-coding
chr16-717	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr16	71736742	71741715	0	NA	intron (intron (N	-14527 NM_01502C	23035 Hs. 709455NM_01502C	ENSG000000PHLPP2	PHLPP1 P	PH domain protein-coding
chr17-54C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr17	54035375	5411418	0	NA	intron (intron (N	-12143 NM_00116C	84268 Hs. 462086NM_03230E	ENSG000000RPAIN	HRIP RIP	RPA inter protein-coding
chr17-161	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr17	16192371	16195499	0	NA	intron (NL2 LINE L	704 NM_00119C	9611 Hs. 462322NM_006311	ENSG000000NCOR1	N-CoR N-	C-nuclear protein-coding
chr17-304	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr17	30422473	30424403	0	NA	intron (intron (N	42960 NM_001195	1362 Hs. 446075NM_001304	ENSG000000CPD	GP180	carboxype protein-coding
chr17-604	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr17	60499919	60500133	0	NA	intron (AluY SINE	26214 NM_001282	10513 Hs. 84084 NM_00638C	ENSG000000APBP2	APP-BP2 E	amyloid t protein-coding
chr17-757	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr17	75702274	75706659	0	NA	intron (MERR102b L	-16993 NM_001321	3691 Hs. 632222NM_000921	ENSG000000ITGB4	CD104 GP1	integrin protein-coding
chr19-118	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	11819380	11822120	0	NA	intron (intron (N	6477 NM_152357	126070 Hs. 418192NM_152357	ENSG000000ZNF440	-	zinc fing protein-coding
chr19-177	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	17726857	17729362	0	NA	exon (NM exon (NM	7953 NM_001308	55201 Hs. 66048 NM_018174	ENSG000000MAP1S	BPY21P1 C	microtubul protein-coding
chr19-192	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	19292784	19293850	0	NA	intron (AluXs1 SI	-20016 NM_001001	53345 Hs. 531624NM_20351C	ENSG000000TM6SF2	-	transmemt protein-coding
chr19-343	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	34396107	34397340	0	NA	intron (intron (N	-7675 NM_001353	84306 Hs. 515344NM_03234C	ENSG000000PDCD2L	-	programme protein-coding
chr19-463	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	46389690	46390284	0	NA	exon (NM exon (NM	24971 NM_03204C	83987 Hs. 97876 NM_03204C	ENSG000000CCDC8	3M3 PPP1	coiled-c protein-coding
chr19-466	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	46605214	46610569	0	NA	intron (intron (N	5819 NM_001325	808 Hs. 515487NM_005184	ENSG000000CALM3	CALM CAMI	calmodulil protein-coding
chr19-49C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr19	49098110	49109054	0	NA	intron (intron (N	-10788 NM_022165	64130 Hs. 221737NM_022165	ENSG000000LIN7B	LIN-7B ML	lin-7 hom protein-coding
chr2-2913	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	29132536	29134313	0	NA	intron (NLIMS LINE	18009 NM_001287	79745 Hs. 122927NM_024692	ENSG000000CLIP4	RSNL2	CAP-Gly c protein-coding
chr2-9673	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	96731928	96734527	0	NA	intron (intron (N	6849 NM_001142	81562 Hs. 655742NM_03080E	ENSG000000LMANL2	MRTN2 VIF	lectin, n protein-coding
chr2-117E	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	1.18E+08	1.18E+08	0	NA	intron (intron (N	6446 NM_006773	8886 Hs. 744922NM_006773	ENSG000000DDX18	Has1 MrD	DEAD-box protein-coding
chr2-1193	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	1.19E+08	1.19E+08	0	NA	intron (intron (N	3706 NM_001075	1622 Hs. 78888 NM_02054E	ENSG000000DBI	ACBD1 ACE	diazepam protein-coding
chr2-1357	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	1.36E+08	1.36E+08	0	NA	intron (intron (N	-18723 NR_163477	1.08E+08 Hs. 591242NM_001365239	LOC10798E-	-	uncharactericncRNA
chr2-1602	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	1.6E+08	1.6E+08	0	NA	intron (MLT1C LTF	-27109 NR_10377E	0.01E+08 Hs. 729532NR_10377E	ENSG000000LINC0247E-	-	long intncRNA
chr2-2308	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr2	2.31E+08	2.31E+08	0	NA	intron (intron (N	-46530 NM_001287	81618 Hs. 111577NM_03092E	ENSG000000ITMC2	BRI3 BRIC	integral protein-coding
chr20-487	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr20	487017	493099	0	NA	intron (AluXs3 SI	-27525 NM_14462E	128637 Hs. 590876NM_14462E	ENSG000000TBC1D20	C20orf14C	TBC1 dom protein-coding
chr21-44C	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr21	44090263	44091091	0	NA	intron (NLIMC5a LI	16353 NM_001351	7109 Hs. 126221NM_003274	ENSG000000TRAPP10	EHOC-1 E	trafficki protein-coding
chr21-462	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr21	46242603	46248135	0	NA	intron (intron (N	16138 NR_11056E	114044 Hs. 655095NR_00277E	ENSG000000MCM3AP-AS	C21orf85	MCM3AP arncRNA
chr22-314	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr22	31419967	31435478	0	NA	intron (AluJo SIN	28118 NM_004147	4733 Hs. 115242NM_001417	ENSG000000CDRG1	NEDD3	developm protein-coding
chr22-324	8.41749	0.04531	0.797588	0.056809	0.954697	0.981636	chr22	32486359	32486601	0	NA	intron (AluJo SIN	11243 NM_001				



chr8-4295	6.684149	-0.05059	0.897367	-0.05638	0.955041	0.981636	chr8	42954124	42954492	+	0	NA	intron (Nintron (N	57330	NM_03241C	84376	Hs.162852NM_03241C	ENSG00000003003	HK3	hook micrprotein-coding	
chr8-6572	6.684149	-0.05059	0.897367	-0.05638	0.955041	0.981636	chr8	65721445	65723039	+	0	NA	intron (Nintron (N	52369	NM_001114F	9650	Hs.584788NM_014637	ENSG00000003003	CHPFR1	FAM mitochondonprotein-coding	
chr1-2127	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr1	21272775	21273062	+	0	NA	intron (Nintron (N	6697	NM_001111F	1889	Hs.195088NM_001397	ENSG00000003003	ECE	endotheliprotein-coding	
chr1-867	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr1	86733012	86740118	+	0	NA	intron (Nintron (N	31989	NM_016009	51100	Hs.136309NM_016009	ENSG00000003003	BiF-1	CG15H3 domainprotein-coding	
chr10-136	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr10	13656528	13657461	+	0	NA	exon (NM exon (NM	50573	NM_001318F	55691	Hs.330466NM_018027	ENSG00000003003	CAFCFA	FFFERM domprotein-coding	
chr10-271	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr10	27129510	27136576	+	0	NA	intron (NMER5A DNA	21341	NM_01426F	10730	Hs.74647	NM_01426F	ENSG00000003003	FTSH	MEG4YME1 likeprotein-coding
chr10-10C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (Nintron (N	11177	NM_001278F	1147	Hs.198999NM_001278	ENSG00000003003	IKBKA	IKK componentprotein-coding	
chr11-12E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	12881940	12884970	+	0	NA	intron (NMIR SINE	106093	NR_038904F	1.01E+08	Hs.153406NR_038904	ENSG00000003003	BLACAT2	long intencRNA	
chr11-467	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	46702496	46706247	+	0	NA	exon (NM exon (NM	3340	NM_001184F	79797	Hs.656931NM_024741	ENSG00000003003	EVR6	RP72 zinc fingprotein-coding	
chr11-47E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	47242367	47242950	+	0	NA	exon (NM exon (NM	47242367	NM_001251F	10062	Hs.438866NM_005699	ENSG00000003003	LXR-a	LXR nuclear rprotein-coding	
chr11-47E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	47232594	47631889	+	0	NA	intron (NAluJr SIN	14818	NM_014342F	23788	Hs.269944NM_014342	ENSG00000003003	HSPC032	Nmitochonprotein-coding	
chr11-59C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	59635780	59644768	+	0	NA	intron (NAluSq2 SI	24500	NM_00255F	5007	Hs.597091NM_00255F	ENSG00000003003	OSBP1	oxysterolprotein-coding	
chr11-85E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	85978670	85983110	+	0	NA	intron (NMIR SINE	88194	NM_00716F	8301	Hs.163899NM_00716F	ENSG00000003003	CALM	CLTF phosphatiprotein-coding	
chr11-111	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr11	1.12E+08	1.12E+08	+	0	NA	intron (Nintron (N	19455	NM_00125F	143903	Hs.503831NM_178834	ENSG00000003003	LAYLN	layilin protein-coding	
chr12-80E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr12	8094512	8096617	+	0	NA	intron (Nintron (N	13290	NM_01550F	25977	Hs.555927NM_01550F	ENSG00000003003	EIEE21	NECAP encrprotein-coding	
chr12-12C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr12	1.21E+08	1.21E+08	+	0	NA	intron (NAluSp SIN	21223	NM_00133C	9921	Hs.442798NM_01486F	ENSG00000003003	RIE2	ring fingprotein-coding	
chr12-13C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr12	1.33E+08	1.33E+08	+	0	NA	intron (NLTR13 LTF	19486	NM_00589F	2802	Hs.507333NM_00589F	ENSG00000003003	GCP170	ME golgin A3protein-coding	
chr13-37E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr13	37205053	37026585	+	0	NA	intron (Nintron (N	22758	NM_18150C	11340	Hs.294041NM_18150C	ENSG00000003003	CIP3	EAP2 exosome cprotein-coding	
chr14-311	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr14	31132557	31135142	+	0	NA	intron (Nintron (N	73944	NM_01538F	25831	Hs.708017NM_01538F	ENSG00000003003	EULLR	HECT domprotein-coding	
chr14-67E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr14	67343096	67353402	+	0	NA	intron (NAluSp SIN	11555	NM_015994F	51382	Hs.272633NM_015994	ENSG00000003003	ATP6M	VATATPase H+protein-coding	
chr14-757	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr14	75783344	75784236	+	0	NA	intron (NL2c LINE	122544	NM_01507F	23093	Hs.709609NM_01507F	ENSG00000003003	CORD19	K1 tubulin rprotein-coding	
chr14-96E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr14	96289591	96290764	+	0	NA	intron (Nintron (N	33967	NM_00071C	623	Hs.525572NM_00071C	ENSG00000003003	B1BRK	B1F bradykiniprotein-coding	
chr15-297	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr15	29758818	29762064	+	0	NA	intron (NAluSz6 SI	60233	NM_00135F	7082	Hs.743999NM_003257	ENSG00000003003	ZO-1	tight jurprotein-coding	
chr15-41C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr15	41076136	41087562	+	0	NA	intron (Nintron (N	34397	NR_10403F	54617	Hs.292949NM_01755F	ENSG00000003003	IN080A	IN IN080 conprotein-coding	
chr15-454	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr15	45410539	45412356	+	0	NA	intron (NAluJo SIN	9111	NR_13664F	79029	Hs.369657NM_02406F	ENSG00000003003	SPATASL1	- spermatocprotein-coding	
chr15-78C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr15	78015446	78016957	+	0	NA	intron (Nintron (N	-21976	NR_02699F	91450	Hs.406766NR_02699F	LOC91450	-	uncharactncRNA	
chr16-21C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr16	21965927	21974077	+	0	NA	intron (Nintron (N	18441	NM_00336F	7385	Hs.528806NM_00336F	ENSG00000003003	UQCRC2	MC3DN5 QC ubiquinolprotein-coding	
chr16-66E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr16	66938205	66939615	+	0	NA	intron (NL2b LINE	3394	NM_00136F	8824	Hs.282977NM_00386F	ENSG00000003003	CES2	CE-2 CES2 carboxylprotein-coding	
chr17-81E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr17	815877	820099	+	0	NA	intron (NAluSz6 SI	35635	NM_01814F	55178	Hs.182722NM_01814F	ENSG00000003003	MRM3	RMTL1 RNW mitochonprotein-coding	
chr17-29E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr17	29542546	29544377	+	0	NA	3' UTR (N3' UTR (N	23576	NM_198147F	116236	Hs.106511NM_198147	ENSG00000003003	ABHD15	- abhydrolprotein-coding	
chr17-47E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr17	47052346	47054544	+	0	NA	IntergeniIntergeni	-74192	NM_20340C	388394	Hs.367999NM_20340C	ENSG00000003003	CRPML	- reprimolprotein-coding	
chr2-325E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr2	32500288	32503713	+	0	NA	intron (Nintron (N	63153	NR_03028F	693143	Hs. NR_03028F	ENSG00000003003	MIR558	tmicroRNA ncRNA	
chr2-170E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	3' UTR (N3' UTR (N	30695	NM_01553C	26003	Hs.431317NM_01553C	ENSG00000003003	GORASP2	GOLPH6 Golgigr protein-coding	
chr2-2061	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr2	2.06E+08	2.06E+08	+	0	NA	intron (NAluSx SIN	16760	NM_00119F	4719	Hs.471207NM_00500F	ENSG00000003003	CNDUFS1	CI-75kD NADH:ubiquinoneprotein-coding	
chr20-38C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr20	38065917	38072634	+	0	NA	intron (Nintron (N	35529	NM_00121F	58490	Hs.278833NM_002121F	ENSG00000003003	RPRD1B	C20orf177 regulatoriprotein-coding	
chr22-20C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr22	20085808	20102567	+	0	NA	intron (Nintron (N	8129	NR_03170F	1E+08	NR_03170F	ENSG00000003003	MIR1306	microRNA ncRNA	
chr3-484	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr3	48441624	48444253	+	0	NA	intron (NMIR SINE	2681	NM_00132F	51372	Hs.356444NM_01593F	ENSG00000003003	TMA7	CCDC72 HS translatiiprotein-coding	
chr3-581C	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr3	58100659	58103115	+	0	NA	intron (Nintron (N	68748	NR_135534F	1.05E+08	Hs.613914NR_135534	ENSG00000003003	FLNB-AS1	- FLNB antncRNA	
chr3-170I	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (NL2a LINE	19216	NM_024947F	80012	Hs.529592NM_024947	ENSG00000003003	PHC3	EDR3 HPH2 polymorphprotein-coding	
chr3-179E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (Nintron (N	6078	NM_03354C	55669	Hs.478383NM_017927	ENSG00000003003	MFN1	hfz01 hfzmitofusirprotein-coding	
chr4-886E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr4	88680665	88681632	+	0	NA	intron (Nintron (N	16681	NM_15375F	266812	Hs.12554	NM_15375F	ENSG00000003003	NAP1L5	DRLM nucleosonprotein-coding
chr4-140E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr4	1.41E+08	1.41E+08	+	0	NA	intron (NL2a LINE	20714	NM_15370F	255520	Hs.45010E	NM_15370F	ENSG00000003003	ELMOD2	9830169G ELMO domprotein-coding
chr5-407E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr5	40769569	40772711	+	0	NA	intron (Nintron (N	-15179	NM_01238F	23548	Hs.34891E	NM_01238F	ENSG00000003003	TTC33	OSRF tetrairicprotein-coding
chr5-7007	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr5	70077387	70080345	+	0	NA	IntergeniAluSx SIN	29343	NM_001297F	6606	Hs.535788NM_000344	ENSG00000003003	SMN1	BCD541 GE survival protein-coding	
chr5-140E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr5	1.41E+08	1.41E+08	+	0	NA	intron (Nintron (N	-40837	NM_00373F	8637	Hs.594084NM_00373F	ENSG00000003003	E1F4EBP3	4E-BP3 4E eukaryotiprotein-coding	
chr6-3377	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr6	33773739	33780973	+	0	NA	intron (Nintron (N	9586	NM_001143F	221496	Hs.44484E	NM_18133F	ENSG00000003003	LEMD2	CTRCT42 ILEM domaiiprotein-coding
chr6-535E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr6	53503084	53511038	+	0	NA	intron (Nintron (N	38040	NM_00149F	2729	Hs.65446E	NM_00149F	ENSG00000003003	GCLC	GCL GCS glutamateprotein-coding
chr7-147E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr7	1.42E+08	1.42E+08	+	0	NA	intron (Nintron (N	5709	NM_00125F	6742	Hs.490394NM_00314F	ENSG00000003003	SSBP1	Mt-SSB SC single stprotein-coding	
chr9-113E	8.896513	0.0438	0.777225	0.056354	0.955059	0.981636	chr9	1.13E+08	1.13E+08	+	0	NA	intron (NL2c LINE	4551	NR_13626F	9128	Hs.744014NM_004697	ENSG00000003003	PRPF4	HSPR4 HPF pre-mRNA protein-coding	



chr21-466	9.375535	0.042429	0.759858	0.055838	0.95547	0.981636	chr21	46647186	46649585	+	0	NA	intron (intron (	12711	NM_206962	3275	Hs.154162	NM_001535	ENSG00000CPRMT2	HRMT1L1	protein	ε	protein-coding	
chr3-4941	9.375535	0.042429	0.759858	0.055838	0.95547	0.981636	chr3	49414689	49415771	+	0	NA	3' UTR (3' UTR (	3024	NM_022171	6988	Hs.517962	NM_022171	ENSG00000TCTA	-	T cell	le	protein-coding	
chr4-2941	9.375535	0.042429	0.759858	0.055838	0.95547	0.981636	chr4	2941606	2941864	+	0	NA	intron (intron (	6189	NR_015453	317648	Hs.398176	NR_015453	ENSG00000NOP14-AS1	C4orf10 FNOP14	antncRNA			
chr5-1347	9.375535	0.042429	0.759858	0.055838	0.95547	0.981636	chr5	135E+08	135E+08	+	0	NA	intron (AluSx S	32282	NM_014822	9879	Hs.406549	NM_014822	ENSG00000DDX46	PRPF5 Prp	DEAD-box	protein-coding		
chr1-1747	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr1	74740018	74741578	+	0	NA	intron (LTR12 L T	-7390	NM_001113C	1429	Hs.83114	NM_001113C	ENSG00000CRYZ	-	crystallin	protein-coding		
chr1-888	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr1	88855457	88860225	+	0	NA	intron (AluSx S	33726	NM_001514	2959	Hs.481852	NM_001514	ENSG00000GTF2B	TF2B TFII	general t	protein-coding		
chr1-108	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr1	109E+08	109E+08	+	0	NA	3' UTR (3' UTR (	17212	NM_001278	23155	Hs.658489	NM_015127	ENSG00000CLCC1	MCLC	chloride	protein-coding		
chr1-155	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr1	156E+08	156E+08	+	0	NA	intron (AluSx S	9634	NM_032292	54856	Hs.656361	NM_032292	ENSG00000GON4L	GON-4 GON	GON-4	lik	protein-coding	
chr1-207	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr1	2.07E+08	2.07E+08	+	0	NA	intron (AluJr S	18708	NR_12534E	1604	Hs.126517	NM_000574	ENSG00000CD55	CHAPLE CFCD55	molε	protein-coding		
chr10-69	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr10	69368389	69370329	+	0	NA	intron (intron (	8777	NM_001057	6865	Hs.88372	NM_001057	ENSG00000TACR2	NK2R NKN	tachykinin	protein-coding		
chr12-19	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr12	19353396	19356885	+	0	NA	intron (intron (	-84352	NM_001114	121536	Hs.126497	NM_153207	ENSG00000AEBP2	-	AE bindir	protein-coding		
chr13-98	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr13	98447277	98449484	+	0	NA	3' UTR (3' UTR (	73745	NM_00357E	8428	Hs.508514	NM_00357E	ENSG00000STK24	HEL-S-95	serine/tl	protein-coding		
chr13-11	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (intron (	5036	NM_00132C	22821	Hs.59307E	NM_00736E	ENSG00000RASA3	GAP1 P4BF	RAS p21	protein-coding		
chr14-58	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr14	58250298	58256143	+	0	NA	intron (AluSx S	8377	NM_00278E	5684	Hs.558799	NM_00278E	ENSG00000PSMA3	H8 P3C3	proteasom	protein-coding		
chr15-48	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr15	48415557	48418075	+	0	NA	intron (intron (	84619	NM_00194E	1854	Hs.52798C	NM_00194E	ENSG00000CDUT	dUTPase	deoxyuric	protein-coding		
chr15-64	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr15	64406014	64408661	+	0	NA	intron (intron (	19501	NM_001321	9325	Hs.50034C	NM_01621E	ENSG00000TRIP4	ASC-1 ASC	thyroid l	protein-coding		
chr15-80	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr15	80753485	80755593	+	0	NA	3' UTR (3' UTR (	-24831	NM_00129E	57214	Hs.45908E	NM_01868E	ENSG00000CCMIP4	CCM1 HVE	cell m	protein-coding		
chr16-17	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr16	1734497	1735144	+	0	NA	promoter-promoter-	-165	NR_03613E	1E+08	NR_03613E	ENSG00000MIR3177	miR-3177	microRNA	ncRNA			
chr16-45	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr16	4506943	4510493	+	0	NA	intron (intron (	12860	NM_001127	3163	Hs.28427E	NM_002134	ENSG00000HMOX2	HO-2	heme oxyg	protein-coding		
chr16-88	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr16	8831109	8832676	+	0	NA	intron (intron (	-17577	NR_14790E	1E+08	Hs.73551E	NR_14790E	LOC10013C-	-	uncharact	ncRNA		
chr16-281	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr16	28164968	28167987	+	0	NA	intron (intron (	45488	NM_015171	23214	Hs.46046E	NM_015171	ENSG00000XP06	EXP6 RAF	exportin	protein-coding		
chr17-31	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr17	31351499	31354636	+	0	NA	intron (AluSx S	-31445	NM_00100C	2123	Hs.59119E	NM_01421C	ENSG00000EV12A	EVDA EVL	ecotropic	protein-coding		
chr17-76	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr17	60446588	60454402	+	0	NA	intron (AluJb S	28006	NM_181707	124773	Hs.129312	NM_181707	ENSG00000C17orf64	-	chromosom	protein-coding		
chr17-60	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr17	76038593	76055776	+	0	NA	intron (AluJb S	6472	NM_00126C	6730	Hs.51449E	NM_01423C	ENSG00000SRP68	-	signal r	protein-coding		
chr18-20	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr18	20978723	20982605	+	0	NA	intron (AluS8 S	131149	NM_00540E	6093	Hs.306307	NM_00540E	ENSG00000ROCK1	P160ROCK	Rho assoc	protein-coding		
chr19-10	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr19	10558967	10560462	+	0	NA	intron (intron (	6296	NM_02300E	6595	Hs.709967	NM_02300E	ENSG00000KR11	-	KR11	homc	protein-coding	
chr19-16	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr19	16650599	16655138	+	0	NA	exon (NM exon (	7276	NM_00130C	79086	Hs.356467	NM_024104	ENSG00000SMI17	C19orf42	small intr	protein-coding		
chr20-38	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr20	3873709	3874424	+	0	NA	non-codir-non-codir	-14715	NM_02496C	80025	Hs.11418C	NM_02496C	ENSG00000PANK2	C20orf48	pantho	protein-coding		
chr21-37	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr21	37142023	37146089	+	0	NA	intron (LIPA5 L	50735	NR_046651	01E+08	Hs.570411	NR_046651	ENSG00000TTC3-AS1	-	TTTC3	antncRNA		
chr22-20	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr22	20044600	20049717	+	0	NA	intron (AluSq2 S	15019	NR_02970E	406961	NR_02970E	ENSG00000MIR185	MIRN185	mi	ncRNA			
chr22-20	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr22	20573977	20579468	+	0	NA	intron (intron (	68675	NM_00129E	51586	Hs.517421	NM_01588E	ENSG00000MED15	ARC105 C	mediator	protein-coding		
chr3-566	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr3	56666906	56672363	+	0	NA	intron (intron (	-5588	NM_015224	23272	Hs.116877	NM_015224	ENSG00000TASOR	C3orf63 F	transcrip	protein-coding		
chr3-940	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr3	94044014	94045113	+	0	NA	intron (SVA_A Ret	-15966	NM_001001	415117	Hs.67976E	NM_001001	ENSG00000STX19	-	syntxin	protein-coding		
chr3-122	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr3	1.22E+08	1.22E+08	+	0	NA	intron (intron (	24830	NR_12540E	1.03E+08	Hs.67505E	NR_12540E	ENSG00000LOC10272E	-	uncharact	ncRNA		
chr3-154	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr3	1.54E+08	1.54E+08	+	0	NA	intron (intron (	35212	NM_02086E	170506	Hs.44627C	NM_02086E	ENSG00000DHX36	DDX36 G4F	DEAH-box	protein-coding		
chr3-183	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (intron (	1190	NR_046727	1.01E+08	NR_046727	YEATS2-AS-	-	YEATS2	antncRNA			
chr5-276	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr5	276514	278122	+	0	NA	TTS (NR_C TTS (NR_C	5672	NM_001267	10016	Hs.50823	NM_01323E	ENSG00000PCDC6	ALG-2 ALC	programme	protein-coding		
chr5-173	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr5	1.73E+08	1.73E+08	+	0	NA	intron (THE1B L T	4668	NM_01398C	662	Hs.14572E	NM_00120E	ENSG00000BNP17	NIP1 SEC2	ECL2	intc	protein-coding	
chr6-155	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr6	1.55E+08	1.55E+08	+	0	NA	exon (NM exon (	17428	NM_01602C	51106	Hs.27990E	NM_01602C	ENSG00000TFB1M	CGI-75 C	transcrip	protein-coding		
chr7-571	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr7	5718781	5723461	+	0	NA	exon (NM exon (	-9211	NR_106934	1.02E+08	NR_106934	ENSG00000MIR6874	hsa-mir-	ε	microRNA	ncRNA		
chr7-358	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr7	35885825	35887498	+	0	NA	intron (intron (	85442	NM_00136E	989	Hs.19134E	NM_00178E	ENSG00000SEPTIN7	CDCl0 CDC	septin 7	protein-coding		
chr7-102	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr7	102E+08	1.02E+08	+	0	NA	TTS (NM_C TTS (NM_C	1606	NR_039677	1.01E+08	NR_039677	ENSG00000MIR4467	-	microRNA	ncRNA			
chr7-105	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	intron (AluSg7 S	20580	NM_02193C	60561	Hs.53138E	NM_02193C	ENSG00000CRINT1	RINT-1	RAD50	intr	protein-coding	
chr8-739	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr8	73957215	73959914	+	0	NA	intron (intron (	13344	NM_001204	6921	Hs.533437	NM_00564E	ENSG00000ELOC	SIII TCFE	elongin C	protein-coding		
chr8-140	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (AluJb S	59395	NR_04071E	54108	Hs.279704	NM_017444	ENSG00000CHRAC1	CHARC1 C	chromatin	protein-coding		
chr8-140	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr8	1.41E+08	1.41E+08	+	0	NA	intron (AluSc S	-28416	NM_012154	27161	Hs.66018E	NM_012154	ENSG00000AG02	C8orf67 EIF	chromat	protein-coding		
chr9-111	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (LTR16A L	-60672	NM_20585E	26248	Hs.38131E	NM_20585E	ENSG00000OR2K2	HSHTPCRH C	olactory	protein-coding		
chr9-136	8.152648	-0.04509	0.810107	-0.05566	0.955611	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (intron (	10761	NM_00308E	6621	Hs.11326E	NM_00308E						



chr2-1087	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	1.09E+08	1.09E+08	+	0	NA	intron (AluSc8 SI	21945	NM_006267	5903	Hs.199561NM_006267	ENSG0000CRANBP2	ADANE ANFRAN	bindiprotein-coding	
chr2-1311	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	35483	NM_001305	55041	Hs.469944NM_017958	ENSG00000PLEKH2	EV22	pleckstriprotein-coding	
chr2-171	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	intron (NL2a LINE	52606	NM_001136	9874	Hs.744917NM_012290	ENSG00000CTLKI	PKU-beta	tousled lprotein-coding	
chr2-1908	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (NTigger16t	17152	NM_014905	2744	Hs.116448NM_014905	ENSG00000GLS	AAD20 CAS	glutamine protein-coding	
chr2-2236	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	2.24E+08	2.24E+08	+	0	NA	intron (Nintron (N	50915	NM_020803	57590	Hs.368355NM_020803	ENSG00000WDFY1	FENS-1 FEWD	repeatprotein-coding	
chr2-2312	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	2.31E+08	2.31E+08	+	0	NA	intron (AluSp SIN	65888	NM_001352	80210	Hs.162411NM_025135	ENSG00000CARMC9	ARM JBTS	armadillcprotein-coding	
chr2-2328	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	2.33E+08	2.33E+08	+	0	NA	intron (AluSc8 SI	35723	NM_001346	389084	Hs.657509NM_020689	ENSG00000SNORC	ASCL830 C	secondaryprotein-coding	
chr2-2335	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr2	2.34E+08	2.34E+08	+	0	NA	intron (NLIP3 LIN	3331	NM_018218	55230	Hs.96513	NM_018218	ENSG00000CUSP40	-	ubiquitinprotein-coding
chr20-365	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr20	36506893	36508728	+	0	NA	non-codirnon-codir	33709	NM_181525	10398	Hs.504687NM_006097	ENSG00000MYL9	LC20 MLC	myosin lprotein-coding	
chr21-366	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr21	36358200	36373502	+	0	NA	intron (AluSq2 SI	19541	NM_005441	8208	Hs.75238	NM_005441	ENSG00000CHAF1B	CAC-1 CAF	chromatirprotein-coding
chr22-298	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr22	29801524	29810619	+	0	NA	intron (Nintron (N	32203	NM_001365	84164	Hs.731754NM_032204	ENSG00000ASCC2	ASC1p100	activatirprotein-coding	
chr22-314	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr22	31408453	31417004	+	0	NA	intron (AluJb SIN	13124	NM_004147	4733	Hs.115242NM_004147	ENSG00000DRG1	NEDD3	developme protein-coding	
chr22-457	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr22	45720187	45720927	+	0	NA	intron (NLIMB2 LIN	39967	NR_039915	1.01E+08	NR_039915	ENSG00000MIR4762	-	microRNA ncRNA	
chr3-5205	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	52059553	52094003	+	0	NA	intron (AluXs1 SI	19971	NM_014674	9695	Hs.224616NM_014674	ENSG00000EDEM1	EDEM	IR degradprotein-coding	
chr3-3067	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	30671026	30671631	+	0	NA	intron (NL2c LINE	64727	NM_003242	7048	Hs.82028	NM_003242	ENSG00000TGFB2	AAT3 FAA	transonprotein-coding
chr3-3313	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	33132261	33135384	+	0	NA	intron (Nintron (N	19864	NM_006371	10491	Hs.517888NM_006371	ENSG00000CRTAP	CASP LEFP	cartilageprotein-coding	
chr3-5265	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	52632602	52634510	+	0	NA	intron (NLIMB3 LIN	52043	NM_001350	55193	Hs.189922NM_018165	ENSG00000PBRM1	BAF180 PE	polybromprotein-coding	
chr3-5265	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	52638168	52645412	+	0	NA	intron (Nintron (N	43809	NM_001350	55193	Hs.189922NM_018165	ENSG00000PBRM1	BAF180 PE	polybromprotein-coding	
chr3-5547	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	55475481	55481045	+	0	NA	intron (Nintron (N	3135	NM_001255	7474	Hs.643088NM_003392	ENSG00000WNT5A	hWNT5A	Wnt famillprotein-coding	
chr3-1327	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	19538	NR_002281	348808	Hs.586111NR_002811	ENSG00000NPHP3-AS1	INCRA001 NPHP3	antncRNA	
chr3-179	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	1.79E+08	1.79E+08	+	0	NA	intron (NHERV17-ir	12939	NM_152242	64393	Hs.371609NM_022470	ENSG00000ZMAT3	PAG608 W	zinc fing protein-coding	
chr3-1978	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr3	1.98E+08	1.98E+08	+	0	NA	exon (NM exon (NM	44552	NM_001365	84859	Hs.518414NM_032775	ENSG00000LRCH3	-	leucine rprotein-coding	
chr4-5821	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr4	5821415	5822124	+	0	NA	exon (NM exon (NM	66044	NM_001288	1400	Hs.135272NM_001315	ENSG00000CRMP1	CRMP-1 DF	collapsirprotein-coding	
chr4-7765	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr4	7765957	7767235	+	0	NA	intron (Nintron (N	12506	NR_026892	84740	Hs.663025NM_032654	ENSG00000AFAP1-AS1	AFAP1-AS AFAP1	antncRNA	
chr4-3985	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr4	39854377	39863008	+	0	NA	intron (AluSq2 SI	119219	NM_001100	23244	Hs.331431NM_015200	ENSG00000PDS5A	PIG54 SCD	PDS5 coheprotein-coding	
chr4-7578	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr4	75781980	75783534	+	0	NA	exon (NM exon (NM	58235	NM_001290	8615	Hs.744877NM_003715	ENSG00000USO1	P15 TAP USO1	vesiprotein-coding	
chr4-1218	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	11131	NM_176824	55212	Hs.591694NM_018190	ENSG00000BBS7	BBS2L1 Bardet-B	Bioprotein-coding	
chr5-1395	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr5	13924460	13925053	+	0	NA	intron (NMIR SINE	19724	NM_001365	1767	Hs.212360NM_001365	ENSG00000DNAH5	CILD3 DN	dynein asprotein-coding	
chr5-4355	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr5	43551586	43553501	+	0	NA	intron (Nintron (N	4534	NM_006451	10605	Hs.482035NM_006451	ENSG00000PAIP1	-	poly (A) tprotein-coding	
chr5-1246	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr5	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	104340	NM_020747	57507	Hs.266616NM_020747	ENSG00000ZNF608	NY-REN-3	zinc fingprotein-coding	
chr5-1297	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	26724	NM_001257	1E+08	Hs.582534NM_001257	ENSG00000CMINAR2	KIAA1024	membrane protein-coding	
chr5-1347	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (AluSq2 SI	13437	NM_014822	9879	Hs.406545NM_014822	ENSG00000DDX46	PRPF5 Pr	DEAD-box protein-coding	
chr5-1678	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr5	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N	21173	NM_001355	345630	Hs.166262NM_001355	ENSG00000FBLL1	-	fibrillarprotein-coding	
chr6-3172	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	31726374	31727492	+	0	NA	TTS (NM_C	2366	NM_001303	23564	Hs.247362NM_013974	ENSG00000DDAH2	DDAH DDA	dimethylprotein-coding	
chr6-4264	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	42648997	42651114	+	0	NA	intron (Nintron (N	72542	NM_000322	5961	Hs.654488NM_000322	ENSG00000PRPH2	AOFMD AV	peripheriprotein-coding	
chr6-5308	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	53085396	53089428	+	0	NA	intron (NMER101-ir	16439	NM_012347	26268	Hs.216655NM_012347	ENSG00000FBX09	FBX9 NY-F	F-box prcprotein-coding	
chr6-7348	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	73485819	73491006	+	0	NA	intron (AluJr SIN	26675	NM_001123	25821	Hs.347614NM_012125	ENSG00000MTO1	CGI-02 C	mitochoncprotein-coding	
chr6-752	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	75262280	75266291	+	0	NA	intron (Nintron (N	13987	NM_001865	1347	Hs.70312	NM_001865	ENSG00000COX7A2	COX7AL C	cytochronprotein-coding
chr6-147	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	1.47E+08	1.47E+08	+	0	NA	intron (Nintron (N	111318	NR_034115	729178	Hs.557608NR_034115	STXBP5-AS-	STXBP5	AS-5 antncRNA	
chr6-1505	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr6	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	39405	NM_001350	25902	Hs.591342NM_015440	ENSG00000MTHFD1L	FTHFSDC1	methylene protein-coding	
chr7-989	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr7	98936515	98942266	+	0	NA	intron (Nintron (N	57693	NR_132754	1.07E+08	NR_132754	SCARNA28	ZLI	small Ca ncRNA	
chr8-8167	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr8	81678343	81678900	+	0	NA	intron (AluSq2 SI	7704	NM_005536	3612	Hs.656694NM_005536	ENSG00000LMPA1	IMP IMPA	inositol protein-coding	
chr9-363	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr9	36338961	36341604	+	0	NA	intron (Nintron (N	59987	NM_194325	152006	Hs.333505NM_022781	ENSG00000CRNF38	-	ring fingprotein-coding	
chr9-920	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr9	92033211	92034553	+	0	NA	intron (Nintron (N	81531	NM_006415	10558	Hs.90458	NM_006415	ENSG00000SPTLC1	HSAN1 HS	serine pprotein-coding
chr9-111	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (Nintron (N	54591	NM_205855	26248	Hs.381312NM_205855	ENSG00000OR2K2	HSHTPCRHC	olfactoryprotein-coding	
chr9-120	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr9	20930	NM_005047	5711	Hs.193725NM_005047	ENSG00000PSMD5	S5B	proteasonprotein-coding							
chr9-124	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chr9	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	12106	NM_002077	2800	Hs.59504	NM_002077	ENSG00000GOLGA1	golgin-97	golgin Alprotein-coding
chrX-457	7.418306	0.046756	0.84522	0.055318	0.955885	0.981636	chrX	45756702	45758220	+	0	NA	Intergen LIME1 LIN	10337	NR_029636	407007	NR_029636	ENSG00000MIR222	MIRN222	microRNA ncRNA	
chr17-305	8.10365	-0.04563	0.825451	-0.05528	0.955914	0.981636	chr17	30500682	30502044	+	0	NA	intron (NLIMC2 LIN	23955	NM_001007	9527	Hs.462688NM_004871	ENSG00000GOSR1	GOLIM2 G	golgi SN/ protein-coding	
chr18-955	8.10365	-0.04563	0.825451	-0.05528	0.955914	0.981636	chr18	9593532	9594078	+	0	NA	exon (NM exon (NM	20754	NR_052003	9989	Hs.743233NM_005134	ENSG00000PPP4R1	MEG1 PP4	(protein tprotein-coding	
chr12-928	9.8545																				



chr3-143c	8.639528	-0.04319	0.791366	-0.05457	0.956478	0.981636	chr3	1.43E+08	1.43E+08	+	0 NA	intron (Nintron (N	21572 NM_00132C	23350 Hs. 596572NM_00108C	ENSG000002SURP	SR140 fSUA2 snRNP	protein-coding	
chr7-538c	8.639528	-0.04319	0.791366	-0.05457	0.956478	0.981636	chr7	5386489	5389698	+	0 NA	exon (NM_exon (NM	35453 NM_00108C	84629 Hs. 520638NM_00101C	ENSG000002NR18	CAGL79 TN trinuclec	protein-coding	
chr7-988c	8.639528	-0.04319	0.791366	-0.05457	0.956478	0.981636	chr7	98896089	98899086	+	0 NA	intron (Nintron (N	15890 NR_132754	1.07E+08	NR_132754	SCARNA28	ZL1	small Ca_ncrNA
chr8-131c	8.639528	-0.04319	0.791366	-0.05457	0.956478	0.981636	chr8	13130651	13132071	+	0 NA	intron (Nintron (N	1928 NM_006094	10395 Hs. 134299NM_006094	ENSG000002DL1C	ARHGAP7 F DL1C	Rho protein-coding	
chr1-258c	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr1	25899968	25901824	+	0 NA	3' UTR (N3' UTR (N	5257 NM_203401	3925 Hs. 209983NM_005563	ENSG000002STM1	Clorf215 stathmin	protein-coding	
chr1-1137	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr1	1.14E+08	1.14E+08	+	0 NA	intron (N LIM1 LINE	38982 NM_006608	10745 Hs. 655824NM_006608	ENSG000002PHTF1	PHTF	putative protein-coding	
chr1-1801	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr1	1.8E+08	1.8E+08	+	0 NA	intron (N Alu Jr SIN	7727 NM_00282E	5768 Hs. 719177NM_00282E	ENSG000002QX01	Q6 QSCN6	quiescin protein-coding	
chr10-305	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr10	30339086	30340960	+	0 NA	intron (Nintron (N	9315 NM_018105	55149 Hs. 173949NM_018105	ENSG000002MTAP	PAPD1 SP miTohcn	protein-coding	
chr10-431	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr10	43182024	43185525	+	0 NA	non-codirnon-codir	28877 NM_00131E	55454 Hs. 657569NM_01859C	ENSG000002CSGALNAC1	CHGN2 ChC	chondroitin protein-coding	
chr10-105	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr10	1.03E+08	1.03E+08	+	0 NA	intron (N THE1B-int	19224 NM_001351	22978 Hs. 97439 NM_01222E	ENSG000002NT5C2	GMP NT5B 5'	nuclec protein-coding	
chr11-115	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr11	11934119	11935017	+	0 NA	intron (N L2a LINE	74071 NM_00101E	27122 Hs. 92475NM_01325E	ENSG000002DKK3	REIC RT5B	dickopf protein-coding	
chr11-777	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr11	77724883	77725437	+	0 NA	intron (N LIMB3 LIN	-87354 NM_001311	1207 Hs. 430733NM_00129E	ENSG000002CLNS1A	CLCI CLNS	chloride protein-coding	
chr12-51C	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr12	51069995	51074181	+	0 NA	intron (Nintron (N	11526 NR_04507E	81566 Hs. 524422NM_03080E	ENSG000002CSRNP2	C12orf2 Cysteine	protein-coding	
chr13-45E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr13	45518997	45521020	+	0 NA	intron (N MERGB DNA	54684 NR_031431	83548 Hs. 507945NM_031431	ENSG000002COG3	SEC3A	component protein-coding	
chr14-31C	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr14	31021632	31022996	+	0 NA	intron (N AluY SINE	-2792 NM_001254	11154 Hs. 293411NM_007077	ENSG000002AP4S1	AP47B CL adaptor	protein-coding	
chr14-501	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr14	50131991	50133629	+	0 NA	intron (N HSMAR2 DN	-16238 NR_04973E	79609 Hs. 558541NM_02455E	ENSG000002VCPKMT	C14orf138 valosin	protein-coding	
chr14-55E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr14	55629695	55630474	+	0 NA	exon (NM_exon (NM	49877 NM_00107E	3895 Hs. 509414NM_00498E	ENSG000002CKTN1	CG1 KNT kinectin	protein-coding	
chr15-494	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr15	49442638	49444591	+	0 NA	intron (N MER63C DN	20372 NM_00200E	2252 Hs. 567268NM_00200E	ENSG000002PGF7	HBGF-7 KC	fibroblas protein-coding	
chr15-717	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr15	71764702	71765732	+	0 NA	intron (Nintron (N	-45337 NM_01634E	10002 Hs. 187354NM_01424E	ENSG000002NR2E3	ESCS PNR nuclear	protein-coding	
chr15-84E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr15	84639099	84642378	+	0 NA	TTS (NR_TTS (NR_1	9278 NR_00485E	54581 Hs. 658114NM_022050	SCAND2P	SCAND2	SCAN dom_e pseudo	
chr16-35E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr16	3523317	3523863	+	0 NA	intron (N MER45A DN	4208695 NM_02479E	23059 Hs. 155999NM_015041	ENSG000002CLUAP1	CFAP22 P clusterin	protein-coding	
chr16-44E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr16	4455936	4457405	+	0 NA	3' UTR (N3' UTR (N	17955 NM_001351	57407 Hs. 288966NM_020677	ENSG000002NMRAL1	HSCARG S NmA	like protein-coding	
chr16-317	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr16	31731386	31731901	+	0 NA	intron (N LIMA9 LIN	18459 NM_00113E	124411 Hs. 528822NM_001004	ENSG000002ZNF720	-	zinc fing protein-coding	
chr17-42C	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr17	4208695	4209907	+	0 NA	intron (Nintron (N	54546 NM_001257	51479 Hs. 696087NM_01637E	ENSG000002ANKFY1	ANKHZN BT ankyrin	protein-coding	
chr17-31E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr17	31358379	31359242	+	0 NA	intron (Nintron (N	-32865 NM_03293E	84440 Hs. 406788NM_03293E	ENSG000002RAB11FIP4	FIP4-Rab1RAB11	fan protein-coding	
chr17-31E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr17	31360478	31362533	+	0 NA	intron (Nintron (N	-30170 NM_03293E	84440 Hs. 406788NM_03293E	ENSG000002RAB11FIP4	FIP4-Rab1RAB11	fan protein-coding	
chr17-35E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr17	35622504	35625650	+	0 NA	intron (N (ATGTCAT)	36755 NM_00103C	163 Hs. 514815NM_00128E	ENSG000002AP2B1	ADTB2 AP1	adaptor protein-coding	
chr17-394	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr17	39428199	39428645	+	0 NA	intron (N AluSc8 SI	22841 NM_004774	5469 Hs. 643754NM_004774	ENSG000002MED1	CRSP1 CRS	mediator protein-coding	
chr18-41E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr18	41957691	41959734	+	0 NA	intron (N (TA)n Sin	3478 NM_00264E	5289 Hs. 464971NM_00264E	ENSG000002PIK3C3	VPS34 Vps	phosphatid protein-coding	
chr19-15E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr19	15355900	15359486	+	0 NA	intron (Nintron (N	22094 NM_00585E	10270 Hs. 594499NM_00585E	ENSG000002AKAP8	AKAP	95 A-kinase	protein-coding
chr19-471	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr19	47154800	47156467	+	0 NA	intron (N AluSq2 SI	24798 NM_00114E	10055 Hs. 515500NM_00550C	ENSG000002SAE1	AOS1 HSPC	SUMO1 act protein-coding	
chr2-107E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr2	10796224	10798677	+	0 NA	intron (Nintron (N	15335 NM_00574E	10130 Hs. 212102NM_00574E	ENSG000002PDIA6	ERP5 P5 I	protein-coding	
chr2-8614	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr2	86142635	86151384	+	0 NA	intron (N AluS6 SI	10998 NR_00437E	69225 Hs. 723087NR_00437E	ENSG000002SNORD94	U94	small nucsnRNA	
chr2-1134	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr2	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	25696 NM_00133C	150472 Hs. 531333NM_17200E	ENSG000002CBWD2	-	COBW dom_e protein-coding	
chr20-34E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr20	34392956	34395045	+	0 NA	intron (N AluS6 SI	30727 NM_001324	83737 Hs. 632272NM_03148E	ENSG000002ITCH	ADMPF ATF	itchy E3 protein-coding	
chr20-34E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr20	34504072	34508638	+	0 NA	intron (N LIMB3 LIN	-10029 NM_00131E	83658 Hs. 59392CNM_01418E	ENSG000002DYNLRB1	B1TH BLP dynein	1 protein-coding	
chr20-44E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr20	44972475	44976020	+	0 NA	non-codirnon-codir	7735 NR_147974	6789 Hs. 472838NM_00628E	ENSG000002CTK4	KRS2 MST1	serine/tl protein-coding	
chr20-49C	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr20	49074352	49077679	+	0 NA	intron (N AluSx SIN	29703 NM_00131E	1434 Hs. 90073 NM_00131E	ENSG000002CSE1L	CAS CSE1 chromoson	protein-coding	
chr21-25E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr21	25982295	25982637	+	0 NA	exon (NM_exon (NM	157924 NM_00113E	351 Hs. 43498CNM_000484	ENSG000002APP	AAA ABET amyloid	l protein-coding	
chr22-451	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr22	45173947	45174574	+	0 NA	intron (N AluJb SIN	9589 NM_15364E	10762 Hs. 475103NM_00717E	ENSG000002CNP50	NPAP60 NF	nucleopor protein-coding	
chr3-112E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr3	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	9732 NM_01417E	29083 Hs. 127496NM_01417E	ENSG000002GTPBP8	HSPC135	GTP bind protein-coding	
chr3-1227	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr3	1.23E+08	1.23E+08	+	0 NA	intron (Nintron (N	38941 NM_017554	54625 Hs. 518202NM_017554	ENSG000002PARP14	ARTD8 BAL	poly (ADP- protein-coding	
chr4-676E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr4	67691476	67693044	+	0 NA	intron (N Tiger2 I	8895 NM_018227	55236 Hs. 212774NM_018227	ENSG000002CUBA6	E1-L2 MOF	ubiquitin protein-coding	
chr4-139E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr4	1.4E+08	1.4E+08	+	0 NA	intron (Nintron (N	10550 NM_00130E	80854 Hs. 480792NM_03064E	ENSG000002SETD7	KMT7 SET7	SET domai protein-coding	
chr5-1284	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr5	1.28E+08	1.28E+08	+	0 NA	intron (N L2b LINE	113846 NM_00119E	2201 Hs. 519294NM_00119E	ENSG000002FBN2	CCA DA9 E	fibrillin protein-coding	
chr5-134E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr5	1.35E+08	1.35E+08	+	0 NA	intron (Nintron (N	25648 NM_00103E	51128 Hs. 432984NM_01610E	ENSG000002SAR1B	ANDD CMR1	secretorin protein-coding	
chr5-179E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr5	1.8E+08	1.8E+08	+	0 NA	intron (N Tiger17e	3845 NM_19886E	23061 Hs. 155822NM_01504E	ENSG000002TBC1D9B	GRAMD9B	TBC1 dom_e protein-coding	
chr6-834E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr6	83423535	83425628	+	0 NA	intron (N MER99 DNA	6470 NM_00239E	4199 Hs. 21160 NM_00239E	ENSG000002CME1	HUMDME H	malic enz protein-coding	
chr8-428E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr8	42860588	42861691	+	0 NA	intron (Nintron (N	-17808 NR_19900E	55145 Hs. 7432 NM_01810E	ENSG000002THAP1	HYD2	THAP dom_e protein-coding	
chr9-332E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr9	33293807	33300920	+	0 NA	intron (Nintron (N	6847 NM_147134	4799 Hs. 413074NM_002504	ENSG000002NFX1	NFX2 TEG-	nuclear t protein-coding	
chr9-361E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr9	36197490	36198665	+	0 NA	intron (N AluSx SIN	7156 NM_001184	1211 Hs. 522114NM_00183E	ENSG000002CLTA	LCA	clathrin protein-coding	
chr9-965C	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636	chr9	96508196	96509341	+	0 NA	intron (Nintron (N	58063 NM_001351	8555 Hs. 40582 NM_003671	ENSG000002CDC14B	CDC14B3 C	cell divi protein-coding	
chr9-128E	7.65791	-0.04549	0.834025	-0.05455	0.956501	0.981636												



chr12-108.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr12	1.09E+08	1.09E+08	+	0 NA	intron (Nintron (N	20392 NM_001161	54434 Hs. 199762NM_018984	ENSG00000SSSH1	SSH1L	slingshotprotein-coding	
chr12-111.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr12	1.11E+08	1.11E+08	+	0 NA	intron (Nintron (N	20630 NM_001291	10019 Hs. 506784NM_005477	ENSG00000SH2B3	IDDM20 LN	SH2B2 adaprotein-coding	
chr15-23C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr15	23029382	23032478	+	0 NA	exon (NM_exon (NM	8639 NM_001354	114791 Hs. 533899NM_052902	ENSG00000TUBGCP5	GCP5	tubulin gprotein-coding	
chr16-678.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr16	67942136	67964038	+	0 NA	intron (NAluSx SIN	-8517 NM_000222	3931 Hs. 387233NM_000222	ENSG00000LCAT	-	lecithin-protein-coding	
chr17-821.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr17	821812	8257410	+	0 NA	intron (Nintron (N	40335 NM_001205	64359 Hs. 527989NM_022463	ENSG00000NXN	NRX TRG-4	nucleorecprotein-coding	
chr17-671.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr17	67128084	67128688	+	0 NA	intron (Nintron (N	83832 NM_000727	786 Hs. 147989NM_000727	ENSG00000CACNG1	CACNLG	calcium vprotein-coding	
chr19-124.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr19	1233370	12359115	+	0 NA	exon (NM_exon (NM	3363 NM_152765	250557 Hs. 346577NM_152765	ENSG00000CBARP	BARP C19c	CACN subprotein-coding	
chr19-144.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr19	14407025	14411239	+	0 NA	TTS (NM_TTS (NM_C	10209 NM_005804	10212 Hs. 311606NM_005804	ENSG00000DDX39A	BAT1 BAT1DEXd	box protein-coding	
chr19-413.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr19	41340823	41341657	+	0 NA	intron (NAluSc8 SI	12682 NM_00066C	7040 Hs. 645227NM_00066C	ENSG00000TGFB1	CED DPD1	transformprotein-coding	
chr19-588.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr19	58392858	58394915	+	0 NA	TTS (NR_ITTS (NR_I	522 NR_162103	1.13E+08	NR_162103	MIR10394	-	microRNA ncRNA
chr2-2061.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr2	2.06E+08	2.06E+08	+	0 NA	3' UTR (N3' UTR (N	-4688 NR_033248	1E+08	Hs. 356055NR_033248	GCSHP3	-	glycine cpsudo
chr20-594.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr20	5942416	5944567	+	0 NA	intron (Nintron (N	7042 NM_01593C	51605 Hs. 128791NM_01593C	ENSG00000TRMT6	CGI-09 GC	tRNA met protein-coding	
chr20-94C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr20	9401366	9404311	+	0 NA	intron (NL2b LINE	95038 NM_000933	5332 Hs. 472101NM_000933	ENSG00000PLCBA	ARCN2D PI	phospholiprotein-coding	
chr20-478.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr20	47248021	47249046	+	0 NA	intron (Nintron (N	-69969 NR_024594	1E+08	Hs. 662547NR_024594	ENSG00000LOC100131	-	shactncRNA
chr22-31C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr22	31090260	31100836	+	0 NA	exon (NM_exon (NM	10552 NM_001207	6525 Hs. 149099NM_006933	ENSG00000SMTN	-	smootheliprotein-coding	
chr3-1001.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr3	10019047	10022717	+	0 NA	intron (NLIMB4 LIN	5254 NR_002788	152302 Hs. 635072NR_002788	ENSG00000CIDCEP1	CICE CIDB	cell deatpseudo	
chr3-256C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr3	25622939	25625295	+	0 NA	intron (Nintron (N	40254 NM_00106E	7155 Hs. 475733NM_00106E	ENSG00000TOP2B	TOP1IB tcDNA	topoiprotein-coding	
chr3-382C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr3	38250348	38253831	+	0 NA	intron (Nintron (N	-13723 NM_00425E	9390 Hs. 225941NM_00425E	ENSG00000SLC22A13	OAT10 OC	solute ce protein-coding	
chr5-126C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr5	1.27E+08	1.27E+08	+	0 NA	intron (NU6 snRNA	41828 NM_001201	501 Hs. 483233NM_00118E	ENSG00000ALDH7A1	ATQ1 EPD	aldehyde protein-coding	
chr6-331F.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr6	33194791	33197390	+	0 NA	intron (Nintron (N	-3622 NM_08068C	1302 Hs. 390171NM_08067E	ENSG00000COL11A2	DFNA13 DF	collagen protein-coding	
chr8-1184.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr8	11842647	11847177	+	0 NA	3' UTR (N3' UTR (N	23175 NM_001190E	1508 Hs. 520899NM_001190E	ENSG00000CTSB	APPS CPSE	cathepsir protein-coding	
chr8-3884.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr8	38840318	38844941	+	0 NA	intron (Nintron (N	37679 NM_001352	6867 Hs. 27924E NM_00628E	ENSG00000TACC1	Gas5	transformprotein-coding	
chr9-863C.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr9	86300437	86304681	+	0 NA	intron (NAluSx SIN	-20021 NM_03094C	81689 Hs. 449291NM_03094C	ENSG00000ISCA1	HBLD2 ISA	iron-sulfprotein-coding	
chr9-1243.8.904371.0.042191.0.778981.0.054162.0.956806.0.981636	chr9	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	22937 NM_00116E	10783 Hs. 197071NM_014397	ENSG00000NEK6	SID6-15 E	NIMA rel protein-coding	
chr10-702.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr10	70212051	70213609	+	0 NA	intron (Nintron (N	20599 NM_02112E	5464 Hs. 437403NM_02112E	ENSG00000PPA1	HEL-S-66	gpyrophosp protein-coding	
chr11-35C.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr11	35513648	35513869	+	0 NA	intron (NMER5B DNA	11858 NM_001001	25891 Hs. 55044 NM_01543C	ENSG00000PAMR1	DKFZP586F	peptidase protein-coding	
chr11-111.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr11	1.13E+08	1.13E+08	+	0 NA	intron (Nintron (N	-24497 NM_00127E	8451 Hs. 339733NM_00358E	ENSG00000CULA4	-	cullin 4 protein-coding	
chr15-29F.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr15	29699526	29701784	+	0 NA	3' UTR (N3' UTR (N	25720 NR_135221	1E+08	Hs. 525722NR_135221	ENSG00000LOC10013C	-	uncharactncRNA
chr15-74F.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr15	74921942	74923328	+	0 NA	intron (NAluJo SIN	15438 NM_00425E	9377 Hs. 40190E NM_00425E	ENSG00000COX5A	COX COX- $\gamma$	cytochdroprotein-coding	
chr2-232E.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr2	2.33E+08	2.33E+08	+	0 NA	non-codirnon-codir	-10464 NM_00134E	389084 Hs. 65750E NM_20689E	ENSG00000SNORC	ASCL830 C	secondarprotein-coding	
chr22-41F.8.904371.0.043377.0.803633.0.053976.0.956954.0.981636	chr22	41646347	41647927	+	0 NA	intron (NAluJo SIN	25842 NM_00128E	2547 Hs. 29249E NM_00146E	ENSG00000XRC6	CTC75 CTC	X-ray re protein-coding	
chr21-46E.11.38962.0.038241.0.710184.0.053846.0.957058.0.981636	chr21	46534619	46535033	+	0 NA	intron (Nintron (N	70256 NM_00627E	6285 Hs. 422181NM_00627E	ENSG00000S100B	NEF S100 S100	cal protein-coding	
chr10-792.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr10	79215359	79219181F	+	0 NA	intron (NAluY SINE	-130199 NM_00572E	10105 Hs. 38107E NM_00572E	ENSG00000PP1F	CYP3 CyP-	peptidyl protein-coding	
chr12-297.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr12	29761753	29762007	+	0 NA	intron (Nintron (N	22062 NM_001367	83857 Hs. 401954NM_03192C	ENSG00000TMTC1	ARG99 OLF	transmet protein-coding	
chr16-214.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr16	21861891	21863276	+	0 NA	IntergeniAluJo SIN	4152 NR_02445E	1E+08	Hs. 648433NR_02445E	LOC10019C	-	uncharactncRNA
chr2-8504.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr2	85044152	85047885	+	0 NA	intron (Nintron (N	21329 NR_14645E	1.01E+08	Hs. 43439E NR_14645E	ENSG00000LINC01964	-	long intencRNA
chr3-4334.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr3	43347471	43349218	+	0 NA	exon (NM_exon (NM	3618 NR_046757	1.01E+08	Hs. 600984NR_046757	SNRK-AS1	-	SNRK antncRNA
chr6-530C.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr6	53091932	53099856	+	0 NA	intron (Nintron (N	24471 NM_012347	26268 Hs. 21665E NM_012347	ENSG00000FBX09	FBX9 NY-F	F-box prcprotein-coding	
chr7-7542.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr7	75420487	75426233	+	0 NA	intron (Nintron (N	13038 NR_10401E	155400 Hs. 436034NM_01033E	ENSG00000NSUN5P1	NSUN5B W	ENSUN5 ps pseudo	
chr9-109C.9.383393.0.040907.0.76005.0.053822.0.957077.0.981636	chr9	1.09E+08	1.09E+08	+	0 NA	intron (NAluSx SIN	-3348 NR_02950E	407036	NR_02950E	ENSG00000MIR32	MIRN32 hs	microRNA ncRNA
chr2-1611.4.461893.0.058388.1.085223.0.053803.0.957092.0.981636	chr2	1.61E+08	1.61E+08	+	0 NA	intron (NAluXs I	-22038 NM_00659E	10716 Hs. 21086E NM_00659E	ENSG00000TBR1	IDDA5 TBF	T-box br protein-coding	
chr7-1001.4.461893.0.058388.1.085223.0.053803.0.957092.0.981636	chr7	1E+08	1E+08	+	0 NA	intron (NAluY SINE	2470 NR_13452E	389541 Hs. 40562E NM_00100E	ENSG00000LAMTOR4	C7orf59	late end protein-coding	
chr15-727.6.468119.0.048923.0.909537.0.053789.0.957103.0.981636	chr15	72738396	72739985	+	0 NA	TTS (NM_TTS (NM_C	-43645 NR_040107	1E+08	Hs. 562587NR_040107	ENSG00000ADPGK-AS1	-	ADPGK antncRNA
chr16-727.6.468119.0.048923.0.909537.0.053789.0.957103.0.981636	chr16	72793421	72793989	+	0 NA	exon (NM_exon (NM	-128735 NR_12633C	1.02E+08	Hs. 63725E NR_12633C	ENSG00000LINC01572	-	long intencRNA
chr9-2647.6.468119.0.048923.0.909537.0.053789.0.957103.0.981636	chr9	2647738	2648931	+	0 NA	exon (NM_exon (NM	-25961 NR_01537E	401491 Hs. 41604E NR_01537E	ENSG00000VLDLR-AS1	line-VLDL	VLDLR antncRNA	
chr20-514.9.326537.0.04207.0.78281.0.053742.0.957141.0.981636	chr20	51618683	51618882	+	0 NA	exon (NM_exon (NM	-55943 NM_00113E	4773 Hs. 74414E NM_01234C	ENSG00000NFATC2	NFAT1 NF	nuclear f protein-coding	
chr11-984.6.725289.0.048.0.893609.0.05372.0.95716.0.981636	chr11	984425	985030	+	0 NA	exon (NM_exon (NM	51991 NM_005961	4588 Hs. 52843E NM_005961	ENSG00000MUC6	MUC-6	mucin 6,  protein-coding	
chr3-182F.6.725289.0.048.0.893609.0.05372.0.95716.0.981636	chr3	1.83E+08	1.83E+08	+	0 NA	intron (N(TTG)n Si	81940 NM_01461E	23200 Hs. 47842E NM_01461E	ENSG00000ATP11B	ATP1F ATF	ATFase p protein-coding	
chr1-7977.9.126408.0.04155.0.775475.0.05358.0.957268.0.981636	chr1	7977719	7978760	+	0 NA	intron (NAluSg SIN	16528 NM_00726E	11315 Hs. 41964C NM_00726E	ENSG00000PARR7	DJ-1 DJ1	Parkinson protein-coding	
chr7-107.9.126408.0.04155.0.775475.0.05358.0.957268.0.981636	chr7	1.07E+08	1.07E+08	+	0 NA	intron (Nintron (N	-108135 NM_00529E	2845 Hs. 657277NM_00529E	ENSG00000GPR22	-	G protei protein-coding	
chr1-363C.8.14479.0.04339.0.809941.0.05357.0.957279.0.981636	chr1	36300690	36305072	+	0 NA	intron (Nintron (N	-3487 NM_00116E	79729 Hs. 52449E NM_02467E	ENSG00000SH3D21	C1orf113	SH3 doma protein-coding	
chr1-467C.8.14479.0.04339.0.809941.0.05357.0.957279.0.981636	chr1	46705376	46707392	+	0 NA	intron (Nintron (N	12730 NM_014774	9813 Hs. 41964C NM_014774	ENSG00000EFCAB14	KIAA0494	EF-hand  protein-coding	
chr1-667E.8.14479.0.04339.0.809941.0.05357.0.957279.0.981636	chr1	66723135	66723637	+	0 NA	intron (Nintron (N	-29073 NM_15266E	200132 Hs. 47922E NM_15266E	ENSG00000CTEX1D1	-	Tctex1  protein-coding	
chr1-150E.8.14479.0.04339.0.809941.0.05357.0.957279.0.981636	chr1	1.51E+08	1.51E+08	+	0 NA	3' UTR (N3' UTR (N	-18386 NM_20704C	2029 Hs. 63245E NM_00443E	ENSG00000CENSA	ARPP-19e	endosulf protein-coding	
chr1-172E.8.14479.0.04339.0.809941.0.05357.0.957279.0.981636	chr1	1.73E+08	1.73E+08	+	0 NA	intron (Nintron (N	46209 NM_01428E	51430 Hs. 20455E NM_0142				



chr5-6236	6.419122	0.048637	0.908994	0.053507	0.957328	0.981636	chr5	62363123	62367582	+	0	NA	exon (NM_exon (NM_00134E+08	38553	NM_00134E	27292	Hs.73166E+08	ENSG000004D1M1	D1M1 D1M1D1M1 rR protein-coding		
chr5-1135	6.419122	0.048637	0.908994	0.053507	0.957328	0.981636	chr5	1.14E+08	1.14E+08	+	0	NA	3' UTR (N3' UTR (N_00134E+08	79848	NM_00134E	64848	Hs.231942	NM_02282E+08	ENSG000004YTHDC2	CAHL HYT YTH domain protein-coding	
chr6-1185	6.419122	0.048637	0.908994	0.053507	0.957328	0.981636	chr6	1.19E+08	1.19E+08	+	0	NA	intron (NLTR10B2 I_002667	30461	NM_002667	5350	Hs.17083E+08	NM_002667	ENSG000004CPLN	CMD1P CM phosphol protein-coding	
chr9-1936	6.419122	0.048637	0.908994	0.053507	0.957328	0.981636	chr9	19363076	19364591	+	0	NA	intron (NAluSx SIN_00101C	16403	NM_00101C	6194	Hs.40807E+08	NM_00101C	ENSG000004RPS6	S6	ribosomal protein-coding
chr9-3404	6.419122	0.048637	0.908994	0.053507	0.957328	0.981636	chr9	34043994	34044982	+	0	NA	intron (NAluS4 SI_001844E	4399	NM_001844E	55833	Hs.49373E+08	NM_01844E	ENSG000004UBAP2	UBAP-2	ubiquitin protein-coding
chr1-3794	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr1	37942425	37944321	+	0	NA	intron (N2b LINE _00135C	-1109	NM_00135C	3633	Hs.449942E+08	NM_00554C	ENSG000004INPP5B	5PTase	inositol protein-coding
chr10-495	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr10	49554775	49559868	+	0	NA	intron (N1MB2 LIN_00145778	4459	NR_145778	1.1E+08	NR_145778	SNORA74C-	-	small nucsnoRNA	
chr10-115	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr10	1.2E+08	1.2E+08	+	0	NA	intron (Nintron (N_00166E	-23818	NR_03983C	1.01E+08	NR_03983C	ENSG000004MIR4682	-	microRNA ncRNA	
chr11-385	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr11	3830014	3831355	+	0	NA	intron (NMIR SINE _00166E	10275	NM_00166E	391	Hs.50172E+08	NM_00166E	ENSG000004CRHOG	ARHG	ras homol protein-coding
chr12-171	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr12	17130	18101	+	0	NA	intron (Nintron (N_00166E	14400	NR_13074E	1E+08	Hs.45957E+08	NR_13074E	ENSG000004WASH8P	-	Wash protein-coding
chr12-505	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr12	50998419	50999774	+	0	NA	intron (Nintron (N_00166E	10119	NM_001174	4891	Hs.50554E+08	NM_000617	ENSG000004SLC11A2	AHMI01 DC	solute c protein-coding
chr12-928	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr12	92854621	92856042	+	0	NA	intron (NAluY SINE_00356E	73964	NM_00356E	8411	Hs.567367E+08	NM_00356E	ENSG000004EEA1	MST105 MS	early enc protein-coding
chr14-102	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr14	1.02E+08	1.02E+08	+	0	NA	IntergeniAluSx SIN_00263C	16748	NM_00263C	51550	Hs.129634E+08	NM_03263C	ENSG000004CINP	-	cyclin d protein-coding
chr16-875	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr16	87539283	87540013	+	0	NA	intron (Nintron (N_00166E	21239	NR_13518C	1.02E+08	Hs.66745E+08	NR_13518C	ENSG000004LOC10192E-	-	uncharacter ncRNA
chr17-312	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr17	31244902	31246509	+	0	NA	intron (NMER21B LI_002544	51534	NM_002544	4974	Hs.113874E+08	NM_002544	ENSG000004OMG	OMGP	oligodenc protein-coding
chr17-365	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr17	36523406	36527576	+	0	NA	intron (Nintron (N_00134E	-9271	NM_00134E	284098	Hs.37888E+08	NM_178517	ENSG000004PIGW	Gwt1 HPMF	phosphat protein-coding
chr18-795	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr18	79931728	79935627	+	0	NA	intron (N1LM4b LIN_00114E	17976	NM_00114E	80148	Hs.288284E+08	NM_02507E	ENSG000004SLC66A2	PQLC1	solute c protein-coding
chr2-2416	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr2	2.42E+08	2.42E+08	+	0	NA	intron (Nintron (N_001271	12290	NM_001271	10494	Hs.516807E+08	NM_006374	ENSG000004STRK25	SOK1 YSK1	serine/t protein-coding
chr3-1025	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	10252889	10253919	+	0	NA	intron (Nintron (N_001476C	11658	NM_00133C	84289	Hs.52917E+08	NM_03232E	ENSG000004ING5	p281NG5	inhibitor protein-coding
chr3-3706	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	3706163	37062137	+	0	NA	intron (Nintron (N_00125E	67800	NM_00125E	4292	Hs.195364E+08	NM_00024E	ENSG000004MLH1	COCA2 FCC	mutL homc protein-coding
chr3-3852	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	38523472	38524159	+	0	NA	intron (Nintron (N_001493E	27475	NR_13493E	9941	Hs.517897E+08	NM_005107	ENSG000004EXO9	ENDOGL1 Exo	endor protein-coding
chr3-1285	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N_001404E	35732	NM_01404E	28976	Hs.56748E+08	NM_01404E	ENSG000004ACAD9	MC1DN20 Nacyl	-CoA protein-coding
chr3-1551	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	1.55E+08	1.55E+08	+	0	NA	intron (Nintron (N_001636	-68210	NR_125399	1.02E+08	Hs.12141E+08	NR_125399	ENSG000004LINC01487-	-	long intencRNA
chr3-3852	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	38523472	38524159	+	0	NA	intron (Nintron (N_001493E	27475	NR_13493E	9941	Hs.517897E+08	NM_005107	ENSG000004EXO9	ENDOGL1 Exo	endor protein-coding
chr3-1285	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N_001404E	35732	NM_01404E	28976	Hs.56748E+08	NM_01404E	ENSG000004ACAD9	MC1DN20 Nacyl	-CoA protein-coding
chr3-1551	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr3	1.55E+08	1.55E+08	+	0	NA	intron (Nintron (N_001636	-68210	NR_125399	1.02E+08	Hs.12141E+08	NR_125399	ENSG000004LINC01487-	-	long intencRNA
chr4-1691	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N_001493E	27475	NR_13493E	9941	Hs.517897E+08	NM_005107	ENSG000004EXO9	ENDOGL1 Exo	endor protein-coding
chr5-6593	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr5	65938775	65940848	+	0	NA	intron (NSVA_D Ret_0028474	5762	NR_028474	1E+08	Hs.60806E+08	NR_028474	LOC100303-	-	LSM3 homc pseudo
chr7-4781	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr7	4781798	4783928	+	0	NA	intron (Nintron (N_001636	5776	NR_03980C	1.01E+08	NR_03980C	ENSG000004MIR4656	-	microRNA ncRNA	
chr8-143C	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chr8	1.43E+08	1.43E+08	+	0	NA	3' UTR (N3' UTR (N_00234E	3261	NM_00234E	4061	Hs.52190E+08	NM_00234E	ENSG000004LY6E	RIG-E RIC	lymphocyt protein-coding
chrX-405	6.947142	0.046743	0.874461	0.053454	0.957371	0.981636	chrX	40599045	40599839	+	0	NA	intron (Nintron (N_00576E	18476	NM_00576E	10159	Hs.49596E+08	NM_00576E	ENSG000004ATP6AP2	APT6M8-9 ATPase	H+ protein-coding
chr10-105	9.862415	0.039729	0.743852	0.053409	0.957406	0.981636	chr10	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N_001324	10865	NM_001324	7511	Hs.39062E+08	NM_02038E	ENSG000004XPNPFP1	NP1 SAMF	X-proly protein-coding
chr12-49C	9.862415	0.039729	0.743852	0.053409	0.957406	0.981636	chr12	49011587	49013171	+	0	NA	intron (NAluSq2 SI_00120E	6397	NM_00120E	5571	Hs.53086E+08	NM_00273E	ENSG000004PRKAG1	AMPKG	protein k protein-coding
chr5-140	4.989133	0.054777	1.028903	0.053238	0.957542	0.981636	chr5	1.4E+08	1.4E+08	+	0	NA	intron (Nintron (N_00194E	11810	NM_00194E	1839	Hs.799	NM_00194E	ENSG000004HBEGF	DTR DTS L	heparin t protein-coding
chr10-994	6.189411	-0.05096	0.957244	-0.05323	0.957546	0.981636	chr10	99405442	99405871	+	0	NA	intron (N1LM4a LI_00207E	24968	NM_00207E	2805	Hs.50075E+08	NM_00207E	ENSG000004GOT1	AST1 ASTC	glutamic- protein-coding
chr17-421	6.189411	-0.05096	0.957244	-0.05323	0.957546	0.981636	chr17	42151553	42151812	+	0	NA	intron (Nintron (N_00458E	3307	NM_00458E	5878	Hs.65038E+08	NM_00458E	ENSG000004CRAB5C	L1880 RAE	RAB5C, me protein-coding
chr12-571	8.855373	0.04192	0.787477	0.053234	0.957546	0.981636	chr12	57149965	57151166	+	0	NA	intron (N2c LINE _001636	-2946	NR_13193E	1.06E+08	Hs.60954E+08	NR_13193E	ENSG000004LRP1-AS	-	LRP1 antncRNA
chr18-415	8.855373	0.04192	0.787477	0.053234	0.957546	0.981636	chr18	41971126	41971631	+	0	NA	intron (Nintron (N_001636	16144	NM_002647	5289	Hs.464971E+08	NM_002647	ENSG000004PIK3C3	VPS34 Vps	phosphat protein-coding
chr2-9937	8.855373	0.04192	0.787477	0.053234	0.957546	0.981636	chr2	99379062	99380404	+	0	NA	intron (N(TTTC)n _0015904	42344	NM_015904	9669	Hs.15868E+08	NM_015904	ENSG000004EIF5B	IF2	eukaryoti protein-coding
chr3-6994	8.855373	0.04192	0.787477	0.053234	0.957546	0.981636	chr3	69948738	69950191	+	0	NA	intron (Nintron (N_00024E	12865	NM_00024E	4286	Hs.166017E+08	NM_00024E	ENSG000004MITF	CMM3 CMM	melanocyt protein-coding
chr17-802	7.369309	0.046499	0.874987	0.053124	0.957618	0.981636	chr17	80251477	80251761	+	0	NA	intron (NAluSx SIN_00125E	-9233	NM_00125E	57674	Hs.19564E+08	NM_020914E	ENSG000004RNF213	AL017 C17	ring fing protein-coding
chr4-3951	7.122032	-0.04815	0.906329	-0.05313	0.957627	0.981636	chr4	39514121	39514333	+	0	NA	intron (Nintron (N_00335E	13212	NM_00335E	7358	Hs.57251E+08	NM_00335E	ENSG000004UGDH	GDH UDP	-CUDP-gluc protein-coding
chr1-151E	6.676291	-0.04832	0.909667	-0.05312	0.95764	0.981636	chr1	1.52E+08	1.52E+08	+	0	NA	intron (N1LM2C LI_005305E	15135	NM_005305E	117145	Hs.16407E+08	NM_005305E	ENSG000004THEM4	CTMP	thioester protein-coding
chr12-645	6.676291	-0.04832	0.909667	-0.05312	0.95764	0.981636	chr12	6499218	6499568	+	0	NA	intron (NAluSx1 SI_001486E	5291	NM_01486E	9918	Hs.5719	NM_01486E	ENSG000004CFAD2	CAP-D2 Cn	non-SMC protein-coding
chr2-6931	6.676291	-0.04832	0.909667	-0.05312	0.95764	0.981636	chr2	69313393	69313648	+	0	NA	IntergeniLIM5 LINE_00205E	73707	NM_00205E	2673	Hs.58030C	NM_00205E	ENSG000004GFPT1	CMS12 CMS	glutamine protein-coding
chr2-1622	6.676291	-0.04832	0.909667	-0.05312	0.95764	0.981636	chr2	1.62E+08	1.62E+08	+	0	NA	intron (NMLT1C LTF_000446E	38849	NM_00446E	2191	Hs.65437E+08	NM_00446E	ENSG000004FAP	DDP1V FAF	fibroblas protein-coding
chr1-174C	7.426164	0.044857	0.84536	0.053063	0.957682	0.981636	chr1	17409153	17411232	+	0	NA	intron (Nintron (N_00113E	28344	NM_00113E	55920	Hs.38				



chr9-1364 7.426164	0.044857	0.84536	0.053063	0.957682	0.981636	chr9	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	-4567 NM_001282	23203 Hs. 495471NM_015166	ENSG000002PMPCA	Alpha-MPF	peptidase protein-coding	
chr6-1664 8.688526	-0.04303	0.814079	-0.05286	0.957847	0.981636	chr6	1.66E+08	1.66E+08	+	0	NA	intron (NLIIPA3 LIN	36160 NR_046799	1.01E+08 Hs. 675696NR_046799	ENSG000002RPS6KA2-1	-	RPS6KA2	incRNA
chr5-132f 9.911413	0.039814	0.75336	0.052848	0.957853	0.981636	chr5	1.33E+08	1.33E+08	+	0	NA	intron (NLIIME3F LI	22955 NR_132124	1.02E+08 Hs. 598812NR_132124	ENSG000002TH2LCRR	TH2-LCR	T helper ncRNA	
chr11-11f 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr11	1.17E+08	1.17E+08	+	0	NA	intron (NMIRb SINE	-57960 NM_000039	335 Hs. 93194 NM_000039	ENSG000002APOA1	apo(a)	apolipoprotein-coding	
chr12-31f 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr12	31281582	31282825	+	0	NA	3' UTR (N3' UTR (N	-42113 NR_026806	79857 Hs. 534485NM_024799	ENSG000002FLJ13224	-	uncharactericncRNA	
chr2-691f 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr2	69184428	69185260	+	0	NA	intron (NMER5B DNA	81162 NR_036073	1E+08 NR_036073	ENSG000002MIR3126	mir-3126	microRNA ncRNA	
chr20-45f 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr20	45949853	45950708	+	0	NA	exon (NM exon (NM	15597 NM_022104	63935 Hs. 472856NM_022104	ENSG000002PCIF1	C20orf67 PDX1	C-terminus protein-coding	
chr6-1334 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr6	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	241758 NM_001301	2070 Hs. 596688NM_004100	ENSG000002EY4A	CMDF1 DFNYA	transprotein-coding	
chr6-1581 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	3' UTR (N3' UTR (N	24192 NM_207118	404672 Hs. 356224NM_207118	ENSG000002GTF2H5	C6orf175 general	tprotein-coding	
chr20-45f 7.212169	-0.04546	0.861475	-0.05277	0.957915	0.981636	chr20	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	32229 NM_138790	153090 Hs. 522378NM_032552	ENSG000002DAB2IP	AF9q34 A1DAB2	inteprotein-coding	
chr12-14f 10.86946	0.037802	0.716849	0.052733	0.957945	0.981636	chr12	14460430	14461216	+	0	NA	exon (NM exon (NM	75542 NM_181352	55729 Hs. 504885NM_018175	ENSG000002ATF7IP	AM ATF-1	activator protein-coding	
chr1-8671 9.613289	-0.04015	0.761979	-0.0527	0.957973	0.981636	chr1	86716659	86717003	+	0	NA	intron (Nintron (N	12255 NM_016005	51100 Hs. 136309NM_016005	ENSG000002SH3GLB1	Bif-1 CGISH3	domain protein-coding	
chr1-1087 9.613289	-0.04015	0.761979	-0.0527	0.957973	0.981636	chr1	1.09E+08	1.09E+08	+	0	NA	intron (NAluJb SIN	7526 NM_007266	6814 Hs. 530436NM_007266	ENSG000002STXP3	MUNC18-3 syntaxin	protein-coding	
chr14-35f 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr14	35102912	35103172	+	0	NA	intron (NAluXs1 SIN	19500 NM_001305	55012 Hs. 530712NM_017917	ENSG000002PPP2R3C	C14orf10 protein	protein-coding	
chr15-494 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr15	49473255	49474640	+	0	NA	intron (NChar1ie21	50705 NM_002005	2252 Hs. 567268NM_002005	ENSG000002PGF7	HBGF-7 KC	fibroblast protein-coding	
chr16-91f 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr16	9121672	9122138	+	0	NA	TTS (NM_CTS (NM_C	30261 NM_014117	29035 Hs. 221497NM_014117	ENSG000002C16orf72	PROO149	chromosome protein-coding	
chr17-49f 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr17	4960284	4961573	+	0	NA	intron (Nintron (N	6889 NM_00489C	9552 Hs. 90436 NM_00489C	ENSG000002CPAG7	ACRP FSA	sperm associated protein-coding	
chr18-13f 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr18	13001854	13002580	+	0	NA	intron (NLIIME4a LI	10855 NM_032142	55125 Hs. 100914NM_018066	ENSG000002CEP192	PPP1R62	centrosome protein-coding	
chr2-698f 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr2	69865934	69867129	+	0	NA	intron (NAluJo SIN	-27425 NR_03786E	11017 Hs. 54649 NM_006857	ENSG000002SNRNP27	27K RY1	small nucprotein-coding	
chr3-450f 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr3	45004408	45005209	+	0	NA	intron (NLIIME3A LI	-21495 NM_00327E	7123 Hs. 476092NM_00327E	ENSG000002CLEC3B	TN TNA	C-type lectin protein-coding	
chr5-5307 7.163172	-0.04587	0.871263	-0.05265	0.958008	0.981636	chr5	53072061	53073076	+	0	NA	intron (NLIIME3E LI	37189 NM_17680E	4338 Hs. 163646NM_004531	ENSG000002MOC52	MCBPE MOc	molybdenum protein-coding	
chr16-151 5.468935	0.051477	0.978048	0.052632	0.958025	0.981636	chr16	15109392	15110383	+	0	NA	TTS (NR_TTS (NR_I	15476 NR_125434	1.01E+08 Hs. 678758NR_125434	ENSG000002LOC100505E	-	uncharactericncRNA	
chr2-219f 5.468935	0.051477	0.978048	0.052632	0.958025	0.981636	chr2	2.19E+08	2.19E+08	+	0	NA	intron (NTiger3b	8636 NM_00131E	23549 Hs. 258551NM_01210C	ENSG000002DNPEP	ASPEP DAF	aspartyl protein-coding	
chr9-121f 5.468935	0.051477	0.978048	0.052632	0.958025	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	22658 NM_00136E	11064 Hs. 652362NM_00701E	ENSG000002CNTRL	CEP1 CEP1	centriole protein-coding	
chr1-211f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr1	21161719	21162674	+	0	NA	intron (Nintron (N	5843 NM_00119E	8672 Hs. 467084NM_00376C	ENSG000002EIF4G3	eIF-4G 3 eukaryoti	protein-coding	
chr1-161f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr1	1.61E+08	1.61E+08	+	0	NA	non-codiron-codir	2096 NM_001013	257177 Hs. 534595NM_001013	ENSG000002CFAP126	Clorf192 cilia	ancprotein-coding	
chr1-240f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr1	2.4E+08	2.4E+08	+	0	NA	intron (Nintron (N	237936 NM_02006E	56776 Hs. 24889 NM_02006E	ENSG000002FMM2	-	formin 2 protein-coding	
chr15-494 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr15	49459884	49460463	+	0	NA	intron (Nintron (N	36481 NM_002005	-2252 Hs. 567268NM_002005	ENSG000002PGF7	HBGF-7 KC	fibroblast protein-coding	
chr18-92f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr18	9225104	9226238	+	0	NA	intron (Nkanga2_a	88108 NM_001204	23253 Hs. 464585NM_01520E	ENSG000002ANKRD12	ANCO-2 AN	ankyrin I protein-coding	
chr19-121 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr19	12216933	12170705	+	0	NA	intron (NAluY SINE	6924 NM_003437	7695 Hs. 479874NM_003437	ENSG000002ZNF136	pH2-20 zinc	finger protein-coding	
chr19-36f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr19	36325727	36326183	+	0	NA	intron (NHERV571-i	5763 NR_03827E	1.01E+08 Hs. 595155NR_03827E	ENSG000002LINC0066E	-	long intencRNA	
chr2-189f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr2	1.9E+08	1.9E+08	+	0	NA	intron (NLIIMEg LIN	27245 NM_001321	5378 Hs. 111745NM_000534	ENSG000002PMS1	HNPC33 PMS1	home protein-coding	
chr6-129f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr6	1.3E+08	1.3E+08	+	0	NA	intron (Nintron (N	77538 NM_03351E	93663 Hs. 486456NM_03351E	ENSG000002ARHGAP18	MacGAP SE	Rho GTPase protein-coding	
chr7-776f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr7	77600210	77601545	+	0	NA	intron (Nintron (N	62834 NM_001131	5782 Hs. 61812 NM_00283E	ENSG000002PTPN12	PTP-PEST protein	tprotein-coding	
chr9-123f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chr9	1.23E+08	1.23E+08	+	0	NA	intron (NMIRb SINE	26785 NR_030331	693185 Hs. 111745NM_000534	ENSG000002MIR600	MIRN600 mi	microRNA ncRNA	
chrX-738f 6.898144	0.046476	0.883123	0.052627	0.958029	0.981636	chrX	73827795	73829393	+	0	NA	non-codiron-codir	24159 NR_001564	7503 Hs. 529901NR_001564	ENSG000002XIST	DXS1089 XIST	inactivincRNA	
chr10-844 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr10	84485613	84486502	+	0	NA	intron (NLIIPA5 LIN	60888 NM_001284	54462 Hs. 461985NM_01899E	ENSG000002CCSER2	FAM190B Coiled-c	protein-coding	
chr14-311 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr14	31167224	31169789	+	0	NA	intron (Nintron (N	39287 NM_01538E	25831 Hs. 708017NM_01538E	ENSG000002HECTD1	EULIR HECT	domain protein-coding	
chr18-95f 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr18	9525990	9530102	+	0	NA	intron (NLIIME1 LIN	52533 NM_00678E	10928 Hs. 528999NM_00678E	ENSG000002RALBP1	RIP1 RLR1	ra1a home protein-coding	
chr2-8531 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr2	85314911	85317966	+	0	NA	IntergeniIntergeni	11551 NM_00136E	10618 Hs. 593382NM_006464	ENSG000002TGOLN2	TGN38 TGN	trans-gol protein-coding	
chr20-51f 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr20	5108223	5110987	+	0	NA	intron (Nintron (N	3471 NM_00100E	29058 Hs. 472024NM_01414E	ENSG000002TMEM230	C20orf30 transmem	protein-coding	
chr5-714f 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr5	71487170	71490155	+	0	NA	intron (NAluSg2 SI	32991 NM_01842E	55814 Hs. 258272NM_01842E	ENSG000002BDP1	DFNB112 FB	double protein-coding	
chr7-139f 8.63167	-0.04155	0.789601	-0.05262	0.958033	0.981636	chr7	1.39E+08	1.39E+08	+	0	NA	intron (NAluSx SIN	26049 NM_02011E	56829 Hs. 133512NM_02011E	ENSG000002ZC3HAV1	ARTD13 FL	zinc finger protein-coding	
chr1-798f 7.905186	0.043194	0.820959	0.052614	0.958039	0.981636	chr1	7983287	7986847	+	0	NA	3' UTR (N3' UTR (N	23356 NM_00726E	11315 Hs. 419646NM_00726E	ENSG000002PARK7	DJ-1 DJ1	Parkinson protein-coding	
chr1-273f 7.905186	0.043194	0.820959	0.052614	0.958039	0.981636	chr1	21267645	21271515	+	0	NA	intron (NMIRb SINE	10035 NM_00111E	1889 Hs. 195088NM_001397	ENSG000002ECE1	ECE	endothelin protein-coding	
chr1-273f 7.905186	0.043194	0.820959	0.052614	0.958039	0.981636	chr1	27324434	27325941	+	0	NA	non-codiron-codir	1313 NR_03392E	644961 Hs. 660887NR_03392E	ACTG1P20	-	actin gauseudo	
chr1-374f 7.905186	0.043194	0.820959	0.052614	0.958039	0.981636	chr1	37480966	37484475	+	0	NA	intron (Nintron (N	2490 NR_10679C	1.02E+08 Hs. NR_10679C	ENSG000002MIR6732	hsa-mir-6	microRNA ncRNA	
chr1-112f 7.905186	0.043194	0.820959	0.052614	0.958039	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	Intergeni(T)n Simp	11600 NR_103744	1.01E+08 Hs. 418285NR_103744	ENSG000002SLC16A1-1	-	SLC16A1	ncRNA
chr10-1																		

chr7-1022	4.940915	0.054491	1.037415	0.052525	0.958111	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	-56269	NM_020979	10603	Hs.48944E	020979	ENSG00000	SH2B2	APS	SH2B adapt protein-coding			
chr10-127	8.193788	-0.04299	0.819623	-0.05246	0.958165	0.981636	chr10	1.27E+08	1.27E+08	+	0	NA	intron (Nintron (N	120643	NM_001035	642938	Hs.613882	NM_001035	ENSG00000	INSY2A	C10orf141	inhibitor protein-coding			
chr17-402	8.193788	-0.04299	0.819623	-0.05246	0.958165	0.981636	chr17	4020928	4022765	+	0	NA	intron (Nintron (N	44743	NR_146884	1.05E+08	Hs.57923E	NR_146884	LINCO197E	-	long intencRNA				
chr19-108	8.193788	-0.04299	0.819623	-0.05246	0.958165	0.981636	chr19	10820090	10822429	+	0	NA	intron (Nintron (N	406976	NR_02958E	406976	NR_02958E	ENSG00000	MIR199A1	MIR-199-5	miRNA ncRNA				
chr16-224	10.82046	0.03761	0.718022	0.05238	0.958226	0.981636	chr16	20259010	22460294	+	0	NA	intron (NAluJr SIN	-21937	NR_02746C	1E+08	Hs.70957E	NR_02746C	RNN3P3	-	RRN3 hmc pseudo				
chr4-1854	10.82046	0.03761	0.718022	0.05238	0.958226	0.981636	chr4	1.85E+08	1.85E+08	+	0	NA	intron (NMLT1D LTF	12999	NM_18172E	353322	Hs.508154	NM_18172E	ENSG00000	CANKRD37	Lrp2bp	ankyrin r protein-coding			
chr10-122	3.990729	0.059664	1.140328	0.052321	0.958273	0.981636	chr10	1.26E+08	1.26E+08	+	0	NA	intron (NAluJr4 S1	26642	NM_07846E	56647	Hs.37029E	NM_016567	ENSG00000	BCCP1	TOK-1	TOKBRCA2	anc protein-coding		
chr7-1392	3.990729	0.059664	1.140328	0.052321	0.958273	0.981636	chr7	13928661	13929407	+	0	NA	intron (Nintron (N	57480	NM_00116E	2115	Hs.22634	NM_00495E	ENSG00000	ETV1	ER81	ETS vari	protein-coding		
chr11-635	8.474346	0.043683	0.835736	0.052269	0.958314	0.981636	chr11	63947846	63948570	+	0	NA	intron (NMIR3 SINE	8877	NM_00130C	79829	Hs.52375E	NM_024771	ENSG00000	CNA40	NAT11	NatN(alpha)	protein-coding		
chr7-1022	8.474346	0.043683	0.835736	0.052269	0.958314	0.981636	chr7	1.02E+08	1.02E+08	+	0	NA	intron (NAluSx SIN	9456	NM_001347	1E+08	Hs.40639E	NM_001242713	LOC10028E	-	uncharact	protein-coding			
chr1-3128	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr1	31287397	31294484	+	0	NA	intron (Nintron (N	5848	NM_004814	9410	Hs.33962	NM_004814	ENSG00000	CNRNP40	40K	HPRPF	small nuc	protein-coding	
chr1-3495	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr1	34991737	34992339	+	0	NA	intron (Nintron (N	-6691	NM_00119E	1.01E+08	Hs.53398E	NM_00119E	ENSG00000	TMEM35B	ZMYM6NB	transmemt	protein-coding		
chr1-1825	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr1	1.86E+08	1.86E+08	+	0	NA	intron (NAluSx S1	7964	NM_017847	54953	Hs.37121E	NM_017847	ENSG00000	CDR4	C1orf27	lodr-4	GPC	protein-coding	
chr1-2007	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr1	2.01E+08	2.01E+08	+	0	NA	intron (NAluJr SIN	43288	NM_001297	23271	Hs.23585	NM_20345E	ENSG00000	CAMSAP2	Camsaf2	IL1L	modulip	protein-coding	
chr12-515	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr12	51992328	51992547	+	0	NA	intron (NAluJo SIN	-14509	NM_181711	160622	Hs.40720E	NM_181711	ENSG00000	GRASP	TAMALIN	general i	protein-coding		
chr12-535	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr12	53542282	53543390	+	0	NA	TTS (NM_C	28852	NR_046221	1.01E+08	Hs.63360E	NR_046221	ENSG00000	LOC10065E	-	uncharact	ncRNA		
chr12-575	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr12	57526820	57528999	+	0	NA	exon (NM_exon (NM	10485	NM_052897	114785	Hs.52452E	NM_052897	ENSG00000	CMBD6	-	methyl-C	protein-coding		
chr17-622	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr17	62050931	62052653	+	0	NA	intron (Nintron (N	5386	NM_005121	9969	Hs.28267E	NM_005121	ENSG00000	MED13	ARC250	DF mediator	protein-coding		
chr18-587	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr18	58733210	58734548	+	0	NA	intron (Nintron (N	-62006	NM_00128E	1.02E+08	Hs.64487E	NM_001289967	LOC10192E	-	uncharact	protein-coding			
chr19-981	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr19	9813344	9814413	+	0	NA	intron (NAluSp SIN	5201	NM_00131E	54850	Hs.12439	NM_01770E	ENSG00000	FBXL12	Fb112	F-box	anc protein-coding		
chr2-1825	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr2	1.83E+08	1.83E+08	+	0	NA	intron (Nintron (N	43538	NM_01343E	10787	Hs.60373E	NM_01343E	ENSG00000	NCKAP1	HEM2	NAP1NCK	assoc	protein-coding	
chr3-1081	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr3	1.08E+08	1.08E+08	+	0	NA	intron (NTHEID LTF	31967	NM_01801C	55081	Hs.41219E	NM_01801C	ENSG00000	IFT57	ESRRBL1	I	intraflag	protein-coding	
chr5-394	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr5	39406594	39408744	+	0	NA	intron (Nintron (N	17311	NM_00134E	1601	Hs.696631	NM_00134E	ENSG00000	CDB2	DOC-2	DOC	DAB	adapt	protein-coding
chr7-575	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr7	5758961	5760624	+	0	NA	intron (NAluSg SIN	21871	NM_207111	54476	Hs.48749E	NM_019011	ENSG00000	RNF216	CAHH	TRIP	ring	finger	protein-coding
chr7-135	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr7	1.36E+08	1.36E+08	+	0	NA	intron (Nintron (N	26676	NM_14580E	136319	Hs.60201E	NM_14580E	ENSG00000	MTPN	GCDP	V-1	myotroph	protein-coding	
chr8-2257	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr8	22571030	22572583	+	0	NA	exon (NM_exon (NM	6077	NM_00101E	10174	Hs.52857E	NM_00577E	ENSG00000	SORBS3	SCAM-1	SC	sorbin	ar	protein-coding
chr8-3824	8.384209	0.041702	0.800348	0.052105	0.958445	0.981636	chr8	38245156	38248805	+	0	NA	intron (Nintron (N	15027	NM_00116E	23259	Hs.43496E	NM_015214	ENSG00000	DDHD2	SAMWD1	SF	DDHD	dom	protein-coding
chr1-1837	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr1	1837568	1838699	+	0	NA	intron (NAluSx S1	52954	NM_002074	2782	Hs.43042E	NM_002074	ENSG00000	GNB1	MRD42	G	protein	protein-coding	
chr1-2201	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr1	2.2E+08	2.2E+08	+	0	NA	intron (NAluSg SIN	-18284	NR_029711	406969	NR_029711	ENSG00000	MIR194-1	MIRN194-1	miRNA	ncRNA			
chr10-926	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr10	926392	927237	+	0	NA	intron (NAluSx SIN	4891	NM_001351	23185	Hs.15906E	NM_01515E	ENSG00000	LARP4B	KIAA0217	La	ribon	protein-coding	
chr12-644	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr12	6445178	6447093	+	0	NA	intron (Nintron (N	1250	NM_00124E	939	Hs.355307	NM_00124E	ENSG00000	CD27	S152	S152	CD27	mol	protein-coding
chr13-42	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr13	42304954	42305624	+	0	NA	intron (NMER58B DN	33306	NM_01624E	11215	Hs.10510E	NM_01624E	ENSG00000	AKAP11	AKAP-11	A	kinase	protein-coding	
chr13-495	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr13	49556000	49558289	+	0	NA	intron (Nintron (N	28411	NM_00135E	55213	Hs.508021	NM_018191	ENSG00000	RCBTB1	CLD7	CLL	RCC1	and	protein-coding
chr13-115	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	TTS (NM_C	-34208	NR_02658C	7027	Hs.79353	NM_007111	ENSG00000	TFDP1	DILC	DP1		transcrip	protein-coding
chr16-508	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr16	5083958	5086141	+	0	NA	3' UTR (N3' UTR (N	12746	NM_20140C	196483	Hs.406461	NM_20140C	ENSG00000	EEF2KMT	EFM3	FAM5	eukaryot	i	protein-coding
chr16-895	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr16	89309922	89312036	+	0	NA	intron (NLM14 LINE	-10154	NM_00124E	1E+08	Hs.65699E	NM_001242885	LOC100287E	-	uncharact	protein-coding			
chr17-425	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr17	4288952	4291119	+	0	NA	intron (Nintron (N	572	NM_00119C	4092	Hs.465087	NM_005904	ENSG00000	SMAD7	CRCS3	MAI	SMAD	famip	protein-coding
chr19-465	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr19	46677161	46677961	+	0	NA	TTS (NR_C	16083	NR_040041	1.01E+08	Hs.434327	NR_040041	ENSG00000	DACT3-AS1	DACT3	antncRNA			
chr19-471	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr19	47183145	47184727	+	0	NA	intron (Nintron (N	-43006	NR_03615E	1E+08	NR_03615E	ENSG00000	MIR3190	mir-3190	microRNA	ncRNA			
chr2-9655	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr2	96598003	96599007	+	0	NA	intron (Nintron (N	39486	NR_04765E	55683	Hs.516341	NM_017991	ENSG00000	KANSL3	KIAA1310	KAT8	reg	protein-coding	
chr20-335	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr20	3368019	33689493	+	0	NA	intron (NAluY SINE	38906	NM_00100E	25943	Hs.51685E	NM_00100E	ENSG00000	C20orf194	-	chromoson	protein-coding		
chr22-194	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr22	19458665	19459679	+	0	NA	intron (Nintron (N	-10940	NM_17379E	128977	Hs.65956E	NM_17379E	ENSG00000	C22orf39	-	chromoson	protein-coding		
chr4-2541	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr4	25411355	25412981	+	0	NA	intron (NMER21C LI	34905	NM_01336E	29945	Hs.15217E	NM_01336E	ENSG00000	ANAPCA4	APC4	anaphase	protein-coding		
chr4-4195	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr4	41939331	41940287	+	0	NA	intron (Nintron (N	4380	NM_01812E	55161	Hs.31082	NM_01812E	ENSG00000	TMEM33	1600019D1	transmemt	protein-coding		
chr4-570	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr4	57055354	57056585	+	0	NA	intron (Nintron (N	-53793	NR_034081	255130	Hs.691061	NR_034081	ENSG00000	IGFBP7-AS	-	IGFBP7	ar	ncRNA	
chr4-1054	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr4	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	38832	NM_17686E	27068	Hs.654957	NM_00690E	ENSG00000	PPA2	HSPC124	Spyrophos	protein-coding		
chr5-789	5.947958	0.048755	0.93718	0.052023	0.95851	0.981636	chr5	7893898	7896700	+	0	NA	intron (Nintron (N	26151	NR_13448E	4552	Hs.481551								



chr17-286	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr17	28650538	28652602	+	0	NA	intron (NMIRb SINE	-6411 NM_001363	9703 Hs. 151761NM_01468C	ENSG0000CKIAA0100	BCOX BCOX KIAA0100	protein-coding		
chr17-350	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr17	35022631	35026767	+	0	NA	intron (Nintron (N	37143 NM_001017	117584 Hs. 13680	NR_005717	ENSG00000RFFL	CARP-2 Caring	fingerprotein-coding	
chr17-372	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr17	37250278	37251829	+	0	NA	intron (NAluY SINE	6252 NR_132772	1.07E+08	NR_132772	SNORA90	-	small nucsnoRNA	
chr17-387	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr17	38793491	38796461	+	0	NA	intron (NAluXs LI	4929 NM_003556	8396 Hs. 266060	ENSG00000PIP4K2B	PI5P4KB F	phosphatiprotein-coding		
chr17-602	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr17	60201782	60203887	+	0	NA	intron (NMLT1C LST	28811 NR_002995	677681	NR_002995	ENSG00000SCARNA20	ACA66	small Ca <sub>v</sub> ncRNA	
chr18-294	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr18	2945601	2946868	+	0	NA	non-codiron-codir	389 NR_026655	727896 Hs. 67312	NR_026659	LOC727896	-	cysteine pseudo	
chr18-577	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr18	57700021	57703354	+	0	NA	intron (NAluXs SIN	71476 NM_001242	1.01E+08	Hs. 660645	NR_001242804	LOC1005050	-	uncharactprotein-coding
chr19-365	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr19	36910790	36911759	+	0	NA	intron (NAluSz SIN	4767 NM_001171	374899 Hs. 720312	NR_001037	ENSG00000ZNF829	-	zinc fingerprotein-coding	
chr19-435	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr19	43552649	43554251	+	0	NA	exon (NM exon (NM	20262 NM_174945	284346 Hs. 213534	NR_174945	ENSG00000ZNF575	-	zinc fingerprotein-coding	
chr2-1214	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr2	1.21E+08	1.21E+08	+	0	NA	intron (NAluJo SIN	-121652 NM_104555	29842 Hs. 156471	NR_014555	ENSG00000TFCP2L1	CRTR1 LBF	transcripprotein-coding	
chr2-162C	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr2	1.62E+08	1.62E+08	+	0	NA	intron (Nintron (N	50462 NM_001935	1803 Hs. 368912	NR_001935	ENSG00000DPP4	ADABP ADC	dipeptidprotein-coding	
chr22-425	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr22	42572275	42575244	+	0	NA	non-codiron-codir	8252 NR_002184	91695 Hs. 534041	NR_002184	ENSG00000RRP7BP	RRP7B dJ	ribosomalpseudo	
chr3-1495	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr3	1.5E+08	1.5E+08	+	0	NA	intron (NLMCa LIN	19913 NM_002625	5217 Hs. 91747	NR_002625	ENSG00000PFN2	D3S1319E	profilin protein-coding	
chr4-176C	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr4	17606468	17608846	+	0	NA	3' UTR (N3' UTR (N	-6984 NM_025205	80306 Hs. 73196	NR_025205	ENSG00000MED28	1500003D1	mediator protein-coding	
chr4-169C	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr4	1.69E+08	1.69E+08	+	0	NA	intron (Nintron (N	-86545 NM_032783	84869 Hs. 659311	NR_032783	ENSG00000CBR4	SDR45C1	carbonyl protein-coding	
chr6-1167	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr6	1.17E+08	1.17E+08	+	0	NA	intron (NLMB5 LIN	33778 NM_001366	3841 Hs. 182971	NR_002266	ENSG00000KPN45	IPOA6 SRF	karyopherin-coding	
chr6-1597	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr6	1.6E+08	1.6E+08	+	0	NA	intron (Nintron (N	-2724 NM_173515	154197 Hs. 349077	NR_173515	ENSG00000PNLDC1	HsPNLDC1	PARN likeprotein-coding	
chr7-1557	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr7	1.56E+08	1.56E+08	+	0	NA	intron (Nintron (N	57657 NM_053043	155435 Hs. 59181	NR_053043	ENSG00000RBM33	PRR8	RNA bindiprotein-coding	
chr8-5395	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr8	53930899	53932330	+	0	NA	intron (NLP1A7 LIN	50742 NR_104578	8601 Hs. 368733	NR_003702	ENSG00000RGS20	RGS21 ZG	regulatorprotein-coding	
chr8-125C	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr8	1.25E+08	1.25E+08	+	0	NA	intron (Nintron (N	40673 NM_003125	6713 Hs. 71465	NR_003125	ENSG00000SCSLE	-	squalene protein-coding	
chr9-2691	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr9	26910037	26911435	+	0	NA	intron (NAluJb SIN	-17908 NM_001167	79886 Hs. 178357	NR_024825	ENSG00000CAAP1	C9orf82 Caspase	εprotein-coding	
chr9-109C	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr9	1.09E+08	1.09E+08	+	0	NA	intron (NAluSz SIN	29692 NM_032012	23731 Hs. 308074	NR_032012	ENSG00000TMEM245	C9orf5 CC	transmemprotein-coding	
chr9-1207	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	15481 NM_012164	26190 Hs. 494985	NR_012164	ENSG00000FBXW2	FBW2 FwdZ	F-box ancprotein-coding	
chr9-1208	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr9	1.21E+08	1.21E+08	+	0	NA	exon (NM exon (NM	10958 NM_104601	26147 Hs. 460124	NR_015651	ENSG00000PHF19	MTF2L1 PC	PHD fingerprotein-coding	
chr9-1278	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chr9	1.28E+08	1.28E+08	+	0	NA	intron (NMIRb SINE	7078 NM_001278	2022 Hs. 76753	NR_000115	ENSG00000CENG	END HHT1	endoglin protein-coding	
chrX-4798	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chrX	47987483	47989474	+	0	NA	intron (NMSTB LTR	15511 NM_006962	7569 Hs. 18969	NR_006962	ENSG00000ZNF182	HHZ150 KC	zinc fingerprotein-coding	
chrX-5362	6.42698	0.046447	0.903742	0.051394	0.959012	0.981636	chrX	53624188	53630495	+	0	NA	intron (NTiger20a	59378 NM_031407	10075 Hs. 13690	NR_031407	ENSG00000HUW1	ARF-BP1 F	HECT, UB <sup>a</sup> protein-coding	
chr1-6654	9.870273	0.038255	0.745402	0.051322	0.959069	0.981636	chr1	66547665	66547870	+	0	NA	intron (NL2a LINE	13614 NM_032291	84251 Hs. 132121	NR_032291	ENSG00000SGIP1	-	SH3 domainprotein-coding	
chr18-29C	9.870273	0.038255	0.745402	0.051322	0.959069	0.981636	chr18	2930598	2931388	+	0	NA	intron (Nintron (N	15630 NR_026655	727896 Hs. 67312	NR_026659	LOC727896	-	cysteine pseudo	
chr12-10C	5.419938	0.051265	0.999194	0.051306	0.959081	0.981636	chr12	1E+08	1E+08	+	0	NA	intron (NAluS6 SI	9814 NR_048568	64341 Hs. 115088	NR_022495	ENSG00000ACTR6	ARP6 CDA	actin relprotein-coding	
chr17-535	5.419938	0.051265	0.999194	0.051306	0.959081	0.981636	chr17	5392392	5394365	+	0	NA	intron (NAluJr SIN	-26263 NM_00116C	84268 Hs. 46208	NR_032305	ENSG00000CRPAIN	HRIP RIP	RPA interprotein-coding	
chr6-8721	5.419938	0.051265	0.999194	0.051306	0.959081	0.981636	chr6	87216878	87217908	+	0	NA	intron (Nintron (N	61828 NM_015021	23036 Hs. 44480	NR_015021	ENSG00000ZNF292	NblA00365	zinc fingerprotein-coding	
chr6-1175	5.419938	0.051265	0.999194	0.051306	0.959081	0.981636	chr6	1.18E+08	1.18E+08	+	0	NA	intron (Nintron (N	43100 NM_001366	285761 Hs. 658304	NR_173674	ENSG00000DCLD1	dJ94G16	discoidin protein-coding	
chr7-103C	5.419938	0.051265	0.999194	0.051306	0.959081	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	intron (NLM4a LI	22335 NM_001161	83787 Hs. 287412	NR_031905	ENSG00000CARMC10	PNAS-112	armadillprotein-coding	
chr10-225	4.469751	0.055152	1.075785	0.051266	0.959113	0.981636	chr10	22539091	22539793	+	0	NA	intron (Nintron (N	-101513 NR_036533	1E+08 Hs. 7444	NR_036533	LOC100495	-	uncharactncRNA	
chr1-4098	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr1	40995382	40999747	+	0	NA	intron (Nintron (N	9045 NM_001301	1503 Hs. 473087	NR_001905	ENSG00000CTPS1	CTPS GATL	CTP syntprotein-coding	
chr12-1318	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (Nintron (N	9774 NM_004592	6433 Hs. 308171	NR_004592	ENSG00000SFSWAP	SFRS8 SW	splicing protein-coding	
chr13-778	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr13	77768316	77768657	+	0	NA	exon (NM exon (NM	92972 NR_046715	1.01E+08 Hs. 56928	NR_046715	ENSG00000MYCBP2-AS	-	MYCBP2 arncRNA	
chr15-282	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr15	28210172	28210889	+	0	NA	intron (N(TACA)n S	-112125 NM_000275	4948 Hs. 654411	NR_000275	ENSG00000OCA2	BEY BEY1	OCA2 mēlprotein-coding	
chr16-864	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr16	86494573	86497424	+	0	NA	intron (Nintron (N	12862 NR_033925	400550 Hs. 44882	NR_033925	ENSG00000FENDRR	FOXF1-AS1	FOXF1 ad <sub>v</sub> ncRNA	
chr17-307	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr17	30735967	30736729	+	0	NA	intron (NSVA_F Ret	26740 NR_144395	440423 Hs. 62888	NR_024187	SUZ12P1	SUZ12P	SUZ12 psepseudo	
chr2-1125	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr2	1.13E+08	1.13E+08	+	0	NA	3' UTR (N3' UTR (N	-12411 NM_001137	84172 Hs. 745127	NR_019014	ENSG00000POLR1B	RPA123 RF	RNA polynprotein-coding	
chr2-1135	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr2	1.14E+08	1.14E+08	+	0	NA	intron (NHAL1 LINE	-23772 NR_148507	440900 Hs. 66220	NR_034125	ENSG00000LINC01191	VIN Inc- <sup>β</sup>	long intncRNA	
chr2-1864	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr2	1.86E+08	1.86E+08	+	0	NA	intron (NLM3G LI	9547 NM_018471	55854 Hs. 74118	NR_018471	ENSG00000ZC3H15	HT010 LEF	zinc fingerprotein-coding	
chr20-375	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr20	37998101	37999114	+	0	NA	intron (NMIRc SINE	34849 NM_001303	9675 Hs. 65548	NR_014657	ENSG00000CTTI1	KIAA0406 TELO2	intprotein-coding	
chr20-385	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr20	38573842	38574590	+	0	NA	exon (NM exon (NM	-6981 NR_130907	149685 Hs. 36802	NR_174905	ENSG00000ADIG	SMAP1	adipogenprotein-coding	
chr3-3736	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr3	37367275	37367965	+	0	NA	TTS (NM_C TTS (NM_C	-18649 NM_178344	339883 Hs. 47594	NR_178335	ENSG00000C3orf35	APRG1	chromosonprotein-coding	
chr5-1707	8.136932	-0.04169	0.813248	-0.05126	0.959117	0.981636	chr5	1.77E+08	1.77E+08	+	0	NA	intron (Nintron (N	41241 NM_001031	53917 Hs. 16258	NR_130781	ENSG00000CRAB24	-	RAB24, meprotein-coding	
chr1-1707	6.717431	-0.04589	0.895829	-0.05122	0.959147	0.981636	chr1	1.71E+08	1.71E+08	+	0	NA	intron (Nintron (N	58669 NM_006902	5396 Hs. 28341	NR_006902	ENSG00000PRXR1	AGOTC PHC	paired reprotein-coding	
chr17-786	6.717431	-0.04589	0.895829	-0.05122	0.959147	0.981636	chr17	78699985	78700861	+	0	NA	exon (NM exon (NM	16609 NM_001292	9267 Hs. 19121	NR_004762	ENSG00000CYTH1	B2-1 CYT	cytohesin protein-coding	
chr2-552	6.717431	-0.04589	0.895829	-0.05122	0.959147	0.981636	chr2	55252516	552											

chr9-1225 7.204311	-0.04353	0.861341	-0.05054	0.95969	0.981636	chr9	1.23E+08	1.23E+08	0 NA	intron (N)IMEF LIN	-34539 NM_005294	2844 Hs. 722036NM_005294	ENSG000000GPR21	-	G protein-coding
chr1-3884 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr1	38849394	38851393	0 NA	intron (N)Alu SINE	9379 NM_001271	64121 Hs. 532461NM_022157	ENSG000000RRAGC	GTR2 RAGC	Ras relatprotein-coding
chr1-1761 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr1	1.76E+08	1.76E+08	0 NA	intron (N)AluSc SIN	91624 NM_001001	64326 Hs. 523744NM_022457	ENSG000000COP1	RNFWD2 RNF COP1 E3	protein-coding
chr11-77 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr11	773608	774519	0 NA	exon (NM exon (NM	3424 NM_00131E	347862 Hs. 218362NM_182612	ENSG000000GATD1	PDDC1	glutamine protein-coding
chr13-366 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr13	36878091	36878621	0 NA	intron (N)Tigger3a	41882 NM_00590E	4093 Hs. 123115NM_00590E	ENSG000000SMAD9	MADH6 MAI SMAD	fam protein-coding
chr16-861 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr16	86145	90947	0 NA	intron (N)intron (N	10321 NM_00101E	4350 Hs. 459596NM_002434	ENSG000000MPG	AAG ADPG N-methyl	protein-coding
chr16-587 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr16	58721974	58723865	0 NA	intron (N)intron (N	11397 NM_00128E	2806 Hs. 599477NM_002088	ENSG000000GOT2	KAT4 KAT1	glutamic protein-coding
chr17-366 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr17	3663686	3665050	0 NA	intron (N)intron (N	4210 NM_014604	30851 Hs. 12956 NM_014604	ENSG000000TAX1BP3	TIP-1 TIF Tax1	binc protein-coding
chr19-13C 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr19	13083378	13084078	0 NA	intron (N)intron (N	19130 NM_00558E	4066 Hs. 46446 NM_00558E	ENSG000000LYL1	bHLHa18	LYL1 basiprotein-coding
chr19-18F 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr19	18535844	18537005	0 NA	intron (N)AluJo SIN	7149 NM_012181	23770 Hs. 173464NM_012181	ENSG000000FKBP8	FKBP38 FKFBP	prolprotein-coding
chr2-113F 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr2	1.14E+08	1.14E+08	0 NA	intron (N)AluX3 SI	-9115 NR_026821	654412 Hs. 64026CNR_026821	ENSG000000FAM138B	F379 bA3E	family wincRNA
chr2-1961 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr2	1.96E+08	1.96E+08	0 NA	intron (N)Charlie7	23032 NM_00422E	9262 Hs. 88297 NM_00422E	ENSG000000STK17B	DRAK2	serine/tl protein-coding
chr3-144E 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr3	14468504	14468786	0 NA	intron (N)intron (N	66039 NM_001134	6533 Hs. 529488NM_00304E	ENSG000000SLC6A6	TAUT	solute c protein-coding
chr5-149E 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr5	1493332	1494802	0 NA	intron (N)intron (N	16789 NR_10672E	1.02E+08 NR_10672E	ENSG000000MIR6075	hsa-mir-ε	microRNA ncRNA
chr6-113E 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr6	1.14E+08	1.14E+08	0 NA	intron (N)intron (N	-17905 NR_12584E	1.02E+08 Hs. 12928CNR_12584E	ENSG000000HDAC2-AS2	HDAC2	ancncRNA
chr7-993E 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr7	99399503	99400759	0 NA	intron (N)intron (N	8466 NM_014891	11333 Hs. 63229E NM_014891	ENSG000000PDAP1	MASP28 PFDGFA	ass protein-coding
chr8-144E 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr8	1.44E+08	1.44E+08	0 NA	TTS (NM_TTS (NM_1	788 NR_03063E	1E+08 NR_03063E	ENSG000000MIR939	HMRN939 hmicroRNA	ncRNA
chr9-1314 7.434022	0.042935	0.849669	0.050531	0.959699	0.981636	chr9	1.31E+08	1.31E+08	0 NA	intron (N)intron (N	24933 NM_01331E	84726 Hs. 74395E NM_01331E	ENSG000000PRRC2B	BAT2L BAI	proline r protein-coding
chr12-78C 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr12	78007009	78007965	0 NA	intron (N)intron (N	176593 NM_01490E	89795 Hs. 655301NM_01490E	ENSG000000NAV3	POMF1L1 Sneur	nc protein-coding
chr12-9118 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr12	91103257	91103608	0 NA	3' UTR (N3' UTR (N	8062 NM_00234E	4060 Hs. 40647E NM_00234E	ENSG000000CLUM	LDC SLRR2	lumican protein-coding
chr14-21E 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr14	21222456	21226458	0 NA	intron (N)intron (N	-17557 NR_038971	283624 Hs. 52521CNR_038971	ENSG000000LINC00641	-	long intncRNA
chr17-42E 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr17	42951433	42952197	0 NA	exon (NM exon (NM	12639 NM_001261	80755 Hs. 31740E NM_001261	ENSG000000AARS1	-	alanyl-tf protein-coding
chr17-68E 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr17	68250929	68254406	0 NA	intron (N)AluJo SIN	-4624 NM_016627	51321 Hs. 29356C NM_016627	ENSG000000CAMZ2	-	archaelys protein-coding
chr20-56E 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr20	56517148	56521319	0 NA	TTS (NM_TTS (NM_C	5496 NM_00101E	200232 Hs. 504907NM_00101E	ENSG000000FAM209A	C20orf10E	familyp protein-coding
chr22-314 6.623812	-0.03994	0.79101	-0.0505	0.959726	0.981636	chr22	31468976	31471612	0 NA	intron (N)AluSg SIN	19262 NM_001164	56478 Hs. 51755E NM_01984E	ENSG000000EIF4ENF1	EIF4E T Clas	eukaryotiprotein-coding
chr1-677E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr1	67701470	67705980	0 NA	3' UTR (N3' UTR (N	19874 NM_001924	1647 Hs. 80409 NM_001924	ENSG000000GADD45A	DDIT1 GAI	growth ar protein-coding
chr1-108E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr1	1.09E+08	1.09E+08	0 NA	intron (N)intron (N	12981 NM_00127E	23155 Hs. 65848E NM_015127	ENSG000000CLCC1	MCLC	chloride protein-coding
chr11-62E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr11	62661754	62663017	0 NA	TTS (NR_TTS (NR_1	2831 NR_104411	1.02E+08 Hs. 9061 NM_00128E	ENSG000000C11orf98	C11orf48	chromoson protein-coding
chr11-72E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr11	72028127	72029581	0 NA	intron (N)intron (N	14560 NR_10417E	1E+08 Hs. 713607NR_10417E	ENSG000000LOC10012E	-	uncharactncRNA
chr12-28E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr12	2801109	2803158	0 NA	intron (N)intron (N	7163 NM_002014	2288 Hs. 52418E NM_002014	ENSG000000FKBP4	FKBP51 FKFBP	prolprotein-coding
chr12-21E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr12	21512152	21514846	0 NA	intron (N(T)n Simp	11710 NM_01607E	51026 Hs. 6227E NM_01607E	ENSG000000GOLT1B	CGI-141 Colgi	trε protein-coding
chr12-12E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr12	1.22E+08	1.22E+08	0 NA	intron (N)intron (N	-61238 NM_00135E	65082 Hs. 48788E NM_02291E	ENSG000000VPS33A	MPSPS	VPS33A c protein-coding
chr15-67E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr15	67174121	67175774	0 NA	intron (N)intron (N	8792 NM_00114E	4088 Hs. 72798E NM_00590E	ENSG000000SMAD3	HSPC193 FSMAD	fam protein-coding
chr16-14E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr16	14574979	14578561	0 NA	intron (N)intron (N	53490 NM_00258E	5073 Hs. 253197NM_00258E	ENSG000000PARN	DAN DKCBε	poly(A)-s protein-coding
chr17-82E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr17	82463039	82461972	0 NA	intron (N)AluJb SIN	2414 NM_01233E	26502 Hs. 25652E NM_01233E	ENSG000000NARF	TOP2	nuclear f protein-coding
chr18-23E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr18	23576015	23577324	0 NA	intron (N)LR12C LI	9837 NM_000271	4864 Hs. 46477E NM_000271	ENSG000000NCP1	NPC POG2 NPC	intrε protein-coding
chr19-57E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr19	5703788	5709831	0 NA	intron (N)intron (N	13337 NR_07639E	9361 Hs. 35026E NM_00479E	ENSG000000LONP1	CODASS LC lon	peptiprotein-coding
chr19-137 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr19	13771268	13772504	0 NA	intron (N)intron (N	-2570 NM_014047	28974 Hs. 23161E NM_014047	ENSG000000C19orf53	HSPC023 L chromoson	protein-coding
chr2-199E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr2	2E+08	2E+08	0 NA	intron (N)Alu SINE	-16966 NM_00136E	79568 Hs. 154494NM_02452E	ENSG000000MAIP1	COrf47	matrix A protein-coding
chr2-233E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr2	2.33E+08	2.33E+08	0 NA	intron (N)MER47A DN	5844 NM_00119C	55054 Hs. 52932E NM_01797E	ENSG000000ATG16L1	APG16L AI	autophagy protein-coding
chr20-59E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr20	50592859	50594336	0 NA	intron (N)intron (N	7811 NR_03037E	693230 NR_03037E	ENSG000000MIR645	MIRN645 hmicroRNA	ncRNA
chr20-50E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr20	59037155	59038317	0 NA	intron (N)intron (N	5050 NM_01604E	51012 Hs. 65686E NM_01604E	ENSG000000PRELID3B	C20orf45 PREL1	don protein-coding
chr22-504 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr22	50447543	50449124	0 NA	exon (NM exon (NM	26702 NM_00297E	6305 Hs. 589924NM_00297E	ENSG000000SBF1	CMT4B3 DESET	bindiprotein-coding
chr3-433E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr3	43339430	43342187	0 NA	intron (N)intron (N	11154 NR_046757	1.01E+08 Hs. 600984NR_046757	SNRK-AS1	-	SNRK antincRNA
chr3-491E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr3	49121664	49122972	0 NA	exon (NM exon (NM	-1380 NM_001351	10869 Hs. 25559E NM_00667E	ENSG000000USP19	ZMYND9	ubiquitiprotein-coding
chr3-503E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr3	50355180	50356160	0 NA	intron (N)intron (N	3851 NM_007024	11070 Hs. 91566 NM_007024	ENSG000000TMEM115	PL6	transmemt protein-coding
chr3-1017 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr3	1.02E+08	1.02E+08	0 NA	intron (N)intron (N	8900 NM_02454E	79598 Hs. 44413E NM_02454E	ENSG000000CEP97	2810403BC	centroson protein-coding
chr3-186E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr3	1.86E+08	1.86E+08	0 NA	exon (NM exon (NM	29056 NM_004454	2119 Hs. 43697 NM_004454	ENSG000000ETV5	ERM	ETS variε protein-coding
chr4-5684 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr4	5684119	5686108	0 NA	intron (N(AC)n Sin	22446 NM_147127	132884 Hs. 87306 NM_147127	ENSG000000EVC2	ELN WAD	Evc cilie protein-coding
chr5-347E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr5	34769850	34770698	0 NA	intron (N)intron (N	-68890 NM_14472E	153657 Hs. 43574E NM_14472E	ENSG000000TTC23L	MC25-1	tetratric protein-coding
chr5-419E 7.913044	0.041391	0.822996	0.050294	0.959888	0.981636	chr5	419								



chr17-498.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr17	49811468	49812439	+ 0 NA	intron (Nintron (N	23272 NM_001199	11143 Hs. 21907 NM_007067	ENSG000000CKAT7	HBO1 HBO#	lysine acprotein-coding
chr19-636.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr19	6364607	6369247	+ 0 NA	intron (NAluJb SIN	5396 NM_006012	8192 Hs. 515092 NM_006012	ENSG000000CLPP	DFNB81 PF	caseinolyprotein-coding
chr19-218.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr19	21825383	21827492	+ 0 NA	intron (NLTR70 LTF	9745 NM_001256	7594 Hs. 534366 NM_003423	ENSG000000ZNF43	HTF6 KOX2	zinc fingprotein-coding
chr19-233.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr19	23337205	23339818	+ 0 NA	IntergeniLIM2 LINE	56960 NM_003430	7644 Hs. 58834 NM_003430	ENSG000000ZNF91	HP7 HTF1	zinc fingprotein-coding
chr2-3401.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr2	3401870	3403256	+ 0 NA	intron (NAluSg SIN	22869 NM_01603C	51112 Hs. 25271 NM_01603C	ENSG000000TRAPP12	CG1-87 PE	traffickingprotein-coding
chr2-2766.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr2	27694800	27695586	+ 0 NA	TTS (NM_C TTS (NM_C	20539 NR_13520C	1E+08 Hs. 515876 NR_13520C	ENSG000000CLINCO146C	-	long intencRNA
chr2-5591.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr2	55913057	55914858	+ 0 NA	intron (NAluSx SIN	9825 NM_001039	2202 Hs. 76224 NM_00410F	ENSG000000EFEMP1	DHRD DRAL	EGF contprotein-coding
chr2-1137.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr2	1.14E+08	1.14E+08	+ 0 NA	intron (Nintron (N	-16447 NR_039942	1.01E+08 Hs. NR_039942	ENSG000000MIR4782	-	microRNA ncRNA
chr20-315.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr20	31561941	31567231	+ 0 NA	intron (NAluJb SIN	8677 NR_046855	1.01E+08 Hs. 373741 NR_046855	ENSG000000HM13-AS1	-	HM13 antncRNA
chr22-245.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr22	24571316	24572907	+ 0 NA	non-codiron-codir	-11639 NM_01243C	2678 Hs. 595809 NM_00526F	ENSG000000GGT1	CD224 D22	gamma-glu protein-coding
chr22-304.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr22	30406493	30406999	+ 0 NA	intron (NAluS6 SI	9728 NM_001204	23541 Hs. 335614 NM_01242F	ENSG000000SECI14L2	C22orf6 SSEC14	likprotein-coding
chr22-415.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr22	41582458	41584761	+ 0 NA	intron (Nintron (N	6231 NM_00267E	5372 Hs. 75835 NM_00267E	ENSG000000PMM1	PMM 1 PMW	phosphome protein-coding
chr3-3161.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr3	31605987	31607015	+ 0 NA	intron (NTHEIB-int	47576 NM_17886E	201595 Hs. 475812 NM_17886E	ENSG000000STT3B	CDGLX SMT3T3	oligprotein-coding
chr3-1496.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr3	1.49E+08	1.49E+08	+ 0 NA	TTS (NM_C TTS (NM_C	42851 NM_03238E	84343 Hs. 558314 NM_03238E	ENSG000000HPS3	BLOC251 SHPS3	biogprotein-coding
chr3-1612.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr3	1.61E+08	1.61E+08	+ 0 NA	intron (Nintron (N	20946 NM_01593E	51068 Hs. 598833 NM_01593E	ENSG000000NMD3	CGI-07	NMD3 ribcprotein-coding
chr3-1727.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr3	1.72E+08	1.72E+08	+ 0 NA	exon (NM_exon (NM	200762 NM_00412E	2693 Hs. 130212 NM_00412E	ENSG000000GHSR	GHPD	growth hprotein-coding
chr3-1837.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr3	1.73E+08	1.73E+08	+ 0 NA	intron (NLA2 LINE	14241 NM_00134E	1894 Hs. 518295 NM_01809E	ENSG000000ECT2	ARHGEF31	epitheliaprotein-coding
chr4-5186.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr4	51863930	51866219	+ 0 NA	intron (NTHEIB-int	20090 NR_12064C	56922 Hs. 47649 NM_02016E	ENSG000000MCCC1	MCC-B MCC	methylcrp protein-coding
chr4-8007.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr4	80001842	80004839	+ 0 NA	intron (Nintron (N	21495 NM_001287	23142 Hs. 605388 NM_01511E	ENSG000000DCUN1D4	-	defectiveprotein-coding
chr5-1347.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr5	1.35E+08	1.35E+08	+ 0 NA	intron (NAluSp SIN	69889 NM_00128E	118429 Hs. 162963 NM_05817E	ENSG000000CANTXR2	CMG-2 CMC	ANTXR celprotein-coding
chr5-1388.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr5	1.39E+08	1.39E+08	+ 0 NA	intron (Nintron (N	39190 NM_01482E	9879 Hs. 406546 NM_01482E	ENSG000000DDX46	PRPF5 Prp	DEAD-box protein-coding
chr6-9051.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr6	90513963	90517033	+ 0 NA	3' UTR (N3' UTR (N	-47391 NM_00129C	1495 Hs. 445981 NM_00190E	ENSG000000CTNNA1	CAP102 MC	catenin aprotein-coding
chr6-1706.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr6	1.71E+08	1.71E+08	+ 0 NA	intron (Nintron (N	13426 NM_00279E	6885 Hs. 594833 NM_00318E	ENSG000000MAP3K7	CSCF FMD2	mi togen-eprotein-coding
chr7-6177.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr7	6170065	6171016	+ 0 NA	exon (NM_exon (NM	1597 NM_001367	5689 Hs. 352768 NM_00279E	ENSG000000PSMB1	HC5 PMSB1	proteasomeprotein-coding
chr7-1731.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr7	17310289	17313428	+ 0 NA	intron (Nintron (N	19265 NM_001367	9265 Hs. 487475 NM_00422E	ENSG000000CYTH3	ARNO3 GRF	cytohesin protein-coding
chr9-3256.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr9	32564687	32565961	+ 0 NA	intron (Nintron (N	13206 NM_001621	196 Hs. 171188 NM_001621	ENSG000000AHR	PRP8 bHLH	aryl h protein-coding
chr9-3418.7.691191	-0.04142	0.832727	-0.04975	0.960325	0.981636	chr9	34184313	34185722	+ 0 NA	intron (NAluS2 SI	7835 NM_18273E	4712 Hs. 493666 NM_00249E	ENSG000000NDUFB6	B17 C1	NADH:ubiq protein-coding
chr12-112.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr12	1.12E+08	1.12E+08	+ 0 NA	3' UTR (N3' UTR (N	5974 NM_001171	51271 Hs. 268963 NM_01652E	ENSG000000UBAP1	NAG20 SPC	ubiquitir protein-coding
chr2-1521.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr2	1.52E+08	1.52E+08	+ 0 NA	intron (Nintron (N	8565 NR_03743C	1.01E+08 Hs. NR_03743C	ENSG000000MIR3657	-	microRNA ncRNA
chr3-4848.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr3	48467261	48468465	+ 0 NA	TTS (NM_C TTS (NM_C	30701 NM_00584E	10254 Hs. 17200 NM_00584E	ENSG000000STAM2	Hbp STAM2	signal tr protein-coding
chr5-1678.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr5	16750525	16752038	+ 0 NA	intron (Nintron (N	1633 NM_03362E	11277 Hs. 707026 NM_00724E	ENSG000000TREG1	AGS1 CRV	three priprotein-coding
chr5-3718.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr5	37183957	37185046	+ 0 NA	intron (Nintron (N	-134358 NM_001034	54463 Hs. 481704 NM_01900C	ENSG000000RETREG1	FAM134B Jret	ubiq protein-coding
chr6-1558.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr6	1.55E+08	1.55E+08	+ 0 NA	intron (NTHEIB LTF	64545 NR_13426E	1.05E+08 Hs. 170993 NR_13426E	ENSG000000LOC105374	-	uncharactncRNA
chr7-1578.8.871089	0.038752	0.781453	0.049589	0.96045	0.981636	chr7	1.57E+08	1.57E+08	+ 0 NA	intron (Nintron (N	7071 NM_01602C	51106 Hs. 279906 NM_01602C	ENSG000000TFB1M	CGI-75 CC	transcrip protein-coding
chrX-1045.6.668433	-0.04587	0.928275	-0.04942	0.960586	0.981636	chrX	10454148	10454347	+ 0 NA	intron (Nintron (N	-88218 NM_005494	10049 Hs. 490746 NM_005494	ENSG000000DNAJB6	DJ4 DnaJ	DnaJ heat protein-coding
chr11-726.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr11	72685502	72686130	+ 0 NA	intron (Nintron (N	113566 NM_00119E	4281 Hs. 27695 NM_000381	ENSG000000MID1	BBB61 FX	midline l protein-coding
chr12-111.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr12	1.12E+08	1.12E+08	+ 0 NA	intron (NAluS2 SI	32255 NM_025247	80724 Hs. 331141 NM_025247	ENSG000000ACAD10	-	acyl-CoA protein-coding
chr15-522.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr15	52055753	52056393	+ 0 NA	intron (Nintron (N	36854 NM_00274E	5597 Hs. 411847 NM_00274E	ENSG000000MAPK6	ERK3 HsT	mi togen-eprotein-coding
chr17-785.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr17	78975953	78977034	+ 0 NA	intron (Nintron (N	3430 NM_005567	3959 Hs. 514533 NM_005567	ENSG000000LGALS3BP	90K BTBD1	galectin protein-coding
chr17-826.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr17	82820005	82820562	+ 0 NA	intron (Nintron (N	19724 NM_02470E	79755 Hs. 464391 NM_02470E	ENSG000000ZNF750	ZFP750	zinc fingprotein-coding
chr4-1475.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr4	1.48E+08	1.48E+08	+ 0 NA	intron (Nintron (N	24682 NM_138364	90826 Hs. 591692 NM_138364	ENSG000000PRMT9	PRMT10	protein aprotein-coding
chr5-4354.5.955815	0.046407	0.940149	0.049361	0.960632	0.981636	chr5	43549216	43550357	+ 0 NA	intron (NAluS2 SIN	7291 NM_006451	10605 Hs. 482033 NM_006451	ENSG000000PAIP1	-	poly(A) t protein-coding
chr16-278.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr16	27682602	27683038	+ 0 NA	intron (NMSTC LTR	36209 NR_14789E	1E+08 Hs. 610277 NR_14789E	LOC100128E	-	uncharactncRNA
chr2-3885.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr2	38856401	38856986	+ 0 NA	intron (NAluJb SIN	19241 NM_19896E	90957 Hs. 468226 NM_19896E	ENSG000000DXH57	DDX57	DEXh-box protein-coding
chr2-2178.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr2	2.18E+08	2.18E+08	+ 0 NA	intron (NAluJr SIN	19584 NR_14579E	1.1E+08 Hs. NR_14579E	SNORA115	-	small nucsnRNA
chr3-4705.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr3	47094674	47097490	+ 0 NA	intron (Nintron (N	67895 NM_01415E	29072 Hs. 517941 NM_012271	ENSG000000SETD2	HBP231 HSE	domaiprotein-coding
chr5-6495.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr5	64962457	64963962	+ 0 NA	intron (NAluSx1 SI	194279 NM_001364	10283 Hs. 371372 NM_00586E	ENSG000000CWC27	NY-CO-10 CWC27	spl protein-coding
chr6-5705.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr6	57057185	57058448	+ 0 NA	IntergeniAluJb SIN	11069 NM_00128E	57691 Hs. 709521 NM_020931	ENSG000000KIAA1586	-	KIAA1586 protein-coding
chr9-1135.5.427796	0.048603	0.984753	0.049356	0.960636	0.981636	chr9	1.14E+08	1.14E+08	+ 0 NA	intron (NLA2c LINE	88124 NM_001633	259 Hs. 436911 NM_001633	ENSG000000CAMP	AIM EDC1	alpha-1-n protein-coding
chr11-726.7.664047	0.041071	0.833565	0.049271	0.960703	0.981636	chr11	72886797	72887485	+ 0 NA	intron (N(AT)n Sin	72730 NM_00131E	89849 Hs. 653188 NM_03338E	ENSG000000ATG16L2	ATG16B Wt	autophagy protein-coding
chr1-331C.7.664047	-0.04178	0.849447	-0.04918	0.9											

chr15-632.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr15	63284390	63285716	+	0	NA	intron (Nintron (N	7448 NM_031301	83464	Hs. 511705	NR_031301	ENSG000004APH1B	APH-1B PFaph-1 honprotein-coding
chr15-846.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr15	84644817	84652584	+	0	NA	intron (Nintron (N	5546 NR_130944	84942	Hs. 745027	NR_032856	ENSG000004WDR73	GAMOS GAW WD repeatprotein-coding
chr15-898.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr15	89883594	89888712	+	0	NA	intron (NAluSc5 SI	-2123 NR_049807	1.01E+08		NR_049807	ENSG000004MIR5009	microRNA ncRNA
chr16-166.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr16	16321359	16322929	+	0	NA	intron (NMIR SINE	-2444 NR_106966	1.02E+08		NR_106966	ENSG000004MIR6511A2	MIR6511A2-microRNA ncRNA
chr16-167.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr16	66744081	66749641	+	0	NA	intron (NMIRb SINE	4748 NM_006141	1783	Hs. 369066	NR_006141	ENSG000004DYNCL1L2	DNCL1L2 Ljdynein cyprotein-coding
chr17-356.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr17	35693916	35695855	+	0	NA	intron (NAluS SIN	-36754 NM_03331E	91608	Hs. 744994	NR_03331E	ENSG000004CRASL10B	RRP17 VTSRAS like protein-coding
chr17-437.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr17	43768333	43774826	+	0	NA	intron (NMIRb SINE	7398 NM_004099	1845	Hs. 181046	NR_004099	ENSG000004DUSP3	VHR dual specprotein-coding
chr18-244.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr18	24440380	24446451	+	0	NA	intron (NFLAM_C SI	16745 NM_018435	55364	Hs. 515317	NR_018435	ENSG000004IMPACT	RWDD5 impact RFPprotein-coding
chr2-6908.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr2	69090261	69094568	+	0	NA	intron (Nintron (N	-11268 NR_036073	1E+08		NR_036073	ENSG000004MIR3126	mir-3126 microRNA ncRNA
chr2-1351.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (Nintron (N	16664 NR_145723	1.1E+08		NR_145723	ENSG000004SNORA40B	small nucsnRNA
chr2-1711.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	intron (Nintron (N	61187 NM_001136	9874	Hs. 744917	NR_001136	ENSG000004TLK1	PKU-beta tousel lprotein-coding
chr2-1862.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr2	1.87E+08	1.87E+08	+	0	NA	Intergeni HERVK-int	35193 NM_018471	55854	Hs. 74118	NR_018471	ENSG000004ZC3H15	HTO10 LEFzinc fingprotein-coding
chr20-508.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr20	50562111	50567094	+	0	NA	intron (NAluS SIN	-21184 NR_03037E	693230		NR_03037E	ENSG000004MIR645	MIRN645 hmicroRNA ncRNA
chr21-392.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr21	39286973	39291414	+	0	NA	intron (NLMIEg LIN	24439 NM_018963	54014	Hs. 62713	NR_018963	ENSG000004BRWD1	C21orf17 bromodome protein-coding
chr22-176.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr22	17609895	17614059	+	0	NA	intron (NLMIM LINE	16772 NM_00169E	529	Hs. 51733	NR_00169E	ENSG000004ATP6V1E1	ARCL2C AIATPase H+protein-coding
chr3-1258.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr3	1.26E+08	1.26E+08	+	0	NA	intron (NMER1 2 DN	5200 NM_003794	8723	Hs. 50724	NR_003794	ENSG000004SNX4	ATG24B sorting rprotein-coding
chr3-1968.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr3	1.97E+08	1.97E+08	+	0	NA	intron (NMER2 B LI	-34415 NR_04663C	1.01E+08		NR_04663C	ENSG000004NCBP2-AS1	NCBP2 antncRNA
chr5-1785.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr5	1.79E+08	1.79E+08	+	0	NA	intron (NLMIPREC2 I	15168 NM_05823C	117608	Hs. 724051	NR_05823C	ENSG000004ZNF354B	KID2 zinc fingprotein-coding
chr6-2464.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr6	24649019	24654604	+	0	NA	intron (NAluS SIN	-5620 NM_00135E	9856	Hs. 26441	NR_01480E	ENSG000004KIAA0319	AAVR DYLLKIAA0319 protein-coding
chr6-7568.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr6	75695666	75697278	+	0	NA	intron (Nintron (N	-52767 NM_00136E	4646	Hs. 149387	NR_00499E	ENSG000004MYO6	DFNA22 DFmyosin VIprotein-coding
chr6-1588.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr6	1.59E+08	1.59E+08	+	0	NA	exon (NM exon (NM	-1367 NR_106981	1.02E+08		NR_106981	ENSG000004MIR7161	hsa-mir-7161 microRNA ncRNA
chr7-5724.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr7	5724052	5726363	+	0	NA	intron (Nintron (N	-13297 NR_106934	1.02E+08		NR_106934	ENSG000004MIR6874	hsa-mir-6874 microRNA ncRNA
chr7-6657.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr7	66571958	66575661	+	0	NA	intron (Nintron (N	18598 NR_111974	493754	Hs. 73240	NR_00293E	ENSG000004CGS1-124K	RAB guanipseudo
chr7-2182.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	intron (Nintron (N	39838 NM_001364	3663	Hs. 521181	NR_03264E	ENSG000004IRF5	SLEB10 interfercprotein-coding
chr7-1514.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr7	1.51E+08	1.51E+08	+	0	NA	intron (Nintron (N	-29047 NR_13177E	155051	Hs. 647104	NR_144727	ENSG000004CRYGN	crystalliprotein-coding
chr8-3908.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr8	39058377	39064633	+	0	NA	intron (NERVL-B4-i	-42820 NR_14598E	1.1E+08		NR_14573E	ENSG000004SNORD38D	small nucsnRNA
chr9-2182.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr9	21822802	21825411	+	0	NA	intron (NLMIP5 LIN	21472 NM_002451	4507	Hs. 19326	NR_002451	ENSG000004MTAP	BDMF DMSFmethylthiuprotein-coding
chr9-3628.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr9	36232851	36235383	+	0	NA	exon (NM exon (NM	24331 NM_00119C	10020	Hs. 5920	NR_00547E	ENSG000004GNE	DMRV GLCN glucosami protein-coding
chr9-1131.8.178072	-0.03956	0.808735	-0.04891	0.960988	0.981636	chr9	1.13E+08	1.13E+08	+	0	NA	exon (NM exon (NM	17504 NM_00186E	1318	Hs. 24030	NR_00186E	ENSG000004SLC31A2	COPT2 CTF solute cprotein-coding
chr17-751.8.441064	0.040043	0.819596	0.048857	0.961033	0.981636	chr17	7511064	7511828	+	0	NA	exon (NM exon (NM	27080 NM_000937	5430	Hs. 270017	NR_000937	ENSG000004PDLR2A	POLR2A POL RNA cypprotein-coding
chr22-458.8.441064	0.040043	0.819596	0.048857	0.961033	0.981636	chr22	45327789	45328973	+	0	NA	intron (Nintron (N	9938 NM_00134E	55007	Hs. 26501	NR_01791E	ENSG000004FAM118A	C22orf8 family wiprotein-coding
chr1-4668.8.129074	-0.03997	0.820188	-0.04873	0.961133	0.981636	chr1	46654658	46656004	+	0	NA	intron (Nintron (N	10545 NM_00125E	64756	Hs. 100874	NR_02274E	ENSG000004ATPAF1	ATP11 ATF ATP syntp protein-coding
chr14-994.8.129074	-0.03997	0.820188	-0.04873	0.961133	0.981636	chr14	99457200	99458113	+	0	NA	intron (Nintron (N	23203 NM_19912E	84193	Hs. 510407	NR_03223E	ENSG000004SETD3	C14orf154SET domaiprotein-coding
chr4-5187.8.129074	-0.03997	0.820188	-0.04873	0.961133	0.981636	chr4	51875948	51877657	+	0	NA	intron (NMER8 DNA	33223 NM_001287	23142	Hs. 60538	NR_01511E	ENSG000004DCUN1D4	defective protein-coding
chr5-1128.8.129074	-0.03997	0.820188	-0.04873	0.961133	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (NAluS SIN	21261 NM_00566E	7905	Hs. 42960	NR_00566E	ENSG000004REEP5	C5orf18 receptor protein-coding
chr6-111.8.129074	-0.03997	0.820188	-0.04873	0.961133	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (NLMIAA4 LI	-86717 NR_03410E	643749	Hs. 48622	NR_03410E	ENSG000004TRAF31P2	C6UAS C6C TRAF31P2 ncRNA
chr4-1094.10.83618	0.034923	0.718446	0.048609	0.961231	0.981636	chr4	1.09E+08	1.09E+08	+	0	NA	intron (NMLTID LTF	-12516 NR_03997E	1.01E+08		NR_03997E	ENSG000004SEC24B-AS	1/2-SBSRN SEC24B arncRNA
chr7-1029.8.829134	0.036514	0.751348	0.048598	0.96124	0.981636	chr7	1.03E+08	1.03E+08	+	0	NA	Intergeni Intergeni	10630 NM_001114	1E+08	Hs. 61025	NR_001114	ENSG000004UPK3BL1	UPK3BL UF uprolakiprotein-coding
chr8-9424.9.829134	0.036514	0.751348	0.048598	0.96124	0.981636	chr8	94249616	94249845	+	0	NA	3' UTR (N3' UTR (N	12589 NR_08617E	2669	Hs. 65446	NR_005261	ENSG000004GEM	KIR GFP bindiprotein-coding
chr9-4102.9.829134	0.036514	0.751348	0.048598	0.96124	0.981636	chr9	41023076	41023847	+	0	NA	intron (NLMIPA2 LIN	31200 NR_03400E	1E+08	Hs. 23186	NR_03400E	ENSG000004FRG1HP	FRG1HP FSHD regipseudo
chr1-1237.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr1	12378507	12380415	+	0	NA	intron (Nintron (N	-127785 NR_00302E	677805	Hs. 65845	NR_00302E	ENSG000004SNORA59A	ACA59 small nucsnRNA
chr1-2685.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr1	26893067	26896734	+	0	NA	intron (NMIRb SINE	-4617 NM_01806E	57407	Hs. 14333	NR_01806E	ENSG000004GPN2	ATPBD1B GPN-loop protein-coding
chr1-3912.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr1	39125928	39126917	+	0	NA	intron (NMLT1C LTF	42255 NM_01209E	23499	Hs. 47247	NR_01209E	ENSG000004MACF1	ABP620 AC microtub protein-coding
chr1-3938.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr1	39388866	39390985	+	0	NA	intron (NCharlie E	-19148 NR_01503E	643314	Hs. 65876	NR_01503E	ENSG000004KIAA0754	KIAA0754 protein-coding
chr1-6661.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr1	66610069	66612944	+	0	NA	intron (Nintron (N	-16934 NR_03606C	1E+08		NR_03606C	ENSG000004MIR3117	mir-3117 microRNA ncRNA
chr1-8896.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr1	88960537	88966032	+	0	NA	intron (NLa LINE	29345 NM_00116E	494115	Hs. 48189	NR_01961C	ENSG000004RBMX1	RBM1 RBMX like protein-coding
chr10-805.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr10	80512036	80515670	+	0	NA	intron (NMERS8 DN	22089 NR_120661	1.02E+08	Hs. 59366	NR_120661	ENSG000004LOC101925	uncharactercncRNA
chr10-100.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr10	1E+08	1E+08	+	0	NA	intron (NAluJr SIN	2968 NM_001001	282991	Hs. 34906	NR_17380E	ENSG000004BLOC1S2	BLOS2 BOFbiogenesiprotein-coding
chr10-100.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr10	1.03E+08	1.03E+08	+	0	NA	exon (NM exon (NM	18106 NM_001591E	51063	Hs. 24154	NR_01591E	ENSG000004CALHM2	FAM26B calcium Iprotein-coding
chr11-918.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr11	9187851	9193762	+	0	NA	intron (NHALLb LIN	74520 NR_14596E	23258	Hs. 50185	NR_01521E	ENSG000004DENND5A	EIEE49 RA DENN dome protein-coding
chr11-684.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr11	68043314	68045575	+	0	NA	promoter-promoter-	-350 NR_106811	1.02E+08		NR_106811	ENSG000004MIR6753	hsa-mir-6753 microRNA ncRNA
chr11-754.6.91386	0.042419	0.873996	0.048534	0.96129	0.981636	chr11	75412872	75415802	+	0	NA	intron (NAluJ SINE						



chr17-676.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr17	6760137	6763590	+	0 NA	intron (Nintron (N	5817 NM_001353	54739 Hs. 44197E	110752:ENSG00000XAF1	BIRC4BP FXIAP	asc protein-coding	
chr17-788.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr17	7853337	7854278	+	0 NA	3' UTR (N3' UTR (N	-1259 NM_203411	92162 Hs. 389666E	NR_203411:ENSG00000TMEM88	-	transmembrane protein-coding	
chr17-766.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr17	76092776	76095045	+	0 NA	intron (Nintron (N	4166 NR_10692E	1.02E+08	NR_10692E:ENSG00000MIR6868	hsa-mir-6	microRNA ncRNA	
chr19-1074.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	6746579	6752733	+	0 NA	intron (NAluJo SIN	9976 NR_110231	9322 Hs. 515094N	00424:ENSG00000TRIP10	CIP4 HSTF	thyroid l protein-coding	
chr19-678.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	10352271	10355265	+	0 NA	intron (Nintron (N	-14144 NM_00132C	3385 Hs. 65456E	NR_00216E:ENSG00000ICAM3	CD50 CDWE	intercell protein-coding	
chr19-144.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	14463558	14464611	+	0 NA	exon (NM_exon (NM	11270 NM_00095E	5731 Hs. 15936CN	00095E:ENSG00000PTGER1	EPI	prostagl protein-coding	
chr19-144.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	14492474	14492774	+	0 NA	intron (Nintron (N	3502 NM_00571E	10755 Hs. 65501E	NR_00571E:ENSG00000GTPC1	C19orf3 CGIP	PDZ protein-coding	
chr19-387.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	38707948	38711211	+	0 NA	intron (Nintron (N	34945 NM_144691	147968 Hs. 73177E	NR_144691:ENSG00000CAPN12	-	calpain l protein-coding	
chr19-413.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	41302490	41308158	+	0 NA	intron (NMIR SINE	-4848 NM_05284E	90324 Hs. 437497N	05284E:ENSG00000CCDC97	-	coiled-c protein-coding	
chr19-588.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr19	58311765	58315134	+	0 NA	intron (NAluSg7 SI	8075 NR_14444E	1.05E+08	Hs. 435404N	14444E:ENSG00000ERVK3-1	-	endogeno ncRNA
chr2-2733.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr2	27339137	27343584	+	0 NA	intron (NLMIB4 LIN	5818 NR_038427	1.01E+08	Hs. 66650E	NR_038427:ENSG00000GTF3C2-AS	-	GTF3C2 arncRNA
chr2-2191.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr2	2.19E+08	2.19E+08	+	0 NA	exon (NM_exon (NM	2372 NM_001321	79137 Hs. 516707N	02429E:ENSG00000RETREG2	C2orf17 Freticulo	protein-coding	
chr2-230.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr2	2.3E+08	2.3E+08	+	0 NA	intron (Nintron (N	-21214 NM_00120E	6672 Hs. 36905E	NR_00311E:ENSG00000SP100	Lysp100b	SP100 nuc protein-coding	
chr20-323.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr20	32214870	32217592	+	0 NA	intron (NMIR3 SINE	8351 NM_01535E	23509 Hs. 47240E	NR_01535E:ENSG00000POFUT1	DD2 FUT1	intron (C protein-coding	
chr20-573.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr20	57365658	57371100	+	0 NA	intron (Nintron (N	-8881 NM_00119C	1E+08	NR_00119C:ENSG00000MTRNR2L3	HN3	MT-RNR2 l protein-coding	
chr3-1003.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr3	1E+08	1E+08	+	0 NA	intron (Nintron (N	33142 NM_01482C	9868 Hs. 22725E	NR_01482C:ENSG00000TOMM70	TOMM70A T	transloc protein-coding	
chr5-1727.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr5	17274446	17277772	+	0 NA	3' UTR (N3' UTR (N	58478 NM_006317	10409 Hs. 201641N	006317:ENSG00000CBASP1	CAP-23 C	brain ab protein-coding	
chr5-109.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr5	1.09E+08	1.09E+08	+	0 NA	intron (NAluSq2 SI	-17564 NR_14904C	285638 Hs. 532104N	NR_14904C:ENSG00000LOC28563E	-	uncharactncRNA	
chr5-1501.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr5	1.5E+08	1.5E+08	+	0 NA	intron (NMLT1K LTF	-6059 NM_005211	1436 Hs. 58621E	NR_005211:ENSG00000CSF1R	C-FMS CD1	colony s protein-coding	
chr5-1501.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr5	1.5E+08	1.5E+08	+	0 NA	intron (NMIR3 SINE	20723 NM_00135E	5159 Hs. 509067N	00260E:ENSG00000PDGFRB	CD140B E	platelet protein-coding	
chr6-8221.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr6	82219860	82225351	+	0 NA	intron (NTigger 3e	25139 NM_00130C	25998 Hs. 30642E	NR_001552E:ENSG00000IBTK	BTD26 BT	inhibitor protein-coding	
chr6-834.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr6	83405952	83407534	+	0 NA	intron (NMLT2D LTF	24308 NM_00239E	4199 Hs. 21160	NR_00239E:ENSG00000CME1	HUMNDME	malic enz protein-coding	
chr6-898.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr6	89860908	89863349	+	0 NA	exon (NM_exon (NM	32228 NM_01211E	9994 Hs. 55821E	NR_01211E:ENSG00000CASP8AP2	CED-4 FL	caspace ε protein-coding	
chr7-446.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr7	44696292	44700530	+	0 NA	intron (Nintron (N	-50155 NM_00130C	83637 Hs. 77978	NR_03144E:ENSG00000ZM122	NET27 TR	zinc fing protein-coding	
chr7-1573.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr7	1.57E+08	1.57E+08	+	0 NA	intron (NLMIB8 LIN	-77543 NM_005494	10049 Hs. 49074E	NR_005494:ENSG00000DNAJB6	DJ4 DnaJ DnaJ	heat protein-coding	
chr8-670.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr8	67053094	67060020	+	0 NA	exon (NM_exon (NM	5576 NM_006837	10987 Hs. 49191E	NR_006837:ENSG00000COPS5	CSN5 JAB1	COP9 sigr protein-coding	
chr8-6717.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr8	67178999	67180391	+	0 NA	intron (Nintron (N	95847 NM_001291	79848 Hs. 370147N	02479C:ENSG00000CSPP1	CSPP JBT5	centrosom protein-coding	
chr9-5655.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr9	5659627	5661184	+	0 NA	intron (NLP1A11 LI	31286 NM_00120E	57589 Hs. 21152CN	02082E:ENSG00000CIC1	CIP150 KIR1	C1 homc protein-coding	
chr9-122.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr9	1.22E+08	1.22E+08	+	0 NA	intron (NAluSc SIN	-14022 NM_01436E	26468 Hs. 103137N	01436E:ENSG00000LHX6	LHX6.1	LIM homec protein-coding	
chr9-1243.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr9	1.24E+08	1.24E+08	+	0 NA	intron (NMIR SINE	15753 NM_00116E	10783 Hs. 197071N	014397:ENSG00000NEK6	SID6-151E	NIMA helc protein-coding	
chr9-1243.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr9	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	-27768 NR_02740E	1E+08	Hs. 65498CN	02740E	LOC10012E	uncharactncRNA
chr9-1363.8.664952	-0.03792	0.788471	-0.0481	0.961639	0.981636	chr9	1.36E+08	1.36E+08	+	0 NA	intron (Nintron (N	10516 NM_015597	26086 Hs. 23937CN	015597:ENSG00000GSPM1	AGS3	G protein protein-coding	
chr1-3888.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr1	3888611	3891168	+	0 NA	3' UTR (N3' UTR (N	10383 NM_20735E	339448 Hs. 10383E	NR_20735E:ENSG00000C1orf174	-	chromosom protein-coding	
chr1-6264.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr1	62641129	62642362	+	0 NA	intron (Nintron (N	44225 NM_01449E	27329 Hs. 20915E	NR_01449E:ENSG00000CANGPTL3	ANG-5 ANC	angiopoie protein-coding	
chr1-1124.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr1	1.12E+08	1.12E+08	+	0 NA	intron (Nintron (N	25905 NR_03621C	1E+08	NR_03621C:ENSG00000MIR4256	-	microRNA ncRNA	
chr10-967.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr10	96057205	96060174	+	0 NA	3' UTR (N3' UTR (N	5710 NR_03611E	1E+08	NR_03611E:ENSG00000MIR3157	mir-3157	microRNA ncRNA	
chr11-117.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr11	1.17E+08	1.17E+08	+	0 NA	intron (NAluSz SIN	12265 NM_01495E	22897 Hs. 50400E	NR_01495E:ENSG00000CCEP164	NPHP15	centrosom protein-coding	
chr13-197.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr13	19756725	19758506	+	0 NA	intron (NMERS1B LI	25330 NM_001354	55269 Hs. 21319E	NR_00104E:ENSG00000PSPC1	PSP1	paraspeck protein-coding	
chr13-957.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr13	95592629	95594120	+	0 NA	intron (Nintron (N	40654 NM_006984	9071 Hs. 53437E	NR_006984:ENSG00000CLDN10	CPTREL3 E	claudin l protein-coding	
chr13-111.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr13	1.11E+08	1.11E+08	+	0 NA	intron (Nintron (N	38838 NM_00135E	79587 Hs. 50872E	NR_024537:ENSG00000CARS2	COXP27 C	cysteiny l protein-coding	
chr14-10.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr14	1.03E+08	1.03E+08	+	0 NA	intron (NLM1D2 LIN	50129 NM_00182E	1152 Hs. 173724N	00182E:ENSG00000CKB	B-C BCK C	retaine protein-coding	
chr16-224.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr16	2242402	2246724	+	0 NA	intron (Nintron (N	7024 NM_00117E	1632 Hs. 40343E	NR_00191E:ENSG00000CEC1	DCI	enoyl-CoA protein-coding	
chr17-167.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr17	16018663	16020138	+	0 NA	intron (NLM1E3Cz I	19576 NM_01777E	54902 Hs. 46231E	NR_01777E:ENSG00000TTC19	20102040I	tetratric protein-coding	
chr19-157.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr19	1595324	1599735	+	0 NA	3' UTR (N3' UTR (N	-4664 NM_001281	53615 Hs. 17872E	NR_00392E:ENSG00000MBD3	-	methyl-C protein-coding	
chr19-107.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr19	10254460	10256174	+	0 NA	intron (N2b LINE	3103 NM_01595E	51073 Hs. 27962E	NR_01595E:ENSG00000MRPL4	CGI-28 L	ami tochon protein-coding	
chr19-367.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr19	36918210	36919365	+	0 NA	intron (NLM1B3 LIN	2455 NM_001204	374900 Hs. 40422N	NR_19853E:ENSG00000ZNF568	ZFP568	zinc fing protein-coding	
chr2-3707.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr2	37037330	37038662	+	0 NA	exon (NM_exon (NM	46376 NM_019024	54497 Hs. 744084N	019024:ENSG00000HEATR5B	-	HEAT repc protein-coding	
chr2-2087.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr2	2.08E+08	2.08E+08	+	0 NA	intron (Nintron (N	36351 NM_00117E	200576 Hs. 744997N	01504C:ENSG00000CIKPYVE	CFD FAB1	phosphoi protein-coding	
chr3-4907.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr3	49030378	49033075	+	0 NA	intron (Nintron (N	-2328 NM_000884	3615 Hs. 65440E	NR_000884:ENSG00000LMPDH2	IMP2 IMF	inosine n protein-coding	
chr4-1222.7.392882	0.040784	0.848977	0.048039	0.961686	0.981636	chr4	1.22E+08	1.22E+08	+	0 NA	intron (NMIR SINE						



chr2-171 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr2	1.71E+08	1.71E+08	+	0	NA	intron (Nintron (N	6434 NM_001136	9874 Hs. 744917NM_01229C	ENSG00000TLK1	PKU-beta tousel lprotein-coding
chr20-344 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr20	34447173	34451962	+	0	NA	intron (Nintron (N	-16758 NR_030374	693229 NR_030374	ENSG00000MIR644A	MIR644 MI microRNA ncRNA
chr3-709 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr3	70963584	70967359	+	0	NA	intron (Nintron (N	99453 NM_001345	27086 Hs. 59368 NM_032682	ENSG00000FOXP1	I2CC4 HSF forkhead protein-coding
chr4-1251 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr4	1251451	1251921	+	0	NA	non-codiron-codir	2247 NR_033333	92070 Hs. 561314NM_052861	CTBP1-DT	C4orf42 CTBP1 divncRNA
chr4-4282 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr4	4282549	4282974	+	0	NA	intron (NAluSx1 S1	6711 NM_001145	55646 Hs. 425427NM_01781C	ENSG00000LYAR	Z4C2C2 ZL1y1 antiviral protein-coding
chr5-959 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr5	95930157	95931893	+	0	NA	intron (Nintron (N	30826 NM_012081	22936 Hs. 192221NM_012081	ENSG00000CELL2	MRCAT1 elongatic protein-coding
chr6-875 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr6	87562125	87564439	+	0	NA	intron (Nintron (N	26705 NM_02032C	57038 Hs. 48591NM_02032C	ENSG00000RARS2	ArgRS DAL arginyl-tprotein-coding
chr6-1007 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr6	10070181	10070181	+	0	NA	intron (NLIPIA11 L1	138286 NM_00682E	10973 Hs. 486031NM_00682E	ENSG00000ASCC3	ASC3 P200 activatir protein-coding
chr7-166 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr7	16621245	16622412	+	0	NA	intron (NAluSx SIN	23926 NM_02031E	57037 Hs. 15737NM_02031E	ENSG00000ANKMY2	ZMYND20 ankryn rprotein-coding
chr7-329 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr7	32926887	32929831	+	0	NA	intron (NMIRe SINE	14820 NM_00350C	441212 Hs. 64808NM_00103C	ENSG00000RP9P	RP9 pseudseudo
chr9-1124 7. 683333	-0.0396	0.834466	-0.04746	0.962148	0.981636	chr9	1.12E+08	1.12E+08	+	0	NA	intron (NLIPIA11 L1	-19342 NM_001287	158405 Hs. 65661NM_13346E	ENSG00000KIAA1958	KIAA1958 protein-coding
chr1-1938 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr1	19385091	19385387	+	0	NA	intron (NLIPIA11 L1	72913 NM_00104C	54896 Hs. 64762NM_01776E	ENSG00000SLC66A1	LAAT-1 L1solute cprotein-coding
chr1-5505 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr1	55099265	55100418	+	0	NA	exon (NM exon (NM	59619 NR_110451	255738 Hs. 18844 NM_17493C	ENSG00000PCSK9	FH3 HCHO1proteiprotein-coding
chr1-788 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr1	78869573	78871495	+	0	NA	intron (Nintron (N	-30007 NM_001321	57602 Hs. 46424NM_02509C	ENSG00000CSP36	DUB1 ubiquitir protein-coding
chr2-1127 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr2	11277704	11277930	+	0	NA	intron (NLIPIB1 LIN	66819 NM_00485C	9475 Hs. 68174NM_00485C	ENSG00000CROCK2	ROCK-II Rho assoc protein-coding
chr20-62 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr20	62263579	62266494	+	0	NA	intron (NLIPIA11 L1	26515 NM_00136E	9885 Hs. 473254NM_01483E	ENSG00000OSBPL2	DFNA67 DN oxysterol protein-coding
chr22-217 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr22	21798533	21799300	+	0	NA	intron (Nintron (N	-63122 NM_01331E	29799 Hs. 51743NM_01331E	ENSG00000CYPEL1	FKSG3 yippe lprotein-coding
chr3-1237 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (NHAL1 LINE	75041 NR_04662E	1.01E+08 Hs. 66731CNR_04662E	ENSG00000MYLK-AS2	MYLK anticncRNA
chr3-1427 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr3	1.43E+08	1.43E+08	+	0	NA	intron (NTiger3 3b	24774 NM_003304	7220 Hs. 250687NM_003304	ENSG00000TRPC1	HTRP-1 TF transient protein-coding
chr4-159 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr4	159929	161338	+	0	NA	intron (NAluSx3 S1	32512 NM_00128E	255403 Hs. 63663NM_00103E	ENSG00000ZNF718	zinc fing protein-coding
chr7-105 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr7	1.05E+08	1.05E+08	+	0	NA	intron (Nintron (N	30925 NM_182931	55904 Hs. 592262NM_01868E	ENSG00000KMT2E	HDCMC04P lysine mprotein-coding
chr7-137 8. 878947	0.037119	0.783217	0.047392	0.962201	0.981636	chr7	1.38E+08	1.38E+08	+	0	NA	intron (NMIRe SINE	32597 NM_00131E	64764 Hs. 49027NM_194071	ENSG00000CREB3L2	BBF2H7 cAMP res protein-coding
chr4-569 9. 151832	-0.03652	0.752813	-0.04739	0.962227	0.981636	chr4	56964873	56965147	+	0	NA	intron (NAluSq2 S1	12596 NM_03231E	84273 Hs. 8715 NM_03231E	ENSG00000CNOA1	C4orf14 Nnitric oprotein-coding
chr1-473 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr1	47369887	47369831	+	0	NA	intron (Nintron (N	35619 NM_00136E	51727 Hs. 731647NM_01630E	ENSG00000CMPK1	CK1 CMK CM cytidine/protein-coding
chr1-201 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr1	2.02E+08	2.02E+08	+	0	NA	intron (NLIPIA11 L1	24480 NM_012134	25802 Hs. 51907NM_012134	ENSG00000LMOD1	ID 64KD E leiomodir protein-coding
chr13-28 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr13	28671880	28673512	+	0	NA	intron (NLTR40b L1	14986 NM_01593E	51371 Hs. 26874NM_01593E	ENSG00000POMP	C13orf12 proteason protein-coding
chr13-491 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr13	49130937	49132814	+	0	NA	intron (NLIPIA11 L1	21558 NM_01492E	22862 Hs. 50801NM_01492E	ENSG00000FNDC3A	FNDC3 HUC fibronectin protein-coding
chr14-20 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr14	20991544	20995517	+	0	NA	intron (NAluSx4 S1	3550 NM_00102E	64745 Hs. 51269NM_022734	ENSG00000METTL17	METTL1D1 methyltr protein-coding
chr15-19 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr15	98939297	98941428	+	0	NA	intron (Nintron (N	65294 NM_00110E	145814 Hs. 592021NM_00110E	ENSG00000PGPEPIL	pyroglutl protein-coding
chr16-15 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr16	15977539	15979221	+	0	NA	intron (NAluJr SIN	28764 NM_00499E	4363 Hs. 391464NM_00499E	ENSG00000ABCC1	ABC29 ABC ATP bindir protein-coding
chr19-13 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr19	13919928	13922220	+	0	NA	intron (NMLT1J LTF	14873 NM_017721	54862 Hs. 26959NM_017721	ENSG00000CC2D1A	FREUD-1 F coiled-cprotein-coding
chr2-552 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr2	55295211	55296358	+	0	NA	exon (NM exon (NM	13465 NR_02725E	344405 Hs. 44529NM_00108C	ENSG00000PRORS1P	NCRNA001 proly1-tf pseudo
chr6-875 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr6	87513349	87521439	+	0	NA	intron (NLIPIA11 L1	44420 NM_00641E	10559 Hs. 42316NM_00641E	ENSG00000SLC35A1	CDGF2 CF sulfte protein-coding
chr7-641 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr7	6418066	6430038	+	0	NA	intron (Nintron (N	23902 NM_13917E	221955 Hs. 48749NM_13917E	ENSG00000CAGLB	DAGLBETA diacylgly protein-coding
chr9-130 9. 151832	-0.0365	0.771274	-0.04733	0.96225	0.981636	chr9	1.31E+08	1.31E+08	+	0	NA	intron (Nintron (N	-10868 NR_10691E	1.02E+08 NR_10691E	ENSG00000MIR6856	hsa-mir-6microRNA ncRNA
chr9-269 9. 151832	0.036507	0.765405	0.047108	0.962427	0.981636	chr9	26919549	26920149	+	0	NA	intron (Nintron (N	-27021 NM_001167	79886 Hs. 178357NM_02482E	ENSG00000CAAP1	C9orf82 C caspase r protein-coding
chr1-122 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr1	12289867	12291759	+	0	NA	intron (Nintron (N	60783 NM_01537E	55187 Hs. 439381NM_01537E	ENSG00000CVP313D	SCAR4 vacuolar protein-coding
chr1-313 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr1	31356427	31357745	+	0	NA	intron (Nintron (N	15990 NM_00410E	2170 Hs. 57637NM_00410E	ENSG00000FABP3	FABP11 H fatty aciprotein-coding
chr10-30 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr10	30334433	30336013	+	0	NA	intron (NAluSx SIN	14115 NM_01810E	55149 Hs. 17394NM_01810E	ENSG00000MTAP	PAPD1 SP1mtohcnc protein-coding
chr10-97 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr10	97719105	97719745	+	0	NA	IntergeniAluSx SIN	5695 NM_031484	83742 Hs. 74407NM_031484	ENSG00000MARVELD1	GB14 MARV MARVEL dc protein-coding
chr11-64 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr11	69665357	69666048	+	0	NA	3' UTR (N3' UTR (N	9651 NM_153451	220064 Hs. 66799NM_153451	ENSG00000LTO1	CIAB1 ORL1TO1 mat protein-coding
chr13-24 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr13	24470798	24472345	+	0	NA	intron (Nintron (N	41207 NM_006437	143 Hs. 74485NM_006437	ENSG00000PARP4	ADPRTL1 poly (ADP)-protein-coding
chr15-40 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr15	40417251	40417895	+	0	NA	intron (NMER44B DN	11776 NR_14892E	3712 Hs. 51364NM_00222E	ENSG00000IVD	ACAD2 isovaleryl protein-coding
chr15-41 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr15	41679077	41680035	+	0	NA	intron (NLIPIA11 L1	-12029 NR_03035E	693211 NR_03035E	ENSG00000MIR626	MIRN626 hmicroRNA ncRNA
chr16-18 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr16	18512183	18514181	+	0	NA	intron (Nintron (N	-18606 NR_03614E	1E+08 NR_03614E	ENSG00000MIR3179-5	microRNA ncRNA
chr17-31 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr17	31335089	31335657	+	0	NA	intron (Nintron (N	-13751 NM_00100C	2123 Hs. 59119NM_01421C	ENSG00000EV12A	EVDA EVI- ecotropic protein-coding
chr19-51 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr19	51978991	51979807	+	0	NA	intron (NHERVK3-ir	7441 NM_02163E	59348 Hs. 40769NM_02163E	ENSG00000ZNF350	ZBRK1 ZFG zinc fing protein-coding
chr2-170 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr2	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	-96472 NR_04568E	140469 Hs. 67190NM_13899E	ENSG00000MYO3B	myosin II protein-coding
chr20-18 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr20	18541554	18543092	+	0	NA	exon (NM exon (NM	-25097 NM_00134E	388789 Hs. 34909NM_00134E	ENSG00000SMIM26	LINC0049E small intr protein-coding
chr20-38 9. 151832	0.04603	0.978012	0.047065	0.962462	0.981636	chr20	38011666	38012502	+	0	NA					



chr6-132:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr6	1.32E+08	1.32E+08	0	NA	intron (NMIR SINE	34023	NM_015525	26002	Hs.6909	NM_015525	ENSG00000	MOXD1	MOX PRO57	monoxyge	protein-coding					
chr7-233:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr7	23301312	23302988	0	NA	intron (NL2b LINE	2811	NM_138444	115416	Hs.87385	NM_138444	ENSG00000	MALSU1	C7orf30	nmitchoncn	protein-coding					
chr7-358:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr7	35898413	35899973	0	NA	intron (Nintron (N	97974	NM_001363	989	Hs.191344	NM_001363	ENSG00000	CEPTIN7	CDIC10	CDX septin 7	protein-coding					
chr7-922:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr7	92218330	92225836	0	NA	intron (Nintron (N	-17985	NR_031616	23554	Hs.16529	NR_031616	ENSG00000	MIR1285-1	MIRN1285	microRNA	ncRNA					
chr7-1208:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr7	92118811	92118811	0	NA	intron (Nintron (N	19967	NM_012338	23554	Hs.16529	NM_012338	ENSG00000	TSPAN12	EVRS NET-	tetraspan	protein-coding					
chr7-121:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr7	1.21E+08	1.21E+08	0	NA	intron (Nintron (N	33571	NM_057168	51384	Hs.272375	NM_057168	ENSG00000	WNT16	Wnt	family	protein-coding					
chr7-1301:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr7	1.3E+08	1.3E+08	0	NA	intron (NALuSx3 SI	-18278	NR_149033	1E+08	Hs.105944	NR_149033	ENSG00000	LOC100128			uncharacter	ncRNA				
chr8-423:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr8	42398723	42406897	0	NA	intron (Nintron (N	10930	NM_005662	7419	Hs.699301	NM_005662	ENSG00000	VDAC3	HD-VDAC3	voltage	protein-coding					
chr8-478:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr8	47891020	47893566	0	NA	intron (NCharlie2f	67843	NM_001081	5591	Hs.491682	NM_006904	ENSG00000	PRKDC	DNA-PKC I	protein	protein-coding					
chr8-125:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr8	1.25E+08	1.25E+08	0	NA	intron (Nintron (N	11383	NM_014844	9897	Hs.270044	NM_014844	ENSG00000	WASHC5	KIAA0196	WASH	com	protein-coding				
chr9-110:8.170214	-0.03786	0.808568	-0.04682	0.962656	0.981636	chr9	1.11E+08	1.11E+08	0	NA	intron (Nintron (N	14118	NM_153366	79987	Hs.522334	NM_153366	ENSG00000	SVFP1	C9orf13	Csushi,	vc	protein-coding				
chr13-32:9.836992	0.035066	0.750189	0.046742	0.962719	0.981636	chr13	32512606	32512988	0	NA	3' UTR (N3' UTR (N	-3402	NR_026928	116828	Hs.658751	NR_026928	ENSG00000	N4BP2L2-1	ICG300	N4BP2L2	ir	ncRNA				
chr1-151:9.638712	-0.03529	0.756642	-0.04663	0.962805	0.981636	chr1	15911321	15912313	0	NA	intron (NALuSx SIN	-63670	NR_024275	729614	Hs.119294	NR_024275	ENSG00000	FLJ37453				uncharacter	ncRNA			
chr2-231:9.638712	-0.03529	0.756642	-0.04663	0.962805	0.981636	chr2	2.31E+08	2.31E+08	0	NA	intron (Nintron (N	78742	NM_001352	80210	Hs.162411	NM_025135	ENSG00000	ARMC9	ARM	JBTS5	armadill	protein-coding				
chr3-979:9.638712	-0.03529	0.756642	-0.04663	0.962805	0.981636	chr3	9795812	9796050	0	NA	intron (NALuSx SIN	2849	NM_001198	10093	Hs.323342	NM_005718	ENSG00000	ARPC4	ARC20	P2C	actin	rel	protein-coding			
chr1-1081:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr1	1.08E+08	1.08E+08	0	NA	intron (Nintron (N	36456	NM_213651	29957	Hs.656877	NM_013388	ENSG00000	SLC25A24	APC1	SCAM	solute	protein-coding				
chr11-57:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr11	57564607	57564983	0	NA	intron (NALuS2 SI	2877	NM_004223	9246	Hs.425777	NM_004223	ENSG00000	UBE2A3	RIG-B UBC	ubiquitin	protein-coding					
chr12-701:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr12	7013165	7013774	0	NA	intron (NL2b LINE	5007	NM_005768	10162	Hs.655248	NM_005768	ENSG00000	LPCAT3	C3F	LPCAI	lysospho	protein-coding				
chr13-951:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr13	95131680	95132641	0	NA	intron (NMER2 DNA	-78184	NR_145733	1.E+08	NR_145733	SNORD13G						small	nucsnRNA			
chr16-68:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr16	68300656	68301174	0	NA	3' UTR (N3' UTR (N	10031	NM_032178	84138	Hs.729522	NM_032178	ENSG00000	SLC7A60S						solute	protein-coding	
chr17-305:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr17	30901889	30904333	0	NA	intron (NALuSx SIN	3127	NM_024683	79736	Hs.31734C	NM_024683	ENSG00000	TEFM	C17orf42	transcri	protein-coding					
chr3-193:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr3	1.94E+08	1.94E+08	0	NA	intron (Nintron (N	-30591	NR_046634	1.01E+08	Hs.679364	NR_046634	ENSG00000	OPAI-AS1						OPAI	antncRNA	
chr3-1967:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr3	1.97E+08	1.97E+08	0	NA	intron (NLIME3D LI	45736	NM_002577	5062	Hs.518533	NM_002577	ENSG00000	PAK2	PAK65 PAK	p21	(RAC1	protein-coding				
chr4-2071:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr4	20713632	20714371	0	NA	intron (NLIP1 LINE	13543	NM_00133C	133015	Hs.479298	NM_145044	ENSG00000	PACRGL	C4orf28	parkin	cc	protein-coding				
chr5-139:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr5	13926588	13927053	0	NA	intron (Nintron (N	17660	NM_00136E	1767	Hs.21236C	NM_00136E	ENSG00000	CNHA5	CILD3	DN	dynein	alpha	protein-coding			
chr6-132:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr6	1.32E+08	1.32E+08	0	NA	intron (Nintron (N	72738	NM_015525	26002	Hs.6909	NM_015525	ENSG00000	MOXD1	MOX PRO57	monoxyge	protein-coding					
chr7-7307:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr7	73071227	73071640	0	NA	IntergeniNALuS2 SI	12805	NM_001351	1.01E+08	Hs.645327	NM_001351	ENSG00000	SPDYE11						speedy/Rl	protein-coding	
chr7-754:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr7	75498555	75499186	0	NA	intron (Nintron (N	5243	NM_00130E	442590	Hs.632298	NM_00109E	ENSG00000	SPDYE5						speedy/Rl	protein-coding	
chr7-1487:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr7	1.49E+08	1.49E+08	0	NA	intron (NALuJb SIN	32695	NM_00137C	8454	Hs.146807	NM_00359E	ENSG00000	CUL1						culin 1	protein-coding	
chr9-106:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr9	1.07E+08	1.07E+08	0	NA	intron (Nintron (N	69230	NM_021224	58499	Hs.370375	NM_021224	ENSG00000	ZNF462	ZFP1P Zf	zinc	finger	protein-coding				
chr9-125:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr9	1.25E+08	1.25E+08	0	NA	intron (NALuSx SIN	18863	NM_005347	3309	Hs.743241	NM_005347	ENSG00000	HSPA5	BIP GRP78	heat	shoc	protein-coding				
chr9-129:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chr9	1.29E+08	1.29E+08	0	NA	intron (NALuJ SINE	15023	NM_03280E	84895	Hs.63269E	NM_03280E	ENSG00000	MIGA2	C9orf54	Fmitogua	protein-coding					
chrX-156:5.914676	0.043734	0.9428	0.046387	0.963001	0.981636	chrX	15688907	15690383	0	NA	intron (NLIMB3 LIN	14187	NR_160542	340591	Hs.732244	NR_026551	ENSG00000	CA5BP1	CASB1	CAE	carbonic	pseudo				
chr10-271:5.963673	0.044016	0.94936	0.046364	0.96302	0.981636	chr10	27139429	27140085	0	NA	intron (NLIM5 LINE	14627	NM_01426E	10730	Hs.74647	NM_01426E	ENSG00000	CYME1L1	FTSH MEG4	YME1	like	protein-coding				
chr1-151:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr1	1.51E+08	1.51E+08	0	NA	intron (NALuSx1 SI	-7849	NM_207171	23126	Hs.489877	NM_01510C	ENSG00000	POGZ	MRD37	WH	pogo	tr	protein-coding			
chr10-10:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr10	1.01E+08	1.01E+08	0	NA	intron (Nintron (N	-4309	NM_01549C	25956	Hs.18889	NM_01549C	ENSG00000	SEC31B	SEC31B-1	SEC31	hon	protein-coding				
chr12-10:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr12	1.05E+08	1.05E+08	0	NA	intron (NALuYb8 SI	23440	NM_00129E	23325	Hs.12144	NM_01527E	ENSG00000	WASHC4	KIAA1033	WASH	com	protein-coding				
chr16-17:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr16	1759698	1760944	0	NA	intron (Nintron (N	9813	NM_00251E	4832	Hs.51406E	NM_00251E	ENSG00000	NME3	DR-nm23	NME	NM23	protein-coding				
chr16-74:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr16	74339841	74343608	0	NA	intron (Nintron (N	26531	NR_02695C	283922	NR_02695C	ENSG00000	LOC283922						pyruvate	pseudo		
chr17-66:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr17	66687778	66690403	0	NA	intron (Nintron (N	-97982	NR_030364	693219	NR_030364	ENSG00000	MIR634	MIRN634						microRNA	ncRNA	
chr19-14:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr19	1412893	1413877	0	NA	intron (Nintron (N	5799	NM_00135E	26528	Hs.22251C	NM_01895E	ENSG00000	DAZAP1						DAZ	assoc	protein-coding
chr4-105:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr4	1.05E+08	1.05E+08	0	NA	intron (NLIP2 LINE	47520	NM_17686E	27068	Hs.654957	NM_00690E	ENSG00000	PPA2	HSPC124	Z	synphos	protein-coding				
chr8-143:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr8	1.43E+08	1.43E+08	0	NA	intron (Nintron (N	4415	NM_001271	286128	Hs.66801E	NM_17383E	ENSG00000	ZFP41	ZNF753 zf	ZFP41	zir	protein-coding				
chr9-128:6.442696	0.042056	0.909273	0.046253	0.963109	0.981636	chr9	1.29E+08	1.29E+08	0	NA	intron (NALuSx SIN	-31112	NM_01490E	22845	Hs.53156E	NM_01										

chr20-36	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr20	36047084	36050019	+	0	NA	non-codirnon-codir	2409 NR_027451	647979 Hs. 743232NR_027451	ENSG00000CNORAD	LINC00657non-codir ncRNA	
chr3-122	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr3	1.23E+08	1.23E+08	+	0	NA	exon (NM exon (NM	5920 NM_001146	83666 Hs. 518200NM_031458	ENSG00000PARP9	ARTD9 BAl poly (ADP- protein-coding	
chr3-132	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr3	1.33E+08	1.33E+08	+	0	NA	intron (Nintron (N	28605 NM_001321	79876 Hs. 170737NM_024818	ENSG00000CUBA5	EIEE44 Scubiquitin protein-coding	
chr3-170	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (Nintron (N	63162 NM_014377	25699 Hs. 231320NM_014377	ENSG00000GPR160	GPCR1 GPCF protein-coding	
chr3-183	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr3	1.84E+08	1.84E+08	+	0	NA	intron (Nintron (N	7981 NM_001351	55688 Hs. 632575NM_018028	ENSG00000YEATS2	- YEATS domain protein-coding	
chr4-249	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr4	2495678	2502645	+	0	NA	intron (NAluSx SI	29708 NM_001188	6047 Hs. 66394 NM_002938	ENSG00000CRNF4	RES4-26 Sring fing protein-coding	
chr4-706	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr4	7063438	7065159	+	0	NA	intron (NAluY SINE	5311 NM_025196	80273 Hs. 443722NM_025196	ENSG00000GRPEL1	GrpE HMGFGrpE like protein-coding	
chr4-122	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr4	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	85824 NM_015312	84162 Hs. 408142NM_015312	ENSG00000K1AA1109	ALKKUS FK1AA1109 protein-coding	
chr4-122	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr4	1.23E+08	1.23E+08	+	0	NA	intron (NTHE1B-int	41381 NM_007088	11162 Hs. 558455NM_007088	ENSG00000NUDT6	ASFGF2 FCnudix hyc protein-coding	
chr5-103	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr5	10394474	10395962	+	0	NA	intron (Nintron (N	-7146 NR_162106	1.13E+08	NR_162106	MIR10397	- microRNA ncRNA
chr5-407	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr5	40773863	40778082	+	0	NA	intron (NLa2 LINE	-20011 NM_012382	23548 Hs. 348918NM_012382	ENSG00000TTC33	OSRF	tetratric protein-coding
chr5-954	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr5	95498386	95500609	+	0	NA	intron (NMSTA LTR	55508 NM_014638	9652 Hs. 482868NM_014638	ENSG00000TTC37	KIAA0372 tetratric protein-coding	
chr5-146	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr5	1.46E+08	1.46E+08	+	0	NA	intron (Nintron (N	66826 NM_018998	54439 Hs. 61441 NM_018998	ENSG00000RBM27	ARRS1 PscRNA bindi protein-coding	
chr5-146	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr5	1.8E+08	1.8E+08	+	0	NA	intron (NLIME4b LI	14402 NR_110566	1.02E+08	NR_110566	ENSG00000LOC101928	- uncharactncRNA
chr6-283	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr6	2835234	2836504	+	0	NA	non-codirnon-codir	5994 NR_073112	1992 Hs. 381167NM_030668	ENSG00000SERPINB1	EI ELANH2 serpin f2 protein-coding	
chr6-264	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr6	26459385	26469175	+	0	NA	intron (NLa2 LINE	6325 NM_007045	11120 Hs. 159028NM_007045	ENSG00000BTN2A1	BK14H9.1 butyroph protein-coding	
chr6-365	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr6	36521429	36522677	+	0	NA	intron (Nintron (N	25426 NM_007271	11329 Hs. 409578NM_007271	ENSG00000CTK38	NDR NDR1 serine/tf protein-coding	
chr6-419	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr6	41932673	41937970	+	0	NA	3' UTR (N3' UTR (N	6527 NM_001287	896 Hs. 534375NM_001287	ENSG00000CCND3	- cyclin D3 protein-coding	
chr6-821	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr6	82168138	82169089	+	0	NA	Intergeni Intergeni	-66848 NR_149138	1.03E+08	Hs. 485841NR_149134	LINC02542	- long intencRNA
chr6-158	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr6	1.58E+08	1.58E+08	+	0	NA	3' UTR (N3' UTR (N	71557 NM_032861	84947 Hs. 154706NM_032861	ENSG00000SERAC1	- serine acprotein-coding	
chr7-203	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr7	203363	206873	+	0	NA	intron (Nintron (N	12547 NM_020222	56975 Hs. 134742NM_020222	ENSG00000GRAM20C	DMP-4 DMF FAM20C acprotein-coding	
chr7-646	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr7	64691236	64692894	+	0	NA	intron (Nintron (N	13001 NR_106898	1.02E+08	NR_106898	ENSG00000MIR6839	hsa-mir-6microRNA ncRNA
chr7-152	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr7	1.52E+08	1.52E+08	+	0	NA	intron (Nintron (N	72721 NM_001371474				
chr7-172	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr7	17274672	17278917	+	0	NA	intron (Nintron (N	29836 NM_001366	137492 Hs. 343878NM_152418	ENSG00000VPS37A	HCRP1 PQE VPS37A sprotein-coding	
chr8-1301	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr8	1.3E+08	1.3E+08	+	0	NA	intron (NLa2 LINE	-47783 NR_045388	1.01E+08	Hs. 106018NR_045388	ENSG00000ASAP1-IT2	- ASAP1 intncRNA
chr8-9	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr8	2836072	2837218	+	0	NA	intron (Nintron (N	7450 NM_014878	9933 Hs. 493308NM_014878	ENSG00000PUM3	HA-8 HLA-pumilio F protein-coding	
chr8-9	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr8	97683054	97684924	+	0	NA	intron (Nintron (N	13420 NR_149094	7507 Hs. 654364NM_000380	ENSG00000XPA	XPI XPAC XPA, DNA protein-coding	
chr8-110	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr8	1.1E+08	1.1E+08	+	0	NA	intron (Nintron (N	-37097 NM_001288	255220 Hs. 147064NM_001008	ENSG00000TXNDC8	SPTRX-3 S thioedox protein-coding	
chr8-114	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr8	1.15E+08	1.15E+08	+	0	NA	intron (NAluY SINE	8574 NM_004888	9550 Hs. 388654NM_004888	ENSG00000ATP6V1G1	ATP6G ATF ATPase H+ protein-coding	
chr8-122	8.657094	-0.03631	0.786711	-0.04615	0.963189	0.981636	chr8	1.22E+08	1.22E+08	+	0	NA	intron (Nintron (N	49040 NM_001346	92399 Hs. 368011NM_138777	ENSG00000MRRF	MRRF MTFR mitoch protein-coding	
chr8-138	8.713949	-0.0376	0.814612	-0.04615	0.96319	0.981636	chr8	13807513	13808288	+	0	NA	intron (NMSTA LTR	12457 NM_023072	65249 Hs. 466018NM_023072	ENSG00000ZSWIM4	- zinc fing protein-coding	
chr8-1379	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	37934745	37940127	+	0	NA	intron (NAluS2 SI	4828 NM_001355	3633 Hs. 449942NM_005548	ENSG00000INPP5B	5PTase inositol protein-coding	
chr8-153	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	53857484	53859764	+	0	NA	intron (NMIRb SINE	-20328 NM_001168	55706 Hs. 476528NM_018087	ENSG00000NDC1	NET3 TMEH NDC1 trar protein-coding	
chr8-166	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	66733715	66735363	+	0	NA	intron (NAluSx SIN	-17920 NM_152668	200132 Hs. 479228NM_152668	ENSG00000CTEX1D1	Tctex1 dc protein-coding	
chr8-196	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	2.2E+08	2.2E+08	+	0	NA	intron (NAluSx SI	-42066 NR_046437	55532 Hs. 284458NM_018718	ENSG00000SLC30A10	HMDPC HMM solute c2 protein-coding	
chr8-216	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	362071	362620	+	0	NA	intron (NCpG	183551 NM_001202	10771 Hs. 292268NM_006624	ENSG00000ZMYND11	BRAM1 BSE zinc fing protein-coding	
chr8-271	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	27109087	27109793	+	0	NA	TTS (NM_C	-8942 NM_014918	22852 Hs. 361041NM_014918	ENSG00000ANKRD26	THC2 ba14ankyrin r protein-coding	
chr8-109	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	69377956	69380830	+	0	NA	intron (NLMs LINE	37525 NM_001057	8665 Hs. 880327NM_001057	ENSG00000TACR2	NK2R NKNA tachykinin protein-coding	
chr8-102	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (Nintron (N	32450 NM_001198	8729 Hs. 290242NM_004198	ENSG00000GBF1	ARF1GEF golgi br protein-coding	
chr8-11	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	35685409	35686857	+	0	NA	intron (Nintron (N	23358 NM_017588	54765 Hs. 192108NM_017588	ENSG00000TRIM44	AN3 DIPB tripartit protein-coding	
chr8-12	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	57525569	57526419	+	0	NA	exon (NM exon (NM	3170 NM_052897	114785 Hs. 524528NM_052897	ENSG00000MBD6	- methyl-Cp protein-coding	
chr8-12	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	88536566	88538108	+	0	NA	intron (NLIPA16 LI	43164 NM_000898	4254 Hs. 1048 NM_000898	ENSG00000CTLG	DCUA DFNAK1 ligar protein-coding	
chr8-21	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	21078247	21085920	+	0	NA	exon (NM exon (NM	-11211 NM_001282	57447 Hs. 525208NM_016258	ENSG00000NDRG2	SYLD NDRG fami protein-coding	
chr8-15	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	78785140	78787635	+	0	NA	intron (NMER45B DN	25077 NM_014272	11173 Hs. 16441 NM_014272	ENSG00000ADAMT57	ADAM-27 ADAM metz protein-coding	
chr8-17	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	5332035	53335633	+	0	NA	intron (NAluSx SIN	50515 NM_001291	9135 Hs. 584784NM_004708	ENSG00000RABEP1	RAB5EP Rabrapatin, protein-coding	
chr8-17	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	7001002	7001552	+	0	NA	intron (Nintron (N	5228 NM_000697	239 Hs. 654431NM_000697	ENSG00000ALOX12	12-LOX 12 arachidor protein-coding	
chr8-17	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	51265212	51267177	+	0	NA	exon (NM exon (NM	5648 NM_016001	51096 Hs. 709327NM_016001	ENSG00000UTP18	CGI-48 WUUTP18 sm protein-coding	
chr8-17	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	62426821	62430504	+	0	NA	intron (NMER21C LI	4777 NM_181728	339175 Hs. 381204NM_181728	ENSG00000METTL2A	METTL2 methyl tr protein-coding	
chr8-17	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	62687874	62692314	+	0	NA	intron (Nintron (N	-16112 NR_147888	1.05E+08	Hs. 446268NR_147888	ENSG00000LOC105371	- uncharactncRNA
chr8-17	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	82582791	82585413	+	0	NA	exon (NM exon (NM	64342 NM_019618	56270 Hs. 132161NM_019618	ENSG00000WDR45B	NEDSBAS WWD repeat protein-coding	
chr8-19	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	34388295	34389042	+	0	NA	intron (Nintron (N	-15730 NM_001355	84306 Hs. 515344NM_032348	ENSG00000PDCD2L	- programme protein-coding	
chr8-2	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	37665296	37667319	+	0	NA	intron (NMER103C I	5892 NM_001277	10602 Hs. 369574NM_006448	ENSG00000CDC42EP3	BORG2 CEF CDC42 eff protein-coding	
chr8-2	6.921718	0.040366	0.876417	0.046058	0.963264	0.981636	chr8	74885363	74886974	+	0	NA	intron (NLa2 LINE	-22963 NR_125792	1.03E+08	Hs. 708648NR_125792	ENSG00000LINC01291	- long intencRNA



chr6-5646 9.143974	-0.03495	0.768154	-0.0455	0.963712	0.981636	chr6	56467794	56477376	+ 0 NA	intron (Nintron (N	-78457 NM_00131E	81578 Hs. 47629	NM_03082C	ENSG00000COL21A1	COLA1L FF collagen protein-coding
chr6-5655 9.143974	-0.03495	0.768154	-0.0455	0.963712	0.981636	chr6	56508152	56509938	+ 0 NA	intron (Nintron (N	-114917 NM_00131E	81578 Hs. 47629	NM_03082C	ENSG00000COL21A1	COLA1L FF collagen protein-coding
chr7-747 9.143974	-0.03495	0.768154	-0.0455	0.963712	0.981636	chr7	74759715	74760866	+ 0 NA	3' UTR (N3' UTR (N	-13672 NM_00026E	653361 Hs. 647047NM_00026E	ENSG00000CNC1	NCF1A NOX neurotrophin protein-coding	
chr6-8967 9.308972	0.035572	0.782431	0.045464	0.963738	0.981636	chr6	89677059	89677505	+ 0 NA	intron (NAluS6 S1	-38535 NM_02046E	572226 Hs. 17727E	NM_02046E	ENSG00000LYRM2	DJ12208.ZLYR motif protein-coding
chr11-636 8.219211	-0.03736	0.822003	-0.04546	0.963745	0.981636	chr11	63647391	63649160	+ 0 NA	intron (NHAL LINE	23101 NM_01545E	25923 Hs. 35671E	NM_01545E	ENSG00000ATL3	HSN1F atlastin protein-coding
chr13-242 8.219211	-0.03736	0.822003	-0.04546	0.963745	0.981636	chr13	24289505	24291059	+ 0 NA	intron (Nintron (N	-16884 NM_00130E	338872 Hs. 362854NM_17854C	ENSG00000C1QTNF9	AQL1 C1QC1q and 1protein-coding	
chr9-1322 8.219211	-0.03736	0.822003	-0.04546	0.963745	0.981636	chr9	1.32E+08	1.32E+08	+ 0 NA	intron (NCharlie2E	86794 NM_001351	23064 Hs. 460317NM_01504E	ENSG00000SETX	ALB1 AOA2 senataxin protein-coding	
chr1-3097 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr1	30978105	30980316	+ 0 NA	intron (Nintron (N	-10973 NR_00306E	692200	NR_00306E	SNORD103C HBS1-251 small nucsnoRNA	
chr1-2367 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr1	2.37E+08	2.37E+08	+ 0 NA	intron (Nintron (N	-33399 NR_03404C	1E+08 Hs. 67737E	NR_03404C	ENSG00000LGALS8-AS-	LGALS8 arncRNA
chr11-337 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr11	33730264	33730618	+ 0 NA	intron (NTigger2b	6038 NM_203331	966 Hs. 27857E	NM_00061E	ENSG00000CD59	16.3A5 1FCDS9 mole protein-coding
chr12-942 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr12	943373	944457	+ 0 NA	intron (Nintron (N	5779 NM_134424	5893 Hs. 41035E	NM_134424	ENSG00000RAD52	- RAD52 hon protein-coding
chr12-121 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr12	12157519	12159075	+ 0 NA	intron (Nintron (N	46345 NR_03605E	1E+08	NR_03605E	ENSG00000MIR1244-1	MIR1244 microRNA ncRNA
chr13-198 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr13	19837572	19838483	+ 0 NA	intron (Nintron (N	25609 NM_00103E	9205 Hs. 53098E	NM_01424E	ENSG00000ZMYM5	HSPC050 zinc fing protein-coding
chr14-241 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr14	24160134	24160636	+ 0 NA	promoter-promoter-	-880 NM_00608E	10379 Hs. 1706	NM_00608E	ENSG00000IRF9	IRF9-9 ISC interferon protein-coding
chr17-181 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr17	18194981	18199899	+ 0 NA	intron (Nintron (N	13612 NM_01775E	54890 Hs. 74413C	NM_01775E	ENSG00000ALKBH5	ABH5 OFO alkB homc protein-coding
chr22-387 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr22	38724145	38725475	+ 0 NA	intron (NMIRb SINE	18866 NM_00428E	9567 Hs. 27692E	NM_00428E	ENSG00000GTPBP1	GP-1 GPI GTP bindi protein-coding
chr4-122 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr4	1.22E+08	1.22E+08	+ 0 NA	intron (Nintron (N	68660 NM_01531E	84162 Hs. 40814E	NM_01531E	ENSG00000KIAA1109	ALKKUS5 FKIAA1109 protein-coding
chr5-137 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr5	13720600	13720932	+ 0 NA	intron (Nintron (N	223714 NM_00136E	1767 Hs. 21236C	NM_00136E	ENSG00000DNAH5	CILD3 DN dynein alpha protein-coding
chr5-361 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr5	36103777	36108352	+ 0 NA	intron (NLMCC LIN	40124 NR_03030E	693165	NR_03030E	ENSG00000MIR580	MIR580 microRNA ncRNA
chr8-253 7.879763	0.037531	0.826219	0.045425	0.963769	0.981636	chr8	25304455	25304787	+ 0 NA	intron (NLMIB6 LIN	-40786 NR_10693E	1.02E+08	NR_10693E	ENSG00000MIR6876	hsa-mir-6876 microRNA ncRNA
chr4-150 5.378798	0.048416	1.068394	0.045317	0.963855	0.981636	chr4	1.5E+08	1.5E+08	+ 0 NA	non-codir non-codir	177997 NM_00104C	166614 Hs. 59168E	NM_15261E	ENSG00000DCLK2	CL2 CLIC8 doublecortin protein-coding
chr11-118 7.188595	-0.03944	0.873951	-0.04513	0.964003	0.981636	chr11	1.18E+08	1.18E+08	+ 0 NA	intron (Nintron (N	7093 NM_00478E	9354 Hs. 75275	NM_00478E	ENSG00000UBE4A	E4 UBOX2 ubiquitin protein-coding
chr20-336 7.188595	-0.03944	0.873951	-0.04513	0.964003	0.981636	chr20	33638614	33638933	+ 0 NA	intron (Nintron (N	-23554 NM_08082E	128864 Hs. 324104NM_08082E	ENSG00000C20orf144	dJ63M2.6 chromosom protein-coding	
chr5-613 7.188595	-0.03944	0.873951	-0.04513	0.964003	0.981636	chr5	61336964	61337411	+ 0 NA	intron (NAluSx1 S1	4929 NM_02092E	57688 Hs. 74493E	NM_02092E	ENSG00000ZSWIM7	AFND NEM zinc fing protein-coding
chr7-9954 7.188595	-0.03944	0.873951	-0.04513	0.964003	0.981636	chr7	99543565	99544026	+ 0 NA	Intergeni Intergeni	8319 NM_145111	221786 Hs. 596587NM_145111	ENSG00000FAM200A	C7orf38 family wiprotein-coding	
chr8-132 7.188595	-0.03944	0.873951	-0.04513	0.964003	0.981636	chr8	1.33E+08	1.33E+08	+ 0 NA	intron (Nintron (N	-2370 NM_00323E	7038 Hs. 654591NM_00323E	ENSG00000CTG	AITD3 TGN thyroglobulin protein-coding	
chr12-504 8.358785	0.036458	0.806889	0.044993	0.964113	0.981636	chr12	50443501	50445551	+ 0 NA	intron (Nintron (N	-12045 NR_13275E	1.07E+08	NR_13275E	SNORD133	CL2142 Z4small nucsnoRNA
chr17-14 8.407783	0.036458	0.811392	0.044933	0.964161	0.981636	chr17	14033660	14034380	+ 0 NA	non-codir non-codir	9522 NR_003261	94158 Hs. 63307E	NR_003261	CDRT15P1	CDRT15P CMT1A dup pseudo
chr2-113 8.407783	0.036458	0.811392	0.044933	0.964161	0.981636	chr2	1.13E+08	1.13E+08	+ 0 NA	intron (NMER135 DN	1738 NR_015377	654433 Hs. 65666C	NR_015377	ENSG00000PAX8-AS1	- PAX8 antncRNA
chr22-451 8.407783	0.036458	0.811392	0.044933	0.964161	0.981636	chr22	45156910	45158115	+ 0 NA	intron (Nintron (N	-4928 NR_038957	1.01E+08	NR_038957	ENSG00000NUP50-DN	NUP50-AS1 NUP50 divncRNA
chr3-1421 8.407783	0.036458	0.811392	0.044933	0.964161	0.981636	chr3	1.42E+08	1.42E+08	+ 0 NA	intron (Nintron (N	-27834 NM_00117E	7029 Hs. 37901E	NM_00628E	ENSG00000TFDP2	DP2 transcrip protein-coding
chr5-346 8.407783	0.036458	0.811392	0.044933	0.964161	0.981636	chr5	34658120	34658605	+ 0 NA	intron (Nintron (N	1871 NM_00114E	26064 Hs. 43140C	NM_01557E	ENSG00000RAI14	NORPEG R retinoic protein-coding
chr1-150 6.872721	0.039974	0.889908	0.04492	0.964171	0.981636	chr1	1.51E+08	1.51E+08	+ 0 NA	Intergeni AluS6 S1	10755 NM_207047	2029 Hs. 63245E	NM_00443E	ENSG00000ENSA	ARPP-19e endosulf protein-coding
chr2-325 6.872721	0.039974	0.889908	0.04492	0.964171	0.981636	chr2	32578374	32578812	+ 0 NA	intron (NAluS6 S1	-3775 NR_12579E	1.04E+08	NR_12579E	ENSG00000BIRC6-AS2	linc-birc6 BIRC6 antncRNA
chr4-139 6.872721	0.039974	0.889908	0.04492	0.964171	0.981636	chr4	1.4E+08	1.4E+08	+ 0 NA	3' UTR (N3' UTR (N	46660 NM_00130E	80854 Hs. 48079E	NM_03064E	ENSG00000SETD7	KMT7 SET7 SET domain protein-coding
chr13-491 7.237593	-0.03902	0.868852	-0.04491	0.96418	0.981636	chr13	49173777	49175739	+ 0 NA	intron (Nintron (N	-45580 NM_001507	2862 Hs. 24812E	NM_001507	ENSG00000MLNR	GPR38 MTL motilin r protein-coding
chr17-504 7.237593	-0.03902	0.868852	-0.04491	0.96418	0.981636	chr17	50484939	50485731	+ 0 NA	non-codir non-codir	6475 NM_01834E	55316 Hs. 8033	NM_01834E	ENSG00000CRSAD1	HemW radical S protein-coding
chr7-2194 7.237593	-0.03902	0.868852	-0.04491	0.96418	0.981636	chr7	219429	220139	+ 0 NA	intron (Nintron (N	27213 NM_00202E	56975 Hs. 13474E	NM_02022E	ENSG00000FAM20C	DMP-4 DMF FAM20C g protein-coding
chr1-2067 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr1	20657758	20659198	+ 0 NA	intron (NMER113 DN	3066 NM_00521E	1650 Hs. 52314E	NM_00521E	ENSG00000DDOST	AGER1 CDC dihydril protein-coding
chr1-179 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr1	1.8E+08	1.8E+08	+ 0 NA	intron (NAluSx SIN	20078 NM_01560E	26092 Hs. 49645E	NM_01560E	ENSG00000TORIAIP1	LAP1 LAP1 torsin 1 protein-coding
chr13-11 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr13	1.11E+08	1.11E+08	+ 0 NA	intron (NAluSx3 S1	18656 NM_00135E	79587 Hs. 50872E	NM_02453E	ENSG00000CAR52	COXP27 cysteiny protein-coding
chr14-64 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr14	64932658	64934245	+ 0 NA	3' UTR (N3' UTR (N	9294 NR_13807E	2877 Hs. 2074	NM_00208E	ENSG00000GPX2	GI-GPx G glutathic protein-coding
chr16-74 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr16	74344089	74344735	+ 0 NA	intron (NAluSx SIN	23843 NR_02695C	283922 Hs. 55872E	NR_02695C	ENSG00000LOC28392	- pyruvate pseudo
chr17-671 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr17	67142529	67143443	+ 0 NA	intron (NAluSx1 S1	98432 NM_000727	786 Hs. 14798E	NM_000727	ENSG00000CACNG1	CACNLG calcium v protein-coding
chr22-17 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr22	17098748	17099174	+ 0 NA	intron (Nintron (N	14002 NM_00128E	23765 Hs. 48353	NM_01433E	ENSG00000IL17RA	CANDF5 C interleuk protein-coding
chr3-149 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr3	1.49E+08	1.49E+08	+ 0 NA	intron (NLMIME2 LIN	-3707 NR_04664E	1.01E+08	NR_04664E	ENSG00000HLTF-AS1	- HLTF antncRNA
chr5-715 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr5	71509127	71510276	+ 0 NA	exon (NM exon (NM	54050 NM_01842E	55814 Hs. 25827E	NM_01842E	ENSG00000BDP1	DFNB112 EB double protein-coding
chr6-135 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr6	1.35E+08	1.35E+08	+ 0 NA	intron (NMLT1F2 LI	33221 NM_001134	54806 Hs. 386684NM_017651	ENSG00000CAH1	AHI-1 JBT Abelson t protein-coding	
chr7-639 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr7	6392167	6392982	+ 0 NA	intron (Nintron (N	18047 NM_00690E	5879 Hs. 41381E	NM_00690E	ENSG00000RAC1	MIG5 MRD4 Rac fami protein-coding
chr7-111 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr7	1.12E+08	1.12E+08	+ 0 NA	intron (Nintron (N	125399 NR_10380E	1.01E+08	NR_10380E	ENSG00000DOCK4-AS1	- DOCK4 antncRNA
chr7-155 6.675476	-0.03772	0.840082	-0.0449	0.964185	0.981636	chr7	1.56E+08	1.56E+08	+ 0 NA	intron (NMIRc SINE	3731 NM_05304E	155435 Hs. 59181E	NM_05304E	ENSG00000CRBM33	

chr8-4315	5.922534	0.04139	0.939939	0.044035	0.964877	0.981636	chr8	43157494	43158964	+	0	NA	intron (AluSc5 SI	17765	NM_15241E	138050	Hs. 600384NM_15241E	ENSG00000CHGSNAT	HGNAT MPS heparan-ε protein-coding	
chr1-8534	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr1	85349075	85350976	+	0	NA	intron (L1ME3Cz L	54481	NM_00133C	23576	Hs. 713411NM_012137	ENSG00000DDAH1	DDAH DDAF dimethylε protein-coding	
chr13-20C	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr13	20058565	20060216	+	0	NA	intron (intron (	-4331	NR_12638C	1.04E+08	Hs. 57801ENR_12638C	ENSG00000LINC01072	long intncRNA	
chr13-30F	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr13	30642477	30645451	+	0	NA	intron (intron (	9759	NM_00132I	10208	Hs. 533831NM_00580C	ENSG00000USPL1	C13orf22 ubiquitin protein-coding	
chr13-41C	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr13	41074667	41079654	+	0	NA	intron (L1PB4 LIN	15651	NM_00118T	11193	Hs. 41130CNM_007187	ENSG00000WBP4	FBP21 WW domain protein-coding	
chr14-34F	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr14	34853636	34853993	+	0	NA	intron (intron (	-20377	NR_16077E	1.12E+08	Hs. 50914CNR_16077E	LOC11226E	uncharactncRNA	
chr14-73H	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr14	73198052	73198592	+	0	NA	intron (intron (	-39184	NR_158677	89932	Hs. 509909NM_17346E	ENSG00000PAPLN	PPN papilin, protein-coding	
chr14-88A	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr14	88410295	88411198	+	0	NA	intron (L1PA7 LIN	25089	NM_01841E	55812	Hs. 52551ENM_01841E	ENSG00000SPATA7	HEL-S-29ε spermatog protein-coding	
chr15-59C	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr15	59088883	59091770	+	0	NA	intron (AluSx1 SI	-14820	NM_00470I	9133	Hs. 19469ENM_00470I	ENSG00000CCNB2	HLT12799 cyclin B2 protein-coding	
chr15-99E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr15	99678251	99679276	+	0	NA	3' UTR (3' UTR (	45875	NM_00113C	4205	Hs. 26867ENM_005587	ENSG00000MEF2A	ADCAD1 RS myocyte ε protein-coding	
chr16-18E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr16	18895826	18896814	+	0	NA	intron (intron (	30084	NM_01841E	23049	Hs. 46017ENM_01509E	ENSG00000SMG1	61E3.4 ATSMG1 nonsprotein-coding	
chr17-54E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr17	5483044	5484581	+	0	NA	intron (intron (	2366	NM_01604I	51009	Hs. 286131NM_01604I	ENSG00000CERL2	CGI-101 Ederlin 2 protein-coding	
chr17-41E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr17	41867922	41869024	+	0	NA	intron (intron (	-3050	NM_01814Z	55175	Hs. 13268	NM_01814Z	ENSG00000KLHL11	kelch likprotein-coding
chr17-60E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr17	60066720	60075970	+	0	NA	intron (L1MC5 LIN	7586	NM_02207C	63897	Hs. 22189ENM_02207C	ENSG00000HEATR6	ABC1 HEAT repeprotein-coding	
chr18-57E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr18	57687867	57689976	+	0	NA	intron (intron (	58590	NM_00124E	1.01E+08	Hs. 66064ENM_00124E	LOC10050E	uncharactprotein-coding	
chr18-79E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr18	79228579	79231154	+	0	NA	intron (L1M4b LIN	21787	NM_00114E	80148	Hs. 288284NM_02507E	ENSG00000SLC66A2	PQLC1 solute cε protein-coding	
chr2-323E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr2	32391801	32400855	+	0	NA	intron (intron (	38915	NM_01625E	57448	Hs. 150107NM_01625E	ENSG00000BIRC6	APOLLON Ebaculovir protein-coding	
chr2-324E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr2	32438894	32444722	+	0	NA	intron (intron (	86280	NM_01625E	57448	Hs. 150107NM_01625E	ENSG00000BIRC6	APOLLON Ebaculovir protein-coding	
chr2-3947	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr2	39475001	39475515	+	0	NA	intron (L1MEi LIN	37842	NR_03787E	728730	Hs. 655344NR_03787E	ENSG00000MAP4K3-D1	MAP4K3 dincRNA	
chr2-2018	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr2	47815391	47815976	+	0	NA	intron (intron (	31728	NM_00128I	2956	Hs. 44505ENM_00017E	ENSG00000MSH6	GTBP GTME mutS homc protein-coding	
chr2-177E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr2	212529	2.02E+08	+	0	NA	intron (L1M87 LIN	-23443	NM_003306E	58538	Hs. 63085	NM_003306E	ENSG00000MPP4	ALS2CR5 Lmembrane protein-coding
chr21-31E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr21	31685387	31688455	+	0	NA	intron (MER1B DNA	27299	NM_000454	6647	Hs. 443914NM_000454	ENSG00000SOD1	ALS ALS1 superoxic protein-coding	
chr21-392	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr21	39223579	39224774	+	0	NA	intron (intron (	-40662	NM_20343E	8624	Hs. 47383ENM_00372C	ENSG00000PSMG1	C21LRP DP proteason protein-coding	
chr3-4804	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr3	48048542	48051270	+	0	NA	intron (AluSx3 SI	38942	NM_00237E	4134	Hs. 51794ENM_00237E	ENSG00000MAP4	microtub protein-coding	
chr3-1701	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr3	1.7E+08	1.7E+08	+	0	NA	intron (L1ME4a LI	66384	NM_024947	80012	Hs. 52959ENM_024947	ENSG00000PHC3	EDR3 HPHε polyhomec protein-coding	
chr3-189E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr3	1.9E+08	1.9E+08	+	0	NA	intron (intron (	133429	NR_03064Z	55763	Hs. 26966ENM_01826I	ENSG00000EXOC1	MIRN944 fmiocrna ncRNA	
chr4-558E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr4	55899399	55900934	+	0	NA	intron (intron (	46786	NM_01826I	2926	Hs. 30976ENM_00209E	ENSG00000GRSF1	BM-102 SE excyst cε protein-coding	
chr4-707E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr4	70792719	70797296	+	0	NA	intron (intron (	44496	NM_00109E	57491	Hs. 50823	NM_02073I	ENSG00000AHRH	AHH AHRH aryl-hydr protein-coding
chr5-360E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr5	360571	366251	+	0	NA	intron (NLTR78 LTF	59235	NM_02073I	51406	Hs. 30624ENM_016167	ENSG00000NOL7	GHR f90 Nucleolar protein-coding	
chr6-1361	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr6	13616840	13624911	+	0	NA	TTS (NM_C	5540	NM_016167	81578	Hs. 47629	NM_03082C	ENSG00000COL21A1	COLA1L FF collagen protein-coding
chr6-5651	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr6	56514723	56515565	+	0	NA	intron (intron (	-121016	NM_00131E	91749	Hs. 40057ENM_15336E	ENSG00000MFSDB4	KIAA1919 major fac protein-coding	
chr6-111E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr6	1.11E+08	1.11E+08	+	0	NA	intron (intron (	104407	NM_15336E	9275	Hs. 647051NM_001707	ENSG00000BCL7B	BAF major protein-coding	
chr7-735E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr7	73538623	73541334	+	0	NA	exon (NM_exon (NM	15847	NM_00010E	1738	Hs. 131711NM_00010E	ENSG00000CLD5	DLDD DLDF dihydroliprotein-coding	
chr7-107E	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr7	1.08E+08	1.08E+08	+	0	NA	intron (L2c LINE	15847	NM_00010E	1738	Hs. 131711NM_00010E	ENSG00000CLD5	DLDD DLDF dihydroliprotein-coding	
chr8-102	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr8	1.02E+08	1.02E+08	+	0	NA	intron (intron (	15192	NR_12541E	1.02E+08	Hs. 49244ENR_12541E	ENSG00000UBR5-AS1	UBR5 anticncRNA	
chr9-1104	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr9	1.1E+08	1.1E+08	+	0	NA	intron (intron (	-78996	NM_00128E	255220	Hs. 147064NM_00100E	ENSG00000TXNDX8	SPTRX-3 Sthioredox protein-coding	
chr9-1114	8.649236	-0.0347	0.788114	-0.04403	0.964884	0.981636	chr9	1.11E+08	1.11E+08	+	0	NA	intron (AluJb SIN	67912	NM_001364	23392	Hs. 36825ENM_00108C	ENSG00000ECPAS	ECM29 KIAEcm29 prc protein-coding	
chr17-634	8.211353	-0.03569	0.814734	-0.04338	0.965063	0.981636	chr17	63418054	63418669	+	0	NA	exon (NM_exon (NM	21906	NM_00133C	1534	Hs. 355264NM_00191E	ENSG00000CYB561	CYB561A1 cytochrom protein-coding	
chr2-1301	8.211353	-0.03569	0.814734	-0.04338	0.965063	0.981636	chr2	1.3E+08	1.3E+08	+	0	NA	intron (intron (	14503	NR_03322C	55627	Hs. 51645ENM_01775I	ENSG00000SMPD4	NET13 NSM synthom protein-coding	
chr1-9171	7.371159	0.06295	1.437577	0.043789	0.965072	0.981636	chr1	91712230	91712501	+	0	NA	exon (NM_exon (NM	173786	NR_036634	7049	Hs. 48239ENM_00324E	ENSG00000TGFB3	BGCAN bet transform protein-coding	
chr3-520	4.915492	0.045552	1.041718	0.043728	0.965122	0.981636	chr3	5217064	5218198	+	0	NA	3' UTR (3' UTR (	29924	NM_014674	9695	Hs. 22461ENM_014674	ENSG00000EDEMI	EDEM ER degrad protein-coding	
chr5-140	4.915492	0.045552	1.041718	0.043728	0.965122	0.981636	chr5	14000613	14001811	+	0	NA	IntergeniL1PA16 LI	-56507	NM_00136E	1767	Hs. 21236CNR_00136E	ENSG00000DNAH5	CILD3 DNε dynein asprotein-coding	
chr11-34E	8.93847	0.033457	0.767167	0.043611	0.965215	0.981636	chr11	34932607	34932870	+	0	NA	intron (L1MC5a LI	-9099	NR_03983E	1.01E+08	Hs. 533444NM_00019I	ENSG00000MIR1343	microRNA ncRNA	
chr1-2381	6.401556	0.039585	0.908688	0.043563	0.965253	0.981636	chr1	23818623	23820386	+	0	NA	intron (AluSx1 SI	5925	NM_00019I	3155	Hs. 533444NM_00019I	ENSG00000CUGL2	HL 3-hydroxy protein-coding	
chr10-35E	6.401556	0.039585	0.908688	0.043563	0.965253	0.981636	chr10	35046650	35049264	+	0	NA	intron (intron (	26326	NM_00119E	8453	Hs. 82919	NM_00359I	ENSG00000CHML2	culin 2 protein-coding
chr12-45E	6.401556	0.039585	0.908688	0.043563	0.965253	0.981636	chr12	45986910	45987360	+	0	NA	intron (FLAM_C SI	3439	NM_00471E	9169	Hs. 210367NM_00471E	ENSG00000SCAF11	CASP11 SF SR-relate protein-coding	
chr12-117	6.401556	0.039585	0.908688	0.043563	0.965253	0.981636	chr12	1.17E+08	1.17E+08	+	0	NA	intron (L1MC5 LIN	9055	NM_01500Z	23014	Hs. 74037ENM_01500Z</			



chr12-48c.6.880579	0.037984	0.882908	0.043021	0.965685	0.981636	chr12	48062645	48063595	+	0 NA	intron (Nintron (N	-42133 NM_001354	5213 Hs. 75160 NM_00028c	ENSG0000CPFKM	ATP-PFK	Chosphofr protein-coding	
chr12-58c.6.880579	0.037984	0.882908	0.043021	0.965685	0.981636	chr12	58907016	58908593	+	0 NA	intron (Nintron (N	11742 NM_00113c	121227 Hs. 25373c	ENSG0000LRIG3	LIG3	leucine r protein-coding	
chr17-59c.6.880579	0.037984	0.882908	0.043021	0.965685	0.981636	chr17	59040608	59041934	+	0 NA	intron (NMIRc SINE	65609 NR_148347	4591 Hs. 57907c	ENSG0000C TRIM37	MUL POB1	tripartit protein-coding	
chr3-129c.6.880579	0.037984	0.882908	0.043021	0.965685	0.981636	chr3	1.3E+08	1.3E+08	+	0 NA	intron (Nintron (N	8149 NM_00130c	132243 Hs. 97358 NM_15383c	ENSG0000CH1FO0	H.8 H1oc H	histor protein-coding	
chr5-722c.6.880579	0.037984	0.882908	0.043021	0.965685	0.981636	chr5	72206039	72207169	+	0 NA	3' UTR (N3' UTR (N	26817 NM_001324	4131 Hs. 33507c	ENSG0000MAP1B	FUT5CH MA	microtub protein-coding	
chr8-899c.6.880579	0.037984	0.882908	0.043021	0.965685	0.981636	chr8	89925002	89925340	+	0 NA	exon (NM_exon (NM	22601 NM_00112c	734 Hs. 43644c	ENSG0000C OSGIN2	C8orf1 h	oxidative protein-coding	
chr10-99c.6.822997	-0.03229	0.75079	-0.04301	0.965694	0.981636	chr10	99950238	99952918	+	0 NA	intron (THEIB-int	-20671 NM_00131c	23268 Hs. 50077c	ENSG0000C DNMBP	HGF6F36 d	ynamn t protein-coding	
chr11-467c.6.822997	-0.03229	0.75079	-0.04301	0.965694	0.981636	chr11	46760229	46764059	+	0 NA	TTS (NR_C TTS (NR_C	355 NR_00305c	692108 Hs. 69325c	ENSG0000C SNORD67	HBII1-166	small nucsnoRNA	
chr12-58c.6.822997	-0.03229	0.75079	-0.04301	0.965694	0.981636	chr12	58889323	58890584	+	0 NA	intron (Nintron (N	29593 NM_00113c	121227 Hs. 25373c	ENSG0000C LRIG3	LIG3	leucine r protein-coding	
chr17-84c.6.822997	-0.03229	0.75079	-0.04301	0.965694	0.981636	chr17	8454707	8458396	+	0 NA	intron (NAluSx SIN	20667 NM_00308c	81565 Hs. 37212c	ENSG0000C NDEL1	EOPA MITF	nude n protein-coding	
chr17-19c.6.822997	-0.03229	0.75079	-0.04301	0.965694	0.981636	chr17	19379822	19384182	+	0 NA	exon (NM_exon (NM	3504 NM_00274c	5598 Hs. 15013c	ENSG0000C MAPK7	BMK1 ERK4	mitogen e protein-coding	
chr3-138c.6.822997	-0.03229	0.75079	-0.04301	0.965694	0.981636	chr3	1.39E+08	1.39E+08	+	0 NA	IntergeniLIM2b LIN	40481 NM_018147	55179 Hs. 17343c	ENSG0000C FAIM	FAIM1	Fas apopt protein-coding	
chr9-338c.6.822997	-0.03229	1.135534	0.042911	0.965773	0.981636	chr9	33866347	33867243	+	0 NA	intron (NLIME3A LI	49635 NM_017811	54926 Hs. 64364c	ENSG0000C UBE2R2	CDC34B E2	ubiquitir protein-coding	
chr17-81c.6.822997	-0.03229	0.789817	-0.04288	0.965794	0.981636	chr17	81575565	81579257	+	0 NA	intron (Nintron (N	1672 NR_13013c	55666 Hs. 44333c	ENSG0000C NPLOC4	NPL4	hmc protein-coding	
chr15-51c.6.822997	-0.03229	0.80706	0.042863	0.965811	0.981636	chr15	51959118	51961472	+	0 NA	intron (Nintron (N	11483 NM_00132c	123169 Hs. 56766c	ENSG0000C LEO1	RDL	LEO1 hmc protein-coding	
chr5-796c.6.822997	-0.03229	0.80706	0.042863	0.965811	0.981636	chr5	79648835	79650097	+	0 NA	intron (Nintron (N	37025 NM_00134c	167153 Hs. 41819c	ENSG0000C TENT2	APD4 GLD2	terminal protein-coding	
chr19-44c.6.822997	-0.03229	1.006124	0.042748	0.965902	0.981636	chr19	4819454	4820237	+	0 NA	intron (NAluS2 SI	11897 NM_18291c	148022 Hs. 29344	ENSG0000C TICAM1	I1AE6 Myf	tol l like protein-coding	
chr20-44c.6.822997	-0.03229	0.868718	-0.04268	0.965959	0.981636	chr20	44498139	44498720	+	0 NA	3' UTR (N3' UTR (N	22555 NM_001261	79183 Hs. 28386c	ENSG0000C TTPAL	C20orf12	alpha toc protein-coding	
chr20-58c.6.822997	-0.03229	0.776428	-0.0426	0.966018	0.981636	chr20	58702872	58704356	+	0 NA	intron (Nintron (N	10814 NM_02466c	79716 Hs. 65486c	ENSG0000C NPEPL1	ba261P9.2	aminopept protein-coding	
chr6-159c.6.822997	-0.03229	0.776428	-0.0426	0.966018	0.981636	chr6	15496540	15497232	+	0 NA	exon (NM_exon (NM	166142 NR_03644c	84062 Hs. 57114c	ENSG0000C DTNBP1	BLOC158 L	dystrobre protein-coding	
chr7-124c.6.822997	-0.03229	0.776428	-0.0426	0.966018	0.981636	chr7	1.29E+08	1.29E+08	+	0 NA	intron (Nintron (N	40334 NR_03405c	23534 Hs. 19361c	ENSG0000C TNPO3	IP012 LG	transpob protein-coding	
chr1-326c.6.822997	-0.03229	0.789096	0.042541	0.966068	0.981636	chr1	32653781	32654964	+	0 NA	intron (NAluJb SIN	3014 NM_00113c	5928 Hs. 16003	ENSG0000C RBBP4	NURF55 RE	RB bindir protein-coding	
chr1-237c.6.822997	-0.03229	0.837309	-0.04237	0.966206	0.981636	chr1	23794259	23795083	+	0 NA	TTS (NM_C TTS (NM_C	3526 NM_00726c	11313 Hs. 53347c	ENSG0000C LYPLA2	APT-2 API	lysophos protein-coding	
chr1-277c.6.822997	-0.03229	0.837309	-0.04237	0.966206	0.981636	chr1	27760367	27760738	+	0 NA	exon (NM_exon (NM	-12667 NM_177424	23673 Hs. 52385c	ENSG0000C STX12	STX13 STY	syntin protein-coding	
chr10-98c.6.822997	-0.03229	0.837309	-0.04237	0.966206	0.981636	chr10	98386711	98387261	+	0 NA	intron (Nintron (N	8321 NR_03161c	1E+08	NR_03161c	ENSG0000C MIR1287	MIRN1287	microRNA ncRNA
chr17-401c.6.822997	-0.03229	0.837309	-0.04237	0.966206	0.981636	chr17	40144273	40145357	+	0 NA	intron (NAluJo SIN	4278 NM_00735c	22794 Hs. 74328c	ENSG0000C CAS3	BTZ MLN51	CASC3 exc protein-coding	
chr20-34c.6.822997	-0.03229	0.837309	-0.04237	0.966206	0.981636	chr20	34409262	34410514	+	0 NA	intron (NFAM SINE	46615 NM_001324	83737 Hs. 63227c	ENSG0000C ITC	ADMPD AIF	itichy E3 protein-coding	
chr7-138c.6.822997	-0.03229	0.837309	-0.04237	0.966206	0.981636	chr7	1.39E+08	1.39E+08	+	0 NA	intron (Nintron (N	66709 NM_01590c	8805 Hs. 49028c	ENSG0000C TRIM24	PTC6 RNFF	tripartit protein-coding	
chr17-55c.6.822997	-0.03229	1.076187	0.042217	0.966326	0.981636	chr17	5537393	5538079	+	0 NA	intron (Nintron (N	-36730 NM_00116c	728392 Hs. 10430c	ENSG0000C LOC72839c	-	uncharact protein-coding	
chr7-5481c.6.822997	-0.03229	1.076187	0.042217	0.966326	0.981636	chr7	5481812	5482263	+	0 NA	intron (Nintron (N	13880 NR_03031c	693174	NR_03031c	ENSG0000C MIR589	MIRN589	hmcRNA ncRNA
chr5-1461c.6.822997	-0.03229	0.723532	-0.04212	0.966402	0.981636	chr5	1.46E+08	1.46E+08	+	0 NA	intron (NAluSc SIN	14856 NM_020117	51520 Hs. 43267c	ENSG0000C LARS	HSPC192 I	leucyl-tf protein-coding	
chr1-586c.6.822997	-0.03229	0.849885	-0.04207	0.966447	0.981636	chr1	58665413	58665987	+	0 NA	intron (Nintron (N	34362 NM_00108c	114803 Hs. 74492c	ENSG0000C MYSM1	2A-DUB 2	My like, protein-coding	
chr16-18c.6.822997	-0.03229	0.818794	-0.04196	0.966528	0.981636	chr16	18875366	18876402	+	0 NA	intron (Nintron (N	50520 NM_01509c	23049 Hs. 46017c	ENSG0000C SMG1	61E.3 A1	SMG1 nons protein-coding	
chr16-53c.6.822997	-0.03229	0.818794	-0.04196	0.966528	0.981636	chr16	53308857	53309717	+	0 NA	intron (NL3 LINE C	61925 NM_001347	643802 Hs. 45133c	ENSG0000C LOC64380c	-	u3 small protein-coding	
chr17-31c.6.822997	-0.03229	0.818794	-0.04196	0.966528	0.981636	chr17	31265526	31266611	+	0 NA	intron (NMIRb SINE	31171 NM_002544	4974 Hs. 11387c	ENSG0000C OMG	OMGP	oligodenc protein-coding	
chr7-151c.6.822997	-0.03229	0.818794	-0.04196	0.966528	0.981636	chr7	1.51E+08	1.51E+08	+	0 NA	intron (NMER21C LI	4997 NM_00136c	51666 Hs. 64708c	ENSG0000C NUB1	BS4 NUB1	negative protein-coding	
chr1-364c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr1	36455846	36456842	+	0 NA	exon (NM_exon (NM	-5859 NM_00133c	127700 Hs. 20220c	ENSG0000C OSCP1	Clorf102	organic s protein-coding	
chr1-550c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr1	55088305	55089974	+	0 NA	intron (NAluSx SIN	48917 NR_110451	255738 Hs. 18844	ENSG0000C PCSK9	FH3 HCHO	proprote protein-coding	
chr1-235c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr1	2.35E+08	2.35E+08	+	0 NA	intron (NAluJb SIN	-43225 NR_03990c	1.01E+08	NR_03990c	ENSG0000C MIR4753	mir-4753	microRNA ncRNA
chr10-997c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr10	99714326	99717216	+	0 NA	intron (NLIME3G LI	-16463 NM_01596c	51076 Hs. 16606	ENSG0000C CUTC	CGI-32	cutC copr protein-coding	
chr14-72c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr14	72956226	72956546	+	0 NA	non-codiron-codir	29922 NM_00135c	26094 Hs. 33149c	ENSG0000C DCAF4	WDR21 WDF	DBD1 and protein-coding	
chr17-77c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr17	77495688	77496689	+	0 NA	intron (NAluSx SIN	21024 NM_00111c	10801 Hs. 11289c	ENSG0000C SEPTIN9	Afl17q25	septin 9 protein-coding	
chr2-2057c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr2	2.06E+08	2.06E+08	+	0 NA	intron (Nintron (N	45900 NM_018534	8828 Hs. 47120c	ENSG0000C CNRP2	NP2 NP2	neuropil protein-coding	
chr5-774c.6.822997	-0.03229	0.811094	-0.04193	0.966556	0.981636	chr5	77484645	77485709	+	0 NA	intron (NERV3-16A3	7139 NM_01826c	55255 Hs. 48257c	ENSG0000C WDR41	MSTP048	WD repeat protein-coding	
chr1-2647c.6.822997	-0.03229	0.843066	0.041775	0.966678	0.981636	chr1	26477509	26477835	+	0 NA	IntergeniIntergeni	5232 NM_005517	3151 Hs. 18116c	ENSG0000C HMG21	HMG17	high mobiprotein-coding	
chr13-48c.6.822997	-0.03229	0.843066	0.041775	0.966678	0.981636	chr13	48084074	48084273	+	0 NA	intron (NAluSz SIN	7036 NR_046511	1.01E+08	Hs. 61624c	ENSG0000C MED4-AS1	MED4-AS	MED4 antncRNA
chr17-281c.6.822997	-0.03229	0.977057	0.041766	0.966685	0.981636	chr17	28142371	28143749	+	0 NA	intron (NAluSc8 SI	-83503 NR_003064	23615 Hs. 15719c	ENSG0000C PYY2	-	peptide l pseudo	
chr12-12c.6.822997	-0.03229	0.792744	-0.04171	0.966729	0.981636	chr12	1.22E+08	1.22E+08	+	0 NA	intron (NAluSx1 SI	-43234 NR_04538c	1.01E+08	Hs. 62425c	ENSG0000C CLIP1-AS1	CLIP1-AS1	antncRNA
chr15-67c.6.822997	-0.03229	0.792744	-0.04171	0.966729	0.981636	chr15	60769779	60772955	+	0 NA	intron (Nintron (N	5765 NM_00590c	4088 Hs. 72798c	ENSG0000C SMAD3	HSPC193 E	SMAD famiprotein-coding	
chr17-35c.6.822997	-0.03229	0.792744	-0.04171	0.966729	0.981636	chr17	35670761	35675127	+	0 NA	intron (Nintron (N	-58695 NM_03331c	91608 Hs. 74499c	ENSG0000C RASL10B	RRP17 VTS	RAS like protein-coding	
chr4-983c.6.822997	-0.03229	0.792744	-0.04171	0.966729	0.981636	chr4	98366176	98367544	+	0 NA	intron (THEIB-int	105476 NM_02115c	5910 Hs. 13285c	ENSG0000C RAP1GDS			

chr12-292.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr12	2928985	2932320	+	0	NA	intron (AluY SINE	-28745	NM_003213	7004	Hs. 94865	NM_003213	ENSG000002TEAD4	EFTR-2 RTTEA	domaiprotein-coding			
chr15-52.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr15	52057739	52060129	+	0	NA	intron (intron (N	39715	NM_002748	5597	Hs. 411847	NM_002748	ENSG000002MAPK6	ERK3 HsTlmitogen-ε	protein-coding			
chr19-144.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr19	14488047	14491766	+	0	NA	intron (intron (N	6221	NM_005716	10755	Hs. 655012	NM_005716	ENSG000002GIPC1	C19orf3 GIPC	PDZ protein-coding			
chr19-219.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr19	21407444	21410334	+	0	NA	TTS (NM_TTS (NM_1	11756	NM_145326	284443	Hs. 656558	NM_145326	ENSG000002ZNF493	ZNF493	zinc finger protein-coding			
chr19-296.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr19	29611795	29612712	+	0	NA	intron (intron (N	5970	NR_027366	10775	Hs. 012877	NR_027366	ENSG000002POP4	POP4	home protein-coding			
chr19-387.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr19	38713514	38730176	+	0	NA	intron (intron (N	22629	NM_144691	147968	Hs. 731777	NM_144691	ENSG000002CAPN12	CAPN12	calpain I protein-coding			
chr2-962.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr2	96299145	96303863	+	0	NA	intron (intron (N	4042	NM_014014	23020	Hs. 246112	NM_014014	ENSG000002SNRNP200	SNRNP200	ASCC3 L1 Esmal1	nucprotein-coding		
chr20-197.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr20	19799927	19803919	+	0	NA	Intergeni Intergeni	-84598	NM_001242	54453	Hs. 472277	NM_001242	ENSG000002C19N2	C19N2	MACS RRAS Ras and F	protein-coding		
chr20-491.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr20	49117422	49118596	+	0	NA	exon (NM_exon (NM_	70361	NM_001322	6780	Hs. 596704	NM_004602	ENSG000002STAU1	STAU1	PPP1R150 staufen c	protein-coding		
chr5-135.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr5	1.35E+08	1.35E+08	+	0	NA	intron (intron (N	30156	NM_138609	9555	Hs. 420272	NM_004893	ENSG000002H2AFY	H2AFY	H2A.y H2M2A	histc protein-coding		
chr6-215.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr6	21595331	21595744	+	0	NA	exon (NM_exon (NM_	1786	NM_003107	6659	Hs. 643913	NM_003107	ENSG000002SOX4	SOX4	EVII6	SRY-box t	protein-coding	
chr9-130.9	177256	-0.03153	0.770276	-0.04093	0.967353	0.981636	chr9	1.3E+08	1.3E+08	+	0	NA	intron (MLT1L LTF	24669	NM_02096C	57720	Hs. 512461	NM_02096C	ENSG000002GPR107	GPR107	GCDRP LUSG	proteir protein-coding		
chr13-32.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr13	32230610	32232850	+	0	NA	intron (intron (N	80224	NM_001133	646799	Hs. 569254	NM_001133	ENSG000002ZARIL	ZARIL	Z3CXXC7 Zyzygo	arprotein-coding		
chr14-100.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	intron (intron (N	4485	NR_00308C	692215	NR_00308C	ENSG000002SNORD112	SNORD112	14q(0)	small	nucsnRNA		
chr17-161.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr17	16140698	16141527	+	0	NA	intron (Kanga2_a	12084	NR_145787	1.1E+08	NR_145787	SNORD163		small	nucsnRNA			
chr17-444.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr17	44472635	44473600	+	0	NA	intron (intron (N	30289	NM_001002	23131	Hs. 463125	NM_001002	ENSG000002GPATCH8	GPATCH8	PKI G-patch	c protein-coding		
chr18-462.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr18	46263005	46264303	+	0	NA	3' UTR (3' UTR (N	-70364	NM_15247C	494470	Hs. 501114	NM_15247C	ENSG000002CRNF165	CRNF165	ARKL2 Arkring	finprotein-coding		
chr18-576.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr18	57657183	57658238	+	0	NA	intron (intron (N	27379	NM_001242	1.01E+08	Hs. 66064E	NM_001242804	LOC100505E		uncharact	protein-coding		
chr21-466.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr21	46362896	46364964	+	0	NA	exon (NM_exon (NM_	39263	NM_001315	5116	Hs. 474066	NM_006031	ENSG000002PCNT	PCNT	KEN MOPD2	pericentri	protein-coding	
chr5-129.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr5	1.3E+08	1.3E+08	+	0	NA	intron (NLIPREC2 I	-120590	NM_001257	1E+08	Hs. 582534	NM_001257	ENSG000002CMINAR2	CMINAR2	KIAA1024 membrane	protein-coding		
chr7-128.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr7	1.29E+08	1.29E+08	+	0	NA	Intergeni AluJr4 SI	-65675	NR_024366	402483	Hs. 72235C	NM_001039682	LINC0100C		long	intcncRNA		
chr9-1347.6	888436	0.035961	0.880705	0.040832	0.96743	0.981636	chr9	1.35E+08	1.35E+08	+	0	NA	intron (intron (N	49193	NR_039691	1.01E+08	NR_039691	ENSG000002MIR3689C	MIR3689C		microRNA	ncRNA		
chr17-171.5	402372	0.040474	0.991571	0.040818	0.967441	0.981636	chr17	17185029	17185801	+	0	NA	3' UTR (3' UTR (N	20918	NM_17883C	201164	Hs. 729079	NM_17883C	ENSG000002PLD6	PLD6	ZUC	phospholip	protein-coding	
chr6-897.5	402372	0.040474	0.991571	0.040818	0.967441	0.981636	chr6	89793243	89793822	+	0	NA	intron (AluJo SIN	26262	NM_014611	23195	Hs. 52994E	NM_014611	ENSG000002MDN1	MDN1	Real	midasin f	protein-coding	
chr6-1484.5	402372	0.040474	0.991571	0.040818	0.967441	0.981636	chr6	1.48E+08	1.48E+08	+	0	NA	intron (AluSx1 SI	-30534	NM_00134C	23328	Hs. 193133	NM_01527E	ENSG000002SASH1	SASH1	CAPOK DUF	SAM and f	protein-coding	
chrX-702.5	402372	0.040474	0.991571	0.040818	0.967441	0.981636	chrX	70286360	70288103	+	0	NA	intron (intron (N	2629	NM_00137C	51248	Hs. 11042	NM_016484	ENSG000002PDZD11	PDZD11	AIPP1 PDZ	PDZ	domaiprotein-coding	
chr3-180.7	895479	0.033779	0.834192	0.040493	0.9677	0.981636	chr3	1.81E+08	1.81E+08	+	0	NA	intron (intron (T) n Simp	18497	NM_00119C	131118	Hs. 230601	NM_145261	ENSG000002DNACJ19	DNACJ19	PAM18 TIM	DnaJ	heat	protein-coding
chr7-7434.7	895479	0.033779	0.834192	0.040493	0.9677	0.981636	chr7	74342150	74342422	+	0	NA	intron (AluSx SIN	52821	NM_00338E	7461	Hs. 64701E	NM_00338E	ENSG000002CLIP2	CLIP2	CLIP CLIF	CAP-Gly	c	protein-coding
chr10-245.8	374501	0.032809	0.810713	0.040469	0.967719	0.981636	chr10	24583824	24586229	+	0	NA	exon (NM_exon (NM_	37871	NM_00136E	57584	Hs. 52419E	NM_020824	ENSG000002ARHGAP21	ARHGAP21	RHO	GTPas	protein-coding	
chr19-34.8	374501	0.032809	0.810713	0.040469	0.967719	0.981636	chr19	3494948	3494944	+	0	NA	intron (AluS6 SI	4828	NM_00114E	83475	Hs. 515064	NM_031304	ENSG000002DOHH	DOHH	HLRC1 hDC	deoxyhyp	protein-coding	
chr1-542.9	664136	-0.03051	0.754327	-0.04045	0.967734	0.981636	chr1	54236994	54238066	+	0	NA	non-codir non-codir	1087	NR_103541	619518	Hs. 59143E	NM_001034	ENSG000002SSBP3-AS1	SSBP3-AS1	C1orf191 SSBP3	antncRNA		
chr15-991.9	664136	-0.03051	0.754327	-0.04045	0.967734	0.981636	chr15	99194100	99193039	+	0	NA	intron (THE1B-int	57362	NM_00128E	64927	Hs. 51319E	NM_02290E	ENSG000002TTC23	TTC23	HCC-8	zetratic	protein-coding	
chr19-11.9	664136	-0.03051	0.754327	-0.04045	0.967734	0.981636	chr19	11606071	11608030	+	0	NA	intron (THE1C-int	9567	NM_14529E	199692	Hs. 52666E	NM_14529E	ENSG000002ZNF627	ZNF627		zinc	finprotein-coding	
chr4-147.9	664136	-0.03051	0.754327	-0.04045	0.967734	0.981636	chr4	1.48E+08	1.48E+08	+	0	NA	intron (MLT1B LTF	130931	NR_039962	1.01E+08	NR_039962	ENSG000002MIR4799	MIR4799		microRNA	ncRNA		
chr7-9941.9	664136	-0.03051	0.754327	-0.04045	0.967734	0.981636	chr7	99419378	99420686	+	0	NA	TTS (NM_TTS (NM_C	10860	NR_162133	1.13E+08	NR_162133	MIR12119		microRNA	ncRNA			
chr1-3571.7	367459	0.034668	0.857162	0.040445	0.967738	0.981636	chr1	35714636	35716164	+	0	NA	3' UTR (3' UTR (N	1511	NM_00134E	127703	Hs. 11202E	NM_152374	ENSG000002C1orf216	C1orf216		chromoson	protein-coding	
chr1-1131.7	367459	0.034668	0.857162	0.040445	0.967738	0.981636	chr1	1.13E+08	1.13E+08	+	0	NA	3' UTR (3' UTR (N	51835	NM_001312	9860	Hs. 448972	NM_01481E	ENSG000002LRIG2	LRIG2	LIG-2 LIC	leucine i	protein-coding	
chr10-87.7	367459	0.034668	0.857162	0.040445	0.967738	0.981636	chr10	87806715	87807367	+	0	NA	intron (NMER3A1 I	11190	NM_001321	84896	Hs. 43594E	NM_03281C	ENSG000002ATAD1	ATAD1	AFDC1 FN	ATPase f	protein-coding	
chr17-39.7	367459	0.034668	0.857162	0.040445	0.967738	0.981636	chr17	39903681	39903920	+	0	NA	TTS (NM_TTS (NM_C	13740	NM_00136E	55876	Hs. 306777	NM_01853C	ENSG000002GSDMB	GSDMB	PP4 gasderm	in	protein-coding	
chr1-5281.7	416456	0.034835	0.862206	0.040402	0.967773	0.981636	chr1	52818615	52819822	+	0	NA	intron (intron (N	-23542	NM_001307	440590	Hs. 65845E	NM_001004	ENSG000002ZYG11A	ZYG11A	ZYG11	zyg-11 f	protein-coding	
chr2-207.7	416456	0.034835	0.862206	0.040402	0.967773	0.981636	chr2	20747093	20747633	+	0	NA	intron (intron (N	-26750	NM_00018E	3053	Hs. 47427C	NM_00018E	ENSG000002SERPIND1	SERPIND1	B225673 Eserpin	f	protein-coding	
chr4-349.7	416456	0.034835	0.862206	0.040402	0.967773	0.981636	chr4	3494345	3503799	+	0	NA	promoter-promoter-	-295	NR_030297	693156	NR_030297	ENSG000002MIR571	MIR571	l	microRNA	ncRNA		
chr5-6957.7	416456	0.034835	0.862206	0.040402	0.967773	0.981636	chr5	69575337	69576184	+	0	NA	intron (Tigger1 I	15515	NM_00109E	728340	Hs. 19135E	NM_00109E	ENSG000002GTF2H2C	GTF2H2C	GTF2H2C_2	GTF2H2 f	protein-coding	
chr9-1344.7	416456	0.034835	0.862206	0.040402	0.967773	0.981636	chr9	1.34E+08	1.34E+08	+	0	NA	intron (intron (N	11167	NM_001291	6256	Hs. 59088E	NM_00295F	ENSG000002RXRA	RXRA	NR2B1	retinoid	protein-coding	
chr19-541.8	853523	0.031903	0.790873	0.040339	0.967823	0.981636	chr19	54106278	54106625	+	0	NA	TTS (NM_TTS (NM_C	3596	NM_004542	4696	Hs. 19826E	NM_004542	ENSG000002NDUFA3	NDUFA3	B9 CI-B9	NADH:ubiq	protein-coding	
chr6-4367.6	937434	0.036004	0.89604	0.040181	0.967949	0.981636	chr6	43673390	43674124	+	0	NA	intron (intron (N	14055	NM_01813E	55168	Hs. 52014E	NM_01813E	ENSG000002MRPS18A	MRPS18A	HumanS18	mitochonc	protein-coding	
chr2-171.7	221877	-0.03502	0.872823	-0.04013	0.967991	0.981636	chr2	1.72E+08	1.72E+08	+	0	NA	intron (NMER5A LI	18897	NM_00370E	8604	Hs. 47060E	NM_00370E	ENSG000002SLC25A12	SL				



chr15-434.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr15	43450684	43453156	+	0	NA	intron (AluS26 SI	41236 NM_001141	7158 Hs. 440966NM_005657	ENSG000002TP53BP1	53BP1 TDF tumor prcprotein-coding	
chr15-446.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr15	44628557	44630691	+	0	NA	intron (MIRB SINE	34038 NM_001166	80208 Hs. 656271NM_025137	ENSG000002SPG11	ALS5 CMT2SPG11 vesprotein-coding	
chr15-671.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr15	67168323	67173345	+	0	NA	intron (intron (	4679 NM_001145	4088 Hs. 727986NM_005902	ENSG000002SMAD3	HSPC193 SMAD famiprotein-coding	
chr16-117.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr16	11759319	11777024	+	0	NA	intron (intron (	-25314 NR_136673	51061 Hs. 313847NM_015914	ENSG000002TXNDC11	EFP1 thiosedolprotein-coding	
chr16-187.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr16	18780756	18779096	+	0	NA	intron (intron (	5408 NM_00103C	6210 Hs. 370504NM_001015	ENSG000002RPS15A	DBA20 SIF ribosomalprotein-coding	
chr16-702.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr16	70255243	70272837	+	0	NA	intron (AluSg SIN	-12100 NM_058215	118460 Hs. 660633NM_058215	ENSG000002EXOSC6	EAP4 MTR:exosome cprotein-coding	
chr16-896.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr16	89877941	89881355	+	0	NA	intron (CPg	6056 NM_014972	22980 Hs. 415342NM_014972	ENSG000002TCF25	FKS626 Hs transcriptiprotein-coding	
chr17-376.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr17	37621112	37624386	+	0	NA	intron (intron (	-7710 NR_106744	1.02E+08	NR_106744	ENSG000002MIR378J	hsa-mir-3 microRNA ncRNA
chr17-511.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr17	51191060	51192844	+	0	NA	intron (intron (	25230 NM_001015	4831 Hs. 463456NM_002512	ENSG000002NM2E	NDKB NDPKNME/NM23 protein-coding	
chr17-576.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr17	57838909	57841146	+	0	NA	intron (intron (	10017 NM_01607C	51649 Hs. 5836	NR_01607C	ENSG000002MRP523	CG1-138 Emiitochonprotein-coding
chr17-82.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr17	82234814	82239644	+	0	NA	TTS (NR_1TTS (NR_1	561 NR_10684E	1.02E+08	NR_10684E	ENSG000002MIR6787	hsa-mir-5 microRNA ncRNA
chr19-491.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr19	49196413	49196989	+	0	NA	exon (NM exon (NM	38909 NM_01763C	54795 Hs. 467101NM_01763C	ENSG000002TRPM4	LTrpC4 PF transientprotein-coding	
chr2-1816.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr2	1.82E+08	1.82E+08	+	0	NA	intron (intron (	9324 NM_001287	6744 Hs. 196982NM_006751	ENSG000002ITPRD2	CS-1 CSI1 ITPR inteprotein-coding	
chr2-1913.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (intron (	145447 NM_001161	4430 Hs. 439622NM_012222	ENSG000002MYO1B	MM1-alpha myosin I protein-coding	
chr20-211.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr20	2116665	2118588	+	0	NA	intron (AluSx1 SI	15799 NM_08083C	140901 Hs. 100057NM_08083C	ENSG000002STK35	CLIK1 STK serine/th protein-coding	
chr21-371.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr21	37151731	37153373	+	0	NA	intron (AluV SINE	41374 NR_046651	1.01E+08	Hs. 570411NR_046651	ENSG000002TTC3-AS1	TTC3 antncRNA
chr3-946.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr3	9469231	9481581	+	0	NA	intron (intron (	77706 NM_00108C	55209 Hs. 288164NM_018187	ENSG000002SETD5	SET domainprotein-coding	
chr3-486.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr3	48606495	48608187	+	0	NA	intron (AluSc SIN	-2191 NR_132776	NR_132776	SNORA94	small nucsnRNA	
chr3-1002.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr3	1E+08	1E+08	+	0	NA	intron (AluSq2 SI	30945 NM_001195	55773 Hs. 477003NM_018305	ENSG000002TBC1D23	NS4ATP1 TBC1 dom protein-coding	
chr4-109.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr4	1.1E+08	1.1E+08	+	0	NA	exon (NM exon (NM	-29855 NM_01791E	55013 Hs. 234145NM_01791E	ENSG000002CMCB	CCDC109B mitochonprotein-coding	
chr5-1126.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr5	1.13E+08	1.13E+08	+	0	NA	intron (AluJb SIN	5149 NM_003133	6728 Hs. 637001NM_003133	ENSG000002SRP19	signal rprotein-coding	
chr5-1404.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr5	1.4E+08	1.4E+08	+	0	NA	exon (NM exon (NM	-50583 NM_003732	8637 Hs. 594084NM_003732	ENSG000002EIF4EBP3	4E-BP3 4E eukaryotiprotein-coding	
chr6-8317.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr6	83179814	83181891	+	0	NA	intron (MER102b I	12413 NM_001195	5238 Hs. 661665NM_015595	ENSG000002PGM3	AGM1 IMD2 phosphoglp protein-coding	
chr7-299.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr7	29934690	29941608	+	0	NA	intron (AluS2 SIN	51652 NM_014766	9805 Hs. 52074CNM_014766	ENSG000002SCRN1	SES1 secernin protein-coding	
chr7-473.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr7	47394085	47397623	+	0	NA	intron (intron (	68949 NR_145811	1.1E+08	NR_145811	SNORD151	small nucsnRNA
chr8-226.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr8	22607640	22616618	+	0	NA	intron (AluS2 SIN	7087 NM_001363	57805 Hs. 744848NM_021174	ENSG000002CCAR2	DBC-1 DBC cell cyclprotein-coding	
chr8-3832.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr8	38328430	38331193	+	0	NA	exon (NM exon (NM	52460 NM_023034	54904 Hs. 434966NM_001777	ENSG000002NSD3	KMT3F KMT nuclear rprotein-coding	
chr9-1912.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr9	19123984	19126090	+	0	NA	intron (LIMB8 LIN	2455 NM_001122	123 Hs. 3416	NR_001122	ENSG000002PLIN2	ADFP ADRF perlipiprotein-coding
chr9-355.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr9	35554920	35561841	+	0	NA	intron (intron (	5498 NM_001287	730112 Hs. 98959	NR_001095	ENSG000002FAM166B	family wiprotein-coding
chr9-954.9.169398	-0.03	0.76716	-0.0391	0.96881	0.981636	chr9	95465191	95469206	+	0	NA	exon (NM exon (NM	3589 NR_038982	1.01E+08	Hs. 661847NR_038982	LOC100507	uncharactncRNA
chr2-1905.9.1204	-0.03035	0.776495	-0.03908	0.968827	0.981636	chr2	1.91E+08	1.91E+08	+	0	NA	intron (MIRc SINE	45044 NM_014905	2744 Hs. 116444NM_014905	ENSG000002GLS	AAD20 CAS glutamine protein-coding	
chr3-437.9.1204	-0.03035	0.776495	-0.03908	0.968827	0.981636	chr3	43576786	43577329	+	0	NA	exon (NM exon (NM	44869 NM_001346	55129 Hs. 656657NM_018075	ENSG000002AN010	SCAR10 TV anacetamir protein-coding	
chr4-519.9.1204	-0.03035	0.776495	-0.03908	0.968827	0.981636	chr4	51901489	51901628	+	0	NA	intron (intron (	58009 NM_001287	23142 Hs. 603388NM_015115	ENSG000002DCUN1D4	defective protein-coding	
chr6-565.9.1204	-0.03035	0.776495	-0.03908	0.968827	0.981636	chr6	56599936	56603422	+	0	NA	intron (intron (	41210 NM_015548	667 Hs. 604915NM_001722	ENSG000002CST	BP240 BP dystonin protein-coding	
chr1-1226.4.931208	0.039953	1.025386	0.038964	0.968919	0.981636	chr1	12287953	12288761	+	0	NA	intron (intron (	58327 NM_015378	55187 Hs. 439381NM_015378	ENSG000002VPS13D	SCAR4 vacuolar protein-coding	
chr10-912.7.65976	-0.03035	0.864465	-0.03893	0.968945	0.981636	chr10	91263852	91264450	+	0	NA	Intergeni THE1B LTF	8920 NM_005398	5507 Hs. 30309CNM_005398	ENSG000002PPP1R3C	PPP1R5 P1 protein protein-coding	
chr1-222.9.607281	-0.02939	0.755856	-0.03888	0.968984	0.981636	chr1	2.23E+08	2.23E+08	+	0	NA	intron (intron (	13774 NM_00130C	375056 Hs. 118474NM_198551	ENSG000002CIA3	ARNT D32CIA SH3 cprotein-coding	
chr16-28.9.607281	-0.02939	0.755856	-0.03888	0.968984	0.981636	chr16	28956696	28957005	+	0	NA	intron (intron (	-1733 NR_039742	1.01E+08	NR_039742	ENSG000002MIR4517	miR-4517 microRNA ncRNA
chr1-436.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr1	43653546	43671398	+	0	NA	intron (AluSg7 SI	12323 NM_014663	9682 Hs. 155983NM_014663	ENSG000002KDMA4	JHDM3A JM lysine deprotein-coding	
chr1-462.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr1	46294471	46298300	+	0	NA	intron (AluSp SIN	6981 NM_006365	10489 Hs. 144941NM_006365	ENSG000002LRR41	MUF1 PPP77 leucine rprotein-coding	
chr10-99.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr10	99893626	99899541	+	0	NA	intron (intron (	17509 NM_00131E	23268 Hs. 500771NM_015222	ENSG000002DNMBP	ARHGAP36 dynamin tprotein-coding	
chr11-636.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr11	63628150	63633788	+	0	NA	intron (intron (	-16500 NM_00112E	11445 Hs. 280881NM_004195	ENSG000002PLAAT3	ADPLA H-F phospholiprotein-coding	
chr11-671.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr11	67184423	67187240	+	0	NA	intron (MLT1A LI	-54183 NM_00125E	22992 Hs. 124147NM_012305	ENSG000002KDM2A	CXXC8 FBI lysine deprotein-coding	
chr14-504.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr14	50443360	50447126	+	0	NA	intron (intron (	-47945 NM_001367	8814 Hs. 280881NM_004195	ENSG000002CDKL1	KKIALRE Cyclin deprotein-coding	
chr14-76.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr14	76004102	76005946	+	0	NA	intron (LIMEF LIN	19261 NM_00125E	112752 Hs. 532625NM_052872	ENSG000002IFT43	C14orf175 intraflag protein-coding	
chr19-17.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr19	17313649	17317422	+	0	NA	intron (AluJr SIN	5972 NM_02405C	79016 Hs. 466154NM_02405C	ENSG000002DDA1	C19orf58 DET1 and protein-coding	
chr19-447.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr19	44750175	44752989	+	0	NA	intron (MIRB SINE	2874 NM_00517E	602 Hs. 31210	NR_00517E	ENSG000002BCL3	BCL4 D19BCL3 trarprotein-coding
chr19-571.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr19	57193064	57195745	+	0	NA	intron (intron (	2904 NM_003417	9422 Hs. 515634NM_003417	ENSG000002ZNF264	zinc fingprotein-coding	
chr2-270.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr2	27066589	27070107	+	0	NA	intron (intron (	3306 NM_001134	1E+08	Hs. 502948NM_001134	ENSG000002OST4	oligosaccprotein-coding
chr2-317.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr22	31702606	31702990	+	0	NA	intron (AluSx SIN	-40234 NM_00132E	23761 Hs. 420555NM_014335	ENSG000002PISD	DJ85816 phosphatiprotein-coding	
chr4-106.9.656278	-0.02903	0.750036	-0.03871	0.969123	0.981636	chr4	1.06E+08	1									

chr3-6902	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr3	69053919	69056871	+	0 NA	3' UTR (N3' UTR (N	-3062 NM_007114	7110 Hs. 267632NM_007114	ENSG000002TMF1	ARA160 T TATA	elenprotein-coding		
chr3-1002	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr3	1E+08	1E+08	+	0 NA	intron (NAluX S	21204 NM_001199	55773 Hs. 477003NM_018306	ENSG000002TBC1D23	NS4ATP1 F TBC1	dom protein-coding		
chr3-1722	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr3	1.72E+08	1.72E+08	+	0 NA	intron (Nintron (N	178295 NM_004122	2693 Hs. 130212NM_004122	ENSG000002GHSR	GHPD	growth hcprotein-coding		
chr4-5588	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr4	55880967	55882514	+	0 NA	intron (NMER4A L	28099 NM_018261	55763 Hs. 269666NM_018261	ENSG000002EXOC1	BM-102 S E	exocyst cprotein-coding		
chr4-1186	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr4	1.19E+08	1.19E+08	+	0 NA	intron (Nintron (N	5402 NM_020961	57721 Hs. 596872NM_020961	ENSG000002METTL14	MeTTL14	methyltra protein-coding		
chr5-6595	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr5	65992150	65993212	+	0 NA	intron (Nintron (N	-47108 NR_028474	1E+08 Hs. 60806CNR_028474	LOC100303	LSM3	homc pseudo		
chr6-2048	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr6	20488919	20491603	+	0 NA	3' UTR (N3' UTR (N	-43746 NM_017774	54901 Hs. 657604NM_017774	ENSG000002CDKAL1	-	CDK5	regt protein-coding	
chr7-3291	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr7	32919940	32921710	+	0 NA	intron (NAluYc S N	22345 NR_003500	441212 Hs. 648086NM_001036	ENSG000002RFP9	-	RFP9	pseud pseudo	
chr7-1314	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr7	1.31E+08	1.31E+08	+	0 NA	intron (N L2a LINE	107559 NM_001018	5420 Hs. 744212NM_005397	ENSG000002PODXL	Gp200 P C	podocaly protein-coding		
chr8-1725	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr8	17294355	17301036	+	0 NA	3' UTR (N3' UTR (N	52777 NM_001363	137492 Hs. 343873NM_152411	ENSG000002VPS37A	BCRP1 PQ E	VPS37A	st protein-coding	
chr9-2074	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr9	2074606	2074805	+	0 NA	intron (NAluJb S N	52760 NM_001285	6595 Hs. 29899CNR_003070	ENSG000002SMARCA2	HAF190 BF SWI SNF	r protein-coding		
chr9-9474	8.67466	-0.02946	0.78865	-0.03736	0.970198	0.981636	chr9	94749281	94750138	+	0 NA	intron (N LIMEb LIN	-9940 NM_001193	84909 Hs. 434255NM_032823	ENSG000002AOPEP	AP-0 APO	aminopept protein-coding		
chr6-1102	10.82647	0.027516	0.736525	-0.03736	0.970198	0.981636	chr6	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	35103 NM_015891	51362 Hs. 428147NM_015891	ENSG000002CDC40	EHB3 PRP1	cell divi protein-coding		
chr8-3824	7.424314	0.032632	0.875952	-0.03754	0.970283	0.981636	chr8	38240341	38240542	+	0 NA	intron (Nintron (N	8488 NM_001164	23259 Hs. 434966NM_015214	ENSG000002DDHD2	SAMMD1 SF	DDHD	dom protein-coding	
chr3-437	7.214019	-0.03283	0.88141	-0.03725	0.970284	0.981636	chr3	43703102	43703782	+	0 NA	intron (NAluSz S N	-11848 NM_001346	5129 Hs. 656657NM_018073	ENSG000002CANO10	SCAR10 T V	anoctami protein-coding		
chr1-328C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr1	32805502	32811657	+	0 NA	intron (Nintron (N	-8863 NM_001256	64766 Hs. 44088CNR_022755	ENSG000002S100BPB	S100BPBR	S100P	bir protein-coding	
chr1-3937	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr1	39379395	39383371	+	0 NA	intron (NAluJo S N	-27522 NM_015038	643314 Hs. 65876CNR_015038	ENSG000002KIAA0754	-	KIAA0754	protein-coding	
chr1-4041	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr1	40414934	40419457	+	0 NA	intron (Nintron (N	20395 NM_001198	64744 Hs. 15200 NM_002273	ENSG000002SMAP2	SMAP1L	small Arf protein-coding		
chr1-150C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr1	1.5E+08	1.5E+08	+	0 NA	intron (Nintron (N	6575 NM_001278	11311 Hs. 44375CNR_002725	ENSG000002VPS45	HI H1 VPS4	vacuolar protein-coding		
chr1-209E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr1	2.1E+08	2.1E+08	+	0 NA	intron (Nintron (N	5570 NM_014388	27042 Hs. 194754NM_014388	ENSG000002UTP25	C1orf107 U	TP25	sm protein-coding	
chr10-87C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr10	87055020	87053933	+	0 NA	intron (NAluXs L S	31932 NM_001146	64316 Hs. 729944NM_001146	ENSG000002FAM25A	ba96C23.5	family wiprotein-coding		
chr11-914	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr11	9141780	9146711	+	0 NA	exon (NM exon (NM	49882 NR_027713	283102 Hs. 689472NR_027713	ENSG000002KRTP41	-	keratin 8	pseudo	
chr11-337	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr11	33707340	33710711	+	0 NA	3' UTR (N3' UTR (N	-8285 NM_001166	1E+08 Hs. 709466NM_001166	ENSG000002C11orf91	-	chromosom	protein-coding	
chr11-118	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr11	1.19E+08	1.19E+08	+	0 NA	intron (NAluSz S N	13194 NM_001257	1656 Hs. 408461NM_004397	ENSG000002DDX6	HLR2 P54	DEAD-box	protein-coding	
chr12-106	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr12	10697318	10704418	+	0 NA	intron (Nintron (N	22455 NM_003651	8531 Hs. 221885NM_003651	ENSG000002YBX3	CSDA CSDA	Y-box	bir protein-coding	
chr12-562	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr12	56271091	56286385	+	0 NA	intron (NAluSc S N	11412 NM_001099	93058 Hs. 4096 NM_144576	ENSG000002COQ10A	-	coenzyme	protein-coding	
chr12-11C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr12	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	6534 NM_001278	10094 Hs. 524741NM_001278	ENSG000002ARPC3	ARC21 p2	actin rel	protein-coding	
chr13-44E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr13	44556663	44557305	+	0 NA	intron (NAluSp S N	-18912 NR_038381	641467 Hs. 624196NR_038381	ENSG000002TSC22D1-1	-	TSC22D1	ancRNA	
chr13-114	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr13	1.14E+08	1.14E+08	+	0 NA	intron (N Tigger17a	13841 NR_049836	1.01E+08 Hs. 624196NR_049836	ENSG000002MIR548AR	-	microRNA	ncRNA	
chr14-213	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr14	21359021	21370121	+	0 NA	intron (Nintron (N	19448 NM_007192	11198 Hs. 213724NM_007192	ENSG000002SUPT16H	CDC68 FAC	SPT16	hon protein-coding	
chr14-52C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr14	52057143	52061067	+	0 NA	intron (N MRB S INE	9954 NM_007361	22795 Hs. 36984CNR_007361	ENSG000002CID2	NID-2	nidogen 2	protein-coding	
chr14-74E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr14	74672618	74676856	+	0 NA	intron (Nintron (N	38343 NM_001038	9870 Hs. 497417NM_014821	ENSG000002AREL1	F1EL1 KI	apoptosis	protein-coding	
chr14-102	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr14	1.02E+08	1.02E+08	+	0 NA	3' UTR (N3' UTR (N	36463 NM_005348	3320 Hs. 525606NM_005348	ENSG000002HSP90AA1	EL52 HEL-	heat	shoc protein-coding	
chr15-77Z	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr15	77257679	77259048	+	0 NA	intron (N LIPA3 LIN	-32959 NR_026813	81698 Hs. 656933NM_030944	LINC00597	C15orf5	long	intencRNA	
chr15-89C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr15	89329413	89333254	+	0 NA	intron (Nintron (N	3466 NM_002693	5428 Hs. 706868NM_002693	ENSG000002POLG	MDP1 MR	RNA	polyn protein-coding	
chr16-16C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr16	16030281	16032145	+	0 NA	intron (Nintron (N	81601 NM_004996	4363 Hs. 391464NM_004996	ENSG000002ABCC1	ABC29 ABC	ATP	bindi protein-coding	
chr17-16C	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr17	16031812	16037348	+	0 NA	intron (NAluJb S N	34756 NM_017775	54902 Hs. 462316NM_017775	ENSG000002TTC19	201020401	tetratric	protein-coding	
chr17-294	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr17	29466673	29469269	+	0 NA	intron (NAluSx S N	77046 NM_025142	57551 Hs. 597434NM_002079	ENSG000002TAOK1	KFC-B MAF	TAO	kinas	protein-coding
chr17-301	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr17	30178119	30186128	+	0 NA	intron (Nintron (N	53574 NM_001046	6532 Hs. 29792 NM_001046	ENSG000002SLC66A1	5-HTT 5-F	tao	cprotein-coding	
chr18-27Z	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr18	2729809	2732846	+	0 NA	intron (Nintron (N	75440 NM_015295	23347 Hs. 8118 NM_015295	ENSG000002SMCHD1	BAMS FSH	E	structure	protein-coding
chr2-2877	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr2	28777699	28790552	+	0 NA	intron (NAluSx3 S	-17659 NM_182756	245711 Hs. 511956NM_182756	ENSG000002SPDYA	RING03 RI	speedy/RI	protein-coding	
chr2-218E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr2	2.19E+08	2.19E+08	+	0 NA	intron (Nintron (N	-26199 NR_032726	84812 Hs. 632525NM_032726	ENSG000002PLCDA	-	phospholip	protein-coding	
chr20-58E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr20	58674971	58676934	+	0 NA	intron (Nintron (N	-13179 NM_001204	79716 Hs. 654866NM_024663	ENSG000002NPEPL1	ba261P9.2	aminopept	protein-coding	
chr21-371	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr21	37160392	37170580	+	0 NA	intron (Nintron (N	28440 NR_046651	1.01E+08 Hs. 570411NR_046651	ENSG000002TTC3-AS1	-	TTC3	antincRNA	
chr22-42E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr22	42597698	42603265	+	0 NA	intron (NAluYml S	14402 NR_10382C	84271 Hs. 505802NM_032311	ENSG000002POLDIP3	PDIP3 PDID	NA	polyn protein-coding	
chr3-690Z	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr3	69037242	69045054	+	0 NA	intron (Nintron (N	7887 NR_036087	1E+08 Hs. 5036087	ENSG000002MIR3136	mir-3136	microRNA	ncRNA	
chr3-123E	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr3	1.24E+08	1.24E+08	+	0 NA	intron (Nintron (N	-8197 NR_046622	1.01E+08 Hs. 667316NR_046622	ENSG000002MYLK-AS2	-	MYLK	antincRNA	
chr4-288Z	9.16154	-0.02847	0.766971	-0.03712	0.97039	0.981636	chr4	2882850	2886916	+	0 NA	intron (Nintron (N	40733 NM_001286	118 Hs. 183706NM_001119					



chr1-1461	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr1	1.46E+08	1.46E+08	+	0	NA	intron (AluJb SIN	5203	NR_001302	1E+08	Hs.714127NM_001039	ENSG00000CNBP10	AB6 AG1 NBPF	memt protein-coding	
chr1-1715	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr1	1.72E+08	1.72E+08	+	0	NA	intron (intron (N	-31854	NR_001368	1.1E+08	NM_001368164	MYOCOS	-	myocilin protein-coding	
chr10-737	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr10	73732867	73733097	+	0	NA	IntergeniCpG	2420	NR_048575	2749	Hs.680699NR_048575	ENSG00000GLUD1P3	C10orf102	glutamate pseudo	
chr10-103	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr10	1.04E+08	1.04E+08	+	0	NA	intron (intron (N	20985	NR_001366	9644	Hs.678727NM_014631	ENSG00000SH3PXD2A	FISH SH3	SH3 and Irfrotein-coding	
chr12-565	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr12	56562199	56565083	+	0	NA	intron (intron (N	41821	NR_002895	5939	Hs.505725NM_002895	ENSG00000RBM52	SCR3	RNA bindi protein-coding	
chr12-928	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr12	92824566	92827825	+	0	NA	exon (NM_exon (NM	89706	NR_001004	440107	Hs.591015NM_001004	ENSG00000PLEKHG7	-	pleckstri protein-coding	
chr12-132	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr12	1.32E+08	1.32E+08	+	0	NA	intron (intron (N	13922	NR_002979	677829	Hs.742405NR_002979	ENSG00000SNORA49	ACA49	small nucsnoRNA	
chr16-218	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr16	21887411	21887944	+	0	NA	IntergeniIntergeni	-20942	NR_024456	1E+08	Hs.648435NR_024456	LOC1001019C	-	uncharactncRNA	
chr16-282	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr16	28396920	28401656	+	0	NA	intron (MIRc SINE	4597	NR_001095	728689	Hs.567374NM_001095	ENSG00000EIF3CL	-	eukaryoti protein-coding	
chr17-152	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr17	15244722	15259526	+	0	NA	promoter-promoter-	-428	NR_039884	1.01E+08	NR_039884	ENSG00000MIR4731	-	microRNA ncRNA	
chr2-3715	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr2	37130342	37142107	+	0	NA	intron (intron (N	11598	NR_001135	5610	Hs.131431NM_002755	ENSG00000EIF2AK2	EIF2AK1	Fukaryoti protein-coding	
chr2-6118	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr2	61181462	61187444	+	0	NA	intron (intron (N	7035	NR_152211	130872	Hs.655602NM_152392	ENSG00000AHS2P	AHA1 AHS	activator pseudo	
chr3-1237	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr3	1.24E+08	1.24E+08	+	0	NA	intron (MIRb SINE	25754	NR_046625	1.01E+08	Hs.667315NR_046625	ENSG00000MYLK-AS2	-	MYLK anticncRNA	
chr3-1254	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr3	1.25E+08	1.25E+08	+	0	NA	intron (AluJo SINE	52561	NR_003794	8723	Hs.507245NM_003794	ENSG00000SNX4	ATG24B	sorting ir protein-coding	
chr5-6152	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr5	61539852	61546339	+	0	NA	intron (intron (N	-94665	NR_161251	285668	Hs.683865NR_126525	ENSG00000C5orf64	-	chromosnncRNA	
chr7-4731	10.1353	-0.02678	0.732669	-0.03656	0.970838	0.981636	chr7	47318537	47321880	+	0	NA	intron (MIRb SINE	144595	NR_145813	1.1E+08	NR_145813	SNORD151	-	small nucsnoRNA	
chr1-2535	10.0863	-0.02716	0.743164	-0.03655	0.970847	0.981636	chr1	25361331	25362152	+	0	NA	TTS (NM_C TTS (NM_C	23407	NR_014133	23585	Hs.705695NM_014133	ENSG00000TMEM50A	IFNRC SMF	transment protein-coding	
chr4-2328	10.0863	-0.02716	0.743164	-0.03655	0.970847	0.981636	chr4	23282091	23282520	+	0	NA	TTS (NM_C TTS (NM_C	36508	NR_001172	57732	Hs.292055NM_020972	ENSG00000ZFVYE28	LST2 LYS1	zinc fing protein-coding	
chr7-1062	8.723657	-0.02898	0.797979	-0.03631	0.971035	0.981636	chr7	1.06E+08	1.06E+08	+	0	NA	exon (NM_exon (NM	31885	NR_005746	10135	Hs.489615NM_005746	ENSG00000NAMP7	111003501	nicotinan protein-coding	
chr1-1352	10.62218	-0.0261	0.719098	-0.0363	0.971047	0.981636	chr1	1352971	13556005	+	0	NA	intron (intron (N	4259	NR_001282	54587	Hs.515687NM_032345	ENSG00000MXRA8	ASP3	matrix re protein-coding	
chr1-2024	10.62218	-0.0261	0.719098	-0.0363	0.971047	0.981636	chr1	2.02E+08	2.02E+08	+	0	NA	intron (AluSz SIN	26153	NR_032103	4660	Hs.444405NM_002481	ENSG00000PPP1R12B	MYPT2 PP1	protein ir protein-coding	
chr13-407	4.460043	0.039136	1.085289	0.03606	0.971234	0.981636	chr13	40722314	40722991	+	0	NA	IntergeniLIMed LIN	5235	NR_031722	1E+08	NR_031722	ENSG00000MIR320D1	MIR320D	1-microRNA ncRNA	
chr5-7094	4.939066	0.037094	1.02923	0.03604	0.97125	0.981636	chr5	70945289	70946206	+	0	NA	intron (intron (N	20806	NR_001297	6606	Hs.535785NM_000344	ENSG00000CSMN1	BCD541 GF	survival protein-coding	
chr13-489	9.210537	-0.02805	0.778579	-0.03602	0.971263	0.981636	chr13	48394606	48395168	+	0	NA	intron (LIPA7 LIN	18226	NR_001162	10161	Hs.123464NM_005767	ENSG00000LPAR6	ARWH1 HYF	lysophos protein-coding	
chr2-1866	8.910379	0.029703	0.825444	0.035984	0.971295	0.981636	chr2	1.87E+08	1.87E+08	+	0	NA	intron (intron (N	44103	NR_001144	3685	Hs.436875NM_002211	ENSG00000ITGAV	CD51 MSK	integrin protein-coding	
chr1-2368	3.932023	0.041261	1.147567	0.035956	0.971318	0.981636	chr1	2.37E+08	2.37E+08	+	0	NA	intron (intron (N	52557	NR_001291	4548	Hs.498187NM_000254	ENSG00000CMT8	HMAG MS c5	methylt protein-coding	
chr13-113	5.418088	0.035368	0.984784	0.035915	0.97135	0.981636	chr13	1.14E+08	1.14E+08	+	0	NA	intron (intron (N	-25896	NR_001366	1.01E+08	Hs.704267NM_001366	ENSG00000C13orf46	-	chromosn protein-coding	
chr14-716	5.418088	0.035368	0.984784	0.035915	0.97135	0.981636	chr14	71661596	71662111	+	0	NA	intron (intron (N	75555	NR_001284	26037	Hs.654657NM_015555	ENSG00000S1PALL1	E6TP1 SP	signal ir protein-coding	
chr19-50	5.418088	0.035368	0.984784	0.035915	0.97135	0.981636	chr19	5036373	5038160	+	0	NA	intron (intron (N	68153	NR_001374	23030	Hs.654815NM_015015	ENSG00000KDM4B	JMJD2B TAN	lysine de protein-coding	
chr2-159	5.418088	0.035368	0.984784	0.035915	0.97135	0.981636	chr2	1.59E+08	1.59E+08	+	0	NA	intron (intron (N	38110	NR_146421	85461	Hs.61590	NR_033394	ENSG00000MTC1C	ROLSB TAB	tetratri protein-coding
chr7-473	5.418088	0.035368	0.984784	0.035915	0.97135	0.981636	chr7	47385311	47386228	+	0	NA	intron (intron (N	79034	NR_145813	1.1E+08	NR_145813	SNORD151	-	small nucsnoRNA	
chr15-225	5.89711	0.033862	0.948962	0.035683	0.971535	0.981636	chr15	22873682	22874140	+	0	NA	intron (AluJb SIN	35270	NR_001008	81614	Hs.591005NM_030922	ENSG00000N1PA2	SLC57A2	N1PA magr protein-coding	
chr15-754	5.89711	0.033862	0.948962	0.035683	0.971535	0.981636	chr15	75473830	75474380	+	0	NA	intron (L2a LINE	-18290	NR_001145	25942	Hs.513035NM_015477	ENSG00000S1N3A	WITKOS	S1N3 trar protein-coding	
chr19-45	5.89711	0.033862	0.948962	0.035683	0.971535	0.981636	chr19	45365420	45367133	+	0	NA	intron (AluSp SIN	4311	NR_001135	2068	Hs.487294NM_000405	ENSG00000ERC2C	COFS2 EM	ERCC exci protein-coding	
chr5-508	5.89711	0.033862	0.948962	0.035683	0.971535	0.981636	chr5	50835008	50835758	+	0	NA	intron (AluSx SIN	134804	NR_104655	1E+08	Hs.519295NR_104655	ENSG00000LINC02105	-	long intncRNA	
chr8-1204	5.89711	0.033862	0.948962	0.035683	0.971535	0.981636	chr8	1.2E+08	1.2E+08	+	0	NA	intron (L3 LINE C	13679	NR_014078	28998	Hs.333825NM_014078	ENSG00000MRPL13	L13 L13A	mitochon protein-coding	
chrX-5355	5.89711	0.033862	0.948962	0.035683	0.971535	0.981636	chrX	53569410	53570481	+	0	NA	intron (MIRc SINE	-12671	NR_029484	406889	NR_029484	ENSG00000MIRLET7F2	LET7F2 M	microRNA ncRNA	
chr15-407	7.383175	0.037074	0.861665	0.035633	0.971575	0.981636	chr15	80134139	80135010	+	0	NA	intron (Tiger2 I	-18425	NR_000137	2184	Hs.73875	NR_000137	ENSG00000FAH	-	fumarylac protein-coding
chr19-801	7.383175	0.037074	0.861665	0.035633	0.971575	0.981636	chr19	40172865	40173922	+	0	NA	intron (AluJg SIN	1726	NR_001142	79934	Hs.130712NM_024875	ENSG00000COQB8	ADCK4 NPF	coenzyme protein-coding	
chr14-716	6.904152	0.031659	0.890377	0.035556	0.971636	0.981636	chr14	71084769	71085752	+	0	NA	intron (LIPA7 LIN	177801	NR_001308	22990	Hs.446555NM_014982	ENSG00000PCNX1	PCNX1 PCNX	pecanex I protein-coding	
chr21-321	6.904152	0.031659	0.890377	0.035556	0.971636	0.981636	chr21	32318679	32319275	+	0	NA	intron (intron (N	27164	NR_001288	56246	Hs.584949NM_178817	ENSG00000MRAP	B27 C21or	melanocor protein-coding	
chr7-439	6.904152	0.031659	0.890377	0.035556	0.971636	0.981636	chr7	4395961	4396108	+	0	NA	intron (intron (N	7244	NR_170688	57541	Hs.632032NM_020781	ENSG00000ZNF398	P51 P71	L1zinc fing protein-coding	
chr18-217	8.341219	0.028972	0.817563	0.035437	0.971731	0.981636	chr18	21789252	21789516	+	0	NA	intron (MLT1C LTF	36401	NR_029675	406922	NR_029675	ENSG00000MIR133A1	MIR133A1	microRNA ncRNA	
chr11-77	6.376132	0.032518	0.919412	0.035368	0.971786	0.981636	chr11	77900241	77901194	+	0	NA	TTS (NM_C TTS (NM_C	59579	NR_001362	28971	Hs.745044NM_024684	ENSG00000AAMD	C11orf67	adipogene protein-coding	
chr15-433	6.376132	0.032518	0.919412	0.035368	0.971786	0.981636	chr15	43340515	43341300	+	0	NA	intron (intron (N	10235	NR_001362	161823	Hs.533915NM_010102	ENSG00000ADAL	-	adenosine protein-coding	
chr4-168	6.376132	0.032518	0.919412	0.035368	0.971786	0.981636	chr4	1.68E+08	1.68E+08	+	0	NA	intron (intron (N	664	NR_001202	8837	Hs.390735NM_003875	ENSG00000CFLAR	CASH CAS	FASP8 anc protein-coding	
chr14-100	6.42513	0.032699	0.925208	0.035343	0.971806	0.981636	chr14	1.01E+08	1.01E+08	+	0	NA	intron (Tiger7 I	38681	NR_017631	55601	Hs.591715NM_017631	ENSG00000DDX60	-	DexD/H-bc protein-coding	
chr16-211	6.42513	0.032699	0.925208	0.035343	0.971806	0.981636	chr16	2111111	2112427	+	0	NA	IntergeniLIPB1 LIN	1589	NR_030617	1E+08	NR_030617	ENSG00000MIR665	MIRN665	1-microRNA ncRNA	
chr2-7565	6.42513	0.032699	0.925208	0.035343	0.971806	0.981636	chr2	75697714	75698907	+	0	NA	exon (NM_exon (NM	-5016	NR_106775	1.02E+08	NR_106775	ENSG00000MIR6511B1	MIR6511B1	microRNA ncRNA	
chr2-1351	6.42513	0.032699	0.925208	0.035343	0.971806	0.981636	chr2	1.35E+08	1.35E+08	+	0	NA	intron (L1ME4c LI	12605	NR_003203	6936	Hs.303805NM_003203	ENSG00000GCFC2	C2orf3 DN	C-rich s protein-coding	
chr5-389	6.666802	-0.02779	0.79328	-0.03504	0																

chr10-121 9.632704	-0.02464	0.753541	-0.0327	0.97391	0.981731	chr10	12149560	12150472	+	0 NA	intron (Nintron (N	-19200 NR_039699	1.01E+08	NR_039699	ENSG000003MIR548AK	-	microRNA ncRNA
chr14-746 9.632704	-0.02464	0.753541	-0.0327	0.97391	0.981731	chr14	74669172	74670547	+	0 NA	intron (Nintron (N	43221 NM_001035		9870 Hs. 497417	NR_014821	ENSG000003AREL1	FIEL1 K1A apoptosis protein-coding
chr21-336 9.632704	-0.02464	0.753541	-0.0327	0.97391	0.981731	chr21	33600493	33603455	+	0 NA	intron (Nintron (N	-13290 NM_017613		29980 Hs. 436341	NR_017613	ENSG000003DONSON	B17 C21or downstree protein-coding
chr7-7434 9.145824	-0.02533	0.775486	-0.03267	0.973938	0.981731	chr7	74345134	74345591	+	0 NA	intron (NAluSz6 S1	55887 NM_003388		7461 Hs. 64701	NR_003388	ENSG000003CLIP2	CLIP CLIF CAP-Gly cprotein-coding
chr19-233 8.707941	-0.02581	0.79121	-0.03262	0.973981	0.981731	chr19	23378992	23380631	+	0 NA	intron (Nintron (N	15660 NM_00343C		7641 Hs. 58834	NR_00343C	ENSG000003ZNF91	HPF7 HTF1zinc fingprotein-coding
chr4-777 8.707941	-0.02581	0.79121	-0.03262	0.973981	0.981731	chr4	7777471	7778611	+	0 NA	non-codir non-codir	23951 NR_02689E		84740 Hs. 66302	NR_02689E	ENSG000003AFAP1-AS1	AFAP1-AS AFAP1 antncRNA
chr1-2007 10.60646	-0.02343	0.718679	-0.0326	0.973994	0.981731	chr1	2.01E+08	2.01E+08	+	0 NA	intron (Nintron (N	21803 NM_001297		23271 Hs. 23585	NR_020345	ENSG000003CAMSAP2	CAMSAP1 Calmodulin protein-coding
chr2-325 10.60646	-0.02343	0.718679	-0.0326	0.973994	0.981731	chr2	32504901	32507133	+	0 NA	intron (NAluJo SIN	-26136 NR_030288		693143	NR_030288	ENSG000003MIR558	MIRN558 miRNA ncRNA
chr5-9551 8.221061	-0.02663	0.817118	-0.03258	0.974006	0.981731	chr5	95518654	95519444	+	0 NA	intron (NLIAMA5 LI	35956 NM_01463E		9652 Hs. 48286	NR_01463E	ENSG000003TTC37	KIAA0372 tetratric protein-coding
chr6-158 8.221061	-0.02663	0.817118	-0.03258	0.974006	0.981731	chr6	1.58E+08	1.58E+08	+	0 NA	intron (Nintron (N	69487 NM_00117E		8871 Hs. 43449	NR_00389E	ENSG000003SYN2J	INPP5F synapto protein-coding
chr16-705 9.194822	-0.02503	0.769296	-0.03254	0.974045	0.981731	chr16	70526400	70526946	+	0 NA	exon (NM exon (NM	-2826 NR_03742C		1E+08	NR_03742C	SNORD111E	SNORD111E microRNA ncRNA
chr17-319 9.194822	-0.02503	0.769296	-0.03254	0.974045	0.981731	chr17	31949097	31951766	+	0 NA	intron (NAluSz6 S1	13424 NM_01535E		23512 Hs. 46273	NR_01535E	ENSG000003SUZ12	CHET9 JJ#SUZ12 polprotein-coding
chr19-444 9.194822	-0.02503	0.769296	-0.03254	0.974045	0.981731	chr19	44490879	44496885	+	0 NA	intron (NMLT1F LTF	6640 NM_01325E		7733 Hs. 22305	NR_01325E	ENSG000003ZNF180	HHZ168 zinc fingprotein-coding
chr2-197 9.194822	-0.02503	0.769296	-0.03254	0.974045	0.981731	chr2	1.94E+08	1.97E+08	+	0 NA	intron (NLIIPA5 LIN	12566 NM_00100E		23451 Hs. 63255	NR_01243E	ENSG000003SF3B1	Hsh155 ML splicing protein-coding
chr8-3774 9.194822	-0.02503	0.769296	-0.03254	0.974045	0.981731	chr8	37741197	37743094	+	0 NA	intron (NAluSc SIN	-4719 NR_125821		1.03E+08	NR_125821	ENSG000003LOC10272E	-
chr1-2098 8.658944	-0.02605	0.80134	-0.03251	0.974065	0.981731	chr1	2.1E+08	2.1E+08	+	0 NA	intron (Nintron (N	9389 NM_01438E		27042 Hs. 19475	NR_01438E	ENSG000003UTP25	Clorf107 UTP25 sm protein-coding
chr1-427 11.58023	-0.02249	0.692857	-0.03246	0.974103	0.981731	chr1	42751678	42753077	+	0 NA	intron (Nintron (N	-12123 NM_00118E		149641 Hs. 49627	NR_00118E	ENSG000003CLDN19	HOMG5 claudin lprotein-coding
chr17-475 6.912101	0.029295	0.9029	0.03246	0.974116	0.981731	chr17	45119805	45121064	+	0 NA	exon (NM exon (NM	-6001 NR_106842		1.02E+08	NR_106842	ENSG000003MIR6784	hsa-mir-6784 microRNA ncRNA
chr1-2296 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr1	2.3E+08	2.3E+08	+	0 NA	intron (Nintron (N	15816 NM_01440E		27097 Hs. 27062	NR_01440E	ENSG000003TAF5L	PAF65B TATA-box protein-coding
chr10-101 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr10	1014851	1018580	+	0 NA	intron (Nintron (N	-5922 NR_02770E		55853 Hs. 72853	NR_01847E	ENSG000003IDI2-AS1	C1orf11C IDI2 antncRNA
chr14-544 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr14	54427717	54430437	+	0 NA	intron (Nintron (N	12297 NM_00577E		10175 Hs. 29460	NR_00577E	ENSG000003CNIH1	CNIH1 CNIH cornichon protein-coding
chr15-484 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr15	48425117	48427649	+	0 NA	intron (Nintron (N	94186 NM_00194E		1854 Hs. 52798	NR_00194E	ENSG000003CUDT	dUTPase deoxyuric protein-coding
chr16-17 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr16	71733624	71734811	+	0 NA	intron (Nintron (N	-9516 NM_01502C		23035 Hs. 70945	NR_01502C	ENSG000003PHLPP2	PHLPP1 PFPH domain protein-coding
chr19-781 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr19	78156322	78157627	+	0 NA	intron (NAluY SINE	-6306 NM_001321		7311 Hs. 5308	NR_00333E	ENSG000003UBA52	CEP52 HUBubiquitin protein-coding
chr8-605 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr8	60592200	60594974	+	0 NA	intron (NLIAMD1 LIN	76600 NM_00286E		5862 Hs. 36901	NR_00286E	ENSG000003RAB2A	LHX RAB2 RAB2A, mcprotein-coding
chr9-332 9.681702	-0.02432	0.750636	-0.0324	0.974154	0.981731	chr9	33262104	33262500	+	0 NA	intron (Nintron (N	2406 NM_00117E		573 Hs. 37748	NR_00432E	ENSG000003BAG1	BAG-1 HAF BCL2 assc protein-coding
chr3-257 4.897926	0.033705	1.0417	0.032356	0.974189	0.981731	chr3	25732249	25733297	+	0 NA	intron (NLIIMEg LIN	50670 NM_018297		55768 Hs. 36896	NR_018297	ENSG000003NGLY1	CDGD CDG1N-glycan protein-coding
chr11-865 10.16858	-0.02369	0.734677	-0.03224	0.974278	0.981731	chr11	86337352	86338185	+	0 NA	intron (NAluSx SIN	35528 NM_00132E		51501 Hs. 28332	NR_016401	ENSG000003CHKESH1	C11orf73 heat shoc protein-coding
chr18-796 10.16858	-0.02369	0.734677	-0.03224	0.974278	0.981731	chr18	79973441	79973981	+	0 NA	exon (NM exon (NM	9068 NM_00113E		44098 Hs. 19158	NR_00113E	ENSG000003HSBP1L1	-
chr19-105 10.16858	-0.02369	0.734677	-0.03224	0.974278	0.981731	chr19	10689835	10689838	+	0 NA	intron (Nintron (N	-12403 NM_03120E		81890 Hs. 63163	NR_03120E	ENSG000003QTRT1	FP3235 Tc heatin tprotein-coding
chr3-639 10.16858	-0.02369	0.734677	-0.03224	0.974278	0.981731	chr3	63994770	63996334	+	0 NA	exon (NM exon (NM	-8470 NR_03828E		1.01E+08	NR_03828E	ENSG000003PSMD6-AS2	-
chr9-137 10.16858	-0.02369	0.734677	-0.03224	0.974278	0.981731	chr9	1.34E+08	1.34E+08	+	0 NA	exon (NM exon (NM	-35024 NR_007101		1757 Hs. 19800	NR_007101	ENSG000003SARDH	BPR-2 DMC sarcosine protein-coding
chr6-144 8.172604	-0.02676	0.832089	-0.03216	0.974346	0.981731	chr6	1.47E+08	1.47E+08	+	0 NA	intron (NLIIME4b LI	-35079 NR_03411E		729178 Hs. 55760	NR_03411E	ENSG000003STXP5-AS	STXP5-AS microRNA ncRNA
chr16-82 10.65546	-0.02314	0.720995	-0.0321	0.974394	0.981731	chr16	82097859	82099906	+	0 NA	TTS (NM TTS (NM C	63629 NM_00215E		3294 Hs. 16279	NR_00215E	ENSG000003HSD17B2	EDH17B2 Hydroxyst protein-coding
chr19-23 10.65546	-0.02314	0.720995	-0.0321	0.974394	0.981731	chr19	23381371	23385255	+	0 NA	intron (NLIIPREC2 I	12518 NM_00343C		7644 Hs. 58834	NR_00343C	ENSG000003ZNF91	HPF7 HTF1zinc fingprotein-coding
chr1-1208 11.14234	-0.02268	0.709255	-0.03198	0.974487	0.981731	chr1	1.21E+08	1.21E+08	+	0 NA	intron (Nintron (N	81583 NM_001351		1.01E+08	NR_001351	ENSG000003CNBP26	-
chr17-29 6.432988	0.030099	0.94274	0.031927	0.97453	0.981731	chr17	29077847	29078723	+	0 NA	intron (NAluSx SIN	-2676 NM_00474C		9220 Hs. 46259	NR_00474C	ENSG000003TIAP1	MAJN SPR2 TGFB1-inc protein-coding
chr17-44 7.247301	-0.02821	0.885455	-0.03186	0.974582	0.981731	chr17	44084830	44085317	+	0 NA	exon (NM exon (NM	14162 NR_02858E		92579 Hs. 29400	NR_13838E	ENSG000003G6P3C	SMN4 UGRF glucosyl-cprotein-coding
chr2-131 7.247301	-0.02821	0.885455	-0.03186	0.974582	0.981731	chr2	1.31E+08	1.31E+08	+	0 NA	3' UTR (N3' UTR (N	42349 NR_001321		130074 Hs. 53467	NR_00100E	ENSG000003FAM168B	MAN1 family wprotein-coding
chr2-4434 11.08549	-0.02166	0.706806	-0.03064	0.975556	0.981731	chr2	44340510	44341009	+	0 NA	intron (NAluSx1 SI	18990 NM_00104E		9581 Hs. 44434	NR_00603E	ENSG000003PREPL	CMS22 prolyl er protein-coding
chr22-408 11.08549	-0.02166	0.706806	-0.03064	0.975556	0.981731	chr22	40825136	40827529	+	0 NA	3' UTR (N3' UTR (N	-6933 NM_00128E		10478 Hs. 47493	NR_00635E	ENSG000003SLC25A17	PMP34 sulfate cprotein-coding
chr1-394 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr1	39426793	39429431	+	0 NA	exon (NM exon (NM	19039 NR_00128E		643314 Hs. 65876	NR_001351	ENSG000003KIAA0754	-
chr1-181 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr1	1.81E+08	1.81E+08	+	0 NA	intron (Nintron (N	18920 NM_00581E		10228 Hs. 51841	NR_00581E	ENSG000003STX6	-
chr10-89 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr10	89337489	89339366	+	0 NA	intron (NMLT2B1 LI	5898 NM_001031		3437 Hs. 47338	NR_00154E	ENSG000003IFIT3	CIG-49 G1 interfeer protein-coding
chr12-27 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr12	27723834	27725725	+	0 NA	intron (Nintron (N	13947 NM_021821		60488 Hs. 71407	NR_021821	ENSG000003MRP35	HDCMD11P mitochon protein-coding
chr16-22 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr16	22505844	22506403	+	0 NA	non-codir non-codir	1674 NR_02445E		1E+08	NR_02445E	LOC10019C	-
chr19-564 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr19	5645307	5648908	+	0 NA	intron (Nintron (N	24024 NM_002967		6294 Hs. 72880	NR_002967	ENSG000003SAFB	HAP HET Scaffold protein-coding
chr2-1514 9.186964	-0.0235	0.769107	-0.03055	0.975626	0.981731	chr2	1.51E+08	1.51E+08	+	0 NA	intron (NAluY SINE	37258 NM_001177		55183 Hs. 53653	NR_018151	ENSG000003CRIF1	-
chr1-240 9.673844	-0.02287	0.749089	-0.03053	0.975642	0.981731	chr1	2.4E+08	2.4E+08	+	0 NA	intron (Nintron (N	25260 NM_02246E		64388 Hs. 98206	NR_02246E	ENSG000003GREM2	CKT5F1B2 gremlin 2 protein-coding
chr14-96 9.673844	-0.02287	0.749															



chr15-645.9.137966	-0.02368	0.784529	-0.03019	0.975916	0.981731	chr15	64979302	64979642	+	0 NA	intron (NL3 LINE C	9998 NM_001127	51324 Hs. 242458NM_016633	ENSG000003PG21	ABHD21 ACSPG21	abf protein-coding		
chr5-7214.7.877913	0.025694	0.85383	0.030093	0.975993	0.981731	chr5	72148715	72149116	+	0 NA	intron (NL2b LINE	-20552 NR_039967	1.01E+08	NR_039967	ENSG000003MIR4803	microRNA ncRNA		
chr16-88C.5.912826	0.028811	0.961138	0.029976	0.976086	0.981731	chr16	88052302	88053198	+	0 NA	intron (N(CCA)n Si	48235 NR_12031C	400553 Hs. 592071NR_12031C	ENSG000003LOC00555	uncharacterncRNA			
chr20-35C.7.726323	-0.02544	0.853724	-0.0298	0.976227	0.981731	chr20	35043473	35043913	+	0 NA	intron (NMER44A DN	49114 NM_015638	26133 Hs. 168073NM_015638	ENSG000003TRPC4AP	C20orf188	transient protein-coding		
chr6-1095.5.863829	0.028343	0.967791	0.029286	0.976636	0.981731	chr6	1.01E+08	1.09E+08	+	0 NA	intron (Nintron (N	9813 NM_00134F	8763 Hs. 52031NM_006011	ENSG000003CD164	DFNA66 MC	CD164 mol protein-coding		
chr4-799F.7.239443	-0.02592	0.894109	-0.02899	0.976869	0.981731	chr4	79982634	79983006	+	0 NA	intron (Nintron (N	90409 NM_00128E	118429 Hs. 162963NM_058172	ENSG000003ANTXR2	CMG-2 CMC	ANTXR cel protein-coding		
chr3-197F.6.342851	0.027223	0.9419	0.028902	0.976943	0.981731	chr3	1.98E+08	1.98E+08	+	0 NA	intron (NAluSx SIN	58000 NM_00136E	84859 Hs. 518414NM_032777	ENSG000003LRCH3	leucine r	protein-coding		
chr21-26F.11.565451	-0.02006	0.696586	-0.02288	0.977025	0.981731	chr21	26923577	26924256	+	0 NA	3' UTR (N3' UTR (N	-30045 NR_03991F	1.01E+08	NR_03991F	ENSG000003MIR4759	microRNA ncRNA		
chr1-215E.12.10039	-0.01947	0.680177	-0.02862	0.977164	0.981731	chr1	2.16E+08	2.16E+08	+	0 NA	intron (NLIPA11 LI	45674 NM_00131E	51133 Hs. 335133NM_016121	ENSG000003KCTD3	NY-REN-4E	potassium protein-coding		
chr20-49C.11.61351	-0.01974	0.690358	-0.02859	0.97719	0.981731	chr20	49269440	49271563	+	0 NA	exon (NM exon (NM	7556 NM_02103E	57169 Hs. 371794NM_02103E	ENSG000003ZNF1	zinc finger	protein-coding		
chr20-50F.11.61351	-0.01974	0.690358	-0.02859	0.97719	0.981731	chr20	50893873	50894389	+	0 NA	exon (NM exon (NM	15660 NM_00128E	23394 Hs. 293733NM_01533E	ENSG000003ADNP	ADNP1 HVT	protein-coding		
chr1-320C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr1	32032779	32047628	+	0 NA	intron (NAluS2 SI	26335 NM_001271	10657 Hs. 445893NM_00655E	ENSG000003KHDRBS1	Sam68 p6E	KH RNA bi protein-coding		
chr1-100C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr1	1E+08	1E+08	+	0 NA	intron (NAluYml SI	5018 NR_03027E	693138	NR_03027E	ENSG000003MIR553	MIRN553 hm	icroRNA ncRNA	
chr1-110C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr1	1.1E+08	1.1E+08	+	0 NA	intron (Nintron (N	10703 NM_00124Z	10768 Hs. 743973NR_006621	ENSG000003AHCYL3	DCAL IRB	adnosyl protein-coding		
chr1-161F.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr1	1.62E+08	1.62E+08	+	0 NA	intron (NLM4 LINE	5438 NM_00724C	11266 Hs. 416216NM_00724C	ENSG000003DUSP12	DUSP1 YVF	dual spec protein-coding		
chr10-114C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr10	1.15E+08	1.15E+08	+	0 NA	intron (Nintron (N	25251 NM_00113E	57700 Hs. 192615NM_02094C	ENSG000003FAM160B1	KIAA1600 family	wiprotein-coding		
chr11-46C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr11	46319849	46321117	+	0 NA	exon (NM exon (NM	-12443 NM_20153E	8525 Hs. 502461NM_00364E	ENSG000003CGKZ	DAGK5 DAC	diacylgly protein-coding		
chr11-47C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr11	47754629	47765439	+	0 NA	intron (Nintron (N	6407 NM_00131E	23360 Hs. 6834 NM_01530E	ENSG000003PNBP4	FBP30	formin bi protein-coding		
chr11-65C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr11	65526335	65528934	+	0 NA	intron (NAluSx1 SI	2551 NM_00104E	57410 Hs. 238833NM_02068C	ENSG000003SCYL1	GKLP HTO1	SCYL1 like protein-coding		
chr12-374C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr12	374048	385166	+	0 NA	intron (Nintron (N	9713 NM_00104E	5927 Hs. 76272 NM_00505E	ENSG000003KDM5A	RBBP-2 RE	lysine de protein-coding		
chr17-35C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr17	35259459	35266281	+	0 NA	intron (NAluJb SIN	19798 NM_14497F	162394 Hs. 585792NM_14497F	ENSG000003SLFN5	schlafen	protein-coding		
chr22-40F.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr22	40845907	40850284	+	0 NA	intron (NCharlie5	8544 NM_00393Z	6767 Hs. 712713NM_00393Z	ENSG000003ST13	AAG2 FAM1	ST13 Hsp7 protein-coding		
chr3-943C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr3	9439503	9452007	+	0 NA	intron (Nintron (N	48055 NM_00108C	55209 Hs. 288164NM_018187	ENSG000003SETD5	SET	domain protein-coding		
chr3-128C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr3	1.28E+08	1.28E+08	+	0 NA	intron (NAluSg7 SI	4532 NM_01333E	29927 Hs. 518233NM_01333E	ENSG000003SEC61A1	HNFJ4 HSE	SEC61 tra protein-coding		
chr5-695E.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr5	69564362	69568775	+	0 NA	intron (Nintron (N	6323 NM_00109E	728340 Hs. 191353NM_00109E	ENSG000003GTF2H2C	GTF2H2C_2	GTF2H2 E protein-coding		
chr5-1324C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr5	1.32E+08	1.32E+08	+	0 NA	intron (NAluS2 SI	5634 NM_00135A	3659 Hs. 436061NM_00219E	ENSG000003IRF1	IRF-1 MAF	interferc protein-coding		
chr5-136C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr5	1.36E+08	1.36E+08	+	0 NA	intron (NAluS2 SI	12389 NM_00035E	7045 Hs. 369397NM_00035E	ENSG000003TGFB1	BIGH3 CDF	transfcr protein-coding		
chr5-149C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr5	1.49E+08	1.49E+08	+	0 NA	exon (NM exon (NM	4197 NM_152407	134266 Hs. 511816NM_152407	ENSG000003GRPEL2	Mt-GrpE2 GrpE	like protein-coding		
chr6-111C.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr6	1.11E+08	1.11E+08	+	0 NA	intron (NMER47A DN	49164 NM_15336E	91749 Hs. 400572NM_15336E	ENSG000003MFS4B	KIAA1919 major	fac protein-coding		
chr7-669F.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr7	66987267	66993901	+	0 NA	intron (Nintron (N	5002 NM_01603E	51119 Hs. 11044E	ENSG000003SBDS	CG1-97	SLBDS rib protein-coding		
chr8-124F.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr8	1.25E+08	1.25E+08	+	0 NA	intron (NTigger1 I	5250 NM_00500E	4715 Hs. 15977 NM_00500E	ENSG000003NDUF9	B22 C1-B2	NADH:ubiq protein-coding		
chr9-356F.10.63975	-0.02046	0.71586	-0.02859	0.977194	0.981731	chr9	35682224	35688826	+	0 NA	exon (NM exon (NM	4400 NM_001301	7169 Hs. 300772NM_00328E	ENSG000003TPM2	AMC1-DA1	tropomyos protein-coding		
chr1-666F.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr1	66679239	66681012	+	0 NA	intron (Nintron (N	51685 NR_03606C	ENSG000003MIR3117	1E+08	NR_03606C	ENSG000003MIR3117	miR-3117	microRNA ncRNA
chr12-56F.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr12	56341523	56358044	+	0 NA	intron (NAluSx SIN	10324 NM_19833Z	6773 Hs. 530595NM_00541E	ENSG000003STAT2	IMD44 ISC	signal tr protein-coding		
chr12-95C.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr12	95001014	95001213	+	0 NA	intron (NAluJo SIN	2584 NM_01883E	55967 Hs. 506374NM_01883E	ENSG000003NDUFA12	B17.2 DAF	NADH:ubiq protein-coding		
chr19-584C.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr19	58414990	58423436	+	0 NA	TTS (NR_TTS (NR_1	10539 NM_00131E	201514 Hs. 439551NM_17354E	ENSG000003ZNF584	zinc finger	protein-coding		
chr2-105F.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr2	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	30228 NM_00128E	79074 Hs. 549577NM_02409E	ENSG000003C2orf49	asw	chromoson protein-coding		
chr2-230C.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr2	2.3E+08	2.3E+08	+	0 NA	intron (NLP18A LI	69538 NM_00120E	6672 Hs. 369056NM_00311E	ENSG000003SP100	lysp100B	SP100 nuc protein-coding		
chr3-179C.11.12663	-0.02007	0.702167	-0.02858	0.977196	0.981731	chr3	1.79E+08	1.79E+08	+	0 NA	intron (Nintron (N	4849 NM_15224C	64393 Hs. 371606NM_02247C	ENSG000003ZMAT3	PAG608 W1z	inc finger protein-coding		
chr13-32F.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr13	32536282	32536773	+	0 NA	exon (NM exon (NM	2268 NM_014887	10443 Hs. 50768C	ENSG000003N4BP2L2	92M18.3 C	NEDD4 bir protein-coding		
chr13-94C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr13	94580384	94583476	+	0 NA	intron (NAluSp SIN	14222 NM_001304	23483 Hs. 12393 NM_01430E	ENSG000003TGDS	CATMANS S	TDP-glucc protein-coding		
chr13-114C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr13	1.14E+08	1.14E+08	+	0 NA	intron (Nintron (N	-7323 NR_03972A	ENSG000003MIR4502	1.01E+08	NR_03972A	ENSG000003MIR4502	microRNA ncRNA	
chr15-484C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr15	48429322	48438338	+	0 NA	intron (Nintron (N	101633 NM_00194E	1854 Hs. 52798C	ENSG000003CDDUT	dUTPase	deoxyuric protein-coding		
chr16-851C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr16	85182365	85186039	+	0 NA	Intergeni Intergeni	-23594 NR_16214Z	1.13E+08	NR_16214Z	MIR12128	microRNA ncRNA		
chr17-161C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr17	16112581	16121115	+	0 NA	intron (NCharlie2	36348 NR_145787	1.1E+08	NR_145787	SNORD163	small nuc	snoRNA	
chr19-57C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr19	57907471	57914600	+	0 NA	intron (NAluS2 SI	5557 NM_001297	147687 Hs. 56771C	ENSG000003ZNF417	zinc finger	protein-coding		
chr2-853C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr2	85320100	85326568	+	0 NA	intron (NAluSx1 SI	4655 NM_00136E	10618 Hs. 593382NM_006464	ENSG000003TGOLN2	TGN38 TGN	trans-gol protein-coding		
chr5-735C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr5	73500135	73506208	+	0 NA	exon (NM exon (NM	4656 NM_001037	689 Hs. 591766NM_001207	ENSG000003CBTF3	BETA-NAC	trans en protein-coding		
chr8-478C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr8	47830144	47830800	+	0 NA	intron (NMTRe SINE	-92308 NM_00519E	1052 Hs. 440823NM_00519E	ENSG000003CEBPD	C/EBP-de	CCAAT tr protein-coding		
chr8-1254C.10.15287	-0.02091	0.731751	-0.02858	0.977201	0.981731	chr8	1.25E+08	1.25E+08	+	0 NA	intron (Nintron (N	1904 NM_00128E						

chr15-235 8.725507	-0.0187	0.800179	-0.02337	0.981354	0.984388	chr15	25087615	25087814	+	0	NA	promoter-promoter-	53 NR_003334	1E+08	NR_003334	ENSG000003NORD116-	HBII-85-2	small	nuc	snoRNA			
chr10-12C 11.10305	-0.01624	0.708184	-0.02293	0.981709	0.984548	chr10	12028819	12029508	+	0	NA	exon (NM exon (NM	13646 NM_015542	26019	Hs. 370688	NR_015542	ENSG000004UPF2	HUPF2 RENUP2	reg	protein-coding			
chr17-28C 11.63893	-0.01579	0.688846	-0.02292	0.981714	0.984548	chr17	28658521	28660186	+	0	NA	intron (NSVA_A Ret	2553 NM_006923	6388	Hs. 51403	ENSG000003CDF2	-	stromal	c	protein-coding			
chr2-241C 11.63893	-0.01579	0.688846	-0.02292	0.981714	0.984548	chr2	2.41E+08	2.41E+08	+	0	NA	intron (Nintron (N	-13409 NM_001282	9855	Hs. 72631	ENSG000003FARP2	FIR FRG FFERM, ARF	protein-coding					
chr1-145E 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr1	1.46E+08	1.46E+08	+	0	NA	TTS (NM_C TTS (NM_C	36881 NM_001371359										
chr1-200E 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr1	2.01E+08	2.01E+08	+	0	NA	intron (NLIPA13 LI	-36584 NM_00529E	2848	Hs. 53431	ENSG000003GPR25	-	G	protein-coding				
chr14-52T 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr14	52717764	52722814	+	0	NA	intron (NALuJr SIN	-9877 NM_00113C	6815	Hs. 36498	NR_145251	ENSG000003STYX	-	serine/t	protein-coding			
chr16-84T 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr16	84485012	84498090	+	0	NA	intron (NALuSz SIN	13108 NM_020947	57707	Hs. 28827	NR_020947	ENSG000003MEA7	KIAA1609 MTOR	asc	protein-coding			
chr17-80C 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr17	80356191	80366089	+	0	NA	intron (N(CATGCAA	-54027 NR_148041	284131	Hs. 38967	ENSG000003ENDOV	-	endonucle	protein-coding				
chr2-241C 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr2	2.41E+08	2.41E+08	+	0	NA	intron (Nintron (N	8877 NM_00132C	3069	Hs. 47185	NR_00533	ENSG000003HDLPB	HBP PROZ2	high	dens	protein-coding		
chr2-241C 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr2	2.41E+08	2.41E+08	+	0	NA	intron (Nintron (N	-6406 NM_001282	9855	Hs. 72631	ENSG000003FARP2	FIR FRG FFERM, ARF	protein-coding					
chr3-184T 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr3	1.84E+08	1.84E+08	+	0	NA	exon (NM exon (NM	-5100 NM_01835E	55324	Hs. 36132	ENSG000003ABCF3	EST201864	ATP	bindi	protein-coding			
chr8-82T 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr8	1.02E+08	1.02E+08	+	0	NA	intron (NLIMEf LIN	26835 NR_12541E	1.02E+08	Hs. 49244	ENSG000003UBR5-AS1	UBR5	antinc	RNA				
chr9-103C 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr9	33337193	33349440	+	0	NA	intron (N(Charlie L	52800 NM_147134	4799	Hs. 41307	NR_002504	ENSG000003CNFX1	NFX2 TEG	nuclear	protein-coding			
chr9-125C 11.15205	-0.01597	0.701665	-0.02276	0.981841	0.984548	chr9	1.25E+08	1.25E+08	+	0	NA	intron (NTHE1B LTF	89486 NM_00133C	26130	Hs. 42376	NR_01563	ENSG000003GAPVD1	GAPX5 GATPase	ac	protein-coding			
chr1-193C 10.66517	-0.01618	0.716503	-0.02259	0.981981	0.984595	chr1	1.93E+08	1.93E+08	+	0	NA	intron (Nintron (N	-49939 NM_00378E	8707	Hs. 51883	NR_00378E	ENSG000003B3GAL72	BETA3GALbeta-1,3-	protein-coding				
chr10-11C 10.66517	-0.01618	0.716503	-0.02259	0.981981	0.984595	chr10	1.12E+08	1.12E+08	+	0	NA	exon (NM exon (NM	12553 NM_022494	64429	Hs. 19699	NR_022494	ENSG000003ZDHH6C	DHHC-6 Zn	inc	protein-coding			
chr19-14C 10.66517	-0.01618	0.716503	-0.02259	0.981981	0.984595	chr19	14514181	14516554	+	0	NA	3' UTR (N3' UTR (N	2495 NM_00130C	3337	Hs. 51521	ENSG000003DNAJB1	HSPF1 HdjDnaJ	heat	protein-coding				
chr22-35C 10.66517	-0.01618	0.716503	-0.02259	0.981981	0.984595	chr22	35263330	35266147	+	0	NA	non-codir non-codir	7245 NM_00136E	10042	Hs. 58881	ENSG000003HMGXB4	HMG2L1 HM	HMG-box	c	protein-coding			
chr15-437 10.17829	-0.01641	0.733713	-0.02237	0.982156	0.984654	chr15	43792723	43796643	+	0	NA	promoter-promoter-	-924 NR_03169E										
chr15-937 10.17829	-0.01641	0.733713	-0.02237	0.982156	0.984654	chr15	99710448	99711263	+	0	NA	intron (Nintron (N	22582 NM_001284	145748	Hs. 56256	ENSG000003LYSMD4	LysM	dom	protein-coding				
chr2-134C 10.17829	-0.01641	0.733713	-0.02237	0.982156	0.984654	chr2	1.34E+08	1.34E+08	+	0	NA	intron (NLIP3 LIN	78290 NM_00241C	4249	Hs. 4988	NR_00241C	ENSG000003MGAT5	GNT-V GNTalpha-1,	protein-coding				
chr7-1394 10.17829	-0.01641	0.733713	-0.02237	0.982156	0.984654	chr7	1.39E+08	1.39E+08	+	0	NA	intron (Nintron (N	24256 NR_03399E	1E+08	Hs. 74444	ENSG000003LOC10012E	-	uncharact	ncRNA				
chr8-424C 10.17829	-0.01641	0.733713	-0.02237	0.982156	0.984654	chr8	42431481	42433110	+	0	NA	intron (N(Tigger1 E	40415 NM_00566E	7419	Hs. 69930	NR_00566E	ENSG000003VDAC3	HD-VDAC3 voltage	c	protein-coding			
chr11-74C 10.12929	-0.01658	0.746642	-0.02221	0.982282	0.984757	chr11	74078043	74078600	+	0	NA	exon (NM exon (NM	-69084 NM_02280C	7352	Hs. 10133	NR_00335E	ENSG000003UCP3	SLC25A9	uncouplir	protein-coding			
chr10-61E 9.69141	-0.01663	0.753747	-0.02207	0.982394	0.984776	chr10	61940211	61942717	+	0	NA	intron (Nintron (N	39765 NM_03219E	84159	Hs. 53529	NR_03219E	ENSG000003ARID5B	DESRT MRF	AT-rich	protein-coding			
chr17-62E 9.69141	-0.01663	0.753747	-0.02207	0.982394	0.984776	chr17	62680003	62680246	+	0	NA	intron (NCpG	-26282 NR_14788E	1.05E+08	Hs. 44626	ENSG000003LOC105371	-	uncharact	ncRNA				
chr2-114E 9.69141	-0.01663	0.753747	-0.02207	0.982394	0.984776	chr2	11451959	11453357	+	0	NA	intron (Nintron (N	13503 NR_10349C	1876	Hs. 60309	NR_19825E	ENSG000003E2F6	E2F-6	E2F	trans	protein-coding		
chr5-150E 9.69141	-0.01663	0.753747	-0.02207	0.982394	0.984776	chr5	1.5E+08	1.5E+08	+	0	NA	intron (Nintron (N	40840 NR_10996E	1436	Hs. 58621	ENSG000003CSF1R	C-FMS CD1	colony	st	protein-coding			
chr1-248E 9.204529	-0.01682	0.771196	-0.02164	0.982733	0.985068	chr1	2.49E+08	2.49E+08	+	0	NA	intron (Nintron (N	7494 NM_02483E	79894	Hs. 52115	NR_02483E	ENSG000003ZNF672	ATP5A1 ATF	ATP	synth	protein-coding		
chr2-238I 9.204529	-0.01682	0.771196	-0.02164	0.982733	0.985068	chr2	2.38E+08	2.38E+08	+	0	NA	intron (Nintron (N	18365 NM_03076E	80895	Hs. 92033	NR_03076E	ENSG000003ILKAP	ILKAP2 II	ILK	assoc	protein-coding		
chr11-64E 12.11795	-0.01445	0.675598	-0.02139	0.982932	0.985177	chr11	64764240	64777359	+	0	NA	intron (Nintron (N	6962 NM_00117E	7536	Hs. 50282	ENSG000003SF1	BBP D1E5	splicing	protein-coding				
chr7-116E 12.11795	-0.01445	0.675598	-0.02139	0.982932	0.985177	chr7	1.17E+08	1.17E+08	+	0	NA	intron (Nintron (N	-36365 NM_00136E	7982	Hs. 36813	NR_01841E	ENSG000003ST7	ST57q FAM	suppress	protein-coding			
chr16-144 5.887402	0.020722	0.977207	0.021205	0.983082	0.985177	chr16	1446484	1446884	+	0	NA	exon (NM exon (NM	-2195 NM_00114E	645811	Hs. 35523	ENSG000003CCDC154	C16orf29	coiled-c	protein-coding				
chr16-15C 11.63107	-0.01456	0.687598	-0.02118	0.983102	0.985177	chr16	15003698	15007596	+	0	NA	intron (Nintron (N	4750 NR_036054	1E+08	Hs. 30605	ENSG000003MIR1972-1	MIR1972 mi	microRNA	ncRNA				
chr18-46C 11.63107	-0.01456	0.687598	-0.02118	0.983102	0.985177	chr18	46079349	46095138	+	0	NA	intron (Nintron (N	11053 NM_001001	498	Hs. 29828	NR_00404E	ENSG000003ATP5F1A	ATP5A1 ATF	ATP	synth	protein-coding		
chr21-38E 11.63107	-0.01456	0.687598	-0.02118	0.983102	0.985177	chr21	38809577	38823976	+	0	NA	intron (Nintron (N	10847 NM_00523E	2114	Hs. 64423	NR_00523E	ENSG000003ETS2	ETS2IT1	ETS	prot	protein-coding		
chr5-553C 11.63107	-0.01456	0.687598	-0.02118	0.983102	0.985177	chr5	55300094	55302950	+	0	NA	intron (NALuSp SIN	6172 NM_00134E	54505	Hs. 59326	NR_01903C	ENSG000003DHX29	DDX29	DEX	box	protein-coding		
chr5-5454 8.717649	-0.01693	0.804853	-0.02104	0.983217	0.985177	chr5	54543338	54544134	+	0	NA	3' UTR (N3' UTR (N	25977 NM_00110E	112574	Hs. 43275	ENSG000003SNX18	SNX18 FAM	sorti	protein-coding				
chr1-842I 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr1	84218976	84219757	+	0	NA	intron (NALuSq2 SI	37734 NM_00124E	5567	Hs. 48732	ENSG000003PRKACB	PKA C-beta	protein-coding					
chr10-68C 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr10	68020761	68022364	+	0	NA	intron (NALuSp SIN	-10679 NR_131184	1E+08	Hs. 131184	POU5F1P5	Oct4-pg5	POU	class	pseudo			
chr11-144 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr11	14469314	14498684	+	0	NA	intron (NLIMC4a LI	15859 NM_016451	1315	Hs. 33927	NR_016451	ENSG000003COPB1	COPB	coater	protein-coding			
chr11-121 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr11	1.21E+08	1.21E+08	+	0	NA	intron (Nintron (N	14171 NM_001024	6309	Hs. 28774	NR_00691E	ENSG000003SC5D	ERG3 S5D	sterol-C	protein-coding			
chr14-52T 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr14	52034461	52042601	+	0	NA	intron (Nintron (N	30528 NM_007361	22795	Hs. 36984	NR_007361	ENSG000003NID2	NID-2	nidogen	protein-coding			
chr14-551 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr14	55138240	55146681	+	0	NA	intron (Nintron (N	5477 NR_00322E	3958	Hs. 53108	NR_00230E	ENSG000003LGLS3	CBP35 GAL	nadogen	protein-coding			
chr15-43C 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr15	43356819	43369894	+	0	NA	intron (NMIRb SINE	6704 NM_15224E	146050	Hs. 41828	NR_15245E	ENSG000003ZSCAN29	ZNF690 Zf	zinc	finger	protein-coding		
chr17-76T 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr17	76717377	76725345	+	0	NA	intron (N(AAACA)n	5065 NM_001081	23210	Hs. 51450	NR_01516E	ENSG000003JMJD6	PSR PTDSF	jumonji	c	protein-coding		
chr18-59C 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr18	59343847	59355816	+	0	NA	intron (Nintron (N	9434 NM_00557C	3998	Hs. 46529	NR_00557C	ENSG000003CLMAN1	ERGIC-53 lectin,	n	protein-coding			
chr2-618T 11.14419	-0.0147	0.70145	-0.02095	0.983282	0.985177	chr2	61870641	61873933	+	0	NA	exon (NM exon (NM	16369 NM_00643C	10575	Hs. 42150	NR_00643C	ENSG000003CCT4	CCT-DELTA7 chaperon	protein-coding				
chr14-55E 6.894444	0.019571	0.934154	0.020951	0.983285	0.985177	chr14	55312757	55312956	+														



chr14-55e	15.09193	-0.00202	0.612748	-0.00329	0.997375	0.997541	chr14	55618840	55621237	+	0 NA	intron (N THE1B-int	39831	NM_001075	3895	Hs.509414NM_004986	ENSG0000CKTN1	CG1 KNT k	kinectin	protein-coding	
chr10-17e	15.59638	0.001554	0.603674	0.002574	0.997947	0.998065	chr10	17229905	17237920	+	0 NA	exon (NM_exon (NM_	-3927	NR_108061	1.01E+08	Hs.740502NR_108066	ENSG0000CVIM-AS1	-	VIM	antisncRNA	
chr9-1014	15.59638	0.001554	0.603674	0.002574	0.997947	0.998065	chr9	1.01E+08	1.01E+08	+	0 NA	intron (N L2c LINE	6219	NM_001278	7743	Hs.50123	NM_003452	ENSG0000CZNF189	-	zinc finger	protein-coding
chr8-9451	13.15227	-0.00156	0.653377	-0.00238	0.998098	0.998192	chr8	94511164	94511678	+	0 NA	exon (NM_exon (NM_	-36306	NM_001205	25788	Hs.30561	NM_006556	ENSG0000CRAD54B	RDH54	RAD54	homprotein-coding
chr10-377	14.11817	-0.00128	0.631062	-0.00203	0.998377	0.998448	chr10	3777691	3784528	+	0 NA	intron (N intron (N	4100	NR_027652	1316	Hs.4055	NM_001306	ENSG0000CKLF6	BCD1 CBA1	Kruppel	protein-coding
chr19-578	15.11736	0.001056	0.612732	0.001724	0.998625	0.998651	chr19	57853305	57868708	+	0 NA	3' UTR (N 3' UTR (N	-6754	NR_144562	1.01E+08	Hs.65482CNR_144562	UBE2CP5	-	ubiquitin	pseudo	
chr11-107	15.08407	-0.00105	0.612516	-0.00172	0.998627	0.998651	chr11	10796252	10807860	+	0 NA	promoter-promoter-	-448	NR_004403	692223	Hs.723086NR_004403	ENSG0000CSNORD97	U97	small	nucsnRNA	
chr20-50e	12.65753	6.04E-05	0.669384	9.02E-05	0.999928	0.999928	chr20	50548513	50548935	+	0 NA	intron (N LIMEi LIN	-37062	NR_030375	693230	NR_030375	ENSG0000CMIR645	MIRN645 t	microRNA	ncRNA	

Supplementary Information

Supplementary Table 8. Genome-wide profiling of differential peaks between senescent cells and counterparts exposed to ML324 (ChIP-seq for H3K9me3).

geneID	baseMea	log2Fold	lfcSE	stat	pvalue	padj	Chr	Start	End	Strand	Peak	Focus	Annotati	Detailed	Distance	Nearest	F	Entrez	ID	Nearest	Nearest	F	Nearest	F	Gene	Na	Gene	Ali	Gene	De	Gene	Type	
chr16-463	1337.821	0.957639	0.124498	7.691982	1.45E-14	2.36E-11	chr16	46385249	46391418	+	0	NA	Intergeni	Intergeni	180764	NR_026556	124149	Hs. 97414	NM_001004299		ANKRD26P1	-									ankyrin ipseudo		
chr13-182	155.23	0.627866	0.215772	7.665826	1.78E-14	2.36E-11	chr13	18211764	18212397	+	0	NA	intron	(HSATI)Sat	16783	NR_027278	26080	Hs. 44858	NR_027278	ENSG00000	FAM230C		LINC00281								family wincRNA		
chr16-463	1994.26	0.969054	0.121511	7.579116	3.48E-14	3.08E-11	chr16	46394248	46395191	+	0	NA	Intergeni	Intergeni	174378	NR_026556	124149	Hs. 97414	NM_001004299		ANKRD26P1	-									ankyrin ipseudo		
chr16-345	977.4214	0.933407	0.129949	7.182895	6.83E-13	3.73E-10	chr16	34576209	34576651	+	0	NA	Intergeni	(AATGGAC)	-194950	NR_158158	1.03E+08	Hs. 69271	(NR_158158)		CCNYL3	-									cyclin Y pseudo		
chr16-345	985.1891	0.934876	0.130222	7.192119	7.01E-13	3.73E-10	chr16	34581384	34583827	+	0	NA	Intergeni	Intergeni	-201125	NR_158158	1.03E+08	Hs. 69271	(NR_158158)		CCNYL3	-									cyclin Y pseudo		
chr16-345	398.8351	1.116115	0.175359	6.33908	2.31E-10	1.03E-07	chr16	34592600	34596135	+	0	NA	Intergeni	(ATGATTC)	-212887	NR_158158	1.03E+08	Hs. 69271	(NR_158158)		CCNYL3	-									cyclin Y pseudo		
chr3-9347	19119.9	0.746191	0.119444	6.247216	4.18E-10	1.59E-07	chr3	93470447	93470718	+	0	NA	Intergeni	SAR SatE	503499	NM_001314	5627	Hs. 64016	NM_00031	ENSG0000C	PROS1		PROS PS2								protein iprotein-coding		
chr16-345	460.984	0.955031	0.158226	6.03587	1.58E-09	5.26E-07	chr16	34584711	34588633	+	0	NA	Intergeni	Intergeni	-205192	NR_158158	1.03E+08	Hs. 69271	(NR_158158)		CCNYL3	-									cyclin Y pseudo		
chr4-7392	208.1846	1.267215	0.159423	5.998106	2.68E-09	7.86E-07	chr4	73906089	73906784	+	0	NA	Intergeni	LIP3 LIN	37043	NM_001511	2919	Hs. 789	NM_001511	ENSG0000C	CXCL1		FSP GRO1								C-X-C motif protein-coding		
chr21-792	216.0886	1.127218	0.189427	5.950681	2.67E-09	7.90E-07	chr21	7924944	7926545	+	0	NA	Intergeni	(ATTCCAT)	-96112	NM_001366	1.03E+08		NM_00133C	ENSG0000C	KCNE1B											potassium protein-coding	
chr1-1251	2923.842	0.69986	0.118592	5.9014	3.60E-09	9.59E-07	chr1	1.25E+08	1.25E+08	+	0	NA	Intergeni	(ATCCAT)	3662312	NR_00395F	647121	Hs. 697682	NR_00395F	ENSG0000C	EMBP1											embigin ipseudo	
chr4-7457	70.92159	1.580935	0.266207	5.883871	1.57E-08	3.81E-06	chr4	74597145	74598143	+	0	NA	Intergeni	TheIB-int	152508	NM_001657	374	Hs. 27083	NM_001657	ENSG0000C	AREG		AR AREG									amphireg protein-coding	
chr21-82	77.82138	1.600935	0.283207	5.652871	1.58E-08	3.82E-06	chr21	8238242	8239161	+	0	NA	intron	(CpG)	-10804	NR_12871F	1.04E+08		NR_12871F	ENSG0000C	MIR6724-2		hsa-mir-6									microRNA ncRNA	
chr21-84	80.48769	1.519658	0.277522	5.475478	4.36E-08	9.68E-06	chr21	8465906	8466762	+	0	NA	Intergeni	CpG	25188	NR_145822	1.07E+08		NR_145822	RNA28SN1		RNA28S4										RNA, 28S rRNA	
chr16-345	369.4686	0.860228	0.15846	5.4312	5.60E-08	1.15E-05	chr16	34571570	34574179	+	0	NA	Intergeni	(GAATG)n	-191394	NR_158158	1.03E+08	Hs. 69271	(NR_158158)		CCNYL3	-										cyclin Y pseudo	
chr22-187	67.48959	1.697298	0.317163	5.351505	8.72E-08	1.66E-05	chr22	18730403	18730687	+	0	NA	Intergeni	AluSc8 S1	-3369	NR_136561	642643		NR_136561	ENSG0000C	FAM230E		LINC01662									family wincRNA	
chr19-74	78.96977	1.471225	0.277574	5.300306	1.16E-07	2.05E-05	chr19	7450649	7451088	+	0	NA	intron	(intron)	11180	NM_00113C	23370	Hs. 465761	NM_01531F	ENSG0000C	ARHGFE18		P114-RhoC									Rho/Rac iprotein-coding	
chr18-106	598.889	0.755311	0.144577	5.224923	1.75E-07	2.91E-05	chr18	106751	110983	+	0	NA	promoter-promoter		-198	NR_03377C	727758	Hs. 58584	NR_03377C	ENSG0000C	ROCK1P1		ROCK1P									Rho assoc pseudo	
chr4-7461	565.6883	0.74311	0.139761	5.201193	1.78E-07	2.97E-05	chr4	74616713	74616924	+	0	NA	Intergeni	AluYg6 S1	171682	NM_001657	374	Hs. 27083	NM_001657	ENSG0000C	AREG		AR AREG									amphireg protein-coding	
chr22-187	58.06839	1.666498	0.329684	5.054834	4.31E-07	6.74E-05	chr22	18896273	18896495	+	0	NA	Intergeni	AluSc8 S1	-1953	NR_136571	1.01E+08	Hs. 63166	NR_136571	FAM230F		LINC01662										family wincRNA	
chr22-12	220.3159	0.911259	0.180555	4.924263	8.47E-07	0.00125	chr22	12691998	12692698	+	0	NA	Intergeni	BSR Beta	794942	NR_110761	1.03E+08	Hs. 65292	NR_110761	LOC10272												uncharactncRNA	
chr16-345	209.8437	0.885876	0.187485	4.725048	2.30E-06	0.00311	chr16	34590197	34590971	+	0	NA	Intergeni	Intergeni	-209104	NR_158158	1.03E+08	Hs. 69271	(NR_158158)		CCNYL3	-										cyclin Y pseudo	
chr1-143	954.515	0.618264	0.131109	4.715658	2.41E-06	0.000311	chr1	1.43E+08	1.43E+08	+	0	NA	Intergeni	Intergeni	190305	NR_027354	645166	Hs. 74418	NR_027354	LSP1P5	-											LSP1 pset pseudo	
chr10-38	105.5385	1.52831	0.24467	4.71178	2.46E-06	0.000311	chr10	38814066	38814283	+	0	NA	Intergeni	(TTCCA)n	117578	NR_04500C	399746	Hs. 742607	NR_04500C	ACTR3BP5		FKSG74										ACTR3B ipseudo	
chr1-143	539.7323	0.693613	0.148042	4.685239	2.80E-06	0.000327	chr1	1.43E+08	1.43E+08	+	0	NA	Intergeni	Intergeni	220714	NR_027354	645166	Hs. 74418	NR_027354	LSP1P5	-												LSP1 pset pseudo
chr21-841	83.01365	1.25844	0.268731	4.682901	2.83E-06	0.000327	chr21	8417753	8421618	+	0	NA	Intergeni	(CT)n Sin	-12845	NR_12871F	1.04E+08		NR_12871F	ENSG0000C	MIR6724-2		hsa-mir-6										microRNA ncRNA
chr5-496	201.9791	0.88438	0.191229	4.624706	3.75E-06	0.000416	chr5	49656727	49661851	+	0	NA	Intergeni	(TCCAT)n	781999	NR_19844F	133418	Hs. 56141	NM_19844F	ENSG0000C	EMB		GP70										embigin protein-coding
chrY-113	154.9628	0.959134	0.209637	4.575216	4.76E-06	0.000491	chrY	11308780	11309700	+	0	NA	Intergeni	BSR Beta	1112350	NR_033667	352887	Hs. 54622	NR_033667	ENSG0000C	GYG2P1		GYG2P										glycogenipseudo
chr4-744	442.1046	0.782491	0.146344	4.438981	4.80E-06	0.000491	chr4	74498802	74499010	+	0	NA	Intergeni	LIM2 LINE	53770	NM_001657	374	Hs. 27083	NM_001657	ENSG0000C	AREG		AR AREG										amphireg protein-coding
chr1-143	456.4059	0.728491	0.159443	4.568982	4.90E-06	0.000491	chr1	1.43E+08	1.43E+08	+	0	NA	Intergeni	Intergeni	228599	NR_027354	645166	Hs. 74418	NR_027354	LSP1P5	-												LSP1 pset pseudo
chr1-143	859.2624	0.61188	0.134027	4.565351	4.99E-06	0.000491	chr1	1.43E+08	1.43E+08	+	0	NA	Intergeni	Intergeni	225059	NR_027354	645166	Hs. 74418	NR_027354	LSP1P5	-												LSP1 pset pseudo
chr1-143	861.5436	0.60632	0.133534	4.540562	5.61E-06	0.000533	chr1	1.43E+08	1.43E+08	+	0	NA	Intergeni	Intergeni	159146	NR_027354	645166	Hs. 74418	NR_027354	LSP1P5	-												LSP1 pset pseudo
chr21-84	81.33793	1.214809	0.270321	4.493945	6.99E-06	0.000642	chr21	8462267	8464656	+	0	NA	Intergeni	CpG	22315	NR_145822	1.07E+08		NR_145822	RNA28SN1		RNA28S4											RNA, 28S rRNA
chr4-1901	435.2916	0.661489	0.151437	4.368082	1.25E-05	0.001089	chr4	1.9E+08	1.9E+08	+	0	NA	intron	(BSR Beta)	4915	NM_00129F	1E+08	Hs. 72874	NR_00120F	ENSG0000C	DUX4		DUX4L										double hc protein-coding
chr21-841	83.19381	1.176564	0.269522	4.36537	1.27E-05	0.001089	chr21	8413209	8414866	+	0	NA	Intergeni	(GA)n Sin	17111	NR_146154	1.1E+08		NR_146154	RNA28SN3													RNA, 28S rRNA
chr21-82	85.05329	1.166188	0.271275	4.298908	1.72E-05	0.001427	chr21	8231679	8232093	+	0	NA	intron	(intron)	-17619	NR_12871F	1.04E+08		NR_12871F	ENSG0000C	MIR6724-2		hsa-mir-6										microRNA ncRNA
chr21-82	81.11978	1.155908	0.269441	4.29002	1.79E-05	0.001441	chr21	8234470	8237329	+	0	NA	intron	(intron)	-13606	NR_12871F	1.04E+08		NR_12871F	ENSG0000C	MIR6724-2		hsa-mir-6										



chr4-491.35.89665	1.03714	0.38641	2.68404	0.007274	0.174109	chr4	49147322	49147735	+	O NA	Intergeni (TCCAT)n	160886	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr4-491.50.48084	0.875923	0.327075	2.678044	0.007405	0.174109	chr4	49118457	49123545	+	O NA	Intergeni (TCCAT)n	134359	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr21-82.78.14614	0.720527	0.269114	2.677406	0.007419	0.174109	chr21	8205089	8221436	+	O NA	promoter-promoter-	-626	NR_003287	1E+08	NR_003287	RNA28SN5	RN28S1 RNA, 28S rRNA	
chr14-17.166.7364	0.535958	0.200289	2.675919	0.007452	0.174109	chr14	17292175	17293039	+	O NA	IntergeniALR/Alph	-1308240	NM_001013	440153	Hs.53488:NM_001013:ENSG00000:OR11H12	-	olfactory protein-coding	
chr10-13.31.60412	1.104161	0.412637	2.675625	0.007459	0.174109	chr10	1.34E+08	1.34E+08	+	O NA	IntergeniCpG	-127266	NM_00108C	441581	Hs.69047:NM_00108C:ENSG00000:FRG2B	-	FSHD regiprotein-coding	
chr22-12.39.57452	0.999502	0.375708	2.660315	0.007807	0.180642	chr22	12693729	12693954	+	O NA	IntergeniCpG	796435	NR_110761	1.03E+08	Hs.65292:NR_110761	LOC102722-	uncharactncRNA	
chr10-42.67.88027	0.758687	0.285923	2.653469	0.007967	0.182758	chr10	42085740	42086729	+	O NA	IntergeniIntergeni	281811	NR_02438C	441666	Hs.25572:NR_02438C:ENSG00000:LOC441666-	-	zinc finpseuso	
chr4-493.29.189	1.102452	0.422514	2.609266	0.009074	0.205691	chr4	49303480	49304037	+	O NA	IntergeniIntergeni	317116	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr21-12.148.0029	0.547554	0.210121	2.605902	0.009163	0.205691	chr21	12034962	12035320	+	O NA	IntergeniALR/Alph	-1003025	NR_02691E	149992	Hs.55864:NM_153773	ANKRD30B C2lorf99 ankyrin ipseudo		
chr21-82.72.00717	0.73403	0.281822	2.604587	0.009199	0.205691	chr21	8249636	8251949	+	O NA	intron (CpG)	1287	NR_12871E	1.04E+08	NR_12871E:ENSG00000:MIR6724-	hsa-mir-6724-microRNA ncRNA		
chrY-113.79.82128	0.701415	0.271055	2.587725	0.009661	0.211226	chrY	11332065	11332297	+	O NA	IntergeniIntergeni	1089409	NR_033667	352887	Hs.546221:NR_033667:ENSG00000:GYG2P1	GYG2P	glycogenipseudo	
chr4-496.31.0989	1.060981	0.410008	2.587711	0.009662	0.211226	chr4	49654730	49657834	+	O NA	Intergeni (GAATG)n	669640	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr1-143.153.7888	0.536175	0.207364	2.585666	0.009719	0.211226	chr1	1.43E+08	1.43E+08	+	O NA	IntergeniIntergeni	215927	NR_027354	645166	Hs.74418:NR_027354	LSP1P5	LSP1 psetpseudo	
chr6-591.616.6632	0.377905	0.146243	2.584093	0.009764	0.211226	chr6	59163307	59163384	+	O NA	IntergeniALR/Alph	-1201764	NR_132994	1.07E+08	Hs.56153:NR_125727:ENSG00000:LINC0068C-	-	long intencRNA	
chrY-568.532.6253	0.562954	0.219017	2.570363	0.010159	0.216975	chrY	56850780	56851016	+	O NA	IntergeniBSR/BetaI	-103357	NM_00584C	10251	Hs.38191:NM_00584C:ENSG00000:SPRY3	spry-3	sprouty protein-coding	
chr4-490.45.13812	0.882643	0.343632	2.568572	0.010212	0.216975	chr4	49094824	49100395	+	O NA	Intergeni (CATT)n	110967	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr4-490.45.19931	0.879535	0.342746	2.566145	0.010284	0.216975	chr4	49091335	49093996	+	O NA	Intergeni (CATT)n	106023	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr19-25.57.42127	0.795919	0.310454	2.563729	0.010355	0.216975	chr19	25339220	25339455	+	O NA	IntergeniALR/Alph	-1175890	NR_00360C	1E+08	Hs.14931:NR_00360C:ENSG00000:HAVCR1P1	-	hepatitis ipseudo	
chr17-26.1060.693	0.37827	0.14771	2.560891	0.010444	0.217046	chr17	26889099	26889598	+	O NA	IntergeniALR/Alph	205808	NR_135673	1.05E+08	Hs.64991:NR_135673	LOC105371-	uncharactncRNA	
chr14-17.44.1853	0.90061	0.3541	2.543375	0.010979	0.225562	chr14	17293992	17294229	+	O NA	IntergeniALR/Alph	-1307007	NM_001013	440153	Hs.53488:NM_001013:ENSG00000:OR11H12	-	olfactory protein-coding	
chr21-84.92.51276	0.637477	0.25077	2.542077	0.01102	0.225562	chr21	8434042	8439078	+	O NA	promoter-promoter-	235	NR_16210E	1.13E+08	NR_16210E	MIR10396-	microRNA ncRNA	
chr17-21.44.42978	0.870158	0.345276	2.520185	0.011729	0.237431	chr17	21972992	21973211	+	O NA	Intergeni (ATGG)n	-229894	NR_14454E	23666	Hs.49991:NR_14454E:ENSG00000:UBBP4	-	ubiquitin ipseudo	
chr7-158.20.03978	1.289115	0.511812	2.51873	0.011778	0.237431	chr7	1.58E+08	1.58E+08	+	O NA	intron (intron)	296834	NR_03896E	1.01E+08	Hs.66126:NR_03896E	LOC10050E-	uncharactncRNA	
chr17-26.834.0117	0.359579	0.14324	2.510323	0.012062	0.241332	chr17	26619430	26620602	+	O NA	IntergeniALR/Alph	469225	NR_135673	1.05E+08	Hs.64991:NR_135673	LOC105371-	uncharactncRNA	
chr21-83.76.2707	0.678223	0.272041	2.493095	0.012663	0.251026	chr21	8392494	8397399	+	O NA	promoter-promoter-	-660	NR_14615E	1.1E+08	NR_14615E:ENSG00000:RNA5-8SN-	-	RNA, 5.8S rRNA	
chr2-161.28.61976	1.060872	0.425751	2.491088	0.012735	0.251026	chr2	1.61E+08	1.61E+08	+	O NA	IntergeniMER21B L	-25954	NR_11059E	1.02E+08	Hs.66648:NR_11059E	LOC10192E-	uncharactncRNA	
chr10-13.24.75264	1.143825	0.460136	2.485839	0.012925	0.252886	chr10	1.34E+08	1.34E+08	+	O NA	IntergeniCpG	-40735	NM_00108C	441581	Hs.69047:NM_00108C:ENSG00000:FRG2B	-	FSHD regiprotein-coding	
chr1-143.132.4453	0.539797	0.217869	2.477627	0.013226	0.256892	chr1	1.43E+08	1.43E+08	+	O NA	IntergeniIntergeni	176896	NR_027354	645166	Hs.74418:NR_027354	LSP1P5	LSP1 psetpseudo	
chr13-16.74.28317	0.681099	0.275448	2.474208	0.013421	0.258785	chr13	16499361	16499620	+	O NA	IntergeniALR/Alph	-1695807	NR_02727E	26080	Hs.44858:NR_02727E:ENSG00000:FAM230C	LINC00281	family wincRNA	
chr4-491.35.33288	0.954049	0.38792	2.459394	0.013917	0.266429	chr4	49143929	49144792	+	O NA	Intergeni (TCCAT)n	157718	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr10-40.382.6345	0.391855	0.159581	2.455524	0.014068	0.267191	chr10	40980955	40981353	+	O NA	IntergeniALR/Alph	1386891	NR_02438C	441666	Hs.25572:NR_02438C:ENSG00000:LOC441666-	-	zinc finpseuso	
chr1-125.111.6982	0.573006	0.233571	2.453235	0.014158	0.267191	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniIntergeni	3648968	NR_00395E	647121	Hs.69768:NR_00395E:ENSG00000:EMB1P1	-	embigin ipseudo	
chr21-83.68.03768	0.700149	0.28654	2.44346	0.014547	0.272606	chr21	8398309	8402921	+	O NA	non-codir-non-codir	3689	NR_146154	1.1E+08	NR_146154	RNA28SN3	RNA, 28S rRNA	
chr10-38.33.01654	0.972795	0.398575	2.440684	0.014659	0.272789	chr10	38526789	38529774	+	O NA	IntergeniIntergeni	100135	NR_024497	399744	Hs.49795:NM_001013665	LINC0099E-	long intencRNA	
chr15-20.18.44122	1.284102	0.529836	2.423585	0.015368	0.283991	chr15	20340307	20342614	+	O NA	Intergeni (AGCAGCC)	58716	NR_03883C	646096	Hs.44878:NR_03883E:ENSG00000:CHEK2P2	-	checkpoir pseudo	
chr21-82.52.29612	0.770448	0.320399	2.404652	0.016188	0.290705	chr21	8257870	8260861	+	O NA	non-codir-non-codir	2584	NR_14612C	1.1E+08	NR_14612C	RNA5-8SN-8S1 FRNA, 5.8S rRNA		
chr4-493.41.49717	0.861599	0.359503	2.39664	0.016546	0.299946	chr4	49331326	49331603	+	O NA	IntergeniIntergeni	344822	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr21-98.24.49776	1.116632	0.466017	2.396119	0.01657	0.299946	chr21	9818836	9819818	+	O NA	intron (SST1 Sate)	1734	NR_038377	441058	Hs.13053:NR_038377	LINC01667-	long intencRNA	
chr5-496.285.275	0.429149	0.179328	2.393092	0.016707	0.300388	chr5	49612239	49617181	+	O NA	IntergeniALR/Alph	826578	NR_19844E	133418	Hs.56141:NM_19844E:ENSG00000:EMB	GP70	embigin protein-coding	
chr4-492.39.14938	0.873678	0.366481	2.383961	0.017127	0.303775	chr4	49628921	49624287	+	O NA	IntergeniIntergeni	296982	NM_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr4-496.23.21414	1.124193	0.471661	2.383475	0.01715	0.303775	chr4	49605029	4962998	+	O NA	Intergeni (GAATG)n	665121	NR_001286	80157	Hs.47970:NM_025087:ENSG00000:CWH43	CWH43-C Cell wall protein-coding		
chr1-228.17.15533	1.307567	0.54903	2.381594	0.017238	0.303775	chr1	2.29E+08	2.29E+08	+	O NA	promoter-promoter-	-332	NR_02336E	1E+08	NR_02336E:ENSG00000:RNA5S3	RN5S3	RNA, 5S rRNA	
chr13-17.44.97342	0.817364	0.345641	2.36478	0.018041	0.315832	chr13	17938650	17939828	+	O NA	IntergeniALR/Alph	-256500	NR_02727E	26080	Hs.44858:NR_02727E:ENSG00000:FAM230C	LINC00281	family wincRNA	
chr17-26.74.36995	0.652367	0.276462	2.3597	0.01829	0.318098	chr17	26398434	26398681	+	O NA	IntergeniALR/Alph	690684	NR_135673	1.05E+08	Hs.64991:NR_135673	LOC105371-	uncharactncRNA	
chr3-924.30.38413	0.976656	0.417803	2.337598	0.019408	0.335357	chr3	92488771	92489132	+	O NA	IntergeniALR/Alph	1485130	NM_001314	5627	Hs.64016	NM_00031E:ENSG00000:PROS1	PROS PS21	protein iprotein-coding
chr20-31.43.71558	0.810873	0.348192	2.328812	0.019869	0.339873	chr20	31070737	31075918	+	O NA	Intergeni (GGAAT)n	-184337	NM_001037	245929	Hs.58079:NM_001037:ENSG00000:DEFB115	DEFB-15	defensin protein-coding	
chr20-31.45.23321	0.796001	0.342136	2.326563	0.019889	0.339873	chr20	31051831	31069353	+	O NA	Intergeni (GGAAT)n	-197072	NM_001037	245929	Hs.58079:NM_001037:ENSG00000:DEFB115	DEFB-15	defensin protein-coding	
chr22-10.18.70441	1.221582	0.529228	2.322717	0.020194	0.339873	chr22	10936435	10936654	+	O NA	IntergeniAluJ SIN	24985	NR_13232C	1.03E+08	NR_13232C	FRG1P	FSHD regipseudo	
chr10-41.27.70526	1.000464	0.430813	2.322272	0.020218	0.339873	chr10	41898644	41900563	+	O NA	Intergeni (AATGG)n	468442	NR_02438C	441666	Hs.25572:NR_02438C:ENSG00000:LOC441666-	-	zinc finpseuso	
chr3-918.49.22328	0.770781	0.332146	2.320607	0.020308	0.339873	chr3	91891250	91891551	+	O NA	IntergeniACRO1 Sat	2082681	NM_001314	5627	Hs.64016	NM_00031E:ENSG		

chr21-104	16.76324	1.078207	0.554932	1.942954	0.052022	0.595334	chr21	10422932	10423215	+	O NA	intron (AluSx)SIN	9541	NM_182481	85318	Hs.545788	NR_182481	BAGE3	CT2.3	BAGE famiprotein-coding
chr19-266	84.33193	0.505273	0.26039	1.940447	0.052325	0.595334	chr19	26504043	26504551	+	O NA	IntergeniALR/Alphe	-1289134	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000001	LOC101927	uncharacteractnRNA
chr4-4911	28.5187	0.817695	0.422057	1.937405	0.052696	0.595334	chr4	49114412	49115632	+	O NA	Intergeni(TCCAT)n	128380	NM_001286	80157	Hs.479703	NR_025087	ENSG00000	CWH43	CWH43-C fcell wallprotein-coding
chr5-477	60.71318	0.587494	0.303515	1.935649	0.052911	0.595334	chr5	47739713	47739935	+	O NA	IntergeniALR/Alphe	-2043444	NR_021072	348980	Hs.353176	NR_021072	ENSG00000	HCN1	BCNG-1 BChyperpolz:protein-coding
chr7-6051	58.72452	0.587991	0.303524	1.935667	0.052921	0.595334	chr7	60517707	60518137	+	O NA	IntergeniALR/Alphe	2786134	NR_003952	643955	Hs.583308	NR_003952	ENSG00000	ZNF733	ZNF733 zinc fingpseudo
chr22-121	18.2837	1.017188	0.525751	1.934734	0.053023	0.595334	chr22	12171044	12172316	+	O NA	IntergeniACRO1 Sat	274274	NR_110761	1.03E+08	Hs.652928	NR_110761	LOC102722	-	uncharacteractnRNA
chr10-418	42.05214	0.679138	0.352768	1.925169	0.054208	0.604519	chr10	41845595	41846536	+	O NA	IntergeniIntergeni	521980	NR_024388	441666	Hs.255729	NR_024388	ENSG00000	LOC441666	zinc fingpseudo
chr22-141	46.54383	0.652161	0.338878	1.924473	0.054295	0.604519	chr22	14170542	14170789	+	O NA	IntergeniALR/Alphe	-1357494	NM_001006	81061	Hs.554706	NR_001006	ENSG00000	OR11H12	OR11H12 colfactoryprotein-coding
chr19-248	98.23847	0.476154	0.247825	1.921329	0.05469	0.606378	chr19	24891532	24891790	+	O NA	IntergeniALR/Alphe	-728214	NR_003605	1E+08	Hs.149312	NR_003605	ENSG00000	HAVCR1P1	hepatitispseudo
chr14-174	39.31538	0.710116	0.370666	1.915787	0.055392	0.610014	chr14	17498868	17499418	+	O NA	IntergeniALR/Alphe	-1101974	NM_001013	440153	Hs.534888	NR_001013	ENSG00000	OR11H12	olfactoryprotein-coding
chr19-266	82.87833	0.506051	0.264528	1.913037	0.055743	0.610014	chr19	26951168	26951399	+	O NA	IntergeniALR/Alphe	-842148	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000	LOC101927	uncharacteractnRNA
chr4-4932	50.17052	0.622166	0.325628	1.910665	0.056048	0.610014	chr4	49321369	49321614	+	O NA	IntergeniIntergeni	334849	NM_001286	80157	Hs.479703	NR_025087	ENSG00000	CWH43	CWH43-C fcell wallprotein-coding
chr12-351	30.9563	0.798962	0.41834	1.909842	0.056154	0.610014	chr12	35133494	35133761	+	O NA	IntergeniALR/Alphe	1111131	NM_032834	84920	Hs.102971	NR_032834	ENSG00000	ALG10	ALG10 DIALG10 al protein-coding
chr5-488	118.9689	0.45212	0.236809	1.909221	0.056234	0.610014	chr5	48860477	48860835	+	O NA	IntergeniALR/Alphe	1580632	NR_198444	133418	Hs.561411	NR_198444	ENSG00000	EMB	GP70 embigin protein-coding
chr4-496	21.74098	0.917308	0.480774	1.907981	0.056394	0.610014	chr4	49647424	49648793	+	O NA	Intergeni(GAATG)n	661466	NM_001286	80157	Hs.479703	NR_025087	ENSG00000	CWH43	CWH43-C fcell wallprotein-coding
chr3-908	26.6054	0.842639	0.444363	1.896285	0.057922	0.615386	chr3	90835879	90836119	+	O NA	IntergeniALR/Alphe	1728378	NR_005233	2042	Hs.123642	NR_005233	ENSG00000	EPH43	EK4 ETK EHPH recep protein-coding
chr19-266	117.1375	0.454218	0.239806	1.894107	0.058211	0.615386	chr19	26353442	26353692	+	O NA	IntergeniALR/Alphe	-1439864	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000	LOC101927	uncharacteractnRNA
chrY-1116	16.41913	0.501099	0.554467	1.89407	0.058216	0.615386	chrY	11194869	11195237	+	O NA	IntergeniAluSx1 S1	125637	NR_033667	352887	Hs.546221	NR_033667	ENSG00000	GYG2P1	GYG2P glycoenipseudo
chr21-104	16.45001	1.046008	0.552295	1.893929	0.058234	0.615386	chr21	10425419	10425988	+	O NA	intron (L1MC5)LIN	12171	NM_182481	85318	Hs.545788	NR_182481	BAGE3	CT2.3	BAGE famiprotein-coding
chr13-167	46.25581	0.637558	0.337049	1.891587	0.058546	0.615386	chr13	16776587	16777463	+	O NA	IntergeniALR/Alphe	-1418272	NR_027278	26080	Hs.448588	NR_027278	ENSG00000	FAM230C	LINC00281family wincRNA
chr22-141	46.48032	1.041811	0.552529	1.885532	0.059358	0.615386	chr22	14150454	14150762	+	O NA	IntergeniALR/Alphe	-1377551	NM_001006	81061	Hs.554706	NR_001006	ENSG00000	OR11H1	OR11H12 colfactoryprotein-coding
chr10-418	25.71405	0.836114	0.444207	1.882263	0.0598	0.615386	chr10	41857801	41861974	+	O NA	Intergeni(ATGGA)n	508158	NR_024388	441666	Hs.255729	NR_024388	ENSG00000	LOC441666	zinc fingpseudo
chr19-256	96.02468	0.465831	0.247576	1.881569	0.059895	0.615386	chr19	25050249	25051413	+	O NA	IntergeniALR/Alphe	-887384	NR_003605	1E+08	Hs.149312	NR_003605	ENSG00000	HAVCR1P1	hepatitispseudo
chr14-166	26.23211	0.826304	0.43931	1.880913	0.059984	0.615386	chr14	16982305	16982973	+	O NA	IntergeniALR/Alphe	-1618478	NR_001013	440153	Hs.534888	NR_001013	ENSG00000	OR11H12	olfactoryprotein-coding
chr10-395	89.90884	0.476016	0.253197	1.880024	0.060105	0.615386	chr10	39986335	39987416	+	O NA	IntergeniALR/Alphe	1290279	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr11-526	52.82625	0.598962	0.318615	1.879894	0.060123	0.615386	chr11	52690099	52690350	+	O NA	IntergeniALR/Alphe	1913774	NM_001004	119749	Hs.553564	NR_001004	ENSG00000	ORC46	olfactoryprotein-coding
chr4-4932	36.18192	0.708844	0.377369	1.878383	0.060329	0.615386	chr4	49328916	49329125	+	O NA	IntergeniACRO1 Sat	343778	NR_001286	80157	Hs.479703	NR_025087	ENSG00000	CWH43	CWH43-C fcell wallprotein-coding
chr13-184	47.70007	0.63952	0.341281	1.873881	0.060947	0.615386	chr13	18002268	18002665	+	O NA	IntergeniALR/Alphe	-192831	NR_027278	26080	Hs.448588	NR_027278	ENSG00000	FAM230C	LINC00281family wincRNA
chr13-167	38.76314	0.684148	0.365263	1.87303	0.061064	0.615386	chr13	16723999	16724328	+	O NA	IntergeniALR/Alphe	-1471134	NR_027278	26080	Hs.448588	NR_027278	ENSG00000	FAM230C	LINC00281family wincRNA
chr1-1241	134.787	0.405227	0.216534	1.871423	0.061286	0.615386	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2604874	NR_003952	647121	Hs.697682	NR_003952	ENSG00000	EMB1P	embigin ipseudo
chr17-266	283.6617	0.319534	0.171143	1.867059	0.061893	0.615386	chr17	26041053	26041344	+	O NA	IntergeniALR/Alphe	1048043	NR_135673	1.05E+08	Hs.649918	NR_135673	LOC105371	-	uncharacteractnRNA
chr4-4926	35.27329	0.712285	0.3816	1.866576	0.061961	0.615386	chr4	49286403	49287435	+	O NA	IntergeniIntergeni	300277	NM_001286	80157	Hs.479703	NR_025087	ENSG00000	CWH43	CWH43-C fcell wallprotein-coding
chr19-266	60.05527	0.567497	0.304305	1.864893	0.062196	0.615386	chr19	26041039	26041446	+	O NA	IntergeniALR/Alphe	-1752189	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000	LOC101927	uncharacteractnRNA
chr1-1245	70.37648	0.525019	0.28166	1.864018	0.062319	0.615386	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	2995394	NR_003952	647121	Hs.697682	NR_003952	ENSG00000	EMB1P	embigin ipseudo
chr20-27	29.26736	0.778767	0.417812	1.863916	0.062334	0.615386	chr20	27331621	27331920	+	O NA	IntergeniALR/Alphe	-1225237	NR_040099	284801	Hs.370699	NR_040099	ENSG00000	MIR663AHC	MIR663A lncRNA
chr4-4928	18.39135	0.979391	0.525479	1.863805	0.062349	0.615386	chr4	49280388	49281356	+	O NA	IntergeniIntergeni	294230	NM_001286	80157	Hs.479703	NR_025087	ENSG00000	CWH43	CWH43-C fcell wallprotein-coding
chr4-5047	33.75452	0.727517	0.390776	1.861725	0.062642	0.615386	chr4	50472300	50472601	+	O NA	IntergeniALR/Alphe	-1370550	NM_001286	23142	Hs.605388	NR_015111	ENSG00000	CUN1D4	defectiveprotein-coding
chr22-13	17.99908	0.983201	0.528429	1.86061	0.062799	0.615386	chr22	13386009	13386357	+	O NA	IntergeniALR/Alphe	1488774	NR_110761	1.03E+08	Hs.652928	NR_110761	LOC102722	-	uncharacteractnRNA
chr10-418	18.93746	0.957767	0.514902	1.860093	0.062872	0.615386	chr10	41885191	41894312	+	O NA	Intergeni(AATGG)n	478274	NR_024388	441666	Hs.255729	NR_024388	ENSG00000	LOC441666	zinc fingpseudo
chr9-447	41.24719	0.667098	0.358721	1.859656	0.062934	0.615386	chr9	44763950	44764446	+	O NA	IntergeniALR/Alphe	1683032	NR_160669	1.03E+08	NR_160669	LOC102722	-	methylencpseudo	
chr20-271	28.78245	0.78445	0.422064	1.858603	0.063083	0.615386	chr20	27143667	27143950	+	O NA	IntergeniALR/Alphe	-934575	NR_040099	284801	Hs.370699	NR_040099	ENSG00000	MIR663AHC	MIR663A lncRNA
chr9-4351	30.29725	0.763521	0.410883	1.858245	0.063134	0.615386	chr9	43511966	43512232	+	O NA	IntergeniALR/Alphe	385933	NR_160669	1.03E+08	NR_160669	LOC102722	-	methylencpseudo	
chr6-5956	224.5186	0.337934	0.182094	1.855818	0.06348	0.616493	chr6	59566187	59566483	+	O NA	IntergeniALR/Alphe	-1604889	NR_132994	1.07E+08	Hs.561538	NR_132994	ENSG00000	LINC00688	long intencnRNA
chr19-27	234.3819	0.329149	0.17857	1.843247	0.065293	0.62737	chr19	27022720	27022981	+	O NA	IntergeniALR/Alphe	-770581	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000	LOC101927	uncharacteractnRNA
chr5-484	59.66073	0.564903	0.306556	1.842737	0.065367	0.62737	chr5	48441498	48441938	+	O NA	IntergeniALR/Alphe	1999570	NR_198444	133418	Hs.561411	NR_198444	ENSG00000	EMB	GP70 embigin protein-coding
chr20-26	177.0331	0.384663	0.208811	1.842163	0.065451	0.62737	chr20	16823810	16824208	+	O NA	IntergeniALR/Alphe	-2634810	NR_040099	284801	Hs.370699	NR_040099	ENSG00000	MIR663AHC	MIR663A lncRNA
chr19-248	54.05869	0.580129	0.3151	1.841092	0.065608	0.62737	chr19	24892787	24893284	+	O NA	IntergeniALR/Alphe	-729588	NR_003605	1E+08	Hs.149312	NR_003605	ENSG00000	HAVCR1P1	hepatitispseudo
chr10-418	20.48654	0.909965	0.494715	1.839374	0.06586	0.62737	chr10	41875315	41877971	+	O NA	Intergeni(ATGGA)n	491402	NR_024388	441666	Hs.255729	NR_024388	ENSG00000	LOC441666	zinc fingpseudo
chr14-174	54.15246	0.576515	0.313608	1.838328	0.066014	0.62737	chr14	17864984	17865312	+	O NA	IntergeniALR/Alphe	-735969	NM_001013	440153	Hs.534888	NR_001013	ENSG00000	OR11H12	olfactoryprotein-coding
chr14-17	20.97031	0.898708	0.490011	1.834056	0.066646	0.631118	chr14	17597225	17597434	+	O NA	IntergeniALR/Alphe	-1003788	NM_001013	440153	Hs.534888	NR_001013	ENSG00000	OR11H12	olfactoryprotein-coding
chr8-857	20.03194	0.918304	0.502401</																	



chr9-605	43.74276	0.571093	0.346463	1.64835	0.099281	0.7392	chr9	60591243	60591519	+	O	NA	IntergeniALR/Alphe	-323026	NM_015667	26165	Hs.123004	NM_015667	ENSG00000	SPATA31A7	AEP1 C9orSPATA31	sprotein-coding
chr19-271	143.7219	0.347222	0.211217	1.64391	0.100195	0.7392	chr19	27130498	27130730	+	O	NA	IntergeniALR/Alphe	-662817	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000	LOC101927	-	uncharactncRNA
chr19-254	102.1126	0.395	0.240319	1.643651	0.100248	0.7392	chr19	25439308	25439602	+	O	NA	IntergeniALR/Alphe	-1276008	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1	-	hepatitispseudo
chr5-474	76.84643	0.403405	0.24547	1.643397	0.100301	0.7392	chr5	47450737	47451920	+	O	NA	IntergeniALR/Alphe	-1754948	NM_021072	348980	Hs.353176	NM_021072	ENSG00000	HCN1	BCNG-1 BChyperpolz	protein-coding
chr1-1237	73.268666	0.453806	0.276801	1.63954	0.101101	0.7392	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2271276	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBP1	-	embigin ipseudo
chr4-494	27.53462	0.712474	0.434725	1.638909	0.101232	0.7392	chr4	49496052	49496304	+	O	NA	IntergeniMER4E1 L1	509536	NM_001286	80157	Hs.479703	NM_025087	ENSG00000	CWH43	CWH43-C fcell wall	protein-coding
chr1-124	45.8997	0.55637	0.339709	1.637783	0.101467	0.7392	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2488381	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBP1	-	embigin ipseudo
chr18-465	17.56894	0.871394	0.532258	1.637165	0.101596	0.7392	chr18	46967060	46969706	+	O	NA	intron (Nintron (N	-3739	NM_001242	1.01E+08	Hs.729822	NM_001242	ENSG00000	ELOA3D	ELOA3L2 telongin /	protein-coding
chr20-273	30.10054	0.669611	0.409688	1.634441	0.102166	0.7392	chr20	27358634	27360558	+	O	NA	IntergeniALR/Alphe	-1150363	NR_040095	284801	Hs.370695	NR_040095	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr1-2652	18.08473	0.855699	0.524001	1.633525	0.102359	0.7392	chr1	2652145	2661704	+	O	NA	intron (Nintron (N	6625145	NM_033467	79258	Hs.591455	NM_033467	ENSG00000	MMEL1	MMEL2 NEI	membrane protein-coding
chr10-395	41.79858	0.576265	0.353021	1.632382	0.102599	0.7392	chr10	39951235	39951549	+	O	NA	IntergeniALR/Alphe	1254796	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chrY-568	18.53989	0.848643	0.520722	1.629742	0.103156	0.7392	chrY	56860336	56861667	+	O	NA	IntergeniLIMEd LIN	-93254	NM_005840	10251	Hs.381912	NM_005840	ENSG00000	SPRY3	spry-3	sprouty fprotein-coding
chr7-600	18.60052	0.841426	0.516668	1.628526	0.103413	0.7392	chr7	60006223	60006422	+	O	NA	IntergeniALR/Alphe	2556141	NM_001155	441234	Hs.533121	NM_001155	ENSG00000	ZNF716	-	zinc fingprotein-coding
chr13-173	39.25107	0.590283	0.362698	1.627478	0.103636	0.7392	chr13	17540080	17540432	+	O	NA	IntergeniALR/Alphe	-655041	NR_027278	26080	Hs.448583	NR_027278	ENSG00000	FAM230C	LINC00281	family wincRNA
chr22-14	26.09546	0.712189	0.438347	1.624716	0.104223	0.7392	chr22	14386492	14386889	+	O	NA	IntergeniALR/Alphe	-1141469	NM_001005	81061	Hs.554706	NM_001005	ENSG00000	OR11H1	OR11H12 Colfactory	protein-coding
chr20-28	51.04685	0.528839	0.325506	1.624666	0.104234	0.7392	chr20	28022764	28023102	+	O	NA	IntergeniALR/Alphe	579732	NR_132315	1E+08	Hs.529357	NR_132315	ENSG00000	FRG1CP	-	FSHD regipseudo
chr4-491	19.60179	0.818032	0.503517	1.624635	0.10424	0.7392	chr4	49135908	49137297	+	O	NA	Intergeni (TCCAT)n	149960	NM_001286	80157	Hs.479703	NM_025087	ENSG00000	CWH43	CWH43-C fcell wall	protein-coding
chr21-123	22.57529	0.763592	0.470238	1.623841	0.10441	0.7392	chr21	12345729	12346095	+	O	NA	IntergeniALR/Alphe	-1294254	NR_026915	149992	Hs.558645	NM_153773	ANKRD30BF	C2lorf99	ankyrin ipseudo	
chr2-898	21.08911	0.788845	0.485811	1.623769	0.104425	0.7392	chr2	89840280	89841172	+	O	NA	Intergeni (TGAA)n	-202819	NR_136325	1.02E+08	Hs.578075	NR_136329	LOC101927	-	lysine mpseudo	
chr13-174	18.63253	0.837994	0.516436	1.622647	0.104665	0.7392	chr13	17445426	17445630	+	O	NA	IntergeniALR/Alphe	-749769	NR_027278	26080	Hs.448583	NR_027278	ENSG00000	FAM230C	LINC00281	family wincRNA
chr21-911	20.11815	0.805644	0.49688	1.621406	0.104931	0.7392	chr21	9111941	9112227	+	O	NA	intron (Nintron (N	9111941	NR_112227	1E+08	Hs.487562	NR_174945	ENSG00000	TEKT4P2	MAFIPL Ti	tektin 4 pseudo
chr22-145	22.08924	0.770582	0.475572	1.620328	0.105162	0.7392	chr22	14984244	14984602	+	O	NA	IntergeniALR/Alphe	-543736	NM_001005	81061	Hs.554706	NM_001005	ENSG00000	OR11H1	OR11H12 Colfactory	protein-coding
chr21-91	24.48462	0.741182	0.457783	1.619069	0.105432	0.7392	chr21	9103646	9104009	+	O	NA	intron (NAluSp SIN	25934	NR_038325	1E+08	Hs.487562	NR_174945	ENSG00000	TEKT4P2	MAFIPL Ti	tektin 4 pseudo
chrY-568	23.51367	0.752236	0.465331	1.618713	0.105509	0.7392	chrY	56843600	56843916	+	O	NA	IntergeniBSR/Betal	-110497	NR_005846	10251	Hs.381912	NM_005840	ENSG00000	SPRY3	spry-3	sprouty fprotein-coding
chr8-857	22.40984	0.797078	0.492617	1.618047	0.105653	0.7392	chr8	85755559	85755809	+	O	NA	IntergeniIntergeni	8215	NR_003594	1E+08	Hs.535055	NR_003594	REX01L2P	-	REX01 li pseudo	
chr21-11	19.11858	0.82784	0.511788	1.617545	0.105761	0.7392	chr21	11334788	11335032	+	O	NA	IntergeniALR/Alphe	813396	NM_199265	7179	Hs.122985	NM_199255	ENSG00000	TPTE	CT44 PTE	transmem protein-coding
chr9-438	21.12055	0.785085	0.485982	1.616942	0.105891	0.7392	chr9	43822664	43822942	+	O	NA	IntergeniALR/Alphe	696637	NR_160669	1.03E+08	Hs.578075	NR_160669	LOC102722	-	methylencpseudo	
chr20-265	28.15919	0.68474	0.423712	1.616048	0.106084	0.7392	chr20	26964000	26964259	+	O	NA	IntergeniALR/Alphe	-754896	NR_040095	284801	Hs.370695	NR_040095	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr12-366	22.54271	0.766442	0.474643	1.614774	0.10636	0.7392	chr12	36678775	36679051	+	O	NA	IntergeniALR/Alphe	-1637861	NM_001011	144245	Hs.529357	NM_001011	ENSG00000	ALG10B	ALG10 KCF	ALG10 al protein-coding
chr5-478	23.63832	0.742216	0.459846	1.614054	0.106516	0.7392	chr5	47896458	47896774	+	O	NA	IntergeniALR/Alphe	-2200236	NM_021072	348980	Hs.353176	NM_021072	ENSG00000	HCN1	BCNG-1 BChyperpolz	protein-coding
chr9-440	18.66341	0.834461	0.517309	1.61308	0.106727	0.7392	chr9	44090804	44091068	+	O	NA	IntergeniALR/Alphe	964770	NR_160669	1.03E+08	Hs.578075	NR_160669	LOC102722	-	methylencpseudo	
chr6-589	24.61041	0.730591	0.453203	1.612058	0.106949	0.7392	chr6	58952907	58953357	+	O	NA	IntergeniALR/Alphe	-991686	NR_132994	1.07E+08	Hs.561535	NR_125727	ENSG00000	LINC0068C	-	long intencRNA
chr1-122	20.11645	0.805517	0.501202	1.607169	0.108017	0.7392	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alphe	994688	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBP1	-	embigin ipseudo
chr9-440	21.66779	0.772043	0.48204	1.601616	0.109241	0.749818	chr9	44064256	44064538	+	O	NA	IntergeniALR/Alphe	938231	NR_160669	1.03E+08	Hs.578075	NR_160669	LOC102722	-	methylencpseudo	
chr20-27	35.82411	0.604884	0.377767	1.601208	0.109331	0.749818	chr20	27054289	27055659	+	O	NA	IntergeniALR/Alphe	-845741	NR_040095	284801	Hs.370695	NR_040095	ENSG00000	MIR663AHC	-	MIR663A lncRNA
chr19-25	71.9822	0.444734	0.278143	1.598943	0.109833	0.751328	chr19	25580581	25583614	+	O	NA	IntergeniALR/Alphe	-1418650	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1	-	hepatitispseudo
chr10-41	33.17064	0.606667	0.406246	1.577041	0.114786	0.75244	chr10	41847792	41848783	+	O	NA	IntergeniIntergeni	519758	NR_02438C	441666	Hs.255725	NR_02438C	ENSG00000	LOC441666	-	zinc fingpseudo
chr19-267	70.51075	0.448755	0.281598	1.593599	0.111026	0.7556	chr19	26714344	26715330	+	O	NA	IntergeniALR/Alphe	-1078594	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000	LOC101927	-	uncharactncRNA
chr19-247	42.00227	0.55869	0.351755	1.589107	0.112036	0.757244	chr19	24742808	24743088	+	O	NA	IntergeniALR/Alphe	-579501	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1	-	hepatitispseudo
chr13-17	32.30337	0.628611	0.396167	1.586732	0.112573	0.757244	chr13	17304358	17305636	+	O	NA	IntergeniALR/Alphe	-890300	NR_027278	26080	Hs.448583	NR_027278	ENSG00000	FAM230C	LINC00281	family wincRNA
chr9-606	37.91702	0.588551	0.371469	1.584389	0.113105	0.757244	chr9	60625747	60625977	+	O	NA	IntergeniALR/Alphe	-288545	NM_015667	26165	Hs.123004	NM_015667	ENSG00000	SPATA31A7	AEP1 C9orSPATA31	sprotein-coding
chr6-591	87.79137	0.408173	0.257953	1.582357	0.113568	0.757244	chr6	59183848	59184095	+	O	NA	IntergeniALR/Alphe	-1222525	NR_132994	1.07E+08	Hs.561535	NR_125727	ENSG00000	LINC0068C	-	long intencRNA
chr22-13	16.17823	0.902932	0.571138	1.580935	0.113893	0.757244	chr22	13589588	13589814	+	O	NA	IntergeniALR/Alphe	1691295	NR_110761	1.03E+08	Hs.652925	NR_110761	LOC102722	-	uncharactncRNA	
chr5-495	142.726	0.349873	0.22143	1.580058	0.114094	0.757244	chr5	49530989	49531244	+	O	NA	IntergeniALR/Alphe	910172	NM_198445	133418	Hs.561411	NM_198445	ENSG00000	EMB	GP70	embigin protein-coding
chr22-15	33.88276	0.613501	0.388499	1.579156	0.1143	0.757244	chr22	15021997	15022198	+	O	NA	IntergeniALR/Alphe	-506620	NM_001005	81061	Hs.554706	NM_001005	ENSG00000	OR11H1	OR11H12 Colfactory	protein-coding
chr10-41	33.17064	0.606667	0.406246	1.577041	0.114786	0.757244	chr10	41847792	41848783	+	O	NA	IntergeniALR/Alphe	865073	NR_02438C	441666	Hs.255725	NR_02438C	ENSG00000	LOC441666	-	zinc fingpseudo
chr5-486	28.2371	0.666385	0.423952	1.571839	0.115988	0.757244	chr5	48617235	48617471	+	O	NA	IntergeniALR/Alphe	1823935	NM_198445	133418	Hs.561411	NM_198445	ENSG00000	EMB	GP70	embigin protein-coding
chr21-11	36.2059	0.618238	0.393478	1.571215	0.116133	0.757244	chr21	11893646	11894061	+	O	NA	IntergeniALR/Alphe	-1144313	NR_026915	149992	Hs.558645	NM_153773	ANKRD30BF	C2lorf99	ankyrin ipseudo	
chr1-1237	73.268666	0.453806	0.276801	1.569053	0.116636	0.757244	chr1	1.24E														

chr21-127	19.03425	0.751012	0.509568	1.47382	0.14053	0.757244	chr21	12720190	12720564	+	O	NA	IntergeniALR/Alpha	-317789	NR_026916	149992	Hs.55864	NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo
chr2-898	18.03184	0.771054	0.523186	1.473767	0.140544	0.757244	chr2	89838074	89838780	+	O	NA	Intergeni(TGGAA)n	-200520	NR_136325	1.02E+08	Hs.57807	NR_136329	LOC101927-		lysine mepseudo
chr21-937	18.03184	0.771054	0.523186	1.473767	0.140544	0.757244	chr21	9371316	9376764	+	O	NA	IntergeniIntergeni	-168990	NR_135512	1.05E+08	Hs.46232	NR_135512	LOC10537-		nuclear ipseudo
chr18-156	19.03312	0.75093	0.509545	1.473725	0.140556	0.757244	chr18	15693226	15693642	+	O	NA	IntergeniALR/Alpha	-367515	NR_027417	644669	Hs.57947	NR_027417	ENSG000001064466	-	ankyrin ipseudo
chr1-123	78.63102	0.393105	0.266792	1.473452	0.140629	0.757244	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alpha	1539418	NR_003955	647121	Hs.69768	NR_003955	ENSG00000006BP1	-	embigin ipseudo
chr13-17	20.55074	0.722987	0.490677	1.473449	0.14063	0.757244	chr13	17078992	17080614	+	O	NA	IntergeniALR/Alpha	-1115494	NR_027278	26080	Hs.44858	NR_027278	ENSG0000000FAM230C	LINC00281	family wincRNA
chr9-435	18.54877	0.759045	0.515677	1.471938	0.141038	0.757244	chr9	43531157	43531544	+	O	NA	IntergeniALR/Alpha	405184	NR_160669	1.03E+08	Hs.160669	NR_160669	LOC10272-		methylenepseudo
chr12-36	18.5482	0.759003	0.515666	1.471889	0.141051	0.757244	chr12	36011114	36011441	+	O	NA	IntergeniALR/Alpha	1988781	NM_032834	84920	Hs.102971	NM_032834	ENSG00000000ALG10	ALG10A	DJALG10 alprotein-coding
chr8-857	18.5482	0.759003	0.515666	1.471889	0.141051	0.757244	chr8	85770281	85771253	+	O	NA	IntergeniMIR[SINE]	5326	NR_003594	1E+08	Hs.53505	NR_003594	REX01L2P	-	REX01 lipseudo
chr5-488	64.89975	0.431701	0.293565	1.470549	0.141413	0.757244	chr5	48866114	48868361	+	O	NA	IntergeniALR/Alpha	1555058	NM_198445	133418	Hs.56141	NM_198445	ENSG00000000EMB	GP70	embigin protein-coding
chr7-5971	19.55061	0.740124	0.503459	1.47008	0.14154	0.757244	chr7	59718357	59718614	+	O	NA	IntergeniALR/Alpha	2268308	NM_001155	441234	Hs.533121	NM_001155	ENSG00000000ZNF716	-	zinc finprotein-coding
chr7-5806	18.54764	0.75896	0.51648	1.469486	0.141701	0.757244	chr7	58067473	58067937	+	O	NA	Intergeni(CCATT)n	617528	NM_001155	441234	Hs.533121	NM_001155	ENSG00000000ZNF716	-	zinc finprotein-coding
chr16-37	20.00577	0.736273	0.501116	1.469268	0.14176	0.757244	chr16	37073734	37074079	+	O	NA	IntergeniALR/Alpha	1327354	NR_033988	400533	Hs.49913	NR_033988	ENSG00000000LINC02167-		long intncRNA
chr20-27	18.06329	0.767538	0.522494	1.46899	0.141835	0.757244	chr20	27220069	27220666	+	O	NA	IntergeniALR/Alpha	-1011134	NR_040095	284801	Hs.37069	NR_040095	ENSG00000000MIR663AH(-)		MIR663A lncRNA
chr21-91	18.06272	0.767492	0.52291	1.467733	0.142177	0.757244	chr21	9109338	9111375	+	O	NA	intron(MLIMB2)LIN	19405	NR_038328	1E+08	Hs.48756	NR_17494	ENSG00000000TEK4P2	MAF1P Tfektin	4 pseudo
chr13-18	19.06513	0.747646	0.509391	1.467726	0.142179	0.757244	chr13	18014970	18016079	+	O	NA	IntergeniALR/Alpha	-179773	NR_027278	26080	Hs.44858	NR_027278	ENSG00000000FAM230C	LINC00281	family wincRNA
chr10-41	117.0736	0.337903	0.230241	1.467606	0.142211	0.757244	chr10	41265303	41265743	+	O	NA	IntergeniALR/Alpha	1102522	NR_02438C	441666	Hs.25572	NR_02438C	ENSG00000000LOC441666-		zinc finpseudo
chr21-112	44.4935	0.513717	0.350188	1.466974	0.142383	0.757244	chr21	11256410	11256611	+	O	NA	IntergeniALR/Alpha	734996	NM_19926C	7179	Hs.12298	NM_199265	ENSG00000000TPTE	CT44 PTE	transmem protein-coding
chr21-128	64.45138	0.430616	0.293552	1.466917	0.142399	0.757244	chr21	12866804	12867093	+	O	NA	IntergeniALR/Alpha	-171218	NR_026916	149992	Hs.55864	NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo
chr13-17	19.48998	0.746879	0.509712	1.465296	0.14284	0.757244	chr13	17225374	17225596	+	O	NA	IntergeniALR/Alpha	-969812	NR_027278	26080	Hs.44858	NR_027278	ENSG00000000FAM230C	LINC00281	family wincRNA
chr22-107	19.03538	0.751106	0.512798	1.464719	0.142998	0.757244	chr22	10738014	10739061	+	O	NA	IntergeniIntergeni	222992	NR_13232C	1.03E+08	NR_132320	FRG1FP	-	FSHD regipseudo	
chr9-436	19.58035	0.736768	0.503039	1.464635	0.143021	0.757244	chr9	43620852	43621538	+	O	NA	IntergeniALR/Alpha	495029	NR_160669	1.03E+08	NR_160669	LOC10272-		methylenepseudo	
chr5-491	93.48197	0.363267	0.248597	1.462717	0.143545	0.757244	chr5	49103386	49103688	+	O	NA	IntergeniALR/Alpha	1337751	NM_198445	133418	Hs.56141	NM_198445	ENSG00000000EMB	GP70	embigin protein-coding
chr4-496	17.57725	0.77647	0.530973	1.462353	0.143645	0.757244	chr4	49637329	49638324	+	O	NA	Intergeni(GAATC)n	651184	NM_00128C	80157	Hs.47970	NM_025087	ENSG00000000CWH43	CWH43-C	cell wallprotein-coding
chr22-141	33.31521	0.57287	0.391972	1.46151	0.143876	0.757244	chr22	14122680	14122926	+	O	NA	IntergeniALR/Alpha	-1405356	NM_001005	81061	Hs.55470	NM_001005	ENSG00000000OR11H1	OR11H12	Colfactoryprotein-coding
chr13-17	20.09728	0.72655	0.497802	1.459517	0.144423	0.757244	chr13	17257731	17258693	+	O	NA	IntergeniALR/Alpha	-937085	NR_027278	26080	Hs.44858	NR_027278	ENSG00000000FAM230C	LINC00281	family wincRNA
chr5-484	21.61377	0.701591	0.481319	1.457644	0.144939	0.757244	chr5	48495931	48496277	+	O	NA	IntergeniALR/Alpha	1945184	NM_198445	133418	Hs.56141	NM_198445	ENSG00000000EMB	GP70	embigin protein-coding
chr13-17	29.18661	0.605834	0.416907	1.453163	0.146179	0.757244	chr13	17927302	17928704	+	O	NA	IntergeniALR/Alpha	-267294	NR_027278	26080	Hs.44858	NR_027278	ENSG00000000FAM230C	LINC00281	family wincRNA
chr19-24	95.56072	0.339969	0.247747	1.452699	0.146232	0.757244	chr19	24894134	24895743	+	O	NA	IntergeniALR/Alpha	-731491	NR_00360C	1E+08	Hs.14931	NR_00360C	ENSG00000000HAVCR1P1	-	hepatitispseudo
chr21-12	29.15573	0.608405	0.418486	1.452965	0.146234	0.757244	chr21	12204650	12204916	+	O	NA	IntergeniALR/Alpha	-833083	NR_026916	149992	Hs.55864	NM_153773	ANKRD30BF	C21orf99	ankyrin ipseudo
chr1-1231	50.81076	0.475435	0.327547	1.4515	0.146641	0.757244	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alpha	1599527	NR_003955	647121	Hs.69768	NR_003955	ENSG00000000EMBP1	-	embigin ipseudo
chr20-27	53.56203	0.456769	0.314762	1.451156	0.146736	0.757244	chr20	27860019	27860492	+	O	NA	IntergeniALR/Alpha	742410	NR_13231E	1E+08	Hs.529357	NR_13231E	ENSG00000000FRG1CP	-	FSHD regipseudo
chr14-17	44.72807	0.496256	0.342559	1.448672	0.147429	0.757244	chr14	17295841	17296551	+	O	NA	IntergeniALR/Alpha	-1304921	NM_00101E	440153	Hs.53488	NM_00101E	ENSG00000000OR11H12	-	olfactoryprotein-coding
chr14-16	36.39693	0.544988	0.376664	1.446881	0.14793	0.757244	chr14	16608047	16609255	+	O	NA	IntergeniALR/Alpha	-1992466	NM_00101E	440153	Hs.53488	NM_00101E	ENSG00000000OR11H12	-	olfactoryprotein-coding
chr5-475	144.0885	0.305292	0.211098	1.44621	0.148118	0.757244	chr5	47547411	47547703	+	O	NA	IntergeniALR/Alpha	-1851177	NM_02107E	348980	Hs.35317	NM_02107E	ENSG00000000HCN1	BCNG-1 B	hyperpolprotein-coding
chr13-16	35.9412	0.544334	0.376641	1.445233	0.148392	0.757244	chr13	16485696	16486990	+	O	NA	IntergeniALR/Alpha	-1708954	NR_027278	26080	Hs.44858	NR_027278	ENSG00000000FAM230C	LINC00281	family wincRNA
chr10-40	35.39453	0.549111	0.380228	1.444164	0.148693	0.757244	chr10	40898300	40898543	+	O	NA	IntergeniALR/Alpha	1649624	NR_02438C	441666	Hs.25572	NR_02438C	ENSG00000000LOC441666-		zinc finpseudo
chr14-17	22.12843	0.692899	0.479887	1.443881	0.148772	0.757244	chr14	17567673	17567908	+	O	NA	IntergeniALR/Alpha	-1033327	NM_00101E	440153	Hs.53488	NM_00101E	ENSG00000000OR11H12	-	olfactoryprotein-coding
chr10-40	27.73075	0.613773	0.425635	1.442015	0.149298	0.757244	chr10	40841572	40841831	+	O	NA	IntergeniALR/Alpha	1526344	NR_02438C	441666	Hs.25572	NR_02438C	ENSG00000000LOC441666-		zinc finpseudo
chr1-122	59.8951	0.434682	0.301461	1.441915	0.149326	0.757244	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alpha	1414776	NR_003955	647121	Hs.69768	NR_003955	ENSG00000000EMBP1	-	embigin ipseudo
chr21-89	39.58489	0.523963	0.36341	1.441799	0.149359	0.757244	chr21	8987032	8988408	+	O	NA	TTS(NR_C	103	NR_16210E	1.13E+08	NR_162105	MIR10396	-	microRNA ncRNA	
chr7-592	74.04838	0.39503	0.27424	1.440457	0.149738	0.757244	chr7	59251605	59251979	+	O	NA	IntergeniALR/Alpha	1801615	NM_001155	441234	Hs.533121	NM_001155	ENSG00000000ZNF716	-	zinc finprotein-coding
chr17-26	17.45769	0.792109	0.550405	1.439137	0.150112	0.757244	chr17	26292298	26292508	+	O	NA	IntergeniALR/Alpha	796838	NR_135673	1.05E+08	Hs.64991	NR_135673	LOC105371-		uncharactncRNA
chr20-27	29.309	0.597106	0.415081	1.438528	0.150284	0.757244	chr20	27056661	27056932	+	O	NA	IntergeniALR/Alpha	-847563	NR_04009E	284801	Hs.37069	NR_04009E	ENSG00000000MIR663AH(-)		MIR663A lncRNA
chr14-17	35.97321	0.542626	0.377517	1.437354	0.150617	0.757244	chr14	17241897	17242129	+	O	NA	IntergeniALR/Alpha	-1359104	NM_00101E	440153	Hs.53488	NM_00101E	ENSG00000000OR11H12	-	olfactoryprotein-coding
chr5-488	133.8833	0.313551	0.218163																		



chr5-494:241.5606	0.239695	0.177893	1.347406	0.177849	0.757244	chr5	49423219	49423479	+	O	NA	IntergeniALR/Alph	1017939	NM_198449	133418	Hs.561411NM_198449	ENSG00000CEMB	GP70	embigin protein-coding
chr3-909:22.95556	0.62574	0.464561	1.34695	0.177996	0.757244	chr3	90909548	90909775	+	O	NA	IntergeniALR/Alph	1802040	NM_005233	2042	Hs.123642NM_005233	ENSG00000EPH3	EK4 ETK EPEH	receptprotein-coding
chr20-26:30.65136	0.545934	0.406184	1.344057	0.17893	0.757244	chr20	26532693	26533669	+	O	NA	IntergeniALR/Alph	-323948	NR_040095	284801	Hs.370695NR_040095	ENSG00000MIR663AH	-	MIR663A lncRNA
chr20-27:30.64909	0.545827	0.40614	1.343937	0.178969	0.757244	chr20	27011712	27018467	+	O	NA	IntergeniALR/Alph	-808556	NR_040095	284801	Hs.370695NR_040095	ENSG00000MIR663AH	-	MIR663A lncRNA
chr22-14:50.38572	0.451123	0.325283	1.34072	0.180011	0.757244	chr22	14520915	14521648	+	O	NA	IntergeniALR/Alph	-1006878	NM_001005	81061	Hs.554706NM_001005	ENSG00000COR11H1	OR11H12 Co	factoryprotein-coding
chr17-26:134.959	0.289264	0.215957	1.339451	0.180424	0.757244	chr17	26299347	26299599	+	O	NA	IntergeniALR/Alph	789768	NR_135673	1.05E+08	Hs.649915NR_135673	LOC105371-	-	uncharactncRNA
chr13-17:21.95316	0.636207	0.475228	1.338741	0.180655	0.757244	chr13	17351160	17352977	+	O	NA	IntergeniALR/Alph	-843229	NR_027278	26080	Hs.448585NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr5-471:23.5011	0.616712	0.46085	1.338206	0.180829	0.757244	chr5	47140622	47140896	+	O	NA	IntergeniALR/Alph	-1444379	NM_021072	348980	Hs.353176NM_021072	ENSG00000HCN1	BCNG-1 B	hyperpolaprotein-coding
chr19-26:46.80408	0.454745	0.340036	1.337345	0.18111	0.757244	chr19	26412831	26413031	+	O	NA	IntergeniALR/Alph	-1380500	NR_110688	1.02E+08	Hs.567934NR_110688	ENSG00000LOC101927-	-	uncharactncRNA
chr21-92:36.95078	0.49667	0.37247	1.333448	0.182385	0.757244	chr21	9251644	9252502	+	O	NA	IntergeniLTR48B L1	-122312	NR_038322	1E+08	Hs.487562NM_174944	ENSG00000TEK4P2	MAFIPL Ti	tektin 4 pseudo
chr10-40:280.5197	0.226086	0.169844	1.331136	0.183144	0.757244	chr10	40593342	40593676	+	O	NA	IntergeniALR/Alph	1745336	NR_024388	441666	Hs.255729NR_024388	ENSG00000LOC441666-	-	zinc fing pseudo
chr21-127:28.64769	0.556299	0.418363	1.329707	0.183615	0.757244	chr21	12791891	12793296	+	O	NA	IntergeniALR/Alph	-245573	NR_026916	149992	Hs.558645NM_153773	ANKRD30B C2lorf99	ankyrin ipseudo	
chrY-112:19.95119	0.660533	0.496923	1.329248	0.183766	0.757244	chrY	11292237	11296471	+	O	NA	IntergeniIntergeni	1129236	NR_033667	352887	Hs.546221NR_033667	ENSG00000GYG2P1	GYG2P	glyconipseudo
chr14-18:20.34459	0.665176	0.500488	1.329055	0.18383	0.757244	chr14	18005410	18005786	+	O	NA	IntergeniALR/Alph	-595519	NM_001013	440153	Hs.534888NM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding
chr11-51:20.95133	0.647734	0.48746	1.328793	0.183916	0.757244	chr11	51575720	51576083	+	O	NA	IntergeniALR/Alph	1166754	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box pseudo
chr22-11:21.49913	0.637478	0.479836	1.328531	0.184003	0.757244	chr22	11879720	11881760	+	O	NA	IntergeniAluSz SIN	-16666	NR_110761	1.03E+08	Hs.652929NR_110761	LOC102722-	-	uncharactncRNA
chr14-16:40.03136	0.477538	0.359472	1.328443	0.184032	0.757244	chr14	16780201	16780853	+	O	NA	IntergeniALR/Alph	-1820590	NM_001013	440153	Hs.534888NM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding
chr5-491:18.9196	0.67803	0.511179	1.326404	0.184706	0.757244	chr5	49117832	49118132	+	O	NA	IntergeniALR/Alph	1323306	NM_198449	133418	Hs.561411NM_198449	ENSG00000EMB	GP70	embigin protein-coding
chr5-489:55.81078	0.412158	0.310931	1.325563	0.184984	0.757244	chr5	48949791	48951004	+	O	NA	IntergeniALR/Alph	1490891	NM_198449	133418	Hs.561411NM_198449	ENSG00000EMB	GP70	embigin protein-coding
chr17-25:390.304	0.205081	0.154765	1.325108	0.185135	0.757244	chr17	25383645	25383941	+	O	NA	IntergeniALR/Alph	1705448	NR_135673	1.05E+08	Hs.649915NR_135673	LOC105371-	-	uncharactncRNA
chr20-27:19.46571	0.665767	0.502939	1.323752	0.185586	0.757244	chr20	27389969	27392052	+	O	NA	IntergeniALR/Alph	-1181777	NR_040095	284801	Hs.370695NR_040095	ENSG00000MIR663AH	-	MIR663A lncRNA
chr20-27:18.43413	0.684014	0.516805	1.323545	0.185654	0.757244	chr20	27932993	27934425	+	O	NA	IntergeniALR/Alph	668956	NR_132313	1E+08	Hs.529357NR_132313	ENSG00000FRG1CP	-	FSHD regipseudo
chr4-18:27.6161	0.564388	0.426831	1.322275	0.186077	0.757244	chr4	18049613	18051023	+	O	NA	IntergeniALR/Alph	-550799	NM_001013	440153	Hs.534888NM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding
chr5-489:53.74422	0.41501	0.313901	1.322104	0.186134	0.757244	chr5	48905902	48906114	+	O	NA	IntergeniALR/Alph	1535280	NM_198449	133418	Hs.561411NM_198449	ENSG00000EMB	GP70	embigin protein-coding
chr19-251:40.63979	0.471133	0.356879	1.320149	0.186785	0.757244	chr19	25172111	25172622	+	O	NA	IntergeniALR/Alph	-1008919	NR_003603	1E+08	Hs.149312NR_003603	ENSG00000HAVCR1P1	-	hepatitispseudo
chr11-51:18.9808	0.671324	0.508812	1.319396	0.187037	0.757244	chr11	51925510	51926266	+	O	NA	IntergeniALR/Alph	1516741	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box pseudo
chr17-25:31.80476	0.531129	0.403033	1.317831	0.18756	0.757244	chr17	25125379	25125636	+	O	NA	IntergeniALR/Alph	1963734	NR_135673	1.05E+08	Hs.649915NR_135673	LOC105371-	-	uncharactncRNA
chr20-27:27.13006	0.566274	0.429707	1.317815	0.187565	0.757244	chr20	27539269	27542138	+	O	NA	IntergeniALR/Alph	1061962	NR_132313	1E+08	Hs.529357NR_132313	ENSG00000FRG1CP	-	FSHD regipseudo
chr13-17:22.56273	0.621034	0.471767	1.31616	0.18804	0.757244	chr13	17474907	17475145	+	O	NA	IntergeniALR/Alph	-720271	NR_027278	26080	Hs.448585NR_027278	ENSG00000FAM230C	LINC00281	family wincRNA
chr6-589:17.46374	0.697113	0.529677	1.31611	0.188137	0.757244	chr6	58971044	58972374	+	O	NA	IntergeniALR/Alph	-1010263	NR_132994	1.07E+08	Hs.561535NR_132994	ENSG00000LINC0068C-	-	long intncRNA
chr22-13:50.63219	0.426077	0.32374	1.316106	0.188138	0.757244	chr22	13863503	13863747	+	O	NA	IntergeniALR/Alph	-1664534	NM_001005	81061	Hs.554706NM_001005	ENSG00000COR11H1	OR11H12 Co	factoryprotein-coding
chr10-40:43.78383	0.452749	0.34402	1.316052	0.188157	0.757244	chr10	40440986	40442603	+	O	NA	IntergeniALR/Alph	1745198	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr14-17:16.94738	0.707963	0.537979	1.315969	0.188185	0.757244	chr14	17437690	17437968	+	O	NA	IntergeniALR/Alph	-1632888	NM_001013	440153	Hs.534888NM_001013	ENSG00000COR11H12	-	olfactoryprotein-coding
chr22-13:16.91763	0.711846	0.541186	1.315344	0.188394	0.757244	chr22	13323879	13324483	+	O	NA	IntergeniALR/Alph	1426775	NR_110761	1.03E+08	Hs.652929NR_110761	LOC102722-	-	uncharactncRNA
chr20-27:17.46317	0.69870	0.530125	1.314916	0.188538	0.757244	chr20	27483401	27487888	+	O	NA	IntergeniALR/Alph	1117021	NR_132313	1E+08	Hs.529357NR_132313	ENSG00000FRG1CP	-	FSHD regipseudo
chr11-51:61.70263	0.388839	0.295928	1.313967	0.188857	0.757244	chr11	51603412	51603668	+	O	NA	IntergeniALR/Alph	1194393	NR_024504	646813	Hs.684175NR_024504	LOC646813-	-	DEXH-box pseudo
chr9-435:21.49743	0.637321	0.485055	1.313914	0.188875	0.757244	chr9	43533738	43533951	+	O	NA	IntergeniALR/Alph	407678	NR_160669	1.03E+08	NR_160669	LOC102722-	-	methylencpseudo
chr21-12:18.43243	0.683939	0.520649	1.313626	0.188972	0.757244	chr21	12509690	12509914	+	O	NA	IntergeniALR/Alph	-528364	NR_026916	149992	Hs.558645NM_153773	ANKRD30B C2lorf99	ankyrin ipseudo	
chr20-27:16.4619	0.715645	0.545629	1.311594	0.189657	0.757244	chr20	27077221	27077420	+	O	NA	IntergeniALR/Alph	-868087	NR_040095	284801	Hs.370695NR_040095	ENSG00000MIR663AH	-	MIR663A lncRNA
chr9-438:28.49102	0.56771	0.433038	1.310993	0.18986	0.757244	chr9	43854864	43855287	+	O	NA	IntergeniALR/Alph	728909	NR_160669	1.03E+08	NR_160669	LOC102722-	-	methylencpseudo
chr19-25:19.52804	0.659338	0.503336	1.309936	0.190217	0.757244	chr19	25751514	25751720	+	O	NA	IntergeniALR/Alph	-1588170	NR_003603	1E+08	Hs.149312NR_003603	ENSG00000HAVCR1P1	-	hepatitispseudo
chr19-26:63.82699	0.385028	0.293947	1.309856	0.190244	0.757244	chr19	26049107	26049336	+	O	NA	IntergeniALR/Alph	-1744210	NR_110688	1.02E+08	Hs.567934NR_110688	ENSG00000LOC101927-	-	uncharactncRNA
chr4-936:18.49475	0.677092	0.517041	1.309554	0.190347	0.757244	chr4	9368109	9368938	+	O	NA	non-codir non-codir	649	NR_027278	391622	Hs.722655NR_027278	ENSG00000USP17L6P	DUB4 USP	ubiquitirpseudo
chr21-12:17.98123	0.686793	0.525005	1.308508	0.190701	0.757244	chr21	12883466	12884137	+	O	NA	IntergeniALR/Alph	-154365	NR_026916	149992	Hs.558645NM_153773	ANKRD30B C2lorf99	ankyrin ipseudo	
chr2-898:16.49278	0.711807	0.545224	1.305532	0.191712	0.757244	chr2	89832331	89833459	+	O	NA	Intergeni(ATTC)n	-194988	NR_136322	1.02E+08	Hs.578075NR_136322	LOC101927-	-	lysine mpseudo
chr21-93:16.49278	0.711807	0.545224	1.305532	0.191712	0.757244	chr21	9300367	9308109	+	O	NA	IntergeniHERVK9-ir	-174477	NR_038322	1E+08	Hs.487562NM_174944	ENSG00000TEK4P2	MAFIPL Ti	tektin 4 pseudo
chr3-908:25.61356	0.577502	0.442524	1.305019	0.191886	0.757244	chr3	90881536	90882088	+	O	NA	IntergeniALR/Alph	1774191	NM_005233	2042	Hs.123642NM_005233	ENSG00000EPH3	EK4 ETK EPEH	receptprotein-coding
chr13-17:																			

chr22-141 42.47046	0.438981	0.352653	1.244797	0.213206	0.757244	chr22	14107278	14107651	+	0 NA	IntergeniALR/Alph	-1420695	NM_001005	81061	Hs.55470c	NM_001005	ENSG00000	COR11H1	OR11H12		Colfactory	protein-coding		
chr22-136 36.68343	0.468454	0.376449	1.244403	0.213351	0.757244	chr22	13638176	13638442	+	0 NA	IntergeniALR/Alph	1740903	NR_110761	1.03E+08	Hs.65292c	NR_110761								
chr1-1224 41.46749	0.439888	0.353533	1.244241	0.213411	0.757244	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alph	1360849	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPI						
chr9-447 41.49724	0.438331	0.352363	1.243977	0.213508	0.757244	chr9	44740829	44741127	+	0 NA	IntergeniALR/Alph	1614812	NR_160669	1.03E+08	NR_160669									
chr21-128 25.81329	0.548742	0.441322	1.243404	0.213719	0.757244	chr21	12817704	12818109	+	0 NA	IntergeniALR/Alph	-220260	NR_026916	149992	Hs.55864c	NM_153773								
chr22-14 18.18038	0.644054	0.518991	1.240972	0.214616	0.757244	chr22	14376671	14378838	+	0 NA	IntergeniALR/Alph	-150405	NM_001005	81061	Hs.55470c	NM_001005	ENSG00000	COR11H1	OR11H12		Colfactory	protein-coding		
chr20-267 45.15594	0.421738	0.340044	1.240244	0.214885	0.757244	chr20	26784756	26785071	+	0 NA	IntergeniALR/Alph	-575680	NR_040099	284801	Hs.37069c	NR_040099	ENSG00000	MIR663AHC						
chr1-1231 34.18154	0.482613	0.389135	1.240221	0.214894	0.757244	chr1	15961119	15960395	+	0 NA	IntergeniALR/Alph	15961119	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPI						
chr14-166 17.66459	0.652919	0.526481	1.240156	0.214918	0.757244	chr14	16635790	16638933	+	0 NA	IntergeniALR/Alph	-1963756	NM_001015	440153	Hs.53488c	NM_001015	ENSG00000	COR11H12						
chr20-268 17.66459	0.652919	0.526481	1.240156	0.214918	0.757244	chr20	26818208	26820931	+	0 NA	IntergeniALR/Alph	-610336	NR_040099	284801	Hs.37069c	NR_040099	ENSG00000	MIR663AHC						
chr21-918 22.7956	0.584926	0.471742	1.239928	0.215002	0.757244	chr21	9181070	9181403	+	0 NA	IntergeniAluSz SIN	-51475	NR_038325	1E+08	Hs.487562	NM_174945	ENSG00000	TEKT4P2	MAFIPL T					
chr22-111 18.17982	0.644013	0.519864	1.238811	0.215416	0.757244	chr22	11929636	11934415	+	0 NA	intron (intron)	34619	NR_110761	1.03E+08	Hs.65292c	NR_110761								
chr10-407 32.05094	0.495546	0.400398	1.237634	0.215852	0.757244	chr10	40755976	40756679	+	0 NA	IntergeniALR/Alph	1611718	NR_02438C	441666	Hs.25572c	NR_02438C	ENSG00000	LOC441666						
chr1-123 25.35982	0.548075	0.443023	1.237127	0.21604	0.757244	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alph	2155010	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPI						
chr10-411 18.57152	0.649393	0.524968	1.237015	0.216082	0.757244	chr10	41278485	41278784	+	0 NA	IntergeniALR/Alph	1089411	NR_02438C	441666	Hs.25572c	NR_02438C	ENSG00000	LOC441666						
chr22-118 21.24822	0.602897	0.487518	1.236665	0.216211	0.757244	chr22	11883138	11883736	+	0 NA	IntergeniIntergeni	-13969	NR_110761	1.03E+08	Hs.65292c	NR_110761								
chr17-26 88.46334	0.320749	0.25941	1.236457	0.216289	0.757244	chr17	26328659	26328911	+	0 NA	IntergeniALR/Alph	760456	NR_135673	1.05E+08	Hs.64991c	NR_135673								
chr14-18 64.75951	0.358784	0.290196	1.236349	0.216329	0.757244	chr14	10725246	10728855	+	0 NA	IntergeniALR/Alph	-528402	NM_001015	440153	Hs.53488c	NM_001015	ENSG00000	COR11H12						
chr20-268 25.35869	0.548017	0.443561	1.235493	0.216647	0.757244	chr20	26865891	26867726	+	0 NA	IntergeniALR/Alph	-657575	NR_040099	284801	Hs.37069c	NR_040099	ENSG00000	MIR663AHC						
chr20-27 16.60156	0.676158	0.547455	1.235093	0.216796	0.757244	chr20	27840157	27843221	+	0 NA	IntergeniALR/Alph	760976	NR_132315	1E+08	Hs.529357	NR_132315	ENSG00000	FRG1CP						
chr10-42 16.63301	0.672333	0.544409	1.234979	0.216838	0.757244	chr10	42093916	42094984	+	0 NA	IntergeniIntergeni	273595	NR_02438C	441666	Hs.25572c	NR_02438C	ENSG00000	LOC441666						
chr20-268 18.21126	0.640627	0.518801	1.234821	0.216897	0.757244	chr20	26827493	26828701	+	0 NA	IntergeniALR/Alph	-618864	NR_040099	284801	Hs.37069c	NR_040099	ENSG00000	MIR663AHC						
chr11-52 17.17968	0.658672	0.533432	1.234782	0.216912	0.757244	chr11	52228068	52228294	+	0 NA	IntergeniALR/Alph	1819034	NR_024504	646813	Hs.68417c	NR_024504								
chr14-17 17.17968	0.658672	0.533432	1.234782	0.216912	0.757244	chr14	17495848	17498036	+	0 NA	IntergeniALR/Alph	-1104175	NM_001015	440153	Hs.53488c	NM_001015	ENSG00000	COR11H12						
chr7-602 85.03836	0.321444	0.260408	1.234384	0.21706	0.757244	chr7	60250524	60250869	+	0 NA	IntergeniALR/Alph	2800519	NM_001155	441234	Hs.533121	NM_001155	ENSG00000	ZNF716						
chr12-34 17.69491	0.649344	0.526125	1.234201	0.217128	0.757244	chr12	34944057	34944435	+	0 NA	IntergeniALR/Alph	921750	NR_032834	84920	Hs.102971	NM_032834	ENSG00000	ALG10	ALG10A D					
chr13-171 18.2107	0.640577	0.519673	1.232653	0.217705	0.757244	chr13	17166434	17166652	+	0 NA	IntergeniALR/Alph	-1028754	NR_027278	26080	Hs.44858c	NR_027278	ENSG00000	FAM230C						
chr20-28 18.2107	0.640577	0.519673	1.232653	0.217705	0.757244	chr20	28331794	28332850	+	0 NA	IntergeniALR/Alph	270343	NR_132315	1E+08	Hs.529357	NR_132315	ENSG00000	FRG1CP						
chr5-484 79.22102	0.327497	0.266144	1.230524	0.218501	0.757244	chr5	48498089	48498367	+	0 NA	IntergeniALR/Alph	1943060	NM_198445	133418	Hs.561411	NM_198445	ENSG00000	EMB						
chr18-207 16.60043	0.676126	0.549468	1.230511	0.218506	0.757244	chr18	20732895	20733216	+	0 NA	IntergeniALR/Alph	378758	NM_005406	6093	Hs.306307	NM_005406	ENSG00000	ROCK1						
chr21-11 16.66445	0.668596	0.543684	1.229752	0.21879	0.757244	chr21	11450079	11450309	+	0 NA	IntergeniALR/Alph	928680	NM_19926C	7179	Hs.12298c	NM_19926C	ENSG00000	TPTE	CT44 PTE					
chr20-27 17.21056	0.650441	0.533411	1.228646	0.219205	0.757244	chr20	27272350	27273415	+	0 NA	IntergeniALR/Alph	-1063649	NR_040099	284801	Hs.37069c	NR_040099	ENSG00000	MIR663AHC						
chr10-38 16.69364	0.664685	0.541176	1.228225	0.219363	0.757244	chr10	38918348	38920911	+	0 NA	Intergeni(GAATG) n	223033	NR_045000	399746	Hs.742607	NR_045000								
chr10-41 26.38914	0.539839	0.439619	1.22797	0.219458	0.757244	chr10	41533473	41534572	+	0 NA	IntergeniALR/Alph	834023	NR_02438C	441666	Hs.25572c	NR_02438C	ENSG00000	LOC441666						
chr5-488 61.67949	0.363872	0.296347	1.227858	0.2195	0.757244	chr5	48850737	48851635	+	0 NA	IntergeniALR/Alph	1590102	NM_198445	133418	Hs.561411	NM_198445	ENSG00000	EMB						
chr21-11 17.18449	0.631257	0.514148	1.227773	0.219532	0.757244	chr21	11703771	11703970	+	0 NA	IntergeniALR/Alph	1182356	NM_19926C	7179	Hs.12298c	NM_19926C	ENSG00000	TPTE	CT44 PTE					
chr5-492 53.72391	0.368418	0.314878	1.227198	0.219748	0.757244	chr5	49234327	49242116	+	0 NA	IntergeniALR/Alph	1197567	NM_198445	133418	Hs.561411	NM_198445	ENSG00000	EMB						
chr5-175 24.90522	0.547374	0.446254	1.226596	0.219974	0.757244	chr5	17525161	17530394	+	0 NA	IntergeniIntergeni	83767	NR_134271	1.03E+08	NR_134271	ENSG00000	LINC02215							
chr13-18 31.65981	0.490268	0.399874	1.226056	0.220177	0.757244	chr13	18018909	18019145	+	0 NA	IntergeniALR/Alph	-176270	NR_027278	26080	Hs.44858c	NR_027278	ENSG00000	FAM230C						
chr14-167 55.80209	0.378958	0.309234	1.225472	0.220397	0.757244	chr14	16729999	16730374	+	0 NA	IntergeniALR/Alph	-1870931	NM_001015	440153	Hs.53488c	NM_001015	ENSG00000	COR11H12						
chr19-24 23.81188	0.561569	0.458986	1.223499	0.221141	0.757244	chr19	24944707	24946356	+	0 NA	IntergeniALR/Alph	-782084	NR_00360C	1E+08	Hs.14931c	NR_00360C	ENSG00000	HAVCR1P1						
chr22-11 16.20929	0.671224	0.548822	1.223025	0.22132	0.757244	chr22	11895722	11897831	+	0 NA	promoter-promoter	-630	NR_110761	1.03E+08	Hs.65292c	NR_110761								
chr1-1231 35.3202	0.643452	0.379254	1.222009	0.221704	0.757244	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alph	1588838	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPI						
chr17-261 30.08268	0.500145	0.409426	1.221578	0.221867	0.757244	chr17	26127964	26128234	+	0 NA	IntergeniALR/Alph	961142	NR_135673	1.05E+08	Hs.64991c	NR_135673								
chr20-27 23.87307	0.556278	0.455493	1.221265	0.221986	0.757244	chr20	27416178	27118378	+	0 NA	IntergeniALR/Alph	-908045	NR_040099	284801	Hs.37069c	NR_040099	ENSG00000	MIR6						



chr20-265	19.41452	0.588743	0.503285	1.1698	0.242081	0.757244	chr20	26922869	26924253	+	O	NA	IntergeniALR/Alph	-714328	NR_04009F	284801	Hs.370699	NR_04009F	ENSG000001MIR663AHC	-	MIR663A	lncRNA	
chr14-166	40.20908	0.421562	0.360379	1.169776	0.242091	0.757244	chr14	16514134	16514355	+	O	NA	IntergeniALR/Alph	-2086873	NM_00101F	440153	Hs.53488C	NM_00101F	ENSG000001C11H12	-	olfactory	protein-coding	
chr21-122	30.25266	0.478457	0.409341	1.168847	0.242465	0.757244	chr21	12224319	12224856	+	O	NA	IntergeniALR/Alph	-813579	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30BF	C21orf99	ankyrin	pseudo	
chr1-1247	61.89366	0.348001	0.298354	1.166401	0.243452	0.757244	chr1	1.25E+08	1.25E+08	+	O	NA	IntergeniALR/Alph	3263118	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr10-412	17.86545	0.610072	0.52363	1.165082	0.243986	0.757244	chr10	41313922	41314295	+	O	NA	IntergeniALR/Alph	1053932	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000001LOC44166E	-	zinc	fin	pseudo
chr5-474	17.86545	0.610072	0.52363	1.165082	0.243986	0.757244	chr5	47403257	47403487	+	O	NA	IntergeniALR/Alph	-1706992	NM_02107Z	348980	Hs.35317E	NM_02107Z	ENSG000001HCN1	BCNG-1	BC	hyperpol	protein-coding
chr20-27	25.65332	0.512194	0.440435	1.162926	0.24486	0.757244	chr20	27021568	27023890	+	O	NA	IntergeniALR/Alph	-813496	NR_04009F	284801	Hs.370699	NR_04009F	ENSG000001MIR663AHC	-	MIR663A	lncRNA	
chr14-166	17.86545	0.610187	0.525497	1.161162	0.245576	0.757244	chr14	16695667	16697219	+	O	NA	IntergeniALR/Alph	-1904674	NM_00101F	440153	Hs.53488C	NM_00101F	ENSG000001C11H12	-	olfactory	protein-coding	
chr19-252	34.97609	0.446927	0.385206	1.160231	0.245955	0.757244	chr19	25207128	25207830	+	O	NA	IntergeniALR/Alph	-1044032	NR_00360F	1E+08	Hs.14931E	NR_00360F	ENSG000001HAVCR1P1	-	hepatitis	pseudo	
chr1-123	19.44597	0.58557	0.505353	1.158734	0.246564	0.757244	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alph	2442840	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr1-124	64.73977	0.335133	0.28942	1.157946	0.246886	0.757244	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alph	2561184	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr20-28	17.89746	0.606703	0.524203	1.157381	0.247117	0.757244	chr20	28366453	28367409	+	O	NA	IntergeniALR/Alph	235734	NR_13231F	1E+08	Hs.529357	NR_13231F	ENSG000001FRG1CP	-	FSHD	regip	pseudo
chr21-121	34.54954	0.443	0.383022	1.156591	0.247439	0.757244	chr21	12199547	12199837	+	O	NA	IntergeniALR/Alph	-838474	NR_02691E	149992	Hs.55864E	NM_153773	ANKRD30BF	C21orf99	ankyrin	pseudo	
chr9-434	17.92721	0.603159	0.522149	1.155148	0.24803	0.757244	chr9	43431280	43431941	+	O	NA	IntergeniALR/Alph	305444	NR_16066E	1.03E+08	Hs.55470E	NM_16066E	LOC10272Z	-	methylenc	pseudo	
chr1-1217	35.09734	0.439752	0.380875	1.154584	0.248261	0.757244	chr1	1.22E+08	1.22E+08	+	O	NA	IntergeniALR/Alph	226991	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr1-1217	23.55757	0.529744	0.459125	1.153813	0.248577	0.757244	chr1	1.22E+08	1.22E+08	+	O	NA	IntergeniALR/Alph	251070	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr1-123	23.55757	0.529744	0.459125	1.153813	0.248577	0.757244	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alph	2089130	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr4-4927	66.38091	0.33225	0.288161	1.153	0.24891	0.757244	chr4	49278678	49278901	+	O	NA	IntergeniALR/Alph	292147	NR_00128E	81057	Hs.47970E	NM_025087	ENSG000001CWH43	CWH43-C	cell	wall	protein-coding
chr22-15	17.38167	0.614608	0.533117	1.152857	0.248969	0.757244	chr22	15018082	15019125	+	O	NA	IntergeniALR/Alph	-509556	NM_00100F	81061	Hs.55470E	NM_00100F	ENSG000001C11H1	OR11H12	Col	factory	protein-coding
chr8-858	16.89506	0.61913	0.537065	1.152803	0.248991	0.757244	chr8	85802068	85806432	+	O	NA	promoter-promoter-	-689	NR_00359F	1E+08	Hs.53505E	NR_00359F	REXO1L2P	-	REXO1	lip	pseudo
chr22-14	29.85869	0.472506	0.409934	1.152637	0.249059	0.757244	chr22	14032195	14032596	+	O	NA	IntergeniALR/Alph	-1495764	NM_00100F	81061	Hs.55470E	NM_00100F	ENSG000001C11H1	OR11H12	Col	factory	protein-coding
chr5-487	106.537	0.275275	0.238963	1.151957	0.249339	0.757244	chr5	48753951	48754193	+	O	NA	IntergeniALR/Alph	1687216	NR_19844E	133418	Hs.561411	NM_19844E	ENSG000001EMB	GP70	embigin	protein-coding	
chr10-406	31.95443	0.619179	0.400985	1.151955	0.24934	0.757244	chr10	40683362	40683668	+	O	NA	IntergeniALR/Alph	1684530	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000001LOC44166E	-	zinc	fin	pseudo
chr21-52	16.89563	0.619179	0.537573	1.151806	0.249401	0.757244	chr21	5232263	5232906	+	O	NA	IntergeniALR/Alph	-77926	NM_00136E	1.03E+08	Hs.44907E	NM_00136E	ENSG000001LOC10272Z	-	periodic	protein-coding	
chr20-27	16.3787	0.627841	0.545715	1.150493	0.249941	0.757244	chr20	27410230	27411129	+	O	NA	IntergeniALR/Alph	1191986	NR_13231F	1E+08	Hs.529357	NR_13231F	ENSG000001FRG1CP	-	FSHD	regip	pseudo
chr10-411	70.08664	0.322194	0.280294	1.149485	0.250356	0.757244	chr10	41124928	41126511	+	O	NA	IntergeniALR/Alph	1242326	NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000001LOC44166E	-	zinc	fin	pseudo
chr1-122	48.69008	0.386668	0.336427	1.149337	0.250417	0.757244	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alph	1403682	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr14-17	17.80142	0.617257	0.537168	1.149094	0.250517	0.757244	chr14	17985736	17985980	+	O	NA	IntergeniALR/Alph	-615259	NM_00101F	440153	Hs.53488C	NM_00101F	ENSG000001C11H12	-	olfactory	protein-coding	
chr13-171	24.13625	0.520658	0.45312	1.149051	0.250535	0.757244	chr13	17114036	17115564	+	O	NA	IntergeniALR/Alph	-1080497	NR_02727E	26080	Hs.44858E	NR_02727E	ENSG000001FAM230C	LINC00281	family	winc	ncRNA
chr1-1247	35.51147	-0.43974	0.382942	-1.14883	0.250832	0.757244	chr1	1.25E+08	1.25E+08	+	O	NA	IntergeniALR/Alph	3279736	NR_00395F	647121	Hs.69768E	NR_00395F	ENSG000001EMB1	-	embigin	pseudo	
chr4-5071	16.37813	0.627803	0.546743	1.14826	0.250861	0.757244	chr4	50711095	50711548	+	O	NA	IntergeniALR/Alph	-1131679	NM_00128E	23142	Hs.60538E	NM_00128E	ENSG000001DCUN1D4	-	defective	protein-coding	
chr9-440	28.67101	0.488116	0.425321	1.14764	0.251117	0.757244	chr9	44059268	44059549	+	O	NA	IntergeniALR/Alph	933242	NR_16066E	1.03E+08	Hs.55470E	NR_16066E	LOC10272Z	-	methylenc	pseudo	
chr19-26	16.92594	0.615476	0.536768	1.146632	0.251534	0.757244	chr19	26018229	26018476	+	O	NA	IntergeniALR/Alph	-1752079	NR_11068E	1.02E+08	Hs.56793E	NR_11068E	ENSG000001LOC10192Z	-	uncharact	ncRNA	
chr5-484	27.2344	0.500032	0.436253	1.146197	0.251714	0.757244	chr5	48438405	48438643	+	O	NA	IntergeniALR/Alph	2002764	NR_19844E	133418	Hs.561411	NM_19844E	ENSG000001EMB	GP70	embigin	protein-coding	
chr22-12	16.40958	0.624065	0.544734	1.145632	0.251947	0.757244	chr22	12868384	12876092	+	O	NA	IntergeniALR/Alph	974832	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272Z	-	uncharact	ncRNA	
chr20-27	16.92651	0.615519	0.537275	1.145631	0.251948	0.757244	chr20	27096171	27097684	+	O	NA	IntergeniALR/Alph	-887894	NR_04009F	284801	Hs.370699	NR_04009F	ENSG000001MIR663AHC	-	MIR663A	lncRNA	
chr5-476	206.4671	0.216358	0.189306	1.1429	0.25308	0.757244	chr5	47648571	47648811	+	O	NA	IntergeniALR/Alph	-1952311	NM_02107Z	348980	Hs.35317E	NM_02107Z	ENSG000001HCN1	BCNG-1	BC	hyperpol	protein-coding
chr22-13	28.31075	0.479744	0.419909	1.142494	0.253249	0.757244	chr22	13631936	13632467	+	O	NA	IntergeniALR/Alph	1734795	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272Z	-	uncharact	ncRNA	
chr18-15	32.45436	0.451475	0.39568	1.14101	0.253866	0.757244	chr18	15551181	15553044	+	O	NA	IntergeniALR/Alph	-226193	NR_02741F	644669	Hs.57947E	NR_02741F	ENSG000001LOC64466E	-	ankyrin	pseudo	
chr20-27	22.58718	0.532888	0.46744	1.140013	0.254281	0.757244	chr20	27712467	27714548	+	O	NA	IntergeniALR/Alph	889158	NR_13231F	1E+08	Hs.529357	NR_13231F	ENSG000001FRG1CP	-	FSHD	regip	pseudo
chr19-26	45.16594	0.386384	0.33903	1.139674	0.254422	0.757244	chr19	26439050	26440183	+	O	NA	IntergeniALR/Alph	-1353815	NR_11068E	1.02E+08	Hs.56793E	NR_11068E	ENSG000001LOC10192Z	-	uncharact	ncRNA	
chr10-40	93.07052	0.288361	0.253179	1.138962	0.254719	0.757244	chr10	40279754	40280243	+	O	NA	IntergeniALR/Alph	1583402	NR_04500C	399746	Hs.742607	NR_04500C	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo
chr14-18	41.28769	0.410323	0.360313	1.138797	0.254788	0.757244	chr14	18060907	18061311	+	O	NA	IntergeniALR/Alph	-540008	NM_00101F	440153	Hs.53488C	NM_00101F	ENSG000001C11H12	-	olfactory	protein-coding	
chr21-11	41.47637	0.401308	0.352528	1.138371	0.254965	0.757244	chr21	11588522	11588851	+	O	NA	IntergeniALR/Alph	1067172	NR_19926C	7179	Hs.12298E	NM_19926C	ENSG000001TPTE	CT44	PTE	transmem	protein-coding
chr20-28	22.55517	0.535585	0.470808	1.137587	0.255293	0.757244	chr20	28194439	28195896	+	O	NA	IntergeniALR/Alph	40798	NR_13231F	1E+08	Hs.529357	NR_13231F	ENSG000001FRG1CP	-	FSHD	regip	pseudo
chr22-13	17.47261	0.603748	0.531171	1.136636	0.25569	0.757244	chr22	13643852	13644143	+	O	NA	IntergeniALR/Alph	1746591	NR_110761	1.03E+08	Hs.65292E	NR_110761	LOC10272Z	-	uncharact	ncRNA	
chr19-26	60.07866	0.340112	0.299235	1.136606	0.255703	0.757244	chr19	26485616	26485852	+	O	NA	IntergeniALR/Alph	-1307697	NR_11068E	1.02E+08	Hs.56793E	NR_11068E	ENSG000001LOC10192Z	-	uncharact	ncRNA	
chr14-17	22.07139	0.537378	0.47301	1.136082	0.255922	0.757244	chr14	17509165	17511076	+	O	NA	IntergeniALR/Alph	-1090997	NM_00101F	440153	Hs.53488C	NM_00101F	ENSG000001C11H12	-			

chr8-458:51.19972	0.35055	0.323291	1.084316	0.278225	0.757244	chr8	45840470	45840759	+0	NA	IntergeniALR/Alpha	777029	NR_146077	389652	NR_146077	ENSG000004ASNSP1	ASNSL1	asparagiri	pseudo
chr13-18:17.58139	0.571652	0.527341	1.084028	0.278353	0.757244	chr13	18013269	18013468	+0	NA	IntergeniALR/Alpha	-181929	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr3-910:24.88265	0.485155	0.447606	1.083888	0.278414	0.757244	chr3	91048944	91049168	+0	NA	IntergeniALR/Alpha	1941435	NM_005233	2042	Hs.12364:NM_005233	ENSG000004EPAH3	EK4 ETK E EPH	recept	protein-coding
chr1-123:19.15908	0.549746	0.507599	1.083032	0.278794	0.757244	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alpha	1769817	NR_003955	647121	Hs.69768:NR_003955	ENSG000004EMBP1	-	emigin	pseudo
chr19-26:68.90982	0.310831	0.287018	1.082966	0.278824	0.757244	chr19	263598831	263599037	+0	NA	IntergeniALR/Alpha	-1434497	NR_110688	1.02E+08	Hs.56793:NR_110688	ENSG000004LOC101927	-	uncharact	ncRNA
chr13-17:18.12807	0.561707	0.518676	1.082964	0.278824	0.757244	chr13	17231269	17233559	+0	NA	IntergeniALR/Alpha	-962883	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr21-121:18.64329	0.55555	0.513001	1.08294	0.278835	0.757244	chr21	12122946	12124387	+0	NA	IntergeniALR/Alpha	-914500	NR_026910	149992	Hs.55864:NM_153773	ANKRD30B C21orf99	ankyrin	pseudo	
chr5-495:52.20325	0.351601	0.325265	1.080967	0.279712	0.757244	chr5	49506291	49506567	+0	NA	IntergeniALR/Alpha	934859	NM_198445	133418	Hs.56141:NM_198445	ENSG000004EMB	GP70	emigin	protein-coding
chr6-593:88.80773	0.274245	0.253855	1.080323	0.279998	0.757244	chr6	59399299	59399655	+0	NA	IntergeniALR/Alpha	-1438031	NR_132994	1.07E+08	Hs.56153:NR_125727	ENSG000004LINC0068C	-	long	intencRNA
chr9-4481:17.61227	0.568164	0.526042	1.080072	0.280111	0.757244	chr9	44817490	44817697	+0	NA	IntergeniALR/Alpha	1691427	NR_160666	1.03E+08	NR_160669	LOC102722	-	methylenc	pseudo
chr22-13:17.61171	0.568118	0.526031	1.080009	0.280138	0.757244	chr22	13516551	13519740	+0	NA	IntergeniALR/Alpha	1620739	NR_110761	1.03E+08	Hs.65292:NR_110761	ENSG000004TPTTE	CT44 PTE	transmem	protein-coding
chr5-484:17.61171	0.568118	0.526031	1.080009	0.280138	0.757244	chr5	48453691	48454422	+0	NA	IntergeniALR/Alpha	1987232	NM_198445	133418	Hs.56141:NM_198445	ENSG000004EMB	GP70	emigin	protein-coding
chr6-596:28.54135	0.452533	0.41906	1.079878	0.280196	0.757244	chr6	59661346	59662142	+0	NA	IntergeniALR/Alpha	-1700298	NR_132994	1.07E+08	Hs.56153:NR_125727	ENSG000004LINC0068C	-	long	intencRNA
chr19-27:18.12693	0.561615	0.520483	1.079026	0.280576	0.757244	chr19	27178379	27178948	+0	NA	IntergeniALR/Alpha	-614768	NR_110688	1.02E+08	Hs.56793:NR_110688	ENSG000004LOC101927	-	uncharact	ncRNA
chr9-4351:18.12693	0.561615	0.520483	1.079026	0.280576	0.757244	chr9	43516621	43516946	+0	NA	IntergeniALR/Alpha	396167	NR_160666	1.03E+08	NR_160669	LOC102722	-	methylenc	pseudo
chr1-123:29.03023	0.452839	0.419805	1.07869	0.280726	0.757244	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alpha	1945835	NR_003955	647121	Hs.69768:NR_003955	ENSG000004EMBP1	-	emigin	pseudo
chr21-11:33.16874	0.428493	0.397325	1.078444	0.280836	0.757244	chr21	11493424	11493847	+0	NA	IntergeniALR/Alpha	972121	NM_199260	7179	Hs.12298:NM_199255	ENSG000004TPTTE	CT44 PTE	transmem	protein-coding
chr5-473:19.15852	0.549677	0.509728	1.078372	0.280868	0.757244	chr5	47375972	47376180	+0	NA	IntergeniALR/Alpha	-1679696	NM_021072	348980	Hs.35317:NM_021072	ENSG000004HCN1	BCNG-1 B hyperpol	protein-coding	
chr17-251:96.81146	0.265766	0.246542	1.077974	0.281045	0.757244	chr17	25139805	25140054	+0	NA	IntergeniALR/Alpha	1949312	NR_135673	1.05E+08	Hs.64991:NR_135673	ENSG000004LOC105371	-	uncharact	ncRNA
chrX-624:22.57772	0.503665	0.467307	1.077802	0.281122	0.757244	chrX	62465467	62465987	+0	NA	IntergeniALR/Alpha	885605	NM_001012	139886	Hs.61278:NM_001012	ENSG000004SPIN4	TDRD28	spindlin	protein-coding
chr19-24:25.85413	-0.47835	0.44395	-1.07748	0.281266	0.757244	chr19	24863116	24863348	+0	NA	IntergeniALR/Alpha	-699785	NR_003608	1E+08	Hs.14931:NR_003608	ENSG000004HAVCR1P1	-	hepatitis	pseudo
chr13-16:27.99694	0.456927	0.424072	1.077475	0.281268	0.757244	chr13	16848772	16849182	+0	NA	IntergeniALR/Alpha	-1346320	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr20-26:17.09535	0.574915	0.534307	1.076002	0.281926	0.757244	chr20	26722837	26723575	+0	NA	IntergeniALR/Alpha	-513973	NR_040095	284801	Hs.37069:NR_040095	ENSG000004MIR663AH	-	MIR663A	lncRNA
chr13-16:23.33584	0.49483	0.460008	1.0757	0.282062	0.757244	chr13	16930417	16930721	+0	NA	IntergeniALR/Alpha	-1264728	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr14-17:21.25483	0.526301	0.489384	1.075435	0.28218	0.757244	chr14	17381885	17382128	+0	NA	IntergeniALR/Alpha	-1219111	NM_001013	440153	Hs.53488:NM_001013	ENSG000004OR11H12	-	olfactory	protein-coding
chr13-17:17.64315	0.564692	0.525843	1.073879	0.282277	0.757244	chr13	17061320	17062739	+0	NA	IntergeniALR/Alpha	-1133268	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr20-20:17.64315	0.564692	0.525843	1.073879	0.282277	0.757244	chr20	21989105	21991016	+0	NA	IntergeniALR/Alpha	612600	NR_132316	1E+08	Hs.52935:NR_132316	ENSG000004FRG1CP	-	FSHD	regipseudo
chr19-26:39.51802	0.391838	0.364895	1.073839	0.282895	0.757244	chr19	26897599	26897860	+0	NA	IntergeniALR/Alpha	-895702	NR_110688	1.02E+08	Hs.56793:NR_110688	ENSG000004LOC101927	-	uncharact	ncRNA
chr12-36:17.64259	0.564647	0.525832	1.073816	0.282905	0.757244	chr12	36367140	36367464	+0	NA	IntergeniALR/Alpha	-1949472	NM_001013	144245	Hs.52935:NM_001013	ENSG000004ALG10	ALG10 KCF	ALG10	protein-coding
chr13-16:52.90376	0.344219	0.320605	1.073657	0.282977	0.757244	chr13	16690045	16690395	+0	NA	IntergeniALR/Alpha	-1505077	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr20-28:16.58012	0.582227	0.542602	1.073026	0.283259	0.757244	chr20	28170803	28173122	+0	NA	IntergeniALR/Alpha	430703	NR_132316	1E+08	Hs.52935:NR_132316	ENSG000004FRG1CP	-	FSHD	regipseudo
chr1-124:16.58012	0.582227	0.542602	1.073026	0.283259	0.757244	chr1	1.24E+08	1.24E+08	+0	NA	IntergeniALR/Alpha	2554076	NR_003955	647121	Hs.69768:NR_003955	ENSG000004EMBP1	-	emigin	pseudo
chr5-492:17.57193	0.51546	0.533091	1.072135	0.283659	0.757244	chr5	49226806	49227952	+0	NA	IntergeniALR/Alpha	1213909	NM_198445	133418	Hs.56141:NM_198445	ENSG000004EMB	GP70	emigin	protein-coding
chr21-10:17.1268	0.57138	0.533001	1.072005	0.283718	0.757244	chr21	10368165	10368958	+0	NA	IntergeniALR/Alpha	-44959	NM_001187	574	Hs.54578:NM_001187	BAGE	BAGE1 CT2B	melano	protein-coding
chr19-26:44.39868	0.369343	0.344864	1.070983	0.284177	0.757111	chr19	26008793	26009024	+0	NA	IntergeniALR/Alpha	-1784523	NR_110688	1.02E+08	Hs.56793:NR_110688	ENSG000004LOC101927	-	uncharact	ncRNA
chr21-11:40.19161	0.383508	0.35856	1.069577	0.28481	0.758295	chr21	11499718	11499932	+0	NA	IntergeniALR/Alpha	978311	NM_199260	7179	Hs.12298:NM_199255	ENSG000004TPTTE	CT44 PTE	transmem	protein-coding
chr22-14:27.54065	0.454561	0.42536	1.068648	0.285228	0.758295	chr22	14930390	14931819	+0	NA	IntergeniALR/Alpha	-597055	NM_001005	81061	Hs.55470:NM_001005	ENSG000004OR11H1	OR11H12 C	olfactory	protein-coding
chr9-438:23.30213	0.497303	0.465379	1.068597	0.285251	0.758295	chr9	43844817	43845131	+0	NA	IntergeniALR/Alpha	718808	NR_160666	1.03E+08	NR_160669	LOC102722	-	methylenc	pseudo
chr10-40:89.47905	0.271016	0.253956	1.067179	0.285891	0.759237	chr10	40019603	40020472	+0	NA	IntergeniALR/Alpha	1323441	NR_045000	399746	Hs.74260:NR_045000	ACTR3BP5	FKSG74	ACTR3B	pseudo
chr19-27:26.99341	0.458985	0.430368	1.066493	0.286201	0.759302	chr19	27008296	27009701	+0	NA	IntergeniALR/Alpha	-784433	NR_110688	1.02E+08	Hs.56793:NR_110688	ENSG000004LOC101927	-	uncharact	ncRNA
chr10-40:45.98911	0.360013	0.338449	1.063716	0.287457	0.761184	chr10	40266972	40269022	+0	NA	IntergeniALR/Alpha	1571401	NR_045000	399746	Hs.74260:NR_045000	ACTR3BP5	FKSG74	ACTR3B	pseudo
chr12-35:16.60931	0.578391	0.544177	1.062874	0.287839	0.761184	chr12	35688783	35689439	+0	NA	IntergeniALR/Alpha	1666615	NM_032834	84920	Hs.10297:NM_032834	ENSG000004ALG10	ALG10A DIALG10	al	protein-coding
chr19-27:38.61052	0.386839	0.364447	1.061442	0.288489	0.761184	chr19	27138456	27140712	+0	NA	IntergeniALR/Alpha	-653847	NR_110688	1.02E+08	Hs.56793:NR_110688	ENSG000004LOC101927	-	uncharact	ncRNA
chr21-11:17.09818	0.57522	0.54194	1.061409	0.288504	0.761184	chr21	11336681	11337196	+0	NA	IntergeniALR/Alpha	815424	NM_199260	7179	Hs.12298:NM_199255	ENSG000004TPTTE	CT44 PTE	transmem	protein-coding
chr22-14:21.7862	0.505644	0.476432	1.061314	0.288547	0.761184	chr22	14796045	14797116	+0	NA	IntergeniALR/Alpha	-731579	NM_001005	81061	Hs.55470:NM_001005	ENSG000004OR11H1	OR11H12 C	olfactory	protein-coding
chr13-16:42.33211	0.370825	0.349459	1.061114	0.288626	0.761184	chr13	16657916	16658560	+0	NA	IntergeniALR/Alpha	-1537059	NR_027278	26080	Hs.44858:NR_027278	ENSG000004FAM230C	LINC00281	family	wincRNA
chr10-40:28.11876	0.448117	0.422734	1.060045	0.289124	0.761208	chr10	40771324	40772361	+0	NA	IntergeniALR/Alpha	1596203	NR_02438C						



chr20-28: 17.84345	0.522306	0.522333	1.001672	0.316502	0.763126	chr20	28380528	28381744	+	O NA	IntergeniALR/Alphe	221529 NR_13231F	1E+08	Hs. 529357NR_13231F	ENSG0000CFRG1CP	-	FSHD	regipseudo
chr22-14f 17.29734	0.532183	0.531434	1.00141	0.316629	0.763126	chr22	14863776	14865305	+	O NA	IntergeniALR/Alphe	-663619 NM_00100F	81061	Hs. 55470fNM_00100F	ENSG0000COR11H1	OR11H12	Colfactory	protein-coding
chr5-476f 37.81067	0.368429	0.368312	1.000317	0.317157	0.763126	chr5	47607622	47608338	+	O NA	IntergeniALR/Alphe	-1911600 NM_02107Z	348980	Hs. 35317fNM_02107Z	ENSG0000HCN1	BCNG-1	BChyperpolz	protein-coding
chr5-487f 38.93603	0.362939	0.362892	1.00013	0.317248	0.763126	chr5	48791255	48792631	+	O NA	IntergeniALR/Alphe	1649345 NM_19844f	133418	Hs. 56141NM_19844f	ENSG0000EMB	GP70	embigin	protein-coding
chr22-14f 21.48827	0.48935	0.489623	0.999443	0.31758	0.763126	chr22	14939638	14939959	+	O NA	IntergeniALR/Alphe	-588361 NM_00100F	81061	Hs. 55470fNM_00100F	ENSG0000COR11H1	OR11H12	Colfactory	protein-coding
chr1-124f 71.10566	0.278355	0.278567	0.99924	0.317678	0.763126	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2648746 NR_00395F	647121	Hs. 69768fNR_00395F	ENSG0000EMB	-	embigin	pseudo
chr5-482f 24.08564	0.459217	0.459634	0.999094	0.317749	0.763126	chr5	48280249	48280723	+	O NA	IntergeniALR/Alphe	2160802 NR_19844f	133418	Hs. 56141NM_19844f	ENSG0000EMB	GP70	embigin	protein-coding
chr8-456f 17.77999	0.530001	0.530532	0.999	0.317795	0.763126	chr8	45651344	45651608	+	O NA	IntergeniALR/Alphe	966167 NR_14607f	389652	NR_14607f	ENSG0000ASNSP1	ASNSL1	asparagip	pseudo
chr22-107f 23.08153	0.461781	0.462366	0.998734	0.317923	0.763126	chr22	10755507	10755921	+	O NA	IntergeniAluJb SIN	205815 NR_13232C	1.03E+08	NR_132320	FRG1FP	-	FSHD	regipseudo
chr5-486f 27.28804	0.426397	0.427135	0.998272	0.318147	0.763126	chr5	48688567	48690249	+	O NA	IntergeniALR/Alphe	1751880 NM_19844f	133418	Hs. 56141NM_19844f	ENSG0000EMB	GP70	embigin	protein-coding
chr20-26f 17.32765	0.528662	0.529617	0.998116	0.318223	0.763126	chr20	26957539	26959873	+	O NA	IntergeniALR/Alphe	-749473 NR_04009F	284801	Hs. 37069fNR_04009F	ENSG0000MIR663AH	BCNG-1	BChyperpolz	protein-coding
chr20-27f 17.32765	0.528662	0.529617	0.998116	0.318223	0.763126	chr20	27206757	27208949	+	O NA	IntergeniALR/Alphe	-998620 NR_04009F	284801	Hs. 37069fNR_04009F	ENSG0000MIR663AH	BCNG-1	BChyperpolz	protein-coding
chr10-40f 21.98819	0.472977	0.474011	0.997819	0.318367	0.763126	chr10	40246748	40248460	+	O NA	IntergeniALR/Alphe	1551008 NR_045000	399746	Hs. 74260fNR_045000	ACTR3BP5	FKSG74	ACTR3B	pseudo
chr1-123f 17.32822	0.528668	0.530122	0.997257	0.31864	0.763126	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alphe	1741761 NR_00395F	647121	Hs. 69768fNR_00395F	ENSG0000EMB	-	embigin	pseudo
chr5-489f 18.90761	0.51009	0.511577	0.997093	0.31872	0.763126	chr5	48924486	48924695	+	O NA	IntergeniALR/Alphe	1516698 NR_19844f	133418	Hs. 56141NM_19844f	ENSG0000EMB	GP70	embigin	protein-coding
chr9-435f 31.52486	0.398613	0.399883	0.996958	0.318785	0.763126	chr9	43546660	43547263	+	O NA	IntergeniALR/Alphe	420795 NR_160666	1.03E+08	NR_160669	LOC10272Z	-	methylenz	pseudo
chr19-27f 16.78042	0.537955	0.539817	0.99655	0.318983	0.763126	chr19	27122346	27122545	+	O NA	IntergeniALR/Alphe	-670986 NR_11068F	1.02E+08	Hs. 56793fNR_11068F	ENSG0000LOC10192Z	-	uncharactncRNA	
chr14-17f 21.98876	0.473027	0.474735	0.996403	0.319054	0.763126	chr14	17915239	17916260	+	O NA	IntergeniALR/Alphe	-685368 NM_00101F	440153	Hs. 53488fNM_00101F	ENSG0000COR11H12	-	olfactory	protein-coding
chr1-123f 23.05292	0.464543	0.466257	0.996325	0.319092	0.763126	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2292329 NR_00395F	647121	Hs. 69768fNR_00395F	ENSG0000EMB	-	embigin	pseudo
chr20-27f 18.39125	0.514846	0.51679	0.996239	0.319134	0.763126	chr20	27983943	27984194	+	O NA	IntergeniALR/Alphe	618597 NR_13231F	1E+08	Hs. 529357NR_13231F	ENSG0000CFRG1CP	-	FSHD	regipseudo
chr20-27f 17.32765	0.528662	0.529617	0.998116	0.319228	0.763126	chr20	12110978	12111799	+	O NA	IntergeniALR/Alphe	-926778 NR_02691F	149992	Hs. 55864fNM_15377Z	ANKRD30BF	C2orf99	ankyrin	pseudo
chr1-123f 41.50308	0.355399	0.357344	0.994558	0.319951	0.763126	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2342126 NR_00395F	647121	Hs. 69768fNR_00395F	ENSG0000EMB	-	embigin	pseudo
chr21-92f 27.28634	0.426294	0.428684	0.994426	0.320016	0.763126	chr21	9259210	9260163	+	O NA	IntergeniIntergeni	-129925 NR_03832Z	1E+08	Hs. 48756fNR_17494F	ENSG0000TEKT4P2	MAFIPL TI	tektin 4	pseudo
chr7-60f 11.13541	0.277443	0.279076	0.994149	0.32015	0.763126	chr7	60591144	6060142	+	O NA	IntergeniALR/Alphe	2712763 NR_00395F	643955	Hs. 58330fNR_00395F	ENSG0000ZNF733P	ZNF733	zinc	finz
chr8-451f 41.62434	0.349365	0.35162	0.993589	0.320423	0.763126	chr8	45187911	45188840	+	O NA	IntergeniALR/Alphe	1429268 NR_14607f	389652	NR_14607f	ENSG0000ASNSP1	ASNSL1	asparagip	pseudo
chr21-11f 16.8113	0.534314	0.537813	0.993494	0.320469	0.763126	chr21	11563630	11564748	+	O NA	IntergeniALR/Alphe	1042679 NR_19926F	7179	Hs. 12298fNR_19926F	ENSG0000TPTE	CT44 PTE	transmem	protein-coding
chr5-476f 22.01964	0.470258	0.473343	0.993483	0.320475	0.763126	chr5	47675470	47676735	+	O NA	IntergeniALR/Alphe	-1979722 NR_02107Z	348980	Hs. 35317fNM_02107Z	ENSG0000HCN1	BCNG-1	BChyperpolz	protein-coding
chr20-29f 17.3591	0.525169	0.529917	0.991039	0.321666	0.763126	chr20	29088471	29088794	+	O NA	intron (intron)	8242 NR_13231F	1.03E+08	NR_132316	FRG1DP	-	FSHD	regipseudo
chr10-41f 33.60473	0.38524	0.388732	0.991017	0.321677	0.763126	chr10	41187901	41188627	+	O NA	IntergeniALR/Alphe	1179781 NR_02438F	441666	Hs. 25572fNR_02438F	ENSG0000LOC44166F	-	zinc	finz
chr4-503f 17.35797	0.525077	0.529895	0.990907	0.321731	0.763126	chr4	50349218	50349434	+	O NA	IntergeniALR/Alphe	1362684 NM_00128F	80157	Hs. 47970fNM_02508F	ENSG0000CWH43	CWH43-C	f cell	wall
chr11-51f 22.04995	0.467475	0.471997	0.990419	0.321969	0.763126	chr11	51951183	51951787	+	O NA	IntergeniALR/Alphe	1542338 NR_02450F	646813	Hs. 68417fNR_02450F	LOC64681F	-	DEXH-box	pseudo
chr10-41f 29.4124	0.415813	0.420076	0.989852	0.322246	0.763126	chr10	41418086	41418388	+	O NA	IntergeniALR/Alphe	949808 NR_02438F	441666	Hs. 25572fNR_02438F	ENSG0000LOC44166F	-	zinc	finz
chr5-175f 16.84274	0.530759	0.536994	0.988389	0.322962	0.763126	chr5	17517590	17524003	+	O NA	IntergeniIntergeni	76786 NR_152427	1.03E+08	NR_13427C	ENSG0000LINC0221F	-	long	intencRNA
chr20-26f 16.84217	0.530711	0.536982	0.988321	0.322995	0.763126	chr20	26948841	26949826	+	O NA	IntergeniALR/Alphe	-740100 NR_04009F	284801	Hs. 37069fNR_04009F	ENSG0000MIR663AH	BCNG-1	BChyperpolz	protein-coding
chr22-14f 17.35967	0.525205	0.531415	0.988315	0.322998	0.763126	chr22	14587364	14587667	+	O NA	IntergeniALR/Alphe	-940644 NM_00100F	81061	Hs. 55470fNM_00100F	ENSG0000COR11H1	OR11H12	Colfactory	protein-coding
chr16-34f 20.48643	0.493902	0.499922	0.987958	0.323173	0.763126	chr16	34276979	34277178	+	O NA	IntergeniALR/Alphe	104402 NR_15815F	1.03E+08	Hs. 69271fNR_15815F	CCNYL3	-	cyclin	Y
chr5-47f 29.9449	0.403664	0.409027	0.98689	0.323697	0.763126	chr5	4788481	4790863	+	O NA	IntergeniALR/Alphe	-1793292 NR_02107Z	348980	Hs. 35317fNM_02107Z	ENSG0000HCN1	BCNG-1	BChyperpolz	protein-coding
chr22-14f 21.50384	0.473386	0.479856	0.986517	0.32388	0.763126	chr22	14146208	14146635	+	O NA	IntergeniALR/Alphe	-1381738 NM_00100F	81061	Hs. 55470fNM_00100F	ENSG0000COR11H1	OR11H12	Colfactory	protein-coding
chr22-14f 16.84161	0.530662	0.538001	0.986359	0.323957	0.763126	chr22	14948438	14948958	+	O NA	IntergeniALR/Alphe	-579461 NM_00100F	81061	Hs. 55470fNM_00100F	ENSG0000COR11H1	OR11H12	Colfactory	protein-coding
chr5-489f 71.69936	0.27306	0.277184	0.985121	0.324565	0.763126	chr5	489870156	48997049	+	O NA	IntergeniALR/Alphe	1471006 NR_19844f	133418	Hs. 56141NM_19844f	ENSG0000EMB	GP70	embigin	protein-coding
chr3-908f 22.59549	0.461793	0.468773	0.98511	0.32457	0.763126	chr3	90874667	90874906	+	O NA	IntergeniALR/Alphe	1767165 NM_00523Z	2042	Hs. 12364fNM_00523Z	ENSG0000EPH3	EK4 ETK E	EPH	recep
chr21-11f 16.77872	0.537927	0.546091	0.98505	0.324599	0.763126	chr21	11516814	11517437	+	O NA	IntergeniALR/Alphe	995611 NM_19926F	7179	Hs. 12298fNR_19926F	ENSG0000TPTE	CT44 PTE	transmem	protein-coding
chr11-53f 16.32638	0.536689	0.544995	0.984759	0.324742	0.763126	chr11	53509096	53509914	+	O NA	IntergeniALR/Alphe	1094493 NM_00100F	119749	Hs. 55356fNM_00100F	ENSG0000COR4C6	-	olfactory	protein-coding
chr20-28f 16.32638	0.536689	0.544995	0.984759	0.324742	0.763126	chr20	28371352	28374310	+	O NA	IntergeniALR/Alphe	229834 NR_13231F	1E+08	Hs. 529357NR_13231F	ENSG0000CFRG1CP	-	FSHD	regipseudo
chrY-568f 16.32582	0.536642	0.545521	0.983724	0.325251	0.763126	chrY	56865487	56871536	+	O NA	IntergeniALR/Alphe	-85744 NM_00584C	10251	Hs. 38191fNM_00584C	ENSG0000SPRY3	spry-3	olfactory	protein-coding
chr10-39f 21.53246	0.470409	0.478737	0.982604	0.325802	0.763126	chr10	39989702	39990776	+	O NA	IntergeniALR/Alphe	1293643 NR_045000	399746	Hs. 74260fNR_045000	ACTR3BP5	FKSG74	ACTR3B	pseudo
chr6-587f 16.84104	0.53061	0.540065	0.982494	0.325857	0.763126	chr6	58731200	58731874	+	O NA	IntergeniALR/Alphe	-770091 NR_13299F	1.07E+08	Hs. 56153fNR_12572Z	ENSG0000LINC0068C	-	long	intencRNA
chr9-439f 25.16198	0.438301	0.446454	0.981399	0.326228	0.763126	chr9	43981627	43981847	+	O NA	IntergeniALR/Alphe	855571 NR_160666	1.03E+08	NR_160669	LOC10272Z	-	methylenz	pseudo
chr20-26f 16.87362	0.527157																	

chr20-27	18.01286	0.486251	0.521257	0.932843	0.350901	0.771949	chr20	27636551	27637602	+	0	NA	IntergeniALR/Alph	965589	NR_13231F	1E+08	Hs.529357NR_13231F	ENSG00000FRG1CP	-	FSHD	regipseudo	
chr19-25	22.7666	0.433393	0.464633	0.932763	0.350942	0.771949	chr19	25348435	25350508	+	0	NA	IntergeniALR/Alph	-186024	NR_00360F	1E+08	Hs.149312NR_00360F	ENSG00000HAVCR1P1	-	hepatitis	pseudo	
chr10-41	33.88095	0.368667	0.395425	0.932332	0.351165	0.771949	chr10	41329702	41329904	+	0	NA	IntergeniALR/Alph	1038242	NR_02438C	441666	Hs.255729NR_02438C	ENSG00000LOC441666	-	zinc	finp	pseudo
chrX-620	33.25949	0.367326	0.394103	0.932056	0.351308	0.771949	chrX	620028972	620030283	+	0	NA	IntergeniALR/Alph	1321705	NM_00101E	139886	Hs.612782NR_00101E	ENSG00000SPIN4	TDRD28	spindlin	protein-coding	
chr9-435	22.21993	0.438226	0.470772	0.930941	0.351884	0.772354	chr9	43585604	43586046	+	0	NA	IntergeniALR/Alph	4596569	NR_160669	1.03E+08	Hs.529357NR_13231F	ENSG00000FRG1CP	-	FSHD	regipseudo	
chr20-28	18.04544	0.483037	0.520149	0.928652	0.353069	0.772354	chr20	28049227	28050735	+	0	NA	IntergeniALR/Alph	552684	NR_13231F	1E+08	Hs.529357NR_13231F	ENSG00000FRG1CP	-	FSHD	regipseudo	
chr21-12	18.04544	0.483037	0.520149	0.928652	0.353069	0.772354	chr21	12257025	12258117	+	0	NA	IntergeniALR/Alph	-780595	NR_02691F	149992	Hs.558644NR_153773	ANKRD30BF	C21orf99	ankyrin	ipseudo	
chr22-13	18.04374	0.482902	0.520114	0.928454	0.353172	0.772354	chr22	13655316	13655946	+	0	NA	IntergeniALR/Alph	1758225	NR_110761	1.03E+08	Hs.652929NR_110761	LOC10272Z	-	uncharact	ncRNA	
chr20-27	18.59097	0.475752	0.513015	0.927365	0.353737	0.772354	chr20	27688376	27688865	+	0	NA	IntergeniALR/Alph	914045	NR_13231F	1E+08	Hs.529357NR_13231F	ENSG00000FRG1CP	-	FSHD	regipseudo	
chr10-40	22.25081	0.435559	0.469882	0.927076	0.353887	0.772354	chr10	40080043	40082761	+	0	NA	IntergeniALR/Alph	1384806	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo
chr20-27	22.25137	0.435598	0.470537	0.925747	0.354578	0.772354	chr20	27537881	27538327	+	0	NA	IntergeniALR/Alph	1064561	NR_13231F	1E+08	Hs.529357NR_13231F	ENSG00000FRG1CP	-	FSHD	regipseudo	
chr19-24	30.20808	0.376771	0.407029	0.925661	0.354622	0.772354	chr19	24848156	24848397	+	0	NA	IntergeniALR/Alph	-684829	NR_00360F	1E+08	Hs.149312NR_00360F	ENSG00000HAVCR1P1	-	hepatitis	pseudo	
chr6-596	17.52851	0.487117	0.526558	0.925058	0.354936	0.772354	chr6	59683252	59683655	+	0	NA	IntergeniALR/Alph	-1722007	NR_132994	1.07E+08	Hs.561539NR_125727	ENSG00000LINC0068C	-	long	intenc	ncRNA
chr7-604	17.52851	0.487117	0.526558	0.925058	0.354936	0.772354	chr7	60400908	60401453	+	0	NA	IntergeniALR/Alph	2902876	NR_00395E	643955	Hs.583309NR_00395E	ENSG00000ZNF733P	ZNF733	zinc	finp	pseudo
chr14-16	17.4965	0.490512	0.530313	0.924948	0.354993	0.772354	chr14	16889979	16890190	+	0	NA	IntergeniALR/Alph	-1711033	NM_00101E	440153	Hs.534888NR_00101E	ENSG00000ORI1H12	-	olfactory	protein-coding	
chr5-487	25.87693	0.409249	0.442711	0.924416	0.35527	0.772354	chr5	48756076	48756298	+	0	NA	IntergeniALR/Alph	1685101	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin	protein-coding	
chr21-11	23.28012	0.431138	0.466657	0.923886	0.355545	0.772354	chr21	11713262	11713687	+	0	NA	IntergeniALR/Alph	1191960	NM_19926C	7179	Hs.122988NM_19925E	ENSG00000TPTE	CT44	PTEN	transmem	protein-coding
chr1-127	109.0333	0.21613	0.234114	0.923184	0.355911	0.772354	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alph	2429015	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB	EMB1	-	embigin	ipseudo
chr15-18	22.24911	0.435455	0.471911	0.922747	0.356139	0.772354	chr15	18545551	18546527	+	0	NA	IntergeniALR/Alph	-1736705	NR_03883C	646096	Hs.448789NR_03883C	ENSG00000CHEK2P2	-	checkpoir	pseudo	
chr6-592	16.95039	0.498756	0.541025	0.921874	0.356594	0.772354	chr6	59217559	59219644	+	0	NA	IntergeniALR/Alph	-1257155	NR_132994	1.07E+08	Hs.561539NR_125727	ENSG00000LINC0068C	-	long	intenc	ncRNA
chr10-40	21.73501	0.437828	0.475598	0.920585	0.357267	0.772354	chr10	40610428	40612734	+	0	NA	IntergeniALR/Alph	1756464	NR_02438C	441666	Hs.255729NR_02438C	ENSG00000LOC441666	-	zinc	finp	pseudo
chr10-40	29.11474	0.382272	0.415492	0.920046	0.357549	0.772354	chr10	40601150	40601654	+	0	NA	IntergeniALR/Alph	1766643	NR_02438C	441666	Hs.255729NR_02438C	ENSG00000LOC441666	-	zinc	finp	pseudo
chr13-17	32.86551	0.360252	0.39159	0.919974	0.357586	0.772354	chr13	17173199	17174252	+	0	NA	IntergeniALR/Alph	-1021572	NR_02727E	26080	Hs.448588NR_02727E	ENSG00000FAM230C	LINC00281	family	winc	ncRNA
chrY-11	17.55939	0.483696	0.525888	0.919769	0.357693	0.772354	chrY	11289000	11289078	+	0	NA	IntergeniIntergeni	1131600	NR_033667	352887	Hs.546221NR_033667	ENSG00000GYC2P1	GYC2P	glycogenip	pseudo	
chr17-26	27.52261	0.398851	0.433754	0.919532	0.357817	0.772354	chr17	26465526	26465743	+	0	NA	IntergeniALR/Alph	623607	NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371	-	uncharact	ncRNA	
chr13-16	17.01272	0.491545	0.534905	0.918938	0.358128	0.772354	chr13	16904428	16905324	+	0	NA	IntergeniALR/Alph	-1293934	NR_02727E	26080	Hs.448588NR_02727E	ENSG00000FAM230C	LINC00281	family	winc	ncRNA
chr5-476	25.97013	0.402232	0.43775	0.918862	0.358168	0.772354	chr5	47636194	47636479	+	0	NA	IntergeniALR/Alph	-1939956	NM_02107Z	348980	Hs.353179NM_02107Z	ENSG00000HCN1	BCNG-1	[B]hyperpol	protein-coding	
chr17-26	36.07131	0.34456	0.375672	0.917182	0.359047	0.77253	chr17	26548951	26549501	+	0	NA	IntergeniALR/Alph	540015	NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371	-	uncharact	ncRNA	
chr10-39	129.6836	0.204303	0.222772	0.917097	0.359092	0.77253	chr10	39967487	39968432	+	0	NA	IntergeniALR/Alph	1271362	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo
chr9-41	28.10663	0.476321	0.519965	0.916063	0.359634	0.77253	chr9	41224934	41225222	+	0	NA	IntergeniIntergeni	-8677	NR_03968E	1.01E+08	NR_03968E	ENSG00000MIR4477A	-	micro	RNA	ncRNA
chr5-484	21.76589	0.435072	0.474967	0.916005	0.359664	0.77253	chr5	48479609	48480534	+	0	NA	IntergeniALR/Alph	1961217	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin	protein-coding	
chr16-34	17.04303	0.487962	0.533571	0.914521	0.360443	0.77253	chr16	34062721	34064881	+	0	NA	IntergeniAluYj4 S	-99777	NR_162093	1.13E+08	NR_162093	MIR9901	-	micro	RNA	ncRNA
chr12-34	26.49338	0.396546	0.433907	0.913898	0.360777	0.77253	chr12	34834858	34835114	+	0	NA	IntergeniALR/Alph	812490	NM_032834	84920	Hs.102971NM_032834	ENSG00000ALG10	ALG10A	[D]ALG10	al	protein-coding
chr7-581	29.1765	0.378139	0.413789	0.913845	0.360798	0.77253	chr7	58181856	58183148	+	0	NA	IntergeniALR/Alph	732325	NM_00115E	441234	Hs.533121NM_00115E	ENSG00000ZNF716	-	zinc	finp	protein-coding
chr19-26	26.00328	0.400048	0.437787	0.913795	0.360825	0.77253	chr19	26488721	26488932	+	0	NA	IntergeniALR/Alph	-1304605	NR_110688	1.02E+08	Hs.567934NR_110688	ENSG00000LOC101927	-	uncharact	ncRNA	
chr10-40	95.35748	0.227123	0.248605	0.913587	0.360934	0.77253	chr10	40412450	40414652	+	0	NA	IntergeniALR/Alph	1716955	NR_045000	399746	Hs.742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo
chr8-458	21.73671	0.43799	0.481185	0.910231	0.362701	0.77253	chr8	45866419	45866767	+	0	NA	IntergeniALR/Alph	715050	NR_146077	389652	NR_146077	ENSG00000ASNSP1	ASNSL1	asparagip	pseudo	
chr19-25	17.58914	0.480157	0.528205	0.909036	0.363331	0.77253	chr19	25840980	25842266	+	0	NA	IntergeniALR/Alph	-1678176	NR_00360F	1E+08	Hs.149312NR_00360F	ENSG00000HAVCR1P1	-	hepatitis	pseudo	
chr5-486	32.92897	0.356674	0.392477	0.908776	0.363468	0.77253	chr5	48696127	48696344	+	0	NA	IntergeniALR/Alph	1745053	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin	protein-coding	
chr11-52	36.08265	0.35108	0.387211	0.90669	0.364571	0.77253	chr11	52323112	52323338	+	0	NA	IntergeniALR/Alph	1914078	NR_024504	646813	Hs.684179NR_024504	LOC646813	-	DEXH	box	pseudo
chr8-858	17.59197	0.480359	0.530757	0.905045	0.365441	0.77253	chr8	85807267	85808822	+	0	NA	IntergeniMLT1F1 L	-4483	NR_003594	1E+08	Hs.535056NR_003594	REXO1L2P	-	REXO1	lip	pseudo
chr21-12	24.97	0.402478	0.444714	0.904972	0.36548	0.77253	chr21	12571974	12573005	+	0	NA	IntergeniALR/Alph	-465677	NR_02691F	149992	Hs.558644NR_153773	ANKRD30BF	C21orf99	ankyrin	ipseudo	
chr11-51	16.5575	0.488862	0.541383	0.902987	0.366533	0.77253	chr11	51795006	51796196	+	0	NA	IntergeniALR/Alph	1386454	NR_024504	646813	Hs.684179NR_024504	LOC646813	-	DEXH	box	pseudo
chr19-26	17.62058	0.476762	0.528159	0.902686	0.366693	0.77253	chr19	26912870	26913508	+	0	NA	IntergeniALR/Alph	-880242	NR_110688	1.02E+08	Hs.567934NR_110688	ENSG00000LOC101927	-	uncharact	ncRNA	
chr1-124	20.73205	0.43965	0.487557	0.901742	0.367194	0.77253	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alph	2861291	NR_00395E	647121	Hs.697682NR_00395E	ENSG00000EMB	EMB1	-	embigin	ipseudo
chr14-17	18.6516	0.468938	0.520446	0.901032	0.367571	0.77253	chr14	17977977	17978260	+	0	NA	IntergeniALR/Alph	-622999	NM_00101E	440153	Hs.534888NR_00101E	ENSG00000ORI1H12	-	olfactory	protein-coding	
chr5-484	21.27872	0.434401	0.482128	0.901006	0.367585	0.77253	chr5	48414025	48414392	+	0	NA	IntergeniALR/Alph	2027080	NM_19844E	133418	Hs.561411NM_19844E	ENSG00000EMB	GP70	embigin	protein-coding	
chr22-14	24.42219	0.406208	0.450965	0.900753	0.36772	0.77253	chr22	14404607	14407328	+	0	NA	IntergeniALR/Alph	-1122192	NR_00100E	81061	Hs.554706NR_00100E	ENSG00000ORI1H1	ORI1H12	[C]olfactory	protein-coding	
chr19-24	31.28613	0.363297	0.403402	0.900583	0.36781	0.77253	chr19	24929888	24931327	+	0	NA	IntergeniALR/Alph	-767160	NR_00360F	1E+08	Hs.149312NR_00360F	ENSG00000HAVCR1P1	-	hepatitis	pseudo	



chr13-17: 17.7288	0.446763	0.524341	0.852048	0.394187	0.77253	chr13	17373537	17375780	+	O NA	IntergeniALR/Alph	-820639	NR_027278	26080	Hs. 44858:NR_027278	ENSG000003FAM230C	LINC00281	family wincRNA
chr1-124: 82.77451	0.225225	0.264376	0.851912	0.394263	0.77253	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alph	3026728	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr18-187: 18.82271	0.434593	0.510504	0.851301	0.394602	0.77253	chr18	18734904	18735299	+	O NA	IntergeniALR/Alph	2376712	NM_005406	6093	Hs. 306307:NM_005406	ENSG000003ROCK1	P160ROCK	Rho assoc protein-coding
chr10-40: 37.92833	0.3135	0.368682	0.850325	0.395144	0.77253	chr10	40599670	40599670	+	O NA	IntergeniALR/Alph	17689430	NR_024388	441666	Hs. 255722:NR_024388	ENSG000003LOC441666	-	zinc fin ipseudo
chr1-122: 21.41951	0.407444	0.479498	0.849731	0.395475	0.77253	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1351013	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr1-124: 17.72823	0.446735	0.525811	0.84961	0.395542	0.77253	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alph	2938015	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr1-123: 41.73917	0.299367	0.352665	0.848872	0.395953	0.77253	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alph	2084346	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr12-37: 31.48755	0.341774	0.402656	0.848799	0.395993	0.77253	chr12	37235338	37240633	+	O NA	IntergeniALR/Alph	-1078789	NM_001011	144245	Hs. 259300:NM_001011	ENSG000003ALG10B	ALG10 KCFALG10	al protein-coding
chr12-37: 21.42008	0.407496	0.480267	0.848478	0.396172	0.77253	chr12	37266624	37266892	+	O NA	IntergeniALR/Alph	-1050016	NM_001011	144245	Hs. 259300:NM_001011	ENSG000003ALG10B	ALG10 KCFALG10	al protein-coding
chr21-127: 17.76025	0.443444	0.522711	0.848354	0.396241	0.77253	chr21	12725269	12726803	+	O NA	IntergeniALR/Alph	-312130	NR_026911	149992	Hs. 55864:NR_153773	ANKRD30BF C21orf99	ankyrin ipseudo	
chr22-14: 17.76025	0.443444	0.522711	0.848354	0.396241	0.77253	chr22	14395521	14396628	+	O NA	IntergeniALR/Alph	-132085	NM_001006	81061	Hs. 554700:NM_001006	ENSG000003OR11H1	OR11H12 Colfactory	protein-coding
chr14-17: 21.99763	0.400458	0.472554	0.847432	0.396754	0.77253	chr14	17052725	17052993	+	O NA	IntergeniALR/Alph	-1548258	NM_001011	440153	Hs. 53488:NM_001011	ENSG000003OR11H12	-	olfactory protein-coding
chr1-121: 52.43178	0.272191	0.321261	0.847259	0.396851	0.77253	chr1	1.22E+08	1.22E+08	+	O NA	IntergeniALR/Alph	256065	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr14-18: 21.93757	0.406962	0.479316	0.847171	0.3969	0.77253	chr14	18066259	18066583	+	O NA	IntergeniALR/Alph	-534696	NM_001011	440153	Hs. 53488:NM_001011	ENSG000003OR11H12	-	olfactory protein-coding
chr21-88: 18.30692	0.437278	0.516176	0.84715	0.396912	0.77253	chr21	8862931	8868354	+	O NA	IntergeniIntergeni	-121357	NR_128711	348980	Hs. 554700:NR_128711	ENSG000003MIR3648	hsa-mir-2	microRNA ncRNA
chr21-12: 25.17085	0.374997	0.443053	0.846392	0.397334	0.77253	chr21	12266369	12268802	+	O NA	IntergeniALR/Alph	-770581	NR_026911	149992	Hs. 55864:NR_153773	ANKRD30BF C21orf99	ankyrin ipseudo	
chr1-123: 28.34521	0.355423	0.420131	0.845982	0.397563	0.77253	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1904068	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr5-47: 25.17029	0.374965	0.443343	0.845767	0.397683	0.77253	chr5	47952831	47954155	+	O NA	IntergeniALR/Alph	-2257113	NM_021072	348980	Hs. 353170:NM_021072	ENSG000003HCN1	BCNG-1 B	hyperpol: protein-coding
chr9-44: 21.9982	0.40049	0.473659	0.845524	0.397818	0.77253	chr9	44147028	44147227	+	O NA	IntergeniALR/Alph	1020961	NR_160669	1.03E+08	NR_160669	LOC102722	-	methylenc pseudo
chr20-29: 18.30635	0.437222	0.517107	0.845515	0.397824	0.77253	chr20	29500852	29501054	+	O NA	IntergeniMSTA LTR	-3619	NR_146067	1.03E+08	NR_146067	FRG1EP	-	FSHD regipseudo
chr20-28: 17.21301	0.449947	0.532292	0.8453	0.397944	0.77253	chr20	28816385	28817766	+	O NA	IntergeniALR/Alph	-214410	NR_132311	1E+08	Hs. 529357:NR_132311	ENSG000003FRG1CP	-	FSHD regipseudo
chr18-79: 17.75911	0.443357	0.524656	0.845044	0.398087	0.77253	chr18	79618662	79620626	+	O NA	IntergeniIntergeni	40362	NR_148949	284240	Hs. 44891:NR_148949	LOC28424	-	uncharactncRNA
chr21-11: 41.80262	0.29655	0.351028	0.844802	0.398221	0.77253	chr21	11641143	11642059	+	O NA	IntergeniALR/Alph	1120087	NM_199260	7179	Hs. 12298:NM_199255	ENSG000003TPTE	CT44 PTE	transmem protein-coding
chr1-122: 45.03761	0.287126	0.340082	0.844284	0.398511	0.77253	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1258736	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr19-26: 32.12799	0.334228	0.395895	0.844233	0.398539	0.77253	chr19	26965800	26968012	+	O NA	IntergeniALR/Alph	-826525	NR_110688	1.02E+08	Hs. 56793:NR_110688	ENSG000003LOC101927	-	uncharactncRNA
chr1-124: 28.92333	0.351005	0.415772	0.844225	0.398544	0.77253	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alph	3228454	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr7-58: 224.5676	0.153669	0.182119	0.844232	0.399099	0.77253	chr7	58797682	58798049	+	O NA	IntergeniALR/Alph	1347688	NM_001155	441234	Hs. 553121:NM_001155	ENSG000003ZNF716	-	zinc fin protein-coding
chr21-11: 44.46289	0.289395	0.343282	0.843023	0.399215	0.77253	chr21	11968826	11969139	+	O NA	IntergeniALR/Alph	-1069184	NR_026911	149992	Hs. 55864:NR_153773	ANKRD30BF C21orf99	ankyrin ipseudo	
chr5-47: 60.58991	0.253465	0.300896	0.842965	0.399248	0.77253	chr5	47604224	47604455	+	O NA	IntergeniALR/Alph	-1907959	NM_021072	348980	Hs. 353170:NM_021072	ENSG000003HCN1	BCNG-1 B	hyperpol: protein-coding
chr1-122: 32.12856	0.332653	0.396767	0.84244	0.399542	0.77253	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1406417	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr11-54: 17.24446	0.446517	0.53052	0.841659	0.399979	0.77253	chr11	54298656	54298870	+	O NA	IntergeniALR/Alph	305235	NM_001004	119749	Hs. 55356:NM_001004	ENSG000003OR4C46	-	olfactory protein-coding
chr1-121: 17.24389	0.44647	0.530509	0.841588	0.400018	0.77253	chr1	1.22E+08	1.22E+08	+	O NA	IntergeniALR/Alph	232824	NR_003955	647121	Hs. 697682:NR_003955	ENSG000003EMPB1	-	embigin ipseudo
chr21-93: 17.79169	0.44014	0.523089	0.841425	0.40011	0.77253	chr21	9360015	9361765	+	O NA	IntergeniCER Satel	-182140	NR_135512	1.05E+08	NR_135512	LOC105375	-	nuclear ipseudo
chr11-94: 20.90259	0.409063	0.486303	0.841169	0.400253	0.77253	chr11	94237872	94239845	+	O NA	IntergeniLIPA4 LIN	-66779	NM_001199	390243	Hs. 55375:NM_001088	ENSG000003IZUM01R	FOLR4 FolIZUM01	re protein-coding
chr10-41: 24.5916	0.380594	0.45281	0.840515	0.40062	0.77253	chr10	41084181	41084400	+	O NA	IntergeniALR/Alph	1283755	NR_024388	441666	Hs. 255722:NR_024388	ENSG000003LOC441666	-	zinc fin pseudo
chr13-17: 27.7974	0.357877	0.425844	0.840396	0.400687	0.77253	chr13	17659813	17660072	+	O NA	IntergeniALR/Alph	-535355	NR_027278	26080	Hs. 44858:NR_027278	ENSG000003FAM230C	LINC00281	family wincRNA
chr6-58: 91.17855	0.211475	0.251753	0.84001	0.400903	0.77253	chr6	58450046	58450908	+	O NA	IntergeniALR/Alph	-489031	NR_132299	1.07E+08	Hs. 56153:NR_125727	ENSG000003LINC0068	-	long intncRNA
chr18-19: 17.79226	0.440176	0.524577	0.839106	0.40141	0.77253	chr18	19658491	19658701	+	O NA	IntergeniALR/Alph	1453217	NR_005406	6093	Hs. 306307:NM_005406	ENSG000003ROCK1	P160ROCK	Rho assoc protein-coding
chr20-27: 20.9346	0.406264	0.484434	0.838637	0.401673	0.77253	chr20	27613897	27614827	+	O NA	IntergeniALR/Alph	988303	NR_132311	1E+08	Hs. 529357:NR_132311	ENSG000003FRG1CP	-	FSHD regipseudo
chr22-14: 31.03238	0.33789	0.403737	0.836905	0.402646	0.77253	chr22	14307405	14308740	+	O NA	IntergeniALR/Alph	-1220087	NM_001006	81061	Hs. 554700:NM_001006	ENSG000003OR11H1	OR11H12 Colfactory	protein-coding
chr20-28: 17.27534	0.443072	0.52982	0.83627	0.403003	0.77253	chr20	28868562	28871424	+	O NA	IntergeniALR/Alph	-210397	NR_132311	1.03E+08	NR_132311	FRG1DP	-	FSHD regipseudo
chr10-40: 27.85973	0.353573	0.422941	0.835986	0.403163	0.77253	chr10	48078269	48079804	+	O NA	IntergeniALR/Alph	1489009	NR_024388	441666	Hs. 255722:NR_024388	ENSG000003LOC441666	-	zinc fin pseudo
chr20-26: 31.0644	0.336001	0.402187	0.835436	0.403472	0.77253	chr20	26050593	26059724	+	O NA	IntergeniALR/Alph	-839235	NR_040099	284801	Hs. 370699:NR_040099	ENSG000003MIR663AH	-	MIR663A lncRNA
chr14-17: 31.06383	0.335974	0.402176	0.83539	0.403498	0.77253	chr14	17911126	17911452	+	O NA	IntergeniALR/Alph	-689828	NM_001011	440153	Hs. 53488:NM_001011	ENSG000003OR11H12	-	olfactory protein-coding
chr12-35: 16.6652	0.457005	0.547094	0.835333	0.40353	0.77253	chr12	35466939	35467386	+	O NA	IntergeniALR/Alph	1444666	NM_032834	84920	Hs. 102971:NM_032834	ENSG000003ALG10	ALG10A DIALG10	al protein-coding
chr10-41: 20.96492	0.403379	0.482949	0.835242	0.403582	0.77253	chr10	41011090	41011491	+	O NA	IntergeniALR/Alph	1356755	NR_024388	441666	Hs. 255722:NR_024388	ENSG000003LOC441666	-	zinc fin pseudo
chr13-17: 16.7281	0.44973	0.538755	0.834758	0.403854	0.77253	chr13	17947873	17949276	+	O NA	IntergeniALR/Alph	-246723	NR_027278	26080	Hs. 44858:NR_027278	ENSG000003FAM230C	LINC00281	family wincRNA
chr22-14: 16.7281	0.44973	0.538755	0.834758	0.403854	0.77253	chr22	14234319	14236688	+	O NA	IntergeniALR/Alph	-1292658	NM_001006	81061				

chr3-937	28.48317	0.335889	0.422835	0.794374	0.426978	0.77253	chr3	93707920	93708854	+	0	NA	IntergeniALR/Alphe	265694	NM_001314	5627	Hs.64016	NM_00031	ENSG00000	PROS1	PROS1	PS21	protein	protein-coding				
chr18-205	25.30995	0.352763	0.444479	0.793653	0.427397	0.77253	chr18	20920124	20922964	+	0	NA	IntergeniALR/Alphe	290269	NM_005406	6093	Hs.306307	NM_00540	ENSG00000	ROCK1	P160ROCK	Rho	assoc	protein-coding				
chr11-532	23.22837	0.367796	0.463472	0.793567	0.427448	0.77253	chr11	53208782	53209058	+	0	NA	IntergeniALR/Alphe	1395078	NM_001004	119749	Hs.553564	NM_00100	ENSG00000	OR4C46			olfactory	protein-coding				
chrX-618	18.99325	0.400855	0.50609	0.792063	0.428324	0.77253	chrX	61821703	61822775	+	0	NA	IntergeniALR/Alphe	1529093	NM_001012	139886	Hs.612782	NM_00101	ENSG00000	SPIN4	TDRD28	spindlin	protein-coding					
chr19-271	49.03739	0.25892	0.326892	0.791848	0.428449	0.77253	chr19	27155416	27156226	+	0	NA	IntergeniALR/Alphe	637610	NR_211068	1.02E+08	Hs.567934	NR_21106	ENSG00000	LOC101927			uncharact	ncRNA				
chr9-434	18.99382	0.400897	0.506552	0.791423	0.428697	0.77253	chr9	43404739	43405154	+	0	NA	IntergeniALR/Alphe	278780	NR_160666	1.03E+08	NR_160669	LOC10272						methylene	pseudo			
chr10-405	18.41457	0.40893	0.516704	0.791421	0.428698	0.77253	chr10	40966719	40967731	+	0	NA	IntergeniALR/Alphe	1400820	NR_02438C	441666	Hs.255722	NR_02438	ENSG00000	LOC441666					zinc	fin	pseudo	
chr10-407	22.71315	0.368525	0.465746	0.791258	0.428794	0.77253	chr10	40715108	40715938	+	0	NA	IntergeniALR/Alphe	1652522	NR_02438C	441666	Hs.255722	NR_02438	ENSG00000	LOC441666					zinc	fin	pseudo	
chr5-473	44.72607	0.271896	0.343864	0.790708	0.429114	0.77253	chr5	47333264	47333476	+	0	NA	IntergeniALR/Alphe	1636990	NM_021072	348980	Hs.353177	NM_02107	ENSG00000	HCN1	BCNG-1	BC	hyperpol	protein-coding				
chr19-263	19.4759	0.402104	0.508906	0.790134	0.429449	0.77253	chr19	26365465	26365668	+	0	NA	IntergeniALR/Alphe	1427865	NR_110688	1.02E+08	Hs.567934	NR_11068	ENSG00000	LOC101927					uncharact	ncRNA		
chr22-132	22.16648	0.371885	0.47077	0.78995	0.429557	0.77253	chr22	13566804	13567041	+	0	NA	IntergeniALR/Alphe	1669516	NR_110761	1.03E+08	Hs.652922	NR_11076	ENSG00000	LOC102722					uncharact	ncRNA		
chr8-8577	18.44602	0.405716	0.513799	0.78964	0.429738	0.77253	chr8	85772118	85779128	+	0	NA	non-codir	non-codir	470	NR_003594	1E+08	Hs.535056	NR_003594	REX01L2P					REX01	lip	pseudo	
chr13-171	22.13786	0.374766	0.475025	0.788939	0.430148	0.77253	chr13	17175128	17175365	+	0	NA	IntergeniALR/Alphe	1020051	NR_027278	26080	Hs.44858	NR_02727	ENSG00000	FAM230C	LINC00281	family	wincRNA					
chr20-277	18.44545	0.405682	0.51473	0.788146	0.430612	0.77253	chr20	27764752	27766026	+	0	NA	IntergeniALR/Alphe	837276	NR_13231E	1E+08	Hs.529357	NR_13231	ENSG00000	FRG1CP					FSHD	regip	pseudo	
chr10-402	31.17148	0.320302	0.406961	0.787058	0.431248	0.77253	chr10	40626293	40263185	+	0	NA	IntergeniALR/Alphe	1566293	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo					
chr11-525	16.36784	0.43477	0.553042	0.786143	0.431784	0.77253	chr11	52550681	52550907	+	0	NA	IntergeniALR/Alphe	2053204	NM_001004	119749	Hs.553564	NM_00100	ENSG00000	OR4C46					olfactory	protein-coding		
chr3-921	18.99495	0.400973	0.510217	0.785888	0.431933	0.77253	chr3	91213803	91214340	+	0	NA	IntergeniALR/Alphe	2106450	NM_00523E	2042	Hs.123642	NM_00523	ENSG00000	EPHA3	EK4 ETK	E EPH	recept	protein-coding				
chr1-1123	19.02413	0.397739	0.506527	0.785227	0.432322	0.77253	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2215157	NR_00395E	647121	Hs.697682	NR_00395	ENSG00000	EMBP1					embigin	pseudo		
chr1-1247	19.02413	0.397739	0.506527	0.785227	0.432322	0.77253	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3249819	NR_00395E	647121	Hs.697682	NR_00395	ENSG00000	EMBP1					embigin	pseudo		
chr10-402	18.47746	0.402558	0.512811	0.785002	0.432452	0.77253	chr10	40284697	40289739	+	0	NA	IntergeniALR/Alphe	1590622	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo					
chr21-887	18.47746	0.402558	0.512811	0.785002	0.432452	0.77253	chr21	8871428	8872191	+	0	NA	IntergeniL2c	LINE1	115190	NR_128711	1.04E+08	NR_128711	ENSG00000	MIR3648	hsa-mir-	microRNA	ncRNA					
chr21-931	18.47746	0.402558	0.512811	0.785002	0.432452	0.77253	chr21	9317371	9321746	+	0	NA	IntergeniLIMA3	LINE1	189797	NR_03832E	1E+08	Hs.487562	NM_17494	ENSG00000	TEKT4P2	MAFIPL Tf	tektin	4	pseudo			
chr20-277	35.04917	0.299496	0.381574	0.784895	0.432515	0.77253	chr20	27716405	27717108	+	0	NA	IntergeniALR/Alphe	885909	NR_13231E	1E+08	Hs.529357	NR_13231	ENSG00000	FRG1CP					FSHD	regip	pseudo	
chr19-256	29.70004	0.323756	0.412603	0.784666	0.432649	0.77253	chr19	25641070	25640383	+	0	NA	IntergeniALR/Alphe	1476829	NR_050360	1E+08	Hs.149312	NR_00360	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr1-1225	28.60782	0.327519	0.417418	0.784631	0.43267	0.77253	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1394132	NR_00395E	647121	Hs.697682	NR_00395	ENSG00000	EMBP1					embigin	pseudo		
chr10-408	28.60669	0.32746	0.417396	0.784531	0.432729	0.77253	chr10	40835166	40835661	+	0	NA	IntergeniALR/Alphe	1532633	NR_02438C	441666	Hs.255722	NR_02438	ENSG00000	LOC441666					zinc	fin	pseudo	
chr5-492	50.1908	0.255556	0.325792	0.784415	0.432797	0.77253	chr5	49245693	49245934	+	0	NA	IntergeniALR/Alphe	1195475	NM_19844E	133418	Hs.561411	NM_19844	ENSG00000	EMB	GP70				embigin	protein-coding		
chr20-267	25.40202	0.345681	0.441226	0.783456	0.433359	0.77253	chr20	26724437	26725594	+	0	NA	IntergeniALR/Alphe	515782	NR_04009E	284801	Hs.370699	NR_04009	ENSG00000	MIR663AH					MIR663A	lncRNA		
chr9-606	38.02971	0.331561	0.423224	0.783417	0.433382	0.77253	chr9	60604847	60605060	+	0	NA	IntergeniALR/Alphe	309454	NM_015667	26165	Hs.123004	NM_01566	ENSG00000	SPATA31A7	AEP1 C9o	SPATA31	s	protein-coding				
chr5-4936	31.84337	0.31113	0.397186	0.783334	0.433431	0.77253	chr5	49366294	49368506	+	0	NA	IntergeniALR/Alphe	1073888	NM_19844E	133418	Hs.561411	NM_19844	ENSG00000	EMB	GP70				embigin	protein-coding		
chr1-1227	142.9741	0.167307	0.213741	0.782753	0.433772	0.77253	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1222505	NR_00395E	647121	Hs.697682	NR_00395	ENSG00000	EMBP1					embigin	pseudo		
chr1-1223	31.2967	0.312609	0.400886	0.779794	0.433512	0.77253	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1006062	NR_00395E	647121	Hs.697682	NR_00395	ENSG00000	EMBP1					embigin	pseudo		
chr19-243	37.79811	0.285938	0.36728	0.778528	0.436258	0.77253	chr19	24816037	24816300	+	0	NA	IntergeniALR/Alphe	652721	NR_00360E	1E+08	Hs.149312	NR_00360	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr5-495	21.68213	0.369982	0.475251	0.7785	0.436274	0.77253	chr5	49555878	49558771	+	0	NA	IntergeniALR/Alphe	883964	NM_19844E	133418	Hs.561411	NM_19844	ENSG00000	EMB	GP70				embigin	protein-coding		
chr20-28	28.02744	0.331502	0.426358	0.777519	0.436852	0.77253	chr20	28473910	28474450	+	0	NA	IntergeniALR/Alphe	128485	NR_13231E	1E+08	Hs.529357	NR_13231	ENSG00000	FRG1CP					FSHD	regip	pseudo	
chr19-25	33.98501	0.30007	0.386078	0.777226	0.437025	0.77253	chr19	25317917	25319074	+	0	NA	IntergeniALR/Alphe	1155048	NR_00360E	1E+08	Hs.149312	NR_00360	ENSG00000	HAVCR1P1					hepatitis	pseudo		
chr14-166	17.96167	0.404358	0.520353	0.777084	0.437109	0.77253	chr14	16686005	16686238	+	0	NA	IntergeniALR/Alphe	1914996	NM_00101E	440153	Hs.53488	NM_00101	ENSG00000	OR11H12					olfactory	protein-coding		
chr18-15	17.96167	0.404358	0.520353	0.777084	0.437109	0.77253	chr18	15505843	15506935	+	0	NA	IntergeniALR/Alphe	180470	NR_027417	644669	Hs.579474	NR_02741	ENSG00000	LOC644666					ankyrin	pseudo		
chr6-585	31.32645	0.310659	0.399972	0.776702	0.437335	0.77253	chr6	58560741	58561589	+	0	NA	IntergeniALR/Alphe	599719	NR_132994	1.07E+08	Hs.561539	NR_12572	ENSG00000	LINC0068					long	intenc	ncRNA	
chr19-266	44.27147	0.268413	0.345599	0.776661	0.437359	0.77253	chr19	268607921	268608214	+	0	NA	IntergeniALR/Alphe	985364	NR_110688	1.02E+08	Hs.567934	NR_11068	ENSG00000	LOC101927					uncharact	ncRNA		
chr12-357	18.47916	0.402703	0.51855	0.776595	0.437398	0.77253	chr12	35786055	35786498	+	0	NA	IntergeniALR/Alphe	1763780	NM_03283A	84920	Hs.102971	NM_03283	ENSG00000	ALG10	ALG10A D	ALG10	al	protein-coding				
chr17-23	19.05558	0.394628	0.508337	0.776312	0.437565	0.77253	chr17	23531109	23531338	+	0	NA	IntergeniALR/Alphe	1008112	NM_00119C	1E+08	Hs.74018	NM_00119	ENSG00000	MTRNR2L1	HN1	MT-RNR2	l	protein-coding				
chr1-1241	54.60042	0.242063	0.311926	0.776029	0.437732	0.77253	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2625353	NR_00395E	647121	Hs.697682	NR_00395	ENSG00000	EMBP1					embigin	pseudo		
chr5-4791	34.01532	0.298292	0.385183	0.774416	0.438685	0.77253	chr5	47912908	47914813	+	0	NA	IntergeniALR/Alphe	2217480	NM_021072	348980	Hs.353177	NM_02107	ENSG00000	HCN1	BCNG-1	BC	hyperpol	protein-coding				
chr6-594	17.32123	0.42034	0.543487	0.773587	0.439175	0.77253	chr6	59404713	59405272	+	0	NA	IntergeniALR/Alphe	1443546	NR_132994	1.07E+08	Hs.561539	NR_12572	ENSG00000	LINC0068					long	intenc	ncRNA	
chr17-251	70.94871	0.216292	0.279804	0.77301	0.439516</																							



chr15-196	17.02046	0.397635	0.536098	0.74172	0.458257	0.773878	chr15	19640129	19641599	+	0	NA	IntergeniALR/Alph	-641880	NR_038836	646096	Hs.448788	NR_038836	ENSG000004CHEK2P2	-	checkpoirpseudo
chr7-582	19.64758	0.370088	0.499683	0.740646	0.458908	0.773878	chr7	58237971	58238218	+	0	NA	IntergeniALR/Alph	787917	NM_001156	441234	Hs.533121	NM_001156	ENSG000004ZNF716	-	zinc_fingprotein-coding
chr1-124	48.11233	0.247629	0.334767	0.739705	0.459479	0.773878	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alph	3389561	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMBP1	-	embigin_pseudo
chr19-26	16.47232	0.402977	0.545012	0.739429	0.459647	0.773878	chr19	26053111	26054021	+	0	NA	IntergeniALR/Alph	-1739865	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chr10-407	29.32447	0.304497	0.412388	0.739056	0.459873	0.773878	chr10	40728317	40728966	+	0	NA	IntergeniALR/Alph	1639104	NR_024388	441666	Hs.255729	NR_024388	ENSG000004LOC441666	-	zinc_fingpseudo
chr1-122	19.67959	0.367164	0.497601	0.737868	0.460595	0.773878	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alph	1000342	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMBP1	-	embigin_pseudo
chr21-11	19.67959	0.367164	0.497601	0.737868	0.460595	0.773878	chr21	11943528	11945172	+	0	NA	IntergeniALR/Alph	-1093816	NR_026910	149992	Hs.558644	NM_153773	ANKR230BF	C21orf99	ankyrin_pseudo
chr5-475	43.37615	0.254434	0.344876	0.737755	0.460663	0.773878	chr5	47583167	47584355	+	0	NA	IntergeniALR/Alph	-1887381	NM_021072	348980	Hs.353176	NM_021072	ENSG000004HCN1	BCNG-1	BC(hyperpol)protein-coding
chr6-592	22.88426	0.341354	0.463341	0.736723	0.461291	0.773878	chr6	59283368	59285706	+	0	NA	IntergeniALR/Alph	-1323091	NR_132994	1.07E+08	Hs.561539	NR_125727	ENSG000004LINC0068C	-	long_intencRNA
chr1-123	22.88369	0.341318	0.46333	0.736662	0.461328	0.773878	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alph	1812138	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMBP1	-	embigin_pseudo
chr20-26	33.62588	0.290677	0.394665	0.736515	0.461417	0.773878	chr20	26610253	26610471	+	0	NA	IntergeniALR/Alph	-401129	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AH	-	MIR663A_lncRNA
chr14-171	34.70223	0.281499	0.382551	0.735847	0.461824	0.773878	chr14	17151416	17151772	+	0	NA	IntergeniALR/Alph	-1449523	NM_001010	440153	Hs.534888	NM_001010	ENSG000004C11H12	-	olfactoryprotein-coding
chr20-26	32.01165	0.292064	0.396767	0.73572	0.461901	0.773878	chr20	26529149	26529574	+	0	NA	IntergeniALR/Alph	-320128	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AH	-	MIR663A_lncRNA
chr5-488	22.88313	0.341285	0.46402	0.735498	0.462036	0.773878	chr5	48847443	48847675	+	0	NA	IntergeniALR/Alph	1593729	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	embigin protein-coding
chr5-477	42.87566	0.258848	0.351949	0.735472	0.462052	0.773878	chr5	47738527	47738743	+	0	NA	IntergeniALR/Alph	-2042255	NM_021072	348980	Hs.353176	NM_021072	ENSG000004HCN1	BCNG-1	BC(hyperpol)protein-coding
chr7-588	225.5063	0.134167	0.182449	0.735366	0.462117	0.773878	chr7	58818464	58818831	+	0	NA	IntergeniALR/Alph	1368470	NM_001156	441234	Hs.533121	NM_001156	ENSG000004ZNF716	-	zinc_fingprotein-coding
chr19-25	22.85508	0.344108	0.468783	0.734045	0.462921	0.774307	chr19	25879761	25880228	+	0	NA	IntergeniALR/Alph	-1716547	NR_003600	1E+08	Hs.149312	NR_003600	ENSG000004HAVCR1P1	-	hepatitis_pseudo
chr10-41	20.22546	0.363382	0.495134	0.733907	0.463005	0.774307	chr10	41231540	41232264	+	0	NA	IntergeniALR/Alph	1126143	NR_024388	441666	Hs.255729	NR_024388	ENSG000004LOC441666	-	zinc_fingpseudo
chr19-25	32.04366	0.29027	0.395726	0.733513	0.463246	0.774307	chr19	25087989	25090298	+	0	NA	IntergeniALR/Alph	-925696	NR_003600	1E+08	Hs.149312	NR_003600	ENSG000004HAVCR1P1	-	hepatitis_pseudo
chr17-26	18.34372	-0.38034	0.519521	-0.7321	0.464108	0.774691	chr17	26522137	26522377	+	0	NA	IntergeniALR/Alph	566984	NR_135673	1.05E+08	Hs.649919	NR_135673	LOC105371	-	uncharactncRNA
chrX-606	22.91514	0.338791	0.462872	0.731932	0.46421	0.774691	chrX	60691088	60692269	+	0	NA	IntergeniALR/Alph	2659654	NM_001010	139886	Hs.612782	NM_001010	ENSG000004SPIN4	TDRD28	spindlin protein-coding
chr10-401	31.94054	0.305369	0.417371	0.731649	0.464383	0.774691	chr10	40101700	40101946	+	0	NA	IntergeniALR/Alph	1405227	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B_pseudo
chr19-25	19.71104	0.364224	0.498099	0.731228	0.46464	0.774691	chr19	25274916	25276192	+	0	NA	IntergeniALR/Alph	-1121107	NR_003600	1E+08	Hs.149312	NR_003600	ENSG000004HAVCR1P1	-	hepatitis_pseudo
chr20-26	22.36733	0.341359	0.468984	0.727869	0.466694	0.77628	chr20	26682555	26683121	+	0	NA	IntergeniALR/Alph	-473605	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AH	-	MIR663A_lncRNA
chr1-124	42.31312	0.253895	0.349669	0.726102	0.467777	0.778438	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alph	3104247	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMBP1	-	embigin_pseudo
chr5-490	22.94602	0.336228	0.463074	0.72608	0.46779	0.778438	chr5	49044907	49045106	+	0	NA	IntergeniALR/Alph	1396288	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	embigin protein-coding
chr9-638	18.58511	0.375107	0.517205	0.725259	0.468293	0.778438	chr9	63816670	63819888	+	0	NA	non-codir non-codir	-1295	NR_039688	1.03E+08	Hs.641018	NR_039688	ENSG000004MIR4477B	-	microRNA_ncRNA
chr14-17	19.19411	0.364818	0.5033	0.724852	0.468543	0.778438	chr14	17267006	17268332	+	0	NA	IntergeniALR/Alph	-1333448	NM_001010	440153	Hs.534888	NM_001010	ENSG000004C11H12	-	olfactoryprotein-coding
chr5-483	19.19468	0.364861	0.503761	0.724275	0.468897	0.778438	chr5	48333308	48335096	+	0	NA	IntergeniALR/Alph	2107086	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	embigin protein-coding
chr1-121	22.39878	0.338769	0.467775	0.724213	0.468935	0.778438	chr1	1.22E+08	1.22E+08	+	0	NA	IntergeniALR/Alph	93514	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMBP1	-	embigin_pseudo
chr19-26	51.62806	0.231925	0.320458	0.723729	0.469232	0.778446	chr19	26842726	26843730	+	0	NA	IntergeniALR/Alph	-950203	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chr5-495	22.39991	0.338848	0.469248	0.722109	0.470227	0.77961	chr5	49568766	49569772	+	0	NA	IntergeniALR/Alph	872019	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	embigin protein-coding
chr5-475	18.58681	0.375337	0.502121	0.721633	0.47052	0.77961	chr5	47509245	47509859	+	0	NA	IntergeniALR/Alph	-1813172	NM_021072	348980	Hs.353176	NM_021072	ENSG000004HCN1	BCNG-1	BC(hyperpol)protein-coding
chr20-26	16.567	0.39231	0.544373	0.720664	0.471116	0.780005	chr20	26935661	26935885	+	0	NA	IntergeniALR/Alph	-726540	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AH	-	MIR663A_lncRNA
chr20-26	21.85211	0.341479	0.474532	0.719612	0.471764	0.780005	chr20	26492232	26494517	+	0	NA	IntergeniALR/Alph	-284141	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AH	-	MIR663A_lncRNA
chrX-604	36.35895	0.270657	0.37647	0.718934	0.472182	0.780005	chrX	60403677	60404348	+	0	NA	IntergeniALR/Alph	-2493379	NM_007156	7789	Hs.550099	NM_007156	ENSG000004XZDA	ZNF896	zinc_fingprotein-coding
chr19-25	19.22556	0.361806	0.503774	0.71819	0.47264	0.780005	chr19	25299739	25300645	+	0	NA	IntergeniALR/Alph	-1136745	NR_003600	1E+08	Hs.149312	NR_003600	ENSG000004HAVCR1P1	-	hepatitis_pseudo
chr9-436	18.58738	0.375475	0.523052	0.717854	0.472847	0.780005	chr9	43642011	43642367	+	0	NA	IntergeniALR/Alph	516023	NR_160669	1.03E+08	Hs.641018	NR_160669	LOC102722	-	methylencpseudo
chr3-930	23.12135	-0.33311	0.464091	-0.71778	0.472895	0.780005	chr3	93039078	93039324	+	0	NA	IntergeniALR/Alph	934880	NM_001314	5627	Hs.64016	NM_000310	ENSG000004PROS1	PROS1	PROS1protein_coding
chr14-17	19.71166	0.358147	0.498987	0.717749	0.472912	0.780005	chr14	17493227	17493455	+	0	NA	IntergeniALR/Alph	-1197776	NM_001010	440153	Hs.534888	NM_001010	ENSG000004C11H12	-	olfactoryprotein-coding
chr7-591	25.08652	0.318861	0.444444	0.717438	0.473104	0.780005	chr7	59148624	59149855	+	0	NA	IntergeniALR/Alph	1699062	NM_001156	441234	Hs.533121	NM_001156	ENSG000004ZNF716	-	zinc_fingprotein-coding
chr11-53	18.67832	0.365528	0.510131	0.716536	0.47366	0.78044	chr11	53976930	53977942	+	0	NA	IntergeniALR/Alph	626562	NM_001004	119749	Hs.553564	NM_001004	ENSG000004OR4C46	-	olfactoryprotein-coding
chr11-51	21.88299	0.338785	0.473255	0.71586	0.474078	0.780644	chr11	51703196	51703427	+	0	NA	IntergeniALR/Alph	1294164	NR_024504	646813	Hs.684179	NR_024504	LOC646813	-	DEXH-box_pseudo
chr17-25	68.58307	0.205539	0.287374	0.715232	0.474466	0.7808	chr17	25115349	25115596	+	0	NA	IntergeniALR/Alph	1973769	NR_135673	1.05E+08	Hs.649919	NR_135673	LOC105371	-	uncharactncRNA
chr8-450	33.7307	0.276258	0.386672	0.714451	0.474949	0.781111	chr8	45039184	45039618	+	0	NA	IntergeniALR/Alph	1578242	NR_146077	389652	NR_146077	ENSG000004ASNSP1	ASNSL1	asparagipseudo	
chr1-123	26.21358	0.312923	0.438743	0.713226	0.475706	0.781258	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alph	1878537	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMBP1	-	embigin_pseudo
chr20-26	24.54042	0.320922	0.450089	0.713017	0.475835	0.781258	chr20	26440940	26442327	+	0	NA	IntergeniALR/Alph	-232400	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AH	-	MIR663A_lncRNA
chr22-13	21.84984	0.341392	0.479043	0.712654	0.47606	0.781258	chr22	13359040	13359253	+	0	NA	IntergeniALR/Alph	1461740	NR_110761	1.03E+08	Hs.652929	NR_110761	LOC102722	-	uncharactncRNA
chr11-51	28.35522	0.299493	0.420553	0.712141	0.476377	0.781258	chr11	51409752	51409974	+	0	NA	IntergeniALR/Alph	1000716	NR_024504	646813	Hs.684179	NR_024504	LOC6		

chr22-137	18.14343	-0.35131	0.523139	-0.67154	0.501877	0.786204	chr22	13741327	13741546	+	O	NA	IntergeniALR/Alphe	-1786723	NM_001006	81061	Hs.55470c	NM_001006	ENSG00000C	OR11H1	Colfatoryprotein-coding		
chr20-288	16.67578	0.361666	0.538571	0.671528	0.501884	0.786204	chr20	28876175	28877743	+	O	NA	IntergeniALR/Alphe	-203431	NR_132316	1.03E+08	Hs.55470c	NM_001006	ENSG00000C	FRG1DP	FSHD	regipseudo	
chrX-6207	19.87931	0.332794	0.496187	0.670703	0.50241	0.786204	chrX	62074740	62075452	+	O	NA	IntergeniALR/Alphe	1276236	NM_001012	139886	Hs.612782	NM_001012	ENSG00000C	SPIN4	TDRD28	spindlin protein-coding	
chr1-1247	148.0935	0.142021	0.290991	0.670529	0.502521	0.786204	chr1	1.25E+08	1.25E+08	+	O	NA	IntergeniALR/Alphe	3206061	NR_003955	647121	Hs.697682	NR_003955	ENSG00000C	EMBPP1	-	embigin ipseudo	
chr11-534	69.38159	0.191702	0.285956	0.670389	0.50261	0.786204	chr11	53456744	53456998	+	O	NA	IntergeniALR/Alphe	1147127	NM_001004	119749	Hs.553564	NM_001004	ENSG00000C	OR4C46	-	olfactoryprotein-coding	
chr5-4982	21.74868	-0.32032	0.478145	-0.66992	0.50291	0.786204	chr5	49828223	49828495	+	O	NA	IntergeniALR/Alphe	612929	NM_198444	133418	Hs.561411	NM_198444	ENSG00000C	EMB	GP70	embigin protein-coding	
chr20-264	41.35831	0.342277	0.361731	0.669771	0.503004	0.786204	chr20	26484563	26484792	+	O	NA	IntergeniALR/Alphe	-275444	NR_040099	284801	Hs.370699	NR_040099	ENSG00000C	MIR663AHC	-	MIR663A lncRNA	
chr5-4805	19.91076	0.292989	0.494581	0.667028	0.504754	0.786204	chr5	48093610	48093895	+	O	NA	IntergeniALR/Alphe	2347536	NM_198444	133418	Hs.561411	NM_198444	ENSG00000C	EMB	GP70	embigin protein-coding	
chr20-264	44.80832	0.227103	0.34065	0.666675	0.50498	0.786204	chr20	26523033	26523517	+	O	NA	IntergeniALR/Alphe	-314042	NR_040099	284801	Hs.370699	NR_040099	ENSG00000C	MIR663AHC	-	MIR663A lncRNA	
chr7-6061	19.33321	0.335743	0.504143	0.665966	0.505433	0.786204	chr7	60618684	60619039	+	O	NA	IntergeniALR/Alphe	2685195	NR_003952	643955	Hs.583308	NR_003952	ENSG00000C	ZNF733P	ZNF733	zinc finipseudo	
chr20-288	16.70609	0.358125	0.537843	0.665855	0.505504	0.786204	chr20	28820977	28821467	+	O	NA	IntergeniALR/Alphe	-2185097	NR_132316	1E+08	Hs.529355	NR_132316	ENSG00000C	FRG1CP	-	FSHD	regipseudo
chr22-148	16.70609	0.358125	0.537843	0.665855	0.505504	0.786204	chr22	14858720	14859124	+	O	NA	IntergeniALR/Alphe	-669237	NM_001006	81061	Hs.55470c	NM_001006	ENSG00000C	OR11H1	OR11H12	Colfatoryprotein-coding	
chr2-9215	19.91019	0.329588	0.495433	0.665797	0.505541	0.786204	chr2	92197201	92198000	+	O	NA	IntergeniALR/Alphe	256467	NR_027714	440888	Hs.730239	NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr5-4854	19.3012	0.338825	0.508986	0.665687	0.505611	0.786204	chr5	48540092	48540405	+	O	NA	IntergeniALR/Alphe	1901040	NM_198444	133418	Hs.561411	NM_198444	ENSG00000C	EMB	GP70	embigin protein-coding	
chrX-6095	25.22562	0.29713	0.446508	0.665453	0.505761	0.786204	chrX	60950116	60951190	+	O	NA	IntergeniALR/Alphe	2400679	NM_001012	139886	Hs.612782	NM_001012	ENSG00000C	SPIN4	TDRD28	spindlin protein-coding	
chr1-1246	52.48267	0.210524	0.316846	0.664438	0.50641	0.786204	chr1	1.25E+08	1.25E+08	+	O	NA	IntergeniALR/Alphe	3167815	NR_003955	647121	Hs.697682	NR_003955	ENSG00000C	EMBPP1	-	embigin ipseudo	
chr11-521	19.33434	0.33587	0.505984	0.663797	0.50682	0.786204	chr11	52183466	52183708	+	O	NA	IntergeniALR/Alphe	1774441	NR_024504	646813	Hs.684179	NR_024504	LOC646813	-	DEXH-box pseudo		
chr5-492	48.68374	0.219205	0.330396	0.663467	0.507034	0.786204	chr5	49208426	49208716	+	O	NA	IntergeniALR/Alphe	1232717	NM_198444	133418	Hs.561411	NM_198444	ENSG00000C	EMB	GP70	embigin protein-coding	
chr7-5887	16.15942	0.362332	0.547184	0.662176	0.507858	0.786204	chr7	58879794	58880003	+	O	NA	IntergeniALR/Alphe	1429721	NM_001155	441234	Hs.533121	NM_001155	ENSG00000C	ZNF716	-	zinc finipseudo	
chr10-402	27.94708	0.281431	0.425384	0.661593	0.508232	0.786204	chr10	40213435	40213647	+	O	NA	IntergeniALR/Alphe	1516945	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chrX-6076	16.15999	0.362391	0.547776	0.661567	0.508249	0.786204	chrX	60758068	60760021	+	O	NA	IntergeniALR/Alphe	60758068	NM_001012	139886	Hs.612782	NM_001012	ENSG00000C	SPIN4	TDRD28	spindlin protein-coding	
chr19-256	16.15885	0.362288	0.547754	0.661407	0.508351	0.786204	chr19	25526965	25528210	+	O	NA	IntergeniALR/Alphe	-1364140	NR_003606	1E+08	Hs.149312	NR_003606	ENSG00000C	HAVCR1P1	-	hepatitisipseudo	
chr14-167	21.52386	0.324915	0.491554	0.660995	0.508615	0.786204	chr14	16795163	16795414	+	O	NA	IntergeniALR/Alphe	-1805829	NM_001013	440153	Hs.534888	NM_001013	ENSG00000C	OR11H12	-	olfactoryprotein-coding	
chr10-401	30.66626	0.268387	0.406399	0.660403	0.508995	0.786204	chr10	40157645	40158999	+	O	NA	IntergeniALR/Alphe	1461726	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr5-4771	34.53999	0.252911	0.3833	0.659825	0.509366	0.786204	chr5	47718398	47719665	+	O	NA	IntergeniALR/Alphe	-2022651	NM_021072	348980	Hs.353176	NM_021072	ENSG00000C	HCN1	BCNG-1	BC hyperpol:protein-coding	
chr20-268	16.15829	0.362259	0.549497	0.659255	0.509732	0.786204	chr20	26884002	26886503	+	O	NA	IntergeniALR/Alphe	-676019	NR_040099	284801	Hs.370699	NR_040099	ENSG00000C	MIR663AHC	-	MIR663A lncRNA	
chr12-351	22.60134	0.309588	0.469183	0.658715	0.510079	0.786204	chr12	35128575	35129331	+	O	NA	IntergeniALR/Alphe	1106457	NM_032834	84920	Hs.102971	NM_032834	ENSG00000C	ALG10	ALG10A	DIALG10	alprotein-coding
chr1-1232	22.63052	0.306349	0.465404	0.658243	0.510382	0.786204	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alphe	1711304	NR_003955	647121	Hs.697682	NR_003955	ENSG00000C	EMBPP1	-	embigin ipseudo	
chr5-478	31.27526	0.263847	0.401114	0.657785	0.510676	0.786204	chr5	47855296	47857108	+	O	NA	IntergeniALR/Alphe	-2159822	NM_021072	348980	Hs.353176	NM_021072	ENSG00000C	HCN1	BCNG-1	BC hyperpol:protein-coding	
chr19-264	16.73811	0.35472	0.539335	0.657699	0.510732	0.786204	chr19	26405198	26405653	+	O	NA	IntergeniALR/Alphe	-1388006	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000C	LOC101927	-	uncharactcRNA	
chr5-4756	36.71364	0.24461	0.372073	0.657425	0.510908	0.786204	chr5	47565193	47565512	+	O	NA	IntergeniALR/Alphe	-1868972	NM_021072	348980	Hs.353176	NM_021072	ENSG00000C	HCN1	BCNG-1	BC hyperpol:protein-coding	
chr8-458	19.94051	0.326689	0.492228	0.657382	0.510935	0.786204	chr8	45829548	45829774	+	O	NA	IntergeniALR/Alphe	787982	NR_146077	389652	NR_146077	ENSG00000C	ASNSP1	ASNSL1	asparaginipseudo		
chrX-5925	28.0077	0.271163	0.421556	0.657359	0.51095	0.786204	chrX	59239676	59241388	+	O	NA	IntergeniALR/Alphe	-1329899	NM_007156	7789	Hs.550094	NM_007156	ENSG00000C	ZXD4	ZNF896	zinc finipseudo	
chr7-594	18.34611	0.346364	0.527583	0.65651	0.511496	0.786204	chr7	59449346	59449644	+	O	NA	IntergeniALR/Alphe	1999318	NM_001155	441234	Hs.533121	NM_001155	ENSG00000C	ZNF716	-	zinc finipseudo	
chr20-272	16.18973	0.358766	0.546392	0.656445	0.511538	0.786204	chr20	27225182	27227070	+	O	NA	IntergeniALR/Alphe	-1016893	NR_040099	284801	Hs.370699	NR_040099	ENSG00000C	MIR663AHC	-	MIR663A lncRNA	
chr22-136	22.05183	0.310864	0.47376	0.656164	0.511719	0.786204	chr22	13627936	13628532	+	O	NA	IntergeniALR/Alphe	1730828	NR_110761	1.03E+08	Hs.652929	NR_110761	LOC102722	-	uncharactcRNA		
chr3-9157	116.0784	0.152964	0.233124	0.656151	0.511727	0.786204	chr3	91572734	91573034	+	O	NA	IntergeniALR/Alphe	2401197	NM_001314	5627	Hs.64016	NM_000314	ENSG00000C	PROS1	PROS	PS21	protein-coding
chr7-6001	104.9163	0.160388	0.244879	0.654967	0.512489	0.786204	chr7	60019356	60019743	+	O	NA	IntergeniALR/Alphe	2569372	NM_001155	441234	Hs.533121	NM_001155	ENSG00000C	ZNF716	-	zinc finipseudo	
chr11-536	32.83765	0.258058	0.395075	0.653187	0.513636	0.787273	chr11	53620763	53621085	+	O	NA	IntergeniALR/Alphe	983074	NM_001004	119749	Hs.553564	NM_001004	ENSG00000C	OR4C46	-	olfactoryprotein-coding	
chr19-271	19.97365	0.324104	0.496424	0.652877	0.513836	0.787723	chr19	27138803	27189703	+	O	NA	IntergeniALR/Alphe	-604178	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000C	LOC101927	-	uncharactcRNA	
chr1-1241	31.30614	0.261967	0.401311	0.652778	0.5139	0.787723	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2607381	NR_003955	647121	Hs.697682	NR_003955	ENSG00000C	EMBPP1	-	embigin ipseudo	
chr19-261	19.42698	0.326762	0.502214	0.650643	0.515277	0.788362	chr19	26137593	26138629	+	O	NA	IntergeniALR/Alphe	-1655320	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG00000C	LOC101927	-	uncharactcRNA	
chr1-1236	16.76785	0.351111	0.539638	0.650642	0.515277	0.788362	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2128981	NR_003955	647121	Hs.697682	NR_003955	ENSG00000C	EMBPP1	-	embigin ipseudo	
chr18-168	16.76785	0.351111	0.539638	0.650642	0.515277	0.788362	chr18	16855004	16855402	+	O	NA	IntergeniALR/Alphe	-1529284	NR_027417	644669	Hs.579474	NR_02					





chr8-8564	17.59215	0.28374	0.526968	0.538444	0.59027	0.808207	chr8	85645401	85645760	+	O NA	IntergeniHSMAR2 DN	10096 NR_003594	1E+08	Hs.535056NR_003594	REXO1L2P	-	REXO1 l k pseudo
chr11-542	20.31304	0.263848	0.49006	0.5384	0.590301	0.808207	chr11	54270106	54271153	+	O NA	IntergeniALR Alphe	333369 NM_001004	119749	Hs.553564NM_001004	ENSG000000C0R4C46	-	olfactory protein-coding
chr10-40	28.47344	0.2269	0.422221	0.537396	0.590994	0.808207	chr10	40086856	40087370	+	O NA	IntergeniALR Alphe	1390517 NR_045000	399746	Hs.742607NR_045000	ACTR3BP5 FKS	FG74	ACTR3B p pseudo
chr11-517	20.31911	0.263772	0.490896	0.537327	0.591042	0.808207	chr11	51793531	51793774	+	O NA	IntergeniALR Alphe	1384505 NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEX box pseudo
chr19-255	54.83574	0.367724	0.311226	0.537307	0.591056	0.808207	chr19	25211520	25211770	+	O NA	IntergeniALR Alphe	-1048198 NR_020360	1E+08	Hs.149312NR_00360	ENSG000000HAVCR1P1	-	hepatitis pseudo
chr13-173	36.14666	0.202845	0.377618	0.53717	0.59115	0.808207	chr13	17389770	17389987	+	O NA	IntergeniALR Alphe	-805419 NR_027278	26080	Hs.44858NR_027278	ENSG000000FAM230C	LINC00281	family w ncRNA
chr20-277	43.30183	0.185397	0.345308	0.536902	0.591335	0.808207	chr20	27711142	27711596	+	O NA	IntergeniALR Alphe	891296 NR_13231F	1E+08	Hs.529357NR_13231F	ENSG000000FRG1CP	-	FSHD reg pseudo
chr17-251	21.98564	0.288259	0.481036	0.536882	0.591349	0.808207	chr17	25796411	25796637	+	O NA	IntergeniALR Alphe	1292717 NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371	-	uncharact ncRNA
chr5-467	23.03458	-0.24899	0.464206	-0.53639	0.591691	0.808259	chr5	46721258	46721593	+	O NA	IntergeniALR Alphe	-1025045 NM_021072	348980	Hs.353176NM_021072	ENSG000000HCN1	BCNG-1 B C	hyperpol protein-coding
chr10-408	17.6236	0.280509	0.524363	0.534951	0.592683	0.808497	chr10	40829612	40831738	+	O NA	IntergeniALR Alphe	1537370 NR_02438C	441666	Hs.255729NR_02438C	ENSG000000LOC441666	-	zinc fin pseudo
chr17-266	33.3915	0.209957	0.392515	0.5349	0.592719	0.808497	chr17	26067647	26068068	+	O NA	IntergeniALR Alphe	1021384 NR_135673	1.05E+08	Hs.649918NR_135673	LOC105371	-	uncharact ncRNA
chr20-288	28.44369	0.229073	0.42832	0.534818	0.592776	0.808497	chr20	28544833	28545032	+	O NA	IntergeniALR Alphe	57733 NR_13231F	1E+08	Hs.529357NR_13231F	ENSG000000FRG1CP	-	FSHD reg pseudo
chr3-912	27.98589	0.229178	0.429423	0.53369	0.593556	0.808567	chr3	91242585	91242626	+	O NA	IntergeniALR Alphe	2138434 NM_00523E	2042	Hs.123642NM_00523E	ENSG000000EPH3	EK4 ETK E	EPH rece protein-coding
chr5-484	25.20418	0.236748	0.443721	0.533552	0.593651	0.808567	chr5	48452305	48452556	+	O NA	IntergeniALR Alphe	1988858 NM_19844E	133418	Hs.561411NM_19844E	ENSG000000EMB	GP70	embigin pr tein-coding
chr1-124	16.47897	-0.29445	0.551996	-0.53343	0.593739	0.808567	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR Alphe	2551597 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr13-168	18.20285	0.275866	0.519729	0.530789	0.595565	0.810454	chr13	16536101	16536324	+	O NA	IntergeniALR Alphe	-1659085 NR_027278	26080	Hs.44858NR_027278	ENSG000000FAM230C	LINC00281	family w ncRNA
chr21-127	19.73662	0.268096	0.505321	0.530546	0.595734	0.810454	chr21	12711699	12711929	+	O NA	IntergeniALR Alphe	-326352 NR_02691E	149992	Hs.55864E NM_153773	ANKRD30B C2lorf99	ankyrin  pseudo	
chr22-134	17.04775	0.285824	0.539325	0.529966	0.596135	0.810586	chr22	1578049 NR_110761	1.03E+08	Hs.652929NR_110761	LOC10272E	-	uncharact ncRNA					
chr11-53	20.88833	0.259875	0.49086	0.529427	0.596509	0.81068	chr11	53519613	53519917	+	O NA	IntergeniALR Alphe	1084233 NM_001004	119749	Hs.553564NM_001004	ENSG000000C0R4C46	-	olfactory protein-coding
chr19-27	39.39666	0.192584	0.364128	0.528892	0.59688	0.81077	chr19	27098638	27098875	+	O NA	IntergeniALR Alphe	-694675 NR_11068E	1.02E+08	Hs.567934NR_11068E	ENSG000000LOC101927	-	uncharact ncRNA
chr1-124	34.29331	-0.20399	0.386312	-0.52806	0.59746	0.810795	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR Alphe	2788793 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr10-40	17.07636	0.282136	0.534362	0.527987	0.597508	0.810795	chr10	40377877	40379220	+	O NA	IntergeniALR Alphe	1681952 NR_045000	399746	Hs.742607NR_045000	ACTR3BP5 FKS	FG74	ACTR3B p pseudo
chr1-124	30.3748	0.258202	0.489518	0.527461	0.597874	0.810831	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR Alphe	3061937 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr10-40	22.51531	0.246497	0.467674	0.527071	0.598144	0.810831	chr10	40371476	40372388	+	O NA	IntergeniALR Alphe	1675336 NR_045000	399746	Hs.742607NR_045000	ACTR3BP5 FKS	FG74	ACTR3B p pseudo
chr1-124	17.10837	0.278848	0.531662	0.524484	0.599942	0.812069	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR Alphe	2511281 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr2-928	25.26764	0.232272	0.443079	0.524222	0.600124	0.812069	chr2	92874419	92874790	+	O NA	IntergeniALR Alphe	933471 NR_027714	440888	Hs.730239NM_001032412	ACTR3BP2 FKS	FG73	ACTR3B p pseudo
chr19-24	25.95519	-0.22974	0.438491	-0.52393	0.600328	0.812069	chr19	24933790	24934002	+	O NA	IntergeniALR Alphe	-770449 NR_029360E	1E+08	Hs.149312NR_00360	ENSG000000HAVCR1P1	-	hepatitis pseudo
chr19-268	19.76354	0.264828	0.505656	0.523732	0.600465	0.812069	chr19	26823512	26823748	+	O NA	IntergeniALR Alphe	-969801 NR_11068E	1.02E+08	Hs.567934NR_11068E	ENSG000000LOC101927	-	uncharact ncRNA
chr7-588	19.82756	0.259019	0.495346	0.522906	0.60104	0.812069	chr7	58884865	58885129	+	O NA	IntergeniALR Alphe	1434820 NM_00115E	441234	Hs.533121NM_00115E	ENSG000000ZNF716	-	zinc fin protein-coding
chr7-588	24.68782	0.234684	0.449172	0.522482	0.601335	0.812069	chr7	58802802	58803148	+	O NA	IntergeniALR Alphe	13582807 NM_00115E	441234	Hs.533121NM_00115E	ENSG000000ZNF716	-	zinc fin protein-coding
chr7-593	17.68593	0.274039	0.524682	0.522295	0.601465	0.812069	chr7	59328510	59329424	+	O NA	IntergeniALR Alphe	1878790 NM_00115E	441234	Hs.533121NM_00115E	ENSG000000ZNF716	-	zinc fin protein-coding
chr21-107	21.71225	-0.24882	0.476439	-0.52225	0.601499	0.812069	chr21	10794542	10814490	+	O NA	IntergeniL LINE	283002 NR_19926C	7179	Hs.122988NM_19925E	ENSG000000TPTE	CT44 PTE	transmem protein-coding
chr5-483	18.88492	-0.27783	0.532672	-0.52157	0.601967	0.812289	chr5	48325069	48325315	+	O NA	IntergeniALR Alphe	2116096 NM_19844E	133418	Hs.561411NM_19844E	ENSG000000EMB	GP70	embigin pr tein-coding
chr10-41	24.7187	0.232327	0.447732	0.518898	0.603832	0.813425	chr10	41438905	41440469	+	O NA	IntergeniALR Alphe	928358 NR_02438C	441666	Hs.255729NR_02438C	ENSG000000LOC441666	-	zinc fin pseudo
chr4-500	17.13869	0.275456	0.53105	0.518701	0.603969	0.813425	chr4	50066875	50068795	+	O NA	IntergeniALR Alphe	1081193 NM_00128E	80157	Hs.479700NM_025087	ENSG000000CWH43	CWH43-3 C	cell wall protein-coding
chr19-25	34.56614	0.198615	0.383113	0.518424	0.604163	0.813425	chr19	25667752	25667956	+	O NA	IntergeniALR Alphe	-1504407 NR_00360E	1E+08	Hs.149312NR_00360	ENSG000000HAVCR1P1	-	hepatitis pseudo
chr10-41	29.60984	0.214576	0.414103	0.51817	0.60434	0.813425	chr10	41466442	41466900	+	O NA	IntergeniALR Alphe	901374 NR_02438C	441666	Hs.255729NR_02438C	ENSG000000LOC441666	-	zinc fin pseudo
chr1-124	17.13982	0.275551	0.532172	0.517786	0.604608	0.813425	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR Alphe	3202994 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr1-124	16.7364	0.193509	0.374266	0.517037	0.60513	0.813425	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR Alphe	3160243 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr11-51	16.5617	0.280542	0.542715	0.516923	0.60521	0.813425	chr11	51614119	51615075	+	O NA	IntergeniALR Alphe	1205450 NR_024504	646813	Hs.684175NR_024504	LOC646813	-	DEX box pseudo
chr20-26	19.85788	0.256089	0.495471	0.51686	0.605254	0.813425	chr20	26859852	26860072	+	O NA	IntergeniALR Alphe	-650729 NR_04009E	284801	Hs.370699NR_04009E	ENSG000000MIR663AH	-	MIR663A l ncRNA
chr7-595	40.67471	0.18445	0.357288	0.51625	0.60568	0.813586	chr7	5942265	5942511	+	O NA	IntergeniALR Alphe	2092211 NM_00115E	441234	Hs.533121NM_00115E	ENSG000000ZNF716	-	zinc fin protein-coding
chr5-484	46.61075	0.175392	0.340098	0.515711	0.606056	0.813681	chr5	48424557	48424796	+	O NA	IntergeniALR Alphe	2016612 NM_19844E	133418	Hs.561411NM_19844E	ENSG000000EMB	GP70	embigin pr tein-coding
chr19-25	82.56732	0.134853	0.262748	0.513239	0.607784	0.81386	chr19	25636208	25636454	+	O NA	IntergeniALR Alphe	-1472884 NR_00360E	1E+08	Hs.149312NR_00360	ENSG000000HAVCR1P1	-	hepatitis pseudo
chr19-26	26.92323	0.220552	0.429818	0.513128	0.607862	0.81386	chr19	26288073	26289743	+	O NA	IntergeniALR Alphe	-1504523 NR_11068E	1.02E+08	Hs.567934NR_11068E	ENSG000000LOC101927	-	uncharact ncRNA
chr6-590	16.59202	0.276988	0.539859	0.513075	0.607899	0.81386	chr6	59059751	59060574	+	O NA	IntergeniALR Alphe	-1098716 NR_132994	1.07E+08	Hs.561539NR_125727	ENSG000000LINC0068C	-	long int ncRNA
chr21-12	21.39222	0.250745	0.488878	0.5129	0.608022	0.81386	chr21	12007811	12008110	+	O NA	IntergeniALR Alphe	-1030206 NR_02691E	149992	Hs.55864E NM_153773	ANKRD30B C2lorf99	ankyrin  pseudo	
chr1-124	30.25199	0.290937	0.470607	0.512838	0.608065	0.81386	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR Alphe	3140874 NR_00395E	647121	Hs.697682NR_00395E	ENSG000000EMB1	-	embigin  pseudo
chr22-13	24.7221	0.232608	0.453777	0.512604	0.608228	0.81386												



chr11-52	24.95157	0.20137	0.44473	0.459	0.646234	0.833686	chr11	52071729	52072688	+	O	NA	IntergeniALR/Alphe	1663061	NR_024504	646813	Hs.684179	NR_024504	LOC646813	-	DEXH-box pseudo
chr11-53	22.77849	0.212876	0.463923	0.458861	0.646334	0.833686	chr11	53306319	53307889	+	O	NA	IntergeniALR/Alphe	1296894	NM_001004	119749	Hs.553564	NM_001004	ENSG000004OR4C46	-	olfactory protein-coding
chr14-17	22.78019	0.212985	0.466184	0.456869	0.647765	0.835128	chr14	17209945	17210203	+	O	NA	IntergeniALR/Alphe	-1391043	NM_001013	440153	Hs.534888	NM_001013	ENSG000004OR11H12	-	olfactory protein-coding
chr19-24	16.21692	-0.25479	0.560025	-0.45497	0.649131	0.836287	chr19	24632695	24632953	+	O	NA	IntergeniALR/Alphe	-469377	NR_003603	1E+08	Hs.149312	NR_003603	ENSG000004HAVCR1P1	-	hepatitis pseudo
chr11-51	30.48486	0.186051	0.409134	0.454745	0.649293	0.836287	chr11	51506786	51507011	+	O	NA	IntergeniALR/Alphe	1097751	NR_024504	646813	Hs.684179	NR_024504	LOC646813	-	DEXH-box pseudo
chr11-52	28.31007	0.191586	0.422284	0.45369	0.650052	0.836652	chr11	52428265	52428557	+	O	NA	IntergeniALR/Alphe	2019264	NR_024504	646813	Hs.684179	NR_024504	LOC646813	-	DEXH-box pseudo
chr1-123	17.88792	0.237243	0.523165	0.453477	0.650205	0.836652	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2480906	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr5-4967	16.82365	-0.24629	0.543774	-0.45292	0.650607	0.836765	chr5	49672852	49673155	+	O	NA	IntergeniALR/Alphe	768285	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr5-487	22.23069	0.212551	0.47114	0.451143	0.651887	0.838005	chr5	48784834	48786749	+	O	NA	IntergeniALR/Alphe	1655497	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr19-25	27.76397	0.1911	0.424231	0.450463	0.652377	0.83823	chr19	25870257	25870509	+	O	NA	IntergeniALR/Alphe	-1706936	NR_003603	1E+08	Hs.149312	NR_003603	ENSG000004HAVCR1P1	-	hepatitis pseudo
chr1-124	17.33954	0.237466	0.527978	0.449766	0.652879	0.838471	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2764470	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr1-123	29.38982	0.184765	0.412439	0.447982	0.654166	0.839719	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alphe	1715750	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr14-17	20.63912	0.220814	0.493903	0.44708	0.654817	0.840149	chr14	17392962	17393172	+	O	NA	IntergeniALR/Alphe	-1208050	NM_001013	440153	Hs.534888	NM_001013	ENSG000004OR11H12	-	olfactory protein-coding
chr2-924	16.76256	0.241342	0.540601	0.446433	0.655285	0.840343	chr2	92482285	92482550	+	O	NA	IntergeniALR/Alphe	541284	NR_027714	440888	Hs.730239	NM_001032412	ACTR3BP2	FKSG73	ACTR3B ps pseudo
chr5-489	25.06686	-0.19946	0.448773	-0.44446	0.656713	0.841629	chr5	48960928	48961191	+	O	NA	IntergeniALR/Alphe	1480229	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr20-26	38.20227	0.162415	0.365674	0.444152	0.656933	0.841629	chr20	26501668	26502020	+	O	NA	IntergeniALR/Alphe	-292611	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AHC	-	MIR663A lncRNA
chr7-5981	17.37099	0.234243	0.527923	0.443707	0.657254	0.841629	chr7	59816742	59817195	+	O	NA	IntergeniALR/Alphe	2366791	NM_001159	441234	Hs.533121	NM_001159	ENSG000004ZNF716	-	zinc finger protein-coding
chr5-485	16.73338	0.245318	0.553397	0.443295	0.657552	0.841629	chr5	47540993	47541226	+	O	NA	IntergeniALR/Alphe	-1844729	NM_021072	348980	Hs.353176	NM_021072	ENSG000004HCN1	BCNG-1	BC hyperpol protein-coding
chr19-26	22.84252	0.207926	0.469556	0.442809	0.657904	0.841674	chr19	26360670	26360900	+	O	NA	IntergeniALR/Alphe	-1432646	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chr5-474	16.79231	0.237792	0.537898	0.442076	0.658434	0.841948	chr5	47480912	47481357	+	O	NA	IntergeniALR/Alphe	-1784754	NM_021072	348980	Hs.353176	NM_021072	ENSG000004HCN1	BCNG-1	BC hyperpol protein-coding
chr7-586	28.84314	0.184123	0.417502	0.44101	0.659206	0.84253	chr7	58657766	58658002	+	O	NA	IntergeniALR/Alphe	1207707	NM_001159	441234	Hs.533121	NM_001159	ENSG000004ZNF716	-	zinc finger protein-coding
chr1-122	28.23415	0.187713	0.427776	0.438811	0.660798	0.843545	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alphe	1096812	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr5-493	84.26663	0.116457	0.259085	0.438649	0.660916	0.843545	chr5	49351635	49351914	+	O	NA	IntergeniALR/Alphe	1089514	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr19-26	23.88968	0.201055	0.458565	0.438444	0.661065	0.843545	chr19	26051801	26052109	+	O	NA	IntergeniALR/Alphe	-1741476	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chr1-123	24.46383	0.198901	0.453944	0.438163	0.661268	0.843545	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2431137	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chrX-585	26.09251	0.191477	0.438897	0.436268	0.662642	0.844266	chrX	58540919	58555112	+	O	NA	IntergeniALR/Alphe	-637582	NM_007156	7789	Hs.550094	NM_007156	ENSG000004ZXA	ZNF896	zinc finger protein-coding
chr5-495	156.6328	0.109177	0.210417	0.436134	0.662739	0.844266	chr5	49563517	49563771	+	O	NA	IntergeniALR/Alphe	877644	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr20-26	26.09081	0.191375	0.438862	0.436071	0.662785	0.844266	chr20	26438021	26438357	+	O	NA	IntergeniALR/Alphe	-228956	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AHC	-	MIR663A lncRNA
chr5-483	72.46686	-0.12142	0.29261	-0.43479	0.663717	0.845048	chr5	48355529	48355770	+	O	NA	IntergeniALR/Alphe	2085639	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr19-26	24.52786	0.194363	0.44857	0.433294	0.664801	0.84561	chr19	26437149	26438058	+	O	NA	IntergeniALR/Alphe	-1355828	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chrX-613	30.00108	0.181538	0.418974	0.433293	0.664802	0.84561	chrX	61304169	61304475	+	O	NA	IntergeniALR/Alphe	2047010	NM_001012	139886	Hs.612782	NM_001012	ENSG000004SPIN4	TDRD28	spindlin protein-coding
chr5-485	31.1253	0.180563	0.417132	0.432866	0.665112	0.84561	chr5	48507078	48507309	+	O	NA	IntergeniALR/Alphe	1934095	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr20-26	31.1053	0.173597	0.402106	0.431719	0.665946	0.84561	chr20	26551376	26551655	+	O	NA	IntergeniALR/Alphe	-342582	NR_040099	284801	Hs.370699	NR_040099	ENSG000004MIR663AHC	-	MIR663A lncRNA
chr1-123	22.90144	0.202645	0.469422	0.431691	0.665966	0.84569	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2000164	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr19-26	16.8552	0.231129	0.535681	0.431468	0.666128	0.84569	chr19	26489812	26491782	+	O	NA	IntergeniALR/Alphe	-1302654	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chrX-611	26.73125	0.18555	0.430627	0.430882	0.666554	0.845828	chrX	61113243	61113824	+	O	NA	IntergeniALR/Alphe	2237799	NM_001012	139886	Hs.612782	NM_001012	ENSG000004SPIN4	TDRD28	spindlin protein-coding
chr1-124	19.60527	0.214764	0.498997	0.430392	0.666911	0.845877	chr1	1.25E+08	1.25E+08	+	O	NA	IntergeniALR/Alphe	3171862	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr10-41	16.27651	0.234704	0.546679	0.429326	0.667686	0.846457	chr10	41840858	41842044	+	O	NA	IntergeniALR/Alphe	526594	NR_02438C	441666	Hs.255729	NR_02438C	ENSG000004LOC441666	-	zinc finger pseudo
chr2-936	30.8469	-0.17306	0.404108	-0.42825	0.66847	0.847047	chr2	93612209	93612474	+	O	NA	IntergeniALR/Alphe	596078	NR_146105	728034	Hs.448588	NR_146105	BMS1P14	-	BMS1 pset pseudo
chr13-17	21.8081	0.201832	0.474404	0.425771	0.670275	0.84893	chr13	17936661	17936887	+	O	NA	IntergeniALR/Alphe	-258523	NR_027278	26080	Hs.448588	NR_027278	ENSG000004FAM230C	LINC00281	family wncRNA
chr5-5001	32.62827	-0.16808	0.395325	-0.42516	0.67072	0.849089	chr5	50016692	50016950	+	O	NA	IntergeniALR/Alphe	424467	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr1-124	33.37176	0.164401	0.388772	0.422874	0.672387	0.85054	chr1	1.24E+08	1.24E+08	+	O	NA	IntergeniALR/Alphe	2979790	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr5-483	30.63869	0.17611	0.417014	0.422313	0.672796	0.85054	chr5	48321979	48322224	+	O	NA	IntergeniALR/Alphe	2119187	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr19-26	21.74294	0.206911	0.491683	0.420822	0.673885	0.85054	chr19	26674417	26674665	+	O	NA	IntergeniALR/Alphe	-1118890	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000004LOC101927	-	uncharactncRNA
chr1-123	26.21546	0.182637	0.434409	0.420426	0.674174	0.85054	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alphe	1913989	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr1-122	26.21603	0.182668	0.435029	0.419897	0.67456	0.85054	chr1	1.23E+08	1.23E+08	+	O	NA	IntergeniALR/Alphe	1035186	NR_003955	647121	Hs.697682	NR_003955	ENSG000004EMB1	-	emigin pseudo
chr7-601	21.26199	0.201325	0.479572	0.419802	0.67463	0.85054	chr7	60100933	60101322	+	O	NA	IntergeniALR/Alphe	2650950	NM_001159	441234	Hs.533121	NM_001159	ENSG000004ZNF716	-	zinc finger protein-coding
chr5-494	52.71629	0.132946	0.317032	0.419346	0.674963	0.85054	chr5	49492262	49493479	+	O	NA	IntergeniALR/Alphe	948418	NM_198444	133418	Hs.561411	NM_198444	ENSG000004EMB	GP70	emigin protein-coding
chr17-23	16.33884	0.227769	0.543206	0.419306	0.674993	0.85054	chr17	23453743	23453942	+	O	NA	IntergeniALR/Alphe	930731	NM_001199	1E+08	Hs.740188	NM_001199	ENSG000004MTRNR2L1	HN1	MT-RNR2 lprotein-coding
chr19-26	16.33884	0.227769	0.543206	0.419306	0.674																

chr19-268 39.86078	-0.12911	0.359938	-0.3587	0.719822	0.87656	chr19	26818302	26818516	+	O NA	IntergeniALR/Alph	-975022 NR_110688	1.02E+08	Hs. 567934NR_110687	ENSG0000CLOC101927-	uncharactncRNA			
chr13-161 36.36914	0.133886	0.375745	0.35632	0.721601	0.87656	chr13	16736413	16736664	+	O NA	IntergeniALR/Alph	-1458759 NR_027278	26080	Hs. 44858:NR_027278	ENSG0000C FAM230C	LINC00281	family wncRNA		
chr1-124 54.78947	0.11141	0.31289	0.356067	0.72179	0.87656	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alph	2964625 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr17-231 29.25599	0.148411	0.417023	0.355882	0.721929	0.87656	chr17	23143681	23144077	+	O NA	IntergeniALR/Alph	620768	NR_00119C	1E+08	Hs. 74018:NR_00119C	ENSG0000C MTRNR2L1	HNI	MT-RNR2	lprotein-coding
chrX-6161 65.85291	0.102725	0.28883	0.355661	0.722095	0.87656	chrX	61614907	61615295	+	O NA	IntergeniALR/Alph	1736231 NR_001019	139886	Hs. 612782:NR_001019	ENSG0000C SPIN4	TD RD28	spindlin	protein-coding	
chr19-268 52.52998	0.114777	0.322826	0.355537	0.722188	0.87656	chr19	26802671	26802901	+	O NA	IntergeniALR/Alph	-990645 NR_110688	1.02E+08	Hs. 567934NR_110687	ENSG0000C LOC101927-	uncharactncRNA			
chr2-934 17.0875	0.189992	0.534237	0.355446	0.722256	0.87656	chr2	93432421	93432801	+	O NA	IntergeniALR/Alph	775808 NR_146107	728034	NR_146105	BMS1P14	-	BMS1	pseudo	
chr17-225 16.50882	0.192095	0.541856	0.354514	0.722954	0.87656	chr17	22548350	22549146	+	O NA	IntergeniALR/Alph	425637 NR_00119C	1E+08	Hs. 74018:NR_00119C	ENSG0000C MTRNR2L1	HNI	MT-RNR2	lprotein-coding	
chr19-271 23.69656	0.161298	0.455276	0.354286	0.723125	0.87656	chr19	27141622	27143552	+	O NA	IntergeniALR/Alph	-650844 NR_110688	1.02E+08	Hs. 567934NR_110687	ENSG0000C LOC101927-	uncharactncRNA			
chr5-477 23.69656	0.161298	0.455276	0.354286	0.723125	0.87656	chr5	47748978	47751034	+	O NA	IntergeniALR/Alph	-2053626 NR_021072	348980	Hs. 35317:NR_021072	ENSG0000C HCN1	BCNG-1	BC hyperpol	protein-coding	
chr5-482 21.49316	0.168837	0.476705	0.354175	0.723208	0.87656	chr5	48241475	48242323	+	O NA	IntergeniALR/Alph	2199389 NR_198445	133418	Hs. 56141:NR_198445	ENSG0000C EMB	GP70	embigin	protein-coding	
chr1-124 23.696	0.161262	0.45562	0.353939	0.723385	0.87656	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alph	2695295 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr7-584 23.696	0.161262	0.45562	0.353939	0.723385	0.87656	chr7	58433908	58435615	+	O NA	IntergeniALR/Alph	984584 NR_001155	441234	Hs. 53312:NR_001155	ENSG0000C ZNF716	-	zinc fin	protein-coding	
chr13-175 19.28863	0.178018	0.503751	0.353385	0.7238	0.876664	chr13	17943918	17944322	+	O NA	IntergeniALR/Alph	-251177 NR_027278	26080	Hs. 44858:NR_027278	ENSG0000C FAM230C	LINC00281	family wncRNA		
chr11-518 24.08986	-0.16001	0.454971	-0.35169	0.72507	0.877803	chr11	51855832	51856061	+	O NA	IntergeniALR/Alph	1446799 NR_024504	646813	Hs. 68417:NR_024504	LOC646813	-	DEXH-box	pseudo	
chr14-161 35.38487	0.132772	0.380975	0.348505	0.727461	0.880297	chr14	16770023	16770275	+	O NA	IntergeniALR/Alph	-1830968 NR_001019	440153	Hs. 53488:NR_001019	ENSG0000C OR11H12	-	olfactory	protein-coding	
chr1-123 18.18688	-0.18039	0.518747	-0.34774	0.728035	0.880376	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1768704 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr5-487 19.32178	0.175258	0.504285	0.347537	0.728188	0.880376	chr5	48765953	48766154	+	O NA	IntergeniALR/Alph	1675235 NR_198445	133418	Hs. 56141:NR_198445	ENSG0000C EMB	GP70	embigin	protein-coding	
chr7-6001 20.94649	0.167473	0.483216	0.346579	0.728907	0.880621	chr7	60016928	60017133	+	O NA	IntergeniALR/Alph	2566853 NR_001155	441234	Hs. 53312:NR_001155	ENSG0000C ZNF716	-	zinc fin	protein-coding	
chr1-123 41.74726	-0.12733	0.36759	-0.34639	0.729053	0.880621	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1809362 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr11-54 19.32235	0.175274	0.506724	0.345896	0.729421	0.880667	chr11	54221939	54222718	+	O NA	IntergeniALR/Alph	2566853 NR_001155	119749	Hs. 55356:NR_001009	ENSG0000C ORC4C6	-	olfactory	protein-coding	
chr11-53 16.57001	0.185245	0.539588	0.343308	0.731367	0.882615	chr11	53454475	53455704	+	O NA	IntergeniALR/Alph	1148909 NR_001004	119749	Hs. 55356:NR_001009	ENSG0000C ORC4C6	-	olfactory	protein-coding	
chr20-26 18.77398	0.173826	0.50836	0.341936	0.732399	0.883398	chr20	26582124	26584211	+	O NA	IntergeniALR/Alph	-374029 NR_040095	284801	Hs. 37069:NR_040095	ENSG0000C MIR663AHC	-	MIR663A	lncRNA	
chr5-491 20.97681	0.167443	0.482318	0.341564	0.732679	0.883398	chr5	49129139	49129355	+	O NA	IntergeniALR/Alph	1249041 NR_198445	133418	Hs. 56141:NR_198445	ENSG0000C EMB	GP70	embigin	protein-coding	
chr20-27 25.38587	0.151574	0.445098	0.340541	0.733449	0.883552	chr20	27906140	27906625	+	O NA	IntergeniALR/Alph	696283 NR_132315	1E+08	Hs. 529357NR_132315	ENSG0000C FRG1CP	-	FSHD	regipseudo	
chr2-925 27.01001	0.147116	0.432042	0.340512	0.733471	0.883552	chr2	92549367	92550647	+	O NA	IntergeniALR/Alph	608874 NR_027714	440888	Hs. 73023:NR_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo	
chr8-449 24.33757	0.155515	0.457548	0.339887	0.733942	0.883719	chr8	44958124	44958435	+	O NA	IntergeniALR/Alph	1659364 NR_146077	389652	NR_146077	ENSG0000C ASNSP1	ASNSL1	asparagip	pseudo	
chr20-29 40.95582	-0.12024	0.354842	-0.33885	0.734724	0.883928	chr20	29884986	29886222	+	O NA	IntergeniALR/Alph	-5141 NR_039685	1.01E+08	NR_039685	ENSG0000C MIR4477A	-	microRNA	ncRNA	
chr1-124 40.3848	0.120708	0.356307	0.338774	0.73478	0.883928	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alph	3174211 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr1-123 18.7171	0.173643	0.514377	0.337579	0.73568	0.884607	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1494472 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr7-603 23.21165	0.155043	0.459874	0.337143	0.736009	0.884607	chr7	60383157	60383396	+	O NA	IntergeniALR/Alph	2920780 NR_003955	643955	Hs. 58330:NR_003955	ENSG0000C ZNF733P	ZNF733	zinc fin	pseudo	
chr7-594 21.00825	0.162104	0.482152	0.33621	0.736712	0.884898	chr7	59400249	59441443	+	O NA	IntergeniALR/Alph	1990668 NR_001155	441234	Hs. 53312:NR_001155	ENSG0000C ZNF716	-	zinc fin	protein-coding	
chr1-122 35.94599	0.162262	0.375739	0.33594	0.736916	0.884898	chr1	1.22E+08	1.22E+08	+	O NA	IntergeniALR/Alph	757578 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr10-41 16.60259	0.181971	0.543626	0.334735	0.737825	0.885413	chr10	41408350	41409072	+	O NA	IntergeniALR/Alph	959334 NR_02438C	441666	Hs. 25572:NR_02438C	ENSG0000C LOC441666	-	zinc fin	pseudo	
chr19-24 27.65046	0.142335	0.42557	0.334457	0.738035	0.885413	chr19	24605343	24605546	+	O NA	IntergeniALR/Alph	-441997 NR_003606	1E+08	Hs. 14931:NR_003606	ENSG0000C HAVCR1P1	-	hepatitis	pseudo	
chr10-41 28.22858	0.141732	0.424585	0.333814	0.73852	0.885413	chr10	41237286	41237589	+	O NA	IntergeniALR/Alph	1130608 NR_02438C	441666	Hs. 25572:NR_02438C	ENSG0000C LOC441666	-	zinc fin	pseudo	
chr10-40 31.50775	0.133323	0.400668	0.333251	0.738945	0.885413	chr10	40315259	40315534	+	O NA	IntergeniALR/Alph	1618800 NR_04500C	399746	Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo	
chr1-125 16.60316	0.181983	0.547321	0.332498	0.739513	0.885413	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniIntergeni	3595100 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr11-53 18.80655	0.170928	0.514516	0.332211	0.73973	0.885413	chr11	53176513	53176728	+	O NA	IntergeniALR/Alph	1427378 NR_001004	119749	Hs. 55356:NR_001009	ENSG0000C ORC4C6	-	olfactory	protein-coding	
chr9-628 16.95387	-0.17834	0.537008	-0.3321	0.739815	0.885413	chr9	62841631	62844802	+	O NA	intron (L1P1Ba)LI	2571 NR_13501C	442421	Hs. 58534:NR_024496	PTGER4P2	-	PTGER4P2	pseudo	
chr17-24 16.98645	-0.18121	0.546062	-0.33184	0.740007	0.885413	chr17	24391218	24391424	+	O NA	IntergeniALR/Alph	1868210 NR_00119C	1E+08	Hs. 74018:NR_00119C	ENSG0000C MTRNR2L1	HNI	MT-RNR2	lprotein-coding	
chr19-25 27.10209	0.140719	0.427722	0.328996	0.742159	0.887575	chr19	25837910	25839213	+	O NA	IntergeniALR/Alph	-1675114 NR_003606	1E+08	Hs. 14931:NR_003606	ENSG0000C HAVCR1P1	-	hepatitis	pseudo	
chr1-122 18.25762	0.169252	0.515118	0.328569	0.742481	0.887575	chr1	1.22E+08	1.22E+08	+	O NA	IntergeniALR/Alph	734485 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr19-26 36.00775	0.123044	0.375403	0.327766	0.743088	0.887704	chr19	26385323	26386248	+	O NA	IntergeniALR/Alph	-1407646 NR_110688	1.02E+08	Hs. 567934NR_110687	ENSG0000C LOC101927-	uncharactncRNA			
chr1-123 74.45611	0.091281	0.279025	0.327143	0.74356	0.887704	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alph	2030596 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr19-25 41.57475	0.118844	0.363321	0.327104	0.743589	0.887704	chr19	25733804	25734016	+	O NA	IntergeniALR/Alph	-1570463 NR_003606	1E+08	Hs. 14931:NR_003606	ENSG0000C HAVCR1P1	-	hepatitis	pseudo	
chr1-122 39.3977	0.119043	0.366462	0.324844	0.745299	0.889346	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alph	1413581 NR_003955	647121	Hs. 697682NR_003955	ENSG0000C EMBP1	-	embigin ipseudo		
chr20-28 20.49189	0.157747	0.487576	0.323533	0.746292	0.890131	chr20	28521783	28521714	+	O NA	IntergeniALR/Alph	78187 NR_132315	1E+08	Hs. 529357NR_132315	ENSG0000C FRG1CP	-	FSHD	regipseudo	
chr15-17 17.53085	-0.16943	0.527569	-0.32115	0.748095	0.891445	chr15	17024484	17028930	+	O NA									



chr2-9246	31.22256	0.108214	0.403808	0.267984	0.788712	0.909871	chr2	92468644	92469174	+	0	NA	IntergeniALR/Alphe	527776	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo				
chr5-4946	45.76973	0.09025	0.336964	0.267833	0.788828	0.909871	chr5	49464927	49466069	+	0	NA	IntergeniALR/Alphe	975790	NR_198449	133418	Hs.561411	NR_198449	ENSG000000000000	EMB	GP70	embigin	protein-coding				
chr21-107	20.66187	0.129994	0.486278	0.267325	0.789219	0.909927	chr21	10745909	10750550	+	0	NA	IntergeniALR/Alphe	226715	NR_199260	7179	Hs.122988	NR_199259	ENSG000000000000	TPTE	CT44	PTEN	transmem	protein-coding			
chr7-584	17.8203	0.142591	0.538349	0.264867	0.791112	0.911715	chr7	58430730	58441024	+	0	NA	IntergeniALR/Alphe	980700	NR_001159	441234	Hs.533121	NR_001159	ENSG000000000000	ZNF716	-	-	zinc	fin	protein-coding		
chr1-1242	28.34169	-0.11192	0.425062	-0.26329	0.792326	0.911923	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2687936	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	BCNG-1	BC	hyperpol	protein-coding			
chr14-17	18.45847	0.134995	0.512762	0.263271	0.792342	0.911923	chr14	17344384	17344861	+	0	NA	IntergeniALR/Alphe	-1256495	NR_001010	440153	Hs.534888	NR_001010	ENSG000000000000	COR11H12	-	-	olfactory	protein-coding			
chr5-467	27.97314	0.111559	0.425629	0.262105	0.793241	0.911923	chr5	46756735	46757105	+	0	NA	IntergeniALR/Alphe	-1060540	NR_021072	348980	Hs.353176	NR_021072	ENSG000000000000	HCN1	BCNG-1	BC	hyperpol	protein-coding			
chr1-1245	38.45846	0.096367	0.368272	0.261674	0.793573	0.911923	chr1	46669238	46669575	+	0	NA	IntergeniALR/Alphe	3393844	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	BCNG-1	BC	hyperpol	protein-coding			
chr2-925	22.92646	0.121035	0.462862	0.261493	0.793712	0.911923	chr2	92592042	92592490	+	0	NA	IntergeniALR/Alphe	651133	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo				
chr5-483	20.69388	0.127382	0.487169	0.261474	0.793727	0.911923	chr5	48356632	48357790	+	0	NA	IntergeniALR/Alphe	2084077	NR_198449	133418	Hs.561411	NR_198449	ENSG000000000000	EMB	GP70	embigin	protein-coding				
chr5-466	25.16074	0.115905	0.443335	0.261438	0.793755	0.911923	chr5	46669238	46669575	+	0	NA	IntergeniALR/Alphe	-973026	NR_021072	348980	Hs.353176	NR_021072	ENSG000000000000	HCN1	BCNG-1	BC	hyperpol	protein-coding			
chrX-613	25.16017	0.115863	0.443321	0.260764	0.794275	0.911923	chrX	61390675	61391024	+	0	NA	IntergeniALR/Alphe	1960483	NR_001010	139886	Hs.612782	NR_001010	ENSG000000000000	SPIN4	TDRD28	-	-	spindlin	protein-coding		
chr7-587	16.25508	0.141366	0.544593	0.259581	0.795187	0.911923	chr7	58706928	58708626	+	0	NA	IntergeniALR/Alphe	1257600	NR_001159	441234	Hs.533121	NR_001159	ENSG000000000000	ZNF716	-	-	zinc	fin	protein-coding		
chr7-597	16.25508	0.141366	0.544593	0.259581	0.795187	0.911923	chr7	59754184	59756119	+	0	NA	IntergeniALR/Alphe	2304974	NR_001159	441234	Hs.533121	NR_001159	ENSG000000000000	ZNF716	-	-	zinc	fin	protein-coding		
chr1-1241	26.78998	0.11398	0.440176	0.258942	0.79568	0.911923	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2636015	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	-	-	embigin	ps	pseudo		
chr10-404	44.17759	0.089278	0.345373	0.258497	0.796023	0.911923	chr10	40893772	40893972	+	0	NA	IntergeniALR/Alphe	1474173	NR_024380	441666	Hs.255729	NR_024380	ENSG000000000000	L0C441666	-	-	zinc	fin	ps	pseudo	
chr19-26	30.7096	0.104611	0.405335	0.258085	0.796342	0.911923	chr19	26056210	26056531	+	0	NA	IntergeniALR/Alphe	-1737061	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000000000000	L0C101927	-	-	uncharact	ncRNA	-	-	
chr5-495	19.0686	0.131615	0.510382	0.257875	0.796504	0.911923	chr5	49589268	49590194	+	0	NA	IntergeniALR/Alphe	851557	NR_198449	133418	Hs.561411	NR_198449	ENSG000000000000	EMB	GP70	embigin	protein-coding				
chr10-395	30.20013	-0.10762	0.41933	-0.25665	0.797447	0.911923	chr10	39965083	39965286	+	0	NA	IntergeniALR/Alphe	1268588	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo				
chr5-492	34.83923	-0.10079	0.392801	-0.25659	0.797492	0.911923	chr5	49218769	49219002	+	0	NA	IntergeniALR/Alphe	1222403	NR_198449	133418	Hs.561411	NR_198449	ENSG000000000000	EMB	GP70	embigin	protein-coding				
chr15-19	21.74105	0.124356	0.485402	0.256191	0.797803	0.911923	chr15	19527355	19527656	+	0	NA	IntergeniALR/Alphe	-755239	NR_195283	646096	Hs.448789	NR_038839	ENSG000000000000	CHEK2P2	-	-	checkpoir	pseudo			
chr5-464	144.8113	-0.05433	0.212138	-0.2561	0.797873	0.911923	chr5	46433391	46433765	+	0	NA	IntergeniALR/Alphe	-738198	NR_021072	348980	Hs.353176	NR_021072	ENSG000000000000	HCN1	BCNG-1	BC	hyperpol	protein-coding			
chr5-492	32.97306	0.099989	0.390774	0.255874	0.798048	0.911923	chr5	49260429	49261153	+	0	NA	IntergeniALR/Alphe	1180497	NR_198449	133418	Hs.561411	NR_198449	ENSG000000000000	EMB	GP70	embigin	protein-coding				
chr10-40	25.73603	0.115433	0.451356	0.255746	0.798147	0.911923	chr10	40001929	40002158	+	0	NA	IntergeniALR/Alphe	1305447	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo				
chr7-587	24.0062	0.116133	0.457502	0.253842	0.799617	0.912967	chr7	58794972	58795175	+	0	NA	IntergeniALR/Alphe	1344896	NR_001159	441234	Hs.533121	NR_001159	ENSG000000000000	ZNF716	-	-	zinc	fin	protein-coding		
chr1-122	16.28652	0.13801	0.544602	0.253414	0.799948	0.912967	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1388768	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	-	-	embigin	ps	pseudo		
chr6-595	16.28539	0.137905	0.54458	0.253231	0.800089	0.912967	chr6	59561812	59562487	+	0	NA	IntergeniALR/Alphe	1600303	NR_132994	1.07E+08	Hs.561539	NR_125727	ENSG000000000000	LINC00680	-	-	long	int	ncRNA		
chr22-14	17.29855	-0.13397	0.531466	-0.25208	0.80098	0.913224	chr22	14655244	14655516	+	0	NA	IntergeniALR/Alphe	-872779	NR_001000	81061	Hs.554700	NR_001000	ENSG000000000000	COR11H1	OR11H12	(o	l	f	actory	protein-coding	
chr15-17	29.69275	0.104088	0.415062	0.250778	0.801986	0.913224	chr15	17009112	17009372	+	0	NA	IntergeniALR/Alphe	-3273502	NR_038839	646096	Hs.448789	NR_038839	ENSG000000000000	CHEK2P2	-	-	checkpoir	pseudo			
chr1-123	29.11464	0.104023	0.415027	0.250642	0.802091	0.913224	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2371184	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	-	-	embigin	ps	pseudo		
chr20-28	53.73815	0.078878	0.315214	0.250236	0.802405	0.913224	chr20	28643719	28646096	+	0	NA	IntergeniALR/Alphe	-42242	NR_132310	1E+08	Hs.529357	NR_132310	ENSG000000000000	FRG1CP	-	-	FSHD	regip	pseudo		
chr17-26	36.31683	0.093603	0.375244	0.249446	0.803016	0.913224	chr17	26624975	26626420	+	0	NA	IntergeniALR/Alphe	463544	NR_135673	1.05E+08	Hs.649918	NR_135673	LOC105371	-	-	-	-	uncharact	ncRNA		
chr1-1234	48.15897	0.082881	0.332767	0.249066	0.80331	0.913224	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1949635	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	-	-	embigin	ps	pseudo		
chr19-27	43.08255	0.086192	0.346193	0.24897	0.803384	0.913224	chr19	27091437	27092983	+	0	NA	IntergeniALR/Alphe	-701221	NR_110688	1.02E+08	Hs.567934	NR_110688	ENSG000000000000	L0C101927	-	-	uncharact	ncRNA			
chr5-475	36.38632	-0.09431	0.379675	-0.2484	0.803828	0.913224	chr5	47500844	47501061	+	0	NA	IntergeniALR/Alphe	-1804572	NR_021072	348980	Hs.353176	NR_021072	ENSG000000000000	HCN1	BCNG-1	BC	hyperpol	protein-coding			
chr3-919	17.94325	0.129382	0.521561	0.248066	0.804083	0.913224	chr3	91926218	91926445	+	0	NA	IntergeniALR/Alphe	2047750	NR_001314	5627	Hs.64016	NR_000310	ENSG000000000000	PROS1	PROS	PS21	protein	protein-coding			
chr16-22	16.65924	-0.13544	0.547091	-0.24756	0.804474	0.913224	chr16	22570444	22571468	+	0	NA	intron (n	intron (n	25258	NR_003670	653786	Hs.56494	NR_003670	ENSG000000000000	OTOA	P1	-	-	OTOA	ps	pseudo
chr1-123	24.82625	-0.11083	0.448101	-0.24734	0.804648	0.913224	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1512645	NR_003959	647121	Hs.697682	NR_003959	ENSG000000000000	EMB	-	-	embigin	ps	pseudo		
chr12-34	16.31684	0.13455	0.544359	0.247172	0.804775	0.913224	chr12	34792872	34793217	+	0	NA	IntergeniALR/Alphe	770548	NR_032834	84920	Hs.102971	NR_032834	ENSG000000000000	ALG10	ALG10A	DI	ALG10	al	protein-coding		
chr2-928	17.94381	0.129459	0.523766	0.24717	0.804776	0.913224	chr2	92854553	92855098	+	0	NA	IntergeniALR/Alphe	913692	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo				
chr5-480	16.89382	0.133742	0.543205	0.24621	0.80552	0.913642	chr5	48013865	48014073	+	0	NA	IntergeniALR/Alphe	-2317589	NR_021072	348980	Hs.353176	NR_021072	ENSG000000000000	HCN1	BCNG-1	BC	hyperpol	protein-coding			
chr3-910	16.3157	0.134416	0.54684	0.245805	0.805833	0.913642	chr3	91094176	91094707	+	0	NA	IntergeniALR/Alphe	1986820	NR_005230	2042	Hs.123642	NR_005230	ENSG000000000000	EPHA3	EK4	ETK	EPH	recep	protein-coding		
chr2-930	23.68588	-0.11255	0.45872	-0.24536	0.806175	0.913642	chr2	93003783	93004042	+	0	NA	IntergeniALR/Alphe	9602779	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo				
chr21-12	26.57448	-0.10689	0.436594	-0.24482	0.806597	0.913731	chr21	12226333	12226569	+	0	NA	IntergeniALR/Alphe	-811715	NR_026910	149992	Hs.55864	NR_153773	ANKRD30B	C21orf99	ankyrin	ps	pseudo				
chr20-29	58.19027	0.074104	0.303345	0.24429	0.807007	0.913806	chr20	29261791	29263962	+	0	NA	IntergeniALR/Alphe	154085	NR_037925	647476	Hs.274541	NR_037925	FRG2EP	-	-						

chr2-9292	16.51939	0.096785	0.546414	0.177127	0.859409	0.940789	chr2	92926924	92927177	+	0	NA	IntergeniALR/Alphe	985917	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo		
chr2-9293	17.03707	-0.09437	0.534007	-0.17671	0.859733	0.940789	chr2	92934719	92935768	+	0	NA	IntergeniALR/Alphe	994110	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo		
chr19-256	22.0963	0.083122	0.471472	0.176303	0.860056	0.940789	chr19	25618814	25619063	+	0	NA	IntergeniALR/Alphe	-1455491	NR_003606	440888	Hs.149312	NR_003606	ENSG00000	HAVCR1P1	-	hepatitis	pseudo		
chr1-124	20.43901	0.086097	0.488582	0.176217	0.860123	0.940789	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2703141	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr20-285	20.44014	0.086178	0.498514	0.176047	0.860257	0.940789	chr20	28552122	28554482	+	0	NA	IntergeniALR/Alphe	49363	NR_13231F	647121	Hs.529357	NR_13231F	ENSG00000	FRG1CP	-	FSHD	regipseudo		
chr10-407	18.78285	0.089703	0.510941	0.175563	0.860637	0.940789	chr10	40766237	40766510	+	0	NA	IntergeniALR/Alphe	1601672	NR_02438C	441666	Hs.255729	NR_02438C	ENSG00000	LOC441666	-	zinc	fin	pseudo	
chr5-497	28.61074	-0.07345	0.41883	-0.17538	0.860781	0.940789	chr5	49773885	49774099	+	0	NA	IntergeniALR/Alphe	667296	NR_19844F	133418	Hs.561411	NR_19844F	ENSG00000	EMB	GP70	embigin	protein-coding		
chr1-124	28.03602	-0.07669	0.437614	-0.17524	0.860888	0.940789	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3007699	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr1-1247	38.42145	0.063673	0.36533	0.174289	0.861638	0.94098	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3218506	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr11-53	73.32499	0.048085	0.276159	0.174122	0.86177	0.94098	chr11	53207336	53207594	+	0	NA	IntergeniALR/Alphe	1396533	NR_001004	119749	Hs.553564	NR_001004	ENSG00000	OR4C46	-	olfactory	protein-coding		
chr1-124	18.75555	-0.08731	0.510339	-0.17108	0.864159	0.943202	chr1	1.24E+08	1.24E+08	+	0	NA	IntergeniALR/Alphe	2899093	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr19-26	22.12548	0.080496	0.471952	0.17056	0.864569	0.943263	chr19	26507466	26507949	+	0	NA	IntergeniALR/Alphe	-1285724	NR_11068F	1.02E+08	Hs.567934	NR_11068F	ENSG00000	LOC101927	-	uncharactncRNA			
chr1-122	27.23618	0.074	0.436452	0.169549	0.865365	0.943589	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1476114	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr5-494	39.53037	0.060953	0.360074	0.169279	0.865577	0.943589	chr5	49499145	49499382	+	0	NA	IntergeniALR/Alphe	942025	NR_19844F	133418	Hs.561411	NR_19844F	ENSG00000	EMB	GP70	embigin	protein-coding		
chr10-406	29.99956	0.068529	0.409083	0.167518	0.866962	0.94207	chr10	40647454	40647743	+	0	NA	IntergeniALR/Alphe	1720447	NR_02438C	441666	Hs.255729	NR_02438C	ENSG00000	LOC441666	-	zinc	fin	pseudo	
chr11-53	19.36398	-0.08451	0.504639	-0.16747	0.867002	0.94207	chr11	53899298	53899743	+	0	NA	IntergeniALR/Alphe	704478	NR_001004	119749	Hs.553564	NR_001004	ENSG00000	OR4C46	-	olfactory	protein-coding		
chr1-122	19.86447	-0.08392	0.501915	-0.16721	0.867209	0.94207	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1175737	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr2-932	27.12484	0.072412	0.43647	0.165904	0.868233	0.94491	chr2	93286111	93286611	+	0	NA	IntergeniALR/Alphe	922058	NR_146107	728034	NR_146105	BMS1P14	-	BMS1	pseu	pseudo			
chr5-465	26.33	-0.07349	0.444108	-0.16548	0.868565	0.94491	chr5	46524135	46524408	+	0	NA	IntergeniALR/Alphe	-827891	NR_021072	348980	Hs.353176	NR_021072	ENSG00000	HCN1	BCNG-1	[BC	hyperpol	protein-coding	
chr14-17	20.5019	0.080717	0.491273	0.164302	0.869494	0.945534	chr14	17064963	17065193	+	0	NA	IntergeniALR/Alphe	-1536039	NR_00101F	440153	Hs.53488C	NR_00101F	ENSG00000	OR11H12	-	olfactory	protein-coding		
chr1-124	27.76642	0.069044	0.422929	0.163251	0.870321	0.946047	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3386901	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr19-26	23.23667	0.075065	0.463701	0.161883	0.871398	0.946832	chr19	26502230	26502616	+	0	NA	IntergeniALR/Alphe	-1291008	NR_11068F	1.02E+08	Hs.567934	NR_11068F	ENSG00000	LOC101927	-	uncharactncRNA			
chr5-495	22.18951	0.075626	0.472478	0.160063	0.872831	0.948002	chr5	49572659	49574944	+	0	NA	IntergeniALR/Alphe	867487	NR_19844F	133418	Hs.561411	NR_19844F	ENSG00000	EMB	GP70	embigin	protein-coding		
chr1-123	72.3918	-0.04622	0.290524	-0.15908	0.873606	0.948455	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1601279	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr8-445	27.79843	0.067096	0.424055	0.158225	0.874279	0.9488	chr8	44594356	44595530	+	0	NA	IntergeniALR/Alphe	1302501	NR_00100F	340441	Hs.531576	NR_00100F	ENSG00000	POTEA	A26A1	[CTI	POTE	anky	protein-coding
chr1-124	19.34567	0.078769	0.503457	0.156457	0.875673	0.949896	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3343248	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr20-28	31.75063	0.062189	0.398548	0.156038	0.876003	0.949896	chr20	28528750	28529027	+	0	NA	IntergeniALR/Alphe	73777	NR_13231F	647121	Hs.529357	NR_13231F	ENSG00000	FRG1CP	-	FSHD	regipseudo		
chr5-498	19.30392	-0.07884	0.509338	-0.15479	0.876986	0.950571	chr5	49896724	49897010	+	0	NA	IntergeniALR/Alphe	544421	NR_19844F	133418	Hs.561411	NR_19844F	ENSG00000	EMB	GP70	embigin	protein-coding		
chr10-40	27.21861	0.066089	0.428201	0.154342	0.87734	0.950571	chr10	40507780	40508164	+	0	NA	IntergeniALR/Alphe	1811376	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo		
chr5-489	21.01958	-0.07401	0.483318	-0.15313	0.878295	0.951218	chr5	48902732	48903115	+	0	NA	IntergeniALR/Alphe	1538365	NR_19844F	133418	Hs.561411	NR_19844F	ENSG00000	EMB	GP70	embigin	protein-coding		
chr7-613	19.27078	-0.07624	0.503077	-0.15154	0.879546	0.952186	chr7	61378519	61379499	+	0	NA	IntergeniALR/Alphe	1925047	NR_003955	643955	Hs.58330F	NR_003955	ENSG00000	ZNF733P	ZNF733	zinc	fin	pseudo	
chr3-911	25.59578	-0.06662	0.441611	-0.15085	0.880096	0.952394	chr3	91152293	91152514	+	0	NA	IntergeniALR/Alphe	2044782	NR_00523F	2042	Hs.123642	NR_00523F	ENSG00000	EPH3A	EK4	[ETK	[EPH	recep	protein-coding
chr1-124	55.35813	0.046844	0.311619	0.150323	0.88051	0.952454	chr1	1.25E+08	1.25E+08	+	0	NA	IntergeniALR/Alphe	3402739	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr19-26	50.93519	0.048239	0.322406	0.149622	0.881063	0.952665	chr19	26024094	26024311	+	0	NA	IntergeniALR/Alphe	-1769229	NR_11068F	1.02E+08	Hs.567934	NR_11068F	ENSG00000	LOC101927	-	uncharactncRNA			
chrX-606	33.03537	-0.05904	0.403481	-0.14632	0.883669	0.954061	chrX	60654455	60654909	+	0	NA	IntergeniALR/Alphe	2696650	NR_00101F	139886	Hs.612782	NR_00101F	ENSG00000	SPIN4	TDRD28	spindlin	protein-coding		
chr10-411	32.8893	0.057151	0.391698	0.145905	0.883996	0.954061	chr10	41117444	41118079	+	0	NA	IntergeniALR/Alphe	1250284	NR_02438C	441666	Hs.255729	NR_02438C	ENSG00000	LOC441666	-	zinc	fin	pseudo	
chr14-106	19.2399	-0.07347	0.503999	-0.14577	0.884105	0.954061	chr14	1.07E+08	1.07E+08	+	0	NA	IntergeniALR/Alphe	98598	NR_049827	1.01E+08	NR_049827	ENSG00000	MIR5195	-	microRNA	ncRNA			
chr5-472	26.67364	0.063235	0.434715	0.145462	0.884346	0.954061	chr5	47299167	47299399	+	0	NA	IntergeniALR/Alphe	-1602903	NR_021072	348980	Hs.353176	NR_021072	ENSG00000	HCN1	BCNG-1	[BC	hyperpol	protein-coding	
chr2-925	17.14114	0.077454	0.534104	0.145017	0.884697	0.954061	chr2	92516603	92517825	+	0	NA	IntergeniALR/Alphe	576081	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo		
chr2-930	18.6326	-0.07551	0.522232	-0.14458	0.88504	0.954061	chr2	93049894	93050876	+	0	NA	IntergeniALR/Alphe	1109252	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo		
chr19-27	17.7507	0.075606	0.523141	0.144524	0.885087	0.954061	chr19	27095956	27096787	+	0	NA	IntergeniALR/Alphe	-697066	NR_11068F	1.02E+08	Hs.567934	NR_11068F	ENSG00000	LOC101927	-	uncharactncRNA			
chr9-606	17.14057	0.077444	0.536492	0.144352	0.885223	0.954061	chr9	60602817	60603293	+	0	NA	IntergeniALR/Alphe	-311352	NR_015667	26165	Hs.123004	NR_015667	ENSG00000	SPATA31A7	AEP1	[C9or	SPATA31	s	protein-coding
chr2-925	27.28452	-0.06147	0.42798	-0.14362	0.885799	0.954296	chr2	92588763	92589501	+	0	NA	IntergeniALR/Alphe	647999	NR_027714	440888	Hs.730239	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo		
chr1-122	92.16148	0.035756	0.250617	0.142673	0.886548	0.954458	chr1	1.23E+08	1.23E+08	+	0	NA	IntergeniALR/Alphe	1392312	NR_003955	647121	Hs.697682	NR_003955	ENSG00000	EMBPP1	-	embigin	pseudo		
chr5-495	103.3646	0.033665	0.239752	0.141668	0.887342	0.954458	chr5	49576831	49577101	+	0	NA	IntergeniALR/Alphe	864322	NR_19844F	133418	Hs.561411	NR_19844F	ENSG00000	EMB	GP70	embigin	protein-coding		
chr11-51	21.0939	0.06825	0.482022	0.14159	0.887404	0.954458	chr11	51704395	51705514	+	0	NA	IntergeniALR/Alphe	1295807	NR_024504	646813	Hs.684179	NR_024504	LOC646813	-	DEXH	box	pseudo		
chr7-597	21.0939	0.06825	0.482022	0.14159	0.887404	0.954458	chr7	59785771	59786034	+	0	NA	IntergeniALR/Alphe	2335725	NR_00115F	441234	Hs.533121	NR_00115F	ENSG00000	ZNF716	-	zinc	fin	protein-coding	
chr1-124	58.79624	0.043167	0.305803	0.141161	0.887743	0.954458	chr																		



chr21-802	16.20219	0.051066	0.545651	0.093587	0.925437	0.965721	chr21	8021542	8022750	+	O NA	IntergeniALR/Alphe	-175474	NR_038958	1.01E+08	Hs. 426704	NR_038958	LOC100507-	uncharactncRNA	
chr1-1235	17.35257	-0.04853	0.529085	-0.09173	0.926911	0.966879	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2036147	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr1-1221	17.88866	0.047489	0.522928	0.090813	0.927641	0.967262	chr1	1.22E+08	1.22E+08	+	O NA	IntergeniALR/Alphe	609338	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr1-1233	19.07162	-0.04568	0.508589	-0.08981	0.928434	0.967711	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alphe	1832223	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr7-5831	16.23307	0.04771	0.545565	0.087451	0.930313	0.968711	chr7	58316230	58316529	+	O NA	IntergeniALR/Alphe	866202	NM_001155	441234	Hs. 533121	NM_001155	ENSG000000ZNF716	zinc finprotein-coding	
chr19-265	21.26331	0.042244	0.483459	0.087378	0.930371	0.968711	chr19	26575072	26575303	+	O NA	IntergeniALR/Alphe	-1218244	NR_110688	1.02E+08	Hs. 567934	NR_110688	ENSG000000LOC101927-	uncharactncRNA	
chr5-492	49.55836	0.0285	0.327249	0.08709	0.9306	0.968711	chr5	49203149	49203429	+	O NA	IntergeniALR/Alphe	1237999	NM_198444	133418	Hs. 561411	NM_198444	ENSG000000EMB	embigin protein-coding	
chr5-4875	32.81497	-0.03407	0.392659	-0.08677	0.93085	0.968711	chr5	48790045	48790289	+	O NA	IntergeniALR/Alphe	1651121	NM_198444	133418	Hs. 561411	NM_198444	ENSG000000EMB	embigin protein-coding	
chr1-124	60.39697	0.026129	0.304105	0.085922	0.931528	0.969037	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2948039	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr2-925	19.03791	-0.04308	0.509139	-0.08461	0.932573	0.969513	chr2	92533592	92534575	+	O NA	IntergeniALR/Alphe	592950	NR_027714	440888	Hs. 730239	NM_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr7-595	27.54299	0.035813	0.426018	0.084064	0.933005	0.969513	chr7	59526079	59527087	+	O NA	IntergeniALR/Alphe	2076406	NM_001155	441234	Hs. 533121	NM_001155	ENSG000000ZNF716	zinc finprotein-coding	
chr2-926	19.60772	0.04186	0.498503	0.083971	0.933079	0.969513	chr2	92632176	92633599	+	O NA	IntergeniALR/Alphe	691754	NR_027714	440888	Hs. 730239	NM_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr10-40	31.06787	-0.0331	0.402913	-0.08216	0.934522	0.970633	chr10	40567551	40567810	+	O NA	IntergeniALR/Alphe	1800365	NR_024380	441666	Hs. 255729	NR_024380	ENSG000000LOC441666-	zinc finpseudo	
chr5-490	23.58777	-0.03821	0.469236	-0.08143	0.935099	0.970845	chr5	49083122	49083367	+	O NA	IntergeniALR/Alphe	1358044	NM_198444	133418	Hs. 561411	NM_198444	ENSG000000EMB	embigin protein-coding	
chr19-26	25.2801	0.03577	0.441126	0.08054	0.935808	0.970845	chr19	26355531	26355821	+	O NA	IntergeniALR/Alphe	-1437755	NR_110688	1.02E+08	Hs. 567934	NR_110688	ENSG000000LOC101927-	uncharactncRNA	
chr18-16	241.5171	0.014398	0.178797	0.080525	0.93582	0.970845	chr18	16265850	16266213	+	O NA	IntergeniALR/Alphe	-940112	NR_027417	644669	Hs. 579474	NR_027417	ENSG000000LOC644666-	ankyrin ipseudo	
chr3-9117	19.63916	0.03912	0.497924	0.078566	0.937377	0.972082	chr3	91177444	91177958	+	O NA	IntergeniALR/Alphe	2070080	NM_005233	2042	Hs. 123642	NM_005233	ENSG000000EPAH3	EK4 ETK E EPH receptor protein-coding	
chr2-925	24.77375	-0.03244	0.452163	-0.07572	0.93964	0.974048	chr2	92558764	92559062	+	O NA	IntergeniALR/Alphe	617780	NR_027714	440888	Hs. 730239	NM_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr7-5911	43.64168	-0.02592	0.345217	-0.07507	0.940158	0.974206	chr7	59111297	59111883	+	O NA	IntergeniALR/Alphe	1661413	NM_001155	441234	Hs. 533121	NM_001155	ENSG000000ZNF716	zinc finprotein-coding	
chr7-581	17.983	0.038468	0.521406	0.073777	0.941188	0.974693	chr7	58198384	58198621	+	O NA	IntergeniALR/Alphe	748325	NM_001155	441234	Hs. 533121	NM_001155	ENSG000000ZNF716	zinc finprotein-coding	
chr5-480	31.00555	-0.02959	0.403077	-0.07341	0.941481	0.974693	chr5	48005507	48005719	+	O NA	IntergeniALR/Alphe	-2309233	NM_021072	348980	Hs. 353176	NR_021072	ENSG000000HCN1	BCNG-1 B Chyperpol:protein-coding	
chr1-236	16.14987	-0.03979	0.546934	-0.07275	0.942008	0.974693	chr1	2.37E+08	2.37E+08	+	O NA	intron (intron)	27437	NM_001278	88	Hs. 498178	NM_001100	ENSG000000ACTN2	CMD1A C actinin 2 protein-coding	
chr21-12	42.32416	0.025571	0.354163	0.072201	0.942442	0.974693	chr21	12245149	12245414	+	O NA	IntergeniALR/Alphe	-792885	NR_026916	149992	Hs. 558649	NM_153773	ANKRD30B C21orf99	ankyrin ipseudo	
chr20-28	17.86836	-0.03763	0.512353	-0.07218	0.94246	0.974693	chr20	28884030	28889998	+	O NA	IntergeniALR/Alphe	-193378	NR_132316	1.03E+08	Hs. 740188	NR_132316	FRG1DP	FSHD regipseudo	
chr5-470	23.04356	0.032988	0.462525	0.071321	0.943143	0.974825	chr5	47074226	47074446	+	O NA	IntergeniALR/Alphe	-1377956	NM_021072	348980	Hs. 353176	NR_021072	ENSG000000HCN1	BCNG-1 B Chyperpol:protein-coding	
chr18-19	23.04299	0.032955	0.464078	0.071012	0.943388	0.974825	chr18	19426399	19426758	+	O NA	IntergeniALR/Alphe	1685235	NM_005400	6093	Hs. 306307	NM_005400	ENSG000000ROCK1	P160ROCK Rh assoc protein-coding	
chr19-25	67.06784	-0.02049	0.290107	-0.07064	0.943686	0.974825	chr19	25955267	25955266	+	O NA	IntergeniALR/Alphe	-1791701	NR_003606	1E+08	Hs. 149312	NR_003606	ENSG000000HAVCR1P1	hepatitis:pseudo	
chr2-926	17.40432	0.035992	0.527472	0.068235	0.945598	0.975325	chr2	92622874	92625785	+	O NA	IntergeniALR/Alphe	683196	NR_027714	440888	Hs. 730239	NM_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr12-35	19.70149	0.033571	0.499944	0.06715	0.946643	0.975325	chr12	35614815	35615520	+	O NA	IntergeniALR/Alphe	1592671	NR_032834	84920	Hs. 102971	NM_032834	ENSG000000ALG10	ALG10A D ALG10 al protein-coding	
chr22-15	19.09079	0.034003	0.507251	0.067034	0.946554	0.975325	chr22	15054057	15054297	+	O NA	IntergeniALR/Alphe	-473982	NM_001000	81061	Hs. 554706	NM_001000	ENSG000000COR11H1	OR11H12 C ofactory protein-coding	
chrX-595	20.77953	0.0325	0.486443	0.066812	0.946731	0.975325	chrX	59501238	59504425	+	O NA	IntergeniALR/Alphe	-1592198	NM_007150	7789	Hs. 550094	NM_007150	ENSG000000ZXDA	ZNF896	zinc finprotein-coding
chr1-124	17.22735	-0.03605	0.539496	-0.06681	0.946731	0.975325	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	3360226	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr1-124	21.38796	0.031979	0.478684	0.066806	0.946736	0.975325	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	3255992	NR_003955	441666	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr10-40	21.38796	0.031979	0.478684	0.066806	0.946736	0.975325	chr10	40837427	40838060	+	O NA	IntergeniALR/Alphe	1530302	NR_024380	441666	Hs. 255729	NR_024380	ENSG000000LOC441666-	zinc finpseudo	
chr18-16	34.37963	-0.02518	0.385498	-0.06532	0.94792	0.976167	chr18	16008586	16008883	+	O NA	IntergeniALR/Alphe	-682815	NR_027417	644669	Hs. 579474	NR_027417	ENSG000000LOC644666-	ankyrin ipseudo	
chr5-493	23.60194	-0.02986	0.462641	-0.06454	0.948541	0.976428	chr5	49383151	49383641	+	O NA	IntergeniALR/Alphe	1057761	NM_198444	133418	Hs. 561411	NM_198444	ENSG000000EMB	embigin protein-coding	
chr1-124	44.57288	0.02162	0.342144	0.06319	0.949615	0.977156	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	3367901	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr5-477	22.95979	-0.02854	0.464522	-0.06143	0.951017	0.977635	chr5	47731357	47731809	+	O NA	IntergeniALR/Alphe	-2035203	NM_021072	348980	Hs. 353176	NR_021072	ENSG000000HCN1	BCNG-1 B Chyperpol:protein-coding	
chr22-13	30.4653	0.024884	0.406803	0.061169	0.951225	0.977635	chr22	13785364	13785621	+	O NA	IntergeniALR/Alphe	-1742667	NM_001000	81061	Hs. 554706	NM_001000	ENSG000000COR11H1	OR11H12 C ofactory protein-coding	
chr5-492	27.08896	0.026082	0.430731	0.060552	0.951716	0.977635	chr5	49256773	49257117	+	O NA	IntergeniALR/Alphe	1184343	NM_198444	133418	Hs. 561411	NM_198444	ENSG000000EMB	embigin protein-coding	
chr1-124	25.40305	0.026908	0.44613	0.060315	0.951905	0.977635	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	3235588	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr7-604	17.80717	-0.03155	0.524041	-0.0602	0.951995	0.977635	chr7	60421222	60421440	+	O NA	IntergeniALR/Alphe	2882725	NR_003955	643955	Hs. 583308	NR_003955	ENSG000000ZNF733P	ZNF733	zinc finpseudo
chr21-83	51.46958	-0.01929	0.322335	-0.05984	0.952285	0.977635	chr21	8385781	8387075	+	O NA	intron (intron)	-1934	NR_128716	1.04E+08	Hs. 128716	NR_128716	ENSG000000MIR6724-	hsa-mir-2 microRNA ncRNA	
chr19-25	63.54629	-0.01694	0.297189	-0.057	0.954542	0.978096	chr19	25271153	25271381	+	O NA	IntergeniALR/Alphe	-1107820	NR_003606	1E+08	Hs. 149312	NR_003606	ENSG000000HAVCR1P1	hepatitis:pseudo	
chr1-123	17.46665	0.0298	0.527514	0.056491	0.954951	0.978096	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alphe	1917074	NR_003955	647121	Hs. 697682	NR_003955	ENSG000000EMB1	embigin ipseudo	
chr17-2	17.46608	0.02975	0.527503	0.056397	0.955025	0.978096	chr17	23267491	23267701	+	O NA	IntergeniALR/Alphe	744485	NM_001190	1E+08	Hs. 740188	NR_001190	ENSG000000MTRNR2L1	HN1	MT-RNR2 l protein-coding
chr2-927	17.46608	0.02975	0.527503	0.056397	0.955025	0.978096	chr2	92755302	92756056	+	O NA	IntergeniALR/Alphe	814546	NR_027714	44088					

Supplementary Information

Supplement Table 9. Genome-wide profiling of differential peaks between senescent cells and counterparts exposed to ML324 (ChIP-seq for H3K36me3).

geneID	baseMea	log2Fold	lfcSE	stat	pvalue	padj	Chr	Start	End	Stranc	Peak	ε	Focus	Annotati	Detailed	Distance	Nearest	F	Entrez	ID	Nearest	U	Nearest	F	Nearest	E	Gene	Nar	Gene	Ali	Gene	De	Gene	Type		
chr16-382	770.5261	0.972888	0.075115	12.95205	2.29E-38	8.61E-35	chr16	38276157	38276483	+	0	NA	Intergeni	ALR Alphe	2529768	NR_033985	400533	Hs.49913	ENR_033985	ENSG000004	LINC02167	-											long intencRNA			
chr17-266	842.7855	0.757288	0.07	10.81843	2.82E-27	5.30E-24	chr17	26603798	26604053	+	0	NA	Intergeni	ALR Alphe	485316	NR_135673	1.05E+08	Hs.64991	ENR_135673	ENSG000004	LOC105371	-												uncharactcRNA		
chr5-487	302.3381	0.985717	0.129479	7.612972	2.68E-14	3.36E-11	chr5	48732109	48732399	+	0	NA	Intergeni	ALR Alphe	1709304	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70											embigin protein-coding		
chr19-265	262.9757	1.028475	0.138631	7.418793	1.18E-13	1.11E-10	chr19	26331628	26331985	+	0	NA	Intergeni	ALR Alphe	-1461625	NR_146733	1.02E+08	Hs.56793	ENR_110687	ENSG000004	LOC101927	-												uncharactcRNA		
chr5-4961	231.2037	1.087339	0.152058	7.15083	8.63E-13	6.49E-10	chr5	49612258	49615611	+	0	NA	Intergeni	ALR Alphe	827354	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70											embigin protein-coding		
chr5-4965	196.4947	1.058742	0.164615	6.431619	1.26E-10	7.92E-08	chr5	49630809	49632109	+	0	NA	Intergeni	ALR Alphe	809829	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70											embigin protein-coding		
chr19-271	133.2163	1.30337	0.204471	6.374352	1.84E-10	9.88E-08	chr19	27146759	27146980	+	0	NA	Intergeni	ALR Alphe	-646562	NR_146733	1.02E+08	Hs.56793	ENR_110687	ENSG000004	LOC101927	-												uncharactcRNA		
chr1-123	271.1514	0.855162	0.135126	6.328639	2.47E-10	1.16E-07	chr1	1.24E+08	1.24E+08	+	0	NA	Intergeni	ALR Alphe	2407205	NR_003955	647121	Hs.69768	ENR_003955	ENSG000004	EMB	-	GP70											embigin ppsudo		
chr5-4961	174.3077	-0.99273	0.158584	-6.26001	3.33E-10	1.39E-07	chr5	49616438	49617194	+	0	NA	Intergeni	ALR Alphe	824472	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70												embigin protein-coding	
chr4-739C	172.1431	1.101746	0.175044	6.278116	3.40E-10	1.41E-07	chr4	73906089	73906784	+	0	NA	Intergeni	LIPA3 LIN	37043	NR_001511	2919	Hs.789	NR_001511	ENSG000004	CXCL1	-	FSP GRO1	C-X-C	mot										protein-coding	
chr4-745	165.1044	1.031746	0.186044	6.278036	3.42E-10	1.42E-07	chr4	74597145	74598143	+	0	NA	Intergeni	THE1B-int	152508	NR_001657	374	Hs.27083	ENR_001657	ENSG000004	AREG	-	AR AREGB	amphireg											protein-coding	
chr10-405	210.9468	-0.99273	0.158584	-6.26001	3.33E-10	1.45E-07	chr10	40980950	40981326	+	0	NA	Intergeni	ALR Alphe	1386907	NR_02438C	441666	Hs.25572	ENR_02438C	ENSG000004	LOC441666	-												zinc fingpsudo		
chr17-266	396.1376	-0.68484	0.110748	-6.18377	6.26E-10	2.14E-07	chr17	26619531	26620055	+	0	NA	Intergeni	ALR Alphe	469448	NR_135673	1.05E+08	Hs.64991	ENR_135673	ENSG000004	LOC105371	-													uncharactcRNA	
chr1-1247	131.1533	-1.23744	0.205448	-6.02312	1.71E-09	5.18E-07	chr1	1.25E+08	1.25E+08	+	0	NA	Intergeni	ALR Alphe	3222330	NR_003955	647121	Hs.69768	ENR_003955	ENSG000004	EMB	-												embigin ppsudo		
chr4-746	142.15	1.367431	0.204347	6.023018	3.85E-10	1.45E-07	chr4	74616713	74616924	+	0	NA	Intergeni	AluYg6 SI	171682	NR_001657	374	Hs.27083	ENR_001657	ENSG000004	AREG	-	AR AREGB	amphireg											protein-coding	
chr17-23C	347.2216	-0.710663	0.18125	-6.01589	1.79E-09	5.18E-07	chr17	23016338	23016540	+	0	NA	Intergeni	ALR Alphe	493328	NR_00119C	1E+08	Hs.74018	ENR_00119C	ENSG000004	MTRNR2L1	-	HNI	MT-RNR2	l										protein-coding	
chr17-268	281.1627	-0.81174	0.137685	-5.89562	3.73E-09	1.00E-06	chr17	26880960	26885887	+	0	NA	Intergeni	ALR Alphe	205818	NR_135673	1.05E+08	Hs.64991	ENR_135673	ENSG000004	LOC105371	-													uncharactcRNA	
chr6-591f	262.8307	-0.80019	0.137833	-5.80552	6.42E-09	1.61E-06	chr6	59163123	59163346	+	0	NA	Intergeni	ALR Alphe	-1201788	NR_132994	1.07E+08	Hs.56153	ENR_125727	ENSG000004	LINC0068C	-													long intencRNA	
chr5-4964	161.8593	-1.0534	0.182829	-5.76165	8.33E-09	1.96E-06	chr5	49643674	49646210	+	0	NA	Intergeni	ALR Alphe	796346	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70												embigin protein-coding	
chr10-405	209.013	-0.90897	0.158577	-5.73203	9.92E-09	2.20E-06	chr10	40556268	40556895	+	0	NA	Intergeni	ALR Alphe	1811464	NR_02438C	441666	Hs.25572	ENR_02438C	ENSG000004	LOC441666	-												zinc fingpsudo		
chr5-4954	118.5783	1.226714	0.215531	5.691578	1.26E-08	2.63E-06	chr5	49547195	49547490	+	0	NA	Intergeni	ALR Alphe	893946	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70												embigin protein-coding	
chr5-485	229.7896	0.86783	0.153364	5.686361	1.53E-08	3.02E-06	chr5	48589523	48589723	+	0	NA	Intergeni	ALR Alphe	1851665	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70												embigin protein-coding	
chr5-4964	111.6384	1.23595	0.221868	5.570662	2.54E-08	4.77E-06	chr5	49642240	49642817	+	0	NA	Intergeni	ALR Alphe	798760	NR_198445	133418	Hs.56141	ENR_198445	ENSG000004	EMB	-	GP70													embigin protein-coding
chr10-405	181.1677	0.922596	0.170121	5.423171	5.86E-08	1.05E-05	chr10	40593352	40593603	+	0	NA	Intergeni	ALR Alphe	1774568	NR_02438C	441666	Hs.25572	ENR_02438C	ENSG000004	LOC441666	-													zinc fingpsudo	
chr5-464	60.87076	1.632742	0.302364	5.399921	6.67E-08	1.14E-05	chr5	46434582	46434946	+	0	NA	Intergeni	ALR Alphe	-738384	NR_021072	348980	Hs.35317	ENR_021072	ENSG000004	HCN1	-	BCNG-1 BC	hyperpol											protein-coding	
chr5-479	137.1194	1.07577	0.199947	5.380283	7.44E-08	1.22E-05	chr5	47982825	47983163	+	0	NA	Intergeni	ALR Alphe	-2286614	NR_021072	348980	Hs.35317	ENR_021072	ENSG000004	HCN1	-	BCNG-1 BC	hyperpol											protein-coding	
chr10-408	169.6754	0.96256	0.179625	5.358711	8.38E-08	1.31E-05	chr10	40892151	40892527	+	0	NA	Intergeni	ALR Alphe	1475706	NR_02438C	441666	Hs.25572	ENR_02438C	ENSG000004	LOC441666	-													zinc fingpsudo	
chr4-744	145.2174	0.985251	0.185621	5.31487	8.84E-08	1.34E-05	chr4	74498802	74499010	+	0	NA	Intergeni	LIM2 LINE	53770	NR_001657	374	Hs.27083	ENR_001657	ENSG000004	AREG	-	AR AREGB	amphireg											protein-coding	
chr1-1217	133.0313	-1.07427	0.203394	-5.28169	1.28E-07	1.93E-05	chr1	1.22E+08	1.22E+08	+	0	NA	Intergeni	ALR Alphe	252637	NR_003955	647121	Hs.69768	ENR_003955	ENSG000004	EMB	-													embigin ppsudo	
chr10-414	123.694	-1.11654	0.211969	-5.26748	1.38E-07	2.00E-05	chr10	41405822	41406021	+	0	NA	Intergeni	ALR Alphe	962124	NR_02438C	441666	Hs.25572	ENR_02438C	ENSG000004	LOC441666	-													zinc fingpsudo	
chr1-1247	128.6484	-1.10302	0.210132	-5.24916	1.53E-07	2.06E-05	chr1	1.25E+08	1.25E+08	+	0	NA	Intergeni	ALR Alphe	3259081	NR_003955	647121	Hs.69768	ENR_003955	ENSG000004	EMB	-													embigin ppsudo	
chr10-402	102.437	-1.21436	0.231359	-5.24884	1.53E-07	2.06E-05	chr10	40267807	40268087	+	0	NA	Intergeni	ALR Alphe	1571351	NR_04500C	399746	Hs.74260	NR_045000	ACTR3BP5	FKSG74	-														ACTR3B ppsudo
chr1-1247	170.08757	-1.44511	0.279619	-5.16814	2.36E-07	3.07E-05	chr1	1.25E+08	1.25E+08	+	0	NA	Intergeni	ALR Alphe	3251931	NR_003955	647121	Hs.69768	ENR_003955	ENSG000004	EMB	-														embigin ppsudo
chr10-401	145.177	1.015933	0.197807	5.13598	2.81E-07	3.52E-05	chr10	40135068	40135333	+	0	NA	Intergeni	ALR Alphe	1438604	NR_04500C	399746	Hs.74260	NR_045000	ACTR3BP5	FKSG74	-														ACTR3B ppsudo
chr5-488	109.7955	1.1345	0.223599	5.073822	3.90E-07	4.73E-05	chr5	48850749	48850994	+	0	NA	Intergeni	ALR																						



chr10-40: 24.69934	1.187364	0.320292	3.707132	0.00021	0.007171	chr10	40367454	40368623	+	0 NA	IntergeniALR/Alph	1671442 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr1-124: 69.53782	1.010731	0.274086	3.687641	0.000226	0.007669	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alph	2515484 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr12-37: 63.06965	1.060742	0.287901	3.684392	0.000229	0.007669	chr12	37237603	37238561	+	0 NA	IntergeniALR/Alph	-1078692 NM_001013	144245 Hs. 259305NM_001013	ENSG000000CALG10B	ALG10 KCF	ALG10	alprotein-coding
chr11-53: 17.18073	1.521699	0.413139	3.683239	0.00023	0.007669	chr11	53509604	53509886	+	0 NA	IntergeniALR/Alph	1094253 NM_001004	119749 Hs. 553564NM_001004	ENSG000000OR4C6	-	olfactory	protein-coding
chr10-40: 23.45979	1.203594	0.327194	3.678535	0.000235	0.007693	chr10	40633542	40633977	+	0 NA	IntergeniALR/Alph	1734288 NR_02438C	441666 Hs. 255725NR_02438C	ENSG000000LOC441666	-	zinc	fingerpseud
chr7-55: 16.68248	1.564241	0.425315	3.677841	0.000235	0.007697	chr7	5528433	5530459	+	0 NA	intron (ncpG)	1155 NM_001101	60 Hs. 520644NM_001101	ENSG000000ACTB	BRWS1 PS1	actin	betprotein-coding
chr1-124: 12.7867	1.820345	0.221177	3.678282	0.00024	0.007782	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alph	2731658 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr19-27: 43.714	1.816097	0.343619	3.667132	0.000245	0.007889	chr19	27065031	27065528	+	0 NA	IntergeniALR/Alph	-728152 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG000000LOC101927	-	uncharactncRNA	
chr19-27: 23.91647	1.183219	0.323773	3.654473	0.000258	0.008218	chr19	27008326	27009103	+	0 NA	IntergeniALR/Alph	-784717 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG000000LOC101927	-	uncharactncRNA	
chr2-92: 21.64682	1.243399	0.340859	3.649246	0.000263	0.008311	chr2	92550084	92550747	+	0 NA	IntergeniALR/Alph	609282 NR_027714	440888 Hs. 730233NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo
chr1-123: 27.03532	1.138686	0.312421	3.644711	0.000268	0.008394	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alph	1628105 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr11-65: 14.71425	-1.77169	0.487157	-3.6368	0.000276	0.008585	chr11	65423118	65425808	+	0 NA	non-codirnon-codir	1665 NR_028272	283131 Hs. 523788NR_002802	ENSG000000NEAT1	LINC00084	nuclear	ncRNA
chr10-40: 33.01611	-1.20144	0.330999	-3.62975	0.000284	0.00875	chr10	40462784	40463063	+	0 NA	IntergeniALR/Alph	1766327 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr5-45: 28.97682	-1.13207	0.312432	-3.62341	0.000291	0.008895	chr5	48538105	48538413	+	0 NA	IntergeniALR/Alph	1903029 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr19-26: 56.71801	-1.08159	0.299023	-3.61706	0.000298	0.008972	chr19	26967507	26967995	+	0 NA	IntergeniALR/Alph	-825680 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG000000LOC101927	-	uncharactncRNA	
chr19-27: 30.59296	-1.14365	0.316188	-3.61701	0.000298	0.008972	chr19	27091791	27092829	+	0 NA	IntergeniALR/Alph	-701121 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG000000LOC101927	-	uncharactncRNA	
chr18-16: 18.9417	-1.35147	0.375786	-3.59638	0.000323	0.009637	chr18	16677690	16677909	+	0 NA	IntergeniALR/Alph	-135180 NR_027417	644669 Hs. 579474NR_027417	ENSG000000LOC644669	-	ankyrin	fpseudo
chr5-49: 19.95058	-1.29305	0.359842	-3.59339	0.000326	0.009646	chr5	49419249	49419511	+	0 NA	IntergeniALR/Alph	1021908 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr5-48: 55.49304	-1.08693	0.302595	-3.59202	0.000328	0.009646	chr5	48929424	48930402	+	0 NA	IntergeniALR/Alph	1511375 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr19-25: 55.96873	-1.08097	0.301604	-3.58407	0.000338	0.009868	chr19	25052059	25051340	+	0 NA	IntergeniALR/Alph	-887352 NR_003603	1E+08 Hs. 149312NR_003603	ENSG000000HAVCR1P1	-	hepatitis	pseudo
chr2-92: 16.89831	-1.49048	0.416746	-3.57647	0.000348	0.010081	chr2	92934828	92935157	+	0 NA	IntergeniALR/Alph	993859 NR_027714	440888 Hs. 730233NM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo
chr10-40: 28.83369	-1.11317	0.311675	-3.57158	0.000355	0.010193	chr10	40080123	40080384	+	0 NA	IntergeniALR/Alph	1383657 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr7-59: 74.55807	-0.9411	0.263818	-3.56723	0.000361	0.010219	chr7	59734599	59735003	+	0 NA	IntergeniALR/Alph	2284624 NM_001155	441234 Hs. 533121NM_001155	ENSG000000ZNF716	-	zinc	fingerprotein-coding
chr10-40: 50.95375	-1.12732	0.316048	-3.56693	0.000361	0.010219	chr10	40412688	40414995	+	0 NA	IntergeniALR/Alph	1717245 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr5-47: 21.39138	-1.21763	0.342024	-3.56006	0.000371	0.010412	chr5	47694883	47696328	+	0 NA	IntergeniALR/Alph	-1999225 NM_021072	348980 Hs. 353176NM_021072	ENSG000000HCN1	BCNG-1 BC	hyperpolaprotein-coding	
chr1-124: 34.26229	-1.19163	0.335767	-3.54896	0.000387	0.01078	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alph	2829607 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr1-124: 37.78298	-1.26407	0.356518	-3.54561	0.000392	0.010838	chr1	1.24E+08	1.24E+08	+	0 NA	IntergeniALR/Alph	2645233 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr1-122: 85.63958	0.875482	0.24765	3.53516	0.000408	0.011194	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alph	1222498 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr5-49: 36.30397	1.22974	0.348568	3.527068	0.00042	0.011394	chr5	49479027	49479228	+	0 NA	IntergeniALR/Alph	962161 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr19-25: 57.07312	1.065266	0.320664	3.526624	0.000421	0.011394	chr19	25439330	25439541	+	0 NA	IntergeniALR/Alph	-1275988 NR_003603	1E+08 Hs. 149312NR_003603	ENSG000000HAVCR1P1	-	hepatitis	pseudo
chr5-49: 37.36705	1.244513	0.353746	3.518096	0.000435	0.011683	chr5	49182269	49183335	+	0 NA	IntergeniALR/Alph	1258486 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr10-40: 27.72905	1.087227	0.310135	3.50566	0.000455	0.012086	chr10	40975909	40976161	+	0 NA	IntergeniALR/Alph	1392014 NR_02438C	441666 Hs. 255725NR_02438C	ENSG000000LOC441666	-	zinc	fingerpseud
chr5-48: 13.919	1.800542	0.513803	3.504342	0.000458	0.012086	chr5	48241487	48242221	+	0 NA	IntergeniALR/Alph	2199434 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr1-19: 13.94376	1.798564	0.513371	3.503441	0.000459	0.012086	chr1	1.93E+08	1.93E+08	+	0 NA	intron (intron)	1827 NM_002922	5997 Hs. 78944 NM_002922	ENSG000000CRGS2	GOS8	regulator	protein-coding
chr10-40: 25.21855	1.105248	0.316039	3.499083	0.000467	0.0122	chr10	40595496	40596559	+	0 NA	IntergeniALR/Alph	1772018 NR_02438C	441666 Hs. 255725NR_02438C	ENSG000000LOC441666	-	zinc	fingerpseud
chr19-26: 19.08459	1.291787	0.370342	3.487924	0.000487	0.012633	chr19	26918117	26918364	+	0 NA	IntergeniALR/Alph	-875191 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG000000LOC101927	-	uncharactncRNA	
chr10-40: 18.55495	1.320191	0.379409	3.479602	0.000502	0.012943	chr10	40400425	40400712	+	0 NA	IntergeniALR/Alph	1703972 NR_045000	399746 Hs. 742607NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr6-59: 51.80495	1.088129	0.311718	3.468833	0.000523	0.013381	chr6	59586841	59587042	+	0 NA	IntergeniALR/Alph	-1625495 NR_132994	1.07E+08 Hs. 561535NR_125727	ENSG000000LINC0068C	-	long	intcncRNA
chr7-58: 25.73494	1.088011	0.314078	3.464146	0.000532	0.013524	chr7	58893059	58893259	+	0 NA	IntergeniALR/Alph	1442982 NM_001155	441234 Hs. 533121NM_001155	ENSG000000ZNF716	-	zinc	fingerprotein-coding
chr19-26: 32.3993	1.119429	0.323382	3.461634	0.000537	0.01356	chr19	26549334	26550173	+	0 NA	IntergeniALR/Alph	-1243678 NR_146733	1.02E+08 Hs. 567934NR_110687	ENSG000000LOC101927	-	uncharactncRNA	
chr19-25: 42.18876	1.189438	0.345864	3.439036	0.000584	0.014645	chr19	25736921	25737124	+	0 NA	IntergeniALR/Alph	-1573575 NR_003603	1E+08 Hs. 149312NR_003603	ENSG000000HAVCR1P1	-	hepatitis	pseudo
chr5-49: 16.10882	1.496103	0.435676	3.433977	0.000595	0.014823	chr5	49459379	49459706	+	0 NA	IntergeniALR/Alph	981746 NM_198445	133418 Hs. 561411NM_198445	ENSG000000EMB	GP70	embigin	protein-coding
chr11-51: 15.12912	1.590037	0.463645	3.429431	0.000605	0.014974	chr11	51770378	51770586	+	0 NA	IntergeniALR/Alph	1361335 NR_024504	646813 Hs. 684175NR_024504	LOC646813	-	DEX	box pseudo
chr1-124: 33.17996	-1.12286	0.328194	-3.42133	0.000623	0.015327	chr1	1.25E+08	1.25E+08	+	0 NA	IntergeniALR/Alph	3167745 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr1-122: 57.67907	-1.01455	0.297047	-3.41547	0.000637	0.015558	chr1	1.23E+08	1.23E+08	+	0 NA	IntergeniALR/Alph	1126228 NR_003955	647121 Hs. 697682NR_003955	ENSG000000EMB1	-	embigin	fpseudo
chr1-125: 15.62979	-1.59104	0.466586	-3.40996	0.00065	0.015774	chr1	1.46E+08	1.46E+08	+	0 NA	intron (intron)	31303 NR_104217	1.02E+08 Hs. 534675NR_104217	ENSG000000NBPF25P	WI2-925H NBPF	memt	pseudo
chr6-37: 11.88799	-2.12293	0.623399	-3.40542	0.000661	0.015936	chr6	37171230	37171598	+	0 NA	exon (NM exon)	1262 NM_001243	5292 Hs. 81170 NM_002644	ENSG000000PIM1	PIM	Pim-1	prcprotein-coding
chr15-10: 13.64676	-1.76172	0.52014	-3.38701	0.000707	0.016734	chr15	1.02E+08	1.02E+08	+	0 NA	IntergeniCpG	-12823 NM_001321	1E+08 Hs. 104864NM_001321551	LOC100128	-	putative	protein-coding
chr5-49: 18.39723	-1.29074	0.381202	-3.38596	0.000709	0.016734	chr5	49545496	49546353	+	0 NA	IntergeniALR/Alph	895364 NM_198445					

chr5-4735	16.98896	1.223098	0.402111	3.041694	0.002353	0.037994	chr5	47358734	47359982+	0	NA	IntergeniALR/Alphe	-1662978	NM_021072	348980	Hs.35317c	NM_021072	ENSG00000	HCN1	BCNG-1	BC	hyperpolaprotein-coding	
chr15-494	8.326801	2.697719	0.890537	3.029318	0.002451	0.039416	chr15	49423717	49427312+	0	NA	intron (N(AAATTAT)R	2272	NM_002005	2252	Hs.567262	NM_002005	ENSG00000	FGF7	HbGF-7	KC	fibroblasprotein-coding	
chr19-256	16.00485	1.285899	0.425691	3.020735	0.002522	0.04026	chr19	25837936	25839035+	0	NA	IntergeniALR/Alphe	-1675038	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1			hepatitispseudo	
chr1-1217	53.73945	0.93823	0.310637	3.02034	0.002525	0.04026	chr1	1.22E+08	1.22E+08+	0	NA	IntergeniALR/Alphe	231238	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr7-5914	16.04199	1.284316	0.425915	3.015425	0.002566	0.040745	chr7	59149122	59149760+	0	NA	IntergeniALR/Alphe	1699264	NM_001155	441234	Hs.533121	NM_001155	ENSG00000	ZNF716			zinc fingprotein-coding	
chr19-248	39.27837	1.069288	0.355021	3.0119	0.002596	0.041048	chr19	24893005	24893298+	0	NA	IntergeniALR/Alphe	-729704	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1			hepatitispseudo	
chr1-1494	15.53357	1.321067	0.438824	3.01047	0.002608	0.041069	chr1	1.49E+08	1.5E+08+	0	NA	exon (NM exon (NM	39111	NM_001351	1.01E+08	Hs.44508C	NM_001351	ENSG00000	NBPF19			NBPF memtprotein-coding	
chr10-395	35.58207	1.01878	0.339276	3.002806	0.002675	0.041942	chr10	39983438	39983710+	0	NA	IntergeniALR/Alphe	1286978	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74			ACTR3B pspseudo	
chr19-271	27.54304	0.916511	0.30566	2.998461	0.002713	0.042368	chr19	27139682	27140680+	0	NA	IntergeniALR/Alphe	-653250	NR_146735	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr20-264	26.2721	0.916897	0.307347	2.98239	0.00286	0.044473	chr20	26468721	26469385+	0	NA	IntergeniALR/Alphe	-259820	NR_040099	284801	Hs.370699	NR_040099	ENSG00000	MIR663AHC-			MIR663A lncRNA	
chr1-1225	19.71725	1.048084	0.352655	2.971979	0.002959	0.04582	chr1	1.23E+08	1.23E+08+	0	NA	IntergeniALR/Alphe	1063707	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr5-4881	35.34122	1.003037	0.337896	2.968482	0.002993	0.045975	chr5	48810888	48811807+	0	NA	IntergeniALR/Alphe	1629941	NM_198444	133418	Hs.561411	NM_198444	ENSG00000	EMB	GP70		embigin protein-coding	
chr10-395	45.45395	0.981231	0.330556	2.968425	0.002993	0.045975	chr10	39986368	39987336+	0	NA	IntergeniALR/Alphe	1290256	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74			ACTR3B pspseudo	
chr10-401	18.74552	1.0898	0.367446	2.965881	0.003018	0.046	chr10	40157670	40158953+	0	NA	IntergeniALR/Alphe	1461715	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74			ACTR3B pspseudo	
chr1-1245	30.90716	-0.92535	0.312132	-2.96461	0.003031	0.046	chr1	1.25E+08	1.25E+08+	0	NA	IntergeniALR/Alphe	2995430	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr20-275	19.22476	-1.06722	0.36	-2.96451	0.003032	0.046	chr20	27966984	27967183+	0	NA	IntergeniALR/Alphe	635582	NR_13231F	1E+08	Hs.529357	NR_13231F	ENSG00000	FRG1CP			FSHD regipseudo	
chr5-486	21.28495	-0.99371	0.335575	-2.96121	0.003064	0.046132	chr5	48603636	48604534+	0	NA	IntergeniALR/Alphe	1837203	NM_198444	133418	Hs.561411	NM_198444	ENSG00000	EMB	GP70		embigin protein-coding	
chr1-1221	221.29512	-0.99334	0.335558	-2.96207	0.003074	0.046132	chr1	1.23E+08	1.23E+08+	0	NA	IntergeniALR/Alphe	1258730	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr1-1217	37.97445	-1.03707	0.350376	-2.95987	0.003078	0.046132	chr1	1.22E+08	1.22E+08+	0	NA	IntergeniALR/Alphe	245491	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr16-865	10.32421	-2.05692	0.695211	-2.9587	0.003089	0.046132	chr16	86510703	86518334+	0	NA	3' UTR (N3' UTR (N	3991	NM_001451	2294	Hs.155591	NM_001451	ENSG00000	FOXP1	ACDMPV	FK	forkhead protein-coding	
chr1-8556	14.03441	-1.44228	0.48782	-2.95657	0.003111	0.046268	chr1	85580922	85583536+	0	NA	exon (NM exon (NM	1468	NM_001554	3491	Hs.8867	NM_001554	ENSG00000	CCN1	CYR61	GI	cellular protein-coding	
chr2-4322	10.30962	-2.05548	0.695896	-2.95371	0.00314	0.046278	chr2	43222536	43225508+	0	NA	3' UTR (N3' UTR (N	2584	NM_006887	678	Hs.503093	NM_006887	ENSG00000	ZFP36L2	BRF2	ERF-	ZFP36 rirprotein-coding	
chr4-1375	10.30962	-2.05548	0.695896	-2.95371	0.00314	0.046278	chr4	1.38E+08	1.38E+08+	0	NA	intron (N(TAT)n Si	6453	NM_019035	54510	Hs.591691	NM_019035	ENSG00000	PCDH18	PCDH68L	protopctd protein-coding		
chr19-25	17.7592	-1.13645	0.384861	-2.95287	0.003148	0.046278	chr19	25021130	25021580+	0	NA	IntergeniALR/Alphe	-857908	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1			hepatitispseudo	
chr1-1225	17.27554	-1.1628	0.394756	-2.94562	0.003223	0.047192	chr1	1.23E+08	1.23E+08+	0	NA	IntergeniALR/Alphe	1000952	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr1-1247	22.19832	-0.9613	0.326983	-2.93991	0.003283	0.047796	chr1	1.25E+08	1.25E+08+	0	NA	IntergeniALR/Alphe	3220783	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr5-488	70.38132	-0.79721	0.271227	-2.93928	0.00329	0.047796	chr5	48860545	48860791+	0	NA	IntergeniALR/Alphe	1580620	NM_198444	133418	Hs.561411	NM_198444	ENSG00000	EMB	GP70		embigin protein-coding	
chr6-5938	58.57665	-0.85511	0.292187	-2.92658	0.003427	0.04958	chr6	59383276	59383494+	0	NA	IntergeniALR/Alphe	-1421939	NR_132994	1.07E+08	Hs.561535	NR_125727	ENSG00000	LINC0068C-			long intencRNA	
chr8-445	38.58886	-1.03985	0.355442	-2.92551	0.003439	0.04958	chr8	44594451	44594671+	0	NA	IntergeniALR/Alphe	1302119	NM_001005	340441	Hs.531575	NM_001005	ENSG00000	POTEA	A26A1	CTI	POTE ankyprotein-coding	
chr1-124	34.03288	-0.96207	0.330431	-2.91155	0.003596	0.051653	chr1	1.24E+08	1.24E+08+	0	NA	IntergeniALR/Alphe	2486311	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr2-9237	16.1915	-1.21819	0.418824	-2.90861	0.00363	0.051944	chr2	92374494	92374819+	0	NA	IntergeniALR/Alphe	433523	NR_027714	440888	Hs.730235	NM_01032412	ACTR3BP2	FKSG73			ACTR3B pspseudo	
chr19-362	12.99414	-1.5419	0.530855	-2.90457	0.003678	0.05242	chr19	36280523	36281852+	0	NA	IntergeniSST1 Sate	-30156	NR_029389	1E+08	Hs.46655C	NR_029389	LOC100134-				uncharactncRNA	
chr1-1227	15.73261	-1.24944	0.430728	-2.90077	0.003723	0.05286	chr1	1.23E+08	1.23E+08+	0	NA	IntergeniALR/Alphe	1203522	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr19-265	15.21977	-1.2832	0.445241	-2.88203	0.003951	0.055764	chr19	26519309	26519508+	0	NA	IntergeniALR/Alphe	-1274023	NR_146735	1.02E+08	Hs.567934	NR_110687	ENSG00000	LOC101927-			uncharactncRNA	
chr1-1242	12.05159	1.66485	0.577553	2.881596	0.003957	0.055764	chr1	1.24E+08	1.24E+08+	0	NA	IntergeniALR/Alphe	2702645	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr1-1241	34.83254	0.971084	0.337469	2.877549	0.004008	0.056273	chr1	1.24E+08	1.24E+08+	0	NA	IntergeniALR/Alphe	2648738	NR_003956	647121	Hs.697682	NR_003956	ENSG00000	EMB1P1			embigin fpseudo	
chr10-415	12.02241	1.662685	0.578774	2.872772	0.004069	0.056919	chr10	41380177	41380376+	0	NA	IntergeniALR/Alphe	987769	NR_02438C	441666	Hs.255725	NR_02438C	ENSG00000	LOC44166C-			zinc fingpseudo	
chr5-4771	19.97244	0.990772	0.348252	2.868818	0.00412	0.057028	chr5	47718440	47719621+	0	NA	IntergeniALR/Alphe	-2022655	NM_021072	348980	Hs.35317c	NM_021072	ENSG00000	HCN1	BCNG-1	BC	hyperpolaprotein-coding	
chr11-522	24.73775	0.893646	0.31155	2.868391	0.004126	0.057028	chr11	52839828	52840055+	0	NA	IntergeniALR/Alphe	1764057	NM_001004	119749	Hs.553564	NM_001004	ENSG00000	OR4C46			olfactoryprotein-coding	
chr19-255	19.98262	0.998618	0.348263	2.867429	0.004138	0.057028	chr19	25317925	25319026+	0	NA	IntergeniALR/Alphe	-1155028	NR_003603	1E+08	Hs.149312	NR_003603	ENSG00000	HAVCR1P1			hepatitispseudo	
chr9-4352	20.51225	0.981493	0.342302	2.867328	0.00414	0.057028	chr9	43524994	43525251+	0	NA	IntergeniALR/Alphe	398957	NR_160666	1.03E+08	Hs.561411	NR_160666	ENSG00000	EMB	LOC102724-			methylenepseudo
chr5-4897	34.47718	0.952062	0.332153	2.86634	0.004152	0.057028	chr5	48973351	48974271+	0	NA	IntergeniALR/Alphe	1467477	NM_198444	133418	Hs.561411	NM_198444	ENSG00000	EMB	GP70		embigin protein-coding	
chr17-614	9.055475	2.267945	0.792576	2.861485	0.004217	0.057699	chr17	61400302	61409492+	0	NA	intron (NCPg-11505	5054	NM_005994	6909	Hs.531085	NM_005994	ENSG00000	TBX2	VETD		T-box traprotein-coding	
chr10-405	53.51789	0.874875	0.30588	2.860186	0.004234	0.057726	chr10	40971781	40971989+	0	NA	IntergeniALR/Alphe	1396160	NR_02438C	441666	Hs.255725	NR_02438C	ENSG00000	LOC44166C-			zinc fingpseudo	
chr5-4735	18.49008	1.058431	0.370397	2.857555	0.004269	0.057932	chr5																



chr2-5587	9.229497	1.851922	0.744944	2.485989	0.012919	0.136295	chr2	55873504	55875065	+0	NA	intron (Nintron (N	49498	NM_001036	2202	Hs.76224	NM_004105	ENSG000004EFEMP1	DHRD DRAI	EGF contaprotein-coding	
chr1-1967	9.715362	1.75495	0.706476	2.48409	0.012988	0.136295	chr1	1.97E+08	1.97E+08	+0	NA	intron (THEIC-int	-35669	NM_021022	10878	Hs.709217	NM_021022	ENSG000004CFHR3	CFHL3 DOW	comlemerprotein-coding	
chr10-40	10.6725	1.594231	0.64188	2.483689	0.013003	0.136295	chr10	40389388	40390526	+0	NA	IntergeniALR/Alphe	1693361	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr11-534	10.6725	1.594231	0.64188	2.483689	0.013003	0.136295	chr11	53416348	53416621	+0	NA	IntergeniALR/Alphe	1187514	NM_001004	119749	Hs.553564	NM_001004	ENSG000004CRK46	-	olfactoryprotein-coding	
chr2-1331	9.200316	1.848395	0.745197	2.480411	0.013123	0.137173	chr2	1.33E+08	1.33E+08	+0	NA	intron (Nintron (N	-11131	NR_110294	1.02E+08	Hs.661917	NR_110294	ENSG000004NCAP5-AS-	-	NKAP5	arncRNA
chr17-48	10.6703	1.590637	0.642801	2.474542	0.013341	0.138154	chr17	48542138	48543626	+0	NA	3' UTR (N3' UTR (N	-1469	NR_102277	1.01E+08	Hs.17180	NR_102277	ENSG000004HOXB-AS1	HOXB30S	HOXB	cluscncRNA
chr18-54	9.686182	1.751671	0.708124	2.473678	0.013373	0.138154	chr18	54924912	54927104	+0	NA	intron (MamRep187	32040	NM_001144	80323	Hs.12079	NM_002514	ENSG000004CCDC68	SE57-1	coiled-cpprotein-coding	
chr19-12	9.686182	1.751671	0.708124	2.473678	0.013373	0.138154	chr19	12247360	12250793	+0	NA	IntergeniAluSg4 S1	45536	NM_001355	51710	Hs.296731	NM_016264	ENSG000004ZNF44	GIOT-2 KC	zinc fingerprotein-coding	
chr19-257	9.17555	1.854632	0.750047	2.472689	0.01341	0.138154	chr19	25711233	25711466	+0	NA	IntergeniALR/Alphe	-1547902	NR_003603	1E+08	Hs.149312	NR_003603	ENSG000004HAVCR1P1	-	hepatitispseudo	
chr17-554	9.713155	1.750557	0.708066	2.472309	0.013424	0.138154	chr17	55413069	55414359	+0	NA	intron (Nintron (N	8121	NM_012325	23531	Hs.46348	NM_012325	ENSG000004MMD1	MMA MMD1	monocyte protein-coding	
chr7-1117	8.685269	1.956728	0.791568	2.471965	0.013437	0.138154	chr7	1.12E+08	1.12E+08	+0	NA	intron (NLMef LIN	-31010	NR_103800	1.01E+08	Hs.67751	NR_103800	ENSG000004DOCK4-AS1	-	DOCK4	antncRNA
chr1-122	10.68268	1.588423	0.643736	2.467509	0.013606	0.139126	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alphe	1148295	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr2-931	10.68268	1.588423	0.643736	2.467509	0.013606	0.139126	chr2	93100686	93100915	+0	NA	IntergeniALR/Alphe	1107619	NR_146107	728034	NR_146105	BMS1P14	-	BMS1	pspseudo	
chr1-178	9.698564	1.748887	0.709558	2.46468	0.013714	0.139849	chr1	1.79E+08	1.79E+08	+0	NA	intron (NLIAPA2 LIN	-26125	NM_004673	9068	Hs.591474	NM_004673	ENSG000004ANGPTL1	ANG3 ANGF	angiopoicprotein-coding	
chr1-123	15.62421	1.0452	0.425051	2.458996	0.013933	0.141698	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alphe	1531124	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr3-9157	51.98639	0.758009	0.308593	2.456337	0.014036	0.142092	chr3	91572763	91572986	+0	NA	IntergeniALR/Alphe	2401207	NM_001314	5627	Hs.64016	NM_000313	ENSG000004PROS1	PROS PS21	protein Sprotein-coding	
chr1-124	12.95208	1.276654	0.519797	2.456064	0.014047	0.142092	chr1	1.24E+08	1.24E+08	+0	NA	IntergeniALR/Alphe	2659994	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr10-401	21.34862	0.806655	0.3296	2.447376	0.01439	0.145174	chr10	40847368	40848517	+0	NA	IntergeniALR/Alphe	1520103	NR_02438C	441666	Hs.25572	NR_02438C	ENSG000004LOC441666	-	zinc	fingerpseudo
chr5-489	15.15515	1.072556	0.438788	2.444361	0.014511	0.145855	chr5	48902736	48903032	+0	NA	IntergeniALR/Alphe	1538404	NM_198445	133418	Hs.561411	NM_198445	ENSG000004EMB	GP70	embigin	protein-coding
chr5-473	15.14056	-1.072	0.438668	-2.44376	0.014535	0.145855	chr5	47325082	47326421	+0	NA	IntergeniALR/Alphe	-1629371	NM_021072	348980	Hs.35317	NM_021072	ENSG000004HCN1	BCNG-1 BC	hyperpolaprotein-coding	
chr6-3667	12.44145	-1.32212	0.541588	-2.44119	0.014639	0.146507	chr6	36678787	36686308	+0	NA	intron (Nintron (N	3833	NM_00038E	1026	Hs.370771	NM_00038E	ENSG000004CDKN1A	CAP20 CDK	hypercyclin deprotein-coding	
chr12-124	15.12376	-1.07023	0.438872	-2.4386	0.014744	0.147171	chr12	1.25E+08	1.25E+08	+0	NA	exon (NM exon (NM	1640	NM_021005	7316	Hs.52034	NM_021005	ENSG000004UBC	HMG20	ubiquitinprotein-coding	
chr1-124	43.99295	-0.81111	0.332956	-2.43608	0.014848	0.147808	chr1	1.24E+08	1.24E+08	+0	NA	IntergeniALR/Alphe	2579739	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr1-122	26.60997	-0.73595	0.302831	-2.43024	0.015089	0.149813	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alphe	1163975	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr19-265	18.36489	-0.88953	0.366823	-2.42495	0.015311	0.151616	chr19	26924473	26925713	+0	NA	IntergeniALR/Alphe	-868338	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG000004LOC101927	-	uncharactncRNA	
chr20-27	17.89141	-0.90594	0.375187	-2.41463	0.015751	0.155569	chr20	27054773	27055564	+0	NA	IntergeniALR/Alphe	-845935	NR_04009E	284801	Hs.37069	NR_04009E	ENSG000004MIR663AHC	-	MIR663A	lncRNA
chr1-124	17.83746	-0.906	0.37552	-2.41265	0.015837	0.156006	chr1	1.24E+08	1.24E+08	+0	NA	IntergeniALR/Alphe	2935592	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr6-5927	90.66336	-0.59065	0.245367	-2.40721	0.016075	0.157935	chr6	59276231	59276430	+0	NA	IntergeniALR/Alphe	-1314884	NR_132994	1.07E+08	Hs.56153	NR_125727	ENSG000004LINC0068C	-	long	intencRNA
chr1-234	11.44274	-1.42189	0.592242	-2.40086	0.016357	0.15993	chr1	2.35E+08	2.35E+08	+0	NA	3' UTR (N3' UTR (N	2842	NM_18297E	359948	Hs.35026	NM_18297E	ENSG000004IRF2BP2	CVID14	interfercprotein-coding	
chr12-921	11.42815	-1.42065	0.591959	-2.39992	0.016399	0.15993	chr12	92141869	92145285	+0	NA	promoter-promoter-	-746	NR_132341	256021	Hs.651357	NM_00125E	ENSG000004LINC0161E	C12orf79	long	intencRNA
chr1-122	17.337	-0.92339	0.384781	-2.39977	0.016405	0.15993	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alphe	1035182	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr2-925	36.84323	-0.82181	0.342821	-2.39719	0.016521	0.160647	chr2	92994221	92994573	+0	NA	IntergeniALR/Alphe	1053264	NR_027714	440888	Hs.73023	NR_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo
chr2-1504	8.432036	-1.90616	0.796401	-2.39455	0.016641	0.16139	chr2	1.5E+08	1.5E+08	+0	NA	intron (Nintron (N	7526	NM_00516E	390	Hs.6838	NM_00516E	ENSG000004RND3	ARHE Rho	Rho familprotein-coding	
chr1-124	16.86352	-0.94175	0.394621	-2.38648	0.01701	0.164551	chr1	1.25E+08	1.25E+08	+0	NA	IntergeniALR/Alphe	3000511	NR_003956	647121	Hs.69768	NR_003956	ENSG000004EMB1P1	-	embigin	fpseudo
chr10-40	13.65599	-1.16189	0.487738	-2.3822	0.01721	0.165859	chr10	40396881	40397628	+0	NA	IntergeniALR/Alphe	1700558	NR_045000	399746	Hs.742607	NR_045000	ACTR3BP5	FKSG74	ACTR3B	pspseudo
chr5-495	10.91531	-1.479	0.620988	-2.38168	0.017234	0.165859	chr5	49134512	49136221	+0	NA	IntergeniALR/Alphe	1305922	NM_198445	133418	Hs.561411	NM_198445	ENSG000004EMB	GP70	embigin	protein-coding
chr1-1717	10.92769	-1.47699	0.620748	-2.37937	0.017342	0.166478	chr1	1.72E+08	1.72E+08	+0	NA	intron (Nintron (N	33023	NR_033704	8674	Hs.6651	NM_00376E	ENSG000004VAMP4	VAMP-4 V	vesicle aprotein-coding	
chr1-2064	10.94008	-1.47494	0.6226	-2.36901	0.017836	0.170781	chr1	2.06E+08	2.06E+08	+0	NA	intron (Nintron (N	-49059	NM_00119E	9641	Hs.32104	NM_01400E	ENSG000004IKBK	IKK-E IKK	inhibitorprotein-coding	
chr9-965	8.415238	-1.89851	0.802096	-2.36693	0.017936	0.171304	chr9	96538999	96539222	+0	NA	exon (NM exon (NM	27271	NM_001351	8555	Hs.40582	NM_003671	ENSG000004C14B1	CDC14B3	cell diviprotein-coding	
chr17-554	10.41486	-1.54206	0.651803	-2.36583	0.01799	0.17138	chr17	55403434	55405405	+0	NA	intron (Nintron (N	17416	NM_01232E	23531	Hs.46348	NM_01232E	ENSG000004MMD	MMA MMD1	monocyte protein-coding	
chr19-271	13.1825	-1.19573	0.507541	-2.35594	0.018476	0.175569	chr19	27105822	27105653	+0	NA	IntergeniALR/Alphe	-687239	NR_146733	1.02E+08	Hs.567934	NR_110687	ENSG000004LOC101927	-	uncharactncRNA	
chr4-87	9.902017	-1.61548	0.686209	-2.35421	0.018562	0.175615	chr4	1.07E+08	1.07E+08	+0	NA	IntergeniCpG-2170E	-1174	NM_00524E	2195	Hs.481371	NM_00524E	ENSG000004FAT1	CDHF7 CDF	FAT atypiprotein-coding	
chr17-404	9.443124	-1.6968	0.720823	-2.35397	0.018574	0.175615	chr17	40443944	40458809	+0	NA	intron (NCR1_Mam I	7926	NM_00155E	3487	Hs.46299	NM_00155E	ENSG000004IGFBP4	BP-4 HT2	insulin lprotein-coding	
chr5-477	15.83563	-0.98204	0.4185	-2.34657	0.018947	0.17869	chr5	47735194	47736041	+0	NA	IntergeniALR/Alphe	-2039237	NM_021072	348980	Hs.35317	NM_021072	ENSG000004HCN1	BCNG-1 BC	hyperpolaprotein-coding	
chr11-52	20.03611	-0.80011	0.341682	-2.34167	0.019198	0.180601	chr11	52690121	52690618	+0	NA	IntergeniALR/Alphe	1913629	NM_001004	119749	Hs.553564	NM_001004	ENSG000004CRK46	-	olfactoryprotein-coding	
chr1-122	15.37895	-1.00574	0.43055	-2.33594	0.019494	0.182936	chr1	1.23E+08	1.23E+08	+0	NA	IntergeniALR/Alphe									

chr1-1452	12.58629	-1.10483	0.525303	-2.10323	0.035446	0.277606	chr1	1.45E+08	1.45E+08	0	NA	intron (Nintron (N	58061	NM_00127E	1E+08	Hs.44508	NC_00127E	ENS00000	NCBPFP20	-	NBPF memt	protein-coding		
chr12-652	12.58629	-1.10483	0.525303	-2.10323	0.035446	0.277606	chr12	6534857	6538393	0	NA	intron (Nintron (N	1361	NM_00125E	2597	Hs.544577	NC_00204E	ENS00000	GAPDH	G3PD	[GAP]	glyceralc	protein-coding	
chr12-352	28.28536	-0.63205	0.300576	-2.10279	0.035485	0.277606	chr12	35030728	35030959	0	NA	IntergeniALR/Alphe	1008347	NM_032834	84920	Hs.102971	NC_032834	ENS00000	CALG10	ALG10A	[DIALG10]	al	protein-coding	
chr1-8905	9.91415	-1.43315	0.682606	-2.09953	0.03577	0.279257	chr1	89052675	89053086	0	NA	3' UTR (N3' UTR (N	12328	NM_00205E	2633	Hs.62661	NC_00205E	ENS00000	GBP1	-	guanylate	protein-coding		
chr1-1245	14.80174	-0.92812	0.443283	-2.09375	0.036282	0.282659	chr1	1.25E+08	1.25E+08	0	NA	IntergeniALR/Alphe	3042236	NR_00395E	647121	Hs.697682	NR_00395E	ENS00000	EMBP1	-	embigin	fpseudo		
chr19-245	12.10263	-1.14234	0.548322	-2.08333	0.037221	0.289384	chr19	24944763	24946356	0	NA	IntergeniALR/Alphe	-782112	NR_00360E	1E+08	Hs.149312	NR_00360E	ENS00000	HAVCR1P1	-	hepatitis	pseudo		
chr8-1026	12.10042	-1.13977	0.547906	-2.08023	0.037505	0.290989	chr8	1.03E+08	1.03E+08	0	NA	non-codiron-codir	3864	NM_00103E	7071	Hs.435001	NC_00565E	ENS00000	KLF10	EGR-alpha	Kruppel	l	protein-coding	
chr11-615	12.08583	-1.13865	0.548473	-2.07604	0.03789	0.293376	chr11	61963776	61967191	0	NA	TTS (NM_TTS (NM_C	2151	NM_00203E	2495	Hs.52491C	NC_00203E	ENS00000	FTH1	FHC	[FTH]	Ferritin	protein-coding	
chr10-408	17.05213	-0.79884	0.387206	-2.06309	0.039104	0.302151	chr10	40835250	40835639	0	NA	IntergeniALR/Alphe	1532601	NR_02438C	441666	Hs.25572E	NR_02438C	ENS00000	LOC44166E	-	zinc fing	pseudo		
chr20-261	11.5752	-1.18009	0.573572	-2.05744	0.039644	0.305694	chr20	26557899	26558615	0	NA	IntergeniALR/Alphe	-349024	NR_04009E	284801	Hs.37069E	NR_04009E	ENS00000	MIR663AHC	-	MIR663a	hncRNA		
chr1-1234	12.0195	-1.14085	0.556597	-2.04969	0.040395	0.310849	chr1	1.23E+08	1.23E+08	0	NA	IntergeniALR/Alphe	1916830	NR_00395E	647121	Hs.697682	NR_00395E	ENS00000	EMBP1	-	embigin	fpseudo		
chr19-255	11.5584	-1.17595	0.575779	-2.04237	0.041115	0.315747	chr19	25963839	25964852	0	NA	IntergeniALR/Alphe	-1800898	NR_00360E	1E+08	Hs.149312	NR_00360E	ENS00000	HAVCR1P1	-	hepatitis	pseudo		
chr19-277	11.08933	-1.22247	0.599237	-2.04005	0.041346	0.316226	chr19	27188814	27189689	0	NA	IntergeniALR/Alphe	-604180	NR_04009E	1.02E+08	Hs.567934	NR_110687	ENS00000	LOC101927	-	uncharact	ncRNA		
chr5-477	11.08933	-1.22247	0.599237	-2.04005	0.041346	0.316226	chr5	47700281	47701093	0	NA	IntergeniALR/Alphe	-2004307	NM_02107E	348980	Hs.35317E	NC_02107E	ENS00000	HCHN1	BCNG-1	[BC]	hyperpol	protein-coding	
chr19-124	11.10172	-1.22062	0.599034	-2.03765	0.041585	0.31741	chr19	1249884	1252405	0	NA	intron (NCpG-1301C	2591	NM_177401	90007	Hs.46552E	NC_177401	ENS00000	MIDN	-	midnoln	protein-coding		
chr5-5594	11.08713	-1.21927	0.599742	-2.033	0.042053	0.319687	chr5	55945996	55947339	0	NA	intron (NAluSz SIN	48296	NM_00136E	3572	Hs.53208E	NC_002184	ENS00000	IL6ST	CD130	[CDW]	interleuk	protein-coding	
chr6-3072	11.08713	-1.21927	0.599742	-2.033	0.042053	0.319687	chr6	30723332	30725788	0	NA	non-codiron-codir	2922	NM_00129E	203068	Hs.63648C	NC_178014	ENS00000	TUBB	CDCBM6	[CS]	tubulin	l	protein-coding
chr1-1838	8.093219	-1.61243	0.794387	-2.02977	0.042379	0.32152	chr1	1.84E+08	1.84E+08	0	NA	intron (NLMIB1 LIN	-3086	NM_001297	23179	Hs.49714E	NC_01514E	ENS00000	RGL1	RGL		guanip	protein-coding	
chr2-9256	11.06015	-1.21977	0.60173	-2.0271	0.042652	0.322934	chr2	92564348	92564553	0	NA	IntergeniALR/Alphe	623317	NR_027714	440888	Hs.73023E	NC_001032412	ACTR3BP2	FKSG73	ACTR3B	ps	pseudo		
chr1-1224	8.1224	-1.61674	0.798519	-2.02468	0.0429	0.323001	chr1	1.22E+08	1.22E+08	0	NA	IntergeniALR/Alphe	968809	NR_00395E	647121	Hs.697682	NR_00395E	ENS00000	EMBP1	-	embigin	fpseudo		
chr18-838	8.078629	-1.6103	0.795395	-2.02453	0.042916	0.323001	chr18	8386795	8388614	0	NA	intron (Nintron (N	-20670	NR_02441E	1E+08	Hs.66665E	NR_02441E	ENS00000	LOC100192	-	uncharact	ncRNA		
chr19-267	11.09951	-1.21738	0.601376	-2.02433	0.042937	0.323001	chr19	26753253	26754252	0	NA	IntergeniALR/Alphe	-1039679	NR_14673E	1.02E+08	Hs.567934	NR_110687	ENS00000	LOC101927	-	uncharact	ncRNA		
chr5-484	15.98489	-0.82941	0.409997	-2.02296	0.043077	0.323001	chr5	48414003	48414324	0	NA	IntergeniALR/Alphe	2027125	NM_19844E	133418	Hs.561411	NC_19844E	ENS00000	CEMB	GP70		embigin	protein-coding	
chr19-255	13.30037	-0.99825	0.493727	-2.02187	0.04319	0.323001	chr19	25956140	25957281	0	NA	IntergeniALR/Alphe	-1793263	NR_00360E	1E+08	Hs.149312	NR_00360E	ENS00000	HAVCR1P1	-	hepatitis	pseudo		
chr19-578	8.095427	-1.61824	0.800911	-2.02049	0.043332	0.323001	chr19	57511265	57511494	0	NA	intron (NLMIE1 LIN	11441	NR_13070E	374928	Hs.57957E	NC_19854E	ENS00000	ZNF773	ZNF419B		zinc fing	protein-coding	
chr12-111	8.091012	-1.60673	0.795271	-2.02036	0.043346	0.323001	chr12	1.11E+08	1.11E+08	0	NA	3' UTR (N3' UTR (N	15703	NM_00108E	79600	Hs.211511	NC_02454E	ENS00000	TCTN1	JBTS13	[TF]	ectonic	protein-coding	
chr5-4952	10.58888	-1.26789	0.62756	-2.02035	0.043347	0.323001	chr5	49526974	49528359	0	NA	IntergeniALR/Alphe	913622	NR_19844E	133418	Hs.561411	NC_19844E	ENS00000	EMB	GP70		embigin	protein-coding	
chr10-588	8.076421	-1.60455	0.798357	-2.00982	0.04445	0.329084	chr10	58811826	58812035	0	NA	intron (NLMIE3 LINE	96915	NR_02750E	728640	Hs.72920E	NR_02750E	FAM133CP	-	family	wipseudo			
chr13-958	8.076421	-1.60455	0.798357	-2.00982	0.04445	0.329084	chr13	95115244	95115894	0	NA	intron (Nintron (N	-94775	NR_14573E	1.1E+08	Hs.697682	NR_14573E	ENS00000	SNORD13G	-	small	nucsnRNA		
chr6-1338	8.606058	-1.52376	0.758407	-2.00916	0.04452	0.329084	chr6	1.34E+08	1.34E+08	0	NA	TTS (NM_TTS (NM_C	4042	NM_00320E	6943	Hs.78061	NC_00320E	ENS00000	TCF21	POD1	[bHLH]	transcrip	protein-coding	
chr1-1823	10.10301	-1.31993	0.65786	-2.00641	0.044813	0.329084	chr1	1.82E+08	1.82E+08	0	NA	intron (Nintron (N	5424	NM_00103E	2752	Hs.13201E	NC_00206E	ENS00000	GLUL	GLNS	[GS]	Fglutamat	protein-coding	
chr16-864	10.10301	-1.31993	0.65786	-2.00641	0.044813	0.329084	chr16	86488680	8649127E+08	0	NA	intron (NLMIE3A LI	18882	NR_036444	400550	Hs.44882E	NR_03392E	ENS00000	PENRR	FOXF1-AS1	FOXF1	ad	ncRNA	
chr12-123	8.591468	-1.52177	0.758469	-2.00636	0.044817	0.329084	chr12	1.23E+08	1.23E+08	0	NA	intron (Nintron (N	1247	NR_036187	1E+08	Hs.697682	NR_036187	ENS00000	MIR4304	-	microRNA	ncRNA		
chr2-848	8.051656	-1.61179	0.804029	-2.00464	0.045001	0.329084	chr2	84835693	84835892	0	NA	TTS (NM_TTS (NM_C	45292	NM_00108C	129293	Hs.469134	NC_00108C	ENS00000	TRABD2A	C2orf89	[T]	TraB	dom	protein-coding
chr1-1217	10.07604	-1.32067	0.658917	-2.00443	0.045038	0.329084	chr1	1.22E+08	1.22E+08	0	NA	IntergeniALR/Alphe	234025	NR_00395E	647121	Hs.697682	NR_00395E	ENS00000	EMBP1	-	embigin	fpseudo		
chr1-1226	10.07604	-1.32067	0.658917	-2.00443	0.045038	0.329084	chr1	1.23E+08	1.23E+08	0	NA	IntergeniALR/Alphe	1134302	NR_00395E	647121	Hs.697682	NR_00395E	ENS00000	EMBP1	-	embigin	fpseudo		
chr2-462	10.07604	-1.32067	0.658917	-2.00443	0.045038	0.329084	chr2	46298721	46299493	0	NA	intron (NCpG	1700	NM_00143C	2034	Hs.46841C	NC_00143C	ENS00000	EPAS1	ECYT4	[HIF]	endothelip	protein-coding	
chr1-2356	10.08842	-1.31833	0.658713	-2.00137	0.045352	0.329498	chr1	2.36E+08	2.36E+08	0	NA	intron (NHERV10E	-20154	NM_00109E	2786	Hs.159711	NC_00448E	ENS00000	GN4	-	G	protein	protein-coding	
chr17-501	10.08842	-1.31833	0.658713	-2.00137	0.045352	0.329498	chr17	50184723	50200752	0	NA	intron (Nintron (N	8902	NM_00008E	1277	Hs.12792E	NC_00008E	ENS00000	COL1A1	EDSARTH1		collagen	protein-coding	
chr1-2276	9.106514	-1.44997	0.724791	-2.00053	0.045443	0.329498	chr1	2.28E+08	2.28E+08	0	NA	exon (NM_exon (NM	42989	NR_03675E	401983	Hs.68181E	NR_03675E	ZNF847P	-	zinc fing	pseudo			
chr7-5944	9.590173	-1.37914	0.690046	-1.99862	0.04565	0.329498	chr7	59440414	59441309	0	NA	IntergeniALR/Alphe	1990684	NM_00115E	441234	Hs.533121	NC_00115E	ENS00000	ZNF716	-	zinc fing	protein-coding		
chr2-22	12.8145	-1.02623	0.513489	-1.99855	0.045657	0.329498	chr2	20447894	20449244	0	NA	3' UTR (N3' UTR (N	1495	NM_00440E	388	Hs.50287E	NC_00404C	ENS00000	RHOB	ARH6	[ARH]	homol	protein-coding	
chr9-110	8.049448	-1.60597	0.803729	-1.99815	0.045701	0.329498	chr9	1.11E+08	1.11E+08	0	NA	exon (NM_exon (NM	76667	NM_15336E	79987	Hs.522334	NC_15336E	ENS00000	SVEP1	C9orf13	[C]	sushi,	vc	protein-coding
chr1-2331	8.633031	-1.52252	0.762307	-1.99726	0.045797	0.329498	chr1	2.33E+08	2.33E+08	0	NA	intron (NLMIE3B LI	123579	NR_014801	80003	Hs.37060E	NC_014801	ENS00000	PCNX2	PCNX2		pecanex	2	protein-coding
chr4-119	8.603851	-1.51852	0.760548	-1.99661	0.045867	0.329498	chr4	1.2E+08	1.2E+08	0	NA	intron (Nintron (N	67523	NR_03763C	645513	Hs.67754E	NR_03763C	ENS00000	LOC64551E	-	septin 7	pseudo		
chr4-119	8.603851	-1.51852	0.760548	-1.99661	0.045867	0.329498	chr4	1.2E+08	1.2E+08	0	NA	intron (Nintron (N	67523	NR_03763C	645513	Hs.67754E	NR_03763C	ENS00000	LOC64551E	-	septin 7	pseudo		
chr17-416	12.79991	-1.02526	0.514292	-1.99353	0.046203	0.331165	chr17	41689500	41693207	0	NA	3' UTR (N3' UTR (N	2468	NM_005801	10209	Hs.15058C	NC_005801	ENS00000	E1F1	A121	[EIF]	eukaryoti	protein-coding	
chr10-405	10.07383	-1.3167	0.660957	-1.99211	0.046359	0.331652	chr10	40378442	40379131	0	NA	IntergeniALR/Alphe	1682190	NR_04500C	399746	Hs.742607	NR_04500C	ACTR3BP5	FKSG74	ACTR3B	ps	pseudo		
chr11-515	15.00298	-0.86639	0.435777																					



chr18-318	8.790505	-1.37874	0.74338	-1.85469	0.063641	0.397808	chr18	31851878	31852401	+	O NA	intron (AluJb SIN	90989 NM_01493E	22878 Hs. 202001NM_01493E	ENSG00000TRAPPC8	GSGL HsT2	traffickiprotein-coding	
chr5-483E	12.04623	-1.00967	0.545429	-1.85115	0.064148	0.400313	chr5	48356698	48357775	+	O NA	IntergeniALR/Alphe	2084052 NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	emigin protein-coding	
chr7-821E	9.330317	-1.31367	0.710962	-1.84774	0.06464	0.402716	chr7	82124182	82124576	+	O NA	intron (MER51A LI	115202 NR_110077	1.02E+08 Hs. 57134E	NR_110077	ENSG00000LOC101927-		uncharactcRNA
chr7-100C	14.25726	-0.84109	0.456789	-1.84131	0.065576	0.407872	chr7	1E+08	1E+08	+	O NA	intron (Nintron (N	8022 NM_01771E	7551 Hs. 435302NM_01771E	ENSG00000ZNF3-	A8-51 HF.	zinc fingprotein-coding	
chr10-43C	11.54798	-1.04302	0.570268	-1.82899	0.067401	0.417842	chr10	43642429	43646871	+	O NA	exon (NM exon (NM	778 NR_047557	414197 Hs. 60583E	NR_047557	ENSG00000ZNF32-AS1 ZNF320S1 ZNF32	antncRNA	
chr2-926E	11.54798	-1.04302	0.570268	-1.82899	0.067401	0.417842	chr2	92624184	92625662	+	O NA	IntergeniALR/Alphe	683790 NR_027714	440888 Hs. 73023E	NR_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo
chr17-16E	11.54577	-1.04013	0.569781	-1.82549	0.067927	0.41902	chr17	16525050	16567530	+	O NA	intron (NLMC4 LIN	9414 NM_02065E	57336 Hs. 99724	NR_02065E	ENSG00000ZNF287	ZKSCAN3	zinc fingprotein-coding
chr17-64E	11.54577	-1.04013	0.569781	-1.82549	0.067927	0.41902	chr17	64498996	64505865	+	O NA	intron (Nintron (N	-1117 NR_03996E	1.01E+08	NR_03996E	ENSG00000MIR5047		microRNA ncRNA
chr19-26E	11.521	-1.0434	0.571621	-1.82534	0.067949	0.41902	chr19	26584213	26584842	+	O NA	IntergeniALR/Alphe	-1208904 NR_14673E	1.02E+08 Hs. 567934	NR_110687	ENSG00000LOC101927-		uncharactcRNA
chr19-26E	11.55018	-1.04598	0.573211	-1.82476	0.068037	0.41902	chr19	26631766	26632414	+	O NA	IntergeniALR/Alphe	-1161341 NR_14673E	1.02E+08 Hs. 567934	NR_110687	ENSG00000LOC101927-		uncharactcRNA
chr4-146E	11.49403	-1.04384	0.575524	-1.81373	0.06972	0.428687	chr4	1.46E+08	1.46E+08	+	O NA	intron (Nintron (N	71983 NM_001371071					
chr1-156E	11.04752	-1.07663	0.595837	-1.80693	0.070774	0.434457	chr1	1.56E+08	1.56E+08	+	O NA	intron (NCpG	10022 NM_001257	4000 Hs. 594444	NM_00557E	ENSG00000CLMNA	CDCD1 CDE	lamin A/C (protein-coding
chr6-329E	11.03293	-1.07526	0.596019	-1.80406	0.071221	0.436492	chr6	32972393	32982059	+	O NA	intron (Nintron (N	4142 NM_00119E	6046 Hs. 75243	NR_005104	ENSG00000BRD2	BRD2-IT1	bromodom protein-coding
chr17-43E	11.07449	-1.07618	0.597484	-1.80119	0.071672	0.438016	chr17	43939994	43400986	+	O NA	3' UTR (N3' UTR (N	1470 NM_00116E	379 Hs. 18315E	NR_001661	ENSG00000ARL4D	ARF4 ARI	ADP ribosprotein-coding
chr5-490E	11.03735	-1.08178	0.600743	-1.80074	0.071744	0.438016	chr5	49076030	49077019	+	O NA	IntergeniALR/Alphe	1364764 NM_19844E	133418 Hs. 561411	NM_19844E	ENSG00000EMB	GP70	emigin protein-coding
chr16-22E	15.98243	-0.73482	0.408174	-1.80026	0.071819	0.438016	chr16	22534046	22537849	+	O NA	exon (NM exon (NM	-9751 NR_00367E	653786 Hs. 56494E	NR_00367E	ENSG00000OTOAP1		OTOA psseudo
chr7-730E	11.01834	-1.07387	0.597325	-1.79779	0.07221	0.439685	chr7	73041265	73042262	+	O NA	IntergeniAluJr SIN	-12001 NR_00366E	728524 Hs. 57127E	NR_001023562	SPDYEBP		speedy/Rlpseudo
chr1-123E	13.27756	-0.88677	0.494115	-1.79467	0.072706	0.441994	chr1	1.23E+08	1.23E+08	+	O NA	IntergeniALR/Alphe	-1870538 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000CEMBP1		emigin psseudo
chr5-485E	19.17979	-0.62528	0.349004	-1.79161	0.073195	0.442425	chr5	48505017	48506150	+	O NA	IntergeniALR/Alphe	1935705 NM_19844E	133418 Hs. 561411	NM_19844E	ENSG00000EMB	GP70	emigin protein-coding
chr1-122E	10.53468	-1.11563	0.624048	-1.78773	0.073819	0.447128	chr1	1.22E+08	1.22E+08	+	O NA	IntergeniALR/Alphe	818845 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000CEMBP1		emigin psseudo
chr1-160E	10.54706	-1.11359	0.623866	-1.78498	0.074264	0.447128	chr1	1.6E+08	1.6E+08	+	O NA	intron (Nintron (N	5111 NR_03649E	5824 Hs. 51723E	NR_002857	ENSG00000PEX19	D1S2223E	peroxisomprotein-coding
chr1-171E	10.54706	-1.11359	0.623866	-1.78498	0.074264	0.447128	chr1	1.72E+08	1.72E+08	+	O NA	intron (Nintron (N	6917 NR_03370A	8674 Hs. 6651	NR_00376E	ENSG00000VAMP4	VAMP-4 V	vesicle aprotein-coding
chr12-104	10.54706	-1.11359	0.623866	-1.78498	0.074264	0.447128	chr12	1.04E+08	1.04E+08	+	O NA	intron (Nintron (N	18618 NM_00100E	493861 Hs. 659857	NR_00100E	ENSG00000EID3	NS4EB NSF	EP300 intrprotein-coding
chr15-40E	10.54706	-1.11359	0.623866	-1.78498	0.074264	0.447128	chr15	40573527	40574446	+	O NA	exon (NM exon (NM	4687 NM_15226E	27079 Hs. 17331	NM_15226E	ENSG00000RPU5D2	C15orf19	RNA psuicprotein-coding
chr10-40E	10.52009	-1.11413	0.62487	-1.78297	0.074591	0.448377	chr10	40658214	40659018	+	O NA	IntergeniALR/Alphe	1709429 NR_02438E	441666 Hs. 25572E	NR_02438E	ENSG00000LOC44166E-		zinc fingpsudo
chr19-26E	10.50771	-1.11619	0.627207	-1.77962	0.075137	0.449288	chr19	26688322	26689695	+	O NA	IntergeniALR/Alphe	-1104393 NR_14673E	1.02E+08 Hs. 567934	NR_110687	ENSG00000LOC101927-		uncharactcRNA
chr16-47E	8.051406	-1.39259	0.783582	-1.77721	0.075533	0.449288	chr16	4757551	4757818	+	O NA	intron (NLMC4 LIN	113616 NR_11090E	1.02E+08 Hs. 63465E	NR_11090E	ITFG1-AS1-		ITFG1 antncRNA
chr2-189E	8.051406	-1.39259	0.783582	-1.77721	0.075533	0.449288	chr2	1.9E+08	1.9E+08	+	O NA	intron (Nintron (N	16546 NM_01458E	30061 Hs. 64300E	NR_01458E	ENSG00000SLC40A1	FPN1 HFE4	solute cprotein-coding
chr4-714E	8.051406	-1.39259	0.783582	-1.77721	0.075533	0.449288	chr4	71408375	71410444	+	O NA	intron (THE1A-int	70356 NM_00375E	8671 Hs. 5462	NR_00375E	ENSG00000SLC44A	HNBC1 KNE	solute cprotein-coding
chr1-147E	8.053614	-1.39288	0.788335	-1.77371	0.076111	0.449288	chr1	1.48E+08	1.48E+08	+	O NA	exon (NM exon (NM	22144 NR_11193E	1E+08 Hs. 69657E	NR_003377	PDZK1P1	PDZ	domaipseudo
chr2-203E	10.04882	-1.15839	0.653434	-1.77277	0.076267	0.449288	chr2	2.03E+08	2.03E+08	+	O NA	intron (NLMC4 LI	89698 NM_001114	65065 Hs. 64884E	NR_19894E	ENSG00000NBAL1	A530083C	neurobeacprotein-coding
chr1-204E	10.51788	-1.11054	0.626815	-1.77171	0.076443	0.449288	chr1	2.04E+08	2.04E+08	+	O NA	3' UTR (N3' UTR (N	7240 NM_03283E	84919 Hs. 30437E	NR_03283E	ENSG00000PPP1R15B	CREP MSSC	protein fprotein-coding
chr10-40E	10.54486	-1.10999	0.626663	-1.77127	0.076517	0.449288	chr10	40081253	40082143	+	O NA	IntergeniALR/Alphe	1385102 NR_04500E	399746 Hs. 742607	NR_04500E	ACTR3BP5	FKSG74	ACTR3B pspseudo
chr1-124E	12.76031	-0.90599	0.511559	-1.77104	0.076554	0.449288	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	3248683 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000CEMBP1		emigin psseudo
chr1-149E	10.03423	-1.15675	0.653606	-1.7698	0.076761	0.449288	chr1	1.49E+08	1.49E+08	+	O NA	intron (Nintron (N	19050 NM_001037	400818 Hs. 44508E	NR_001037	ENSG00000NBPF9	AEO1	NBPF memtprotein-coding
chr1-243E	10.03423	-1.15675	0.653606	-1.7698	0.076761	0.449288	chr1	2.43E+08	2.43E+08	+	O NA	intron (NLM5 LINE	-37445 NR_029401	731275 Hs. 72235E	NR_029401	ENSG00000LINC01347-		long intncRNA
chr17-29E	10.02184	-1.15904	0.655053	-1.76938	0.076831	0.449288	chr17	29631747	29632821	+	O NA	exon (NM exon (NM	-10861 NM_03285A	84940 Hs. 14304E	NR_03285A	ENSG00000COR06		coronin fprotein-coding
chr3-172E	10.0612	-1.1561	0.654527	-1.76632	0.077342	0.449288	chr3	1.72E+08	1.72E+08	+	O NA	intron (Nintron (N	95096 NR_198407	2693 Hs. 13021E	NR_00412E	ENSG00000GHSR	GHPD	growth hcprotein-coding
chr5-143E	10.0612	-1.1561	0.654527	-1.76632	0.077342	0.449288	chr5	14343294	14343493	+	O NA	intron (NLM2 LIN	-120599 NR_14581E	1.1E+08	NR_14581E	SNORD170		small ncusnoRNA
chr7-592E	10.04661	-1.15446	0.6547	-1.76333	0.077844	0.449288	chr7	59274995	59275528	+	O NA	IntergeniALR/Alphe	1825084 NM_00115E	441234 Hs. 533121	NM_00115E	ENSG00000ZNF716		zinc fingprotein-coding
chr1-173E	10.01964	-1.1551	0.655236	-1.76287	0.077922	0.449288	chr1	1.74E+08	1.74E+08	+	O NA	3' UTR (N3' UTR (N	-17930 NR_152521	60674 Hs. 53185E	NR_00257E	ENSG00000GAS5	NCRNA000E	growth arncRNA
chr1-124E	9.550567	-1.20865	0.685715	-1.76261	0.077966	0.449288	chr1	1.25E+08	1.25E+08	+	O NA	IntergeniALR/Alphe	3031306 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000CEMBP1		emigin psseudo
chr19-95E	14.98594	-0.76428	0.433627	-1.76252	0.077981	0.449288	chr19	9522759	9537725	+	O NA	intron (AluJb SIN	8403 NM_02410E	79088 Hs. 38647E	NR_02410E	ENSG00000ZNF426	K-RBP	zinc fingprotein-coding
chr3-183E	8.551862	-1.32471	0.751627	-1.76246	0.077991	0.449288	chr3	1.84E+08	1.84E+08	+	O NA	intron (MERSB DNV	58630 NR_03965E	1.01E+08	NR_03965E	ENSG00000MIR4448		microRNA ncRNA
chr13-44E	10.00725	-1.15739	0.656695	-1.76245	0.077993	0.449288	chr13	4432851	4434705	+	O NA	3' UTR (N3' UTR (N	3080 NM_06022E	8848 Hs. 43638E	NR_06022E	ENSG00000TSC22D1	Ptg-2 TGf	TSC2 donprotein-coding
chr1-520E	8.564245	-1.3216	0.751523	-1.75856	0.078653	0.449288	chr1	52024187	52024523	+	O NA	intron (Nintron (N	9455 NM_138417	112970 Hs. 47603E	NR_138417	ENSG00000CT112	SBB181 T	CT112 chrprotein-coding
chr1-124E	8.566453	-1.32682	0.754615	-1.75827	0.078702	0.449288	chr1	1.24E+08	1.24E+08	+	O NA	IntergeniALR/Alphe	2549267 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000CEMBP1		emigin psseudo
chr20-27E	12.74351	-0.90278	0.513508	-1.75806	0.078737	0.449288	chr20	27099525	27100070	+	O NA	IntergeniALR/Alphe	-890564 NR_04009E	284801 Hs. 37069E	NR_04009E	ENSG00000MIR663AHC-		MIR663A lncRNA
chr1-178E	8.549655	-1.31954	0.750575	-1.75803	0.078742	0.449288	chr1	1.79E+08	1.79E+08	+	O NA	intron (NLMed LIN	61731 NM_00467E	9068 Hs. 591474	NR_00467E	ENSG00000ANGPTL1	ANG3 ANG	angiopoieprotein-coding
chr1-236E	8.549655	-1.31954	0.750575	-1.75803	0.078742	0.449288	chr1	2.36E+08	2.36E+08	+	O NA	intron (NAluSq SIN	35971 NM_00250E	4811 Hs. 356624	NR_00250E	ENSG00000NID1	NID	nidogen lprotein-coding
chr2-512E	8.549655	-1.31954	0.750575	-1.75803	0.078742	0.449288	chr2	1.12E+08	1.12E+08	+	O NA	intron (Nintron (N	54930 NM_00505A	84220 Hs. 44693E	NR_00505A	ENSG00000RGPD5	BS-63 BS	RANBP2 lprotein-coding
chr4-542E	8.549655	-1.31954	0.750575	-1.75803	0.078742	0.449288	chr4	54277889	54280267	+	O NA	intron (Nintron (N	45118 NM_001347	5156 Hs. 74615	NR_00620E	ENSG00000PDGFR	CD140A P	lplatelet protein-coding
chr4-119E	8.549655	-1.31954	0.750575	-1.75803	0.078742	0.449288	chr4	1.19E+08	1.2E+08	+								

chr1-2155	9.749604	-1.09693	0.667961	-1.64221	0.100547	0.49789	chr1	2.16E+08	2.16E+08	0	NA	intron (Nintron (N	13054	NM_016121	51133	Hs.33513	ENSG00000CKTD3	NY-REN-4	potassium protein-coding		
chr19-467	9.749604	-1.09693	0.667961	-1.64221	0.100547	0.49789	chr19	46773856	46783675	0	NA	exon (NM exon (NM	6049	NM_00114E	6510	Hs.631582	ENSG00000SLCIA5	AAAT ASCI	solute caprotein-coding		
chr11-684	8.252651	-1.25449	0.763984	-1.64203	0.100583	0.49789	chr11	68428293	68430709	0	NA	intron (Nintron (N	-31251	NM_00135E	55291	Hs.503022	ENSG00000PPP6R3	C11orf23	protein fprotein-coding		
chr13-236	8.252651	-1.25449	0.763984	-1.64203	0.100583	0.49789	chr13	23658641	23662293	0	NA	exon (NM exon (NM	81107	NM_018647	55504	Hs.149168	ENSG00000TNFRSF19	TAJ TAJ-ε	TNF receptor protein-coding		
chr3-584	8.252651	-1.25449	0.763984	-1.64203	0.100583	0.49789	chr3	58406641	58412073	0	NA	intron (Nintron (N	24772	NM_00092E	5162	Hs.161357	ENSG00000PDHB	PDBHD PDF	tyrinate protein-coding		
chr16-68	12.47569	-0.85655	0.521655	-1.64198	0.100593	0.49789	chr16	68540875	68546606	0	NA	intron (N L2c LINE	13449	NR_130977	146198	Hs.461074	ENSG00000ZFP90	FIK NK10 ZFP90	zif protein-coding		
chr7-753	12.47569	-0.85655	0.521655	-1.64198	0.100593	0.49789	chr7	75361451	75366802	0	NA	intron (N AluSx SIN	4926	NR_04058E	54441	Hs.63231	CNM_018991	STAG3L1	stromal apseudo		
chr11-515	12.50266	-0.85632	0.521799	-1.64111	0.100776	0.49789	chr11	51948627	51949492	0	NA	IntergeniALR/Alphe	1539912	NR_024504	646813	Hs.68417E	NR_024504	LOC646813	DEXH-box	pseudo	
chr2-189	9.776577	-1.09628	0.668197	-1.64065	0.100871	0.49789	chr2	1.89E+08	1.89E+08	0	NA	intron (N MER106A I	10394	NR_037401	1.01E+08	NR_037401	ENSG00000MIR3606	mir-3606	microRNA ncRNA		
chr6-283	9.265946	-1.14644	0.699172	-1.63972	0.101064	0.49789	chr6	28363180	28366884	0	NA	intron (Nintron (N	-8761	NM_00113E	64288	Hs.65641E	CNM_03089E	ENSG00000ZSCAN31	ZNF20-Lp	zinc fingprotein-coding	
chr1-1231	9.280536	-1.14834	0.700823	-1.63856	0.101306	0.49789	chr1	1.23E+08	1.23E+08	0	NA	IntergeniALR/Alphe	1666479	NR_00395E	647121	Hs.69768E	NR_00395E	ENSG00000EMB1	-	embigin fpseudo	
chr1-1971	12.48807	-0.85527	0.521977	-1.63852	0.101313	0.49789	chr1	1.97E+08	1.97E+08	0	NA	intron (N AluSx1 S1	13941	NM_194314	360023	Hs.52943E	NM_194314	ENSG00000ZBTB41	FRBZ1 ZNF	zinc fingprotein-coding	
chr1-5507	8.265033	-1.25128	0.763929	-1.63795	0.101432	0.49789	chr1	55073514	55073804	0	NA	intron (Nintron (N	33437	NR_110451	255738	Hs.18844	NM_17493E	ENSG00000PCSK9	FH3 HCHO1	proteiteprotein-coding	
chr12-58	8.265033	-1.25128	0.763929	-1.63795	0.101432	0.49789	chr12	58880104	58880789	0	NA	intron (Nintron (N	39100	NM_00113E	121227	Hs.2537E	CNM_15337E	ENSG00000LRIG3	LIG3	leucine iprotein-coding	
chr15-49	8.265033	-1.25128	0.763929	-1.63795	0.101432	0.49789	chr15	49613927	49615156	0	NA	intron (N LOR1a LTF	6277	NM_00133C	196951	Hs.17295E	NM_15264E	ENSG00000PAM227B	C15orf33	family wiprotein-coding	
chr4-412	8.265033	-1.25128	0.763929	-1.63795	0.101432	0.49789	chr4	41260372	41267496	0	NA	intron (Nintron (N	7006	NM_004181	7345	Hs.518731	CNM_004181	ENSG00000UCHL1	HEL-117	fubiquitirprotein-coding	
chr5-128	8.265033	-1.25128	0.763929	-1.63795	0.101432	0.49789	chr5	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	205983	NM_00199E	2201	Hs.519294	NM_00199E	ENSG00000PBN2	CCA DA9	fibrillirprotein-coding	
chr4-54	8.78008	-1.19576	0.731675	-1.63674	0.101685	0.49789	chr4	54261390	54267811	0	NA	intron (Nintron (N	30640	NM_001347	5156	Hs.74615	NM_00620E	ENSG00000FDGPA	CD140A PL	platelet protein-coding	
chr1-155	9.251356	-1.14457	0.69931	-1.63671	0.101691	0.49789	chr1	1.55E+08	1.55E+08	0	NA	intron (N AluS8 S1	5000	NM_00127E	23623	Hs.22649E	NM_01432E	ENSG00000RUSC1	NESCA	RUN and Sprotein-coding	
chr1-2024	9.251356	-1.14457	0.69931	-1.63671	0.101691	0.49789	chr1	2.02E+08	2.02E+08	0	NA	intron (N AluS8 S1	-13381	NM_03210A	4660	Hs.44440E	NM_002481	ENSG00000PPP1R12B	MYPT2 PP1	protein fprotein-coding	
chr22-41	9.278329	-1.1438	0.699032	-1.63627	0.101784	0.49789	chr22	41304874	41305178	0	NA	intron (N AluSx1 S1	-2657	NM_001317	5905	Hs.18380C	NM_00288E	ENSG00000RANGAP1	Fug1 RAN	Ran GTPase protein-coding	
chr3-149	9.278329	-1.1438	0.699032	-1.63627	0.101784	0.49789	chr3	1.49E+08	1.49E+08	0	NA	intron (Nintron (N	3846	NM_01422C	4071	Hs.35131E	NM_01422C	ENSG00000TM4SF1	H-16 L6	M transment protein-coding	
chr1-109	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr1	1.09E+08	1.09E+08	0	NA	intron (N LIMB4 LIN	-33245	NM_00126E	343263	Hs.44340E	NM_00101C	ENSG00000MYBPHL	-	myosin biiprotein-coding	
chr1-2064	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr1	2.06E+08	2.06E+08	0	NA	intron (Nintron (N	-14890	NM_18266E	83593	Hs.49757E	NM_031437	ENSG00000RASSF5	Maxp1 NOF	Ras assocprotein-coding	
chr1-2305	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr1	2.31E+08	2.31E+08	0	NA	intron (N LIME3F LI	50180	NM_02452E	79573	Hs.42478E	NM_02452E	ENSG00000TTC13	-	tetratric protein-coding	
chr17-42	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr17	42581686	42582808	0	NA	non-codiron-codir	-4416	NR_104567C	29893	Hs.38301E	NM_01329C	ENSG00000PSCM3IP	GT198 HOF	PSCM3 intrprotein-coding	
chr2-420	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr2	42051672	42060789	0	NA	intron (Nintron (N	8209	NM_13837C	91461	Hs.40854E	NM_13837C	ENSG00000PKDC	SGK493 V1	protein kprotein-coding	
chr2-229	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr2	2.3E+08	2.3E+08	0	NA	intron (Nintron (N	-103393	NM_13907E	92737	Hs.234074	NM_13907E	ENSG00000DNER	UNQ26 bet	delta/not protein-coding	
chr7-7704	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr7	77044912	77045589	0	NA	intron (N LTR45B LI	5770	NR_02805E	1E+08	Hs.29299E	NM_001129851	PMS2P9	PMS2L17	FPM51	hpcpseudo
chr9-1104	8.76549	-1.19554	0.730771	-1.636	0.10184	0.49789	chr9	1.1E+08	1.1E+08	0	NA	intron (N MLT2A2 LI	83345	NR_15336E	79987	Hs.522334	NM_15336E	ENSG00000SVEP1	C9orf13 C	(sushi, hvc)	protein-coding
chr5-935	9.761987	-1.09453	0.669166	-1.63565	0.101912	0.49789	chr5	93536466	93537248	0	NA	intron (N THE1B LTF	34486	NR_10982E	441094	Hs.457407	NR_01536E	ENSG00000NR2F1-AS1	-	NR2F1 antncRNA	
chr5-128	8.753107	-1.19847	0.732752	-1.63557	0.10193	0.49789	chr5	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	218669	NM_00104E	6558	Hs.16258E	NM_00104E	ENSG00000SLC12A2	BSC BSC2	solute caprotein-coding	
chr8-117	9.292919	-1.145683	0.700683	-1.635094	0.102029	0.49789	chr8	1.18E+08	1.18E+08	0	NA	intron (Nintron (N	90762	NR_14579E	1.1E+08	NR_14579E	NR_14579E	ENSG00000SNCR168	-	small nucsnRNA	
chr4-499	8.23806	-1.252319	0.766195	-1.634465	0.102161	0.49789	chr4	49987791	49988390	0	NA	IntergeniALR/Alphe	1001448	NM_00128E	80157	Hs.47970E	NM_02508E	ENSG00000CWH43	CWH43-C	F cell wall protein-coding	
chr7-817	8.23806	-1.252319	0.766195	-1.634465	0.102161	0.49789	chr7	81751249	81752888	0	NA	3' UTR (N3' UTR (N	17979	NM_00101C	3082	Hs.39653C	NM_000601	ENSG00000HGF	DFNB39 F	hepatocyt protein-coding	
chr9-4377	17.40263	0.615215	0.376421	-1.63438	0.102179	0.49789	chr9	43777445	43777877	0	NA	IntergeniALR/Alphe	651495	NR_160669	1.03E+08	NR_160669	LOC102724-	-	methylenepseudo		
chr1-121	9.735014	-1.095169	0.67054	-1.633263	0.102414	0.49789	chr1	1.21E+08	1.21E+08	0	NA	intron (Nintron (N	10584	NR_10418E	1.01E+08	Hs.56852E	NR_10418E	ENSG00000SRGAP2-AS-	-	SRGAP2 arncRNA	
chr1-171	9.263738	-1.141926	0.699172	-1.633255	0.102415	0.49789	chr1	1.72E+08	1.72E+08	0	NA	intron (N LIME1 LI	15186	NR_03370A	8674	Hs.6651	NM_00376E	ENSG00000VAMP4	VAMP-4 V	vesicle aprotein-coding	
chr1-180	9.263738	-1.141926	0.699172	-1.633255	0.102415	0.49789	chr1	1.8E+08	1.8E+08	0	NA	intron (N LIME2 LI	25559	NM_00282E	5768	Hs.71917E	NM_00282E	ENSG00000QSOX1	Q6 QSCN6	quiescin protein-coding	
chr2-189	9.263738	-1.141926	0.699172	-1.633255	0.102415	0.49789	chr2	1.89E+08	1.89E+08	0	NA	intron (Nintron (N	56910	NR_037401	1.01E+08	NR_037401	ENSG00000MIR3606	mir-3606	microRNA ncRNA		
chr2-11	9.263738	-1.141926	0.699172	-1.633255	0.102415	0.49789	chr2	26837463	26844796	0	NA	exon (NM exon (NM	4280	NM_00698E	9510	Hs.643357	NM_00698E	ENSG00000ADAMT5	C3-C5 MET	ADAM metaprotein-coding	
chr4-496	9.263738	-1.141926	0.699172	-1.633255	0.102415	0.49789	chr4	1.2E+08	1.2E+08	0	NA	intron (N TGAA N S	21477	NM_03343C	8654	Hs.647971	NM_0108E	ENSG00000PDEA5	CGB-68E	phosphodi protein-coding	
chr2-1124	9.238973	-1.147243	0.702691	-1.632641	0.102544	0.49789	chr2	1.12E+08	1.12E+08	0	NA	intron (N AluS8 S1	22922	NM_005054	84220	Hs.46963C	NM_005054	ENSG00000RGPD5	BS-63 BS	RANBP2 liprotein-coding	
chr17-554	8.750899	-1.193518	0.731848	-1.630829	0.102926	0.49789	chr17	55406343	55411609	0	NA	intron (N AluSz SIN	12859	NM_01232E	23531	Hs.46348E	NM_01232E	ENSG00000MMD	MMA MMD1	monocyte protein-coding	
chr4-542	8.750899	-1.193518	0.731848	-1.630829	0.102926	0.49789	chr4	54285235	54299083	0	NA	intron (N LIPA11 LI	-40733	NR_14716C	1.05E+08	Hs.157697	NR_14716C	LINC0228E-	-	long intencRNA	
chr9-438	8.750899	-1.193518	0.731848	-1.630829	0.102926	0.49789	chr9	43830184	43830603	0	NA	IntergeniALR/Alphe	704227	NR_16066E	1.03E+08	NR_160669	LOC102724-	-	methylenepseudo		
chr1-1805	8.738517	-1.196445	0.733835	-1.630402	0.103017	0.49789	chr1	1.81E+08	1.81E+08	0	NA	exon (NM exon (NM	4006	NM_02095C	57710	Hs.73481E	NM_02095C	ENSG00000KIAA1614	-	KIAA1614 protein-coding	
chr13-32	8.250443	-1.249091	0.766144	-1.63036	0.103025	0.49789	chr13	32239091	32241078	0	NA	intron (Nintron (N	71870	NM_00113E	646799	Hs.569254	NM_00113E	ENSG00000ZAR1L	Z3CCXC7	zygot aprotein-coding	
chr13-95	8.250443	-1.249091	0.766144	-1.63036	0.103025	0.49789	chr13	95097608	95098083	0	NA	intron (N LIME2 LI	-112499	NR_145733	1.1E+08	NR_145733	SNORD13G	-	small nucsnRNA		
chr16-67	8.250443	-1.249091	0.766144	-1.63036	0.103025	0.49789	chr16	67545194	67546624	0	NA	intron (Nintron (N	8447	NM_00119E	79567	Hs.152717	NM_02451E	ENSG00000RIPOR1	FAM65A	RHO familiprotein-coding	
chr17-291	8.250443	-1.249091	0.766144	-1.63036	0.103025	0.49789	chr17	29108391	29111758	0	NA	exon (NM exon (NM	30315	NM_00134E	399687						



chr1-1562	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr1	1.56E+08	1.56E+08	0	NA	intron (AluJo SIN	-7608 NM_001272	79957	Hs.23587	ENSG000002PAQR6	PRdelta	progesterone-protein-coding	
chr1-2017	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr1	2.02E+08	2.02E+08	0	NA	intron (AluY SINE	-23645 NR_031599	1E+08	NR_031599	ENSG000002MIR1231	MIRN1231	microRNA ncRNA	
chr1-2028	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr1	2.03E+08	2.03E+08	0	NA	exon (NM_exon (NM	-5445 NM_002871	5877	Hs.90875	NM_002871	ENSG000002CRABIF	MSS4 RASC	RAB interprotein-coding
chr1-2029	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr1	2.03E+08	2.03E+08	0	NA	intron (N LIPB3 LIN	12579 NM_001290	51094	Hs.5298	NM_015999	ENSG000002ADIPOR1	ACDCR1 CC	adiponectin-protein-coding
chr11-51F	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr11	51523027	51523950	0	NA	IntergeniALR/Alphe	1114341 NR_024504	646813	Hs.684175	NR_024504	LOC646813	DEXH-box	pseudo
chr11-66C	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr11	66053395	66069441	0	NA	intron (NMIR3 SINE	8274 NR_145738	1.1E+08	NR_145738	SNORD13F	-	small nucsnoRNA	
chr17-31F	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr17	31373745	31374231	0	NA	intron (N intron (N	-17687 NM_032932	84440	Hs.40678E	NM_032932	ENSG000002RAB11F1P4	Rab11	fanprotein-coding
chr17-80S	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr17	80350829	80355093	0	NA	exon (NM_exon (NM	-62206 NM_001352	284131	Hs.38967E	NM_173627	ENSG000002ENDOV	-	endonucleprotein-coding
chr19-377	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr19	37737261	37740659	0	NA	exon (NM_exon (NM	-19199 NM_03268E	84775	Hs.116622	NM_03268E	ENSG000002ZNF607	-	zinc fingprotein-coding
chr19-57E	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr19	57698819	57706889	0	NA	intron (N intron (N	6350 NR_11097E	7710	Hs.64637E	NM_003444	ENSG000002ZNF154	pH2-92	zinc fingprotein-coding
chr2-1214	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr2	1.21E+08	1.21E+08	0	NA	intron (N intron (N	-83215 NR_02334E	1E+08	Hs.68963E	NR_02334E	ENSG000002RNU4ATAC	MOPD1 RFW	RNA, U4at5nRNA
chr22-36E	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr22	36278886	36301624	0	NA	intron (AluJr SIN	-3348 NR_106877	1.02E+08	NR_106877	ENSG000002MIR6819	hsa-mir-ε	microRNA ncRNA	
chr3-134F	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr3	1.34E+08	1.34E+08	0	NA	intron (N intron (N	-1585 NR_10688E	1.02E+08	NR_10688E	ENSG000002MIR6827	hsa-mir-ε	microRNA ncRNA	
chr5-151E	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr5	1.52E+08	1.52E+08	0	NA	intron (N intron (N	-10235 NR_10987E	1.02E+08	Hs.57102E	NR_10987E	ENSG000002CLMAT3	CTB-113P	colorectncRNA
chr6-821F	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr6	82198736	82200899	0	NA	intron (NL2c LINE	47927 NM_001300	25998	Hs.30642E	NM_01552E	ENSG000002IBTK	BTBD26 B1	inhibitorprotein-coding
chr7-445E	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr7	44567257	44572729	0	NA	intron (N intron (N	4545 NM_001257	54606	Hs.65476E	NM_01908E	ENSG000002DDX56	DDX21 DD	DEAD-box protein-coding
chr9-122F	9.479573	-1.03634	0.681333	-1.52104	0.128249	0.538991	chr9	1.22E+08	1.22E+08	0	NA	intron (NMER58A DN	5232 NM_001271	5742	Hs.20197E	NM_00096E	ENSG000002PTGS1	COX1 COX	prostaglandin-protein-coding
chr4-8734	9.963232	-0.99457	0.654132	-1.52045	0.128399	0.538991	chr4	87344815	87345408	0	NA	intron (AluJo SIN	-22229 NM_17813E	345275	Hs.284414	NM_17813E	ENSG000002HSD17B13	HMFN0376	hydroxystprotein-coding
chr10-40E	9.990205	-0.99401	0.653937	-1.52004	0.1285	0.538991	chr10	40545676	40546475	0	NA	IntergeniALR/Alphe	1821970 NR_02438C	441666	Hs.25572E	NR_02438C	ENSG000002LOC44166E	-	zinc fingpseudo
chr1-124F	9.469398	-1.04323	0.687341	-1.51777	0.129072	0.538991	chr1	1.24E+08	1.24E+08	0	NA	IntergeniALR/Alphe	2846695 NR_00395E	647121	Hs.69768E	NR_00395E	ENSG000002EMBP1	-	embigin fpseudo
chr1-564S	8.495459	-1.12947	0.744583	-1.51692	0.129287	0.538991	chr1	56493952	56496811	0	NA	3' UTR (N3' UTR (N	80418 NR_14716E	1.05E+08	Hs.183974	NR_14716E	ENSG000002LINC01767	-	long intncRNA
chr1-2064	8.495459	-1.12947	0.744583	-1.51692	0.129287	0.538991	chr1	2.06E+08	2.06E+08	0	NA	intron (N intron (N	-64578 NM_00119E	9641	Hs.32104E	NM_01400E	ENSG000002IKBKE	IKK-ε IKK	inhibitorprotein-coding
chr13-95E	8.495459	-1.12947	0.744583	-1.51692	0.129287	0.538991	chr13	95205828	95213365	0	NA	promoter-promoter-	-748 NR_14573E	1.1E+08	NR_14573E	SNORD13G	-	small nucsnoRNA	
chr19-12E	8.495459	-1.12947	0.744583	-1.51692	0.129287	0.538991	chr19	12318068	12322723	0	NA	intron (AluJb SIN	13238 NM_14527E	147837	Hs.66351C	NM_14527E	ENSG000002ZNF154	-	zinc fingprotein-coding
chr19-18E	8.495459	-1.12947	0.744583	-1.51692	0.129287	0.538991	chr19	18386690	18389759	0	NA	intron (N intron (N	1662 NR_03615E	1E+08	NR_03615E	ENSG000002MIR3189	mir-3189	microRNA ncRNA	
chr17-67E	8.981325	-1.08141	0.713061	-1.51658	0.129374	0.538991	chr17	6764278	6774769	0	NA	intron (NLIMed LIN	-6692 NM_15323C	162517	Hs.368364	NM_15323C	ENSG000002FBX03	CT144 Fbx	F-box prcprotein-coding
chr4-185I	8.510049	-1.13161	0.746696	-1.51549	0.129648	0.538991	chr4	1.85E+08	1.85E+08	0	NA	3' UTR (N3' UTR (N	19258 NM_001151	291	Hs.24650E	NM_001151	ENSG000002LIC25A4	AAC1 ANT	solute cprotein-coding
chr14-10C	8.497667	-1.13466	0.748742	-1.51543	0.129664	0.538991	chr14	1.01E+08	1.01E+08	0	NA	promoter-promoter-	-326 NR_00320E	767588	NR_00320E	ENSG000002SNORD114	14q (I1-1C	small nucsnoRNA	
chr11-62F	9.491956	-1.03384	0.68264	-1.51448	0.129905	0.538991	chr11	62593855	62598975	0	NA	intron (N intron (N	4835 NM_00133C	9219	Hs.17304E	NM_00473E	ENSG000002MTA2	MTA11 P1	metastasiaprotein-coding
chr2-105F	9.491956	-1.03384	0.68264	-1.51448	0.129905	0.538991	chr2	1.05E+08	1.05E+08	0	NA	3' UTR (N3' UTR (N	9455 NM_02409E	79074	Hs.549577	NM_02409E	ENSG000002Corf49	asw	chromosonprotein-coding
chr8-672E	9.491956	-1.03384	0.68264	-1.51448	0.129905	0.538991	chr8	67225417	67227682	0	NA	intron (NMIR SINE	117232 NM_006421	10565	Hs.65690E	NM_006421	ENSG000002ARFGEP1	ARFGEP1 EADP	ribosprotein-coding
chr8-994F	9.010506	-1.08542	0.71676	-1.51433	0.129941	0.538991	chr8	99432410	99434053	0	NA	intron (N intron (N	103499 NR_03032E	693184	NR_03032E	ENSG000002MIR599	MIRN599	microRNA ncRNA	
chr4-119I	9.464983	-1.03449	0.683239	-1.51411	0.13	0.538991	chr4	1.2E+08	1.2E+08	0	NA	intron (N intron (N	62692 NR_03343C	8654	Hs.647971	NM_00108E	ENSG000002PDE5A	CGB-PDE	phosphodiaprotein-coding
chr5-371E	9.464983	-1.03449	0.683239	-1.51411	0.13	0.538991	chr5	37121395	37121648	0	NA	intron (N intron (N	-127525 NR_13426E	1.05E+08	Hs.17099E	NR_13426E	ENSG000002LOC105374	-	uncharactncRNA
chr7-552E	9.464983	-1.03449	0.683239	-1.51411	0.13	0.538991	chr7	55200102	55203631	0	NA	intron (N intron (N	-12917 NR_047551	1.01E+08	Hs.72048E	NR_047551	ENSG000002EGFR-AS1	-	EGFR antncRNA
chr1-128E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr1	35381441	35381992	0	NA	exon (NM_exon (NM	240 NR_02961E	406955	NR_02961E	ENSG000002MIR181B1	MIRN181B1	microRNA ncRNA	
chr1-198E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr1	1.99E+08	1.99E+08	0	NA	TTS (NR_C TTS (NR_C	8103 NM_00128E	252839	Hs.181444	NM_01645E	ENSG000002TMEM9	DERM4 TME	transmemprotein-coding
chr1-2011	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr1	2.07E+08	2.07E+08	0	NA	3' UTR (N3' UTR (N	-38352 NM_15375E	29949	Hs.661017	NM_013371	ENSG000002LINC119	IL-10C MC	interleukprotein-coding
chr1-230E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr1	2.31E+08	2.31E+08	0	NA	intron (N intron (N	49426 NR_110681	1.02E+08	Hs.63892E	NR_110681	ENSG000002LOC101927	-	uncharactncRNA
chr10-73I	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr10	73174758	73182877	0	NA	intron (N intron (N	10698 NR_17334E	317662	Hs.408577	NM_17334E	ENSG000002FAM149B1	KIAA0974	family wiprotein-coding
chr12-57I	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr12	51723957	51723926	0	NA	intron (N intron (N	-1343 NR_031597	1E+08	NR_031597	ENSG000002MIR1228	MIRN1228	microRNA ncRNA	
chr16-16C	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr16	16097884	16127555	0	NA	intron (N intron (N	110752 NM_001171	368	Hs.44218E	NM_001171	ENSG000002ABCC6	ABC34 AR	ATP bindiprotein-coding
chr17-81E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr17	817722	820297	0	NA	intron (AluXs1 SI	36656 NM_001317	55178	Hs.18272E	NM_01814E	ENSG000002MRM3	RMTL1 RN	mitochondncprotein-coding
chr17-80S	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr17	80385201	80391645	0	NA	intron (N intron (N	-26744 NM_00135E	284131	Hs.38967E	NM_173627	ENSG000002ENDOV	-	endonucleprotein-coding
chr17-80E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr17	80995030	80997843	0	NA	intron (N intron (N	4959 NM_024591	79643	Hs.51456E	NM_024591	ENSG000002CHMP6	VPS20	charged nprotein-coding
chr2-702E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr2	70274883	70277280	0	NA	intron (AluXs1 SI	17143 NM_001317	6637	Hs.465167	NM_00309E	ENSG000002SNRFP	SMG Sm-G	small nucprotein-coding
chr21-26E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr21	26927428	26927975	0	NA	intron (NL2a LINE	-26260 NR_03991E	1.01E+08	NR_03991E	ENSG000002MIR4759	-	microRNA ncRNA	
chr21-20E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr22	27063583	27065635	0	NA	intron (N intron (N	-9504 NM_00018E	3053	Hs.47427E	NM_00018E	ENSG000002SERPIND1	D22S673 E	serpin fprotein-coding
chr5-476E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr5	47631951	47633692	0	NA	IntergeniALR/Alphe	-1936441 NM_02107E	348980	Hs.35317E	NM_02107E	ENSG000002HCN1	BCNG-1 B	hyperpoleprotein-coding
chr7-111E	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr7	1.2E+08	1.2E+08	0	NA	intron (N intron (N	135431 NR_10380E	1.01E+08	Hs.67751E	NR_10380E	ENSG000002DOCK4-AS1	-	DOCK4 antncRNA
chr9-1274	8.480868	-1.12735	0.744634	-1.51397	0.130034	0.538991	chr9	33216 NM_00100E	90678	Hs.49518E	NM_138361	ENSG000002LRSM1	90678	Hs.49518E	NM_138361	ENSG000002LRSM1	CMT2P RF	leucine rprotein-coding	
chr5-128E	8.468486	-1.13037	0.746662	-1.513															

chr2-3073	10.20825	-0.90599	0.634768	-1.42727	0.153502	0.570268	chr2	2.37E+08	2.37E+08	0	NA	intron (Nintron (N	56858	NM_057165	1293	Hs.23324	CNM_004366	ENS00000	COL6A3	BTHLM1	DIYcollagen protein-coding		
chr20-586	10.20825	-0.90599	0.634768	-1.42727	0.153502	0.570268	chr20	58908372	58912472	0	NA	intron (Nintron (N	18259	NR_132272	2778	Hs.12589	NR_00051	ENS00000	GNAS	AHO C20rGNAS	comp protein-coding		
chr3-757	10.20825	-0.90599	0.634768	-1.42727	0.153502	0.570268	chr3	75737578	75744829	0	NA	intron (Nintron (N	2923	NR_036235	1E+08	NR_036235	ENS00000	CIR4273	-	microRNA	ncRNA		
chr3-128	10.20825	-0.90599	0.634768	-1.42727	0.153502	0.570268	chr3	1.28E+08	1.28E+08	0	NA	exon (NM exon (NM	8659	NR_046646	1.01E+08	Hs.58160	NR_046646	ENS00000	RUVBL1-AS	RUVBL1	arnRNA		
chr19-250	10.23522	-0.90552	0.63629	-1.42312	0.1547	0.570268	chr19	25058553	25059514	0	NA	IntergeniALR/Alphe	89558	NR_003603	1E+08	Hs.14931	NR_003603	ENS00000	HAVCR1P1	-	hepatitis pseudo		
chr1-146	10.19366	-0.90434	0.635696	-1.4226	0.154851	0.570268	chr1	1.47E+08	1.47E+08	0	NA	intron (N LIPA4 LIN	42213	NM_001275	149013	Hs.66698	NM_001275	ENS00000	NCBP12	COA51 KI NCBP	memt protein-coding		
chr11-57	10.19366	-0.90434	0.635696	-1.4226	0.154851	0.570268	chr11	57801447	57817908	0	NA	intron (Nintron (N	47875	NM_001206	1500	Hs.16601	NM_001331	ENS00000	CTNND1	B2C52 CAS	catenin cprotein-coding		
chr5-958	10.19366	-0.90434	0.635696	-1.4226	0.154851	0.570268	chr5	95886105	95901734	0	NA	intron (Nintron (N	41687	NR_026936	202299	Hs.8373	NM_17561	ENS00000	LINC01554	C5orf27 F	long intencrNA		
chr1-201	10.22063	-0.90388	0.635722	-1.42181	0.15508	0.570268	chr1	2.02E+08	2.02E+08	0	NA	intron (N AluJo SIN	8531	NM_006335	10440	Hs.20716	NM_006335	ENS00000	TIMM17A	TIM17 TIM	translocaprotein-coding		
chr19-441	10.22063	-0.90388	0.635722	-1.42181	0.15508	0.570268	chr19	44143241	44158782	0	NA	intron (N AluSg SIN	9457	NM_006633	10780	Hs.23599	NM_006633	ENS00000	ZNF234	HZF4 ZNF2	zinc fingprotein-coding		
chr21-63	9.785251	0.954811	0.675417	1.413661	0.157461	0.570268	chr21	6332954	6333847	0	NA	IntergeniLIMB1 LIN	66064	NM_001322	1.03E+08	Hs.74398	NR_001322	047	LNC012724	-	uncharactprotein-coding		
chr1-154	9.70999	-0.93976	0.664981	-1.41321	0.157595	0.570268	chr1	1.55E+08	1.55E+08	0	NA	promoter-promoter-	790	NR_046666	1.01E+08	NR_046666	ENS00000	UBE2Q1-AS	-	UBE2Q1	arnRNA		
chr2-925	9.70999	-0.93976	0.664981	-1.41321	0.157595	0.570268	chr2	92533517	92534424	0	NA	IntergeniALR/Alphe	592837	NR_027714	440888	Hs.73023	CNM_001032412	ACTR3BP2	FKSG73	ACTR3B	pspseudo		
chr6-3061	9.724589	-0.94156	0.666513	-1.41266	0.157755	0.570268	chr6	30619549	30622441	0	NA	intron (Nintron (N	3155	NM_014046	28973	Hs.65532	CNM_014046	ENS00000	MRPS18B	C6orf14 F	mitochncprotein-coding		
chr18-352	12.43387	-0.73541	0.520748	-1.41221	0.157888	0.570268	chr18	35242559	35255020	0	NA	3' UTR (N3' UTR (N	7755	NM_001135	84307	Hs.59106	NM_032347	ENS00000	ZNF397	ZNF47 ZSC	zinc fingprotein-coding		
chr20-294	17.3732	-0.53058	0.375804	-1.41187	0.157989	0.570268	chr20	29457938	29459789	0	NA	TTS (NR_TTS (NR_1	10346	NR_134504	1.05E+08	Hs.70227	NR_134504	LOC105375	-	uncharactncRNA			
chr1-155	9.695408	-0.93797	0.665149	-1.41017	0.15849	0.570268	chr1	1.56E+08	1.56E+08	0	NA	intron (Nintron (N	6816	NR_106796	1.02E+08	NR_106796	ENS00000	MIR6738	hsa-mir-6	microRNA	ncRNA		
chr1-202	9.695408	-0.93797	0.665149	-1.41017	0.15849	0.570268	chr1	2.4E+08	2.4E+08	0	NA	intron (Nintron (N	166232	NM_001305	56776	Hs.24889	NM_020066	ENS00000	PMN2	-	formin 2 protein-coding		
chr12-57	9.695408	-0.93797	0.665149	-1.41017	0.15849	0.570268	chr12	57820511	57829592	0	NA	promoter-promoter-	359	NR_029847	407016	NR_029847	ENS00000	MIR26A2	MIRN26A2	microRNA	ncRNA		
chr18-124	9.695408	-0.93797	0.665149	-1.41017	0.15849	0.570268	chr18	12426802	12430050	0	NA	intron (Nintron (N	4348	NR_136514	1.05E+08	Hs.51528	NR_136514	LOC105371	-	uncharactncRNA			
chr10-43	9.722381	-0.93743	0.664846	-1.40999	0.158543	0.570268	chr10	43614916	43617401	0	NA	intron (Nintron (N	9720	NM_145312	220992	Hs.14744	CNM_145312	ENS00000	ZNF485	-	zinc fingprotein-coding		
chr14-71	10.19145	-0.90053	0.639125	-1.409	0.158834	0.570268	chr14	71064429	71065655	0	NA	intron (N LIPA7 LIN	157583	NM_001308	22990	Hs.44655	CNM_014982	ENS00000	PCNX1	PCNX PCNX	pecanex lprotein-coding		
chr1-173	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr1	1.74E+08	1.74E+08	0	NA	intron (Nintron (N	30247	NR_000488	462	Hs.75599	NM_000488	ENS00000	SERPINC1	AT3 AT3D	serpin faprotein-coding		
chr1-250	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr1	2.04E+08	2.04E+08	0	NA	intron (Nintron (N	29087	NR_003015	677843	Hs.67613	NR_003015	ENS00000	SNORA77	ACA63 SNC	small ncRNA		
chr10-93	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr10	93371767	93376127	0	NA	intron (N LIPA6 LIN	108387	NM_013451	26509	Hs.60208	CNM_013451	ENS00000	MYOF	FERL13	myoferlir	protein-coding	
chr11-281	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr11	28173004	28174771	0	NA	intron (N LIMC3 LIN	65499	NM_001297	196074	Hs.24332	CNM_152635	ENS00000	METTL15	METT5D1	methytra	protein-coding	
chr12-571	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr12	57152614	57171574	0	NA	intron (Nintron (N	14475	NR_131938	1.06E+08	Hs.60954	CNR_131938	ENS00000	LRP1-AS	-	LRP1	antincRNA	
chr21-38	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr21	38807544	38823689	0	NA	intron (Nintron (N	9687	NM_005235	2114	Hs.64423	CNM_005235	ENS00000	ETS2	ETS2I1	ETS protc	protein-coding	
chr3-521	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr3	52198972	52215594	0	NA	intron (N AluY SINE	9123	NM_000688	211	Hs.47630	CNM_000688	ENS00000	ALAS1	ALAS ALAS	5'-amino	protein-coding	
chr3-187	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr3	1.88E+08	1.88E+08	0	NA	intron (Nintron (N	6736	NM_001134	604	Hs.47858	NM_001705	ENS00000	BCL6	BCL5 BCL6	trarp	protein-coding	
chr5-393	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr5	39370700	39394709	0	NA	exon (NM exon (NM	18209	NM_001737	735	Hs.65444	CNM_001737	ENS00000	CC9	ARM15 C9	complemer	protein-coding	
chr9-127	9.707791	-0.93564	0.665015	-1.40695	0.159443	0.570268	chr9	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	54470	NM_022833	64855	Hs.52240	NM_022833	ENS00000	LIBAN2	C9orf88 F	liban ap	protein-coding	
chr7-408	9.21175	-0.97764	0.697793	-1.40104	0.161201	0.570268	chr7	40839918	40840392	0	NA	intron (N MER5A DN	139784	NR_110283	1.02E+08	Hs.63976	NR_110283	ENS00000	LINC0145C	-	long intencrNA		
chr5-488	9.224133	-0.97504	0.696155	-1.40061	0.16133	0.570268	chr5	48836112	48836587	0	NA	IntergeniALR/Alphe	1604939	NM_198445	133418	Hs.56141	CNM_198445	ENS00000	CEMB	GP70	embigin	protein-coding	
chr1-211	9.693201	-0.93383	0.666888	-1.40029	0.161428	0.570268	chr1	2.11E+08	2.11E+08	0	NA	TTS (NM_CTS (NM_C	13286	NM_004615	7188	Hs.52393	CNM_004615	ENS00000	TRAF5	MGC-3978	TNF recep	protein-coding	
chr14-22	9.19716	-0.97569	0.696972	-1.3999	0.161544	0.570268	chr14	22839411	22847356	0	NA	exon (NM exon (NM	6798	NM_004995	4323	Hs.2399	NM_004995	ENS00000	MMP14	MMP-14 M	matrx	protein-coding	
chr1-205	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr1	2.05E+08	2.05E+08	0	NA	intron (Nintron (N	14839	NM_030952	81788	Hs.49751	CNM_030952	ENS00000	CNUAK2	SNARK	NUAK	famiprotein-coding	
chr13-414	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr13	41459394	41471770	0	NA	intron (N MR3 SINE	8032	NM_014055	28984	Hs.50786	CNM_014055	ENS00000	RCR2A	C13orf15	regulator	protein-coding	
chr17-751	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr17	75112124	75174851	0	NA	exon (NM exon (NM	28666	NM_000937	5430	Hs.27001	CNM_000937	POLR2A	POLR2L POLR	polyn	protein-coding		
chr19-48	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr19	48381501	48389685	0	NA	intron (Nintron (N	5958	NM_006801	10945	Hs.51551	CNM_006801	ENS00000	KDEL1R1	ERD2 ERD2	KDEL	endc	protein-coding
chr2-41	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr2	41244946	41285041	0	NA	intron (N L2c LINE	11943	NR_106949	1.02E+08	NR_106949	ENS00000	MIR6889	hsa-mir-6	microRNA	ncRNA		
chr5-143	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr5	14364063	14398855	0	NA	intron (Nintron (N	82524	NR_145815	1.1E+08	NR_145815	SNORD170	-	small ncRNA				
chr7-134	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr7	1.34E+08	1.34E+08	0	NA	intron (N MRB SINE	12177	NM_001628	231	Hs.52121	CNM_001628	ENS00000	AKR1B1	ADR ALDR1	aldo-ketc	protein-coding	
chr8-102	9.209542	-0.97311	0.69534	-1.39947	0.161672	0.570268	chr8	1.02E+08	1.02E+08	0	NA	intron (Nintron (N	28266	NR_125415	1.02E+08	Hs.49244	NR_125415	ENS00000	UBR5-AS1	-	UBR5	antincRNA	
chr12-29	9.238723	-0.977	0.698901	-1.39791	0.162139	0.570268	chr12	2909387	2910920	0	NA	intron (N AluYk4 SI	19262	NM_001166	7289	Hs.65533	CNM_003324	ENS00000	TULP3	TUBL3	TUB	like	protein-coding
chr18-24	9.213045	-1.06337	0.760919	-1.39748	0.162268	0.570268	chr18	24097070	24097413	0	NA	intron (N HSMAR2 DN	16086	NM_001292	125488	Hs.12857	CNM_153211	ENS00000	TTC39C	C18orf17	tetratric	protein-coding	
chr1-669	8.225428	-1.06025	0.758848	-1.39718	0.16236	0.570268	chr1	66998216	66999062	0	NA	TTS (NM_CTS (NM_C	55509	NM_015135	23169	Hs.21364	CNM_015135	ENS00000	SLC35D1	SHKND U	solute cap	protein-coding	
chr1-168	8.225428	-1.06025	0.758848	-1.39718	0.16236	0.570268	chr1	1.68E+08	1.68E+08	0	NA	intron (N L2 LINE I	28363	NR_031702	1E+08	NR_031702	ENS00000	CIR12155B2	MIRN1255B	microRNA	ncRNA		
chr12-22	8.198455	-1.06112	0.759745	-1.39667	0.162512	0.570268	chr12	22056629	22057208	0	NA	intron (Nintron (N	10700	NM_018688	55907	Hs.31134	CNM_018688	ENS00000	CMAS	CSS1	cytidine	protein-coding	
chr8-118	8.198455	-1.06112	0.759745	-1.39667	0.162512	0.570268	chr8	1.19E+08	1.19E														



chr11-111	8.20863	-1.05264	0.760922	-1.38338	0.166549	0.570268	chr11	1.12E+08	1.12E+08	0 NA	intron (Nintron (N	19505 NM_00125E	143903 Hs. 503831NM_178834	ENSG00000CLAYN	-	layilin protein-coding		
chr17-738	8.20863	-1.05264	0.760922	-1.38338	0.166549	0.570268	chr17	7389387	7393029	0 NA	intron (Nintron (N	3317 NM_001366	57048 Hs. 534591NM_02036C	ENSG00000PLSCR3	-	phospholiprotein-coding		
chr6-111	8.20863	-1.05264	0.760922	-1.38338	0.166549	0.570268	chr6	1.11E+08	1.11E+08	0 NA	intron (Nintron (N	-85063 NR_03411C	643749 Hs. 48622ENR_03410E	ENSG00000CTRAF3IP2	C6UAS C6c	TRAF3IP2 ncRNA		
chr6-1572	8.20863	-1.05264	0.760922	-1.38338	0.166549	0.570268	chr6	1.57E+08	1.57E+08	0 NA	exon (NM exon (NM	122994 NM_01845E	729515 Hs. 157212NM_01845E	ENSG00000TMEM242	BMO33 C6c	transmembrane protein-coding		
chr7-647C	8.20863	-1.05264	0.760922	-1.38338	0.166549	0.570268	chr7	64706147	64707135	0 NA	exon (NM exon (NM	27577 NR_10689E	1.02E+08	NR_10689E	ENSG00000MIR6839	hsa-mir-610	microRNA ncRNA	
chr8-327F	8.20863	-1.05264	0.760922	-1.38338	0.166549	0.570268	chr8	32759252	32761593	0 NA	3' UTR (N3' UTR (N	38587 NM_00132Z	3084 Hs. 453951NM_00449E	ENSG00000CNRG1	ARIA GGF	neuregulin protein-coding		
chr1-2064	8.694496	-1.00635	0.729543	-1.38216	0.166922	0.571023	chr1	2.06E+08	2.06E+08	0 NA	promoter-promoter-	79 NR_10691E	1.02E+08	NR_10691E	ENSG00000MIR6769B	hsa-mir-610	microRNA ncRNA	
chr2-189C	9.196244	-0.96658	0.70091	-1.37903	0.167885	0.573718	chr2	1.89E+08	1.89E+08	0 NA	intron (Nintron (N	15613 NR_037401	1.01E+08	NR_037401	ENSG00000MIR3606	hsa-mir-3606	microRNA ncRNA	
chr7-107F	8.721469	-1.00757	0.730857	-1.37861	0.168014	0.573718	chr7	1.08E+08	1.08E+08	0 NA	intron (NAluSc8 SI	5735 NM_002291	3912 Hs. 65058E	NM_002291	ENSG00000CLAMB1	CLM LIS5	laminin sprotein-coding	
chr16-18F	9.639254	-0.93487	0.679094	-1.37665	0.168622	0.575271	chr16	1.8338489	1.8338804	0 NA	intron (Nigger6a	-2786 NM_00128E	1.01E+08	Hs. 63656E	NM_00128E	ENSG00000NIPPA8	LCR16a9 N	nuclear rprotein-coding
chr12-11F	8.667523	-1.00907	0.734038	-1.37468	0.169223	0.575385	chr12	1.12E+08	1.12E+08	0 NA	exon (NM exon (NM	-21445 NR_106921	1.02E+08	NR_106921	ENSG00000MIR6861	hsa-mir-610	microRNA ncRNA	
chr4-113F	8.667523	-1.00907	0.734038	-1.37468	0.169223	0.575385	chr4	1.14E+08	1.14E+08	0 NA	exon (NM exon (NM	76628 NM_02459C	79642 Hs. 22895	NM_02459C	ENSG00000CARSJ	ASJ	arylsulfatase protein-coding	
chr1-666E	8.19404	-1.05033	0.764529	-1.37383	0.169495	0.575385	chr1	66666577	66667549	0 NA	intron (Nintron (N	38623 NR_03606C	1E+08	NR_03606C	ENSG00000CIR3117	mir-3117	microRNA ncRNA	
chr2-958E	8.19404	-1.05033	0.764529	-1.37383	0.169495	0.575385	chr2	95893183	95893477	0 NA	intron (Nintron (N	-66349 NR_103734	150759 Hs. 50346E	NR_103734	LINC0034Z	NCRNA0034	long intencRNA	
chr7-128E	8.19404	-1.05033	0.764529	-1.37383	0.169495	0.575385	chr7	1.29E+08	1.29E+08	0 NA	IntergeniIntergeni	-22247 NR_02436E	402483 Hs. 72235C	NM_001039682	LINC0100C	-	long intencRNA	
chr3-122A	8.250193	-1.05393	0.767288	-1.37358	0.169573	0.575385	chr3	1.22E+08	1.22E+08	0 NA	intron (NAluYg6 SI	22941 NM_002264	3836 Hs. 16100E	NM_002264	ENSG00000CPNA1	IPOA5 NP1	karyopher protein-coding	
chr11-10F	8.706879	-1.00542	0.733112	-1.37145	0.170236	0.576568	chr11	1.08E+08	1.08E+08	0 NA	exon (NM exon (NM	102027 NM_152587	160140 Hs. 65318C	NM_152587	ENSG00000C11orf65	-	chromosom protein-coding	
chr4-141E	8.706879	-1.00542	0.733112	-1.37145	0.170236	0.576568	chr4	1.41E+08	1.41E+08	0 NA	intron (Nintron (N	12509 NM_014487	27309 Hs. 12076E	NM_014487	ENSG00000CNF330	HSA6591 N	zinc fing protein-coding	
chr5-432E	8.679905	-1.00618	0.733982	-1.37085	0.17042	0.576568	chr5	43293779	43294120	0 NA	intron (NAluSx SIN	19232 NM_001324	3157 Hs. 39772E	NM_00213C	ENSG00000HMGC51	HMGC5	3-hydroxy protein-coding	
chr11-51F	16.34532	-0.54275	0.396027	-1.37049	0.170534	0.576568	chr11	51963373	51963612	0 NA	IntergeniALR/Alphe	1554435 NR_024504	646813 Hs. 68417E	NR_024504	LOC646813	-	DEXH-box pseudo	
chr1-231E	8.221013	-1.04938	0.767321	-1.36759	0.171441	0.578595	chr1	2.31E+08	2.31E+08	0 NA	intron (NMSTB1 LTF	14754 NM_15237E	128061 Hs. 743464NM_15237E	ENSG00000Clorf131	-	chromosom protein-coding		
chr5-682E	8.221013	-1.04938	0.767321	-1.36759	0.171441	0.578595	chr5	68293328	68293708	0 NA	intron (Nintron (N	941 NM_00124Z	5295 Hs. 13222E	NM_181504	ENSG00000PIK3R1	AGM7 GRB1	phosphoir protein-coding	
chr2-22Z	8.692288	-1.00321	0.737616	-1.36007	0.173809	0.585389	chr2	22306489	22307065	0 NA	intron (Nintron (N	8679 NR_02729E	96610 Hs. 449601NM_080926	BMS1P20	IGL IGLV BMS1	pset pseudo		
chr3-183E	8.179449	-1.04793	0.770688	-1.35974	0.173912	0.585389	chr3	1.84E+08	1.84E+08	0 NA	intron (Nintron (N	-18660 NR_04657E	1.01E+08	Hs. 57069E	NR_04657E	ENSG00000ABC5-AS1	-	chromosom antncRNA
chr20-27J	13.62144	-0.64303	0.472914	-1.35971	0.173921	0.585389	chr20	27758540	27758824	0 NA	IntergeniALR/Alphe	843983 NR_13231E	1E+08	Hs. 529357NR_13231E	ENSG00000FRG1CP	-	FSHD regipseudo	
chr3-180E	9.190537	-0.9617	0.710761	-1.35306	0.176036	0.591978	chr3	1.81E+08	1.81E+08	0 NA	intron (NAluSp SIN	28133 NM_00136E	8087 Hs. 478407NM_005087	ENSG00000CFXR1	FXR1P	FMRI	autc protein-coding	
chr9-128E	8.677698	-1.00088	0.744529	-1.34432	0.178846	0.59423	chr9	1.28E+08	1.28E+08	0 NA	intron (NLTR13A LI	3653 NM_00131E	375757 Hs. 259594NM_00104C	ENSG00000CSW15	C9orf119 N	SW15	homc protein-coding	
chr4-183E	8.191832	-1.04453	0.77724	-1.3439	0.17898	0.59423	chr4	1.83E+08	1.83E+08	0 NA	exon (NM exon (NM	-20773 NR_12647E	1.02E+08	Hs. 57071E	NR_12647E	ENSG00000WWC2-AS1	-	WWC2 antncRNA
chr17-39J	10.93692	-0.79566	0.592662	-1.34252	0.179426	0.59423	chr17	39200746	39204971	0 NA	intron (NMIR SINE	2535 NM_00133C	6143 Hs. 381061NM_000981	ENSG00000RPL19	L19	ribosomal protein-coding		
chr1-232E	8.164859	-1.04542	0.779643	-1.34089	0.179956	0.59423	chr1	2.43E+08	2.43E+08	0 NA	intron (Nintron (N	80665 NR_039824	1.01E+08	NR_039824	ENSG00000MIR4677	mir-4677	microRNA ncRNA	
chr1-225J	10.92233	-0.79421	0.592854	-1.33964	0.180362	0.59423	chr1	2.26E+08	2.26E+08	0 NA	intron (NAluSg SIN	10663 NM_00113C	6726 Hs. 51142E	NM_00313E	ENSG00000SRP9	ALURBP	signal rprotein-coding	
chr18-49J	10.92233	-0.79421	0.592854	-1.33964	0.180362	0.59423	chr18	49489068	49492177	0 NA	TTS (NR_CTS (NR_C	307 NM_00136E	6139 Hs. 29365E	NM_00098E	ENSG00000RPL17	L17 PD-1	ribosomal protein-coding	
chr19-11J	10.92233	-0.79421	0.592854	-1.33964	0.180362	0.59423	chr19	11770240	11785813	0 NA	intron (NAluSg2a	11026 NM_15235E	126068 Hs. 67513E	NM_15235E	ENSG00000CNF441	-	zinc fing protein-coding	
chr8-130E	10.92233	-0.79421	0.592854	-1.33964	0.180362	0.59423	chr8	13082422	13101003	0 NA	intron (Nintron (N	24532 NM_001164	10395 Hs. 13429E	NM_006094	ENSG00000DLC1	ARHGAP7 D	LDC1	Rho protein-coding
chr5-699J	13.17714	-0.65627	0.490712	-1.33738	0.181099	0.59423	chr5	69913813	69916129	0 NA	intron (NAluJo SIN	-10951 NR_157804	1.02E+08	Hs. 63401E	NR_157804	LOC10192E	-	putative pseudo
chr1-246J	10.93471	-0.79242	0.593544	-1.33507	0.181852	0.59423	chr1	24645332	24659660	0 NA	non-codiron-codir	8917 NM_00136E	10250 Hs. 18192	NR_00583E	ENSG00000SRRM1	160-KD P	serine ar protein-coding	
chr1-144E	10.93471	-0.79242	0.593544	-1.33507	0.181852	0.59423	chr1	1.45E+08	1.45E+08	0 NA	intron (Nintron (N	174388 NR_027354	645166 Hs. 74418E	NR_027354	LSP1P5	-	LSP1 pset pseudo	
chr2-928E	10.93471	-0.79242	0.593544	-1.33507	0.181852	0.59423	chr2	92823857	92824740	0 NA	IntergeniALR/Alphe	883165 NR_027714	440888 Hs. 73023E	NR_001032412	ACTR3BP2	FKSG73	ACTR3B pspseudo	
chr6-365E	10.93471	-0.79242	0.593544	-1.33507	0.181852	0.59423	chr6	36595116	36610684	0 NA	non-codiron-codir	8538 NR_003017	6428 Hs. 405144NM_003017	ENSG00000SRSF3	SFRS3 SR	serine ar protein-coding		
chr16-32Z	13.14796	-0.65442	0.490469	-1.33427	0.182116	0.59423	chr16	3221576	3233748	0 NA	intron (NTHEID LTF	7496 NM_00114E	7752 Hs. 63222E	NM_003454	ENSG00000ZNF200	-	zinc fing protein-coding	
chr14-71J	10.89315	-0.79125	0.597059	-1.32524	0.185091	0.59423	chr14	71102312	71102533	0 NA	intron (NAluJb SIN	194963 NM_00130E	22990 Hs. 44655E	NM_01498E	ENSG00000PCNX1	PCNX PCN	pecanex I protein-coding	
chr1-123E	10.42408	-0.8195	0.620232	-1.32127	0.18641	0.59423	chr1	1.24E+08	1.24E+08	0 NA	IntergeniALR/Alphe	2451193 NR_00395E	647121 Hs. 69768E	NR_00395E	ENSG00000EMB1	-	embigin pset pseudo	
chr9-127J	10.42408	-0.8195	0.620232	-1.32127	0.18641	0.59423	chr9	1.28E+08	1.28E+08	0 NA	3' UTR (N3' UTR (N	3953 NM_001261	1025 Hs. 15042E	NM_001261	ENSG00000CDK9	C-2K CDC	cyclin d protein-coding	
chr5-483E	10.45106	-0.81911	0.620262	-1.31983	0.186892	0.59423	chr5	48364399	48365273	0 NA	IntergeniALR/Alphe	207645E NM_19844E	133418 Hs. 561411NM_19844E	ENSG00000EMB	GP70	embigin protein-coding		
chr1-154J	10.43647	-0.81752	0.620088	-1.31839	0.187372	0.59423	chr1	1.54E+08	1.54E+08	0 NA	3' UTR (N3' UTR (N	-10195 NM_00115E	91181 Hs. 67639E	NR_20730E	ENSG00000NUP210L	-	nucleopor protein-coding	
chr1-157J	10.43647	-0.81752	0.620088	-1.31839	0.187372	0.59423	chr1	1.57E+08	1.57E+08	0 NA	TTS (NM_CTS (NM_C	4574 NR_00156C	360155 Hs. 49180E	NR_00156C	ENSG00000CYCSP52	HC6 HCP2	CYCS	pset pseudo
chr12-56E	10.43647	-0.81752	0.620088	-1.31839	0.187372	0.59423	chr12	56637816	56645633	0 NA	intron (NAluSc8 SI	2030 NR_00304E	692090 Hs. 67513E	NR_00304E	SNORD59B	U59B	small nucsnoRNA	
chr12-11J	10.43647	-0.81752	0.620088	-1.31839	0.187372	0.59423	chr12	1.12E+08	1.12E+08	0 NA	intron (Nintron (N	3138 NM_00132C	6128 Hs. 52866E	NM_00097C	ENSG00000RPL6	L6 SHUJUN	ribosomal protein-coding	
chr1-156J	10.42187	-0.81592	0.620997	-1.31389	0.188883	0.59423	chr1	10760 NM_001271	4209 Hs. 314327	0 NA	intron (Nintron (N	10760 NM_001271	4209 Hs. 314327	NR_00592C	ENSG00000MRF2D	-	myocyte protein-coding	
chr1-201E	10.42187	-0.81592	0.620997	-1.31389	0.188883	0.59423	chr1	2.02E+08	2.02E+08	0 NA	intron (Nintron (N	-7253 NR_106797	1.02E+08	NR_106797	ENSG00000MIR6739	hsa-mir-610	microRNA ncRNA	
chr1-224E	10.42187	-0.81592	0.620997	-1.31389	0.188883	0.59423	chr1	2.24E+08	2.24E+08	0 NA	intron (NLMIB8 LIN	7681 NR_03989E	1.01E+08	NR_03989E	ENSG00000MIR4742	mir-4742	microRNA ncRNA	
chr10-91E	10.3949	-0.81629	0.623518	-1.30917	0.190477	0.59423	chr10	91628713	91632250	0 NA	exon (NM exon (NM	2590 NM_00539E	5507 Hs. 30309E	NM_00539E	ENSG00000PPP1R3C	PPP1R5 P	PI protein-coding	
chr19-25J	17.6138	-0.48571	0.371255	-1.30829	0.190776	0.59423	chr19	25108820	25109029	0 NA	IntergeniALR/Alphe	-94547 NR_00360E	1E+08	Hs. 14931E	NR_00360E	ENSG00000HAVCR1P1	-	hepatitis pseudo
chr1-233E	14.86075	-0.56514	0.433037	-1.30506	0.191873													

chr1-3517.9.396197	-0.87097	0.683348	-1.27456	0.202465	0.59423	chr1	35175358	35191998	+	NA	3' UTR (N3' UTR (N	9467 NR_136703	6421 Hs. 355934NM_005066	ENSG000003FPQ	POMP100 F	splicing protein-coding
chr1-2582.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	25825373	25834614	+	NA	intron (Nintron (N	-6387 NR_024498	646471 Hs. 727271NR_024498	LOC646471	-	uncharactercncRNA
chr1-2688.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	26832566	26836498	+	NA	intron (NL2c LINE	7844 NM_032288	84243 Hs. 523731CNM_032288	ENSG000003ZDHC18	DHHC-18 Z	inc zinc fingprotein-coding
chr1-4368.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	43689254	43705141	+	NA	intron (NL2a LINE	10144 NR_033827	1E+08 Hs. 655566NR_033827	KDMA4-AS1-	KDMA4	antncRNA
chr1-8421.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	84218796	84219642	+	NA	intron (NLIM4A LI	37587 NR_001242	5567 Hs. 487326NM_002731	ENSG000003PRKACB	PKA C-beta	protein-coding
chr1-9458.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	94531025	94533508	+	NA	intron (Nintron (N	9493 NM_001995	2152 Hs. 62192 NM_001995	ENSG000003CF3	CD142 TF	coagulatiprotein-coding
chr1-1548.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	1.55E+08	1.55E+08	+	NA	intron (Nintron (N	14515 NM_001193	103 Hs. 12341 NM_001111	ENSG000003ADAR	ADAR1 AGS	adenosineprotein-coding
chr1-1627.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	1.63E+08	1.63E+08	+	NA	intron (Nintron (N	-20436 NM_001304	51478 Hs. 492926NM_016371	ENSG000003HSD17B7	PRAP SDR	hydroxystprotein-coding
chr1-1688.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	1.68E+08	1.68E+08	+	NA	intron (Nintron (N	66479 NM_001267	23432 Hs. 27180NM_007366	ENSG000003GPR161	RE2	G proteirprotein-coding
chr1-1808.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	1.8E+08	1.8E+08	+	NA	intron (NAluSx LIN	-78877 NM_001004	5768 Hs. 719176NM_002826	ENSG000003QSOX1	Q6 QSCN6	quiescin protein-coding
chr1-2226.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr1	2.23E+08	2.23E+08	+	NA	intron (NLIMEg LI	12480 NM_001300	375056 Hs. 118474NM_198551	ENSG000003MIA3	ARNT D32	MIA SH3 cprotein-coding
chr10-378.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr10	37951752	37957700	+	NA	intron (Nintron (N	21254 NR_138066	219749 Hs. 499425NM_145011	ENSG000003ZNF25	KOX19 Zfz	inc zinc fingprotein-coding
chr11-868.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr11	8683320	8686973	+	NA	promoter-promoter-	-293 NR_002977	677826 Hs. 745552NR_002977	ENSG000003SNORA3B	AC3-2 S	small nucsnoRNA
chr11-647.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr11	64761282	64777349	+	NA	exon (NM exon (NM	8446 NM_001178	7536 Hs. 502825NM_004632	ENSG000003SF1	BBP D115	splice protein-coding
chr12-104.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr12	1.04E+08	1.04E+08	+	NA	intron (Nintron (N	43389 NM_001008	493861 Hs. 659857NM_001008	ENSG000003EID3	NS4EB NSE	EP300 intrprotein-coding
chr12-108.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr12	1.09E+08	1.09E+08	+	NA	intron (Nintron (N	5632 NM_00132C	23479 Hs. 615131NM_014301	ENSG000003ISCU	CCD120 H4C	coiled-cpseuso
chr17-203.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr17	20304462	20308143	+	NA	intron (NLIMed LI	-14872 NR_023380	348254 Hs. 462477NR_023380	CCDC144CC	CCDC144C	coiled-cpseuso
chr17-395.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr17	39983756	39999726	+	NA	intron (Nintron (N	10934 NM_002808	5709 Hs. 12970 NM_002808	ENSG000003PSMD3	P58 RPN3	proteasoneprotein-coding
chr2-952.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr2	95209551	95217792	+	NA	IntergeniIntergeni	47862 NM_001282	7549 Hs. 590916NM_021088	ENSG000003ZNF2	A1-5 ZNF2	inc zinc fingprotein-coding
chr20-388.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr20	3854181	3867260	+	NA	intron (NAluSg SI	13886 NR_037921	57506 Hs. 570362NM_020746	ENSG000003MAVS	CARDIF I	mitochondncprotein-coding
chr20-538.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr20	53564468	53578060	+	NA	intron (NAluSg SI	11833 NM_006526	7764 Hs. 15504CNM_006526	ENSG000003ZNF217	ZABCI	inc zinc fingprotein-coding
chr3-2728.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr3	27298436	27301464	+	NA	intron (NTHE1B-int	69433 NM_199347	152110 Hs. 506115NM_152534	ENSG000003NEK10	-	NIMA releprotein-coding
chr3-7572.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr3	75728666	75729659	+	NA	TTS (NM_C	-9118 NR_036235	1E+08 NR_036235	ENSG000003MIR4273	-	microRNA ncRNA
chr4-868.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr4	8683320	8686973	+	NA	intron (Nintron (N	-77884 NM_005958	4543 Hs. 243467NM_005958	ENSG000003MTNR1A	MEL-1A-R	melatoninprotein-coding
chr8-1318.8.924921	-0.90496	0.710032	-1.27454	0.202474	0.59423	chr8	13109183	13114847	+	NA	intron (NAluJo SI	4229 NM_001164	10395 Hs. 134296NM_006094	ENSG000003DLC1	ARHGAP7 F	DLC1 Rho protein-coding
chr1-2478.8.426673	-0.94397	0.740975	-1.27395	0.202679	0.59423	chr1	2.47E+08	2.47E+08	+	NA	exon (NM exon (NM	-30076 NM_020394	57116 Hs. 669895NM_020394	ENSG000003ZNF695	SBZF3	inc zinc fingprotein-coding
chr12-121.8.426673	-0.94397	0.740975	-1.27395	0.202679	0.59423	chr12	1.21E+08	1.21E+08	+	NA	intron (Nintron (N	21061 NM_001217	10645 Hs. 297345NM_006546	ENSG000003CAMK2C	CAMK2C CAM	calcium/cprotein-coding
chr13-102.8.426673	-0.94397	0.740975	-1.27395	0.202679	0.59423	chr13	1.03E+08	1.03E+08	+	NA	intron (Nintron (N	32987 NR_160411	7174 Hs. 432424NM_003291	ENSG000003TPP2	TPP-2 TPF	tripepticprotein-coding
chr2-2737.8.426673	-0.94397	0.740975	-1.27395	0.202679	0.59423	chr2	27373107	27378983	+	NA	intron (Nintron (N	4399 NM_001201	130557 Hs. 515872NM_144631	ENSG000003ZNF513	HMFT0656 z	inc zinc fingprotein-coding
chr3-5322.8.426673	-0.94397	0.740975	-1.27395	0.202679	0.59423	chr3	53221251	53242314	+	NA	intron (Nintron (N	24240 NM_001064	7086 Hs. 89643NM_001064	ENSG000003TKF	HEL-S-48	transketprotein-coding
chr17-241.12.14705	-0.67978	0.533704	-1.2737	0.202768	0.59423	chr17	24188150	24188723	+	NA	IntergeniALR/Alphe	1665325 NM_00119C	1E+08 Hs. 740188NM_00119C	ENSG000003MTRNR2L1	HNI	MT-RNR2 lprotein-coding
chr10-126.8.42888	-0.94915	0.745867	-1.27255	0.203177	0.59423	chr10	1.27E+08	1.27E+08	+	NA	intron (NLA_A_Mam	80136 NM_00129C	1793 Hs. 159193NM_00138C	ENSG000003DOCK1	DOCK1 D	cdedicatorprotein-coding
chr6-1315.8.42888	-0.94915	0.745867	-1.27255	0.203177	0.59423	chr6	1.32E+08	1.32E+08	+	NA	3' UTR (N3' UTR (N	2485 NM_001901	1490 Hs. 410037NM_001901	ENSG000003CCN2	CTGF HCS2	cellular protein-coding
chr14-218.8.453646	-0.94325	0.742068	-1.27111	0.20369	0.59423	chr14	21387433	21387632	+	NA	intron (NAluSp SI	-3513 NM_007192	11198 Hs. 213724NM_007192	ENSG000003SPT16H	CDC68 FAC	SPT16 honprotein-coding
chr2-9228.8.453646	-0.94325	0.742068	-1.27111	0.20369	0.59423	chr2	92296775	92297631	+	NA	IntergeniALR/Alphe	356070 NR_027714	440888 Hs. 730233NM_001032412	ACTR3BP2	FKSG73	ACTR3B psseudo
chr4-3868.8.453646	-0.94325	0.742068	-1.27111	0.20369	0.59423	chr4	38681032	38683025	+	NA	intron (Nintron (N	-17400 NR_026804	79667 Hs. 29275 NM_024614	ENSG000003KLF3-AS1	-	KLF3 antncRNA
chr1-1567.8.951894	-0.90433	0.711453	-1.27111	0.203693	0.59423	chr1	1.57E+08	1.57E+08	+	NA	intron (NAluSq2 SI	22838 NM_005975	5546 Hs. 516944NM_005975	ENSG000003PRCC	RCCP1 TPF	proline rprotein-coding
chr14-321.8.951894	-0.90433	0.711453	-1.27111	0.203693	0.59423	chr14	32153786	32157830	+	NA	3' UTR (N3' UTR (N	-46237 NR_004394	26827 NR_004394	ENSG000003RNU6-1	RNU6 RNU6A,	U6 ssnRNA
chr9-1104.8.951894	-0.90433	0.711453	-1.27111	0.203693	0.59423	chr9	1.1E+08	1.1E+08	+	NA	intron (Nintron (N	-77303 NR_00128E	255220 Hs. 147064NM_001003	ENSG000003TXND8	SRP18-3 S	thioredoxprotein-coding
chr9-1218.8.951894	-0.90433	0.711453	-1.27111	0.203693	0.59423	chr9	1.21E+08	1.21E+08	+	NA	intron (Nintron (N	6038 NM_000177	2934 Hs. 522377NM_000177	ENSG000003CGSN	ADF AGEL	gelsolin protein-coding
chr1-6655.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr1	66534475	66542547	+	NA	intron (Nintron (N	4358 NM_032291	84251 Hs. 132121NM_032291	ENSG000003SGIP1	-	SH3 domaiprotein-coding
chr1-1537.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr1	1.54E+08	1.54E+08	+	NA	intron (Nintron (N	-14752 NR_145826	11000 Hs. 438725NM_02433C	ENSG000003SLC27A3	ACSVL3 F	soluble cprotein-coding
chr1-1568.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr1	1.57E+08	1.57E+08	+	NA	intron (Nintron (N	-48503 NR_030527	768220 NR_030527	ENSG000003MIR765	MIRN765 f	microRNA ncRNA
chr1-2057.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr1	2.06E+08	2.06E+08	+	NA	intron (Nintron (N	17250 NM_173854	254428 Hs. 20274 NM_173854	ENSG000003SLC41A1	MgIE	soluble cprotein-coding
chr1-2112.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr1	2.11E+08	2.11E+08	+	NA	intron (Nintron (N	-30312 NM_004615	7188 Hs. 52393CNM_004615	ENSG000003TRAF5	MGC-3978C	TNF receprotein-coding
chr1-2156.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr1	2.16E+08	2.16E+08	+	NA	intron (NL2c LINE	41996 NM_016121	51133 Hs. 335133NM_016121	ENSG000003CKTD3	NY-REN-4	potassiumprotein-coding
chr11-351.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr11	35176062	35190687	+	NA	intron (Nintron (N	20424 NR_145794	1E+08 NR_145794	SNORD164	-	small nucsnoRNA
chr18-938.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr18	9388544	9392364	+	NA	intron (NAluY SINE	55681 NR_020648	57045 Hs. 514688NM_020648	ENSG000003TWSG1	TSG	twisted protein-coding
chr19-488.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr19	48904183	48919917	+	NA	intron (NAluJr SI	6841 NR_046633	1E+08 Hs. 569933NR_046633	ENSG000003NUCB1-AS1	-	NUCB1 antncRNA
chr2-1115.8.439055	-0.94105	0.740954	-1.27006	0.204065	0.59423	chr2	11195171	11203140	+	NA	intron (NAluSz SI	43688 NR_104231	130814 Hs. 274415NM_152391	ENSG000003SLC66A3	C2orf22 F	soluble cprotein-coding
chr2-3928.8.439055	-0.94105	0.740954	-1													



chr15-851	10.16643	-0.75691	0.634085	-1.1937	0.232596	0.59423	chr15	85190784	85194205	+	O	NA	IntergeniMamGypLTF	42287	NR_158175	1.02E+08	Hs.68166E	NR_158179	LOC101925	-	golgin A2pseudo
chr1-1384	10.13946	-0.75728	0.634401	-1.1937	0.232596	0.59423	chr1	1384692	1398441	+	O	NA	TTS (NM_C	6776	NR_00135C	81669	Hs.515704	NR_030937	ENS00000CCNL2	ANIA-6B	Cyclin L2protein-coding
chr1-1205	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr1	1.21E+08	1.21E+08	+	O	NA	non-codiron-codir	-109016	NR_003242	767846	Hs.65718E	NR_003242	ENS00000PFN1P2	C1orf152	profilin pseudo
chr1-149C	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr1	1.49E+08	1.49E+08	+	O	NA	intron (N	8211	NR_001037	400818	Hs.44508C	NR_001037	ENS00000BNBP9	AEO1	NBPF memtprotein-coding
chr11-965	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr11	9694034	9696150	+	O	NA	intron (N	31015	NR_001297	23075	Hs.15302E	NR_01505E	ENS00000SWAP70	HSPC321	switchingprotein-coding
chr16-56E	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr16	56933289	56945498	+	O	NA	intron (N	7251	NR_01468E	9709	Hs.14639E	NR_01468E	ENS00000CHERPUD1	HERP	Mif1homocysteprotein-coding
chr17-16C	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr17	1669801	1683784	+	O	NA	intron (N	8075	NR_00644E	10594	Hs.18136E	NR_00644E	ENS00000PRPF8	HPRP8	PRF pre-mRNA protein-coding
chr19-93C	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr19	9335224	9345573	+	O	NA	intron (N	15703	NR_001202	1.01E+08	Hs.728944	NR_00117E	ENS00000ZNF559-5A	-	ZNF559-5A protein-coding
chr2-3874	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr2	38744530	38750440	+	O	NA	intron (N	3876	NR_001031	6432	Hs.30909C	NR_00627E	ENS00000SRSP7	9G8	AAG3 serine arprotein-coding
chr20-35T	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr20	35700208	35740984	+	O	NA	intron (N	21191	NR_008074E	140823	Hs.472564	NR_008074E	ENS00000ROMO1	hso0rf52	reactive protein-coding
chr3-1295	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr3	1.29E+08	1.29E+08	+	O	NA	intron (N	-7612	NR_106884	1.02E+08	NR_106884	ENS00000MIR6826	hsa-mir-6	microRNA ncRNA	
chr3-1571	10.15184	-0.75522	0.634271	-1.19069	0.233777	0.59423	chr3	1.57E+08	1.57E+08	+	O	NA	intron (N	8165	NR_00130E	57018	Hs.4859	NR_020307	ENS00000CCNL1	ANIA6A	B cyclin L1protein-coding
chr19-521	12.37968	-0.61699	0.520587	-1.18518	0.235948	0.59423	chr19	52031860	52047999	+	O	NA	intron (N	8632	NR_00132E	9668	Hs.655934	NR_01465C	ENS00000ZNF432	-	zinc fingprotein-coding
chr19-29C	10.13725	-0.75351	0.636053	-1.18466	0.23615	0.59423	chr19	29144007	2918752	+	O	NA	intron (N	9471	NR_00131E	126295	Hs.59137E	NR_17348C	ENS00000ZNF57	ZNF424	zinc fingprotein-coding
chr6-4424	10.13725	-0.75351	0.636053	-1.18466	0.23615	0.59423	chr6	44248009	44256614	+	O	NA	intron (N	1974	NR_03979C	1.01E+08	NR_03979C	ENS00000MIR4647	mir-4647	microRNA ncRNA	
chr20-392	10.16423	-0.75312	0.636289	-1.18362	0.236655	0.59423	chr20	3920258	3920859	+	O	NA	intron (N	-2995	NR_03172E	1E+08	NR_03172E	ENS00000MIR103B2	MIR103-2	microRNA ncRNA	
chr19-707	12.36509	-0.61588	0.520776	-1.18263	0.236956	0.59423	chr19	7070639	7092325	+	O	NA	intron (N	11779	NR_001044	79230	Hs.59138C	NR_024341	ENS00000ZNF557	-	zinc fingprotein-coding
chr19-44C	12.36509	-0.61588	0.520776	-1.18263	0.236956	0.59423	chr19	44026622	44035356	+	O	NA	intron (N	4700	NR_00112E	7673	Hs.27984C	NR_01336C	ENS00000PRPF22	-	zinc fingprotein-coding
chr1-185E	9.668186	-0.78227	0.663879	-1.17833	0.238665	0.59423	chr1	1.85E+08	1.85E+08	+	O	NA	intron (N	66062	NR_01767E	54823	Hs.13418E	NR_01767E	ENS00000SWT1	C1orf26	SWT1 RNA protein-coding
chr1-150E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	1.46E+08	1.46E+08	+	O	NA	intron (N	10279	NR_00130E	10623	Hs.51576E	NR_00646E	ENS00000POLR3C	RPC3	RPC RNA polynprotein-coding
chr1-145C	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	1.5E+08	1.5E+08	+	O	NA	intron (N	19194	NR_00469E	9129	Hs.11776	NR_00469E	ENS00000PRPF3	HPRP3	PRF pre-mRNA protein-coding
chr1-151E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	1.51E+08	1.51E+08	+	O	NA	intron (N	27453	NR_00113E	8394	Hs.655131	NR_003557	ENS00000PIP5K1A	-	phosphatiprotein-coding
chr1-153E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	1.54E+08	1.54E+08	+	O	NA	intron (N	2892	NR_00103C	6232	Hs.546291	NR_00103C	ENS00000RPS27	DBA17	MPS ribosomalprotein-coding
chr1-156E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	1.56E+08	1.56E+08	+	O	NA	exon (NM	16969	NR_015327	23381	Hs.516837	NR_015327	ENS00000SMG5	EST1B	LPTSMG5 nonsprotein-coding
chr1-171E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	1.72E+08	1.72E+08	+	O	NA	intron (N	52832	NR_01517E	23215	Hs.494614	NR_01517E	ENS00000PRRC2C	BAT2	iso proline rprotein-coding
chr1-203E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr1	2.04E+08	2.04E+08	+	O	NA	intron (N	-28951	NR_003094	6635	Hs.33461E	NR_003094	ENS00000SNRPE	HYPT11	S small nucprotein-coding
chr10-37E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr10	37827040	37838741	+	O	NA	exon (NM	24720	NR_14799E	57209	Hs.52842E	NR_02104E	ENS00000ZNF248	BAI62G10	zinc fingprotein-coding
chr11-18E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr11	18394728	18408903	+	O	NA	intron (N	5549	NR_00116E	3939	Hs.2795	NR_00556E	ENS00000LDHA	GSD11	HEL lactate cprotein-coding
chr14-102	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr14	1.03E+08	1.03E+08	+	O	NA	intron (N	67247	NR_003094E	81693	Hs.534494	NR_03094E	ENS00000AMN	PRU1028	epsilon amino asnoRNA
chr19-39C	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr19	3972125	3985074	+	O	NA	intron (N	3973	NR_00260E	26812	NR_00260E	ENS00000SNORD37	RNU37	U37 small nucsoRNA	
chr19-21E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr19	21806262	21822540	+	O	NA	intron (N	21781	NR_00342E	7594	Hs.53436E	NR_00342E	ENS00000ZNF43	HTF6	KOX2 zinc fingprotein-coding
chr19-37E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr19	37372264	37390523	+	O	NA	intron (N	10294	NR_003245E	84503	Hs.59094C	NR_003245E	ENS00000ZNF527	-	zinc fingprotein-coding
chr19-38E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr19	38834494	38848755	+	O	NA	intron (N	38834	NR_00153E	3191	Hs.64490E	NR_00153E	ENS00000HNRNPL	HNRNPL	P C heterogprotein-coding
chr2-4634	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr2	46346469	46363407	+	O	NA	intron (N	39229	NR_14699E	1.05E+08	Hs.57016E	NR_14699E	ENS00000LINC0182C	-	long intencRNA
chr2-197E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr2	1.97E+08	1.97E+08	+	O	NA	intron (N	30195	NR_00130E	23451	Hs.632554	NR_01243E	ENS00000SF3B1	Hsh155	ML splicing protein-coding
chr3-184E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr3	1.84E+08	1.84E+08	+	O	NA	intron (N	-4824	NR_001351	55324	Hs.36132E	NR_01835E	ENS00000ABCFC3	EST201864	ATP bindi protein-coding
chr3-184E	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr3	1.84E+08	1.84E+08	+	O	NA	intron (N	4708	NR_00127E	5708	Hs.518464	NR_00280E	ENS00000PSMD2	P97	RPN1 proteasonprotein-coding
chr6-2744	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr6	27449514	27467764	+	O	NA	intron (N	14259	NR_00131E	7738	Hs.158174	NR_00714E	ENS00000ZNF184	kr-ZNF3	zinc fingprotein-coding
chr6-1324	9.653595	-0.78043	0.663149	-1.17685	0.239254	0.59423	chr6	1.32E+08	1.32E+08	+	O	NA	intron (N	50323	NR_00132E	8417	Hs.59314E	NR_00356E	ENS00000STX7	RNU37	U37 small nucsoRNA
chr22-411	9.62883	-0.78506	0.668442	-1.17446	0.240211	0.59423	chr22	41176917	41178904	+	O	NA	exon (NM	19591	NR_110514	1.02E+08	Hs.517517	NR_110514	EP300-AS1	EP300	antcRNA
chr9-436E	20.03271	-0.39356	0.335505	-1.17304	0.240782	0.59423	chr9	43680400	43680705	+	O	NA	IntergeniALR/Alphe	554836	NR_16066E	1.03E+08	NR_160669	LOC102724	-	methylenepseudo	
chr1-191E	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr1	19181106	19202358	+	O	NA	intron (N	18534	NR_02076E	23352	Hs.14807E	NR_02076E	ENS00000UBR4	RBAF600	Zubiquitin rprotein-coding
chr1-2374	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr1	23749471	23761248	+	O	NA	intron (N	11993	NR_00319E	6924	Hs.15535	NR_00319E	ENS00000CELOA	SIII	SIII elongin rprotein-coding
chr14-23C	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr14	23058834	23069507	+	O	NA	exon (NM	-6632	NR_14498E	64403	Hs.15591E	NR_02247E	ENS00000CDH24	CDH11L	cadherin protein-coding
chr16-89E	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr16	89219061	89236208	+	O	NA	exon (NM	9931	NR_001201	197320	Hs.64738E	NR_182531	ENS00000ZNF778	-	zinc fingprotein-coding
chr17-80E	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr17	80287439	80314267	+	O	NA	intron (N	40001	NR_020954	57674	Hs.19564E	NR_020914	ENS00000RNF213	ALO17	C17 ring fingprotein-coding
chr19-29E	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr19	2929643	2940788	+	O	NA	intron (N	9756	NR_002121E	58492	Hs.38004	NR_002121E	ENS00000ZNF77	pT1	zinc fingprotein-coding
chr22-39E	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr22	39310458	39319007	+	O	NA	promoter-promoter-	578	NR_000027	116937	NR_000027	ENS00000SNORD83A	RNU83A	U8 small nucsoRNA	
chr5-476E	9.639005	-0.77859	0.664222	-1.17218	0.241124	0.59423	chr5	47626449	47627365	+	O	NA	IntergeniALR/Alphe	-1930527	NR_02107E	348980	Hs.35317E	NR_02107E	ENS00000HCN1	BCNG-1	BC hyperpol protein-coding
chr1-587E	9.665978	-0.77814	0.664282	-1.17141	0.241436	0.59423	chr1	58781060	58782790	+	O	NA	3' UTR (N	2122	NR_00222E	3725	Hs.696684	NR_00222E	ENS00000JUN	AP-1	AP1 Jun protcprotein-coding
chr2-465E	9.665978	-0.77814	0.664282	-1.17141	0.241436	0.59423	chr2	46576755	46577164	+	O	NA	intron (N	3279	NR_10418E	1.01E+08					

chr2-1891	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr2	1.89E+08	1.89E+08	0	NA	intron (Nintron (N	23305 NR_036076	1E+08	NR_036076	ENS00000C	MIR3129	mir-3129	microRNA	ncRNA	
chr2-2312	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr2	2.31E+08	2.31E+08	0	NA	intron (Nintron (N	36985 NM_001291	80210 Hs. 162411	NR_025136	ENS00000C	ARMC9	ARM JBT5	armadillo protein-coding		
chr22-302	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr22	30240178	30246086	0	NA	3' UTR (N3' UTR (N	-3078 NR_148946	91370 Hs. 658999	NR_052856	ENS00000C	LOC91370	-	uncharacterized	ncRNA	
chr22-352	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr22	35286444	35290946	0	NA	intron (Nintron (N	-10580 NM_001136	10043 Hs. 47470E	NR_005488	ENS00000C	TGM1	-	target of protein-coding		
chr3-1723	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr3	1.72E+08	1.72E+08	0	NA	intron (Nintron (N	68626 NM_001136	2693 Hs. 13021E	NR_004122	ENS00000C	GHSR	GHPD	growth h protein-coding		
chr5-347E	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr5	34795751	34806432	0	NA	intron (Nintron (N	-38073 NM_14472E	153657 Hs. 435742	NR_14472E	ENS00000C	TTC23L	MC25-1	tetratric protein-coding		
chr7-138E	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr7	1.39E+08	1.39E+08	0	NA	intron (Nintron (N	95123 NM_01590E	8805 Hs. 490287	NR_00385E	ENS00000C	TRIM24	PTC6 RNFE	tripartite protein-coding		
chr8-306E	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr8	30690500	30693205	0	NA	intron (NAluJb SIN	33666 NM_00209E	2961 Hs. 77100	NR_00209E	ENS00000C	GTF2E2	FE TFE2E	general protein-coding		
chr8-1177	8.65489	-0.83558	0.724076	-1.15399	0.248504	0.59423	chr8	1.18E+08	1.18E+08	0	NA	intron (Ntigger3a	118349 NR_14579E	1.1E+08	NR_14579E	SNORD168	-	small nucsnoRNA			
chr1-155E	8.156642	-0.87115	0.754963	-1.15399	0.248543	0.59423	chr1	1.56E+08	1.56E+08	0	NA	exon (NM exon (NM	21842 NM_15228E	23208 Hs. 32984	NR_15228E	ENS00000C	SYT11	SYT12 syt	synaptotagmin protein-coding		
chr1-2064	8.156642	-0.87115	0.754963	-1.15399	0.248543	0.59423	chr1	2.06E+08	2.06E+08	0	NA	intron (NAluJo SIN	9641 Hs. 32104E	NR_01400E	ENS00000C	IKKBE	IKK-E IKK	inhibitor protein-coding			
chr10-294	8.156642	-0.87115	0.754963	-1.15399	0.248543	0.59423	chr10	29468948	29470746	0	NA	TTS (NR_1TTS (NR_1	59604 NR_11092E	1.03E+08	NR_00393C	ENS00000C	SVIL-AS1	-	SVIL anticRNA		
chr10-10E	8.156642	-0.87115	0.754963	-1.15399	0.248543	0.59423	chr10	1.02E+08	1.02E+08	0	NA	intron (NMER102a I	17634 NM_00573E	10121 Hs. 153961	NR_00573E	ENS00000C	ACTRIA	ARPI Arp	actin rel protein-coding		
chr13-11C	8.156642	-0.87115	0.754963	-1.15399	0.248543	0.59423	chr13	1.1E+08	1.1E+08	0	NA	intron (Nintron (N	31312 NM_00126E	1E+08	NR_00403E	ENS00000C	COL4A2-AS-	-	COL4A2 as protein-coding		
chr19-447	8.156642	-0.87115	0.754963	-1.15399	0.248543	0.59423	chr19	44749896	44752989	0	NA	intron (Nintron (N	2734 NM_00517E	602 Hs. 31210	NR_00517E	ENS00000C	BCL3	BCL4 D19E	BCL3 trar protein-coding		
chr16-667	8.609824	-0.77479	0.671991	-1.15297	0.248923	0.59423	chr16	66739779	66740001	0	NA	intron (Nintron (N	11719 NM_00614E	1783 Hs. 36906E	NR_00614E	ENS00000C	DYNC1L12	DNCL12 Lly	dnein cy protein-coding		
chr20-19E	8.144259	-0.8742	0.75882	-1.15205	0.249302	0.59423	chr20	19819067	19819426	0	NA	IntergenimLTI1A LTF	-67275 NM_00124E	54453 Hs. 47227	NR_01899E	ENS00000C	CRIN2	MACS RASS	Ras and F protein-coding		
chr1-198	8.138549	-0.80215	0.69636	-1.15193	0.249352	0.59423	chr1	1.99E+08	1.99E+08	0	NA	intron (Nintron (N	38283 NR_04007E	1E+08	NR_11077	NR_04007E	MIR181A1E	-	MIR181A1	ncRNA	
chr4-8281	9.138549	-0.80215	0.69636	-1.15193	0.249352	0.59423	chr4	82817126	82833490	0	NA	intron (NL2c LINE	-26451 NM_02490E	79966 Hs. 379191	NR_02490E	ENS00000C	SCD5	ACOD4 FAI	stearoyl- protein-coding		
chr1-150E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr1	1.5E+08	1.5E+08	0	NA	intron (Nintron (N	7743 NM_01899E	54460 Hs. 40588	NR_01899E	ENS00000C	MRPS21	MDSO16 MF	mitochondon protein-coding		
chr1-151E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr1	1.51E+08	1.51E+08	0	NA	intron (Nintron (N	-2356 NR_13197E	1.02E+08	NR_63404E	NR_13197E	GBAT2	-	glioblastncRNA		
chr1-178E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr1	1.79E+08	1.79E+08	0	NA	intron (NL2a LINE	33871 NM_00467E	9068 Hs. 591474	NR_00467E	ENS00000C	ANGPTL1	ANG3 ANG	angiopoie protein-coding		
chr10-587	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr10	5876109	5888211	0	NA	intron (Nintron (N	-7412 NM_00125E	84893 Hs. 49854E	NR_03280E	ENS00000C	FBH1	FBXO18 Ft	F-box DN protein-coding		
chr11-151E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr11	72227101	72238527	0	NA	intron (Nintron (N	8047 NM_00156E	3636 Hs. 52387E	NR_00156E	ENS00000C	INPPL1	OPSM SDI	inositol protein-coding		
chr11-12E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr11	1.23E+08	1.23E+08	0	NA	intron (NMLT1F2 LI	-53944 NM_15320E	3312 Hs. 180414	NR_00659E	ENS00000C	HSPA8	HEL-33 Hf	heat shoc protein-coding		
chr12-49C	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr12	49001318	49005815	0	NA	exon (NM exon (NM	-4191 NM_01508E	23109 Hs. 591044	NR_01508E	ENS00000C	DDN	-	dendrin protein-coding		
chr13-30C	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr13	30460445	30462691	0	NA	3' UTR (N3' UTR (N	2759 NM_00131E	3146 Hs. 43410E	NR_00212E	ENS00000C	HMG1B	HMG-1 HMC	high mob protein-coding		
chr16-44E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr16	4468453	4469588	0	NA	intron (Nintron (N	5605 NM_00135E	57407 Hs. 28896E	NR_02067E	ENS00000C	NMRAL1	HSCARG SE	NmrA like protein-coding		
chr17-50C	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr17	50075689	50085524	0	NA	intron (NL2c LINE	-14131 NM_00119E	5164 Hs. 256667	NR_00261E	ENS00000C	PDK2	PDHK2 PDF	pyruvate protein-coding		
chr19-10E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr19	1029787	1038974	0	NA	intron (NCpC	-5723 NR_09191E	10347 Hs. 134514	NR_01911E	ENS00000C	ABC7	ABCA-SSN ATP	bindi protein-coding		
chr2-1331	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr2	1.33E+08	1.33E+08	0	NA	intron (NLIPI LINE	-164770 NR_11029E	1.02E+08	NR_661917	NR_11029E	ENS00000C	NCKAP5-AS-	-	NCKAP5 arncRNA	
chr3-491E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr3	49108066	49118903	0	NA	intron (NAluSc8 SI	7454 NM_00135E	10869 Hs. 25559E	NR_00667E	ENS00000C	USP19	ZMYND9	ubiquitin protein-coding		
chr3-9984	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr3	99847608	99851292	0	NA	exon (NM exon (NM	-25585 NR_11082E	1.02E+08	NR_74161E	NR_11082E	HP09053	-	uncharacterized	ncRNA	
chr4-541E	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr4	5416740	5418635	0	NA	intron (NHALIM8 LI	-106882 NR_12651E	10141 Hs. 17797E	NR_00575E	ENS00000C	LINC01587C	4orf6 aC	long intencRNA		
chr5-1511	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr5	1.51E+08	1.51E+08	0	NA	intron (NMADE1 DN	8808 NM_00119E	309 Hs. 412117	NR_00115E	ENS00000C	ANXA6	ANX6 CBP	annexin A protein-coding		
chr8-1447	8.142051	-0.86884	0.754965	-1.15083	0.249801	0.59423	chr8	1.45E+08	1.45E+08	0	NA	intron (NMLTR14B LI	7993 NM_03058E	80778 Hs. 631854	NR_03058E	ENS00000C	ZNF34	KOX32	zinc fing protein-coding		
chr10-57E	9.165522	-0.80162	0.697026	-1.15006	0.25012	0.59423	chr10	5795457	5797291	0	NA	intron (Nintron (N	17060 NM_00149E	2665 Hs. 29905E	NR_00149E	ENS00000C	CGD12	HEL-S-46E	GDP discs protein-coding		
chr10-93E	9.165522	-0.80162	0.697026	-1.15006	0.25012	0.59423	chr10	93354606	93357032	0	NA	intron (Nintron (N	126515 NM_01345E	26509 Hs. 60208E	NR_01345E	ENS00000C	MYOF	FERIL3	myoferlin protein-coding		
chr1-154	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr1	1.54E+08	1.54E+08	0	NA	intron (Nintron (N	-36904 NR_14785E	1.02E+08	NR_61708E	NR_14785E	ENS00000C	IL6R-AS1	-	IL6R anticRNA	
chr1-1787	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr1	1.79E+08	1.79E+08	0	NA	intron (Ntigger2 I	72493 NM_00467E	9068 Hs. 591474	NR_00467E	ENS00000C	ANGPTL1	ANG3 ANG	angiopoie protein-coding		
chr14-96E	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr14	96258335	96259977	0	NA	intron (NBLACKJACK	2946 NM_00071E	623 Hs. 52557E	NR_00071E	ENS00000C	BDRKB1	B1BRK B1F	bradykinin protein-coding		
chr2-1021	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr2	1.02E+08	1.02E+08	0	NA	intron (Nintron (N	3384 NM_00087E	3554 Hs. 17198E	NR_00087E	ENS00000C	IL1R1	CD121A D2	interleukin protein-coding		
chr3-172E	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr3	1.72E+08	1.72E+08	0	NA	intron (Nintron (N	115626 NM_19840E	2693 Hs. 13021E	NR_00412E	ENS00000C	GHSR	GHPD	growth h protein-coding		
chr5-166E	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr5	1.6665381	1.6669340	0	NA	intron (Nintron (N	-50302 NM_00103E	54463 Hs. 481704	NR_01900E	ENS00000C	RETREG1	FAM134B J	reticuloc protein-coding		
chr8-1334	8.169024	-0.86815	0.75499	-1.14989	0.25019	0.59423	chr8	1.33E+08	1.33E+08	0	NA	intron (Nintron (N	108557 NM_03003E	6482 Hs. 374257	NR_03003E	ENS00000C	ST3GAL1	Gal-Nac6E	ST3 beta protein-coding		
chr1-4054	8.6403	-0.83342	0.725293	-1.14908	0.250522	0.59423	chr1	40544123	40547591	0	NA	intron (Nintron (N	14220 NM_15237E	127396 Hs. 524767	NR_15237E	ENS00000C	ZNF684	AL55 CMT2	SPG11 ves protein-coding		
chr1-150E	8.6403	-0.83342	0.725293	-1.14908	0.250522	0.59423	chr1	1.5E+08	1.5E+08	0	NA	non-codiron-codir	2688 NM_00107E	51107 Hs. 10840E	NR_01602E	ENS00000C	APH1A	6530402N	cap-1 hom protein-coding		
chr1-1537	8.6403	-0.83342	0.725293	-1.14908	0.250522	0.59423	chr1	1.54E+08	1.54E+08	0	NA	intron (Nintron (N	-2509 NR_14582E	11000 Hs. 43872E	NR_02433E	ENS00000C	SLC27A3	ACSVL3 F	solute c protein-coding		
chr14-74E	8.6403	-0.83342	0.725293	-1.14908	0.250522	0.59423	chr14	74887439	74904735	0	NA	intron (NAluJo SIN	14171 NM_00124E	1743 Hs. 52545E	NR_00193E	ENS00000C	DLST	DLTS	dihydrolyl protein-coding		
chr15-60E	8.6403	-0.83342	0.725293	-1.14908	0.250522	0.59423	chr15	60344708	60349745	0	NA	TTS (NM_1TTS (NM_1	50760 NM_00100E	302 Hs. 51160E	NR_00403E	ENS00000C	ANXA2	ANX2 ANX	annexin A protein-coding		
chr15-64E	8.6403	-0.83342	0.725293	-1.14908	0.250522	0.59423	chr15	6413420													





chr2-1632	8.870725	-0.73732	0.708663	-1.04044	0.298136	0.59423	chr2	1632500	1636186	+0.00686	0 NA	intron (Nintron (N	110172	NM_012293	7837	Hs.332197NM_012293	ENSG00000CPXD	ASGD7	COF peroxidase protein-coding	
chr5-1787	8.870725	-0.73732	0.708663	-1.04044	0.298136	0.59423	chr5	1.79E+08	1.79E+08	+0.00000	0 NA	intron (MLT1C LTF	10284	NM_005645	6940	Hs.484324NM_005645	ENSG00000ZNF354A	ENZF	HEL1 zinc finger protein-coding	
chr6-3284	8.870725	-0.73732	0.708663	-1.04044	0.298136	0.59423	chr6	32845261	32851816	+0.00655	0 NA	intron (Nintron (N	-3859	NM_004155	5696	Hs.180062NM_004155	ENSG00000PSMB8	ALDD	D6S2 protease on protein-coding	
chr9-1108	8.870725	-0.73732	0.708663	-1.04044	0.298136	0.59423	chr9	1.11E+08	1.11E+08	+0.00000	0 NA	3' UTR (N3' UTR (N	145968	NM_001366	4593	Hs.521652NM_005592	ENSG00000MUSK	CM59	FADS muscle as protein-coding	
chr4-1028	9.42292	-0.71144	0.685154	-1.03836	0.299102	0.59423	chr4	1.03E+08	1.03E+08	+0.00000	0 NA	promoter-promoter-	-289	NM_001300	7323	Hs.518777NM_00334C	ENSG00000UBE2D3	E2 (17)	K6 ubiquitin protein-coding	
chr2-1195	8.897698	-0.73684	0.709624	-1.03835	0.299109	0.59423	chr2	1.2E+08	1.2E+08	+0.00000	0 NA	intron (Nintron (N	-55836	NR_138472	57669	Hs.369232NM_020909	ENSG00000EPB41L5	BE37	YMO1 erythrocyte protein-coding	
chr1-110	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	1.1E+08	1.1E+08	+0.00000	0 NA	intron (Nintron (N	12532	NM_001242	10768	Hs.743977NM_006621	ENSG00000ACHYL1	DCAL	TRB1 adenosyl protein-coding	
chr1-1557	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	1.56E+08	1.56E+08	+0.00000	0 NA	intron (NAluSx S S	8261	NR_132767	1.07E+08	NR_132767	SCARNA26E	-	small CajncRNA	
chr1-1617	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	1.62E+08	1.62E+08	+0.00000	0 NA	intron (NLM3E3 LI	5874	NM_00724C	11266	Hs.416216NM_00724C	ENSG00000CUSP12	DUSP1	YV dual spec protein-coding	
chr1-168	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	1.68E+08	1.68E+08	+0.00000	0 NA	exon (NM exon (NM	5288	NR_003170Z	1E+08	NR_03170Z	ENSG00000MIR1255B2	MIR1255B	microRNA ncRNA	
chr1-1835	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	1.84E+08	1.84E+08	+0.00000	0 NA	intron (Nintron (N	56216	NM_000433	4688	Hs.587555NM_000433	ENSG00000CNCF2	NCF-2	NO3 neutrophil protein-coding	
chr1-205	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	2.05E+08	2.05E+08	+0.00000	0 NA	intron (Nintron (N	-17431	NM_20337E	388730	Hs.146925NM_20337E	ENSG00000TMEM81	HC3107	KV transmem protein-coding	
chr1-2124	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	2.12E+08	2.12E+08	+0.00000	0 NA	intron (NMER1B DNF	5856	NM_018252	55248	Hs.445386NM_018252	ENSG00000PACC1	Clorf75	Fproton ac protein-coding	
chr1-2226	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	2.23E+08	2.23E+08	+0.00000	0 NA	intron (NMER68 LTF	26110	NM_022831	64853	Hs.156525NM_022831	ENSG00000AIDA	Clorf80	axin inte protein-coding	
chr1-2354	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	2.35E+08	2.35E+08	+0.00000	0 NA	TTS (NM_TTS (NM_)	57256	NM_001277	148789	Hs.498144NM_15249C	ENSG00000B3GALNT2	B3GALNAc-beta-1,3-	protein-coding	
chr1-2468	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr1	2.47E+08	2.47E+08	+0.00000	0 NA	intron (Nintron (N	66502	NR_015422	149134	Hs.720494NM_207326	LINC01341-	-	long intncRNA	
chr10-27	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr10	2.7222837	2.7223345	+0.00507	0 NA	intron (Nintron (N	17395	NM_001301	91452	Hs.530597NM_14569E	ENSG00000ACBD5	-	acyl-CoA protein-coding	
chr10-101	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr10	1.02E+08	1.02E+08	+0.00000	0 NA	intron (NAluS2 S S	17104	NM_01221E	10724	Hs.500842NM_01221E	ENSG00000OGA	MEA5	MGEF0-GlcNAc protein-coding	
chr12-558	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr12	55983644	55995613	+0.01197	0 NA	intron (Nintron (N	-7648	NM_001032	6821	Hs.558403NM_00045E	ENSG00000SUOX	-	sulfite c protein-coding	
chr14-101	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr14	1.02E+08	1.02E+08	+0.00000	0 NA	intron (Nintron (N	53732	NM_00137E	1778	Hs.614088NM_00137E	ENSG00000DYNCH1	CMT20	DHC dynein cy protein-coding	
chr15-428	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr15	42954818	42957900	+0.00308	0 NA	intron (NAluS2 S S	-35581	NM_17350C	146057	Hs.646511NM_17350C	ENSG00000CTBK2	SCA11	TTT tau tubul protein-coding	
chr15-484	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr15	48410082	48413586	+0.00350	0 NA	intron (Nintron (N	79637	NM_00194E	1854	Hs.527988NM_00194E	ENSG00000DUT	dUTPase	deoxyuric protein-coding	
chr15-641	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr15	64154322	64162008	+0.00768	0 NA	TTS (NM_TTS (NM_C	4990	NM_00094Z	5479	Hs.434937NM_00094Z	ENSG00000PPIB	B CYP-S1 peptidyl	protein-coding	
chr16-317	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr16	31752777	31762236	+0.00946	0 NA	intron (NLMC4a LI	44277	NM_00113C	124411	Hs.528825NM_001004	ENSG00000CTFZ20	-	zinc finger protein-coding	
chr17-505	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr17	50380092	50396658	+0.01656	0 NA	intron (NAluJr S N	9148	NM_018505	55379	Hs.370927NM_018505	ENSG00000LRRC59	PRO1855	l leucine r protein-coding	
chr17-59	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr17	59665115	59668253	+0.00314	0 NA	intron (Nintron (N	40915	NM_016077	51651	Hs.126777NM_016077	ENSG00000PTRH2	BIT1	CFAF peptidyl-protein-coding	
chr19-118	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr19	11801483	11808352	+0.00687	0 NA	intron (Nintron (N	6395	NM_15235E	126069	Hs.631634NM_15235E	ENSG00000ZNF491	-	zinc finger protein-coding	
chr2-262	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr2	26207896	26221959	+0.01409	0 NA	intron (Nintron (N	29705	NM_00018Z	3030	Hs.516032NM_00018Z	ENSG00000HADHA	ECHA	GBP hydroxyac protein-coding	
chr2-552	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr2	55233157	55237041	+0.00384	0 NA	TTS (NR_CTTS (NR_C	935	NR_039624	1.01E+08	NR_039624	ENSG00000MIR4426	-	microRNA ncRNA	
chr2-690	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr2	69039861	69045590	+0.00573	0 NA	intron (NL2 LINE L	29581	NM_053034	84168	Hs.165855NM_01815E	ENSG00000ANTXR1	ATR GAPO ANTXR	cel protein-coding	
chr2-691	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr2	69101989	69106720	+0.00483	0 NA	TTS (NR_CTTS (NR_C	672	NR_03607E	1E+08	NR_03607E	ENSG00000MIR3126	mir-3126	microRNA ncRNA	
chr2-86	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr2	1.87E+08	1.87E+08	+0.00000	0 NA	intron (Nintron (N	-24073	NM_177454	165215	Hs.288727NM_177454	ENSG00000PAM171B	KIAA1946	family w protein-coding	
chr20-621	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr20	62135401	62141226	+0.00582	0 NA	intron (Nintron (N	5081	NM_00279Z	5688	Hs.182395NM_00279Z	ENSG00000PSMA7	-	S-proteasone protein-coding	
chr22-378	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr22	37862451	37867847	+0.00539	0 NA	intron (NAluJo S N	15730	NM_016091	51386	Hs.446852NM_016091	ENSG00000EIF3L	EIF3E1P	l eukaryoti protein-coding	
chr3-1017	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr3	1.02E+08	1.02E+08	+0.00000	0 NA	intron (NLM3B LIN	7632	NM_00134E	91775	Hs.595959NM_145037	ENSG00000NXPE3	FAM55C	MC neurexophil protein-coding	
chr4-7528	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr4	75282	88293	+0.00111	0 NA	intron (NLM3B2 LIN	28466	NM_182524	152687	Hs.709466NM_182524	ENSG00000ZNF595	-	zinc finger protein-coding	
chr4-186	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr4	1.87E+08	1.87E+08	+0.00000	0 NA	exon (NM exon (NM	-63302	NM_00595E	4543	Hs.243467NM_00595E	ENSG00000MTNR1A	MEL-1A-R	melatonin protein-coding	
chr5-179	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr5	1.8E+08	1.8E+08	+0.00000	0 NA	intron (Nintron (N	1277	NM_001364	3187	Hs.604001NM_00552C	ENSG00000HNRNPH1	HNRPH	HNF heteroge protein-coding	
chr7-649	8.883108	-0.73473	0.708618	-1.03685	0.299807	0.59423	chr7	64978144	64993326	+0.01512	0 NA	intron (NAluSx3 S S	5301	NM_015852	51351	Hs.250593NM_015852	ENSG00000ZNF117	-	HLN HPF zinc finger protein-coding	
chr1-1931	9.32741	-0.71076	0.686088	-1.03596	0.300221	0.59423	chr1	1.93E+08	1.93E+08	+0.00000	0 NA	intron (Nintron (N	3853	NM_02452E	79577	Hs.378999NM_02452E	ENSG00000CDC73	Clorf28	Fcell divi protein-coding	
chr11-65	8.856135	-0.73521	0.709887	-1.03568	0.300354	0.59423	chr11	65337898	65353703	+0.01581	0 NA	exon (NM exon (NM	-8951	NM_14571E	220359	Hs.632121NM_14571E	ENSG00000TIGD3	-	tigger t protein-coding	
chr16-22	8.856135	-0.73521	0.709887	-1.03568	0.300354	0.59423	chr16	2252801	2266480	+0.01479	0 NA	intron (NAluY S INE	7697	NM_00128E	10921	Hs.555642NM_006711	ENSG00000CRNP51	E5.1	RNA bindi protein-coding	
chr19-147	8.856135	-0.73521	0.709887	-1.03568	0.300354	0.59423	chr19	14704769	14723334	+0.01857	0 NA	intron (Nintron (N	24003	NM_00135Z	84449	Hs.515215NM_03243E	ENSG00000ZNF333	-	zinc finger protein-coding	
chr2-2014	8.856135	-0.73521	0.709887	-1.03568	0.300354	0.59423	chr2	2.01E+08	2.01E+08	+0.00000	0 NA	intron (Nintron (N	22857	NM_00120E	55437	Hs.652333NM_018571	ENSG00000STRADB	ALS2CR2	(STE20 rel protein-coding	
chr5-712	8.856135	-0.73521	0.709887	-1.03568	0.300354	0.59423	chr5	71202244	71204595	+0.00235	0 NA	intron (NAluJo S N	4712	NR_02702E	728411	Hs.881818NM_207331	ENSG00000GUSBP1	-	GUSB psepseudo	
chr7-457	8.856135	-0.73521	0.709887	-1.03568	0.300354	0.59423	chr7	45726135	45729223	+0.00309	0 NA	intron (Nintron (N	41339	NR_024271	641977	Hs.723477NR_024271	ENSG00000SEPTIN7P2	SEPT13	SE septin 7 pseudo	
chr6-352	8.843752	-0.73783	0.713006	-1.03481	0.300756	0.59423	chr6	35294482	35295673	+0.00119	0 NA	intron (Nintron (N	-2739	NM_022047	50619	Hs.15476	NR_022047	ENSG00000DEF6	IBP SLAT DEF6	guar protein-coding
chr20-46	9.339793	-0.70836	0.684649	-1.03463	0.300843	0.59423	chr20	4698746	4700813	+0.00067	0 NA	exon (NM exon (NM	13323	NM_00108C	5621	Hs.472012NM_000311	ENSG00000CRNP	ASCR A1Tfprion	prc protein-coding	
chr8-182	8.372477	-0.76554	0.740347	-1.03402	0.301125	0.59423	chr8	18222323	18222599	+0.00027	0 NA	exon (NM exon (NM	793	NM_00116C	9	Hs.591847NM_00066Z	ENSG00000NAT1	AAC1	MAN1N-acetyl protein-coding	
chr8-1334	8.372477	-0.76554	0.740347	-1.03402	0.301125	0.59423	chr8	1.33E+08	1.33E+08	+0.00000	0 NA	3' UTR (N3' UTR (N	113327	NM_003033	6482	Hs.374257NM_003033	ENSG00000ST3GAL1	Gal-1	Nac6S23 beta- protein-coding	
chr1-2171																				



chr19-88c.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr19	8805503	8825919	+	0	NA	intron (AluJr SIN	6352	NM_001304	148156	Hs.349444NM_144693	ENSG000002ZNF558	-	-	zinc	fingerprotein-coding		
chr19-11f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr19	11940268	11943105	+	0	NA	intron (LTR12C LI	16579	NM_144566	90592	Hs.528486NM_144566	ENSG000002ZNF700	-	-	zinc	fingerprotein-coding		
chr19-171f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr19	17158167	17179082	+	0	NA	intron (intron (	-46733	NM_018467	55850	Hs.16187NM_018467	ENSG000002UCE1	D12	MDS03	unconvent	protein-coding		
chr19-36f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr19	36936437	36952799	+	0	NA	intron (MER20 DN	28286	NM_001204	374900	Hs.404222NM_198539	ENSG000002ZNF568	ZFP568	zinc	fingerprotein-coding			
chr2-165f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	1667524	1667387	+	0	NA	intron (intron (	82010	NM_012293	7837	Hs.332197NM_012293	ENSG000002PXDN	ASG7	COF	peroxidase	protein-coding		
chr2-166f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	1667502	1675309	+	0	NA	intron (LIMEd LIN	73110	NM_012293	7837	Hs.332197NM_012293	ENSG000002PXDN	ASG7	COF	peroxidase	protein-coding		
chr2-199f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	1992682	19929339	+	0	NA	intron (MER9a2 LI	-26132	NM_001008	130502	Hs.591547NM_001008	ENSG000002FTC32	-	-	tetratric	protein-coding		
chr2-284f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	28402154	28418676	+	0	NA	intron (intron (	-15743	NR_103831	403150	Hs.562977NR_103831	ENSG000002FLJ31356	-	-	uncharacter	ncRNA		
chr2-471f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	47157155	47173713	+	0	NA	intron (intron (	8773	NM_001305	805	Hs.468442NM_001305	ENSG000002CALM2	CALM	CALM	calmodulin	protein-coding		
chr2-958f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	95874286	95875520	+	0	NA	intron (NLPA3 LIN	-47922	NR_103734	150759	Hs.503463NR_103734	LINC00342	NCRNA0034	long	intcncRNA			
chr2-177f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr2	177E+08	1.77E+08	+	0	NA	intron (MIR SINE	20860	NR_13847C	220988	Hs.516535NM_194247	ENSG000002MIRNPA3	2610510D1	hetero	protein-coding			
chr20-10f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr20	10654623	10664899	+	0	NA	intron (intron (	-10066	NR_10693C	1.02E+08	NR_10693C	ENSG000002MIR6870	hsa-mir-6	microRNA	ncRNA			
chr20-35f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr20	35668339	35676022	+	0	NA	intron (AluY SINE	-7280	NM_001198	10137	Hs.700188NM_006047	ENSG000002RBM12	HRH1HF205	RNA	bindi	protein-coding		
chr20-44f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr20	44902306	44907968	+	0	NA	intron (intron (	-4923	NR_134988	80336	Hs.641481NM_001124	ENSG000002PABPCIL	C20orf11	poly(A)	t	protein-coding		
chr20-63f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr20	63866411	63879581	+	0	NA	intron (AluY SINE	7726	NM_199361	7165	Hs.473296NM_003288	ENSG000002TPD52L2	D54	TPD54	TPD52	lik	protein-coding	
chr22-19f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr22	19381334	19384320	+	0	NA	intron (intron (	48906	NM_00332E	7290	Hs.474206NM_00332E	ENSG000002HIRA	DGCR1	TUF	histone	c	protein-coding	
chr22-50f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr22	50414626	50425676	+	0	NA	intron (ML2c LINE	12709	NR_162128	1.13E+08	MIR_12114	-	-	microRNA	ncRNA			
chr3-946f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr3	9461980	9469190	+	0	NA	intron (intron (	67885	NM_00108C	55209	Hs.288164NM_018187	ENSG000002SETD5	-	-	SET	domai	protein-coding	
chr3-979f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr3	9797419	9809209	+	0	NA	intron (L3 LINE C	-6601	NM_00102E	26140	Hs.726433NM_015644	ENSG000002TLL3	HOTTL	tubulin	t	protein-coding		
chr3-146f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr3	14654797	14667904	+	0	NA	intron (intron (	9588	NM_016474	51244	Hs.517822NM_016474	ENSG000002CCDC174	C3orf19	Fcoiled	cc	protein-coding		
chr3-459f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr3	45950898	45970131	+	0	NA	intron (intron (	17050	NM_006564	10663	Hs.34526NM_006564	ENSG000002CXCR6	BON20	CD1C-X-C	mot	protein-coding		
chr3-113f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr3	1.14E+08	1.14E+08	+	0	NA	intron (LIM5 LINE	-30548	NM_017577	54762	Hs.24583NM_017577	ENSG000002GRAMD1C	-	-	GRAM	doma	protein-coding	
chr4-176f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr4	17620297	17635228	+	0	NA	3' UTR (3' UTR (	13121	NM_02520E	80306	Hs.713966NM_02520E	ENSG000002MED28	1500003D1	mediator	protein-coding			
chr4-707f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr4	70768649	70771778	+	0	NA	intron (Tigger I	35803	NR_001291	22902	Hs.740904NM_014961	ENSG000002RUFY3	RIPX	SINC	RN	and	F	protein-coding
chr5-143f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr5	14306504	14322782	+	0	NA	intron (intron (	-149340	NR_14581E	1.1E+08	NR_14581E	SNORD170	-	-	small	nucsnRNA		
chr5-138f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr5	1.38E+08	1.38E+08	+	0	NA	exon (NM exon (NM	10656	NM_00130C	10902	Hs.519337NM_006699	ENSG000002BRD8	SMAP	SMAF	bromodome	protein-coding		
chr5-179f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr5	1.8E+08	1.8E+08	+	0	NA	intron (LIM3Cz I	10382	NM_01617E	51149	Hs.741166NM_01617E	ENSG000002MRN1P	C5orf45	MRN	com	protein-coding		
chr6-369f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr6	36966469	36981742	+	0	NA	intron (intron (	12446	NM_001271	23787	Hs.485262NM_014341	ENSG000002MTC1H	CGI-64	P	mitochon	c	protein-coding	
chr6-152f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr6	1.52E+08	1.52E+08	+	0	NA	intron (intron (	-22724	NR_120501	1.01E+08	Hs.571203NR_120501	SYNE1-AS1	-	-	SYNE1	antncRNA		
chr7-128f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr7	1.29E+08	1.29E+08	+	0	NA	IntergeniAluJo SIN	-6198	NR_02436E	402483	Hs.722396NM_001039682	LINC100C	-	-	long	intcncRNA		
chr8-705f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr8	70573030	70607416	+	0	NA	intron (intron (	17446	NM_001317	23471	Hs.491988NM_014294	ENSG000002TRAM1	PNAS8	TR	transloc	protein-coding		
chr8-981f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr8	98118864	98131068	+	0	NA	intron (intron (	7126	NM_01502E	10940	Hs.252828NM_01502E	ENSG000002POP1	ANXD2	POP1	homc	protein-coding		
chr8-102f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr8	1.02E+08	1.02E+08	+	0	NA	intron (L2c LINE	68739	NR_12541E	1.02E+08	Hs.492446NR_12541E	ENSG000002RUB5-AS1	-	-	UBR5	antncRNA		
chr9-108f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr9	1.09E+08	1.09E+08	+	0	NA	intron (intron (	16846	NM_006687	10881	Hs.123533NM_006687	ENSG000002ACTL7A	-	-	actin	lik	protein-coding	
chr9-121f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr9	1.21E+08	1.21E+08	+	0	NA	exon (NM exon (NM	29425	NM_000177	2934	Hs.522377NM_000177	ENSG000002GSN	ADF	AGEL	gelsolin	protein-coding		
chr9-138f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr9	1.28E+08	1.28E+08	+	0	NA	intron (AluSp SIN	11694	NM_001131	25792	Hs.740904NM_014961	ENSG000002RUFY3	LSFR1	NP	CDKRNA	ir	protein-coding	
chr9-128f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr9	1.28E+08	1.28E+08	+	0	NA	intron (intron (	-5813	NM_00131E	375757	Hs.259594NM_00104C	ENSG000002SWI5	C9orf119	SWI5	homc	protein-coding		
chr9-132f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr9	1.32E+08	1.32E+08	+	0	NA	intron (intron (	84515	NM_001351	23064	Hs.460317NM_01504E	ENSG000002SETX	ALSA	AOA2	senataxi	protein-coding		
chr9-133f.8.370269	-0.76043	0.738656	-1.02948	0.303256	0.59423	chr9	1.33E+08	1.33E+08	+	0	NA	intron (MIRc SINE	16759	NM_001271	5900	Hs.106188NM_006266	ENSG000002RAGDGS	RGD5	AL	guani	protein-coding		
chr3-446f.11.5946	-0.57111	0.55509	-1.02886	0.303545	0.59423	chr3	44650666	44662284	+	0	NA	intron (AluSx1 SI	7743	NM_00342C	7584	Hs.288658NM_00342C	ENSG000002ZNF35	HF.10	HF1	zinc	fingerprotein-coding		
chr11-12f.8.895491	-0.7321	0.711638	-1.02875	0.303596	0.59423	chr11	1.23E+08	1.23E+08	+	0	NA	intron (MIR1_Am	-22861	NM_153201	3312	Hs.180414NM_006597	ENSG000002HSPAB	HEL-33	HE	heat	shoc	protein-coding	
chr20-29f.13.78087	-0.47818	0.464993	-1.02835	0.303785	0.59423	chr20	29481298	29483859	+	0	NA	intron (intron (	14756	NR_146067	1.03E+08	NR_146067	FRG1EP	-	-	FSHD	regipseudo		
chr2-171f.8.345504	-0.76616	0.745732	-1.02739	0.304236	0.59423	chr2	1.71E+08	1.71E+08	+	0	NA	intron (AluYc SIN	-24965	NM_00113C	9874	Hs.744917NM_012293	ENSG000002TLK1	PKU-beta	tousled	l	protein-coding		
chr4-147f.8.397242	-0.75986	0.74037	-1.02633	0.304738	0.59423	chr4	1.48E+08	1.48E+08	+	0	NA	intron (intron (	93235	NR_03996E	1.01E+08	NR_03996E	ENSG000002MIR4799	-	-	microRNA	ncRNA		
chr6-281f.8.397242	-0.75986	0.74037	-1.02633	0.304738	0.59423	chr6	28115006	28119591	+	0	NA	IntergeniIntergeni	-7258	NM_00132C	80345	Hs.656641NM_025231	ENSG000002ZSCAN16	ZNF392	Z	zinc	fingerprotein-coding		
chr8-706f.8.397242	-0.75986	0.7403																					

chr12-791.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr12	7917590	7935474	+0	NA	intron (Nintron (N	9655	NM_006931	6515	Hs.41924CNM_006931	ENSG00000SLC2A3	GLUT3	solute carrier protein-coding	
chr15-603.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr15	60350534	60362489	+0	NA	intron (Nintron (N	41475	NM_001002	302	Hs.51160FN_00403E	ENSG00000ANXA2	ANX2	ANX2 amexin A protein-coding	
chr15-925.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr15	92931043	92990931	+0	NA	intron (Nintron (N	56588	NR_03613E	1E+08	NR_03613E	ENSG00000MIR3175	mir-3175	microRNA ncRNA	
chr17-18E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr17	18666786	18681103	+0	NA	intron (Nintron (N	8370	NM_00136E	2310	Hs.59212E	NM_00136E134	FOXO3B	FKHLR1P1	forkhead protein-coding
chr17-28E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr17	28969960	28925612	+0	NA	intron (Nintron (N	8624	NR_11080E	1.02E+08	Hs.66570E	NR_11080E	ENSG00000LOC101927	U83	uncharactericnRNA
chr17-801.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr17	80132313	80145418	+0	NA	intron (Nintron (N	8263	NM_01474E	9775	Hs.38964E	NM_01474E	ENSG00000EIF4A3	DDX48	Faleukaryotiprotein-coding
chr19-48E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr19	4837094	4845158	+0	NA	intron (Nintron (N	9384	NM_18291E	148022	Hs.29344	NM_014261	ENSG00000TTCAM1	I1AE6	Myf toll like protein-coding
chr2-262E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr2	26222422	26239777	+0	NA	intron (Nintron (N	13533	NM_00018E	3030	Hs.61603E	NM_00018E	ENSG00000HADHA	GLG3	glyoxalase protein-coding
chr2-101.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr2	1.01E+08	1.01E+08	+0	NA	intron (Nintron (N	2830	NM_00099E	6160	Hs.46947E	NM_00099E	ENSG00000RPL31	L31	ribosomal protein-coding
chr2-200E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr2	2.01E+08	2.01E+08	+0	NA	intron (Nintron (N	7176	NM_00132E	1195	Hs.40407E	ENSG00000CLK1	CLK	CLK/CLKC like protein-coding	
chr2-218E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr2	2.18E+08	2.18E+08	+0	NA	intron (Nintron (N	15613	NM_00132E	151306	Hs.160954N	NR_17069E	ENSG00000GPBAR1	BG37	GPCF protein-coding
chr3-500E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr3	50090063	50121102	+0	NA	non-codiron-codir	4594	NR_04538E	1.01E+08	Hs.43948E	NR_04538E	ENSG00000RBM5-AS1	LUST	RBM5 anticnRNA
chr5-150E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr5	1.51E+08	1.51E+08	+0	NA	intron (Nintron (N	5741	NM_00184E	55696	Hs.713564N	NR_01804E	ENSG00000RBM22	Cwc2	ZC3F RNA bindiprotein-coding
chr6-315E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr6	31529647	31541049	+0	NA	intron (Nintron (N	1101	NR_00314E	692233	NR_00314E	ENSG00000SNORD117	U83	small nucsnoRNA	
chr6-635E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr6	63576260	63583859	+0	NA	exon (NM exon (NM	8047	NM_00346E	7803	Hs.22777E	NM_00346E	ENSG00000PTP4A1	HH72	PRL-protein tprotein-coding
chr7-2351.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr7	23512135	23522091	+0	NA	intron (Nintron (N	14868	NM_00136E	29896	Hs.44565E	NM_01329E	ENSG00000TRA2A	AWMS1	HIS transformprotein-coding
chr7-261E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr7	26188508	26195513	+0	NA	intron (Nintron (N	6736	NM_00213E	3181	Hs.48774E	NM_00213E	ENSG00000HNRNP2B1	HNRNP2B1	Heterogeprotein-coding
chr7-662E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr7	66287094	66287732	+0	NA	intron (Nintron (N	82079	NM_00359E	8460	Hs.421194N	NR_00359E	ENSG00000TPST1	TANG012A	tyrosyl pprotein-coding
chr7-754E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr7	75426723	75442472	+0	NA	intron (Nintron (N	24275	NR_10401E	155400	Hs.436034N	NR_0103E	ENSG00000NSUN5P1	NSUN5B	WEINSUN5 pseudo
chr8-116E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr8	1.17E+08	1.17E+08	+0	NA	intron (Nintron (N	26559	NR_03388E	644660	Hs.706174N	NR_03388E	ENSG00000CAD21-AS1	Corf84	1RAD21 anticnRNA
chr9-9214.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr9	92142573	92145603	+0	NA	intron (Nintron (N	2621	NR_02734E	158314	Hs.14994E	NR_02734E	LINC0047E	C9orf44	long intncRNA
chr9-128E.9.597192	-0.62376	0.663515	-0.94008	0.347176	0.59423	chr9	1.29E+08	1.29E+08	+0	NA	intron (Nintron (N	4310	NM_00124E	6418	Hs.43668E	NM_00301E	ENSG00000SET	2P2PA	I2FSET nucleprotein-coding
chr10-50C.9.582601	-0.62184	0.665624	-0.93422	0.350192	0.59423	chr10	50097180	50102099	+0	NA	intron (Nintron (N	31685	NM_00100E	387680	Hs.36528E	NM_01823E	ENSG00000WASHC2A	FAM21A	WASH comp protein-coding
chr12-561.9.582601	-0.62184	0.665624	-0.93422	0.350192	0.59423	chr12	56158949	56163016	+0	NA	intron (Nintron (N	2623	NM_02101E	4637	Hs.63271E	NM_02101E	ENSG00000MYL6	ESMLC	LCI myosin liprotein-coding
chr2-226E.9.582601	-0.62184	0.665624	-0.93422	0.350192	0.59423	chr2	2.27E+08	2.27E+08	+0	NA	intron (Nintron (N	12952	NM_00554E	3667	Hs.47150E	NM_00554E	ENSG00000IRS1	HIRS-1	insulin iprotein-coding
chr9-127E.9.08656	-0.64535	0.694407	-0.92936	0.352704	0.59423	chr9	1.28E+08	1.28E+08	+0	NA	intron (Nintron (N	2181	NM_00128E	30815	Hs.10967E	NM_01344E	ENSG00000ST6GALNAC	SIAT7-F	ST6 protein-coding
chr12-13E.11.81044	-0.50475	0.543583	-0.92857	0.353113	0.59423	chr12	1.33E+08	1.33E+08	+0	NA	intron (Nintron (N	16217	NM_00130E	7699	Hs.421155E	NM_00344E	ENSG00000ZNF140	pH2-39	zinc fingprotein-coding
chr1-394E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	39451899	39475036	+0	NA	intron (Nintron (N	28169	NM_18180E	353500	Hs.47249E	NM_18180E	ENSG00000BMP8A	3	bone morpprotein-coding
chr1-117E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	1.18E+08	1.18E+08	+0	NA	intron (Nintron (N	54574	NM_01768E	54834	Hs.31080E	NM_01768E	ENSG00000GDAP2	MACROD3	Sc gangliosiprotein-coding
chr1-150E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	1.51E+08	1.51E+08	+0	NA	intron (Nintron (N	33267	NM_00119E	405	Hs.63244E	NM_00166E	ENSG00000ARNT	HIF-1	beta1 hydprotein-coding
chr1-156E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	1.56E+08	1.56E+08	+0	NA	intron (Nintron (N	7848	NM_01532E	23381	Hs.51683E	NM_01532E	ENSG00000SMG5	EST1B	LP1SMG5 nonsprotein-coding
chr1-160E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	1.6E+08	1.6E+08	+0	NA	TTS (NR_CTS (NR_C	22526	NR_14761E	1E+08	Hs.65764E	NR_14761E	ENSG00000LOC100287	1	uncharactericnRNA
chr1-169E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	1.7E+08	1.7E+08	+0	NA	intron (Nintron (N	27353	NM_02042E	57147	Hs.43556E	NM_02042E	ENSG00000SCYL3	PACE-1	PA3CY1 like protein-coding
chr1-1734.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	1.73E+08	1.73E+08	+0	NA	non-codiron-codir	242	NR_12596E	1.02E+08	Hs.67488E	NR_12596E	ENSG00000LOC10192E	1	uncharactericnRNA
chr1-232E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr1	2.33E+08	2.33E+08	+0	NA	intron (Nintron (N	7778	NR_13802E	84284	Hs.64271E	NM_03232E	ENSG00000NTPCR	Clorf57	H nucleosicprotein-coding
chr10-14E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr10	14916581	14922559	+0	NA	intron (Nintron (N	34526	NM_00103E	64421	Hs.65593E	NM_02248E	ENSG00000DCLRE1C	A-SCID	DCDNA crossprotein-coding
chr12-53C.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr12	53015392	53042827	+0	NA	intron (Nintron (N	17917	NM_19831E	23371	Hs.6147	NM_01531E	ENSG00000TNS2	C1-TEN	C1tensin 2 protein-coding
chr12-561.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr12	56106400	56114432	+0	NA	exon (NM exon (NM	5857	NM_00619E	5036	Hs.52449E	NM_00619E	ENSG00000PA2G4	EBP1	HG4-proliferaprotein-coding
chr12-567.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr12	56710712	56716257	+0	NA	intron (Nintron (N	11815	NM_00111E	4666	Hs.50573E	NM_00559E	ENSG00000NACA	HSD48	HAC nascent pprotein-coding
chr14-68E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr14	68869644	68894777	+0	NA	intron (Nintron (N	85967	NM_00124E	39075	Hs.85155	NM_00492E	ENSG00000ZFP36L1	BRF1	BergZFP36 rirprotein-coding
chr14-10E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr14	1.04E+08	1.04E+08	+0	NA	intron (Nintron (N	39075	NM_001371231	5685	Hs.251531N	NR_00278E	ENSG00000PSMA4	HC9	Hs1T17proteasoprotein-coding
chr15-78E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr15	78542493	78550107	+0	NA	intron (Nintron (N	5614	NM_00133E	7157	Hs.43746E	NM_00054E	ENSG00000TP53	BCC7	BMF5 tumor prcprotein-coding
chr17-76E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr17	7667929	7676330	+0	NA	intron (Nintron (N	3115	NM_00127E	55175	Hs.13268	NM_01814E	ENSG00000KLHL11	1	kelch likprotein-coding
chr17-41E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr17	41866569	41894935	+0	NA	intron (Nintron (N	15329	NM_01814E	90799	Hs.56971E	NM_13836E	ENSG00000CEP95	CCDC45	centrosoprotein-coding
chr17-64E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr17	64509227	64513317	+0	NA	intron (Nintron (N	4295	NR_13364E	51129	Hs.9613	NM_01610E	ENSG00000ANGPTL4	ARP4	FIAF angiopieprotein-coding
chr19-83E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr19	8368021	8374664	+0	NA	exon (NM exon (NM	7187	NM_00103E	126070	Hs.41819E	NM_15235E	ENSG00000ZNF440	1	zinc fingprotein-coding
chr19-11E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr19	11815588	11836841	+0	NA	intron (Nintron (N	11941	NM_15235E	171392	Hs.26434E	NM_13833E	ENSG00000ZNF675	TBZF	TIZ zinc fingprotein-coding
chr19-23E.9.098943	-0.6429	0.69297	-0.92774	0.353541	0.59423	chr19	23652432	23664											



chr17-182.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr17	18263169	18265581	+0	NA	exon (NM_exon (NM_125170	Hs.655555	139162	ENS00000	MIEF2	MID49	SMC	mitochondrial protein-coding	
chr19-118.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr19	11860696	11870684	+0	NA	promoter-promoter-intron (N_intron (N_90594	Hs.528731	152262	ENS00000	ZNF439			zinc finger protein-coding	
chr2-237.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr2	2.37E+08	2.37E+08	+0	NA	intron (N_intron (N_23505	23324	CNM_004365	ENS00000	COL6A3	BTHLM1	DI	collagen protein-coding	
chr3-538.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr3	53869090	53881012	+0	NA	intron (N_Alus6 S 61445861	41218	CNM_022899	ENS00000	ACTR8	ARPF	IN	actin repressor protein-coding	
chr3-6414.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr3	64145861	64149373	+0	NA	exon (NM_exon (NM_39927	67084	CNR_046702	ENS00000	PRICKLE2			PRICKLE2 ncRNA	
chr6-3441.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr6	34414623	34425359	+0	NA	intron (N_Alus6 S 6078	40662	CNM_001014	ENS00000	CRPS10	DBA9	S10	ribosomal protein-coding	
chr7-839.8.586104	-0.66223	0.723725	-0.91503	0.360174	0.59423	chr7	83994901	83995341	+0	NA	intron (N_L1P2 L1N_199668	252451	NM_006088	ENS00000	SEMA3A	COLL1	HHH	semaphorin protein-coding	
chr12-121.8.627668	-0.66402	0.726024	-0.91462	0.360402	0.59423	chr12	1.21E+08	1.21E+08	+0	NA	exon (NM_exon (NM_18793	29734	NM_006545	ENS00000	CAMK22	CAMK1	CAM	calcium/calmodulin-dependent protein-coding	
chr11-333.8.613077	-0.66178	0.723644	-0.91452	0.360445	0.59423	chr11	33345635	33354083	+0	NA	intron (N_Alus1 S 26249	50226	CNM_012194	ENS00000	KIAA1549	C11orf41	KIAA1549	protein-coding	
chr17-48.8.613077	-0.66178	0.723644	-0.91452	0.360445	0.59423	chr17	28328797	28332156	+0	NA	exon (NM_exon (NM_4996	705431	NM_174887	ENS00000	IFT20			intraflagellar protein-coding	
chr19-277.8.613077	-0.66178	0.723644	-0.91452	0.360445	0.59423	chr19	47728339	47728525	+0	NA	exon (NM_exon (NM_12760	744963	NM_014601	ENS00000	EHD2	PAST2	EH	domain protein-coding	
chr20-344.8.613077	-0.66178	0.723644	-0.91452	0.360445	0.59423	chr20	34438081	34448720	+0	NA	intron (N_Alus6 S 22925	303074	NR_030374	ENS00000	MIR644A	MIR644	M	microRNA ncRNA	
chr21-372.8.613077	-0.66178	0.723644	-0.91452	0.360445	0.59423	chr21	37200009	37203840	+0	NA	3' UTR (N_3' UTR (N_6579	505155	NM_148675	ENS00000	DSCR9	NCRNA0005	Down	synchrRNA	
chr8-6577.8.613077	-0.66178	0.723644	-0.91452	0.360445	0.59423	chr8	65774986	65783570	+0	NA	intron (N_intron (N_9779	527115	NM_022603	ENS00000	PDE7A	HCP1	PDE	phosphodiesterase protein-coding	
chr1-161.8.102446	-0.68887	0.755482	-0.91182	0.361862	0.59423	chr1	1.61E+08	1.61E+08	+0	NA	TTS (NM_C_TTS (NM_C_2097	12707	NM_015268	ENS00000	DNAJC13	PARK21	RNAJ	heat shock protein-coding	
chr3-1324.8.102446	-0.68887	0.755482	-0.91182	0.361862	0.59423	chr3	1.32E+08	1.32E+08	+0	NA	intron (N_intron (N_56269	25960	NM_017837	ENS00000	CP1G	GPI-MT-1	I	phosphatidylinositol protein-coding	
chr1-2677.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr1	26773335	26781916	+0	NA	intron (N_Alus6 S 32373503	353454	NM_018045	ENS00000	BSDC1			BSD domain protein-coding	
chr1-3237.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr1	32373503	32391250	+0	NA	intron (N_Alus6 S 10171	49718	NM_006465	ENS00000	IVNS1ABP	ARA3	FLAF	influenza protein-coding	
chr1-185.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr1	1.85E+08	1.85E+08	+0	NA	exon (NM_exon (NM_32427	497492	NM_002393	ENS00000	MDM4	HDMX	MDM4	regulator protein-coding	
chr1-204.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr1	2.05E+08	2.05E+08	+0	NA	intron (N_intron (N_21088	29734	NM_032324	ENS00000	NTPCR	Clorf57	MDM5	protein-coding	
chr1-232.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr1	2.33E+08	2.33E+08	+0	NA	intron (N_intron (N_23115	43689	NM_007055	ENS00000	POLR3A	ADDD	HLDRNA	polymerase protein-coding	
chr10-77.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr10	77984482	78028319	+0	NA	intron (N_Alus1 S 22430	502302	NM_001752	ENS00000	CCAT			catalase protein-coding	
chr11-34.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr11	3449291	34473437	+0	NA	exon (NM_exon (NM_35191985	527115	NR_145794	ENS00000	SNORD164			small nucleolar RNA	
chr11-61.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr11	61299108	61331322	+0	NA	intron (N_intron (N_17967	6278	NM_015533	ENS00000	TKFC	DAK	NET4E	triokinase protein-coding	
chr11-7.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr11	77842800	77846578	+0	NA	intron (N_L1M4b L1N_3551	74504	CNM_024684	ENS00000	AAMD	C11orf67	AD	lipogenic protein-coding	
chr12-54.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr12	54393791	54411130	+0	NA	intron (N_Alus6 S 11162	344055	NM_015481	ENS00000	ZNF385A	HIF1RZF1	Z	zinc finger protein-coding	
chr12-68.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr12	68808916	68843043	+0	NA	intron (N_intron (N_16955	484551	NM_002392	ENS00000	MDM2	ACTFS	HDM	MDM2	protector protein-coding
chr12-71.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr12	71606029	71638476	+0	NA	intron (N_L2a LINE 41596	24579	NM_144982	ENS00000	ZFC3H1	CCDC131	C	zinc finger protein-coding	
chr12-91.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr12	91554841	91177011	+0	NA	intron (N_Alus6 S 12720	43914	NM_001920	ENS00000	CCDN	CSD	D	decorin protein-coding	
chr13-37.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr13	37032068	37040234	+0	NA	intron (N_Tigger1 E_23336	43581	NM_017565	ENS00000	SUPT20H	C13	C13orf	SPT20	homeobox protein-coding
chr13-11.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr13	1.1E+08	1.1E+08	+0	NA	intron (N_intron (N_86499	13472	NR_148221	ENS00000	LOC105370			uncharacterized ncRNA	
chr14-51.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr14	51701933	51730742	+0	NA	promoter-promoter-intron (N_intron (N_946	44096	NM_005657	ENS00000	TP53BP1	C14orf31	FERM	domain protein-coding	
chr14-71.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr14	71051794	71053940	+0	NA	intron (N_intron (N_145408	51675	NM_014982	ENS00000	PCNX1	PCNX	PCN	pecanexin 1 protein-coding	
chr14-74.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr14	74459675	74694640	+0	NA	intron (N_intron (N_6474	204041	NM_012111	ENS00000	AHSA1	AHA1	C14	activator protein-coding	
chr15-434.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr15	43465930	43483013	+0	NA	intron (N (A)n Simp_18685	44096	NM_005657	ENS00000	TP53BP1	53BP1	TDF	tumor protein-coding	
chr15-447.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr15	44714471	44719801	+0	NA	promoter-promoter-intron (N_intron (N_20980	51675	NR_162102	ENS00000	MIR10393			microRNA ncRNA	
chr16-21.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr16	21178294	21182549	+0	NA	non-coding-non-coding-intron (N_intron (N_16931	38121	NR_001096	ENS00000	ACLY	DNAC3B	B	dynein axonemal protein-coding	
chr17-41.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr17	41894958	41910162	+0	NA	intron (N_intron (N_39698	43705	NM_003152	ENS00000	STAT5A	MGF1	STAT	signal transducer protein-coding	
chr17-42.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr17	42313567	42341941	+0	NA	intron (N_intron (N_3758	43405	NM_001988	ENS00000	ETV4	E1A-F	E1A	ETS	variable protein-coding
chr17-63.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr17	63269981	63272868	+0	NA	exon (NM_exon (NM_12242	43724	NM_014966	ENS00000	ARG	USHA	arylsulfatase protein-coding		
chr17-73.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr17	73204425	73210163	+0	NA	TTS (NM_C_TTS (NM_C_14239	10355	NM_018714	ENS00000	COG1	CDG2G	LDI	component protein-coding	
chr18-361.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr18	36141533	36149724	+0	NA	intron (N_intron (N_51279	8739	NM_018255	ENS00000	ELP2	MRT58	SHI	elongator protein-coding	
chr19-484.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr19	48460558	4863678	+0	NA	intron (N_Alus6 S 12799	14045	NM_005817	ENS00000	CLIN3	M6PRBP1	F	perilipin protein-coding	
chr19-45.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr19	45824975	45852193	+0	NA	exon (NM_exon (NM_85376528	44644	NM_030785	ENS00000	RSLPD6A	RSHL1	RSF	radial glial protein-coding	
chr2-8537.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr2	85376528	85381936	+0	NA	intron (N_Alus6 S 24463	26999	NM_032213	ENS00000	ELMOD3	DFNB88	L	ELMO domain protein-coding	
chr2-855.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr2	85539688	85546719	+0	NA	intron (N_intron (N_4035	516157	NM_005911	ENS00000	CCAT2A	MATA2	MAT	methionin protein-coding	
chr2-109.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr2	1.1E+08	1.1E+08	+0	NA	intron (N_L1M5a L1L_4925	53561	NR_027144	ENS00000	LIMS3-LOC			LIMS3-LOC ncRNA	
chr20-384.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr20	38418617	38433937	+0	NA	promoter-promoter-intron (N_intron (N_25292	608	Hs.517517	NR_110514	EP300-AS1			EP300 antncRNA	
chr3-2391.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr3	23917850	23921798	+0	NA	3' UTR (N_3' UTR (N_2692	38121	NR_001252	ENS00000	RPL15	DBA12	E	ribosomal protein-coding	
chr3-2741.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr3	27417837	27421545	+0	NA	intron (N_intron (N_37087	43075	NM_003615	ENS00000	SLC4A7	NBC2	NBC3	solute carrier protein-coding	
chr4-389.8.598487	-0.65956	0.72372	-0.91135	0.362114	0.59423	chr4	38901371	38945630	+0	NA	intron (N_Alus6 S 55468	59171	CNM_017631	ENS00000	DDX60			DExD/H-box protein-coding	
chr4-770.8.598487	-0.65956	0.72372	-0.91135	0.36211															



chr17-758.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	7591714	7609480	+0	NA	intron (N FLAM_C SI	-10503	NM_006942	6665	Hs.95582	NM_006942	ENS00000CSOX15	SOX20 SOX	SRY-box	tprotein-coding
chr17-286.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	28613895	28632034	+0	NA	intron (N AluSg SIN	-8779	NM_0011174	124923	Hs.729077	NM_14461C	ENS00000RSKR	SGK494	ribosomal	protein-coding
chr17-384.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	38466291	38508917	+0	NA	intron (N AluSx1 SI	59140	NM_001199	57636	Hs.37444	ENS00000CARHGAP23	-	Rho	GTPase	protein-coding
chr17-387.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	38768983	38787411	+0	NA	intron (N intron (N	21708	NM_003555	8396	Hs.28600	ENS00000PIP4K2B	P15P4KB F	phosphatidyl	protein-coding	
chr17-425.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	425668245	42576848	+0	NA	non-coding-non-coding	5170	NM_001256	29893	Hs.38301	ENS00000PSMC31P	GR198 H9F	PSMC3	intron-protein-coding	
chr17-428.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	42834176	42846145	+0	NA	intron (N AluSp SIN	-4420	NM_001158	314	Hs.14310	ENS00000CAOC2	DA02 RAO	amine oxidase	protein-coding	
chr17-758.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	75946081	75958227	+0	NA	intron (N intron (N	-13922	NM_001319	85302	Hs.72066	ENS00000FBF1	Alb FBF	F-1fas	bindinprotein-coding	
chr17-802.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr17	80225999	80242944	+0	NA	intron (N LIMEc LIN	14044	NM_17362E	284129	Hs.4866	ENS00000SLC26A11	-	solute	carboxinprotein-coding	
chr19-241.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	24115168	24123738	+0	NA	intron (N AluSx SIN	32266	NM_00127E	9534	Hs.43440	ENS00000ZNF254	BZMF-5 HI	zinc finger	protein-coding	
chr19-367.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	36392005	36402896	+0	NA	intron (N LIMD LINE	-18249	NM_020917	57677	Hs.35524	ENS00000ZFP14	ZNF531	ZFP14	zinc protein-coding	
chr19-371.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	37147189	37171526	+0	NA	intron (N LIMC5a LIN	13079	NM_19912E	199704	Hs.65923	ENS00000ZNF585A	-	zinc	finger protein-coding	
chr19-371.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	37183031	37201194	+0	NA	intron (N intron (N	18424	NM_15227E	92285	Hs.39056	ENS00000ZNF585B	SZFP41	zinc finger	protein-coding	
chr19-418.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	41267903	41307009	+0	NA	intron (N LIMC4 LIN	22375	NM_001321	11100	Hs.15521	ENS00000HNRNPUL1	E1B-AP5 E	heterologous	protein-coding	
chr19-452.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	45897942	45901358	+0	NA	intron (N AluSx1 SI	2963	NM_001012	339344	Hs.51547	ENS00000MYPO	P42p20	Myb	relatprotein-coding	
chr19-466.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	46672408	46711649	+0	NA	intron (N intron (N	17326	NR_036157	1E+08	NR_036157	ENS00000MIR320E	mir-320e	microRNA	ncRNA	
chr19-492.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr19	49210072	49212003	+0	NA	exon (NM exon (NM	53245	NM_00119E	54795	Hs.46710	ENS00000TRPM4	LTrpC4 PF	transient	protein-coding	
chr2-320.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	32498358	32511511	+0	NA	intron (N intron (N	-27219	NR_03028E	693143	NR_03028E	ENS00000MIR558	MIRN558 f	microRNA	ncRNA	
chr2-697.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	69070052	69074176	+0	NA	intron (N intron (N	131568	NR_036073	1E+08	NR_036073	ENS00000MIR3126	mir-3126	microRNA	ncRNA	
chr2-1602.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	1.6E+08	1.6E+08	+0	NA	intron (N intron (N	-12705	NR_10377E	1.01E+08	Hs.72953	ENS00000LINC0247E	-	long	intencRNA	
chr2-1603.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	1.6E+08	1.6E+08	+0	NA	intron (N AluSx1 SI	-10489	NR_10377E	1.01E+08	Hs.72953	ENS00000LINC0247E	-	long	intencRNA	
chr2-1916.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	1.91E+08	1.91E+08	+0	NA	intron (N intron (N	14528	NM_00113C	4430	Hs.43962	ENS00000MYO1B	MMI	alpha	myosin IF	protein-coding
chr2-2186.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	2.19E+08	2.19E+08	+0	NA	exon (NM exon (NM	6000	NM_02245E	64320	Hs.47140	ENS00000RNF25	A07	ring	finger protein-coding	
chr2-2328.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	2.33E+08	2.33E+08	+0	NA	intron (N intron (N	-40567	NM_00117E	3769	Hs.46733	ENS00000KCNJ13	KIR1.4 K1	potassium	protein-coding	
chr2-2411.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr2	2.41E+08	2.41E+08	+0	NA	intron (N intron (N	5270	NM_00108C	25992	Hs.47183	ENS00000SNED1	IRE-BP1 S	sushi, ni	protein-coding	
chr20-245.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr20	2457067	2469651	+0	NA	promoter-promoter-	-312	NR_003684	1E+08	NR_003684	SNORD119	-	small	nucsnRNA	
chr20-455.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr20	45966031	45969024	+0	NA	exon (NM exon (NM	4376	NM_02209E	63925	Hs.17419	ENS00000ZNF335	MCPH10 N	zinc	finger protein-coding	
chr22-414.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr22	41664055	4167703	+0	NA	intron (N MR SINE	4613	NM_03275E	84844	Hs.47498	ENS00000PHF5A	E1 Rds3 PHD	finger	protein-coding	
chr3-1523.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr3	15239842	15244194	+0	NA	intron (N intron (N	-12166	NR_046084	1.01E+08	Hs.74502	ENS00000SH3BP5-AS	-	SH3BP5	arnRNA	
chr3-1203.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr3	1.2E+08	1.2E+08	+0	NA	intron (N intron (N	-9666	NR_029584	406975	NR_029584	ENS00000MIR198	MIRN198	microRNA	ncRNA	
chr3-1493.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr3	1.49E+08	1.49E+08	+0	NA	intron (N intron (N	-29993	NR_04664E	1.01E+08	Hs.74242	ENS00000HLTF-AS1	-	HLTF	antincRNA	
chr5-3493.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr5	34932619	34947162	+0	NA	intron (N intron (N	10297	NM_19428E	134218	Hs.13188	ENS00000DNAJC21	BMF53 DN	DnaJ	heat	protein-coding
chr5-1517.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr5	1.52E+08	1.52E+08	+0	NA	intron (N MER4A LITF	-3134	NR_109873	1.02E+08	Hs.57102	ENS00000CLMAT3	CTB-113P	icolactancRNA	-	
chr5-1548.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr5	1.55E+08	1.55E+08	+0	NA	intron (N intron (N	-23685	NR_039667	1.01E+08	NR_039667	ENS00000MIR378H	-	microRNA	ncRNA	
chr6-247.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr6	24701156	24719966	+0	NA	intron (N AluSp SIN	8593	NM_03093E	81688	Hs.74485	ENS00000C6orf62	Nb1a00237	chromosom	protein-coding	
chr6-2597.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr6	25972156	25986485	+0	NA	intron (N LIMS LINE	16518	NM_00635E	10475	Hs.58485	ENS00000TRIM38	RNF15 ROF	tripartit	protein-coding	
chr6-2646.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr6	26462673	26469934	+0	NA	intron (N intron (N	8348	NM_00704E	11120	Hs.15902	ENS00000BTN2A1	BK14H9.1	butyrophil	protein-coding	
chr6-4266.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr6	42662166	42664488	+0	NA	exon (NM exon (NM	59270	NM_00032E	5961	Hs.65448	ENS00000PRPH2	AOFMD AV	peripheri	protein-coding	
chr7-5214.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr7	5214439	5233425	+0	NA	intron (N intron (N	9663	NM_00103E	26100	Hs.12236	ENS00000WIPI2	ATG18B At	mid	repeat	protein-coding
chr7-2331.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr7	23316651	23319935	+0	NA	intron (N AluJb SIN	18954	NM_13844E	115416	Hs.87385	ENS00000MALSU7	C7orf30	AT	titonchonc	protein-coding
chr7-7603.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr7	76054689	76067302	+0	NA	intron (N intron (N	12889	NM_00591E	4191	Hs.52096	ENS00000MDH2	EIEE51 M	malate de	protein-coding	
chr7-1391.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr7	1.4E+08	1.4E+08	+0	NA	intron (N intron (N	85637	NM_00135E	154790	Hs.57806	ENS00000CLEC2L	-	C-type	leprotein-coding	
chr8-1411.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr8	1.41E+08	1.41E+08	+0	NA	intron (N L2c LINE	12143	NM_00136E	22898	Hs.18166	ENS00000DENND3	-	DENN	domer	protein-coding
chr9-3326.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr9	33266114	33282237	+0	NA	intron (N AluJb SIN	9126	NM_01641C	51510	Hs.63531	ENS00000CHMP5	C9orf83 C	charged n	protein-coding	
chr9-1228.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr9	1.23E+08	1.23E+08	+0	NA	intron (N intron (N	25618	NR_003071	692206	Hs.69325	ENS00000SNORD90	HBII-295	small	nucsnRNA	
chr9-1364.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chr9	1.36E+08	1.36E+08	+0	NA	intron (N intron (N	-16304	NM_152571	158055	Hs.51261	ENS00000C9orf163	-	chromosom	protein-coding	
chrX-1673.8.100238	-0.68354	0.752372	-0.90852	0.363604	0.59423	chrX	16752516	16761624	+0	NA	intron (N intron (N	-29362	NM_00116E	55787	Hs.55596	ENS00000TXLNG	CXorf15 E	taxilin	protein-coding	
chr8-6725.8.559131	-0.66269	0.729479	-0.90845	0.363642	0.59423	chr8	67291617	67292320	+0	NA	exon (NM exon (NM	51813	NM_006421	10565	Hs.65690	ENS00000ARFGEF1	ARFGEF1 E	ADP	ribos	protein-coding
chr10-615.8.129419	-0.68838	0.757877	-0.9083	0.363721	0.59423	chr10	61940257	61943283	+0	NA	intron (N intron (N	40071	NM_03219E	84159	Hs.53529	ENS00000ARID5B	DESRT MR	FAT-rich	protein-coding	
chr7-1436.8.075473	-0.6894																			





chr1-1602.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr1	1.6E+08	1.6E+08	0 NA	intron (Nintron (N	-3720 NR_12372E	729867 Hs. 674191NR_12372E	ENSG000001CLOC729867	-	uncharactncRNA	
chr1-1798.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr1	1.8E+08	1.8E+08	0 NA	intron (NLMIME3Cz L	13531 NM_001345	163590 Hs. 571797NM_022347	ENSG000001TOR1AIP2	IFRG15 LU	torsin 1 protein-coding	
chr1-2260.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr1	2.26E+08	2.26E+08	0 NA	intron (NAluSx SIN	6835 NR_00231E	440926 Hs. 533624NR_002315	H3F3AP4	p13	H3 historpseudo	
chr1-2351.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr1	2.35E+08	2.35E+08	0 NA	intron (NLMIME4b LI	15986 NM_001346	23029 Hs. 535224NM_015014	ENSG000001RBM34	-	RNA bindiprotein-coding	
chr10-4578.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr10	45754555	45754555	0 NA	intron (NAluSx SIN	41971 NM_001351	643479 Hs. 522900NM_001351234	FAM25E	FAM25D	family wiprotein-coding	
chr11-185.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr11	18554308	18557852	0 NA	intron (Nintron (N	23438 NM_001261	55293 Hs. 407991NM_018314	ENSG000001UEVLD	ATTP UEV:UEV	and lprotein-coding	
chr11-348.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr11	34076140	34101676	0 NA	intron (Nintron (N	-16721 NM_001144	55226 Hs. 577281NM_024662	ENSG000001NAT10	ALP Kre3E	acetyltprotein-coding	
chr11-576.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr11	57659517	57662811	0 NA	intron (Nintron (N	3402 NM_006811	10978 Hs. 523687NM_006831	ENSG000001CLP1	HEAB HLI	cleavage protein-coding	
chr11-108.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr11	1.08E+08	1.08E+08	0 NA	intron (NLMIP3 LINE	50745 NM_001351	472 Hs. 367437NM_000051	ENSG000001ATM	AT1 ATA ATM	serirprotein-coding	
chr11-127.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr11	1.26E+08	1.26E+08	0 NA	intron (Nintron (N	9393 NM_001330	9538 Hs. 643514NM_00487E	ENSG000001E124	EPG4 PIGEI24	autcprotein-coding	
chr12-577.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr12	57747183	57751288	0 NA	promoter-promoter-	-553 NR_106817	NR_106817	ENSG000001MIR6759	Hsa-gm-ε	microRNA ncRNA	
chr14-498.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr14	49807369	49851414	0 NA	exon (NM exon (NM	23397 NM_00471E	9147 Hs. 655964NM_00471E	ENSG000001CNEMF	NY-CO-1 S	nuclear eprotein-coding	
chr14-747.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr14	74778921	74785520	0 NA	intron (NM exon (NM	18904 NM_01958E	56252 Hs. 531111NM_01958E	ENSG000001YLRPM1	C14orf17C YLP	motifprotein-coding	
chr16-278.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr16	2753621	2776180	0 NA	exon (NM exon (NM	12262 NM_01633E	23524 Hs. 433433NM_01633E	ENSG000001SRM2	300-KD C	serine/arprotein-coding	
chr16-223.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr16	22344000	22352984	0 NA	intron (NMER5B DNF	26127 NM_001802	1039 Hs. 513433NM_001802	ENSG000001CDR2	CDR62 Yo	cerebellaprotein-coding	
chr16-245.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr16	24956180	24970680	0 NA	intron (Nintron (N	51939 NM_018054	55114 Hs. 37379E	ENSG000001ARHGAP17	MSTO66 MS	Rho GTPasprotein-coding	
chr16-307.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr16	30700102	30739772	0 NA	intron (NLMIPA16 LI	9400 NR_00296E	677813 Hs. 68971E	ENSG000001SNORA30	ACA30 SNC	small nucsnRNA	
chr16-707.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr16	70554032	70572964	0 NA	intron (Nintron (N	-16397 NM_15245E	146433 Hs. 461214NM_15245E	ENSG000001LR34	C16orf77 C	interleukprotein-coding	
chr17-388.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr17	38800815	38815607	0 NA	intron (NAluSx3 SI	-8306 NM_00355E	8396 Hs. 26060E	ENSG000001PIP4K2B	PIP54KB P	phosphatiprotein-coding	
chr17-488.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr17	48916351	48943521	0 NA	TTS (NM_C	14906 NM_001317	11267 Hs. 12724E	ENSG000001SNF8	Dot3 EAP:SNF8	subprotein-coding	
chr17-758.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr17	75845161	75853032	0 NA	intron (Nintron (N	-4379 NM_19924E	201294 Hs. 41045 NM_19924E	ENSG000001UNC13D	FHL3 HLH:unc-13	hprotein-coding	
chr17-788.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr17	78808319	78822257	0 NA	intron (NAluSc SIN	25239 NM_001321	57602 Hs. 46424E	ENSG000001USP36	DUB1	ubiquitirprotein-coding	
chr18-358.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr18	35256044	35264821	0 NA	intron (NLMIPA10 LI	19398 NM_00113E	84307 Hs. 591061NM_032347	ENSG000001ZNF397	ZNF47 ZSC	zinc fingprotein-coding	
chr19-758.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr19	5602820	5621750	0 NA	intron (Nintron (N	10491 NM_01464E	9667 Hs. 65539E	ENSG000001SAFB2	-	scaffold protein-coding	
chr19-358.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr19	35651026	35659143	0 NA	intron (NAluSc8 SI	6761 NM_00186E	1340 Hs. 43166E	ENSG000001COX6B1	COX6B CO	cytochoenprotein-coding	
chr19-477.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr19	47729963	47742974	0 NA	exon (NM exon (NM	-9078 NM_01571E	29997 Hs. 421907NM_01571E	ENSG000001NOP53	GLTSCR2 FN	OP53 ritprotein-coding	
chr2-8611.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr2	86115272	86139556	0 NA	intron (Nintron (N	-8456 NR_00437E	692225 Hs. 723087NR_00437E	ENSG000001SNORD94	U94	small nucsnRNA	
chr20-458.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr20	45325806	45336285	0 NA	intron (NMER41B LI	17379 NM_00299E	6385 Hs. 632267NM_00299E	ENSG000001SDCA4	SYND4	syndcan protein-coding	
chr20-492.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr20	49242372	49275786	0 NA	intron (NAluJo SIN	18528 NM_02103E	57169 Hs. 371794NM_02103E	ENSG000001ZNF1X1	-	zinc fingprotein-coding	
chr22-411.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr22	41123924	41167309	0 NA	intron (Nintron (N	51885 NR_110514	1.02E+08 Hs. 517517NR_110514	EP300-AS1	-	EP300 antncRNA	
chr3-1695.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr3	1.7E+08	1.7E+08	0 NA	intron (NAluSx1 SI	18489 NM_00326E	7095 Hs. 74485E	ENSG000001SEC62	Dtrp1 HTF	SEC62 honprotein-coding	
chr3-1978.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr3	1.98E+08	1.98E+08	0 NA	intron (Nintron (N	4730 NM_00131E	6165 Hs. 529631NM_00099E	ENSG000001RPL35A	DBA5 L35	ribosomalprotein-coding	
chr4-7598.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr4	75954437	75983046	0 NA	intron (Nintron (N	-12049 NR_00299E	1.02E+08 Hs. 63757E	NR_12590E	ENSG000001LOC10192E	-	uncharactncRNA
chr4-7701.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr4	77016926	77021841	0 NA	intron (Nintron (N	55527 NM_00134E	10983 Hs. 518827NM_00683E	ENSG000001CCNI1	CCNI1 CY	cyclin I protein-coding	
chr5-728.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr5	72861092	72877076	0 NA	intron (NBLACKJACK	-9507 NR_03996E	1.01E+08 Hs. 430661NM_00219E	ENSG000001IRF1	IRF-1 MAF	interfercprotein-coding	
chr5-1324.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr5	1.32E+08	1.32E+08	0 NA	intron (NAluJb SIN	12545 NM_183401	9604 Hs. 48361E	ENSG000001CRNF14	ARA54 HFE	ring fingprotein-coding	
chr5-1418.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr5	56456370	56460458	0 NA	3' UTR (N3' UTR (N	-64286 NR_00131E	81578 Hs. 47629 NM_03082E	ENSG000001COL21A1	COLA1L P	collagen protein-coding	
chr7-4727.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr7	47276345	47276804	0 NA	3' UTR (N3' UTR (N	188229 NR_145813	1.1E+08 NR_145813	SNORD151	-	small nucsnRNA	
chr7-728.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr7	72831117	72839756	0 NA	intron (Nintron (N	6063 NR_024111	155370 Hs. 58505E	ENSG000001SBDSP1	SBDSP	SBDS psetpseudo	
chr8-3046.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chr8	30469935	30472107	0 NA	intron (Nintron (N	-85620 NR_04620E	1E+08 Hs. 12681E	NR_04620E	ENSG000001RBPMS-AS1	-	RBPMS antncRNA
chrX-2408.8.814322	-0.56779	0.708431	-0.80148	0.422853	0.619909	chrX	24055807	24069315	0 NA	exon (NM exon (NM	7605 NM_00141E	1968 Hs. 539684NM_00141E	ENSG000001EIF2S3	EIF2 EIF2	eukaryotprotein-coding	
chr1-1863.8.841295	-0.56744	0.709741	-0.7995	0.423999	0.619909	chr1	1.86E+08	1.86E+08	0 NA	intron (Nintron (N	3282 NM_00329E	7175 Hs. 27964E	ENSG000001TPR	-	translocaprotein-coding	
chr11-888.8.841295	-0.56744	0.709741	-0.7995	0.423999	0.619909	chr11	88330805	88332716	0 NA	intron (NMER21A LI	5976 NM_001114	1075 Hs. 12806E	ENSG000001CTSC	CPP1 DPP	cathepsirprotein-coding	
chr2-1897.8.841295	-0.56744	0.709741	-0.7995	0.423999	0.619909	chr2	1.89E+08	1.89E+08	0 NA	intron (Nintron (N	68142 NR_03607E	NR_03607E	ENSG000001MIR3129	mir-3129	microRNA ncRNA	
chr5-957.8.841295	-0.56744	0.709741	-0.7995	0.423999	0.619909	chr5	95736284	95739936	0 NA	intron (NLMIME3 LIN	-6008 NM_00134E	83890 Hs. 50499 NM_03195E	ENSG000001SPATA9	NYD-SP16	spermatogprotein-coding	
chr1-1012.8.826705	-0.56525	0.709885	-0.7963	0.425857	0.619909	chr1	10129457	10133484	0 NA	intron (NAluSx SIN	-79100 NM_00136E	23095 Hs. 97858 NM_015074	ENSG000001KIF1B	CMT2 CMT	kinesin fprotein-coding	
chr1-1507.8.826705	-0.56525	0.709885	-0.7963	0.425857	0.619909	chr1	1.51E+08	1.51E+08	0 NA	exon (NM exon (NM	3655 NM_00120E	1893 Hs. 81071 NM_00442E	ENSG000001ECMI1	URBWD	extracellprotein-coding	
chr1-125.8.826705	-0.56525	0.709885	-0.7963	0.425857	0.619909	chr10	12209701	12212658	0 NA	intron (Nintron (N	14991 NM_06020E	8872 Hs. 41284E	ENSG000001CDC123	C10orf7 C	cell diviprotein-coding	
chr5-5526.8.826705	-0.56525	0.709885	-0.7963	0.425857	0.619909	chr5	55262804	55275064	0 NA	intron (Nintron (N	-35217 NR_12534E	10309 Hs. 3041 NM_021147	ENSG000001CCNO	CCNU CILL	cyclin O protein-coding	
chr8-2898.8.826705	-0.56525	0.709885	-0.7963	0.425857	0.619909	chr8	28999299	29000749	0 NA	intron (NLMIM4 LINE	109025 NM_001324	79618 Hs. 56356E	ENSG000001HMBOX1	HNF1LA H	homeobox protein-coding	
chr15-729.8.774966	-0.57071	0.716878	-0.7961	0.425971	0.619909	chr15	72781634	72782199	0 NA	promoter-promoter-	-919 NR_040107	ENSG000001ADPGK-AS1	-	ADPGK antncRNA		
chr2-2025.8.799731	-0.5656	0.71094	-0.79556	0.426286	0.619909	chr2	2.03E+08	2.03E+08</								



chr2-1278.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr2	1.28E+08	1.28E+08	0	NA	intron (Nintron (N	-8596 NM_00480E	5433 Hs. 71534E	ENSG000001POLR2D	HSRBP4 HSR	RNA polyn	protein-coding	
chr20-398.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr20	3989272	3990004	0	NA	intron (NMLTII LTF	25920 NM_001134	11237 Hs. 54757E	ENSG000001RNF24	GIL	ring fing	protein-coding	
chr20-458.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr20	45960585	45962594	0	NA	intron (Nintron (N	10614 NM_02209E	63925 Hs. 17419E	ENSG000001ZNF335	MCPH10 N1	zinc fing	protein-coding	
chr20-498.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr20	49651191	49656524	0	NA	intron (Nintron (N	60019 NM_004477E	9334 Hs. 370487	ENSG000001B4GLT5	B4GL1 T5	beta-1,4-	protein-coding	
chr3-9458.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr3	94529155	9459839	0	NA	intron (NAluSx SIN	58675 NM_00108C	55209 Hs. 208816	ENSG000001SETD5	SET	domaipro	tein-coding	
chr3-1335.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr3	1.34E+08	1.34E+08	0	NA	intron (Nintron (N	8252 NM_00128E	55573 Hs. 51826E	ENSG000001CDV3	H41	CDV3 homc	protein-coding	
chr4-3155.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr4	3155770	3165253	0	NA	intron (Nintron (N	-83858 NM_00133C	345222 Hs. 442291	ENSG000001MSANTD1	C4orf44	Ryb/SANT	protein-coding	
chr5-3468.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr5	34687362	34695233	0	NA	intron (Nintron (N	3738 NM_00114E	26064 Hs. 43140C	ENSG000001RAI14	NORPEG Rf	retinoic	protein-coding	
chr5-8348.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr5	83494040	83494243	0	NA	intron (Nintron (N	22397 NM_00438E	1462 Hs. 643801	ENSG000001VCAN	CSPG2 ER	versican	protein-coding	
chr5-1408.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr5	1.41E+08	1.41E+08	0	NA	intron (Nintron (N	-3786 NM_14472E	153527 Hs. 350194	ENSG000001ZMAT2	Ptg-12 S	zinc fing	protein-coding	
chr6-3328.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr6	33201539	33205253	0	NA	intron (Nintron (N	-1259 NM_014234	7923 Hs. 41505E	ENSG000001HSD17B8	D6S2245E	hydroxyst	protein-coding	
chr7-6694.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr7	66947980	66951731	0	NA	intron (Nintron (N	28630 NM_017994	55069 Hs. 48847E	ENSG000001TMEM248	C7orf42	transmemt	protein-coding	
chr7-9941.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr7	99410468	99422367	0	NA	TTS (NM_C	7245 NR_162133	1.13E+08	NR_162133	MIR12119	-	microRNA	ncRNA
chr8-1985.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr8	19830309	19845999	0	NA	intron (NAluSx SIN	20738 NM_01814E	55174 Hs. 512627	ENSG000001INTS10	C8orf35 I	integratc	protein-coding	
chr8-1028.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr8	1.03E+08	1.03E+08	0	NA	intron (Nintron (N	27265 NR_14902C	401472	NR_149020	GASAL1	GASL1	growth	arncRNA
chr9-3298.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr9	32982815	32989915	0	NA	intron (NAluSx SIN	15211 NM_00119E	54840 Hs. 20158	ENSG000001APT	AOA AOA1	aprataxir	protein-coding	
chr9-3504.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr9	35043074	35069114	0	NA	TTS (NM_C	13854 NM_20329E	138724 Hs. 14825C	ENSG000001C9orf131	-	chromoson	protein-coding	
chr9-1258.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr9	1.25E+08	1.25E+08	0	NA	intron (Nintron (N	93207 NM_001354	26130 Hs. 42376	ENSG000001GAPVD1	GAPEX5 G	GTGase	protein-coding	
chr9-1314.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr9	1.31E+08	1.31E+08	0	NA	intron (Nintron (N	-16899 NR_002914	26786	NR_002914	ENSG000001SNORD62A	RNU62 U6	small	nucsnRNA
chr9-1333.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr9	1.33E+08	1.33E+08	0	NA	TTS (NM_C	1103 NR_00001E	26813	NR_00001E	ENSG000001SNORD36C	RNU36C U	small	nucsnRNA
chr9-1364.8.328456	-0.58262	0.738045	-0.78941	0.429873	0.619909	chr9	1.36E+08	1.36E+08	0	NA	exon (NM	7902 NM_01516C	23203 Hs. 495471	ENSG000001PMPCA	Alpha-MP	peptidase	protein-coding	
chr2-3885.8.2891	-0.58578	0.742654	-0.78876	0.43025	0.619909	chr2	38859962	38862239	0	NA	exon (NM	14834 NM_00132E	90957 Hs. 46822E	ENSG000001DHX57	DDX57	DEXH-box	protein-coding	
chr2-5812.8.2891	-0.58578	0.742654	-0.78876	0.43025	0.619909	chr2	58123590	58123834	0	NA	intron (NAluJb SIN	77000 NM_00113C	7444 Hs. 71529E	ENSG000001VRK2	-	VRK serir	protein-coding	
chr10-458.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr10	45825512	45827468	0	NA	exon (NM	-9166 NM_001351	643479 Hs. 52290C	ENSG000001P13E234	FAM25E	FAM25D	family	wiprotein-coding
chr11-354.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr11	35447502	35449885	0	NA	intron (NLIPIA10 LI	-28635 NM_00125E	6506 Hs. 50233E	ENSG000001SLCIA2	EAAT2 E1E	solute	carrier	protein-coding
chr19-258.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr19	25275012	25275862	0	NA	Intergeni	-111990 NR_00360E	1E+08	NR_00360E	ENSG000001HACLIP1	-	hepatitis	pseudo
chr19-482.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr19	4841835	48418440	0	NA	intron (Nintron (N	2541 NR_07302E	6141 Hs. 515517	ENSG000001RPLV1	DBA18 L1	ribosomal	protein-coding	
chr19-538.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr19	53568650	53579582	0	NA	intron (NAluSx SIN	18809 NM_00107E	55422 Hs. 185674	ENSG000001ZNF331	RITA ZNF	zinc fing	protein-coding	
chr5-1507.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr5	1.51E+08	1.51E+08	0	NA	intron (NAluJb SIN	-17998 NM_018047	55696 Hs. 713564	ENSG000001RBM22	Cwc2 ZC3	RNA bindi	protein-coding	
chr6-5358.8.301483	-0.58301	0.739381	-0.78851	0.430396	0.619909	chr6	53502795	53511557	0	NA	intron (NAluJb SIN	37925 NM_001197	2729 Hs. 65446E	ENSG000001GCLC	GCL GC3	glutamate	protein-coding	
chr18-701.8.839087	-0.56265	0.714243	-0.78775	0.430843	0.619909	chr18	70102876	70103177	0	NA	intron (NSVA_A Ret	102661 NM_17363C	25914 Hs. 65480E	ENSG000001RRTN	MSSP	rotatin	protein-coding	
chr1-4628.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr1	46284904	46286234	0	NA	exon (NM	17797 NR_00636E	10489 Hs. 144941	ENSG000001LRC41	MUF1 PP7	leucine	protein-coding	
chr1-1108.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr1	1.1E+08	1.1E+08	0	NA	intron (NAluSx SIN	-5470 NR_102697	1.01E+08	NR_102697	LAMTOR5-A-	LAMTOR5	ancRNA	
chr1-1471.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr1	1.47E+08	1.47E+08	0	NA	intron (Nintron (N	12213 NR_10387C	5565 Hs. 50732	ENSG000001PRKAB2	-	protein	kprotein-coding	
chr1-1698.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr1	1.7E+08	1.7E+08	0	NA	TTS (NM_C	40470 NM_002042E	57147 Hs. 43556E	ENSG000001SCYL3	PACE-1 P	PCy1	like	protein-coding
chr10-108.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr10	1E+08	1E+08	0	NA	intron (Nintron (N	-5605 NM_001347	10613 Hs. 150087	ENSG000001ERLIN1	C10orf69	ER lipid	protein-coding	
chr11-477.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr11	47716586	47733995	0	NA	intron (Nintron (N	-9921 NM_02478E	79841 Hs. 147377	ENSG000001AGBL2	CCP2	ATP/GTP	protein-coding	
chr12-534.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr12	53479220	53480817	0	NA	3' UTR (N3' UTR (N	15550 NR_109828E	1.02E+08	NR_109828E	ENSG000001PCBP2-OT1	UC3A T	PCBP2	ovncRNA
chr12-108.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr12	1E+08	1E+08	0	NA	intron (NAluJb SIN	7178 NR_04856E	64431 Hs. 11508E	ENSG000001ACTR6	ARP6 C3A	actin	protein-coding	
chr12-111.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr12	1.1E+08	1.1E+08	0	NA	intron (Nintron (N	45435 NM_17066E	488 Hs. 50675E	ENSG000001ATP2A2	ATP2B DAF	ATPase	protein-coding	
chr14-684.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr14	68915112	68922055	0	NA	intron (NAluJ SINE	60719 NM_00110E	87 Hs. 23575E	ENSG000001ACTN1	BDLP15	actinin	protein-coding	
chr15-488.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr15	48462027	48466318	0	NA	intron (Nintron (N	131975 NM_001194E	1854 Hs. 52798C	ENSG000001DUPT	DUPTase	deoxyuric	protein-coding	
chr15-641.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr15	64112108	64133792	0	NA	intron (Nintron (N	26968 NM_00309E	6642 Hs. 188634	ENSG000001SNX1	Hs1T7379	sorting	protein-coding	
chr16-281.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr16	28146463	28153746	0	NA	intron (Nintron (N	61861 NM_00127C	23214 Hs. 46046E	ENSG000001XPO6	EXP6 RAN	exportin	protein-coding	
chr16-717.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr16	71753270	71759751	0	NA	intron (Nintron (N	1977 NR_00305E	69211 Hs. 46046E	ENSG000001SNORD71	HB11-239	small	nucsnRNA	
chr17-365.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr17	36579181	36590279	0	NA	intron (NAluJr SIN	-7149 NM_002430E	79154 Hs. 46285E	ENSG000001DHR511	ARPG836	dehydroge	protein-coding	
chr17-428.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr17	42816303	42822117	0	NA	intron (Nintron (N	4669 NM_00131E	8678 Hs. 716464	ENSG000001BECN1	ATG6 VPS	beclin 1	protein-coding	
chr17-768.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr17	76037657	76069986	0	NA	promoter-promoter-	-165 NM_00126E	6730 Hs. 51449E	ENSG000001SRP68	-	signal	reprotein-coding	
chr19-438.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr19	43888275	43997995	0	NA	intron (Nintron (N	8847 NR_139808E	7711 Hs. 27956E	ENSG000001ZNF155	pHZ-96	zinc	protein-coding	
chr2-2738.8.313866	-0.58026	0.739423	-0.78475	0.432602	0.619909	chr2	27339065	27343231	0	NA	intron (NAluSx SIN	5606 NR_038427	1.01E+08	NR_038427	ENSG000001GTF3C2-AS-	-	GTF3C2	arncRNA

chr6-131e	9.07172	-0.48341	0.696287	-0.69427	0.487511	0.640316	chr6	1.32E+08	1.32E+08	0	NA	exon (NM_exon (NM_25908 NM_00127C	9439 Hs. 29679	NM_00483C	ENS00000	CMD23	ARC130 CFmediator protein-coding
chr1-171f	9.030157	-0.48154	0.694257	-0.6936	0.487934	0.640316	chr1	1.72E+08	1.72E+08	0	NA	intron (N Tigger3b  -36054 NM_001366	1.11E+08	NM_001368164	MYOCOS	- myocilin protein-coding	
chr1-2237	9.030157	-0.48154	0.694257	-0.6936	0.487934	0.640316	chr1	2.24E+08	2.24E+08	0	NA	intron (N intron (N_61574 NM_00174E	824 Hs. 35089	NM_00174E	ENS00000	CAPN2	CANP2 CAN calpain 2 protein-coding
chr13-145	9.030157	-0.48154	0.694257	-0.6936	0.487934	0.640316	chr13	45335224	45340489	0	NA	promoter-promoter- 247 NR_002967	677814 Hs. 37459	NR_002967	ENS00000	SNORA31	ACT31 SNC small nucsnoRNA
chr19-197	9.030157	-0.48154	0.694257	-0.6936	0.487934	0.640316	chr19	19709566	19723480	0	NA	intron (N AluSz6 SI 16591 NR_002103C	7561 Hs. 65993	NM_002103C	ENS00000	ZNF14	GIOA3-4 KC zinc finger protein-coding
chr3-869f	9.030157	-0.48154	0.694257	-0.6936	0.487934	0.640316	chr3	86967274	86969443	0	NA	intron (N intron (N_22791 NM_00132C	389136 Hs. 60650	NM_00132C	ENS00000	VGLL3	VGL-3 VGL vestigial protein-coding
chr4-102f	9.030157	-0.48154	0.694257	-0.6936	0.487934	0.640316	chr4	1.03E+08	1.03E+08	0	NA	intron (N intron (N_126316 NM_00590E	4126 Hs. 48041	NM_00590E	ENS00000	MANBA	MANB1 mannosidase protein-coding
chr1-168f	9.05713	-0.48127	0.694083	-0.69339	0.488062	0.640316	chr1	1.68E+08	1.68E+08	0	NA	intron (N intron (N_1128 NR_03170Z	1E+08	NR_03170Z	ENS00000	MIR1255B	MIR1255B-microRNA ncRNA
chr15-32f	9.05713	-0.48127	0.694083	-0.69339	0.488062	0.640316	chr15	32846805	32848439	0	NA	intron (N AluY SINE -128757 NR_109767	1E+08 Hs. 61054	NR_109767	ENS00000	LOC100131-	uncharactericncRNA
chr15-92f	9.05713	-0.48127	0.694083	-0.69339	0.488062	0.640316	chr15	92923258	92929872	0	NA	intron (N intron (N_22301 NR_00313E	1E+08	NM_00313E	ENS00000	MIR3175	mir-3175 microRNA ncRNA
chr16-554	9.05713	-0.48127	0.694083	-0.69339	0.488062	0.640316	chr16	55487716	55494764	0	NA	intron (N MLT1C LTF 9683 NR_001127	4313 Hs. 51361	NM_00453C	ENS00000	CMP2	CLG4 CLG4 matrix mcp protein-coding
chr5-132f	9.05713	-0.48127	0.694083	-0.69339	0.488062	0.640316	chr5	1.33E+08	1.33E+08	0	NA	exon (NM_exon (NM_22723 NM_052971	116842 Hs. 33758	NM_052971	ENS00000	LEAP2	LEAP-2 liver enr protein-coding
chr8-390f	9.05713	-0.48127	0.694083	-0.69339	0.488062	0.640316	chr8	39053619	39057051	0	NA	intron (N LIME4a LI -36650 NR_14598E	1.1E+08	NR_14573E	ENS00000	SNORD38D	- small nucsnoRNA
chr2-2317	9.076136	-0.49292	0.71107	-0.69321	0.488178	0.640316	chr2	2.32E+08	2.32E+08	0	NA	promoter-promoter- -366 NR_12871C	1.04E+08	NR_12871C	ENS00000	MIR1244-	hsa-mir-1244 microRNA ncRNA
chr1-246f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr1	24660520	24679183	0	NA	intron (N intron (N_26272 NM_00136E	10250 Hs. 18192	NM_00583E	ENS00000	SRRM1	160-KD PC serine ar protein-coding
chr1-1147	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr1	1.15E+08	1.15E+08	0	NA	intron (N AluJb SIN -4848 NM_002524	4893 Hs. 48650	NM_002524	ENS00000	NRAS	ALP54 CML NRAS prot protein-coding
chr10-46f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr10	46006776	46018171	0	NA	intron (N intron (N_7064 NM_00114E	8031 Hs. 64365	NM_00543E	ENS00000	CNCOA4	AR470 ELF nuclear r protein-coding
chr10-97f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr10	97650665	97659200	0	NA	intron (N HALIME LI 14246 NM_01842E	55361 Hs. 25300	NM_01842E	ENS00000	PI4KA2	PI4K11 PI phosphatid protein-coding
chr14-102	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr14	1.02E+08	1.02E+08	0	NA	3' UTR (N3' UTR (N_5926 NM_00534E	3320 Hs. 52560	NM_00534E	ENS00000	HSP90AA1	EL52 HEL-heat shoc protein-coding
chr15-78f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr15	78878188	78904897	0	NA	exon (NM_exon (NM_18553 NM_00126E	10933 Hs. 37450	NM_006791	ENS00000	MORF4L1	Eaf3 FWPC mortality protein-coding
chr16-214	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr16	21465146	21473280	0	NA	intron (N intron (N_-32313 NR_02746C	1E+08 Hs. 70957	NR_02746C	RRN3P3	- RRN3 homcpseudo	
chr16-754	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr16	75410330	75412592	0	NA	intron (N intron (N_22042 NM_006324	10428 Hs. 46136	NM_006324	ENS00000	CFDP1	BCNT BUCE craniofac protein-coding
chr17-424	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr17	42474006	42482958	0	NA	exon (NM_exon (NM_-16291 NR_04984E	1.01E+08	NR_04984E	ENS00000	MIR548AT	- microRNA ncRNA
chr17-58f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr17	58002913	58006431	0	NA	3' UTR (N3' UTR (N_6426 Hs. 68714	NM_006924	ENS00000	SRSF1	ASF SF2 serine ar protein-coding	
chr18-34f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr18	3456201	3461055	0	NA	TTS (NM_C TTS (NM_C_4854 NM_173211	7050 Hs. 37355	NM_003244	ENS00000	TGIF1	HPF4 TGIF1 induc protein-coding
chr19-47f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr19	47352500	47364698	0	NA	intron (N AluJo SIN 9284 NM_014681	9704 Hs. 15170	NM_014681	ENS00000	DHX34	DDX34 HRF DEXH-box protein-coding
chr2-227f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr2	2.28E+08	2.28E+08	0	NA	66981 NM_004504	3267 Hs. 35296	NM_004504	ENS00000	AGFG1	HRB HRB FArGAP wiprotein-coding
chr2-29f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr2	29547043	29549456	0	NA	intron (N intron (N_5406 NM_00100Z	8563 Hs. 75361	NM_00367E	ENS00000	THOC5	C22orf19 THO compl protein-coding
chr5-388f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr5	38874010	38889503	0	NA	exon (NM_exon (NM_35744 NM_00132E	9180 Hs. 12065	NM_00399E	ENS00000	OSMR	IL-31R-beoncostatiprotein-coding
chr5-149f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr5	1.5E+08	1.5E+08	0	NA	intron (N intron (N_41619 NM_001271	1452 Hs. 52986	NM_00189Z	ENS00000	CNSK1A1	CK1 CK1a casein iprotein-coding
chr7-755f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr7	75510070	75526205	0	NA	intron (N ATn Sin 9986 NR_02805E	5387 Hs. 65987	NM_00539E	ENS00000	PMS2P3	PMS2L3 PMS1 homcpseudo
chr9-124f	9.04254	-0.47914	0.694219	-0.69019	0.490074	0.640316	chr9	1.24E+08	1.24E+08	0	NA	intron (N intron (N_1771 NM_00279E	5695 Hs. 21347	NM_00279E	ENS00000	PSMB7	Z proteasom protein-coding
chr6-151f	9.015566	-0.47939	0.696734	-0.68806	0.491416	0.640316	chr6	1.5E+08	1.5E+08	0	NA	intron (N AluSz SIN 8824 NM_00135C	25902 Hs. 59134	NM_01544C	ENS00000	MTF5DL	FTF ZFSDCI1 methyleneprotein-coding
chr10-29f	9.069513	-0.47886	0.696686	-0.68734	0.491867	0.640316	chr10	29654479	29658065	0	NA	intron (N intron (N_-21301 NM_02173E	6840 Hs. 49920	NM_003174	ENS00000	CSVL	- supervill protein-coding
chr2-390f	9.069513	-0.47886	0.696686	-0.68734	0.491867	0.640316	chr2	39022335	39023249	0	NA	exon (NM_exon (NM_-62448 NR_02838E	375196 Hs. 65903	NR_02838E	ENS00000	LOC37519E	uncharactericncRNA
chr1-400f	9.027949	-0.47699	0.696698	-0.68464	0.493572	0.640316	chr1	40059313	40076435	0	NA	intron (N intron (N_27023 NM_00135C	10487 Hs. 37058	NM_006367	ENS00000	CAP1	CAP CAP1-cyclase ar protein-coding
chr13-331	9.027949	-0.47699	0.696698	-0.68464	0.493572	0.640316	chr13	33128915	33130233	0	NA	exon (NM_exon (NM_56517 NM_178007	90627 Hs. 15655	NM_052851	ENS00000	STARD13	ARHGAP37 STAR relaprotein-coding
chr6-434	9.027949	-0.47699	0.696698	-0.68464	0.493572	0.640316	chr6	43440043	43440748	0	NA	intron (N L2a LINE 5853 NR_106894	1.02E+08	NR_106894	ENS00000	MIR6780B	hsa-mir-6780 microRNA ncRNA
chr2-1521	9.484634	-0.46474	0.681761	-0.68167	0.495448	0.640316	chr2	1.52E+08	1.52E+08	0	NA	intron (N AluSc SIN 31022 NM_00584Z	10254 Hs. 17200	NM_00584Z	ENS00000	STAM2	Hbp STAM2 signal tr protein-coding
chr1-235f	9.531908	-0.49347	0.724678	-0.68095	0.495903	0.640316	chr1	2.35E+08	2.35E+08	0	NA	intron (N LIPA3 LIN 19665 NM_001287	6905 Hs. 74499	NM_00319E	ENS00000	TBCE	HRD KCS1 tubulin f protein-coding
chr19-384	9.988593	-0.47963	0.704415	-0.68089	0.495941	0.640316	chr19	38405334	38405535	0	NA	intron (N intron (N_2299 NM_17490E	147965 Hs. 35516	NM_17490E	ENS00000	FAM98C	- family wiprotein-coding
chr16-554	9.558881	-0.49317	0.72444	-0.68076	0.496021	0.640316	chr16	55495634	55499087	0	NA	intron (N MER113 DN -11712 NM_01783E	54947 Hs. 46085	NM_01783E	ENS00000	LPAT2	AGPAT11 lysophosph protein-coding
chr17-31f	9.558881	-0.49317	0.72444	-0.68076	0.496021	0.640316	chr17	31973645	31974619	0	NA	intron (N AluJb SIN -33251 NM_001321	114659 Hs. 51407	NM_05288E	ENS00000	LRRC37B	LRRC37 leucine r protein-coding
chr19-13f	9.558881	-0.49317	0.72444	-0.68076	0.496021	0.640316	chr19	1362361	1363775	0	NA	intron (N LIMD2 LIN 5649 NM_00136E	84939 Hs. 51501	NM_03222C	ENS00000	PWP3A	EXPAND1 PWPW domaprotein-coding
chr3-584f	9.558881	-0.49317	0.72444	-0.68076	0.496021	0.640316	chr3	58424799	58431966	0	NA	intron (N intron (N_5450 NM_00092E	5162 Hs. 16135	NM_00092E	ENS00000	PDHB	PDH pyruvate protein-coding
chr4-107f	9.558881	-0.49317	0.72444	-0.68076	0.496021	0.640316	chr4	1.08E+08	1.08E+08	0	NA	intron (N MSTD LTR  19527 NM_00544Z	9061 Hs. 36861	NM_00544Z	ENS00000	PAPSS1	ATPSK1 P3'3'-phosp protein-coding
chr1-1634	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	1634422	1657869	0	NA	intron (N LIM4a2 LI 12859 NM_03349C	984 Hs. 65122	NM_001787	ENS00000	CDK11B	CDC2L1 Cyclin deprotein-coding
chr1-320f	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	32037402	32060922	0	NA	intron (N intron (N_-25219 NM_00131E	55116 Hs. 25544	NM_01805E	ENS00000	TMEM39B	- transmem protein-coding
chr1-6704	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	67046087	67051405	0	NA	intron (N intron (N_5402 NM_01513E	23169 Hs. 21364	NM_01513E	ENS00000	SLC35D1	SHNKND UC solute caprotein-coding
chr1-146f	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	1.47E+08	1.47E+08	0	NA	intron (N LTR5_Hs I 10579 NM_00127E	149013 Hs. 66698	NM_00127E	ENS00000	NBPF12	COAS1 KI1 NBPF memt protein-coding
chr1-149f	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	1.5E+08	1.5E+08	0	NA	intron (N AluSx SIN -33564 NM_00114E	10903 Hs. 42514	NM_006697	ENS00000	MTMR11	CRA myotubulaprotein-coding
chr1-151f	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	1.51E+08	1.51E+08	0	NA	intron (N intron (N_7837 NM_00119E	5298 Hs. 63246	NM_002651	ENS00000	PI4KB	NPK1 PI4b phosphatid protein-coding
chr1-153f	9.544291	-0.49087	0.723204	-0.67874	0.497304	0.640316	chr1	1.54E+08	1.54E+08	0	NA	intron (N MRB SINE -4299 NM_01485E	9909 Hs. 74487	NM_01485E	ENS00000	DENN4B	KIAA0476 DENN domaprotein-coding
chr1-171f	9.544291	-0.49087	0.723204														



chr12-577.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr12	57794894	57797248	0	NA	intron (Nintron (N	13284	10102	Hs.632704NM_00572c	ENS00000	TSFM	EFTS EFTS	translprotein-coding	
chr14-504.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr14	50443148	50447021	0	NA	exon (NM exon (NM	-47786	8814	Hs.280881NM_00419c	ENS00000	CDKL1	KKIALRE F	cyclin deprotein-coding	
chr15-658.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr15	65876579	65883873	0	NA	intron (Nintron (N	10735	8766	Hs.321541NM_00466c	ENS00000	CAB11A	YL8	RAB11A, nprotein-coding	
chr2-652.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr2	65259132	65259344	0	NA	intron (NAluJo SIN	31543	10097	Hs.643727NM_00572c	ENS00000	ACTR2	ARP2	actin relprotein-coding	
chr2-1751.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr2	1.75E+08	1.75E+08	0	NA	3' UTR (N3' UTR (N	3534	518	Hs.429	NR_00168c	ENS00000	ATP5MC3	ATP5G3 PE	ATP synthprotein-coding
chr4-5702.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr4	57021284	57023016	0	NA	intron (Nintron (N	43254	5431	Hs.602757NM_00093c	ENS00000	POLR2B	POL2RB RF	RNA polynprotein-coding	
chr5-959.8.556674	-0.48826	0.724714	-0.67373	0.500485	0.640316	chr5	95902973	95916319	0	NA	intron (Nintron (N	52205	22936	Hs.192221NM_01208c	ENS00000	ELL2	MRCRAT1	elongaticprotein-coding	
chr7-1305.8.048225	-0.50956	0.759126	-0.67125	0.502064	0.640316	chr7	1.31E+08	1.31E+08	0	NA	intron (NLCz LINE	10626	378805	Hs.15055c	ENS00000	LINC-PINT	LINCRNA-F	long intencRNA	
chr4-999.8.060633	-0.50667	0.755779	-0.6704	0.502604	0.640316	chr4	99905941	99906682	0	NA	intron (NLS LINE C	-11765	8649	Hs.43333c	ENS00000	LAMTOR3	MAP2K1 P1	late endcprotein-coding	
chr12-327.8.046042	-0.50416	0.752819	-0.66969	0.503053	0.640316	chr12	32739908	32740259	0	NA	exon (NM exon (NM	15814	51067	Hs.505231NM_01593c	ENS00000	YARS2	CGI-04 ML	tyrosyl-tprotein-coding	
chr12-102.8.046042	-0.50416	0.752819	-0.66969	0.503053	0.640316	chr12	1.02E+08	1.02E+08	0	NA	intron (N(SVA_A Ret	-27384	51019	Hs.405692NM_01605c	ENS00000	WASHC3	CCG53 CC	WASH compprotein-coding	
chr17-638.8.046042	-0.50416	0.752819	-0.66969	0.503053	0.640316	chr17	63829392	63837943	0	NA	exon (NM exon (NM	5061	6603	Hs.250581NM_00307c	ENS00000	SMARCD2	BAF60B CF	SWI/SNF rprotein-coding	
chr20-195.8.046042	-0.50416	0.752819	-0.66969	0.503053	0.640316	chr20	19965514	19967700	0	NA	intron (NAluSq2 SI	-50683	51126	Hs.39878c	ENS00000	NAA20	NAT3 NAT	(alpha)-protein-coding	
chr8-1407.8.046042	-0.50416	0.752819	-0.66969	0.503053	0.640316	chr8	1.41E+08	1.41E+08	0	NA	intron (NAluS26 SI	5271	5747	Hs.35657c	ENS00000	PTK2	FADK FAK	protein tprotein-coding	
chr16-160.8.502727	-0.48883	0.730153	-0.66949	0.503182	0.640316	chr16	16030281	16030930	0	NA	intron (NLMC5 LIN	80989	4363	Hs.391464NM_00499c	ENS00000	ABCC1	ABC29 ABC	ATP bindiprotein-coding	
chr12-115.8.542083	-0.48593	0.726107	-0.66923	0.503348	0.640316	chr12	1.16E+08	1.16E+08	0	NA	3' UTR (N3' UTR (N	187501	693205	NR_030351	ENS00000	MIR620	MIRN620	microRNA ncRNA	
chr18-101.8.542083	-0.48593	0.726107	-0.66923	0.503348	0.640316	chr18	10538802	10542419	0	NA	intron (Nintron (N	14583	8774	Hs.464622NM_00382c	ENS00000	CNAPG	GAMMASNAF	NSF attacprotein-coding	
chr2-727.8.542083	-0.48593	0.726107	-0.66923	0.503348	0.640316	chr2	72763211	72764126	0	NA	intron (NAluSz SIN	62365	23233	Hs.303454NM_01518c	ENS00000	EXOC6B	SEC15B SE	exocyst protein-coding	
chr6-564.8.542083	-0.48593	0.726107	-0.66923	0.503348	0.640316	chr6	56461937	56466301	0	NA	intron (Nintron (N	-69991	81578	Hs.47629	NR_03082c	ENS00000	COL21A1	COLA1L F	collagen protein-coding
chr5-704.8.583647	-0.48791	0.73056	-0.66786	0.504221	0.640316	chr5	70496148	70496776	0	NA	intron (NMIR3 SINE	4306	1E+08	Hs.665231NR_03396c	ENS00000	GUSBP9	-	GUSB pseupseudo	
chr1-408.8.51511	-0.48621	0.728657	-0.66726	0.504603	0.640316	chr19	40708504	40710255	0	NA	intron (NLMC5a LI	5740	79934	Hs.13071c	ENS00000	COQB8	ADCK4 NP	coenzyme protein-coding	
chr1-3284.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr1	32845726	32848174	0	NA	intron (NAluSp SIN	21637	64766	Hs.44088c	ENS00000	S100PPP	S100PPBP	S100P	birprotein-coding
chr1-114.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr1	1.15E+08	1.15E+08	0	NA	3' UTR (N3' UTR (N	13757	10286	Hs.22960	NR_00587c	ENS00000	BCAS2	DAM1 SPF	2C preprotein-coding
chr11-157.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr11	5706230	5709800	0	NA	intron (Nintron (N	18225	10346	Hs.50177c	ENS00000	TRIM22	GPSTAF50	tripartitprotein-coding	
chr12-193.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr12	19370570	19372284	0	NA	3' UTR (N3' UTR (N	-68065	121536	Hs.126497NM_15320c	ENS00000	AEBP2	-	AE bindirprotein-coding	
chr12-297.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr12	29757469	29758742	0	NA	intron (Nintron (N	25837	83857	Hs.401954NM_03192c	ENS00000	TMTC1	ARG99 OLF	transmentprotein-coding	
chr14-36.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr14	36309419	36311710	0	NA	intron (NLCz LINE	10073	51562	Hs.308647NM_01518c	ENS00000	CMBIP	-	MAP3K12	tprotein-coding
chr17-207.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr17	-2078907	2081373	0	NA	intron (Nintron (N	8621	23293	Hs.44834c	ENS00000	SMG6	C17orf31	SMG6 nonsprotein-coding	
chr17-294.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr17	29495310	29506233	0	NA	intron (NLMB4 LIN	66266	116236	Hs.10651c	ENS00000	ABHD15	-	abhydrola	protein-coding
chr18-63.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr18	63388777	63404091	0	NA	intron (NAluJb SIN	26042	9525	Hs.12655c	ENS00000	VPS4B	MIG1 SKD	1 vacuolar protein-coding	
chr19-39.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr19	3953190	3968397	0	NA	TTS (NR_C TTS (NR_C	719	693222	NR_030367	ENS00000	MIR637	MIRN637	microRNA ncRNA	
chr2-2307.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr2	2.31E+08	2.31E+08	0	NA	intron (NAluSx1 SI	30578	51719	Hs.60393c	ENS00000	CAB39	CGI-66 MC	calcium tprotein-coding	
chr2-2381.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr2	2.38E+08	2.38E+08	0	NA	intron (NLMC5a LI	21443	151176	Hs.24951	NR_15252c	ENS00000	ERFE	C1QNF15	erythrofeprotein-coding
chr3-4597.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr3	45976256	45981262	0	NA	intron (Nintron (N	17065	79443	Hs.200227NM_02451c	ENS00000	FYCO1	CATC2 CT	FYVE and protein-coding	
chr5-407.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr5	40760728	40765420	0	NA	intron (Nintron (N	-7113	23548	Hs.34891c	ENS00000	TTCC3	OSRF	tetratricprotein-coding	
chr6-411.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr6	4115536	4125706	0	NA	intron (NAluSx SIN	14847	10455	Hs.15250	NR_00611c	ENS00000	CEC12	ACBD2 DRS	enoyl-CoA protein-coding
chr6-565.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr6	56588331	56594082	0	NA	intron (Nintron (N	51683	667	Hs.60491c	ENS00000	CDST	BP240 BP	dystonin protein-coding	
chr6-150.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr6	1.51E+08	1.51E+08	0	NA	intron (Nintron (N	20638	25902	Hs.59134c	ENS00000	CTHFD1L	FTHFSDC1	methyleneprotein-coding	
chr7-262.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr7	26204997	26212318	0	NA	intron (NAluSq2 SI	6912	11335	Hs.38118c	ENS00000	CBX3	HECH HPI	chromoboxprotein-coding	
chr7-762.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr7	77627018	77629458	0	NA	intron (Nintron (N	68027	101E+08	Hs.72451	NR_03836c	ENS00000	CAPTR	RSBN1L-AS	Alu-mediencRNA
chr7-871.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr7	87164553	87177330	0	NA	intron (Nintron (N	18387	9988	Hs.19612c	ENS00000	DMT1F	DMP1 DMT	f cyclin D protein-coding	
chr8-2537.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr8	25376795	25379498	0	NA	intron (NMER2 C LI	-16634	105E+08	NR_159962	LOC10537c	-	uncharactncRNA		
chr8-6724.8.058425	-0.50135	0.752905	-0.66588	0.505486	0.640316	chr8	67247189	67253274	0	NA	intron (NLCz LINE	93550	10565	Hs.65690c	ENS00000	ARFGF1	ARFGEP1 E	ADP ribosprotein-coding	
chr22-11.8.5761	0.247374	0.372541	0.664018	0.506679	0.640316	chr22	11905785	11906098	0	NA	intron (NAluSx4 SI	8535	6E+08	Hs.65292c	NR_110761	LOC10272c	-	uncharactncRNA	
chr1-178.8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr1	1785022	1797824	0	NA	intron (NAluSp SIN	-11392	56220	Hs.65479c	ENS00000	CNADK	dJ283E3.1N	AD kinaseprotein-coding	
chr1-1107.8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr1	11072523	11097741	0	NA	intron (NLIPI3 LIN	-14543	10218	Hs.14655c	ENS00000	ANGPTL7	AngX CDT	angiopoicprotein-coding	
chr1-112.8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr1	11203229	11204695	0	NA	intron (NMLT1G LI	14607	200081	Hs.17987	NR_17585c	ENS00000	TXLNA	IL14 TXL	taxilin tprotein-coding
chr1-321.8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr1	32180516	32198495	0	NA	intron (Nintron (N	9830	7579	Hs.44270c	ENS00000	ZSCAN20	KOX29 ZFF	zinc fingprotein-coding	
chr1-3347.8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr1	33479369	33482474	0	NA	intron (NTigger12c	8276	79729	Hs.52449c	ENS00000	SH3D21	Clorf113	SH3	domaiprotein-coding
chr1-362.8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr1	36285737	36299737	0	NA	intron (Nintron (N	-13631	115353	Hs.40094	NR_05294c	ENS00000	LRRC42	dJ167A19.	leucine rprotein-coding
chr1-539.8																			

chr2-1054	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr2	95097225	95106190	+0	NA	exon (NM_exon (NM_19850	19850	NR_001321	64969	Hs.655255	NR_031902	ENSG000003MRP55	MRP-S5	SE	mitochondrial protein-coding	
chr2-1084	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr2	1.08E+08	1.09E+08	+0	NA	intron (NM_LIMC5a LI	33290	NR_13529C	644903	Hs.474938	NR_003265	ENSG000003GCC2-AS1			GCC2 anticrRNA	
chr2-162C	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr2	1.62E+08	1.62E+08	+0	NA	intron (NMIR3 SINE	37459	NR_00193E	1803	Hs.368912	NR_00193E	ENSG000003DPP4	ADABP	ADC	dipeptidylprotein-coding	
chr2-169F	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr2	1.7E+08	1.7E+08	+0	NA	intron (NALuSx1 SI	26780	NR_00479Z	9360	Hs.470544	NR_00479Z	ENSG000003PP1G	CARS-Cyp	peptidyl	protein-coding	
chr2-2017	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr2	2.02E+08	2.02E+08	+0	NA	intron (NALuSx1 SI	40622	NR_00306E	58538	Hs.63085	NR_00306E	ENSG000003MPP4	ALS2CR3	Lumebriane	protein-coding	
chr2-231C	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr2	2.31E+08	2.31E+08	+0	NA	intron (NALuSx1 SI	7668	NR_002807	5707	Hs.3887	NR_002807	ENSG000003PSMD1	P112 Rpn2	protease	protein-coding	
chr20-114	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr20	1123754	1130523	+0	NA	intron (NALuSx1 SI	8536	NR_001322	9491	Hs.471917	NR_006814	ENSG000003PSMF1	P131	protease	protein-coding	
chr20-304	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr20	3047626	3049617	+0	NA	TTS (NM_CTTs (NM_C	2569	NR_00318E	64949	Hs.18946	NR_030811	ENSG000003MRP526	C20orf19	5	mitochondrial protein-coding	
chr20-354	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr20	35403963	35410066	+0	NA	intron (NALIMB3 LIN	4959	NR_018244	55245	Hs.72629C	NR_018244	ENSG000003UQCC1	BFZB	C20c	ubiquinol protein-coding	
chr20-621	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr20	62124345	62134434	+0	NA	intron (NALuSx1 SI	6914	NR_14470C	149986	Hs.105379	NR_14470C	ENSG000003LSM142E	C20orf40	LSM	family protein-coding	
chr21-347	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr21	34797116	34800038	+0	NA	intron (NMER2 DNA	52752	NR_03888E	1.01E+08	Hs.120175	NR_03888E	ENSG000003LINC0142E	lincRNA-t	-	long intencRNA	
chr21-371	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr21	37131042	37175501	+0	NA	exon (NM_exon (NM_	40655	NR_046651	1.01E+08	Hs.570411	NR_046651	ENSG000003TTC3-AS1			TTC3 anticrRNA	
chr22-26E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr22	26500096	26511488	+0	NA	intron (NALuSx1 SI	6276	NR_01214E	24144	Hs.20225	NR_01214E	ENSG000003TFIP11	NTRI	STIF	tuftelin protein-coding	
chr22-40F	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr22	40822769	40851958	+0	NA	intron (NALuSx1 SI	-17964	NR_00128E	10478	Hs.474938	NR_00635E	ENSG000003SLC25A17	PMP34		solute carrier protein-coding	
chr3-9387	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr3	9387725	9395257	+0	NA	intron (NALuSx1 SI	5132	NR_132781	440944	Hs.598958	NR_00101E	ENSG000003THUMP3D3	ASET5D5-AS1	THUMP3	ancRNA	
chr3-1014	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr3	10148851	10154690	+0	NA	3' UTR (NM_3' UTR (N	9992	NR_19815E	7428	Hs.517792	NR_000551	ENSG000003VHL	HRCAL1	RC	von Hippel protein-coding	
chr3-154F	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr3	15431509	15438186	+0	NA	intron (NALuSx1 SI	7249	NR_03308E	85403	Hs.71673E	NR_03308E	ENSG000003CEAF1			ELL assoc protein-coding	
chr3-163F	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr3	16375800	16378340	+0	NA	intron (NALuSx1 SI	111858	NR_00135E	92106	Hs.65544E	NR_138381	ENSG000003OXNAD1			oxidoreductase protein-coding	
chr3-124E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr3	1.25E+08	1.25E+08	+0	NA	intron (NALuSx1 SI	53533	NR_02073C	57493	Hs.47742C	NR_02073C	ENSG000003HEG1	HEG	MST1	heart dev protein-coding	
chr4-150F	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr4	15057715	15068264	+0	NA	intron (NALuSx1 SI	60508	NR_001177	132864	Hs.656937	NR_18248E	ENSG000003CPEB2	CPE-BP2	C	cytoplasm protein-coding	
chr4-253E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr4	25388749	25398616	+0	NA	intron (NALuSx1 SI	16419	NR_013367	29945	Hs.15217E	NR_013367	ENSG000003ANAPC4	APC4		anaphase protein-coding	
chr4-7081	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr4	70819049	70838298	+0	NA	intron (NALuSx1 SI	10830	NR_00109E	2926	Hs.30976E	NR_00209E	ENSG000003GRSF1			G-rich Rb protein-coding	
chr4-758C	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr4	75807515	75813943	+0	NA	intron (NALuSx1 SI	86207	NR_00371E	8615	Hs.744877	NR_00371E	ENSG000003USO1	P115 TAP	USO1	vesicle protein-coding	
chr5-143E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr5	14323538	14342502	+0	NA	intron (NALuSx1 SI	-130963	NR_14581E	1.1E+08	Hs.120175	NR_03888E	ENSG000003LINC0142E			small ncRNA	
chr5-7211	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr5	72114625	72121125	+0	NA	intron (NALuSx1 SI	10400	NR_00590E	4131	Hs.33507E	NR_00590E	ENSG000003MAP1B	FUTSCH	M	microtubule protein-coding	
chr5-127E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr5	1.28E+08	1.28E+08	+0	NA	intron (NALuSx1 SI	14380	NR_00128E	133619	Hs.48325E	NR_13080E	ENSG000003PRR1			proline r protein-coding	
chr5-132E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr5	1.33E+08	1.33E+08	+0	NA	intron (NALuSx1 SI	32719	NR_132124	1.02E+08	Hs.59881E	NR_132124	ENSG000003TH2LCRR	TH2-LCR		T helper ncRNA	
chr6-1224	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr6	1.22E+08	1.22E+08	+0	NA	intron (NALuSx1 SI	17716	NR_02075E	57515	Hs.14666E	NR_02075E	ENSG000003SERINC1	TDEL	L	TDF serine r protein-coding	
chr6-148E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr6	1.49E+08	1.49E+08	+0	NA	exon (NM_exon (NM_	35569	NR_100134E	23328	Hs.19313E	NR_01527E	ENSG000003SASH1	CAPOK	DUF	SAM and S protein-coding	
chr7-474C	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr7	47437787	47440834	+0	NA	intron (NALuSx1 SI	25493	NR_14581E	1.1E+08	Hs.120175	NR_03888E	ENSG000003SNORD151			small ncRNA	
chr7-100C	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr7	1E+08	1E+08	+0	NA	intron (NALuSx1 SI	10356	NR_00134E	7586	Hs.61536E	NR_00343E	ENSG000003ZKSCAN1	KOX18	PHZ	zinc finger protein-coding	
chr7-103E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr7	1.01E+08	1.01E+08	+0	NA	intron (NALuSx1 SI	7055	NR_00101E	402682	Hs.53484E	NR_00101E	ENSG000003UFSP1	UFSP		UFMI spec protein-coding	
chr7-100F	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr7	1.03E+08	1.03E+08	+0	NA	intron (NALuSx1 SI	16319	NR_00280E	5701	Hs.43736E	NR_00280E	ENSG000003PCMC2	MSS1	Nbl	protease protein-coding	
chr7-116E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr7	1.17E+08	1.17E+08	+0	NA	intron (NALuSx1 SI	-38079	NR_00136E	7982	Hs.368131	NR_01841E	ENSG000003ST7	ETS7q	FA	suppressin protein-coding	
chr8-226E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr8	22605905	22616618	+0	NA	intron (NALuSx1 SI	6219	NR_0021174	57805	Hs.74484E	NR_021174	ENSG000003CCAR2	DBC-1	DBC	cell cycl protein-coding	
chr8-9814	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr8	98147769	98148988	+0	NA	intron (NALuSx1 SI	30538	NR_01502E	10940	Hs.25282E	NR_01502E	ENSG000003POP1	ANXD2		POP1 hom protein-coding	
chr8-1237	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr8	1.24E+08	1.24E+08	+0	NA	intron (NALuSx1 SI	14747	NR_001317	157769	Hs.459174	NR_14496E	ENSG000003FAM91A1			family wiprotein-coding	
chr8-1254	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr8	1.25E+08	1.25E+08	+0	NA	exon (NM_exon (NM_	4132	NR_00128E	10221	Hs.444947	NR_02519E	ENSG000003TRIB1	C8FW	GIG	tribbles protein-coding	
chr8-144E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr8	1.45E+08	1.45E+08	+0	NA	3' UTR (NM_3' UTR (N	18853	NR_00136E	58500	Hs.532277	NR_021061	ENSG000003ZNF250	ZFP647	Zn	zinc finger protein-coding	
chr9-2691	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr9	26918508	26926349	+0	NA	intron (NALuSx1 SI	-24562	NR_00109E	80173	Hs.14540E	NR_02510E	ENSG000003IFT74	BBS20	CCI	intraflag protein-coding	
chr9-2721	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr9	27212821	27215258	+0	NA	intron (NALuSx1 SI	68754	NR_002667E	158035	Hs.201554	NR_02667E	ENSG000003LINC00032E	C9orf14	N	long intencRNA	
chr9-332E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr9	33251846	33263059	+0	NA	intron (NALuSx1 SI	7256	NR_00117E	573	Hs.377484	NR_00432E	ENSG000003BAG1	BAG-1	HAF	BCL2 assoc protein-coding	
chr9-113E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chr9	1.13E+08	1.13E+08	+0	NA	intron (NALuSx1 SI	10804	NR_001371234								
chrX-138E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chrX	1385906	1391495	+0	NA	intron (NALuSx1 SI	3413	NR_00163E	293	Hs.350927	NR_00163E	ENSG000003SLC25A6	AAC3	AIF	solute carrier protein-coding	
chrX-108E	8.043835	-0.49887	0.7529	-0.66259	0.507591	0.640316	chrX	24069332	24079129	+0	NA	intron (NALuSx1 SI	19274	NR_00141E	1968	Hs.539684	NR_00141E	ENSG000003EIF2S3	EIF2	ENT	eukaryot protein-coding	
chr4-554E	8.554466	-0.48323	0.730719	-0.66131	0.508413	0.641139	chr4	55465915	55466598	+0	NA	intron (THEIB LTF	70299	NR_01847E	55858	Hs.47976E	NR_01847E	ENSG000003TMEM165	CDGK2	FTZ	transmem protein-coding	
chr1-252E	9.213405	0.452444	0.691349	0.654437	0.51283	0.646457	chr1	2522689	2522984	+0	NA	intron (NALuSx1 SI	3760	NR_01821E	55229	Hs.26156	NR_01821E	ENSG000003PANK4			pantothier protein-coding	
chr8-241F	10.75754	-0.3889	0.594454	-0.65421	0.512974	0.646457	chr8	241556	248678	+0	NA	intron (NALuSx1 SI	12661	NR_00104E	169270	Hs.59138E	NR_17353E	ENSG000003ZNF596			zinc finger protein-coding	
chr1-170F	10.76992	-0.38719	0.59434	-0.65146	0.514747	0.647824	chr1	1.71E+08	1.71E+08	+0	NA	intron (NALuSx1 SI	-8698	NR_12595E	1.02E+08	Hs.67666E	NR_12595E	ENSG000003GORAB-AS1	GORAB		GORAB anticrRNA	
chr19-40C	10.76992	-0.38719	0.59434	-0.65146	0.514747	0																



chr1-666	8.787099	-0.40441	0.710591	-0.56912	0.569274	0.676573	chr1	66630018	66630640	+0	0 NA	intron (Nintron (N	1889 NR_03606C	1E+08	NR_03606C	ENS00000C	MIR3117	mir-3117	microRNA ncRNA		
chr1-1804	8.787099	-0.40441	0.710591	-0.56912	0.569274	0.676573	chr1	1.8E+08	1.8E+08	+0	0 NA	intron (NLM1E LIN	27214 NM_03236C	84320 Hs.	200051NM_03236C	ENS00000C	ACBD6	-	acyl-CoA protein-coding		
chr6-1354	8.787099	-0.40441	0.710591	-0.56912	0.569274	0.676573	chr6	1.35E+08	1.35E+08	+0	0 NA	intron (NLM3D3 LIN	15672 NM_001134	54806 Hs.	386684NM_017651	ENS00000C	AHI1	AHI-1 JBI	Abelson tprotein-coding		
chr1-3348	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr1	33483724	33489191	+0	0 NA	intron (Nintron (N	18312 NM_145238	7579 Hs.	44270E	NR_145238	ENS00000C	ZSCAN20	KOX29 ZFF	zinc fingerprotein-coding	
chr1-1536	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr1	1.54E+08	1.54E+08	+0	0 NA	intron (NAluSx SIN	4868 NM_001024	6284 Hs.	51650E	NR_00597E	ENS00000C	S100A13	-	S100 calprotein-coding	
chr1-1625	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr1	1.63E+08	1.63E+08	+0	0 NA	intron (NMER20 DN	21939 NM_17586E	127933 Hs.	12731CNM_144624	ENS00000C	UHMK1	KIS KIST U2AF	homcprotein-coding		
chr1-1735	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr1	1.74E+08	1.74E+08	+0	0 NA	intron (NAluSx SIN	1838 NM_00130C	149041 Hs.	30258 NM_172071	ENS00000C	RC3H1	RNF198 RCR	ring fingerprotein-coding		
chr1-2351	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr1	2.35E+08	2.35E+08	+0	0 NA	intron (NAluSx SIN	11255 NR_00295E	677802 Hs.	74474E	NR_00295E	ENS00000C	SNORA14B	ACA14B	small nucsnoRNA	
chr11-433	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr11	43336134	43337823	+0	0 NA	intron (NAluYml SI	-21907 NM_001307	55761 Hs.	19118E	NR_01825E	ENS00000C	TTC17	-	tetratricprotein-coding	
chr11-614	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr11	61436304	61442016	+0	0 NA	intron (NMLT1J LTF	9035 NM_017841	54949 Hs.	313247NM_017841	ENS00000C	SDHAF2	C1lorf79	succinateprotein-coding		
chr15-682	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr15	68289850	68292166	+0	0 NA	exon (NM exon (NM	13263 NM_01532E	10116 Hs.	36273E	NR_01532E	ENS00000C	FEM1B	F1A-ALPHA	fem-1 honprotein-coding	
chr16-482	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr16	48259410	48264595	+0	0 NA	intron (Nintron (N	-14463 NM_00137C	85320 Hs.	652267NM_03258E	ENS00000C	ABCC11	EWWD MRPE	ATP bindi protein-coding		
chr16-896	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr16	89643664	89648440	+0	0 NA	exon (NM exon (NM	11656 NM_00108E	5119 Hs.	589427NM_00276E	ENS00000C	CHMP1A	CHMP1	PCF charged nprotein-coding		
chr17-136	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr17	13630113	1364876	+0	0 NA	intron (NMER20 DN	36278 NM_006761	7531 Hs.	513851NM_006761	ENS00000C	YWHAE	14-3-3E	tyrosine protein-coding		
chr17-388	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr17	38845417	38853191	+0	0 NA	3' UTR (N3' UTR (N	2354 NR_145761	1.1E+08	NR_145761	ENS00000C	SNORA21B	-	small nucsnoRNA		
chr19-408	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr19	40007287	40016331	+0	0 NA	intron (NMLT1C LTF	14749 NM_001297	339327 Hs.	12500E	NR_178544	ENS00000C	ZNF546	ZNF49	zinc fingerprotein-coding	
chr2-8531	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr2	85319480	85327457	+0	0 NA	intron (NAluSx1 SI	4521 NM_00120E	10618 Hs.	59338E	NR_006464	ENS00000C	TGOLN2	TGN38 TG	trans-golprotein-coding	
chr2-1772	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr2	1.77E+08	1.77E+08	+0	0 NA	intron (Nintron (N	6608 NR_13847C	220988 Hs.	51653E	NR_194247	ENS00000C	HNRNP3A	2610510D	heterogolprotein-coding	
chr2-2225	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr2	2.23E+08	2.23E+08	+0	0 NA	intron (Nintron (N	49197 NM_001354	2181 Hs.	65577E	NR_004457	ENS00000C	ACSL3	ACS3 FAC1	acyl-CoA protein-coding	
chr20-39C	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr20	3908079	3919362	+0	0 NA	intron (NLM1B7 LIN	-3774 NR_02951E	406896	NR_02951E	ENS00000C	MIR103A2	MIR103-2	microRNA ncRNA		
chr3-1514	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr3	1.02E+08	1.02E+08	+0	0 NA	intron (Nintron (N	4153 NM_00098E	6152 Hs.	47702E	NR_00098E	ENS00000C	RPL24	HEL-5-31	(ribosomal) protein-coding	
chr5-1341	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr5	1.34E+08	1.34E+08	+0	0 NA	intron (NAluSx SIN	12689 NM_17067E	6500 Hs.	17162E	NR_00693C	ENS00000C	SKP1	EMC19 OCF	S-phase kprotein-coding	
chr6-2822	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr6	28227076	28235130	+0	0 NA	intron (NMER44B DN	5828 NM_00629E	7746 Hs.	100921NM_00629E	ENS00000C	ZSCAN9	PRD51 ZNF	zinc fingerprotein-coding		
chr6-7562	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr6	75659481	75663443	+0	0 NA	intron (NMLP1A1 LI	59582 NM_00110C	26054 Hs.	485784NM_015571	ENS00000C	SENPE6	SSP1 SUSF	SUMO specprotein-coding		
chr8-8354	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr8	8354229	8368756	+0	0 NA	intron (NHERV1-int	24752 NM_00136E	157285 Hs.	58386E	NR_00108C	ENS00000C	PRAG1	NACK PEAK	PEAK1 relprotein-coding	
chr9-1132	8.772509	-0.40216	0.709418	-0.56688	0.570795	0.676573	chr9	1.13E+08	1.13E+08	+0	0 NA	intron (NAluJb SIN	15784 NM_13928E	246184 Hs.	72764E	NR_13928E	ENS00000C	CDC26	ANAP29	cell divi protein-coding	
chr1-2077	8.745536	-0.40236	0.710807	-0.56606	0.571351	0.676573	chr1	2.08E+08	2.08E+08	+0	0 NA	intron (NHE1C LTF	470726	NR_02983E	ENS00000C	VEZF1	MIRN21C	microRNA ncRNA			
chr11-115	8.745536	-0.40236	0.710807	-0.56606	0.571351	0.676573	chr11	1.19E+08	1.19E+08	+0	0 NA	exon (NM exon (NM	-2070 NM_00210E	3014 Hs.	47787E	NR_00210E	ENS00000C	H2AFX	H2A.X H2A	histcprotein-coding	
chr4-558E	8.745536	-0.40236	0.710807	-0.56606	0.571351	0.676573	chr4	55868444	55869468	+0	0 NA	intron (Nintron (N	15306 NM_178237	55763 Hs.	26966E	NR_018261	ENS00000C	EXOC1	BM-102 SE	exocyst cprotein-coding	
chr8-8374	8.745536	-0.40236	0.710807	-0.56606	0.571351	0.676573	chr8	8374261	8384186	+0	0 NA	intron (Nintron (N	7021 NM_00136E	157285 Hs.	58386E	NR_00108C	ENS00000C	PRAG1	NACK PEAK	PEAK1 relprotein-coding	
chr1-1008	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr1	1.01E+08	1.01E+08	+0	0 NA	intron (NMLT1J LTF	3673 NM_001144	148867 Hs.	53390E	NR_13349E	ENS00000C	SLC30A7	ZNT7 ZnT	solute cprotein-coding	
chr1-149C	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr1	1.49E+08	1.49E+08	+0	0 NA	IntergeniLIMC2 LIN	-14225 NM_001277	400818 Hs.	44508C	NR_001037	ENS00000C	NBP9F	AEO1	NBPF	menfprotein-coding
chr11-13C	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr11	1.31E+08	1.31E+08	+0	0 NA	intron (Nintron (N	12900 NM_001301	399979 Hs.	444024NM_01475E	ENS00000C	SNX19	CHET8	sorting rprotein-coding		
chr12-34E	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr12	346579	386553	+0	0 NA	intron (Nintron (N	22754 NM_00104E	5927 Hs.	76272 NM_00505E	ENS00000C	KDM5A	RBBP-2 RE	lysine deprotein-coding		
chr14-674	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr14	67343227	67353951	+0	0 NA	intron (NAluSg SIN	11215 NM_015994	51382 Hs.	27263C	NR_015994	ENS00000C	ATPGV1D	ATP6M VAI	ATPase Hprotein-coding	
chr2-1514	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr2	1.51E+08	1.51E+08	+0	0 NA	intron (Nintron (N	60153 NM_001177	55183 Hs.	536537NM_018151	ENS00000C	RIF1	-	replicati protein-coding		
chr9-1101	8.757918	-0.39989	0.710806	-0.56259	0.573716	0.676573	chr9	1.1E+08	1.1E+08	+0	0 NA	intron (Nintron (N	13233 NM_00113E	445815 Hs.	59190E	NR_00720E	ENS00000C	PALM2-AK	AKAP-2 AK	PALM2-AK	protein-coding
chr10-102	8.784891	-0.39967	0.712159	-0.5612	0.574659	0.676573	chr10	1.02E+08	1.02E+08	+0	0 NA	intron (NAluSg SIN	16862 NM_024541	79591 Hs.	16004 NM_024541	ENS00000C	ARMH3	C1oorf76	armadil11cprotein-coding		
chr10-924	8.726468	-0.41476	0.742961	-0.55826	0.576668	0.676573	chr10	92454766	92455156	+0	0 NA	intron (Nintron (N	36300 NR_03824E	1.01E+08	Hs.	56877E	NR_03824E	MARK2P9	-	microtub pseudo	
chr15-988	8.261877	-0.41228	0.740085	-0.55707	0.577478	0.676573	chr15	98829928	98832166	+0	0 NA	intron (NMSTB LTR	46621 NR_039864	1.01E+08	NR_039864	ENS00000C	MIR4714	-	microRNA ncRNA		
chr6-1391	8.261877	-0.41228	0.740085	-0.55707	0.577478	0.676573	chr6	1.39E+08	1.39E+08	+0	0 NA	exon (NM exon (NM	32191 NM_016217	51696 Hs.	197644NM_016217	ENS00000C	HECA	HDCL hdcl	homolprotein-coding		
chr1-669E	8.770301	-0.39738	0.713563	-0.55689	0.577602	0.676573	chr1	66969986	66971824	+0	0 NA	exon (NM exon (NM	40649 NM_001077	57708 Hs.	60543E	NR_02094E	ENS00000C	MIER1	ER1 MI	EFMIER1 tprotein-coding	
chr5-1604	8.770301	-0.39738	0.713563	-0.55689	0.577602	0.676573	chr5	1.6E+08	1.6E+08	+0	0 NA	intron (NLM1E4c LI	6816 NM_001364	10569 Hs.	43534E	NR_00642E	ENS00000C	SLU7	9G8 hSu7	SLU7 hprotein-coding	
chr1-524C	8.27426	-0.4096	0.738605	-0.55456	0.579193	0.676573	chr1	52405438	52420776	+0	0 NA	intron (NMIRb SINE	8505 NM_032864	84950 Hs.	5301 NM_032284	ENS00000C	PRPF38A	PRP38A Prp	mRNA protein-coding		
chr11-831	8.27426	-0.4096	0.738605	-0.55456	0.579193	0.676573	chr11	83189145	83192887	+0	0 NA	TTS (NR_1TTS (NR_1	2653 NR_14900E	1.01E+08	Hs.	58550E	NR_018705	LOC10050E	-	uncharactncRNA	
chr14-49E	8.27426	-0.4096	0.738605	-0.55456	0.579193	0.676573	chr14	49893565	49896697	+0	0 NA	3' UTR (N3' UTR (N	2049 NM_00166E	382 Hs.	52533C	NR_00166E	ENS00000C	ARF6	-	ADP ribos protein-coding	
chr17-517	8.27426	-0.4096	0.738605	-0.5545																	





chr4-7695.8.988344	-0.32091	0.69522	-0.4616	0.644371	0.731633	chr4	76995486	77000865	0	NA	intron (Nintron (N	48423	55752	Hs.128199	ENS000000SEPTIN11	11-Sep	septin 11protein-coding
chr1-2332.8.973753	-0.3187	0.696601	-0.45751	0.647303	0.731633	chr1	23321621	23338538	0	NA	intron (Nintron (N	14205	10236	Hs.373765	ENS000000HNRNPR	HNRNPR	hnf heteroer protein-coding
chr17-51(8.973753	-0.3187	0.696601	-0.45751	0.647303	0.731633	chr17	5105201	5110721	0	NA	intron (Nintron (N	-3974	1.02E+08	Hs.66004ENR_135657	ENS000000LOC10192E-		uncharactcncRNA
chr19-56(8.973753	-0.3187	0.696601	-0.45751	0.647303	0.731633	chr19	56372750	56377780	0	NA	intron (Nintron (N	-6882	79149	Hs.177688	ENS000000ZSCAN5A	ZNF495	ZS zinc fingprotein-coding
chr7-6731(8.973753	-0.3187	0.696601	-0.45751	0.647303	0.731633	chr7	6731596	6746398	0	NA	intron (NAluSp SIN	3692	441194	Hs.71559	ENS000000PMS2CL	PMS2P13	PMS2 C-tepsudo
chr7-102(8.973753	-0.3187	0.696601	-0.45751	0.647303	0.731633	chr7	1.03E+08	1.03E+08	0	NA	promoter-promoter-exon (NM exon (NM	-54601	441273	Hs.65642ENM_001031	ENS000000SPDYE2	SPDYB2-L1	speedy/R1protein-coding
chr1-178(9.000726	-0.31857	0.696443	-0.45742	0.647366	0.731633	chr1	1.78E+08	1.78E+08	0	NA	intron (NAluJb SIN	-54601	84066	Hs.534501	ENS000000TEX35	Clorf49	testis exprotein-coding
chr17-16(9.000726	-0.31857	0.696443	-0.45742	0.647366	0.731633	chr17	16031812	16037348	0	NA	intron (NAluJb SIN	34756	54902	Hs.46231ENM_01777E	ENS000000TTC19	201020401	tetratric protein-coding
chr3-641(9.000726	-0.31857	0.696443	-0.45742	0.647366	0.731633	chr3	64196289	64199312	0	NA	intron (NLIPIA13 LI	10256	101E+08	Hs.67084CNR_04670E	ENS000000PRICKLE2-		PRICKLE2 ncRNA
chr3-142(9.000726	-0.31857	0.696443	-0.45742	0.647366	0.731633	chr3	1.42E+08	1.42E+08	0	NA	intron (NAluSq2 SI	104819	54464	Hs.43510CENM_019001	ENS000000XRN1	1-Sep 5'-3'	excpprotein-coding
chr6-5647(9.000726	-0.31857	0.696443	-0.45742	0.647366	0.731633	chr6	56475480	56483982	0	NA	intron (NLIPIB4 LIN	-85603	81578	Hs.47629	ENS000000COL21A1	COL1A1	FF collagen protein-coding
chr6-570(9.000726	-0.31857	0.696443	-0.45742	0.647366	0.731633	chr6	57098118	57105146	0	NA	exon (NM exon (NM	11444	26036	Hs.48562ENM_01555E	ENS000000ZNF451	COASTER	zinc fingprotein-coding
chr1-222(8.986136	-0.31635	0.697832	-0.45333	0.650313	0.731633	chr1	2.23E+08	2.23E+08	0	NA	intron (Nintron (N	11595	64853	Hs.15662ENM_022831	ENS000000AIDA	Clorf80	axin inteprotein-coding
chr5-6964(8.959163	-0.31645	0.700537	-0.45173	0.651466	0.731633	chr5	69645753	69646096	0	NA	non-codiron-codir	14779	1.02E+08	Hs.63401ENR_157804	ENS000000LOC10192E-		putative pseudo
chr1-1461(11.21397	-0.25602	0.570586	-0.44869	0.653657	0.731633	chr1	1.46E+08	1.46E+08	0	NA	intron (Nintron (N	41260	388677	Hs.65515ENM_20345E	ENS000000NOTCH2NL2	NOTCH2NL2	NOTCH notch 2 protein-coding
chr19-39(8.490095	-0.32337	0.725298	-0.44584	0.655712	0.731633	chr19	39972016	39984868	0	NA	intron (Nintron (N	7277	5704	Hs.211594	ENS000000PSMC4	MIP224	HSF proteasoneprotein-coding
chr3-710(8.490095	-0.32337	0.725298	-0.44584	0.655712	0.731633	chr3	71012667	71016586	0	NA	intron (NLIPIA5 LIN	50298	27086	Hs.59368	ENS000000FOX1	12CC4	HSF forkhead protein-coding
chr8-1728(8.490095	-0.32337	0.725298	-0.44584	0.655712	0.731633	chr8	17284373	17292888	0	NA	intron (NLIPIA7 LIN	41672	137492	Hs.34387	ENS000000VPS37A	HCRP1	PQE VPS37A sprotein-coding
chr6-1387(8.517068	-0.32324	0.728097	-0.44395	0.657077	0.731633	chr6	1.39E+08	1.39E+08	0	NA	intron (NAluJb SIN	-7417	345930	Hs.66060ENM_001077	ENS000000ECTZL	ARHGAP32	epitheliaprotein-coding
chr8-115(8.531659	-0.32571	0.733851	-0.44384	0.657162	0.731633	chr8	1.16E+08	1.16E+08	0	NA	exon (NM exon (NM	48480	7227	Hs.65701ENM_01411E	ENS000000TRPS1	CG79	LGCF transcrip protein-coding
chr11-57(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr11	57295406	57303856	0	NA	TTS (NM_CTS (NM_C	25321	85456	Hs.53073CENM_03339E	ENS000000TNKS1BP1	TAB18	tankyrase protein-coding
chr14-241(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr14	24137567	24139539	0	NA	TTS (NM_CTS (NM_C	2359	5720	Hs.75348	ENS000000PSME1	HEL-S-12E	proteasoneprotein-coding
chr14-751(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr14	75133372	75135804	0	NA	3' UTR (N3' UTR (N	-7540	91754	Hs.7200	ENS000000CNEK9	APUG	LCCS NIMA relaprotein-coding
chr19-40(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr19	40443314	40442496	0	NA	3' UTR (N3' UTR (N	1193	29946	Hs.51541ENM_01336E	ENS000000SERTAD3	RBT1	SERTA donprotein-coding
chr19-44(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr19	44324778	44341965	0	NA	intron (Nintron (N	23309	7771	Hs.48589	ENS000000ZNF112	ZFP112	Zn zinc fingprotein-coding
chr19-58(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr19	58410968	58424292	0	NA	non-codiron-codir	8956	201514	Hs.439551ENM_17354E	ENS000000ZNF584		zinc fingprotein-coding
chr7-416(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr7	41688807	41690941	0	NA	exon (NM exon (NM	-4045	285954	Hs.65686ENR_02711E	ENS000000INHBA-AS1		INHBA antncRNA
chr7-102(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr7	1.03E+08	1.03E+08	0	NA	intron (Nintron (N	9231	548644	Hs.61025ENM_00101E	ENS000000POLR2J3	POLR2J2	URNA polynprotein-coding
chr7-102(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr7	1.03E+08	1.03E+08	0	NA	Intergeni Intergeni	10865	1E+08	Hs.61025ENM_001114	ENS000000UPK3BL1	UPK3BL	UVU roluplakim protein-coding
chr9-277(8.475505	-0.32098	0.725369	-0.44251	0.658123	0.731633	chr9	2772469	2779438	0	NA	IntergeniAluSz SIN	58443	169522	Hs.62267ENM_133497	ENS000000CKNV2	KV11.1	kv putakim protein-coding
chr1-1457(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr1	1.46E+08	1.46E+08	0	NA	3' UTR (N3' UTR (N	26857	11126	Hs.488237ENM_00705E	ENS000000CD160	CD160	molprotein-coding
chr12-68(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr12	68648987	68663764	0	NA	exon (NM exon (NM	-29000	1E+08	Hs.72453CNR_03333E	ENS000000SNR070G	U70G	small nucsnoRNA
chr15-92(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr15	92884318	92899256	0	NA	intron (Nintron (N	8491	1.01E+08	Hs.622504ENR_037600	ENS000000LINC0157E-		long intncRNA
chr15-99(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr15	99674504	99677556	0	NA	intron (NAluSx SIN	43052	4205	Hs.26867ENM_00558E	ENS000000MEF2A	ADCAD1	RMycocyte eprotein-coding
chr16-91(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr16	9103029	9110104	0	NA	intron (NAluSx SIN	14922	29035	Hs.221497ENM_01411E	ENS000000Cl6orf72	PREL049	chromosoneprotein-coding
chr17-771(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr17	77142744	77145531	0	NA	intron (Nintron (N	3168	6397	Hs.464184ENM_00300E	ENS000000SECI4L1	PRELID4A	SEC14 likprotein-coding
chr2-182(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr2	1.83E+08	1.83E+08	0	NA	intron (NLIPIA4 LIN	77337	10787	Hs.60373ENM_01343E	ENS000000CNCKAP1	HEM2	NAP1NCK assocprotein-coding
chr3-446(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr3	44627080	44645144	0	NA	intron (NAluY SINE	11076	10168	Hs.15703ENM_00699E	ENS000000ZNF197	D3S1363E	zinc fingprotein-coding
chr4-5787(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr4	5787180	5789487	0	NA	intron (NMLT1F2 LI	77132	2121	Hs.64689ENM_01455E	ENS000000EVC	DWF-1	EVC Evc cilia protein-coding
chr6-136(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr6	1.36E+08	1.36E+08	0	NA	intron (Nintron (N	-19561	113115	Hs.12153ENM_13841E	ENS000000MTFR2	DUFD1	FAM mitochondncprotein-coding
chr7-746(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chr7	74694691	74715277	0	NA	intron (Nintron (N	23984	23984	Hs.110044	ENS000000LOC10192E-		uncharactcncRNA
chrX-411(8.502478	-0.32084	0.725334	-0.44233	0.65825	0.731633	chrX	41189022	41222390	0	NA	intron (Nintron (N	-73033	1E+08	Hs.54611ENR_13561E	ENS000000LINC02601-		long intncRNA
chr6-1297(8.448532	-0.32113	0.731103	-0.43924	0.660491	0.731633	chr6	1.3E+08	1.3E+08	0	NA	intron (NAluSx SIN	3442	93663	Hs.48645ENM_03351E	ENS000000ARHGAP18	MacGAP	SERHO GTPasprotein-coding
chr1-7317(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr1	731747	733490	0	NA	Intergeni Intergeni	-2267	1E+08	Hs.728864ENR_028327	ENS000000LOC10013E-		uncharactcncRNA
chr1-109(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr1	31905188	31920728	0	NA	intron (Nintron (N	24860	8073	Hs.470477ENM_00347E	ENS000000PTCA4A2	HH13	HH17 protein tprotein-coding
chr1-187(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr1	1.09E+08	1.09E+08	0	NA	intron (NTHE1C LTF	37589	6814	Hs.53043ENM_00726E	ENS000000STXP3	MUNC18-3	syntaxin protein-coding
chr1-1481(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr1	1.48E+08	1.48E+08	0	NA	intron (NLTR5_Hs L	-2116	200030	Hs.72158ENM_18337E	ENS000000NBPF11	NBPF24	NBPF memtprotein-coding
chr1-143(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr1	1.49E+08	1.49E+08	0	NA	intron (Nintron (N	59526	400818	Hs.44508CENM_001037	ENS000000NBPF9	NBPF	memtprotein-coding
chr10-73(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr10	73466206	73466490	0	NA	intron (Nintron (N	-29404	59254	Hs.43450ENR_13210E	ENS000000PPP3CB-AS1	USP54-AS1	PPP3CB arncRNA
chr10-737(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr10	73725189	73728241	0	NA	intron (NAluJb SIN	3791	1.14E+08	NR_16042E	ENS000000BMS1P4-AC	BMS1P4-AC	pseudo
chr10-11(8.487887	-0.31845	0.725408	-0.43899	0.660667	0.731633	chr10	1.19E+08	1.19E+08	0	NA	intron (NAluSp SIN	5554	641451	Hs.68865ENR_00291E	ENS000000SNORA19	ACA19	small nucsnoRNA

chr6-1062.9.216561	-0.24179	0.681878	-0.35459	0.722897	0.792848	chr6	1.06E+08	1.06E+08	0	NA	intron (Nintron (N	24476 NR_104402	9474 Hs. 486066	ENSG000004ATG5	APG5	APG5	autophagyprotein-coding	
chr14-226.9.189588	-0.24185	0.683288	-0.35395	0.723376	0.792911	chr14	22601491	22606156	0	NA	intron (Nintron (N	5585 NM_022066	63874 Hs. 445666	ENSG000004ABHD4	ABHD4	ABHD4	abhydrolaseprotein-coding	
chr9-1542.9.189588	-0.24185	0.683288	-0.35395	0.723376	0.792911	chr9	15424788	15426258	0	NA	intron (Nintron (N	2647 NR_161445	6619 Hs. 546299	ENSG000004SNAPC3	PTFbeta	PTFbeta	small nucprotein-coding	
chr2-850f.9.201971	-0.23963	0.68325	-0.35072	0.7258	0.795336	chr2	85052955	85053323	0	NA	intron (Nintron (N	14208 NR_146455	1.01E+08 Hs. 434398	ENSG000004LINC01964			long intencRNA	
chr9-410c.11.42981	-0.19537	0.595357	-0.34928	0.726883	0.796291	chr9	41005071	41012722	0	NA	intron (NMER33 DN	18910 NR_156733	1E+08 Hs. 231861	NR_034006	FRG1HP		FSDH recpseudo	
chr15-67c.9.174998	-0.23966	0.68714	-0.34878	0.727253	0.796465	chr15	67075655	67075872	0	NA	intron (NAluSx1 SI	10161 NM_005902	4088 Hs. 72798	ENSG000004SMAD3	HSPC193	HSPC193	SMAD famiprotein-coding	
chr7-920c.9.214354	-0.23737	0.685517	-0.34627	0.729143	0.798302	chr7	92026509	92028050	0	NA	intron (NSVA_A Ret	86404 NM_005751	10142 Hs. 651221	ENSG000004AKAP9	AKAP-9	AKAP-9	AKA-kinase protein-coding	
chr12-105.9.241327	-0.23725	0.688783	-0.34445	0.730506	0.799562	chr12	1.09E+08	1.09E+08	0	NA	intron (NMER9a3 LI	18188 NM_183415	89910 Hs. 374067	ENSG000004UBE3B	BPD15	BPD15	KO5ubiquitinprotein-coding	
chr15-101.13.62625	-0.16118	0.468928	-0.34373	0.73105	0.799925	chr15	1.02E+08	1.02E+08	0	NA	intron (Nintron (N	4622 NR_003655	374666 Hs. 459577	NR_199163	WASH3P	FAM39DP	WASP famipseudo	
chr1-156.8.708138	-0.2469	0.719407	-0.34319	0.731454	0.800134	chr1	1.57E+08	1.57E+08	0	NA	intron (NAluJb SIN	-45393 NR_030527	768220	NR_030527	ENSG000004MIR765	MIRN765	lincRNA ncRNA	
chr3-111.8.735111	-0.24687	0.721043	-0.34237	0.732071	0.800576	chr3	1.11E+08	1.11E+08	0	NA	intron (Nintron (N	47411 NM_001243	25945 Hs. 293917	NR_015488	ENSG000004NECTIN3	CD113	CD113	CDWnectin cprotein-coding
chr14-607.8.70593	-0.24201	0.712777	-0.33953	0.734208	0.80268	chr14	60717174	60718090	0	NA	intron (Nintron (N	6719 NM_017420	51804 Hs. 97849	NR_017420	ENSG000004SIX4	AREC3	SIX	homecprotein-coding
chr1-1784.8.718313	-0.2396	0.711499	-0.33675	0.736303	0.803932	chr1	1.78E+08	1.78E+08	0	NA	intron (Nintron (N	-70574 NM_032122	84066 Hs. 534501	NR_032122	ENSG000004TEX35	Clorf49	Clorf49	testis exprprotein-coding
chr17-604.8.718313	-0.2396	0.711499	-0.33675	0.736303	0.803932	chr17	60486674	60493916	0	NA	intron (NLMIM2 LI	35945 NM_001282	10513 Hs. 84084	NR_006380	ENSG000004APPBP2	APP-BP2	Famlyoid tprotein-coding	
chr5-3901.8.718313	-0.2396	0.711499	-0.33675	0.736303	0.803932	chr5	39010040	39012848	0	NA	intron (NTHE1C-int	62955 NM_001282	253260 Hs. 407922	NR_152755	ENSG000004RICTOR	AVO3	PIA	RPTOR incprotein-coding
chr8-103c.8.718313	-0.2396	0.711499	-0.33675	0.736303	0.803932	chr8	1.03E+08	1.03E+08	0	NA	intron (NL2c LINE	21795 NR_145795	1.1E+08	NR_145795	SNORD173		small nucsnRNA	
chr14-754.8.69134	-0.23967	0.712883	-0.33662	0.736722	0.803932	chr14	75431502	75432946	0	NA	promoter-promoter-	90 NM_001135	122953 Hs. 196482	NR_130465	ENSG000004JDP2	JUNDM2	Jun dimerprotein-coding	
chr8-427.8.69134	-0.23967	0.712883	-0.33662	0.736722	0.803932	chr8	42276007	42276225	0	NA	intron (NAluSx1 SIN	4814 NM_001190	3551 Hs. 597664	NR_001555	ENSG000004IKKBK	IKK-beta	inhibitorprotein-coding	
chr17-45f.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr17	45513929	45516500	0	NA	promoter-promoter-	-15 NM_001330	1.01E+08 Hs. 559255	NR_001035	ENSG000004ARL17B	ARL17	ARLADP	ribosprotein-coding
chr18-23f.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr18	23516331	23523557	0	NA	intron (Nintron (N	16433 NM_013322	29919 Hs. 464777	NR_013322	ENSG000004RMC1	C18orf8	Regulatorprotein-coding	
chr19-53c.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr19	53064952	53102548	0	NA	intron (NAluJb SIN	3287 NM_001322	90338 Hs. 655967	NR_033288	ENSG000004ZNF160	F11	Hkr1	zinc fingprotein-coding
chr19-53c.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr19	53397530	53415822	0	NA	intron (NAluSx1 SIN	11527 NM_001040	91661 Hs. 657821	NR_001040	ENSG000004ZNF765		zinc fingprotein-coding	
chr3-125f.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr3	1.26E+08	1.26E+08	0	NA	intron (NAluSx1 SI	13073 NR_073435	8723 Hs. 507242	NR_003794	ENSG000004SNX4	ATG24B	sorting rprotein-coding	
chr4-118f.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr4	1.19E+08	1.19E+08	0	NA	intron (NL2c LINE	5333 NR_001318	9871 Hs. 189641	NR_014822	ENSG000004SEC24D	CLCRP2	SEC24	honprotein-coding
chr5-150f.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr5	1.5E+08	1.5E+08	0	NA	intron (Nintron (N	11722 NM_014983	22993 Hs. 719185	NR_014983	ENSG000004HMGXB3	HMGX3	SMF HMG-box cprotein-coding	
chr6-264f.8.703722	-0.23726	0.711607	-0.33342	0.738816	0.803932	chr6	26459271	26461500	0	NA	intron (Nintron (N	2430 NM_007045	11120 Hs. 159022	NR_007045	ENSG000004BTN2A1	BK14H9.1	l ubtrophinprotein-coding	
chr3-1137.8.730696	-0.23719	0.712804	-0.33276	0.739314	0.803932	chr3	1.14E+08	1.14E+08	0	NA	3' UTR (N3' UTR (N	-24398 NR_111981	205717 Hs. 632577	NR_001005	ENSG000004ZNF31	KIAA2018	upstream protein-coding	
chr1-205f.8.716105	-0.23485	0.712913	-0.32942	0.741836	0.803932	chr1	2.06E+08	2.06E+08	0	NA	intron (Nintron (N	9656 NM_001973	2005 Hs. 497520	NR_001973	ENSG000004ELK4	SAP1	ETS	transprotein-coding
chr20-34c.8.716105	-0.23485	0.712913	-0.32942	0.741836	0.803932	chr20	34369013	34375390	0	NA	intron (NAluY SINE	8928 NM_001257	83737 Hs. 632272	NR_031482	ENSG000004ITCH	ADMFD	AIF	itchy E3 protein-coding
chr20-41c.8.689132	-0.23491	0.714479	-0.32878	0.742323	0.803932	chr20	41061330	41063211	0	NA	intron (Nintron (N	33448 NM_003288	7150 Hs. 472737	NR_003288	ENSG000004TOP1	TOP1	DNA topoisprotein-coding	
chr1-1931.8.701515	-0.23247	0.715801	-0.32476	0.74536	0.803932	chr1	1.93E+08	1.93E+08	0	NA	intron (Nintron (N	6319 NM_024525	79577 Hs. 378996	NR_024525	ENSG000004CDC73	Clorf28	cell diviprotein-coding	
chr11-97f.15.35584	-0.13452	0.416372	-0.32307	0.746639	0.803932	chr11	975370	975744	0	NA	intron (NCPg	49687 NR_144510	161 Hs. 19121	NR_012305	ENSG000004AP2A2	ADTBA	Cladaptor rprotein-coding	
chr2-4631.8.674542	-0.23247	0.720273	-0.32275	0.746881	0.803932	chr2	46317137	46317920	0	NA	intron (NTigger1 I	20121 NM_001430	2034 Hs. 468410	NR_001430	ENSG000004EPAS1	ECTY4	HLF	endothelinprotein-coding
chr7-1247.8.207682	-0.2399	0.74489	-0.32206	0.747404	0.803932	chr7	1.25E+08	1.25E+08	0	NA	intron (NAluJb SIN	6576 NM_005302	2861 Hs. 406094	NR_005302	ENSG000004GPR37	EDNRBL	Pg	protein-coding
chr2-6991.8.220664	-0.23726	0.742041	-0.31974	0.749162	0.803932	chr2	69913033	69913322	0	NA	IntergeniIntergeni	-1864 NM_001202	4084 Hs. 468908	NR_002357	ENSG000004MXD1	BHLH538	MAX	dimerprotein-coding
chr6-1345.8.713898	-0.22996	0.719794	-0.31948	0.749365	0.803932	chr6	1.35E+08	1.35E+08	0	NA	exon (NM exon (NM	-18003 NR_037435	1.01E+08	NR_037435	ENSG000004MIR3662	mir-3662	microRNA ncRNA	
chr7-746f.8.713898	-0.22996	0.719794	-0.31948	0.749365	0.803932	chr7	74659290	74659634	0	NA	intron (NAluSx1 SIN	1744 NM_033000	2969 Hs. 647041	NR_001515	ENSG000004GTF2I	BAP135	B1	general tprotein-coding
chr3-111f.8.647569	-0.23239	0.730665	-0.31806	0.750442	0.803932	chr3	1.12E+08	1.12E+08	0	NA	non-codiron-codir	-7479 NM_013255	29114 Hs. 169330	NR_013255	ENSG000004TAGLN3	NP22	NP24	transgeliprotein-coding
chr1-3902.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr1	39028223	39039424	0	NA	intron (NAluSx1 SIN	7183 NM_004552	4725 Hs. 632387	NR_004552	ENSG000004DNLF5	Cl-15k	CINADH	ubiquitinprotein-coding
chr11-91f.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr11	9164878	9166394	0	NA	intron (NAluJr SIN	71273 NR_027713	283102 Hs. 689472	NR_027713	ENSG000004KRT8P41		keratin Epseudo	
chr11-73f.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr11	73014085	73011251	0	NA	intron (NLMIM2 LI	131450 NM_014824	9873 Hs. 744955	NR_014824	ENSG000004CHSD2	NWK	NWK1	FCN and cprotein-coding
chr14-67c.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr14	67682385	67693252	0	NA	intron (NAluSx2 SI	7946 NM_001252	51109 Hs. 719922	NR_016022	ENSG000004RDH11	ARSDR1	CC	retinol cprotein-coding
chr16-30f.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr16	30202276	30205059	0	NA	TTS (NR_CTS (NR_C	3260 NR_002557	613038 Hs. 569582	NR_002557	ENSG000004LOC613038		SAGA compseudo	
chr16-351.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr16	85182103	85187306	0	NA	IntergeniLIM5 LI	-23092 NR_162142	1.13E+08	NR_162142	MIR1218		microRNA ncRNA	
chr19-351.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr19	35156029	35168448	0	NA	intron (Nintron (N	7503 NM_144775	53827 Hs. 333411	NR_014164	ENSG000004FXD5	DYSAD	HSE	FXD5 domeprotein-coding
chr19-351.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr19	39431290	39435574	0	NA	intron (Nintron (N	2517 NM_001020	6217 Hs. 397609	NR_001020	ENSG000004RPS16	S16	ribosomalprotein-coding	
chr19-57f.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr19	57936911	57944907	0	NA	TTS (NM_CTS (NM_C	-5507 NM_001317	147686 Hs. 660722	NR_133460	ENSG000004ZNF418		zinc fingprotein-coding	
chr4-118f.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr4	1.19E+08	1.19E+08	0	NA	intron (NAluJo SIN	11871 NM_001318	9871 Hs. 189641	NR_014822	ENSG000004SEC24D	CLCRP2	SEC24	honprotein-coding
chr6-656f.8.205474	-0.23472	0.740523	-0.31697	0.751265	0.803932	chr6	656308	657146	0	NA								



chr10-68: 9.432396	-0.16888	0.668261	-0.25272	0.800487	0.847323	chr10	68375449	68376209	0	NA	intron (AluSx SIN	31360	NM_017987	55680	Hs.653144NM_017987	ENSG000003RUFY2	RABIP4R ZRUN and Fprotein-coding	
chr19-362: 9.432396	-0.16888	0.668261	-0.25272	0.800487	0.847323	chr19	36226166	36241091	0	NA	intron (LTR5_Hs L	12300	NM_001366	147929	Hs.596338NM_152477	ENSG000003ZNF565	- zinc fingprotein-coding	
chr4-6361: 10.49477	0.154266	0.612851	0.251719	0.801258	0.847901	chr4	63613	63812	0	NA	intron (AluSx3 SI	10391	NM_182524	152687	Hs.709466NM_182524	ENSG000003ZNF595	- zinc fingprotein-coding	
chr4-1508: 8.921765	-0.16501	0.700892	-0.23542	0.813879	0.861014	chr4	1.51E+08	1.51E+08	0	NA	intron (NL1PA4 LIN	119629	NM_001199	987	Hs.480938NM_00672f	ENSG000003LRBA	BGL CDC41LPS respprotein-coding	
chr4-4302: 8.961121	-0.16272	0.701044	-0.2321	0.816457	0.863257	chr4	4302524	4303316	0	NA	exon (NM exon (NM	12669	NR_138481	166793	Hs.419997NM_145291	ENSG000003ZBTB49	ZNF509 zinc fingprotein-coding	
chr3-676: 8.907175	-0.16271	0.701029	-0.2321	0.816458	0.863257	chr3	67608971	67609621	0	NA	intron (intron (N	45318	NM_00384f	8801	Hs.64491fNM_00384f	ENSG000003SUGL2	G-SCS GBE succinateprotein-coding	
chr4-603: 11.02	0.134105	0.582469	0.230235	0.817909	0.863605	chr4	60307	62494	0	NA	intron (AluSx1 SI	8079	NM_182524	152687	Hs.709466NM_182524	ENSG000003ZNF595	- zinc fingprotein-coding	
chr14-101: 8.946531	-0.16042	0.698495	-0.22966	0.818357	0.863605	chr14	1.02E+08	1.02E+08	0	NA	intron (intron (N	14456	NM_00137f	1778	Hs.61408fNM_00137f	ENSG000003DYN5C1H1	CMT20 DHC dynein cyprotein-coding	
chr2-1731: 8.946531	-0.16042	0.698495	-0.22966	0.818357	0.863605	chr2	1.73E+08	1.73E+08	0	NA	non-codiron-codir	83583	NR_03388f	339751	Hs.57008fNR_03388f	ENSG000003MAP3K20	MAP3K20 a ncRNA	
chr9-4697: 8.946531	-0.16042	0.698495	-0.22966	0.818357	0.863605	chr9	4697833	4698748	0	NA	intron (NLIME4a LI	18721	NM_01791f	55664	Hs.66643fNM_01791f	ENSG000003CDC37L1	CDC37B Hf cell diviprotein-coding	
chr1-151: 8.919557	-0.16042	0.698641	-0.22961	0.818394	0.863605	chr1	1.52E+08	1.52E+08	0	NA	intron (LTR12C LI	2152	NM_05305f	117145	Hs.16407fNM_05305f	ENSG000003THEM4	CTMP thioesterprotein-coding	
chr17-45: 8.919557	-0.16042	0.698641	-0.22961	0.818394	0.863605	chr17	45517621	45519917	0	NA	non-codiron-codir	1754	NR_00294f	55073	Hs.59675fNM_018001	LRRRC37A4 LRRRC37 LF leucine rpseudo		
chr19-53: 8.919557	-0.16042	0.698641	-0.22961	0.818394	0.863605	chr19	53337478	53555056	0	NA	intron (NLIM4c LIN	91664	Hs.72067fNM_138374	91664	Hs.72067fNM_138374	ENSG000003ZNF845	- zinc fingprotein-coding	
chr10-124: 8.850522	0.161983	0.710156	0.228096	0.819572	0.864587	chr10	1.25E+08	1.25E+08	0	NA	IntergeniAluSg SIN	-18989	NM_01758f	54764	Hs.59515fNM_01758f	ENSG000003ZNRAN1	TRABID zinc fingprotein-coding	
chr11-62: 8.93194	-0.15813	0.698635	-0.22635	0.820933	0.864587	chr11	62882134	62890033	0	NA	intron (AluSg SIN	4384	NR_03719f	6520	Hs.50276fNM_002394	ENSG000003SLC3A2	4F2 4F2HC solute caprotein-coding	
chr12-71: 8.93194	-0.15813	0.698635	-0.22635	0.820933	0.864587	chr12	71649708	71661837	0	NA	intron (NLIME1 LIN	8076	NM_14498f	196441	Hs.24579fNM_14498f	ENSG000003ZFC3H1	CCDC131 C zinc fingprotein-coding	
chr13-114: 8.93194	-0.15813	0.698635	-0.22635	0.820933	0.864587	chr13	1.14E+08	1.14E+08	0	NA	exon (NM exon (NM	9002	NR_126391	1.04E+08	Hs.56921fNR_126391	LINC01054	long intencRNA	
chr14-94: 8.93194	-0.15813	0.698635	-0.22635	0.820933	0.864587	chr14	94070870	94079445	0	NA	intron (NLIME1 LIN	6045	NM_020414	57062	Hs.51032fNM_020414	ENSG000003DDX24	- DEAD-box protein-coding	
chr16-214: 8.93194	-0.15813	0.698635	-0.22635	0.820933	0.864587	chr16	21445392	21460814	0	NA	intron (intron (N	-18648	NR_02445f	1E+08	Hs.64843fNR_02445f	LOC10019c	uncharactncRNA	
chr17-46: 8.93194	-0.15813	0.698635	-0.22635	0.820933	0.864587	chr17	46213619	46223910	0	NA	intron (AluSg SIN	6610	NM_00119f	284058	Hs.64874fNM_01544f	ENSG000003KANSL1	CENP-36 KAT8 regu protein-coding	
chr5-140: 8.944323	-0.15582	0.701011	-0.22228	0.824096	0.867313	chr5	1.4E+08	1.4E+08	0	NA	intron (AluSg SIN	3223	NM_00262f	5201	Hs.48356fNM_00262f	ENSG000003PPFN1	PDF PDF1 prefoldirprotein-coding	
chr7-139: 8.944323	-0.15582	0.701011	-0.22228	0.824096	0.867313	chr7	1.4E+08	1.4E+08	0	NA	intron (intron (N	8322	NM_00111f	28996	Hs.73141fNM_002274	ENSG000003HIPK2	PROO593 homodomeprotein-coding	
chr2-738: 8.91735	-0.15582	0.701465	-0.22213	0.824212	0.867313	chr2	73831769	73833852	0	NA	intron (MER20 DN	3843	NM_00135f	10617	Hs.46901fNM_00646f	ENSG000003STAMPB	AMSH MICC STAM binprotein-coding	
chr4-395: 8.942115	-0.15105	0.70878	-0.21311	0.831243	0.874466	chr4	39564652	39565221	0	NA	intron (AluJr SIN	37097	NR_04767f	1.01E+08	Hs.64076fNR_04767f	ENSG000003UGDH-AS1	UGDH anticncRNA	
chr1-110: 9.331972	0.144978	0.681929	0.2126	0.831639	0.874625	chr1	1.1E+08	1.1E+08	0	NA	exon (NM exon (NM	2171	NM_00120f	64783	Hs.43594fNM_002276	ENSG000003RBM15	OTT OTT1 RNA bindiprotein-coding	
chr1-538: 8.448282	-0.15344	0.728734	-0.21055	0.833238	0.874625	chr1	53881919	53883486	0	NA	intron (AluJb SIN	7095	NR_13507f	54432	Hs.11923	NM_01898f	ENSG000003YIPF1	DJ167A19. Yip1 dome protein-coding
chr1-242: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr1	24284	24692	0	NA	intron (intron (N	4892	NR_02454f	653635	Hs.44646fNR_02454f	WASH7P	FAM39F Wf WASP fampseudo	
chr1-3294: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr1	32940193	32948643	0	NA	intron (MIRb SINE	20391	NM_00112f	127544	Hs.591504NM_153341	ENSG000003RNF19B	IBRD3 Nf ring fingprotein-coding	
chr1-112: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr1	1.13E+08	1.13E+08	0	NA	intron (intron (N	-24514	NM_02096f	4343	Hs.514941NM_02096f	ENSG000003MOV10	fSAP113 fMov10 RfS protein-coding	
chr1-145: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr1	1.46E+08	1.46E+08	0	NA	intron (AluSg6 SI	36196	NM_01445f	27246	Hs.52355fNM_01445f	ENSG000003RNF115	BCF2 ZNFc ring fingprotein-coding	
chr10-57: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr10	5763457	5770316	0	NA	intron (intron (N	46548	NM_001494	2665	Hs.29905fNM_001494	ENSG000003GDI2	HEL-S-46cGDP disscprotein-coding	
chr10-57: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr10	5780739	5791854	0	NA	intron (AluSx1 SI	27138	NM_001494	2665	Hs.29905fNM_001494	ENSG000003GDI2	HEL-S-46cGDP disscprotein-coding	
chr11-59: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr11	59575638	59603620	0	NA	intron (AluSx1 SI	5529	NR_03612f	1E+08	NR_03612f	ENSG000003MIR3162	mir-3162 microRNA ncRNA	
chr12-11: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr12	1.1E+08	1.1E+08	0	NA	intron (AluSx1 SI	18295	NM_03312f	88455	Hs.52870fNM_03312f	ENSG000003ANKRD13A	ANKRD13 ankyrin rprotein-coding	
chr18-23: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr18	23524507	23546150	0	NA	intron (intron (N	31817	NM_01332f	29919	Hs.46477fNM_01332f	ENSG000003RMC1	C18orf8 F regulator protein-coding	
chr19-19: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr19	19323	190109	0	NA	intron (intron (N	19323	NM_00109f	440515	Hs.35190fNM_00109f	ENSG000003ZNF506	- zinc fingprotein-coding	
chr4-806: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr4	80065382	80069417	0	NA	intron (intron (N	5830	NM_05817f	118429	Hs.16296fNM_05817f	ENSG000003ANTXR2	CMG-2 CMCANTXR celprotein-coding	
chr5-349: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr5	34924574	34926398	0	NA	3' UTR (N' 3' UTR (N	-3983	NM_00101f	134218	Hs.13188fNM_19428f	ENSG000003DNJ1	BMF25 DNJ DnaJ heatprotein-coding	
chr8-644: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr8	6445082	6445908	0	NA	exon (NM exon (NM	38342	NM_00132f	79648	Hs.59380fNM_002459f	ENSG000003MCPH1	BRIT1 MC1microcelprotein-coding	
chr8-9734: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr8	9734422	9736281	0	NA	intron (intron (N	-6321	NR_03032f	693182	NR_03032f	ENSG000003MIR597	MIR597 f microRNA ncRNA	
chr8-127: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr8	1.28E+08	1.28E+08	0	NA	intron (intron (N	4156	NM_00246f	4609	Hs.20245fNM_00246f	ENSG000003MYC	MRTL MYCCMYC protcprotein-coding	
chr9-922: 8.433692	-0.15095	0.727294	-0.20755	0.835578	0.874625	chr9	92278917	92289660	0	NA	intron (NLIMC5 LIN	8259	NR_037424	1.01E+08	NR_037424f	ENSG000003MIR3651	mir-3651 microRNA ncRNA	
chr2-2071: 8.460665	-0.15097	0.730122	-0.20677	0.836192	0.874782	chr2	2.07E+08	2.07E+08	0	NA	exon (NM exon (NM	10088	NM_00127f	8609	Hs.59908	NM_00370f	ENSG000003KLF7	UKLF Kruppel lprotein-coding
chr4-150: 8.460665	-0.15097	0.730122	-0.20677	0.836192	0.874782	chr4	15032953	15033979	0	NA	intron (MIR SINE	30985	NM_00117f	132864	Hs.65693fNM_18248f	ENSG000003CPEB2	CPE-BP2 C cytoplasm protein-coding	
chr11-121: 8.379745	-0.15092	0.738957	-0.20423	0.838172	0.876074	chr11	12162294	12163180	0	NA	promoter-promoter-	658	NM_00128f	9645	Hs.50192fNM_01463f	ENSG000003MICAL2	MICAL-2 f microtub protein-coding	
chr17-68: 8.46074	-0.14848	0.728677	-0.20377	0.838534	0.876074	chr17	68515531	68520386	0	NA	intron (THE1C-int	2564	NM_00127f	5573	Hs.28034fNM_002734	ENSG000003PRKARIA	ACRDY1 A protein kprotein-coding	
chr18-45: 8.46074	-0.14848	0.728677	-0.20377	0.838534	0.876074	chr18	45934692	45950430	0	NA	intron (AluSg6 SI	24768	NM_02096f	57724	Hs.51484fNM_02096f	ENSG000003EPG5	HEEW1 K1f ectopic Fprotein-coding	
chr16-294: 8.419101	-0.14847	0.728883	-0.2037	0.838592	0.876074	chr16	29441897	29449939	0	NA	intron (AAAAG)n	1108	NR_13531f	1E+08	Hs.55270fNR_13531f	ENSG000003SMG1P6	SMG1 psetpseudo	
chr2-738: 8.419101	-0.14847	0.728883	-0.2037	0.838592	0.876074	chr2	73852779	73858867	0	NA	intron (intron (N	25356	NM_00135f	10617	Hs.46901fNM_00646f	ENSG000003STAMPB	AMSH M	

chr19-565	10.88754	-0.05625	0.588049	-0.09566	0.923789	0.945395	chr19	56568505	56581890	+	0 NA	intron (TTT)n S	7729	NM_001001	388566	Hs.20444	ENSG000002ZNF470	CZF-1	zinc fingprotein-coding	
chr17-815	8.632729	-0.06683	0.721005	-0.09269	0.926151	0.947555	chr17	81911773	81916124	+	0 NA	intron (Nintron (N	-2549	NM_001184	5833	Hs.56984	ENSG00000PCYT2	ET	phosphateprotein-coding	
chr22-105	13.04463	-0.0453	0.491756	-0.09213	0.926597	0.947753	chr22	10957519	10957891	+	0 NA	intron (NLIMEc LIN	3824	NR_13232C	1.03E+08	NR_132320	FRG1FP	-	FSHD regipseudo	
chr18-455	9.620033	-0.05833	0.665939	-0.08759	0.930203	0.951183	chr18	45952074	45953518	+	0 NA	intron (Nintron (N	14533	NM_020964	57724	Hs.51484	ENSG00000EPG5	HEEW1 KI	ectopic Fprotein-coding	
chr5-7856	8.657494	-0.06188	0.728669	-0.08491	0.932329	0.9521	chr5	78560236	78560465	+	0 NA	intron (Nintron (N	88422	NM_005775	ENSG00000LHFL2	-	LHFPL tetprotein-coding			
chr8-1254	9.58962	0.056293	0.663175	0.084884	0.932354	0.9521	chr8	12540945	12542058	+	0 NA	intron (NAluSc SIN	104488	NR_040091	1.01E+08	Hs.65689	NR_040091	LOC100506	-	uncharactncRNA
chr1-2066	8.151278	-0.06167	0.74509	-0.08277	0.934036	0.9521	chr1	2.07E+08	2.07E+08	+	0 NA	intron (NAluJr4 S	2012	NM_006689	1939	Hs.49758	ENSG00000EIF2D	HCA56 LG	leukaryotiprotein-coding	
chr9-9208	8.151278	-0.06167	0.74509	-0.08277	0.934036	0.9521	chr9	92080609	92089265	+	0 NA	intron (NLIPA3 LIN	27746	NM_006415	10558	Hs.90458	NM_006415	ENSG00000SPTLC1	HSAN1 HSA	serine pprotein-coding
chr16-150	11.80286	0.044393	0.543446	0.081688	0.934895	0.9521	chr16	15015088	15016908	+	0 NA	intron (Nintron (N	-5601	NR_036265	1E+08	NR_036265	ENSG00000MIR1972-2	-	microRNA ncRNA	
chr2-1135	16.25412	-0.03189	0.396338	-0.080461	0.935871	0.9521	chr2	1.14E+08	1.14E+08	+	0 NA	intron (NAluSp SIN	2840	NR_024077	375260	Hs.44646	NM_19894	ENSG00000WASH2P	FAM39B	WASP famipseudo
chr12-760	8.163661	-0.05914	0.743822	-0.07951	0.936663	0.9521	chr12	76047903	76074333	+	0 NA	intron (Nintron (N	23567	NM_139207	4673	Hs.52459	NM_004537	ENSG00000NAP1L1	NAP1 NAP	nucleosonprotein-coding
chr12-105	8.163661	-0.05914	0.743822	-0.07951	0.936663	0.9521	chr12	1.05E+08	1.05E+08	+	0 NA	intron (Nintron (N	19623	NM_001251	55198	Hs.50660	NM_018171	ENSG00000APPL2	DIP13B	adaptor fprotein-coding
chr12-133	8.163661	-0.05914	0.743822	-0.07951	0.936663	0.9521	chr12	1.33E+08	1.33E+08	+	0 NA	intron (NL2c LINE	6553	NM_015394	7556	Hs.57398	NM_015394	ENSG00000ZNF10	KOX1	zinc fingprotein-coding
chr13-365	8.163661	-0.05914	0.743822	-0.07951	0.936663	0.9521	chr13	36321913	36323471	+	0 NA	intron (NL4_A_Mam	23702	NM_015087	23111	Hs.44041	NM_015087	ENSG00000SPART	SPG20 TAF	spartin protein-coding
chr15-515	8.163661	-0.05914	0.743822	-0.07951	0.936663	0.9521	chr15	51957799	51958505	+	0 NA	intron (Nintron (N	13626	NM_138792	123169	Hs.56766	NM_138792	ENSG00000LEO1	RDL	LEO1 homcprotein-coding
chr17-304	8.163661	-0.05914	0.743822	-0.07951	0.936663	0.9521	chr17	30460830	30463189	+	0 NA	exon (NM exon (NM	-15399	NM_004871	9527	Hs.46268	NM_004871	ENSG00000GOSR1	GOLIM2 GC	golgi SN^protein-coding
chr16-145	11.81746	0.043027	0.54203	0.079381	0.93673	0.9521	chr16	14997243	15013793	+	0 NA	intron (Nintron (N	4879	NR_036054	1E+08	NR_036054	ENSG00000MIR1972-1	MIR1972 f	microRNA ncRNA	
chr17-408	8.190634	-0.05926	0.748631	-0.07916	0.936906	0.9521	chr17	40817043	4081873	+	0 NA	TTS (NM_CTTS (NM_C	-1687	NR_160887	147184	Hs.35316	NM_145274	ENSG00000MEM99	-	transmentncRNA
chr2-9725	9.591828	0.052176	0.659676	0.079093	0.936958	0.9521	chr2	97229833	97231776	+	0 NA	intron (NLIPA3 LIN	-47913	NR_103732	1.01E+08	Hs.73261	NR_103732	LOC100506	-	uncharactncRNA
chr1-1791	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr1	1.79E+08	1.79E+08	+	0 NA	intron (Nintron (N	21501	NM_005158	27	Hs.15947	NM_005158	ENSG00000ABL2	ABLL ARG	ABL protcprotein-coding
chr10-104	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr10	1.04E+08	1.04E+08	+	0 NA	intron (NLIME3A LI	2990	NR_039702	1.01E+08	NR_039702	ENSG00000MIR4482	MIR4482-1	microRNA ncRNA	
chr14-572	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr14	57273821	57275946	+	0 NA	exon (NM exon (NM	5912	NM_018225	55745	Hs.59734	NM_018225	ENSG00000AP5M1	C14orf10	adaptor rprotein-coding
chr15-490	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr15	49041494	49043093	+	0 NA	intron (NLIM3 LINE	4153	NM_014701	9728	Hs.9997	NM_014701	ENSG00000SECISBP21	SBP2L SLA	SECIS birprotein-coding
chr17-542	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr17	51573469	51590707	+	0 NA	intron (NAluJr SIN	-4390	NM_00132C	4927	Hs.58478	NM_002532	ENSG00000NUP88	FADS4	nucleoporprotein-coding
chr17-424	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr17	42460991	42472855	+	0 NA	intron (NAluV SINE	8045	NM_00113C	535	Hs.46307	NM_005177	ENSG00000ATP6VOA1	ATP6N1 A1AT	Pase H^protein-coding
chr19-182	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr19	18349899	18364463	+	0 NA	intron (Nintron (N	16583	NM_00130C	54858	Hs.13177	NM_017712	ENSG00000PGPEP1	PAP-1 PG1	pyroglutaprotein-coding
chr19-515	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr19	51573469	51590707	+	0 NA	intron (NLIM5 LINE	10805	NR_13620E	7728	Hs.11901	NM_007147	ENSG00000ZNF175	OTK18	zinc fingprotein-coding
chr21-295	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr21	29326232	29330279	+	0 NA	intron (Nintron (N	23051	NR_027655	571	Hs.15427	NM_00118E	ENSG00000BACH1	BACH-1 BTBTB	domaiprotein-coding
chr3-1490	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr3	1.49E+08	1.49E+08	+	0 NA	intron (NMERIB DNA	33996	NM_001184	2992	Hs.47789	NM_00413C	ENSG00000GYG1	GSD15 GYC	glycogeniprotein-coding
chr5-3241	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr5	32412408	32415423	+	0 NA	intron (Nintron (N	-19440	NR_03030E	693164	NR_03030E	ENSG00000MIR579	MIR579 f	microRNA ncRNA	
chr8-9101	8.14907	-0.05651	0.743859	-0.07597	0.93944	0.9521	chr8	91014277	91021348	+	0 NA	intron (Nintron (N	23047	NM_01871C	55529	Hs.20251	NM_01871C	ENSG00000PIP4P2	TMEM55A	phosphatiprotein-coding
chr1-1554	8.176043	-0.05661	0.745283	-0.07596	0.93945	0.9521	chr1	1.55E+08	1.55E+08	+	0 NA	exon (NM exon (NM	48032	NR_03418C	645682	Hs.63248	NR_03418C	ENSG00000POU5F1P4	OMT3 OCT4	POU classpseud
chr12-2297	8.176043	-0.05661	0.745283	-0.07596	0.93945	0.9521	chr12	95861521	95863877	+	0 NA	intron (NLIMB3 LIN	3747	NM_00309E	54788	Hs.50001	NM_00309E	ENSG00000NMRFP	SMT Sm F	small rprotein-coding
chr14-506	8.176043	-0.05661	0.745283	-0.07596	0.93945	0.9521	chr14	50659282	50665767	+	0 NA	intron (Nintron (N	5782	NM_02181E	60485	Hs.64284	NM_02181E	ENSG00000SAV1	SAV WW45	salvador protein-coding
chr5-1591	8.176043	-0.05661	0.745283	-0.07596	0.93945	0.9521	chr5	1.59E+08	1.59E+08	+	0 NA	intron (NAluJb SIN	17459	NM_00119E	153830	Hs.34930	NM_14472E	ENSG00000RNF145	-	ring fingprotein-coding
chr7-2297	8.176043	-0.05661	0.745283	-0.07596	0.93945	0.9521	chr7	22974429	22976891	+	0 NA	intron (Nintron (N	38470	NM_00136E	84668	Hs.85603	NM_032581	ENSG00000FAM126A	DRCTNNB1^	family wiprotein-coding
chr8-3895	8.176043	-0.05661	0.745283	-0.07596	0.93945	0.9521	chr8	38991857	38995260	+	0 NA	exon (NM exon (NM	2951	NM_03194C	83877	Hs.7471	NM_03194C	ENSG00000TM2D2	BLP1	TM2 domaiprotein-coding
chr20-114	11.81966	0.040391	0.541903	0.074536	0.940584	0.952993	chr20	1149818	1150098	+	0 NA	intron (NAluJb SIN	31356	NM_00132E	9491	Hs.47191	NM_006814	ENSG00000PSMF1	PI31	proteasonprotein-coding
chr10-725	8.161453	-0.05398	0.745323	-0.07242	0.942265	0.953183	chr10	72339568	72341134	+	0 NA	intron (NAluX SIN	14568	NR_10712E	54788	Hs.50001	NM_00309E	ENSG00000DNABJ12	DJ10	DnaJ heatprotein-coding
chr16-158	8.161453	-0.05398	0.745323	-0.07242	0.942265	0.953183	chr16	15881718	15883795	+	0 NA	intron (N(TATC)n S	5847	NM_001304	123811	Hs.51417	NM_14460C	ENSG00000FOPNL	C16orf63 FGFR10P	l^protein-coding
chr9-1355	8.161453	-0.05398	0.745323	-0.07242	0.942265	0.953183	chr9	1.36E+08	1.36E+08	+	0 NA	Intergeni MLT1A1 LI	-6263	NM_015447	157922	Hs.52249	NM_015447	ENSG00000CAMSAP1	-	calmoduliprotein-coding
chr6-8755	8.188426	-0.05405	0.749537	-0.07211	0.942514	0.953183	chr6	87554259	87554910	+	0 NA	intron (NAluJr SIN	35403	NM_02032C	57038	Hs.48591	NM_02032C	ENSG00000RARS2	ArgRS DAI	arginyl-t^protein-coding
chr1-2235	8.13448	-0.05386	0.747267	-0.07207	0.942544	0.953183	chr1	2.24E+08	2.24E+08	+	0 NA	intron (NMLTID LTF	34500	NR_13211E	441124	Hs.52058	NR_132119	GTF2IP20	-	general tpsudo
chr12-128	8.13448	-0.05386	0.747267	-0.07207	0.942544	0.953183	chr12	12821247	12822982	+	0 NA	intron (Nintron (N	8768	NM_016355	51202	Hs.71993	NM_016355	ENSG00000DDX47	E4-DBP HG	DEAD-box protein-coding
chr2-9435	8.13448	-0.05386	0.747267	-0.07207	0.942544	0.953183	chr2	9435697	9438653	+	0 NA	intron (NAluSx SIN	13521	NM_016207	51692	Hs.51597	NM_016207	ENSG00000CPSF3	CPSF-73 C	cleavage protein-coding
chr4-1025	8.146863	-0.0513	0.748747	-0.06851	0.945381	0.955538	chr4	1.03E+08	1.03E+08	+	0 NA	intron (NLIPA5 LIN	-68662	NR_132602	1.05E+08	Hs.15833	NR_136202	LOC105377	-	uncharactncRNA
chr5-1325	8.146863	-0.0513	0.748747	-0.06851	0.945381	0.955538	chr5	1.32E+08	1.32E+08	+	0 NA	intron (Nintron (N	9755	NM_003687	8572	Hs.42431	NM_003687	ENSG00000PDLIM4	RIL	PDZ and l^protein-coding
chr13-445	9.888832	-0.02946	0.643376	-0.04578	0.963482	0.973572	chr13	44556827	44557478	+	0 NA	intron (NAluSp SIN	-18744	NR_033881	641467	Hs.62419	NR_033881	ENSG00000TSC22D1-A	-	TSC22D1 encRNA
chr9-4095	12.08749	-0.02354	0.529546	-0.04446	0.964536	0.974164	chr9	40998179	41002054	+	0 NA	intron (NAluJb SIN	7855	NR_15673C	1E+08	Hs.23186	NR_034006	FRG1HP	-	FSHD regipseudo
chr16-701	10.06752	0.028221	0.635598	0.0444	0.964585	0.974164	chr16	70159769	70161680	+	0 NA	3' UTR (N3' UTR (N	12724	NR_126007	400541	Hs.46118	NR_126007	ENSG00000LOC400541	-	uncharactncRNA
chr4-5201	8.348107	0.028015	0.742212	0.037746	0.969891	0.979259	chr4	52013993	52014214	+	0 NA	intron (NAluSp SIN	6260	NM_001024	339977	Hs.66145	NM_001024	ENSG00000LRRC66	-	leucine r^protein-coding
chr1-8543	8.362698																			



## Supplementary Information

**Supplementary Table 10. Antibody information for experimental assays.**

Antibody	Source and Identifier	Application
Anti-p-ATM	Abways, cat. no. CY5111	IB
Anti-ATM	Abways, cat. no. CY5207	IB
Anti-H3K9me3	Abcam, cat. no. ab8898	IB, IHC, IF
Anti-H3K36me3	ABclonal, cat. no. A2366	IB, IHC, IF
Anti-H3K9me3	Active Motive, cat. no. 39161	ChIP-seq
Anti-H3K36me3	Active Motive, cat. no. 61101	ChIP-seq
Anti-H3K9me2	Cell Signaling Technology, cat. no. 4658	IB
Anti-H3K36me2	Bioss, cat. no. bsm-53020M	IB
Anti-p16	Abways, cat. no. CY5357	IB
Anti-p21	Abways, cat. no. CY5088	IB
Anti-CXCL8	Proteintech, cat. no. 17038-1-AP	IB
Anti-KDM4A	Abways, cat. no. CY8322	IB, IHC, IF
Anti-KDM4A	abcam, cat. no. ab24545	ChIP-PCR
Anti-KDM4B	Cell Signaling Technology, cat. no. 8639	IB, IHC,IF
Anti-KDM4C	Abcam, cat. no. ab85454	IB
Anti-KDM4D	Abcam, cat. no. ab198209	IB
Anti-SUV39H1	Cell Signaling Technology, cat. no. 8729	IB
Anti-HA	Cell Signaling Technology, cat. no. 3724	IB
Anti-Ubiquitin	Abways, cat. no. CY1295	IB
Anti-γH2AX	Cell Signaling Technology, cat. no. 9718	IB, IF
Anti-H2AX	Cell Signaling Technology, cat. no. 7361	IB
Anti-p-53BP1	Santa Cruz, cat. no. sc-135748	IB, IF
Anti-53BP1	Proteintech, cat. no. 20002-1-AP	IB
Anti-p65	Santa Cruz, cat. no. sc-8008	IB
Anti-Histone H3	Cell Signaling Technology, cat. no. 4499	IB
Anti-Caspase 3 (cleaved)	Cell Signaling Technology, cat. no. 9661	IB, IHC
Anti-Caspase 3	Cell Signaling Technology, cat. no. 9662	IB
Anti-GAPDH	Abways, cat. no. AB0037	IB

Note: IB, immunoblot; IHC, immunohistochemistry; IF, immunofluorescence.

## Supplementary Information

**Supplementary Table 11. Primer sequences for qRT-PCR assays.**

Gene name	Forward (5'-3')	Reverse (5'-3')
<i>IL6</i>	TTCTGCGCAGCTTTAAGGAG	AGGTGCCCATGCTACATTTG
<i>CXCL8</i>	ATGACTTCCAAGCTGGCCGTG	TGTGTTGGCGCAGTGTGGTC
<i>IL-1<math>\alpha</math></i>	AATGACGCCCTCAATCAAAG	TGGGTATCTCAGGCATCTCC
<i>IL-1<math>\beta</math></i>	TGGGTATCTCAGGCATCTCC	TTCTGCTTGAGAGGTGCTGA
<i>GM-CSF</i>	ATGTGAATGCCATCCAGGAG	AGGGCAGTGCTGCTTGTAGT
<i>AREG</i>	AGCTGCCTTTATGTCTGCTG	TTTCGTTCCCTCAGCTTCTCC
<i>CXCL1</i>	CACCCAAGAACATCCAAAG	TAACTATGGGGGATGCAGGA
<i>CXCL3</i>	GGAGCACCAACTGACAGGAG	CCTTCCAGCTGTCCCTAGA
<i>CCL3</i>	TGCAACCAGTTCTCTGCATC	TTTCTGGACCCACTCCTCAC
<i>CCL8</i>	TCACCTGCTGCTTTAACGTG	ATCCCTGACCCATCTCTCCT
<i>MMP1</i>	GGTCTCTGAGGGTCAAGCAG	AGTTCATGAGCTGCAACACG
<i>MMP3</i>	AGGGAACTTGAGCGTGAATC	TCACTTGTCTGTTGCACACG
<i>MMP8</i>	TCTGCAAGGTTATCCCAAGG	CTTGCTGGAAAACCTGCATCA
<i>MMP10</i>	GGCTCTTTCACCTCAGCCAAC	TCCCGAAGGAACAGATTTTG
<i>SPINK1</i>	CCTTGGCCCTGTTGAGTCTA	GCCCAGATTTTTGAATGAGG
<i>WNT16B</i>	GCTCCTGTGCTGTGAAAACA	TGCATTCTCTGCCTTGTGTC
<i>p16<sup>INK4a</sup></i>	CTTCCTGGACACGCTGGT	ATCTATGCGGGCATGGTTAC
<i>P21<sup>CIP1</sup></i>	ATGAAATTCACCCCCTTTCC	CCCTAGGCTGTGCTCACTTC
<i>KDM4A</i>	TGGAATTGGTGGAAAAGGAG	GTCTTCAGTGTGCCAAGCAA
<i>KDM4B</i>	GGACTGACGGCAACCTCTAC	CGTCCTCAAACCTCCACCTG
<i>KDM4C</i>	TGCCTGTCTGTTTTCTCAG	CATGTCGAGCAACTTCAGGA
<i>KDM4D</i>	TTTCCCTATGGCTACCATGC	TCATAGCGTTCAGGTTGCAG
<i>SUV39H1</i>	GTCATGGAGTACGTGGGAGAG	CCTGACGGTCGTAGATCTGG
<i>RPL13A</i>	GTACGCTGTGAAGGCATCAA	CGCTTTTTCTTGTCTGAGGG



## Supplementary Information

### Supplementary Table 12. Basic characteristics and QC of ChIP-seq libraries (CTRL group).

##FastQC	0.11.9						
>>Basic Statistics	pass						
#Measure	Value						
Filename	CTRL-1-3-input_2_val_2.fq.gz						
File type	Conventional base calls						
Encoding	Sanger / Illumina 1.9						
Total Sequences	14693315						
Sequences flagged as poor quality	0						
Sequence length	20-150						
%GC	39						
>>END_MODULE							
>>Per base sequence quality	pass						
#Base	Mean	Median	Lower Quartile	Upper Quartile	10th Percentile	90th Percentile	
1	35.7745	37	37	37	37	37	37
2	35.57287	37	37	37	37	37	37
3	35.75874	37	37	37	37	37	37
4	35.76841	37	37	37	37	37	37
5	35.8496	37	37	37	37	37	37
6	35.8214	37	37	37	37	37	37
7	35.79939	37	37	37	37	37	37
8	35.82203	37	37	37	37	37	37
9	35.81694	37	37	37	37	37	37
	35.857	37	37	37	37	37	37
15-19	35.84111	37	37	37	37	37	37
20-24	35.79981	37	37	37	37	37	37
25-29	35.73897	37	37	37	37	37	37
30-34	35.69198	37	37	37	37	37	37
35-39	35.66943	37	37	37	37	37	37
40-44	35.64014	37	37	37	37	37	37
45-49	35.57315	37	37	37	37	37	37
50-54	35.54193	37	37	37	37	37	37
55-59	35.49454	37	37	37	37	37	37
60-64	35.45118	37	37	37	37	37	37

65-69	35.40584	37	37	37	37	37
70-74	35.39193	37	37	37	37	37
75-79	35.32191	37	37	37	34.6	37
80-84	35.26352	37	37	37	34.6	37
85-89	35.28055	37	37	37	37	37
90-94	35.19622	37	37	37	25	37
95-99	35.13609	37	37	37	25	37
100-104	35.09063	37	37	37	25	37
105-109	35.04995	37	37	37	25	37
110-114	35.01937	37	37	37	25	37
115-119	34.98532	37	37	37	25	37
120-124	34.81667	37	37	37	25	37
125-129	34.79613	37	37	37	25	37
130-134	34.8112	37	37	37	25	37
135-139	34.63038	37	37	37	25	37
140-144	34.56597	37	37	37	25	37
145-149	34.5588	37	37	37	25	37
>>END_MODULE	150 34.41528	37	37	37	25	37



### Supplementary Information

**Supplementary Table 13. Basic characteristics and QC of CHIP-seq libraries (BLEO group).**

##FastQC	0.11.9						
>>Basic Statistics	pass						
#Measure	Value						
Filename	BLEO-2-2-input_2_val_2.fq.gz						
File type	Conventional base calls						
Encoding	Sanger / Illumina 1.9						
Total Sequences	33271794						
Sequences flagged as poor quality	0						
Sequence length	20-150						
%GC	39						
>>END_MODULE							
>>Per base sequence quality	pass						
#Base	Mean	Median	Lower Quartile	Upper Quartile	10th Percentile	90th Percentile	
1	35.82588	37	37	37	37	37	37
2	35.86822	37	37	37	37	37	37
3	35.99687	37	37	37	37	37	37
4	35.97876	37	37	37	37	37	37
5	36.02685	37	37	37	37	37	37
6	36.0085	37	37	37	37	37	37
7	35.97396	37	37	37	37	37	37
8	35.96807	37	37	37	37	37	37
9	35.95195	37	37	37	37	37	37
	35.98313	37	37	37	37	37	37
15-19	36.05518	37	37	37	37	37	37
20-24	36.02828	37	37	37	37	37	37
25-29	35.9411	37	37	37	37	37	37
30-34	35.90737	37	37	37	37	37	37
35-39	35.88251	37	37	37	37	37	37
40-44	35.84138	37	37	37	37	37	37
45-49	35.77285	37	37	37	37	37	37
50-54	35.69475	37	37	37	37	37	37
55-59	35.68489	37	37	37	37	37	37
60-64	35.66751	37	37	37	37	37	37

65-69	35.55309	37	37	37	37	37
70-74	35.55462	37	37	37	37	37
75-79	35.46192	37	37	37	37	37
80-84	35.41105	37	37	37	37	37
85-89	35.37145	37	37	37	37	37
90-94	35.38655	37	37	37	37	37
95-99	35.2612	37	37	37	29.8	37
100-104	35.14181	37	37	37	25	37
105-109	35.09898	37	37	37	25	37
110-114	35.11619	37	37	37	25	37
115-119	34.99176	37	37	37	25	37
120-124	34.8854	37	37	37	25	37
125-129	34.81463	37	37	37	25	37
130-134	34.75972	37	37	37	25	37
135-139	34.60572	37	37	37	25	37
140-144	34.53947	37	37	37	25	37
145-149	34.28972	37	37	37	25	37
	150 34.32601	37	37	37	25	37

>>END\_MODULE



### Supplementary Information

**Supplementary Table 14. Basic characteristics and QC of ChIP-seq libraries (BLEO/ML324 group).**

```

##FastQC                0.11.9
>>Basic Statistics      pass
#Measure                Value
Filename                BLEO-ML324-3-4-H3K36me3_2_val_2.fq.gz
File type               Conventional base calls
Encoding                Sanger / Illumina 1.9
Total Sequences        24178187
Sequences flagged as poor quality  0
Sequence length        20-150
%GC                     42
>>END_MODULE
>>Per base sequence quality  pass
#Base                   Mean      Median   Lower Quartile Upper Quartile 10th Percentile 90th Percentile
1 35.47687              37       37       37       37       37       37
2 35.48851              37       37       37       37       37       37
3 35.59955              37       37       37       37       37       37
4 35.54916              37       37       37       37       37       37
5 35.58892              37       37       37       37       37       37
6 35.60606              37       37       37       37       37       37
7 35.61358              37       37       37       37       37       37
8 35.58155              37       37       37       37       37       37
9 35.60267              37       37       37       37       37       37
   35.6411              37       37       37       37       37       37
15-19                   35.64139  37       37       37       37       37
20-24                   35.60147  37       37       37       37       37
25-29                   35.51056  37       37       37       37       37
30-34                   35.4785   37       37       37       37       37
35-39                   35.458    37       37       37       37       37
40-44                   35.42439  37       37       37       37       37
45-49                   35.31269  37       37       37       34.6     37
50-54                   35.21263  37       37       37       27.4     37
55-59                   35.22509  37       37       37       27.4     37
60-64                   35.21736  37       37       37       27.4     37

```

65-69	35.0841	37	37	37	25	37
70-74	35.09653	37	37	37	25	37
75-79	34.96084	37	37	37	25	37
80-84	34.91946	37	37	37	25	37
85-89	34.85124	37	37	37	25	37
90-94	34.86545	37	37	37	25	37
95-99	34.73031	37	37	37	25	37
100-104	34.61884	37	37	37	25	37
105-109	34.58245	37	37	37	25	37
110-114	34.61261	37	37	37	25	37
115-119	34.43888	37	37	37	25	37
120-124	34.3913	37	37	37	25	37
125-129	34.29534	37	37	37	25	37
130-134	34.19898	37	37	37	25	37
135-139	34.04085	37	37	37	25	37
140-144	33.95945	37	37	37	25	37
145-149	33.69617	37	37	37	25	37
	150 33.7233	37	37	37	25	37

>>END\_MODULE



**Supplementary Information**

**Supplementary Table 15. FastqC output of ChIP-seq libraries (mapping statistics for all).**

<b>Modification</b>	<b>Sample Name</b>	<b>Total Reads</b>	<b>Mapped Reads</b>	<b>% Mapped</b>
None	CTRL-1-1-input	36477776	30693636	84.14%
None	CTRL-1-2-input	36884260	31441905	85.24%
H3K9me3	CTRL-1-1-H3K9me3	44260666	42184447	95.31%
H3K9me3	CTRL-1-2-H3K9me3	51104202	48269305	94.45%
None	CTRL-1-3-input	29386630	27467563	93.47%
None	CTRL-1-4-input	36867136	29086228	78.89%
H3K36me3	CTRL-1-3-H3K36me3	26535286	25394486	95.70%
H3K36me3	CTRL-1-4-H3K36me3	28486164	27626815	96.98%
None	BLEO-2-1-input	59987896	53737650	89.58%
None	BLEO-2-2-input	66543588	60547204	90.99%
H3K9me3	BLEO-2-1-H3K9me3	63076954	61376933	97.30%
H3K9me3	BLEO-2-2-H3K9me3	56499018	54750066	96.90%
None	BLEO-2-3-input	28006786	25085110	89.57%
None	BLEO-2-4-input	33857258	31055106	91.72%
H3K36me3	BLEO-2-3-H3K36me3	37027760	35818900	96.74%
H3K36me3	BLEO-2-4-H3K36me3	40670232	39383872	96.84%
None	BLEO-ML324-3-1-input	43434654	41928500	96.53%
None	BLEO-ML324-3-2-input	48718064	47048384	96.57%
H3K9me3	BLEO-ML324-3-1-H3K9me3	45302648	43662391	96.38%
H3K9me3	BLEO-ML324-3-2-H3K9me3	53378402	51565319	96.60%
None	BLEO-ML324-3-3-input	41647824	40101109	96.29%
None	BLEO-ML324-3-4-input	63531914	60743434	95.61%
H3K36me3	BLEO-ML324-3-3-H3K36me3	52006598	51062341	98.18%
H3K36me3	BLEO-ML324-3-4-H3K36me3	48356374	47514433	98.26%

## Supplementary Information

Supplementary Table 16. Primer sequences for ChIP-PCR assays.

Gene name	Forward (5'-3')	Reverse (5'-3')
<i>IL6</i>	GGCAGGAAACTGTCAAGAGC	GCAGACACCAGGCTCTAAGG
<i>CXCL1</i>	ATCCGAGACACAACGCTCTT	TCTGGGATATTCGCCTTCTG
<i>IL-1<math>\alpha</math></i>	TTGTGATCTTGGGTTGGTCA	ATGTTGGTGGGTGACTGGAT
<i>IL-1<math>\beta</math></i>	CCTGTATCCCAAGTCCAGCA	TGATCACAGCAGCCTCAAAC
<i>AREG</i>	ATCTTGGCTCACTGCGATCT	GCAGGTGGATCATCTCAGGT
<i>MMP3</i>	ATCCCTGGGAGGTCAGATTT	GAAAGGGGGAGGAAGATGAG
<i>p16<sup>INK4a</sup></i>	CAGCACTTTGGGAGGCTAAG	GAGCAATTCTCCTGCCTCAG
<i>p21<sup>CIP1</sup></i>	GGCAGATTCAAGACCTGGAG	AAGTTCTGCCAGAAAGCAA