

BRIEF REPORT

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

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SUMMARY

Base editors can correct disease-causing genetic variants. After a neonate had received a diagnosis of severe carbamoyl-phosphate synthetase 1 deficiency, a disease with an estimated 50% mortality in early infancy, we immediately began to develop a customized lipid nanoparticle–delivered base-editing therapy. After regulatory approval had been obtained for the therapy, the patient received two infusions at approximately 7 and 8 months of age. In the 7 weeks after the initial infusion, the patient was able to receive an increased amount of dietary protein and a reduced dose of a nitrogen-scavenger medication to half the starting dose, without unacceptable adverse events and despite viral illnesses. No serious adverse events occurred. Longer follow-up is warranted to assess safety and efficacy. (Funded by the National Institutes of Health and others.)

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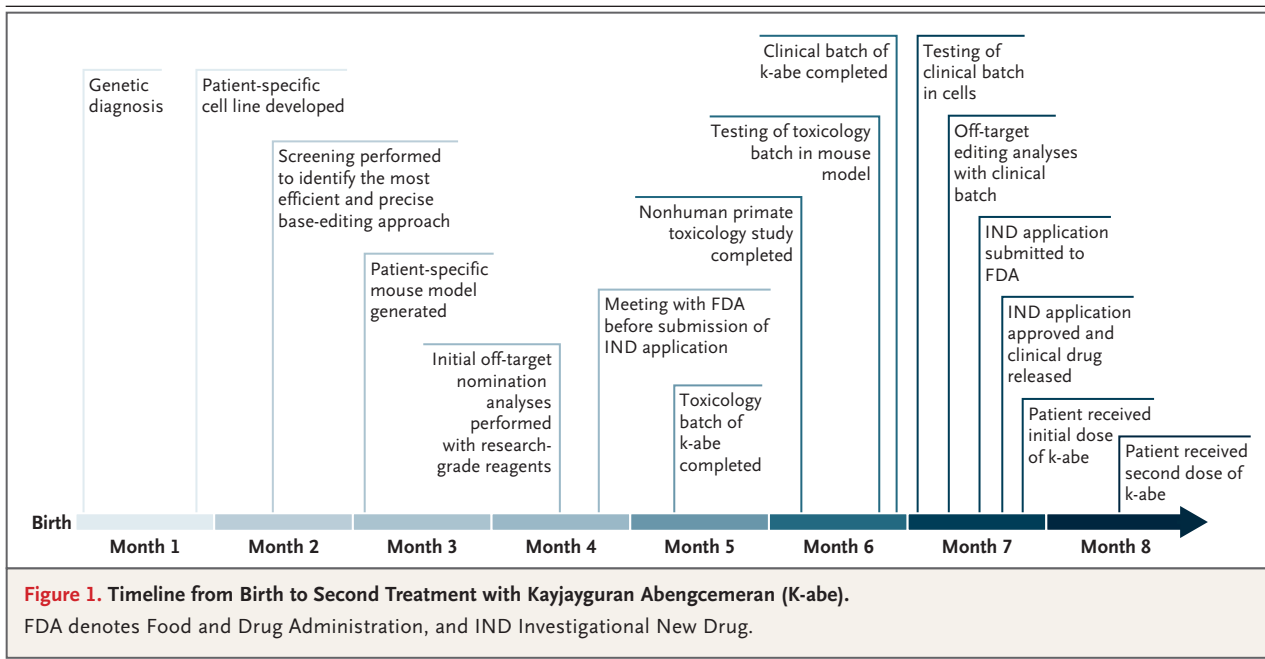
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PROGRAMMABLE GENE-EDITING TECHNOLOGY BASED ON CLUSTERED regularly interspaced short palindromic repeats (CRISPR)–CRISPR-associated protein 9 (Cas9)¹ has matured into therapeutic approaches that are improving the lives of patients with various diseases, such as sickle cell disease, β -thalassemia, and hereditary angioedema.²⁻⁴ Precise, corrective CRISPR-Cas9 technology — namely, base editing (which can effect cytosine-to-thymine changes [cytosine base editing⁵] or adenine-to-guanine changes [adenine base editing⁶]) and prime editing⁷ (which can produce any single-nucleotide change or small insertion or deletion) — can potentially address more than 90% of pathogenic variants in genetic diseases that, although rare individually, collectively affect hundreds of millions of people worldwide.⁸ However, drug-development efforts have largely focused on recurrent variants in a few relatively common genetic diseases on account of the extensive resources needed to develop and bring to market any given therapy.⁹

We developed a workflow for the rapid development of customized, corrective gene-editing therapies for patients with ultrarare or unique “N-of-1” variants (Fig. 1). More specifically, we developed a base-editing therapy, delivered in vivo to hepatocytes through lipid nanoparticles, for a single patient who at birth received a diagnosis of neonatal-onset carbamoyl-phosphate synthetase 1 (CPS1) deficiency,



an ultrarare inborn error of metabolism affecting the urea cycle. CPS1 deficiency affects 1 in 1,300,000 persons¹⁰ and has an estimated mortality of 50% in early infancy.¹¹ Liver transplantation provides a functional urea cycle and improves outcomes.^{12,13} However, hyperammonemic crises and irreversible neurologic injury often occur in infants before they grow large enough to undergo transplantation.¹⁴⁻¹⁶ We administered the customized therapy to our patient twice, at approximately 7 and 8 months of age, with the goal of providing protection against hyperammonemia.

METHODS

STUDIES FOR INVESTIGATIONAL NEW DRUG APPLICATION

Full descriptions of cellular studies, studies in animals, and off-target assessments are provided in the Supplementary Appendix 1, available with the full text of this article at NEJM.org. The institutional animal care and use committee at the University of Pennsylvania and at AmplifyBio approved the studies in mice and nonhuman primates, respectively. Genome-sequencing data from the patient and blood-derived genomic DNA samples from the patient's father were obtained under a human subjects research protocol that was approved by the institutional review board at the University of California, Berkeley.

CLINICAL STUDY

Because the therapy (kayjayguran abengcemeran, or k-abe) was administered as part of clinical care under a single-patient expanded-access Investigational New Drug application, the clinical protocol was reviewed by the institutional review board at Children's Hospital of Philadelphia (CHOP) through alternative procedures. After the initial regulatory review by the Food and Drug Administration (FDA), we received authorization from the FDA to obtain concurrence by the CHOP chairperson of the institutional review board, who then reviewed and approved the study. The patient's parents provided written informed consent. Clinical activities were overseen by a multidisciplinary oversight committee comprising physicians from the CHOP metabolism, hepatology, immunology, gene therapy, and medical ethics services. The investigators vouch for the accuracy and completeness of the data and for the fidelity of the study to the protocol, available at NEJM.org.

RESULTS

CLINICAL PRESENTATION

Symptoms of CPS1 deficiency, including lethargy and respiratory distress, developed in the patient (a male neonate) within the first 48 hours of life. Measurement of blood ammonia revealed a level greater than 1000 μmol per liter (1703 μg per

deciliter; reference range, 9 to 33 μmol per liter [15 to 56 μg per deciliter]). Continuous renal-replacement therapy was initiated promptly. Plasma amino acid profiling revealed a critically elevated level of glutamine, undetectable citrulline, and a normal level of urinary orotic acid, findings suggestive of a proximal urea-cycle defect. Rapid targeted analysis of the patient's genome identified two truncating *CPS1* variants: c.1003C→T (p.Gln335Ter, referred to as Q335X, on the paternal allele) and c.2140G→T (p.Glu714Ter, referred to as E714X, on the maternal allele). The Q335X variant is absent in the Genome Aggregation Database but has been reported in a case of neonatal-onset *CPS1* deficiency.¹⁷

The patient was weaned from continuous renal-replacement therapy and transitioned to long-term therapy that included nitrogen-scavenger medication (glycerol phenylbutyrate), citrulline supplementation (at a dose of 200 mg per kilogram of body weight per day, which remained unchanged throughout his clinical course), and a protein-restricted diet (given as a 1:1 mix of natural protein and essential amino acid formula). The patient had the expected infantile “honeymoon” period¹⁴ from days 50 to 100, after which his biochemical status worsened, leading to a further reduction in protein intake and an increase in the dose of glycerol phenylbutyrate to manage the elevated ammonia and glutamine levels. Each hyperammonemic episode incurred a risk of permanent neurologic damage and death. Given the severity of his disease, the patient was listed for liver transplantation at 5 months of age.

PATIENT-SPECIFIC CUSTOMIZATION OF BASE-EDITING THERAPY

Reliable assessment of base editing of the *CPS1* Q335X variant would ideally use human hepatocytes with the variant; however, human hepatocytes were not available. Therefore, we used the cultured human HuH-7 cell line as a proxy. We synthesized a cassette harboring a 100-bp human genomic segment spanning the *CPS1* Q335X variant, as well as 100-bp segments spanning the patient's other *CPS1* variant and two reference variants in *PAH* to serve as positive controls (Fig. S2A in the Supplementary Appendix 1 [all supplementary figures and tables are available in Supplementary Appendix 1]). We transduced HuH-7 cells with a lentiviral vector containing the cassette, thereby inserting the cassette into the genome. This process

was completed 1 month after the patient's birth.

To develop a patient-specific, bespoke gene editor, we screened various adenine base editors (ABEs) with guide RNAs (gRNAs) tiling the site of the Q335X variant in the lentivirus-transduced HuH-7 cells (Fig. S2B, S2C, and S2D and Fig. S3). We identified an ABE with a preference for NGC protospacer-adjacent motifs, termed NGC-ABE8e-V106W, and a gRNA with the target Q335X adenine in the eighth position of its protospacer sequence as the most efficient and precise base-editing approach; although there was bystander editing of neighboring adenines, all such edits were synonymous (Figs. S4 through S7). This process was completed 2 months after the patient's birth. We named the gRNA used in the lipid nanoparticle therapy (Table S1) “kayjayguran,” the messenger RNA (mRNA) encoding the ABE (Fig. S1 and Table S2) “abengcemeran,” and the therapy “k-abe” (for short).

PRECLINICAL STUDIES

After the initial regulatory review by the FDA, we manufactured a toxicology batch of k-abe (i.e., the batch used for toxicologic testing) and undertook a limited safety study in cynomolgus monkeys to characterize single-dose toxicity of the lipid nanoparticle therapy. A total RNA dose of 1.5 mg per kilogram of body weight was administered intravenously. No clinical signs of toxic effects were present, and there were transient elevations in alanine aminotransferase and aspartate aminotransferase levels to several times the upper limit of the normal range — findings that are consistent with the results of previous studies (Fig. S12).^{18,19} Two weeks after treatment, plasma levels of lipid excipients had fallen more than 99.5% from the peak levels, a development that supported readministration of the therapy at intervals greater than 2 weeks (Fig. S13). The results of the study in cynomolgus monkeys (completed 5 months after the patient's birth) indicated that a dose of 0.1 mg per kilogram was a potentially safe initial clinical dose for the patient.

On learning of the patient's genetic diagnosis, we immediately started generating mouse models to assess the *in vivo* editing efficiency of k-abe. To maximize the chance of success, we used established CRISPR reagents in mouse zygotes to insert a cassette harboring a 100-bp human genomic segment spanning the *CPS1* Q335X variant into

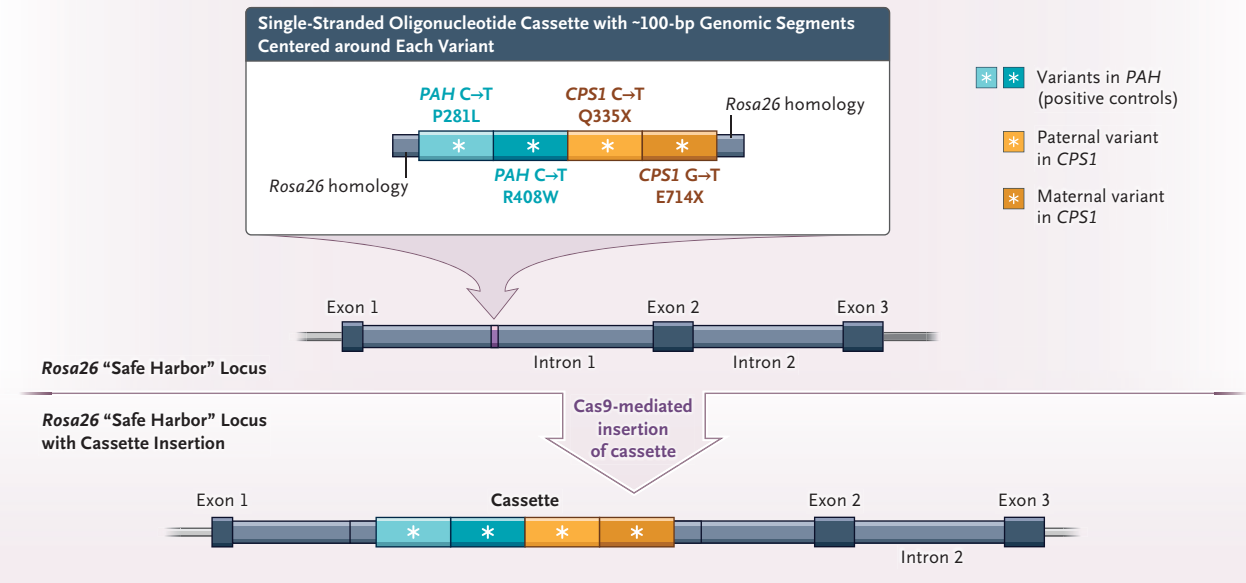
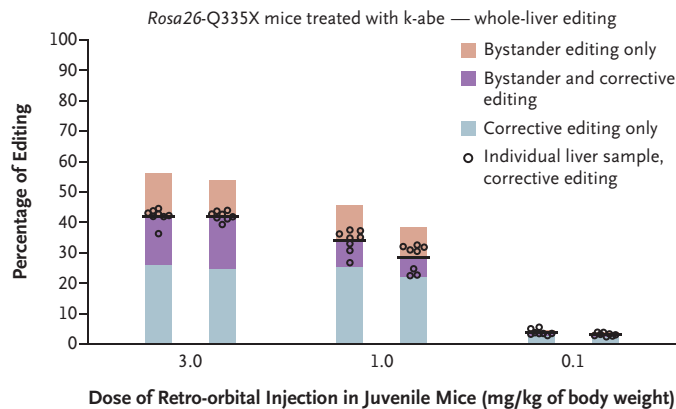
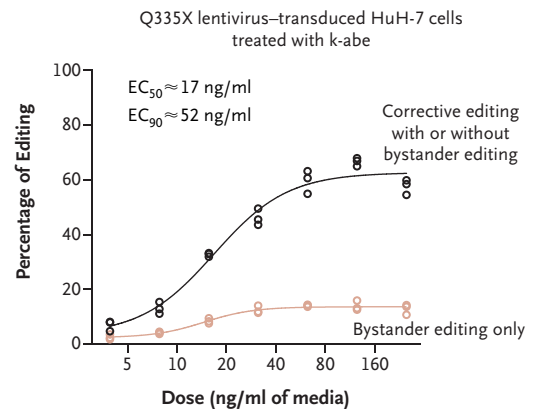
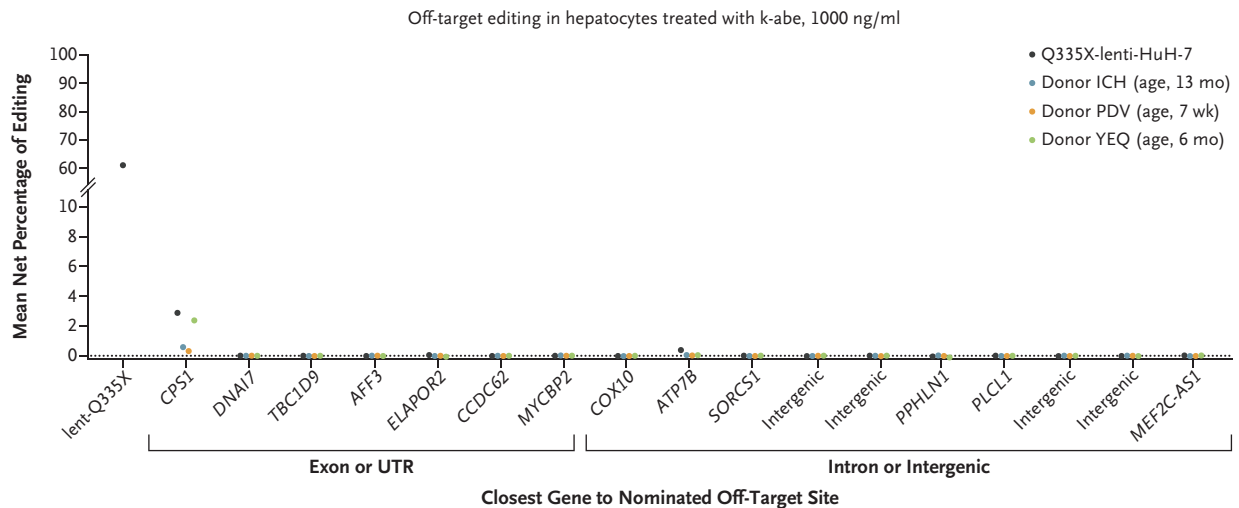
A Engineering a Mouse Model with Four Human Pathogenic Variant Sequences, Including Q335X Variant**B In Vivo Efficacy of Toxicology Batch of K-abe in Mice****C In Vitro Efficacy of Clinical Batch of K-abe in Cells****D Off-Target Assessment of Clinical Batch of K-abe in Cells**

Figure 2 (facing page). Preclinical Studies.

Panel A shows the contents of the single-stranded DNA oligonucleotide cassette inserted into the endogenous mouse *Rosa26* locus in mouse zygotes. Panel B shows the extent of whole-liver corrective adenine base editing of the *CPS1* Q335X variant in *Rosa26*-Q335X mice. Several days after administration of a single dose of k-abe from the toxicology batch, we obtained multiple samples distributed throughout the liver of each juvenile mouse on necropsy. We assessed the extent of editing in eight samples per mouse by sequencing the *Rosa26*-Q335X cassette. The two bars at each dose level (3.0, 1.0, and 0.1 mg per kilogram of body weight) represent two mice. Across the three dose groups, no more than 1% insertional or deletional mutagenesis occurred at the target site. Panel C shows corrective adenine base editing of the *CPS1* Q335X variant in lentivirus-transduced HuH-7 cells treated with k-abe. Editing was determined 3 days after treatment at the stated dose (concentration after dilution with cell medium). The best-fit agonist response curve with variable slope (four-parameter logistic regression) and 50% effective concentration (EC_{50}) and 90% effective concentration (EC_{90}) values were calculated with GraphPad Prism. Panel D shows the evaluation of a high-priority subset of nominated off-target sites for any adenine-to-guanine editing through individual-site targeted amplicon sequencing in the Q335X lentivirus-transduced HuH-7 cells (Q335X-lenti-HuH-7) and in primary human hepatocytes from three male donors (donor ICH [13 months of age], donor PDV [7 weeks of age], and donor YEQ [6 months of age]) after treatment with k-abe at 1000 ng per milliliter of media, as compared with untreated cells. Of 21 high-priority nominated off-target sites, 16 were successfully sequenced and shown here. Cas9 denotes clustered regularly interspaced short palindromic repeats-associated protein 9, and UTR untranslated region.

the *Rosa26* “safe harbor” locus (the same cassette used for the lentivirus-transduced HuH-7 cells) (Fig. 2A). At 5 months after the patient’s birth, we performed a limited dose–response study in which the toxicology batch of k-abe was used in a small number of *Rosa26*-Q335X mice. In this study, we observed up to 42% whole-liver corrective editing, along with the expected synonymous bystander editing (Fig. 2B and Figs. S10 and S11A). Editing was evident at the lowest dose (0.1 mg per kilogram), which further supported that dose as the initial clinical dose for the patient. Subsequent validation of *in vivo* corrective editing in a second mouse model in which the Q335X variant was introduced into the endogenous mouse *Cps1* locus is described in Figures S9 and S11B.

With the clinical batch of k-abe that was produced 5 months after the patient’s birth, we performed a dose–response potency assessment in lentivirus-transduced HuH-7 cells (Fig. 2C and Fig. S8). To assess off-target editing, we performed ONE-seq¹⁸ and CHANGE-seq-BE assays²⁰ using recombinant NGC-ABE8e-V106W protein and kayjayguran, as well as a modified GUIDE-seq²¹ assay using a nuclease version of the editor (Figs. S14 through S18, and see Supplementary Appendix 2), during months 4 and 5. The ONE-seq assay was performed with a synthetic library that had been designed with the patient’s genome as the reference genome. The CHANGE-seq-BE assay was performed with genomic DNA obtained from the patient’s father, who carried the Q335X variant (we were unable to obtain enough genomic DNA from the patient). We prioritized the on-target *CPS1* site and 21 nominated off-target sites for verification with individual-site targeted amplicon sequencing (Fig. 2D and Tables S3 through S6). We exposed lentivirus-transduced HuH-7 cells and primary human hepatocytes from three donors to a supersaturating dose of k-abe. Low-level synonymous bystander editing was evident at the endogenous wild-type *CPS1* genomic site in all four cell lots, a finding that is consistent with the gRNA (kayjayguran) having a 1-base mismatch to the wild-type sequence (the HuH-7 cells retained endogenous wild-type *CPS1* alleles in addition to the transduced *CPS1* Q335X variant sequence). We observed a low level of off-target editing at an intronic site in *ATP7B* in the HuH-7 cells but not in the three primary human hepatocyte lots. *ATP7B* encodes a copper transporter and was not considered to represent biologic risk because its loss of function has not been linked to carcinogenesis.²² Subsequent analysis of a larger set of nominated off-target sites detected no off-target editing in the treated primary human hepatocytes (Fig. S19).

TREATMENT OF THE PATIENT

A single-patient, expanded-access Investigational New Drug application was submitted to the FDA when the patient was 6 months of age, which was approved 1 week later. The patient was presumed to have no cross-reactive immunologic material, and out of concern for the potential development of an immune response to full-length *CPS1* protein, prophylactic immunosuppression with sirolimus and tacrolimus was initiated on days 205

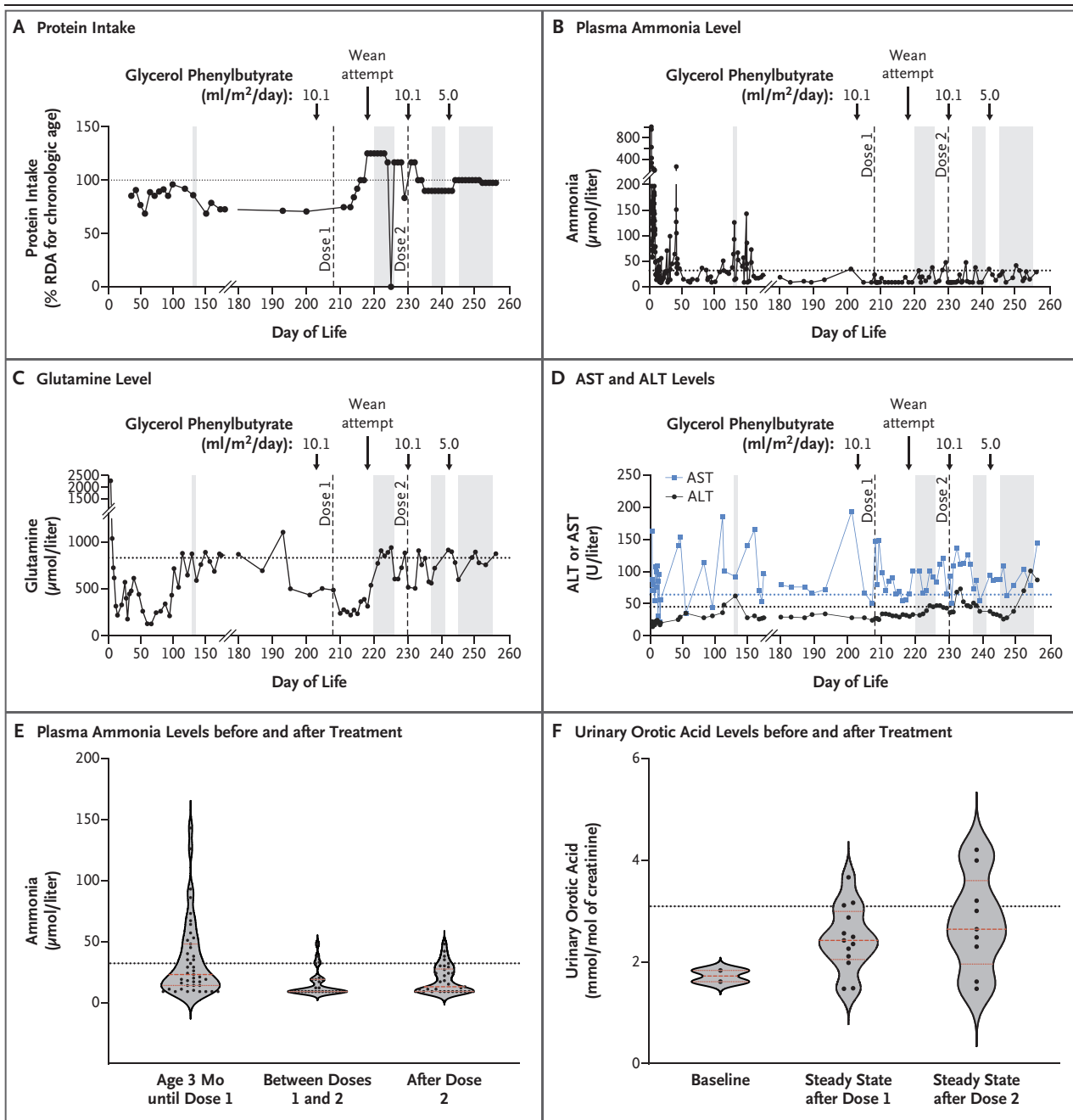


Figure 3. Biochemical Profile before and after Treatment with K-abe.

Shown are the timelines of protein intake (Panel A) and levels of plasma ammonia (Panel B), glutamine (Panel C), aspartate aminotransferase (AST) and alanine aminotransferase (ALT) (Panel D). The gray bars from left to right indicate periods of rotavirus-positive gastroenteritis before treatment, rhinovirus-positive upper respiratory tract infection after dose 1, and two viral illnesses after dose 2 (gastroenteritis followed by a new rhinovirus or enterovirus infection with associated viral transaminitis). In Panels B through F, the dotted horizontal lines indicate upper limits of the normal range for the laboratory value. Panels E and F show violin plots of plasma ammonia levels and urinary orotic acid levels, respectively, before and after treatment. Inside the plots, the red dashed line indicates the median, and the red dotted lines indicate the upper and lower quartiles. The clusters of dots indicate the individual data points. To convert the values for ammonia to micrograms per deciliter, divide by 0.5872. To convert the values for glutamine to micrograms per deciliter, divide by 68.42. RDA denotes recommended dietary allowance.

and 209, respectively, after the patient's birth. We selected this steroid-sparing regimen because corticosteroids can trigger hyperammonemia in patients with CPS1 deficiency. On day 208 after birth, the patient received an intravenous infusion of k-abe at a total RNA dose of 0.1 mg per kilogram. After treatment, it was possible to increase his dietary protein intake. Because the patient was born at 35 weeks' gestation, his prescribed protein goal was sometimes above the recommended daily allowance for chronologic age (Fig. 3A). The patient recovered from a viral respiratory infection without the occurrence of an illness-associated hyperammonemic crisis; however, he received intravenous fluids, which is standard during illness, and was on a protein-free diet for 1 day (day 225 after birth). We were unable to wean him from glycerol phenylbutyrate; we had reduced the dose from 10.1 to 8.1 ml per square meter of body-surface area per day but then restored the original dose because of rising glutamine levels.

Given the incomplete biochemical correction in the patient — and according to the clinical protocol — he received a second dose of k-abe (0.3 mg per kilogram) 22 days after receipt of the first k-abe infusion. The patient had a coughing episode during the second infusion that resolved with nasal suctioning. Transient elevations in alanine aminotransferase and aspartate aminotransferase levels occurred a few days after the second k-abe infusion and recurred a few weeks later during the course of viral illness (Fig. 3D). At 2 weeks after the second infusion, the patient was able to receive a reduced dose of glycerol phenylbutyrate to half the starting dose (from 10.1 to 5.0 ml per square meter per day) without unacceptable adverse effects.

During the 4 weeks after the second infusion of k-abe, two viral infections, each with accompanying vomiting and diarrhea, developed in the patient. In contrast to a gastroenteritis infection that had occurred in the patient before the administration of k-abe, he recovered from the viral infections without a hyperammonemic crisis and was able to continue his full-protein diet during the course of his illnesses. The median blood ammonia levels before the first k-abe dose (23 μmol per liter [39 μg per deciliter]; interquartile range, 14 to 48 μmol per liter [24 to 82 μg per deciliter]), between the first and second doses (9 μmol per liter [15 μg per deciliter]; interquartile range, 9 to

19 μmol per liter [15 to 32 μg per deciliter]), and after the second dose (13 μmol per liter [22 μg per deciliter]; interquartile range, 9 to 28 μmol per liter [15 to 48 μg per deciliter]) support the occurrence of a treatment-related reduction (Fig. 3E). CPS1 contributes to orotic acid synthesis, and patients with CPS1 deficiency often have urinary orotic acid levels at the lower end of the normal range (median level in our patient before the first k-abe dose, 1.7 mmol per mole of creatinine; interquartile range, 1.6 to 1.8); after receipt of the two doses of k-abe, the levels in our patient were often at the high end of the normal range (2.4 mmol per mole of creatinine; interquartile range, 2.0 to 3.0) or above the normal range (2.6 mmol per mole of creatinine; interquartile range, 2.0 to 3.6) (Fig. 3F). The patient's weight increased from 7.14 kg (the 9th percentile) at 207 days after birth (before the first dose), to 8.17 kg (the 26th percentile) at 256 days after birth (the end of the 7-week follow-up period), and his neurologic status was stable.

DISCUSSION

In this study, we describe a personalized base-editing therapy wholly developed in the 6-month span after a patient's birth. The patient was able to receive an increased amount of dietary protein and a reduced dose (to half the starting dose) of a nitrogen-scavenger medication, despite the “stress tests” presented by consecutive viral infections. The short follow-up is a limitation of this study; longer follow-up is needed to assess the safety and efficacy of k-abe, as well as the patient's neurologic health. Liver biopsy to assess for corrective CPS1 editing was deferred because it posed an unacceptable risk to the infant. The potential for germline editing with k-abe could not be evaluated, although a study of a different lipid nanoparticle gene-editing drug did not detect editing in sperm samples from nonhuman primates nor germline transmission of gene edits in female mice to offspring.¹⁹

An advantage of lipid nanoparticle therapies is the potential for readministration,²³ which is contraindicated with adeno-associated virus–delivered therapies, given the immunogenicity of the vector. We opted to start with a very low initial dose of k-abe to evaluate safety, which was followed by a moderately higher second dose. In principle, the

patient could receive additional and higher doses of k-abe in the future, if needed.

Therapies similar to k-abe could be developed for hundreds of hepatic inborn errors of metabolism. Similar to antisense oligonucleotide therapy,^{24,25} corrective gene editing lends itself to rapid customization for individual patients owing to the platform nature of the technology.⁹ Shared components among gene-editing therapies could include the same lipid nanoparticle formulation and mRNA, with the gRNA customized to each patient's variant.

We assessed k-abe for editing efficiency in mice and for safety in nonhuman primates. Such studies might not be necessary for future patient-specific treatments; perhaps cell-based studies would be sufficient. Although k-abe was developed under emergency conditions for a devastating neonatal-onset metabolic disorder, we anticipate that rapid deployment of patient-specific gene-editing therapies will become routine for many genetic diseases.

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Disclosure forms provided by the authors are available with the full text of this article at NEJM.org.

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CLINICAL TRIAL REGISTRATION

The *Journal* requires investigators to register their clinical trials in a public trials registry. The members of the International Committee of Medical Journal Editors (ICMJE) will consider most reports of clinical trials for publication only if the trials have been registered. Current information on requirements and appropriate registries is available at www.icmje.org/about-icmje/faqs/.

Protocol

Protocol for: Musunuru K, Grandinette SA, Wang X, et al. Patient-specific in vivo gene editing to treat a rare genetic disease. *N Engl J Med* 2025;392:2235-43. DOI: 10.1056/NEJMoa2504747

This trial protocol has been provided by the authors to give readers additional information about the work.

This supplement contains the following items:

1. Original protocol, final protocol, summary of changes.
2. Original and final statistical analysis plan.

Title	Single subject IND for severe neonatal-onset carbamoyl phosphate synthetase I deficiency (CPS1 deficiency) in a single patient who harbors the <i>CPS1</i> c.1003C>T, p.Q335X variant in <i>trans</i> with a second variant, <i>CPS1</i> c.2140G>T, p.E714X using LNP.CPS1.Q335X
Drug or Biologic Name	LNP.CPS1.Q335X
FDA IND	31438
Regulatory Sponsor	Sponsor Name: Rebecca Ahrens-Nicklas, MD, PhD
eIRB Number	25-023112
Protocol Date	11 MAR 2025

INTRODUCTION

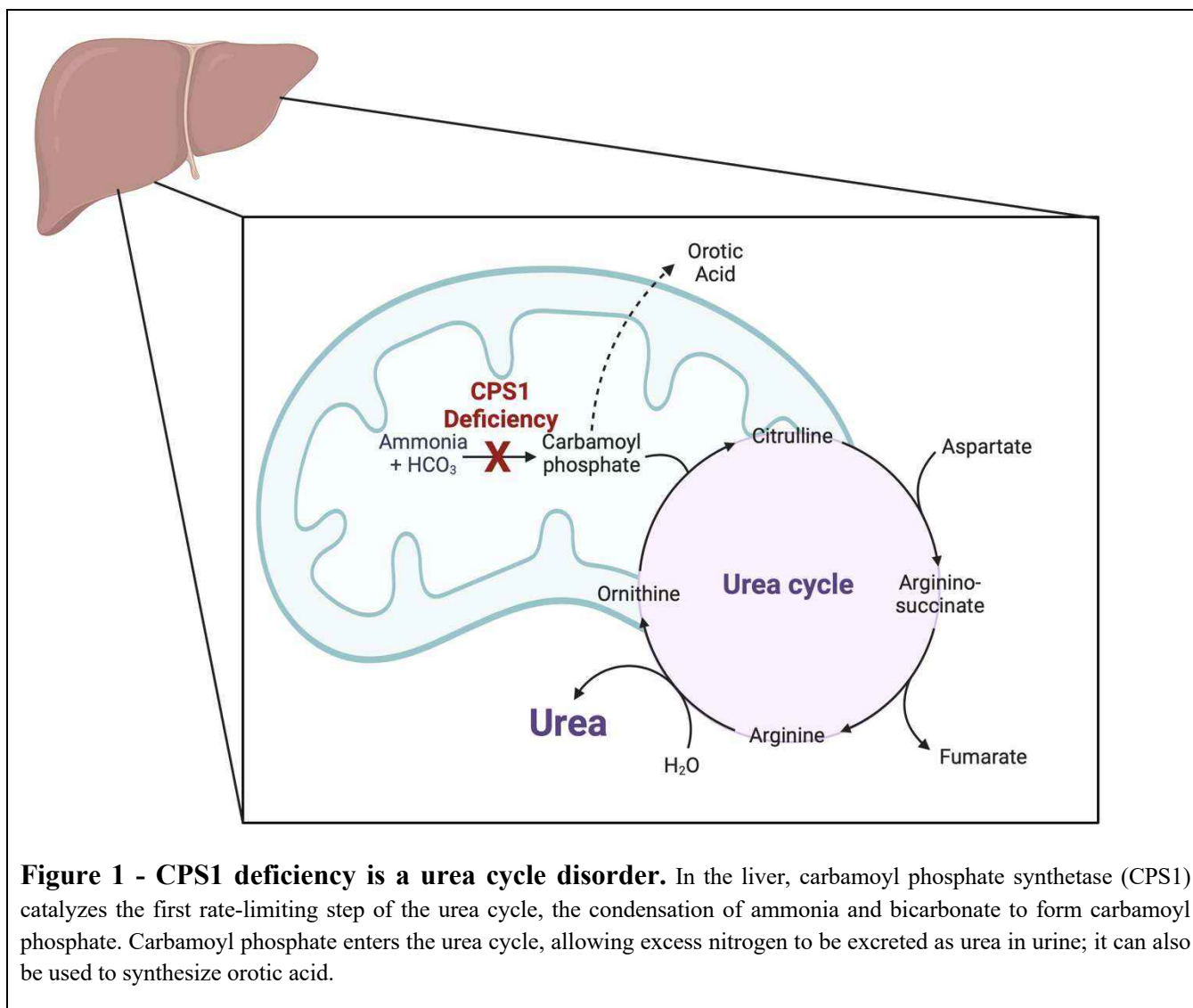
Carbamoyl phosphate synthetase I deficiency (CPS1 deficiency) is a urea cycle disorder (UCD) characterized by life-threatening episodes of hyperammonemia starting in the neonatal period. Despite standard-of-care therapy with ammonia scavenger medications and dietary therapy, patients experience recurrent episodes with any minor physiologic stressors¹.

Each hyperammonemic episode is associated with a high risk of permanent neurologic damage and death. It is estimated that 50% of infants with neonatal-onset UCDs die in early infancy². CPS1 deficiency is an ultra-rare disease with an estimated incidence of 1:1,300,000³.

Current standard of care for CPS1 deficiency

Humans ingest protein to support growth and the synthesis of a number of key macromolecules. Nitrogen waste generated from protein catabolism is converted to ammonia, which under normal physiologic conditions is converted to urea via the urea cycle. Urea can then be excreted in the urine to maintain whole-body nitrogen homeostasis.

Patients with CPS1 deficiency have impaired activity of the first, rate-limiting step of the urea cycle⁴ (**Figure 1**). As such, they experience frequent episodes of neurotoxic hyperammonemia, which can induce cerebral edema and death. Unfortunately, even when treated with the standard of care, most patients have recurrent episodes of severe metabolic decompensations and neurologic injury⁵. It has been noted that among CPS1 patients that survive the neonatal period, more than 80% go on to have recurrent hyperammonemia before their first birthday⁶. Consistent with this data, the CPS1 patient proposed to be treated with LNP.CPS1.Q335X has had multiple episodes of hyperammonemia during the first five months of life. Given this high risk of metabolic decompensation, there is a large unmet need for new effective therapies for CPS1 deficiency, including a clear such need in the present case.



The standard of care focuses on limiting protein intake and catabolism through dietary measures and on reducing ammonia levels through ammonia scavenger medications (**Table 1**). Given that these measures are not very effective, liver transplantation has become the standard of care for severely affected patients at many institutions⁷⁻⁹. As the urea cycle occurs entirely within the liver, transplantation can normalize the metabolic defect. However, transplantation is often delayed by donor availability and the need for neonates to grow to an appropriate size for transplant¹⁰. Patients often are not large enough to be transplant candidates until after their first birthday. During this first year of life, most patients experience irreversible neurologic damage, even with close medical management⁵. Liver transplantation is also associated with acute and chronic risks and challenges.

Table 1. Current supportive therapy for CPS1 deficiency.

Therapeutic aim	Chronic management	Emergent management during decompensations
Reduce toxic ammonia accumulation through scavenger therapy or direct removal	• Oral glycerol phenylbutyrate (Ravicti) • Liver transplantation after patient is large enough, approximately 10 kg	• IV sodium phenylacetate/sodium benzoate (Ammonul) • Dialysis (if needed)
Prevent fasting or inadequate caloric intake, which triggers catabolism of endogenous protein	• Frequent feeds, avoid fasting • Closely monitor caloric need and provide fats and carbohydrates as extra calories as needed	• High-dextrose intravenous fluids • IV lipids
Limit protein intake while avoiding any essential amino acid deficiencies, which trigger catabolism of endogenous protein	• Carefully provide non-essential amino-acid-free medical formula (i.e., “incomplete protein”) to maintain normal essential amino acid levels • Strictly limit intake of natural (i.e., “complete”) protein • Provide supplemental citrulline (an amino acid that generates the essential amino acid arginine in the urea cycle distal to the defect in CPS1 deficiency)	• Stop all protein intake for a limited period of time • Provide IV arginine, an essential amino acid generated in the urea cycle

PATIENT CLINICAL INFORMATION

Brief Clinical History

The patient is a 6-month-old ex-35 1/7 male born via C-section secondary to intrauterine growth restriction (IUGR) and placenta accreta with a diagnosis of carbamoyl phosphate synthetase (CPS1) deficiency and a history of severe hyperammonemia requiring continuous renal replacement therapy (CRRT) and ammonia scavenger therapy, and currently an inpatient at the Children’s Hospital of Philadelphia (CHOP). As of [REDACTED], his length is 59 cm and his weight is 6.3kg. Shortly after birth, he began having

lethargy, increased tone, clonus, and apnea, bradycardia, and desaturation (ABD) events. Initial studies, including head ultrasound, electroencephalography (EEG), and lumbar puncture were normal. Ammonia level obtained due to persistent lethargy revealed an ammonia of >1000 µmol/L (normal range: 9-33 µmol/L) after which he was promptly started on CRRT. Computed tomography (CT) of the head at that time did not demonstrate evidence of cerebral edema. Subsequent plasma amino acid profile demonstrated critically elevated glutamine and undetectable citrulline, suggestive of a proximal urea cycle defect. Follow-up genetic testing via rapid targeted analysis of the genome identified compound heterozygous truncating variants in *CPS1*, c.1003C>T (p.Gln335*) and c.2140G>T p.Glu714*), associated with no residual enzyme activity and severe disease. At that time, he was started on protein restriction, dextrose-containing fluids, intralipids, medical formula, glycerol phenylbutyrate, and sodium benzoate. Since his initial presentation, he has been weaned from CRRT and initiated on chronic ammonia scavenger medications, citrulline replacement, and a protein-restricted diet.

He continues to have life-threatening periods of episodic hyperammonemia despite aggressive therapy. Since his diagnosis, he has had occasional transient elevations in ammonia between 40-100 µmol/L. In addition, his admission has been complicated by bradycardia/desaturation and respiratory acidosis. He is currently awaiting liver transplantation evaluation, as liver transplantation is curative in urea cycle disorders such as CPS1 deficiency. He remains admitted to CHOP for close monitoring and supportive care.

INVESTIGATIONAL PRODUCT INFORMATION

- Integrated DNA Technologies, Inc. (IDT) will perform all stages of manufacturing of the CPS1-001 guide RNA (gRNA) drug substance (DS);
- Aldevron LLC (Aldevron) will perform all stages of manufacturing of the NGC-ABE8e-V106W mRNA DS;
- Aldevron will perform all stages of manufacturing of the LNP.CPS1.Q335X drug product (DP).

DESCRIPTION:

The drug product (DP) is a liver-targeted, lipid nanoparticle (LNP) base editing therapeutic comprising a messenger RNA (mRNA) drug substance (DS) encoding an adenine base editor (ABE), a single guide RNA (gRNA) DS to engage with the ABE once expressed within the target cells, and lipid excipients that provide the LNP delivery system for the nucleic acid DSs. The DP will be administered intravenously.

- **gRNA Drug Substance**

The gRNA DS in the LNP.CPS1.Q335X DP comprises (1) a 20-nucleotide spacer sequence that corresponds to a protospacer DNA sequence matching the region of the *CPS1* gene spanning the Q335X variant, which includes the target adenosine nucleotide to be corrected by the DP, and (2) an 80-nucleotide

tracrRNA domain that complexes with a *Streptococcus pyogenes* Cas9 nickase domain in an ABE. The gRNA DS (also known as CPS1-001) is a 100-mer oligonucleotide comprising 53 ribonucleotides, 47 2'-O-methylribonucleotides, and 6 phosphorothioate backbone modifications at select positions.

- **mRNA Drug Substance**

The mRNA DS in the LNP.CPS1.Q335X DP encodes the adenine base editor 8e protein with a V106W variant in the adenosine deaminase domain and with a version of the *S. pyogenes* Cas9 D10A nickase with a preference for the protospacer-adjacent motif (PAM) NGC (hereafter referred to as NGC-ABE8e-V106W). The mRNA comprises the 5' cap, the 5' untranslated region (UTR), the ABE coding sequence, the 3' UTR, and the 3' polyadenylate tail. The ABE coding sequence, 4818 nucleotides in length, is codon-optimized with uridine minimization and has substitution of all uridines with the modified nucleotide N1-methylpseudouridine.

- **Lipid Nanoparticle Drug Product**

The LNP.CPS1.Q335X DP comprises the mRNA and gRNA DSs and four lipid excipients: an ionizable amino lipid (ALC-0307), cholesterol, 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC), and a PEG-lipid (ALC-0159). The targeted ratio of gRNA to mRNA is 1:1 by weight, -

RATIONALE FOR PROPOSED TREATMENT:

Rationale for the liver as the target organ

The *CPS1* gene is largely expressed in hepatocytes, and correction of the primary genetic defect solely within the liver via organ transplantation is curative in CPS1 deficiency¹¹. *CPS1* is unequivocally the causal gene responsible for CPS1 deficiency, inherited in a recessive manner. Besides the unambiguous human genetic evidence, mouse models with disruption of the *Cps1* gene phenocopy the human disease, manifesting hyperammonemia and death within 24-36 hours of birth^{12,13}. Natural history studies of patients demonstrate two clinical presentations of CPS1 deficiency: neonatal-onset disease, in which hyperammonemia that can cause irreversible brain damage occurs within a few days of birth, with high morbidity and mortality; and late-onset disease, with moderate or mild severe symptoms that emerge later in childhood or adulthood and are elicited by protein-rich meals or situations of high metabolic demand.

Neonatal-onset disease is generally associated with less than 5% of the normal CPS1 activity in liver, whereas late-onset disease is associated with higher residual activity¹⁴. Among a cohort of Japanese patients with CPS1 deficiency, one patient with late-onset disease (13 years of age) was observed to have 4.8% residual hepatic enzyme activity, and another patient with genetically confirmed late-onset disease (13 years of age) had 17% residual activity¹⁴. In the same cohort, three patients with genetically confirmed neonatal-onset disease had 6%, 6.25%, and 11% residual activity, respectively. By extrapolation,

achieving correction of $\approx 10\text{-}15\%$ of the *CPS1* alleles in the hepatocytes of neonatal-onset disease patients with no residual activity (complete loss of function, e.g., a patient with two *CPS1* nonsense variants such as the patient who is the intended recipient of LNP.CPS1.Q335X) should ameliorate disease phenotypes in these patients.

Rationale for a base editing strategy and DP mechanism of action

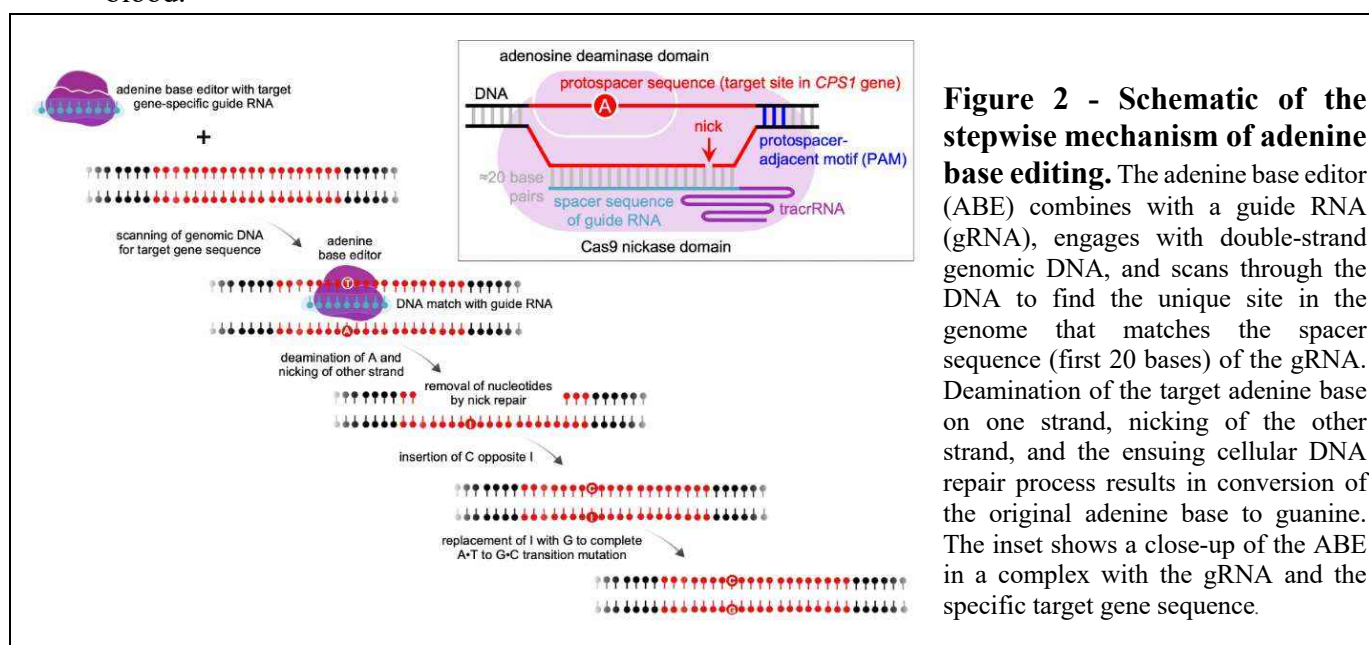
With the LNP.CPS1.Q335X DP, the Sponsor plans to use corrective adenine base editing that introduces an A>G change in the genome, in a highly specific manner, at the site of the Q335X pathogenic variant in the *CPS1* gene in hepatocytes. The expected effect of reverting the variant to wild-type would be to restore functionality to the CPS1 protein product, durably reducing and even normalizing blood ammonia levels in the patient. The DP will comprise LNPs encapsulating an mRNA encoding an adenine base editor (ABE) and a single guide RNA (gRNA) targeting the site of the *CPS1* Q335X variant, in liquid form for IV infusion and delivery to the hepatocytes in the liver. Specifically, the DP will contain NGC-ABE8e-V106W mRNA and a gRNA designated CPS1-001.

The mechanism of action of the DP is as follows:

- (1) The LNPs will be internalized by the hepatocytes following binding of endogenous apolipoprotein E (apoE) to the LNP, leading to engagement of low-density lipoprotein receptor (LDLR) on the plasma membrane and subsequent receptor-mediated endocytosis of the LNP carrying the mRNA and gRNA. Comprehensive nonclinical data have shown that the LNP characteristics of the DP drive the biodistribution profile of the DP.
- (2) After LNP-bound apoE engages with LDLR, endocytosis of the LNP occurs. The subsequent reduction in endosomal pH results in a charge-based interaction of the ionizable lipid with the endosomal membrane, which ultimately results in the release of the mRNA and gRNA cargoes into the cytoplasm^{15,16}.
- (3) The mRNA will be translated into an ABE protein, which comprises a catalytically impaired clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein 9 (Cas9) nuclease domain (that functions as a single-strand nickase and minimizes the production of double-strand breaks) fused with an adenosine deaminase domain^{17,18} (**Figure 2**). The gRNA comprises a tracrRNA domain that complexes with the Cas9 nickase domain and a spacer sequence that corresponds to a protospacer DNA sequence matching the region of the *CPS1* gene spanning the c.1003C>T variant, which includes the target adenosine nucleotide to be corrected. The protospacer is located immediately upstream of the protospacer-adjacent motif (PAM), which is required for ABE activity. The protospacer is chosen to be unique in the genome, enabling a highly specific gRNA that would not bind elsewhere in the genome where it could cause off-target editing.
- (4) Base pairing between the gRNA and the target DNA sequence will result in displacement of the PAM-containing genomic DNA strand to form a single-stranded DNA R-loop, i.e., an editing window, that exposes the target adenosine nucleotide to the deaminase activity of the ABE (**Figure**

2).

- (5) Deamination of adenosine will produce inosine, which is read as guanosine by DNA polymerase during DNA repair.
- (6) To increase efficiency of the DNA repair process, the Cas9 domain will nick the unedited DNA strand to induce a DNA repair mechanism that uses the edited strand as the template for DNA repair, resulting in an adenine-to-guanine substitution. In the case of the LNP.CPS1.Q335X DP, this substitution on the *CPS1* antisense strand will result in a thymine-to-cytosine substitution on the sense strand, reverting the c.1003C>T variant to wild-type.
- (7) Corrected alleles will produce functional CPS1 protein, which will reduce ammonia levels in the blood.



Data from prior human studies using an analogous LNP formulation



Data from prior human studies of repeat dosing of intravenous LNP therapies

The Sponsor is proposing a treatment plan that would allow for repeat dosing of LNP.CPS1.Q335X (see **Dosing Regimen, Figure 3**). While repeat dosing of the LNP formulation that will be used in the LNP.CPS1.Q335X DP has not occurred in human subjects to date, multiple doses of a different LNP gene editing therapy⁹ have been well tolerated in first-in-human trials. Specifically, in a phase 1 clinical trial in subjects with hereditary transthyretin amyloidosis (NCT04601051, NTLA-2001), three individuals in the lowest dose group were later successfully re-dosed with good therapeutic effect¹⁹. After the initial low (0.1 mg/kg) dose, the three subjects experienced a median 52% therapeutic reduction in serum

transthyretin levels. After repeat dosing with a standard 55 mg dose, transthyretin levels were reduced to 90% of baseline. While one individual experienced a mild infusion reaction, the repeat dose was generally well tolerated. There were no clinically significant changes in liver enzymes, platelets, or coagulation parameters.

There is also precedent for repeat intravenous dosing of LNP-encapsulated mRNA DPs in ongoing trials of two rare hepatic inborn errors of metabolism, propionic acidemia (NCT04159103) and methylmalonic acidemia (NCT04899310). Both trials are enrolling older infants who are at least 1 year old or 11 kg in size. While the lipid excipients used in these DPs are different from the lipid excipients that will be used in LNP.CPS1.Q335X, these trials provide proof of concept that repeat LNP dosing in older infants can be well tolerated²⁰. There were no serious adverse events in the initial trial for propionic acidemia, and the treatment-emergent adverse events were those expected for a population of pediatric patients with propionic acidemia. No immune toxicities were noted in the study.

Preliminary findings from GLP non-human primate toxicology study

A short-term GLP toxicology and biodistribution study of the LNP.CPS1.Q335X drug product in juvenile male cynomolgus monkeys was recently completed. non-GMP gRNA DS and mRNA DS formulated with GMP lipids were for the NHP toxicology and biodistribution study. The toxicology batch of drug product was made by the same active pharmaceutical ingredient manufacturers that produced clinical drug product intended for use in the patient.

The GLP NHP study comprised three groups: (1) a biodistribution group that will undergo necropsy at 4 hours following LNP treatment; (2) a short-term single dose toxicology group that will undergo necropsy after 2 weeks of recovery; and (3) a vehicle control group that will undergo necropsy after 2 weeks of recovery. To minimize the risk of infusion reactions, all animals will be pretreated with famotidine, diphenhydramine, and dexamethasone.

For the biodistribution study, animals underwent necropsy at 4 hours after infusion of the LNP.CPS1.Q335X. Tissue samples from a wide variety of organs including (but not limited to) liver, adrenal glands, spleen, lungs, heart, kidney, muscle, testes, and bone marrow were collected and frozen for molecular analysis to detect the mRNA DS. Specimens will also be evaluated via standard histopathologic analysis. Final results are pending.

For the single dose toxicology study, the study endpoint was 14 days after infusion of the LNP.CPS1.Q335X. This timepoint was selected given previously published pharmacokinetic and toxicity studies of a drug with an analogous LNP formulation, which showed clearance of the DP and resolution of ALT elevations by 14 days after dosing^{22,23}. Animals in both the single dose toxicology and vehicle control groups were monitored for several longitudinal in-life laboratory assessments, including serum chemistry, hematology, and coagulation, and clinical assessments prior to necropsy. Upon necropsy, gross examination and detailed histopathologic evaluation of a wide variety of relevant tissues was completed.

All slides will be evaluated by a board-certified pathologist. In addition, samples will be obtained for molecular analysis to detect the mRNA DS.

While full results are pending, a preliminary summary of findings from the toxicology study is as follows. Changes in the clinical pathology data attributed to test article administration were limited to mild alterations in the leukogram (increased neutrophils, decreased lymphocytes and monocytes) that resolved by Day 8 and minimal increases in serum enzyme activity (alanine aminotransferase and aspartate aminotransferase) attributable to hepatocyte damage/stress. The observed changes in the leukogram were minimal to mild and are consistent with a non-specific physiologic stress response and non-adverse. The described serum enzyme elevations were minimal to mild and resolved by the end of study and are therefore considered non-adverse. All other changes are considered spurious and due to normal biological variation, and unrelated to test article administration. As no observable adverse events were detected, the NOAEL is at least 1.5 mg/kg.

Preliminary findings from off-target editing studies

The Sponsor has used three orthogonal methods to nominate candidate off-target sites for the LNP.CPS1.Q335X drug product. Of note, the Sponsor endeavored to adapt these methods as much as possible to the individual genome of the single patient who will be treated with LNP.CPS1.Q335X. The first method was Circularization for High-throughput Analysis of Nuclease Genome-wide Effects by sequencing adapted for adenine base editing (CHANGE-seq-BE)²⁴, a homology-independent biochemical assay that provides an unbiased genome-wide analysis, using genomic DNA obtained from the patient's parent (the parent from whom the *CPS1* Q335X variant was inherited). The second method was OligoNucleotide Enrichment and sequencing (ONE-seq), a homology-dependent biochemical assay that uses a synthetic human genomic library selected by sequence similarity to the protospacer/PAM sequence specified by the adenine base editor (ABE)/guide RNA (gRNA) (i.e., NGC-ABE8e-V108W and CPS1-001)^{23,25}. The overall nomination list comprises the candidate genomic sites identified by CHANGE-seq-BE and/or ONE-seq. The third method was bioinformatic prediction, which relies on sequence similarity between genomic sites and the protospacer/PAM sequence specified by the ABE/gRNA (i.e., NGC-ABE8e-V108W and CPS1-001). This method uses bioinformatic tools such as Cas-OFFinder and GuideScan^{26,27} to identify sites in the reference patient genome (derived from whole-genome sequencing) with up to three mismatches, or up to two mismatches plus up to one RNA or DNA bulge. These sites were added to the overall nomination list if they had not already been nominated by CHANGE-seq-BE or by ONE-seq.

The Sponsor has prioritized assessment of nominated sites that lie in exonic regions of genes, as off-target editing in coding sequences or untranslated regions is the most likely to have functional consequences on gene function and, thereby, influence oncogenic risk. None of the CHANGE-seq-BE-nominated candidate sites were in exonic regions; together, ONE-seq and bioinformatic prediction identified 12 candidate sites in exonic regions. In the initial analysis, the Sponsor has not observed any off-target editing at any nominated exonic site upon assessment in LNP.CPS1.Q335X-treated human hepatocytes *in vitro*. The Sponsor is undertaking a comprehensive assessment of the entire nomination list using the rhAmpSeq

methodology (Integrated DNA Technologies). This analysis is expected to take 1-2 months to complete and as such will not be completed until after the patient has been treated with LNP.CPS1.Q335X. The full report will be submitted to the FDA as an amendment to the IND.

Risk-benefit analysis

The patient's genetic testing results of compound heterozygous truncating variants in *CPS1* are associated with severe CPS1 deficiency, as there is no residual enzyme activity. He has remained admitted as an inpatient at CHOP for monitoring and has intermittent episodes of hyperammonemia without a clear trigger. CPS1 deficiency is typically the most severe urea cycle disorder, as the enzyme is the first step of the urea cycle and is the rate-limiting urea cycle enzyme. When compared to other urea cycle disorders, CPS1 deficiency is associated with a greater incidence of irreversible neurological injury, with one study documenting 6 individuals out of 7 (85%) of individuals with CPS1 deficiency having neurological injury or death immediately after initial presentation and the remaining individual developing severe neurological disease later in life, even with aggressive clinical management. In contrast, the same study identified that only 7/17 patients with citrullinemia type I (41.2%) and 7/24 patients with OTC deficiency (7/24 patients) had similar levels of severe neurological disease or death¹. Therefore, it is imperative that those who are diagnosed with CPS1 deficiency receive curative treatment, such as liver transplantation, as early as possible in life, which can prevent further neurological damage, decrease morbidity and mortality, and increase quality of life.

Studies on liver transplantation in infants have demonstrated that graft survival outcomes are moderate (67-79% at 1 year), and these individuals have higher rates of vascular complications, including thrombosis, necessitating re-transplantation²⁸. Many centers have liver transplantation weight requirements, and historically patients at CHOP are not transplanted until they reach 10 kg in weight. It is documented that infants 0-3 months of age or those < 5 kg in weight have lower survival rates and higher risks of complications²⁹. Although our patient is listed for transplant, his current size puts him at higher risk of post-transplant complications and transplant failure. In addition, his small size severely limits the availability of donor livers. Currently, liver transplantation is the only available cure for CPS1 deficiency, and the patient is at risk of significant morbidity and mortality in the interim between now and when a transplant may be available. As such, consideration of the use of gene editing in this patient is clinically warranted and has the potential to provide a curative therapy before the patient would have access to liver transplantation.

The LNP.CPS1.Q335X DP is designed to treat a single patient with severe neonatal-onset CPS1 deficiency. At initial presentation on day of life 0, he was noted to have a blood ammonia level above the quantification range of the clinical laboratory assay (>1,000 $\mu\text{mol/L}$, normal 9-33 $\mu\text{mol/L}$). He was found to have elevated plasma glutamine, undetectable plasma citrulline, and absent urine orotic acid, consistent with a biochemical diagnosis of CPS1 deficiency. Subsequently he was found to harbor compound heterozygous disease-causing variants in *CPS1*. Despite receiving standard-of-care therapy (**Table 1**), he continues to have episodes of hyperammonemia requiring urgent escalation of care including initiation of a sick day diet and administration of intravenous ammonia scavenger medications. During each of these

events, he experiences a high risk of permanent neurologic damage³⁰. He remains admitted as an inpatient for close monitoring at CHOP. In order to minimize the risk of death and to limit the ongoing permanent neurologic damage he is experiencing, we aim to treat the patient with LNP.CPS1.Q335X DP.

DOSING REGIMEN:

To prioritize the safety of the patient, the dosing plan will begin with a low dose that is still predicted to provide benefit. Pending the full results of the proposed GLP NHP toxicology and biodistribution study, the Sponsor proposes an initial 0.1 mg/kg dose of the LNP.CPS1.Q335X DP administered intravenously. This dose was selected because:

- As per the FDA Guidance for Industry Estimating the Maximum Starting Dose in Initial Clinical Trials for Therapeutics in Adult Healthy Volunteers (2005), the estimated body surface area (BSA) of an NHP (i.e., juvenile male cynomolgus monkey) is 0.25 m². Based on current growth charts, we estimate the BSA of the patient on the intended dosing date (late winter 2025) will be approximately 0.3 m². Therefore, the estimated BSA conversion factor (the ratio of the BSA of NHP to patient) is 0.833. In the GLP NHP toxicology study of LNP.CPS1.Q335X (full results pending, see preliminary findings summary above), no observable adverse events were detected at a dose of 1.5mg/kg (therefore the NOAEL is at least 1.5mg/kg). Using BSA scaling, the human equivalent dose (HED) for the patient is 1.25 mg/kg (1.5mg/kg × 0.833). The proposed starting dose of 0.1 mg/kg therefore represents a safety factor of 12.5. The Sponsor feels this high scaling factor is appropriate to ensure the patient's safety, especially given the inherent uncertainty in scaling drug doses in infants.
- The clinical laboratory testing and evaluations that occur prior to the initial dosing will be considered the baseline period. On day 1, the patient will be given an initial low-dose (0.1 mg/kg) intravenous infusion of the LNP.CPS1.Q335X DP. If the dose of 0.1 mg/kg is well tolerated by the patient, a repeat higher dose can be considered. Up to three total doses can be given (**Figure 3**).
- If the safety profile is favorable, and the patient continues to demonstrate biochemical features of CPS1 deficiency at 21 days after this initial dose, a second administration of the LNP.CPS1.Q335X DP can be considered; 21 days was selected because ALT/AST elevations resolved by 14 days in studies of VERVE-101, and this interval was tolerated in a repeat LNP dosing study in infants with a metabolic disorder²⁰. If clinically indicated, a final third dose can be given. For any repeat dosing (i.e., a second or third dose), a medium dose of 0.3 mg/kg can be considered if the prior dose was well tolerated. If 0.3 mg/kg is well-tolerated for the second dose but the patient has an incomplete biologic response, the clinical oversight committee can consider increasing the last dose to 0.45

mg/kg for the third dose, There must be a minimum of 21 days between doses. The maximum time that may elapse between the first dose and the third dose is 120 days.

The decision to administer a repeat dose will be made by the multidisciplinary clinical oversight committee of experts including metabolic physicians, hepatologists, metabolic dieticians, immunologists, and ethicists (see **Figure 3 and Treatment Monitoring**, below)

Figure 3. Dosing schematic.

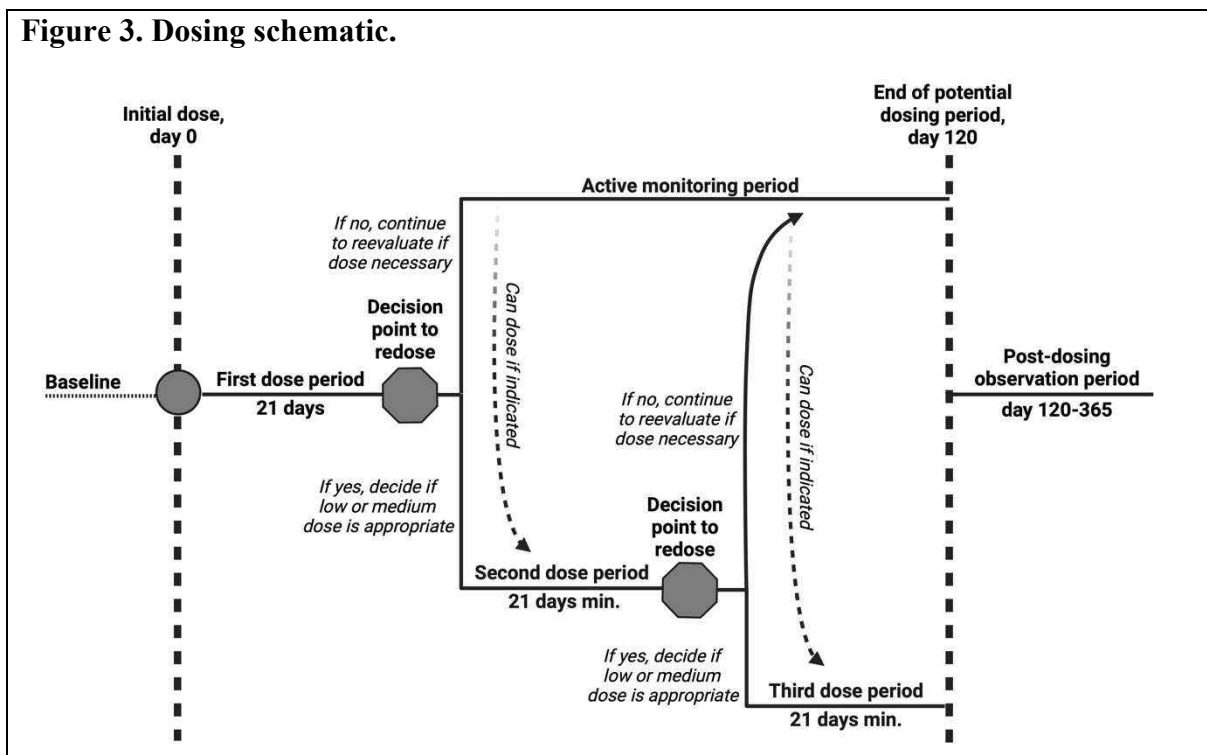


Table 2 - Study activities in the peri-dosing period. All activities can be modified based on the patient's clinical status and needs. Follow up during the post-dosing period (Day 120-365) and LTFU (Day 366- year 15) will be based on the standard of care for patients with CPS1 deficiency.

Schedule of Assessments	Consent	Baseline	Dosing Day ⁷	Peri-Dosing Follow-up Period [†]																					
	Days pre-administration			Days Post administration																					
	Prior to baseline	-7 to -1	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	
CONSENT																									
Informed Consent	X																								
CLINICAL EVALUATIONS																									
Review medical history		X (daily)<-----																							>X
Review medication history		X (daily)<-----																							>X
Review of available clinical laboratory testing		X (daily)<-----																							>X
Review of concomitant medications		X (daily)<-----																							>X
Review of diet		X (daily)<-----																							>X
Weight		X (daily)<-----																							>X
Height		X (weekly)<-----																							>X
Vital signs, including blood pressure		X (daily)<-----																							>X
Physical examination		X (daily)<-----																							>X
SAFETY & EFFICACY EVALUATIONS [§]																									
Review of adverse events		X<-----																							>X
Plasma amino acid quantification		X [‡]	X ^{‡‡} (q24h)--->	X (q24h)---->	X (q24-q48h)----->	X (q48-72h)----->																			
Ammonia		X [‡]	X ^{‡‡} (q4h)--->	X (q8h)---->	X (q12-q24h)----->	X (q48-72h)----->																			
Complete metabolic panel [‡]		X [‡]	X ^{‡‡} (q12h)--->	X (q24h)---->	X (q24-q48h)----->	X (q48-72h)----->																			
CBC w/ differential		X [‡]	X ^{‡‡} (q12h)--->	X (q24h)---->	X (q24-q48h)----->	X (q48-72h)----->																			
Coagulation testing (PT/INR, PTT)		X [‡]	X ^{‡‡} (q24h)--->	X (q24h)---->																					
Creatinine kinase check		X [‡]	X ^{‡‡} (q24h)--->	X (q24h)---->																					
Urine orotic acid analysis		X [‡]	X ^{‡‡} (q24h)--->	X (q24h)---->	X (q24-q48h)----->	X (q48-72h)----->																			
Lipid panel		X [‡]																							
EKG		X																							
ECHO		X																							
MEDICATIONS [§]																									
Sirolimus		X (Day -7 loading doses, followed by 0.5mg/m2/day divided BID) ----->																							
Ammonul [§]		X																							
Methylprednisone [§]		X																							
Diphenhydramine [§]		X																							
Famotidine [§]		X																							
Acetaminophen [§]		X																							
Tacrolimus			X (0.2 mg/kg/day divided BID) ----->																						
Sirolimus trough level**		X (daily beginning on D-5 until goal trough level is achieved, monthly thereafter) ----->																							
Tacrolimus trough level							X (then at least monthly as clinically indicated) ----->																		
Reduction in ammonia scavenger medication										X (if clinically indicated)----->															
CLINICAL INTERVENTIONS [§]																									
Sick day diet			X ^{††}																						
High-dextrose IV fluids			X ^{††}																						
Increase dietary protein											X (if clinically indicated)----->														
LNP.CPS1.Q335X DOSING																									
Administration of LNP.CPS1.Q335X			X																						
FUTURE USE RESEARCH SPECIMENS																									
Blood sample		X		X							X							X							
Urine sample		X	X	X							X							X							
Liver tissue samples ^{§§}			X (liver samples will be collected only if patient undergoes liver transplantation at any time after first dose)																						

¹ If sirolimus goal trough level is achieved prior to Day 0, dosing day can be moved up to facilitate timely dosing of the patient.

² After Day 21, the multidisciplinary clinical oversight committee will review safety and efficacy data to determine if a repeat dose is appropriate.

³ Baseline clinical lab values drawn prior to dosing will be reviewed and used to establish baseline values.

⁴ Laboratory evaluations, immunosuppression protocol, other medications, and clinical interventions can be adapted as per clinical needs.

⁵ Complete metabolic panel will include liver function testing.

⁶ Ammonul, methylprednisone, diphenhydramine, famotidine, and acetaminophen to be administered prior to LNP.CPS1.Q335X administration.

⁷ Sirolimus trough levels will be measured starting two days (Day -5) after sirolimus loading dose is given. After Day -5, trough levels are to be measured daily until goal trough level is achieved. Levels will continue to be measured monthly thereafter to maintain appropriate trough levels.

¹¹ If patient is stable at 24 h post-LNP.CPS1.Q335X administration, transfer to regular diet and wean off fluids.

¹² Plasma amino acid quantification, ammonia, complete metabolic panel (+liver function testing), CBC with differential, coagulation testing, and uric acid analysis are to start 4 hours prior to LNP.CPS1.Q335X administration.

⁸⁸ Liver tissue samples will only be collected upon liver transplant.

Schedule of Administration (see Figure 3, Table 2)

Baseline evaluations (Day -7 to -1):

The patient is currently an inpatient at the Children's Hospital of Philadelphia and continues to have regular laboratory testing, diet analysis, and medication titration as clinically indicated. Baseline evaluations (**Table 2**) will include:

- Clinical laboratory values including blood ammonia levels, urinary orotic acid levels, plasma amino acid quantitation, lipid panel, and liver function testing obtained prior to dosing will be reviewed and used to establish laboratory baselines.
- A 12-lead electrocardiogram (EKG) and echocardiogram (ECHO) will be obtained in the week prior to dosing.
- In addition, diet and medication records will be reviewed.
- Future use for research blood and urine specimens will be collected. The amount of blood collected for research will confer to NIH guidelines. Specifically, no more than 5 mL/kg may be drawn for research purposes in a single day, and no more than 9.5 mL/kg may be drawn over any eight-week period.
- On Day -7 the patient will begin sirolimus regimen (see "Immunosuppression Protocol" for details).

First dose period, Days 0–21:

- On the day of dosing (Day 0) the patient will:
 1. Have safety labs drawn including ammonia, liver function testing, and complete blood counts.
 2. Have a future use for research urine specimen collected.
 3. Transition to a sick-day diet plan and supplementary high-dextrose fluid to support metabolism and minimize risk of decompensation during the 24 hours after dosing.
 4. Prior to steroid dosing, transition from oral Ravicti to more potent nitrogen scavenger (Ammonul) to prevent against metabolic decompensation during steroid dosing.
 - A. The most frequent adverse reaction to Ammonul is infection (12%). Less frequent side effects (occurring between 1 and 10% of patients) include: bradycardia, cardiogenic shock, cardiomyopathy, chest pain, edema, flushing, heart failure, hypertension, hypotension, low cardiac output, myocardial rupture (atria), pericardial effusion, thrombosis, venous thrombosis, alopecia, pruritus, skin blister,

skin rash, urticaria, acidosis, alkalosis, dehydration, fluid retention, hyperammonemia, hyperglycemia, hyperkalemia, hyponatremia, hypervolemia, hypocalcemia, hypoglycemia, hypokalemia, increased serum pH, metabolic acidosis, respiratory acidosis, respiratory alkalosis, abdominal distention, cholestasis, diarrhea, gastrointestinal hemorrhage, nausea, vomiting, anuria, urinary retention, urinary tract infection, anemia, disorder of hemostatic components of blood, disseminated intravascular coagulation, hemangioma, hemorrhage, pancytopenia, thrombocytopenia, hepatic artery stenosis, hepatic failure, hepatotoxicity, jaundice, sepsis, septic shock, injection-site reaction, absent reflexes, acute psychosis, aggressive behavior, agitation, asthenia, ataxia, brain edema, cerebral atrophy, cerebral hemorrhage, cerebral herniation, cerebral infarction, clonus, coma, confusion, decreased mental acuity, encephalopathy, hallucination, impaired consciousness, increased intracranial pressure, paralysis (nerve), seizure, subdural hematoma, tremor, tetany, blindness, kidney failure, aspiration pneumonia, dyspnea, hypercapnia, hyperventilation, Kussmaul respiration, pneumothorax, pulmonary edema, pulmonary hemorrhage, respiratory distress, respiratory failure, tachypnea, variations in blood CO₂ concentration, fever, and multi-organ failure.

5. Receive premedication with methylprednisolone (see “Immunosuppression Protocol” for details), famotidine, acetaminophen, and diphenhydramine.
 - A. The most frequent (occurring in >1% of patients) side effects of famotidine are: headache, dizziness, constipation, and diarrhea. Other side effects that occurred less frequently are: fever, asthenia, fatigue, palpitations, elevated liver enzymes, vomiting, nausea, abdominal discomfort, anorexia, dry mouth, thrombocytopenia, orbital edema, rash, conjunctival injection, bronchospasm, musculoskeletal pain, arthralgia, seizure, hallucinations, depression, anxiety, decreased libido, insomnia, somnolence, pruritus, dry skin, flushing, tinnitus, taste disorder, and impotence. In pediatric patients less than one year of age, agitation was observed in 5/35 patients in a clinical study. Agitation resolved when famotidine was withdrawn.
 - B. The most frequent side effects of diphenhydramine are: urticaria, drug rash, anaphylactic shock, photosensitivity, excessive perspiration, chills, dryness of mouth, nose, and throat, hypotension, headache, palpitations, tachycardia, extrasystoles, hemolytic anemia, thrombocytopenia, agranulocytosis, sedation, sleepiness, dizziness, disturbed coordination, fatigue, confusion, restlessness, excitation, nervousness, tremor, irritability, insomnia, euphoria, paresthesia, blurred vision, diplopia, vertigo, tinnitus, acute labyrinthitis, neuritis, convulsions, epigastric distress, anorexia, nausea, vomiting, diarrhea, constipation, urinary frequency, difficult urination, urinary retention, early menses, thickening of bronchial secretions, tightness of chest or throat and wheezing, nasal stuffiness.

C. The most clinically significant side effects of oral acetaminophen are: acute hepatotoxicity, drug-induced liver injury, liver failure. Other adverse reactions do not have a defined frequency but include: erythema of skin, skin blister, skin rash, acute generalized exanthematous pustulosis, Stevens-Johnson syndrome, toxic epidermal necrolysis, hearing loss, anaphylaxis, hypersensitivity reaction

6. Receive a single IV dose of 0.1 mg/kg LNP.CPS1.Q335X.

- On Day 1 the patient will:
 1. Begin tacrolimus regimen (see “Immunosuppression Protocol” for details)
 2. Have future use for research blood and urine specimens collected. The amount of blood collected for research will confer to NIH guidelines. Specifically, no more than 5 mL/kg may be drawn for research purposes in a single day, and no more than 9.5 mL/kg may be drawn over any eight-week period.
- On Days 1–21 the patient will undergo:
 1. Safety and adverse event monitoring will occur through clinical monitoring and frequent safety labs, including ammonia, liver function testing, and complete blood counts.
 2. Efficacy monitoring with plasma amino acid quantitation, ammonia levels, and urine orotic acid analysis.
- On Days 7–21 the patient may undergo a reduction in ammonia scavenger dosage and/or an increase in dietary protein as clinically indicated.
- On Day 7 the patient will:
 1. Have future use for research blood and urine specimens collected. The amount of blood collected for research will confer to NIH guidelines. Specifically, no more than 5 mL/kg may be drawn for research purposes in a single day, and no more than 9.5 mL/kg may be drawn over any eight-week period.
- On Day 14 the patient will:
 1. Have future use for research blood and urine specimens collected. The amount of blood collected for research will confer to NIH guidelines. Specifically, no more than 5 mL/kg may be drawn for research purposes in a single day, and no more than 9.5 mL/kg may be drawn over any eight-week period.

First timepoint for decision to redose, Day 22

All data collected up to Day 21 will be reviewed, and a decision to re-dose will be made by a multidisciplinary clinical committee of experts including metabolic physicians, hepatologists, metabolic dietitians, immunologists, and ethicists (see **Treatment Monitoring**, below).

1) A repeat escalated dose (0.3 mg/kg) of LNP.CPS1.Q335X will be considered if:

- a. The initial dose was safe and well tolerated, AND
- b. The patient still demonstrates biochemical features of CPS1 deficiency requiring protein-restricted diet and/or ammonia scavenger medications.

2) A repeat unchanged dose of (0.1 mg/kg) of LNP.CPS1.Q335X will be considered if:

- a. The initial dose resulted in transient, mild laboratory abnormalities that have resolved, AND
- b. The patient still demonstrates biochemical features of CPS1 deficiency requiring protein-restricted diet and/or ammonia scavenger medications.

3) A repeat dose will not be considered if:

- a. The initial dose was not well tolerated, as determined by the clinical oversight committee, OR
- b. The patient no longer demonstrates biochemical features of CPS1 deficiency while off all dietary therapy and scavenger medications. If the patient subsequently redevelops biochemical or clinical evidence of disease, and less than 120 days have passed since dose one, repeat dosing can be reconsidered.

If no subsequent dose indicated, Days 22+

The patient will continue to undergo safety, adverse event, and efficacy monitoring through clinical laboratory testing and clinical evaluations. In addition, careful dietary records and medical scavenger doses will be followed. Dietary plans, scavenger medication dosages, and laboratory schedules will be adjusted as per clinical care.

The patient data will be reviewed at a minimum of once a week to evaluate if there is still biochemical or clinical evidence of CPS1 deficiency, and if a repeat dose may be indicated. If a repeat dose is considered after this review, the multidisciplinary clinical committee will review and decide if it is appropriate to offer a subsequent dose. A maximum of three total doses will be provided. There must be a minimum of 21 days between doses.

If a subsequent dose is indicated, Days 22+

If the patient receives a second or third dose, he will undergo a similar appropriate laboratory and monitoring process as occurred with the first dose (**Table 2**). If the previous dose(s) were well tolerated, the clinical team can increase the dose of LNP.CPS1.Q335X to 0.3 mg/kg (second dose) or repeat a 0.3 mg/kg or 0.45mg/kg dose (third dose).

If a third dose is not given by 120 days after the first dose, no further dosing will occur.

EXPLORATORY BIOMARKERS AND PHARMACOGENIC SAMPLES

Blood and urine will be collected for exploratory biomarker research related to metabolic disorders and gene editing. The biomarkers studied will be relevant to the understanding of the pathophysiology of CPS1 deficiency, the mechanism of action, and possible efficacy and toxicities of LNP.CPS1.Q335X.

Blood and urine samples will be collected as described in **Table 2** and in Section “**Schedule of Administration**” above.

Liver specimens will be collected from the participant whose treating physician has ordered a liver biopsy or a liver transplant as part of routine clinical care or if a liver mass was resected, and for which patient consent has been obtained for the sample to be evaluated for editing efficiency. Only existing liver biopsy or resection samples will be utilized if sufficient tissue remains. If there is insufficient available tissue, then no sample will be collected.

IMMUNOSUPPRESSION PROTOCOL

As the components of the LNP drug product - including the lipid excipients, base editor mRNAs and guideRNA are cleared within the first few days after dosing, the likelihood of a prolonged immune response to the drug product itself is low. However, the patient has biallelic null alleles in the *CPS1* gene. Therefore, it is likely he does not currently have any expression of CPS1 protein. If the drug successfully corrects the patient’s pathogenic variant, he may be at risk of developing an immune response to the functional protein. To mitigate the risk of an anti-CPS1 protein response we will treat him with a prophylactic immunosuppressive regimen designed to reduce both potential B-cell and T-cell responses³². This immunosuppressive regimen includes:

- The patient will begin a sirolimus regimen starting on Day -7, with an initial load of 1 mg/m² every 4 hours for 3 total doses. This will be followed by daily enteral dosing at 0.5 mg/m²/day divided BID. The goal trough level is 4-8 ng/mL. Trough levels during the loading period will be measured daily beginning on Day -5 (two days after loading dose is given). If the patient reaches goal trough level prior to day 0, dosing day can be moved up to facilitate timely dosing of the patient. If dose adjustments to obtain the trough goal are not needed, the patient will continue sirolimus at this

dose. Trough levels will continue to be checked at a minimum of monthly intervals, as clinically indicated, to maintain appropriate trough levels. Sirolimus wean is planned to start at 9 months.

- The patient will be administered one dose of methylprednisone (IV, 1 mg/kg) immediately prior to drug product infusion (on Day 0).
- The patient will begin a tacrolimus regimen on Day +1 at a dose of 0.2 mg/kg/day divided BID. The goal trough level is 4-8 ng/mL. Levels will be checked initially after 4 days of treatment and then at a minimum of monthly intervals, as clinically indicated, to maintain appropriate trough levels. If dose adjustments to obtain the goal level are not needed, the patient will continue tacrolimus at this dose. Tacrolimus wean is planned to start at 6 months.

Risks associated with methylprednisone, tacrolimus, and sirolimus

The primary risks associated with the use of methylprednisolone, tacrolimus, and sirolimus are an increased risk of infection and decreased response to vaccinations due to the immunosuppressive effect of the medications. Prescribing information for methylprednisolone, sirolimus, and tacrolimus are appended to this treatment plan (**Appendix 2-4**, respectively).

Sirolimus may interfere with wound healing. If the patient is indicated for a liver transplant after beginning the sirolimus regimen, sirolimus will be stopped prior to surgery and post-surgical wound healing will be closely monitored.

Methylprednisone may induce metabolic decompensation and elevated ammonia levels in patients with CPS1 deficiency. To minimize this risk, the patient will be placed on sick day protein-restricted diet and high dextrose IV fluids prior to receiving the premedication regimen on Day 0 (Dosing Day, see **Schedule of Administration**).

EXPECTED DURATION OF STUDY

The study is expected to last 365 days. The dosing period for the study is up to 120 days. The post-dose observation period will continue through Day 365 +/- 10 days.

The patient will continue to be monitored for long-term safety and efficacy as part of his ongoing care in the Division of Metabolism at CHOP. Long-term follow up will last for 15 years.

CONSENTING AND TREATMENT COMPLIANCE

The investigator will obtain consent and/or assent before initiating treatment, conduct the study in accordance with the treatment plan, and will report unanticipated problems involving risks to subjects or others in accordance with The Children's Hospital of Philadelphia IRB Policies and Procedures and all federal requirements. The study PI will be available to explain the medical aspects of the research, explain the risks and benefits of the intervention, and answer questions during the consenting process. Collection, recording, and reporting of data will be accurate and ensure the privacy, health and welfare of the subject during and after treatment.

TREATMENT MONITORING

- **Multidisciplinary Clinical Oversight Committee**

A clinical oversight committee will meet to review safety and efficacy data at regular, predetermined intervals and will review any major safety events. They will also decide if repeat dosing is appropriate. This clinical oversight committee will comprise:

- 1) At least two attending physicians from the CHOP Metabolism service, including the physician-sponsor;
- 2) A member of the CHOP Ethics consult service;
- 3) An attending physician from the CHOP Hepatology service, to provide input on any liver toxicities and insights into the need and appropriateness for rescue liver transplantation; and
- (4) An attending physician from the CHOP Immunology service, to provide input on any immune toxicities.

- **Treatment Safety Monitoring Plan**

For this individual patient expanded access IND, DP dosing will occur as part of clinical care. The physician-sponsor will be responsible for ensuring the day-to-day safety of the potential patient.

The patient will undergo close clinical monitoring in the peri-dosing period (see representative assessments in **Table 2**). The exact schedule of activities may be adapted as per clinical need.

Safety will be evaluated by:

- Physical examination
 - Vital signs
 - Clinical laboratory evaluations
 - Clinical EKG and ECHO
- **Post-dosing observation period, Days 120–365**

If an additional dose is not given by 120 days after the first dose, no further dosing will occur. The patient will continue to undergo safety, adverse event, and efficacy monitoring through clinical laboratory testing and clinical evaluations. Monitoring will be based on the current clinical care for patients with CPS1-deficiency. During this period, we anticipate visits will occur every 3 months, but may occur more frequently as clinically indicated.

Safety and efficacy will be evaluated by:

- Physical examination
 - Vital signs
 - Clinical laboratory evaluations including: liver function testing, and complete blood counts. plasma amino acid quantitation, ammonia levels, and urine orotic acid analysis. Clinical evaluations may be added or subtracted as clinically indicated.
-
- **Long-term follow-up, Day 366 – 15 years**
The patient will continue to be monitored for long-term safety and efficacy as part of his ongoing care in the Division of Metabolism at CHOP. Monitoring will be based on the current clinical care for patients with CPS1-deficiency. During this period, we anticipate visits will occur every 6 months to 1 year, but may occur more frequently as clinically indicated.

The patient will be evaluated by:

- Physical examination
- Vital signs
- Clinical laboratory evaluations including: liver function testing, and complete blood counts. plasma amino acid quantitation, ammonia levels, and urine orotic acid analysis. Clinical evaluations may be added or subtracted as clinically indicated.

ADVERSE EVENT REPORTING

Adverse events that are non-serious will be reported in the Annual Report or Withdrawal of IND report to the FDA, and in the Continuing Review to the IRB. Serious or life-threatening adverse events directly attributable to the study product will be reported to the FDA and IRB in a prompt manner. FDA Form 3500A will be used for initial and follow-up reporting of possibly related, serious and unexpected adverse drug reactions.

In general, a serious adverse event (SAE) will meet any of the following conditions:

- 1) results in death;

- 2) is life-threatening (places the subject at immediate risk of death from the event as it occurred);
- 3) requires inpatient hospitalization or prolongation of existing hospitalization (hospitalization for a protocol-specified activity or for an elective, pre-planned procedure is not considered an SAE);
- 4) results in persistent or significant disability/incapacity;
- 5) results in a congenital anomaly or a birth defect; or
- 6) based upon appropriate medical judgment, may jeopardize the subject's health and may require medical or surgical intervention to prevent one of the other outcomes listed in this definition (examples of such events include allergic bronchospasm requiring intensive treatment in the emergency room or at home, blood dyscrasias or convulsions that do not result in inpatient hospitalization, or the development of drug dependency or drug abuse).

DRUG/BIOLOGIC ACCOUNTABILITY

Adequate records of study drug receipt and disposition will be maintained by the CHOP Pharmacy. Records of receipts, investigational drug orders, dispensing records, and disposition forms will be examined during the course of the study. The purpose of these records is to ensure regulatory authorities and the Sponsor that the investigational new drug will not be distributed to any person who is not a study subject under the terms and conditions set forth in this protocol. The study medication is to be prescribed by the Investigator or designee and may not be used for any purpose other than that described in this protocol.”

At study completion, all drug supplies including partially used and empty containers will be disposed, or returned to the manufacturer or designee.

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APPENDIX 1 - CERTIFICATE OF ANALYSIS

WILL BE APPENDED IN IND SUBMISSION

APPENDIX 2 – METHYLPREDNISOLONE PRESCRIBING INFORMATION

WILL BE APPENDED IN IND SUBMISSION

APPENDIX 3 – SIROLIMUS PRESCRIBING INFORMATION

WILL BE APPENDED IN IND SUBMISSION

APPENDIX 4 – TACROLIMUS PRESCRIBING INFORMATION

WILL BE APPENDED IN IND SUBMISSION

APPENDIX 5 – DR. AHRENS-NICKLAS’S CV

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Supplementary Appendix

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This appendix has been provided by the authors to give readers additional information about the work.

TABLE OF CONTENTS

1. AUTHOR CONTRIBUTIONS	3
2. DRUG SUBSTANCES AND DRUG PRODUCT	4
Guide RNA drug substance	4
Messenger RNA drug substance	4
Lipid nanoparticle drug product	4
3. CELLULAR STUDIES	4
Proof-of-concept studies in cells	4
Establishing the editing efficiency of the clinical batch of the drug product	6
4. MOUSE STUDIES	7
Transgenic mouse models to test the in vivo efficacy of the drug product	7
In vivo corrective editing with the toxicology batch of the drug product in transgenic mouse models	7
Implications of mouse studies for dose selection for the clinical protocol	8
5. NONHUMAN PRIMATE TOXICOLOGY STUDY	9
Study design	9
Summary of study results	9
Implications of nonhuman primate study for dose selection for the clinical protocol	10
Potential for off-tissue editing	10
6. OFF-TARGET EDITING ANALYSES	10
Nominating and experimentally verifying potential off-target sites for a drug product in a time-limited setting	10
Candidate off-target site nomination in silico using the patient's genome sequence	11
Candidate off-target site nomination using ONE-seq, a patient-variant-aware in vitro assay	11
Candidate off-target site nomination using CHANGE-seq-BE, an in vitro assay, with the patient's father's genomic DNA	12
Candidate off-target site nomination using UNCOVERseq, an in cellulo assay: tissue culture and library preparation	13
Candidate off-target site nomination using UNCOVERseq, an in cellulo assay: bioinformatic analysis	14
Generation of the union set of nominated off-target sites for experimental verification ..	14
Experimental verification of nominated off-target sites: library preparation and bioinformatic analysis	15
Translocation analysis	16
Initial experimental verification of off-target sites in hepatocytes	16
Integrating off-target site nomination data for more comprehensive experimental verification	18

7. SUPPLEMENTARY FIGURES	21
Figure S1. Structure of mRNA Drug Substance	21
Figure S2. Optimization of Base Editing to Correct <i>CPS1</i> Q335X Variant	22
Figure S3. Schematic of Genomic Site of <i>CPS1</i> Q335X Variant	23
Figure S4. High-Throughput PAM Determination Assay (HT-PAMDA) Profiles of SpG and NGC Cas9 Proteins	24
Figure S5. Predicted Corrective Adenine Base Editing of <i>CPS1</i> Q335X Variant	25
Figure S6. Empirical Corrective Adenine Base Editing of <i>CPS1</i> Q335X Variant	26
Figure S7. Calibration of Adenine Base Editing Between Lentiviral Cassettes and Endogenous Loci	27
Figure S8. Corrective Editing of <i>CPS1</i> Q335X Variant After Treatment of HuH-7 Cells with Clinical Batch of K-abe	28
Figure S9. Founder Mouse with Humanized <i>Cps1</i> Q335X Allele	29
Figure S10. Corrective Editing of <i>CPS1</i> Q335X Variant After Treatment of Rosa26-Q335X Transgenic Mouse with Toxicology Batch of K-abe	30
Figure S11. Whole-liver Editing of Rosa26-Q335X Transgenic Mice and <i>Cps1</i> -Q335X Knock-in Mice After Lipid Nanoparticle Treatment	31
Figure S12. Serum Enzymes/Liver Function Tests in Cynomolgus Monkeys Treated with Vehicle Control or with K-abe	32
Figure S13. Plasma Lipid Excipients in Cynomolgus Monkeys Treated with K-abe	33
Figure S14. Three Off-target Site Nomination Methods	34
Figure S15. Off-target Nomination Workflow	35
Figure S16. Determination of Candidate Off-target Site List	36
Figure S17. Origin of UNCOVERseq-nominated Sites	37
Figure S18. Nomination Frequencies of Sites with Patient-specific Variants	38
Figure S19. Candidate Off-target Site Verification in Primary Human Hepatocytes	39
8. SUPPLEMENTARY TABLES	40
Table S1. Guide RNA Sequence	40
Table S2. Abengcemeran mRNA Sequence, not Including 5' Cap or 3' Polyadenylate Tail, and Protein Sequence	41
Table S3. Off-target Editing in Q335X Lentivirus-transduced HuH-7 Cells Treated with 1000 ng/mL of Clinical Batch of K-abe	44
Table S4. Off-target Editing at <i>ATP7B</i> Intronic Site in Q335X Lentivirus-transduced HuH-7 Cells	45
Table S5. mRNA Levels in Q335X Lentivirus-transduced HuH-7 Cells Versus Primary Human Hepatocytes	46
Table S6. Off-target Editing in Primary Human Hepatocytes Treated with 1000 ng/mL of Clinical Batch of K-abe	47
Legends for Supplementary Excel File	48
9. REFERENCES	49

AUTHOR CONTRIBUTIONS

K.M., S.A.G., and R.A.-N. designed the study and analyzed the data, except for the off-target nomination data generated by CHANGE-seq-BE and by UNCOVERseq and the off-target verification data generated by rhAmpSeq, which were analyzed by T.R.H., G.K., and G.R. All of the authors either directly contributed to the gathering of data or oversaw the gathering of data. K.M. and R.A.-N. vouch for the data and the analysis. R.A.-N. served as the sponsor-investigator for the single-patient expanded-access IND application. K.M. wrote the first draft of the paper, with subsequent revisions by R.A.-N. The decision to publish the paper was made jointly by K.M. and R.A.-N.

DRUG SUBSTANCES AND DRUG PRODUCT

Guide RNA drug substance

The guide RNA (gRNA) drug substance in the lipid nanoparticle (LNP) drug product comprised (1) a 20-nucleotide spacer sequence that corresponded to a protospacer DNA sequence matching the region of the *CPS1* gene spanning the Q335X variant, which included the target adenosine nucleotide to be corrected by the drug product, and (2) an 80-nucleotide tracrRNA domain that complexed with a *Streptococcus pyogenes* Cas9 (SpCas9) nickase domain in an adenine base editor (ABE) (**Table S1**). The gRNA drug substance (originally known as CPS1-001, then renamed **kayjayguran**) was a 100-mer oligonucleotide comprising 53 ribonucleotides, 47 2'-O-methylribonucleotides, and 6 phosphorothioate backbone modifications at select positions, manufactured by IDT using proprietary methods.

Messenger RNA drug substance

The messenger RNA (mRNA) drug substance in the LNP drug product encoded the adenine base editor 8e (ABE8e) protein with a V106W variant in the adenosine deaminase domain and with a version of the SpCas9 D10A nickase with a preference for the protospacer-adjacent motif (PAM) NGC (known as **NGC-ABE8e-V106W**) (**Fig. S1, Table S2**). The mRNA drug substance (known as **abengcemeran**) comprised the 5' cap, the 5' untranslated region (UTR), the ABE coding sequence, the 3' UTR, and the 3' polyadenylate tail; it was manufactured by Aldevron using proprietary methods. The ABE coding sequence, 4818 nucleotides in length, was codon-optimized with uridine minimization and had substitution of all uridines with the modified nucleotide N1-methylpseudouridine.

Lipid nanoparticle drug product

The LNP used was previously described,¹ and the specific drug product (originally known as LNP.CPS1.Q335X, then renamed **kayjayguran abengcemeran**, or **k-abe**) was manufactured under cGMP using processes described in Patent Application WO/2020/061426A2 with the lipid components (Acuitas Therapeutics® proprietary ionizable cationic lipid ALC-0307 and PEG-lipid ALC-0159, 1,2-distearoyl-sn-glycero-3-phosphocholine, and cholesterol) being rapidly mixed with an aqueous buffer solution containing gRNA and mRNA in a 1:1 ratio by weight, followed by buffer exchange, sterile filtration, and filling to glass vials for storage until administration. Ionizable cationic lipid and LNP compositions are described in Patent Applications WO/2017/004143A1 and WO/2021/030701A1. The clinical batch of the drug product had an average hydrodynamic diameter of 73 nm with a polydispersity index of 0.07 as determined by dynamic light scattering, 97% total mRNA encapsulation by the RiboGreen fluorescence assay, and a gRNA/mRNA ratio of 1.1 as measured by ultra-performance liquid chromatography (UPLC)-based determinations.

CELLULAR STUDIES

Proof-of-concept studies in cells

To identify a base editing solution for the *CPS1* Q335X variant as quickly as possible following the genetic diagnosis of the patient, we wished to use hepatocytes with the variant. We deemed it unethical to obtain primary hepatocytes from the patient, and other primary cell types (e.g., fibroblasts) were considered inadequate. We instead used the cultured human HuH-7 hepatoma cell line (Japanese Collection of Research Bioresources Cell Bank) as a proxy for human hepatocytes. We used a lentiviral vector to transduce human HuH-7 cells with a ≈100-bp *CPS1*

genomic sequence spanning the Q335X variant, a $\approx$ 100-bp *CPS1* genomic sequence spanning the E714X variant (the patient's second variant), a $\approx$ 100-bp *PAH* genomic sequence spanning the P281L variant, and a $\approx$ 100-bp *PAH* genomic sequence spanning the R408W variant as shown in **Fig. S2A**. The *PAH* P281L and R408W variant sequences, which are pathogenic variants for phenylketonuria (PKU), serve as reference controls due to their having validated base editing solutions that we have previously shown to be efficacious in correcting each variant in vitro in HuH-7 cells and in vivo in humanized mouse models of PKU.^{2,3} For this study, we solely used the *PAH* P281L variant sequence as a reference control, with ABE8.8 and a P281L-specific gRNA (designated PAH1) being the optimized base editing solution.² (For this study, ultimately neither the *CPS1* E714X variant sequence nor the *PAH* R408W variant sequence was used.)

We also attempted to use prime editing to introduce the Q335X variant into the endogenous *CPS1* locus in HuH-7 cells, so as not to have to rely solely on the Q335X lentivirus-transduced HuH-7 cell line for cellular studies. Several attempts were unsuccessful. Accordingly, all cellular corrective editing data were generated using the Q335X lentivirus-transduced HuH-7 cell line.

As shown in **Figs. S2B–2D**, using the Q335X lentivirus-transduced HuH-7 cells, we screened a variety of ABEs in combination with individual candidate gRNAs in plasmid transfection experiments. Seven gRNAs (designated gRNA3 through gRNA9) tiling the site of the Q335X variant, such that the variant adenine base ranged from positions 3 through 9 of the protospacer sequence (**Fig. S3**) that spanned the ABE editing window, were tested with ABEs compatible with the PAMs associated with each of the protospacer sequences: SpG for NGN PAMs, SpRY for all other PAMs (i.e., “near-PAMless”).⁴ ABEs with three different deaminase domains were tested: ABE8.8, with the narrowest editing window, ABE8.20, with an intermediate editing window, and ABE8e, with the broadest window.^{5,6} In the initial screen (**Fig. S2B**), the SpG-ABE8e/gRNA8 combination had the highest corrective editing efficiency for the Q335X variant.

In a secondary transfection screen, we assessed three engineered ABEs with a preference for NGC PAMs (the extended PAM sequence for gRNA8 is AGCC), designated A1, A2, and A3 (**Fig. S2C**). The A1 enzyme encodes SpCas9-LWKYQS, differing from wild-type SpCas9 with the amino acid substitutions D1135L/S1136W/G1218K/E1219Y/R1335Q/T1337S.⁷ A2 encodes SpCas9-MQKSER+ with L1111R/D1135M/S1136Q/G1218K/E1219S/R1335E/T1337R, and A3 encodes eSpGC with L1111R/D1135L/S1136W/G1218K/E1219F/A1285K/R1335E/T1337G (described in Patent Applications WO/2019/040650A1 and WO/2021/151085A2). All versions of the ABE8e editor with gRNA8 displayed highly efficient corrective editing. In the same transfection experiment, the well-established solution for the *PAH* P281L variant (ABE8.8 with the P281L-specific gRNA, designated PAH1) had similar or less corrective editing efficiency for the P281L variant (**Fig. S2C**) compared to the ABE8e editors with gRNA8 for the Q335X variant.

Because ABE8e has been reported to have gRNA-independent off-target RNA and DNA editing, the ABE8e-V106W variant, which largely eliminates this off-target editing of ABE8e,⁶ was used in a final transfection screen. The SpG, A1, A2, and A3 ABE8e editors, without and with the V106W variant, in combination with gRNA8 were tested (**Fig. S2D**). Among the V106W-containing editors, A1-ABE8e-V106W most closely matched the efficiency of the corresponding editor without the V106W variant, with the other V106W-containing editors showing reduced efficiency. In the same transfection experiment, the validated solution for the *PAH* P281L variant (ABE8.8 with PAH1) had similar corrective editing efficiency for the P281L variant (**Fig. S2D**, red horizontal dotted line) compared to the A1-ABE8e-V106W editor with gRNA8 for the Q335X variant. Accordingly, a version of gRNA8 with stabilizing chemical modifications, designated **kayjayguran**, and the A1-ABE8e-V106W editor, designated **NGC-ABE8e-V106W** (which, when encoded in mRNA, is called **abengcemeran**), were chosen for use in the LNP drug product

(also called **kayjayguran abengcemeran**, or **k-abe** for short). NGC-ABE8e-V106W has a more restricted PAM preference relative to SpG: NGC(A/C) versus NGN (**Fig. S4**) as indicated by the HT-PAMDA assay.⁸

Using the BE-Hive machine learning model,⁹ the kayjayguran gRNA was predicted to have substantial bystander editing near the Q335X variant (**Fig. S5**). However, **all of the significantly affected bystander adenine positions represent synonymous variants that do not change the CPS1 amino acid sequence** and were not expected to affect CPS1 function. We performed individual amplicon sequencing and next-generation sequencing (NGS) of the lentiviral cassette with a genomic DNA sample from NGC-ABE8e-V106W/gRNA8 plasmid-treated Q335X lentivirus-transduced HuH-7 cells (**Fig. S6**). We confirmed the presence of bystander editing and found that, indeed, it predominantly resulted in synonymous changes.

A potential criticism of the use of this cell line is that corrective editing activity in lentiviral cassettes stochastically inserted into the genomes of cells might not accurately reflect corrective editing activity in the endogenous gene locus (if the variant were present in the locus). To address this concern, we tested a series of gRNAs targeting the *CPS1* Q335X genomic sequence adjacent to but not overlapping the site of the Q335X variant itself (i.e., in the flanking sequence in lentiviral cassette); we also tested a series of gRNAs targeting the *PAH* P281L genomic sequence adjacent to but not overlapping the site of the P281L variant itself (**Fig. S7**). Thus, each gRNA simultaneously targeted two sites in the lentivirus-transduced HuH-7 cell line—a site in the lentiviral cassette, and the corresponding site in the endogenous gene locus—and editing produced by the gRNA at the two sites, in the same cells, could be directly compared. We found that editing in the lentiviral cassette was consistently and modestly higher than editing in the endogenous locus, averaging ~25% higher across the *CPS1* sequence and the *PAH* sequence. Thus, even though **absolute** lentiviral cassette editing did not perfectly match **absolute** endogenous locus editing, there was a high degree of correlation between the two, allowing us to conclude that **relative** editing among different gRNAs would be similar whether tested in the lentiviral cassette or in the endogenous locus. **This observation validated our choice of kayjayguran as the optimal gRNA for correction of the patient's variant, even though we were unable to test it for corrective editing directly in the endogenous CPS1 locus in HuH-7 cells.**

Establishing the editing efficiency of the clinical batch of the drug product

We did not develop a potency assay for the k-abe drug product, because we do not anticipate that it will be used for any patient besides the single patient who was the focus of this study, and thus no additional clinical batch of k-abe will ever be made in the future.

Nonetheless, to quantitatively and specifically demonstrate the editing efficiency of the single manufactured **clinical batch** of k-abe that was used for the single patient, we used the Q335X lentivirus-transduced HuH-7 cell line for a dose-response assessment with the drug product (**Fig. 2C**). This assay demonstrated a maximum proportion of the desired editing outcome (correction of the Q335X variant +/- synonymous bystander editing) of ~67%, with an EC₅₀ of ~17 ng/mL and an EC₉₀ of ~52 ng/mL. (Of note, the estimated EC₉₀ was used to determine the dose of k-abe with which to assess for off-target editing in HuH-7 cells and, by extension, primary human hepatocytes, as described in the **Off-Target Editing Analyses** section below.) The maximum proportion of overall editing (including editing outcomes in which there was bystander editing without corrective editing) was ~80%. The editing outcomes observed in the sample of cells that achieved the highest level of editing in **Fig. 2C** are shown in **Fig. S8**. Compared to the results in **Fig. S6**, obtained with plasmid transfection of the same Q335X lentivirus-transduced HuH-7 cell line, lower levels of bystander editing relative to the correction

of the Q335X variant were observed with k-abe treatment (e.g., compare the most frequent editing outcome in **Fig. S8** versus that in **Fig. S6**).

MOUSE STUDIES

Transgenic mouse models to test the in vivo efficacy of the drug product

We used mice for the purpose of demonstrating the in vivo hepatic editing efficacy of k-abe, rather than a biological response with respect to functional endpoints (i.e., prolonged survival, reduced blood ammonia levels, etc.) given the need to develop the drug product as quickly as possible following the genetic diagnosis of the patient. We generated two transgenic mouse models that could serve this purpose.

First, we microinjected mouse zygotes with Cas9, a well-validated gRNA targeting the *Rosa26* safe harbor locus, and a single-strand DNA oligonucleotide with ≈ 100 -bp genomic sequences spanning the *CPS1* Q335X variant, the *CPS1* E714X variant, the *PAH* P281L variant, and the *PAH* R408W variant (**Fig. 2A**)—the same cassette used for the Q335X lentivirus-transduced HuH-7 cell line. We obtained two founder mice, both female, in which the genomic segment was introduced into the *Rosa26* locus in some alleles. Both *Rosa26* founder mice achieved germline transmission in their first litters, with multiple F1 offspring in each litter harboring the transgenic allele (these offspring were called ***Rosa26-Q335X*** mice). We were able to use these offspring for a limited dose-response study of the k-abe drug product prior to submission of the single-patient expanded-access Investigational New Drug (IND) application. Of note, although these *Rosa26-Q335X* mice can be considered a patient-specific model because they harbor one copy each of the patient's two variants (Q335X and E714X), the two variants are on the same *Rosa26* allele, and the two copies of the endogenous wild-type *Cps1* locus are intact. Thus, these mice do not have a *CPS1* deficiency phenotype. They cannot be used to test for **therapeutic efficacy** of base editing, but only **editing efficacy**.

Second, we microinjected mouse zygotes with Cas9, a gRNA targeting the endogenous mouse *Cps1* gene near the orthologous site of the *CPS1* Q335X variant, and a single-strand DNA oligonucleotide intended to knock in a humanized segment spanning the Q335X variant and the protospacer/PAM sequences matched to the kayjayguran gRNA, so as to permit the use of the human-specific investigational drug product rather than a mouse-specific proxy drug product. We obtained a female founder mouse in which close to 50% of the alleles in a sample of genomic DNA had the desired humanized segment (**Fig. S9**). The first litter born from this founder mouse did not have any F1 offspring bearing the humanized Q335X allele. The second litter had multiple offspring heterozygous for the humanized Q335X allele (these offspring were called ***Cps1-Q335X*** knock-in mice). Although we did not obtain these offspring in time to perform any studies prior to submission of the single-patient expanded-access IND application, we subsequently performed a limited dose-response study of the k-abe drug product.

In vivo corrective editing with the toxicology batch of the drug product in transgenic mouse models

We tested the **toxicology batch** of k-abe for editing efficiency in vivo in the liver in the F1 *Rosa26-Q335X* mice from the first litters, when they were between 1 and 2 months of age. Due to the small number of mice available, we tested three LNP doses across a broad range (total RNA dose of 3 milligrams per kilogram of body weight [mg/kg], 1 mg/kg, and 0.1 mg/kg) in two mice for each dose. In selecting these doses, we recognized that it was important to:

- document that k-abe could achieve the expected and desired editing outcomes in vivo;

- rule out any unexpected adverse editing outcomes with exposure to a very high dose of k-abe; and
- model the effects of the initial very low dose (0.1 mg/kg) specified in the clinical protocol

The doses were administered intravenously via retro-orbital injection, and upon necropsy several days later, genomic DNA was isolated from eight liver samples per mouse (two per lobe). The editing efficiencies were assessed via targeted amplicon sequencing specific to the *Rosa26-Q335X* cassette, followed by NGS. Despite the small number of mice per group, there was reasonable consistency of the whole-liver editing efficiencies in each group (**Fig. 2B**). At the 3 mg/kg dose, there was mean 42% corrective editing of the Q335X variant; at the 1 mg/kg dose, mean 31% corrective editing; and at the 0.1 mg/kg dose, mean 4% corrective editing. Across the dose groups, indel rates at the target site were $\leq 1\%$. The editing outcomes observed in a representative liver sample from a mouse treated with a 3 mg/kg dose are shown in **Fig. S10**; **by far, the single most frequent editing outcome was correction of the Q335X variant without any bystander editing.** Even in other editing outcomes, **all observed bystander editing resulted in synonymous variants.** The patterns of corrective and bystander editing are consistent with those observed in HuH-7 cells treated with k-abe (see **Fig. S8**). To provide a positive reference control, two F1 *Rosa26-Q335X* mice from a subsequent litter were treated with ABE8.8/PAH1 LNPs, demonstrating correction of the *PAH* P281L variant (**Fig. S11A**).

We subsequently tested the **toxicology batch** of k-abe for editing efficiency in vivo in the liver in a small number of F1 *Cps1-Q335X* knock-in mice when they were 1 month of age. Due to the small number of mice available, we tested two LNP doses (total RNA dose of 3 mg/kg or 1 mg/kg) in two mice for each dose. At the 3 mg/kg dose, there was mean 52% corrective editing of the Q335X variant, and at the 1 mg/kg dose, mean 35% corrective editing (**Fig. S11B**)—modestly higher than the editing observed at the same doses in *Rosa26-Q335X* mice. **This observation validates our use of *Rosa26* transgenic mice to model the in vivo corrective editing efficiency of a drug product.**

Implications of mouse studies for dose selection for the clinical protocol

We note the following reasons why the active dose levels observed in the transgenic mouse models might not translate to the single human patient and were not construed as predictive of **therapeutic efficacy** in the patient.

- The LNP formulation process used for the k-abe drug product was optimized for use in primates rather than for use in mice. Any given LNP formulation can vary widely in activity between species; for example, for LNP particles with the same ratio of the same lipid excipients but formulated to be of different sizes, larger particles preferentially delivered an mRNA cargo into hepatocytes in mice compared to nonhuman primates, whereas smaller particles preferentially delivered an mRNA cargo into hepatocytes in nonhuman primates compared to mice.¹⁰ Thus, the potency of the k-abe drug product observed in mice might be exceeded by the potency in the single human patient.
- No relevant efficacy data were available from the nonhuman primate toxicology study (see next section), because the *CPS1* Q335X variant was not present in the wild-type monkeys available for the study.
- *CPS1*, along with other urea cycle genes, is preferentially expressed in periportal (zone 1) hepatocytes,¹¹ which are the hepatocytes that are most efficiently transduced by LNPs with mRNA cargoes.^{12,13} Thus, corrective editing might preferentially occur in the hepatocytes where *CPS1* is expressed, and a given percentage of whole-liver editing might translate into a substantially higher percentage of functional enzyme activity.

Accordingly, our initial dose selection for the single patient was dictated not by the editing activity findings of a limited dose-response study in mice, but rather by **safety considerations** (see next section).

NONHUMAN PRIMATE TOXICOLOGY STUDY

Study design

The purpose of this Good Laboratory Practice (GLP) study, performed at AmplifyBio, was to evaluate the potential toxicity and biodistribution of the k-abe drug product when administered once via intravenous infusion to cynomolgus monkeys, with samples collected on day 1 (treatment day) and day 15. The **toxicology batch** of k-abe was used as the test article, and phosphate-buffered saline (PBS) was used as the control vehicle. Nine male juvenile cynomolgus monkeys, ranging from 2.6 to 3.7 years of age with body weights ranging from 2.40 to 3.45 kg on day 1, were divided among three treatment groups using a stratified randomization program designed to maintain similar group mean body weights:

- Group 1 = treatment with vehicle control on day 1, necropsy on day 14
- Group 2 = treatment with 1.5 mg/kg test article on day 1, necropsy at 4 hours post-treatment
- Group 3 = treatment with 1.5 mg/kg test article on day 1, necropsy on day 15 (2 weeks)

All animals received 0.5 mg/kg famotidine intramuscularly, 5 mg/kg diphenhydramine intramuscularly, and 1 mg/kg dexamethasone intramuscularly on the day prior to treatment (day 0), and all three agents again up to 2 hours prior to treatment (day 1). This was done to mimic the pre-treatment for the patient specified in the clinical treatment protocol, and such pre-treatment has become standard practice for nonhuman primate studies of LNP gene-editing drug products.^{1,14,15}

The k-abe test article or vehicle control was administered via intravenous infusion over a 30-minute period. Ketamine (targeting 5-20 mg/kg intramuscularly) was used for blood collections, and specimens were collected from the femoral vessel. All animals survived to their scheduled termination and were euthanized by an administration of a barbiturate overdose followed by whole-body perfusion with saline. A necropsy with select tissue harvest was performed. All scheduled necropsies were conducted with a board-certified veterinary pathologist available for consultation.

Summary of study results

Endpoints used to evaluate potential toxicity were survival, clinical observations, body weights, ophthalmic examinations, respiratory rates, snapshot electrocardiographic evaluations, clinical pathology (hematology, serum chemistry, and coagulation), and anatomic pathology, including organ weights, gross observations at necropsy, and microscopic evaluation of selected tissues. Blood was collected for analysis of lipid excipients by BioAgilytix.

Test article related findings included changes in leukocytes (increases in neutrophils coupled with decreases in lymphocytes and monocytes) and minimal increases in serum enzyme activity. These parameters resolved and were considered non-adverse. Test article related findings in anatomic pathology included increased liver weights that corresponded to microscopic findings of minimal, diffuse, cytoplasmic vacuolization of hepatocytes 4 hours after dose administration. Cytoplasmic vacuolization was likely due to the LNP carrier. This was resolved on day 15 and considered non-adverse. No changes in clinical observations, body

weights, ophthalmology, respiratory rates, and electrocardiographic evaluations were associated with administration of the test article.

In final summary, administration of the drug product resulted in no adverse findings. The observed changes in the leukogram were minimal to mild and were consistent with a non-specific physiological stress response and deemed non-adverse. The described serum enzyme elevations were minimal to mild and resolved by the conclusion of the study (**Fig. S12**); therefore, these changes were considered non-adverse. The changes observed 4 hours following dose administration in the liver were transient and non-adverse as they were resolved by day 15.

Implications of nonhuman primate study for dose selection for the clinical protocol

No observable adverse events were detected with a 1.5 mg/kg dose of k-abe; therefore, the no-observed-adverse-effect level (NOAEL) was at least 1.5 mg/kg of the drug product. The estimated body surface area (BSA) conversion factor (the ratio of the BSA of a monkey to the patient) was 0.833. Using BSA scaling, the human equivalent dose (HED) for the patient was 1.25 mg/kg ($1.5 \text{ mg/kg} \times 0.833$). The starting dose of 0.1 mg/kg therefore represented a safety factor of 12.5. We felt that this high scaling factor was appropriate to ensure the patient's safety, especially given the inherent uncertainty in scaling drug doses in infants.

There was >99.5% clearance of both measured lipid excipients in the blood at 2 weeks after treatment compared to peak values (**Fig. S13**). The doses of k-abe chosen for the clinical treatment protocol—ranging from a starting dose of 0.1 mg/kg to as high as 0.45 mg/kg, with successive doses separated by a minimum of 3 weeks—were far lower than the 1.5 mg/kg dose of k-abe assessed in the monkeys. Furthermore, the maximum aggregate dose comprising the three potential doses to be administered to the patient would be substantially lower than the single 1.5 mg/kg dose assessed in the monkeys. Thus, we felt that the proposed repeated dosing presented minimal risk to the patient.

Potential for off-tissue editing

We were unable to assess for off-tissue editing by k-abe in the nonhuman primate toxicology study, because the *CPS1* Q335X variant was not present in the wild-type monkeys available for the study. Prior studies of LNP gene-editing drug products have demonstrated that they largely distribute to the liver but also transduce the spleen and adrenal glands to a lesser extent.^{1,14,15} Because the intended effect of the editing in the patient was to correct the Q335X variant to wild-type, off-tissue editing in these organs was felt to pose acceptable risk. Although the potential for germline editing with k-abe could not be evaluated, a prior study of an LNP gene-editing drug product did not detect editing in sperm samples from treated nonhuman primates, and (though not relevant for our male patient) there was no germline transmission of editing from treated female mice to offspring.¹⁴

OFF-TARGET EDITING ANALYSES

Nominating and experimentally verifying potential off-target sites for a drug product in a time-limited setting

Assessing the potential for unintended genomic alterations (at so-called “off-target sites”) has been an established regulatory requirement in the field since the first gene editing trials in 2009.¹⁶ Despite such an extended track record, no universal framework for such an assessment exists in the field, except that the extent of the effort is made somewhat proportionate to the severity of the clinical picture. Thus, a CAR-T product base-edited at multiple loci advanced to

the clinic for treatment-refractory pediatric T-cell acute lymphoblastic leukemia (T-ALL) after 20 candidate off-target sites were evaluated,¹⁷ whereas some development programs for in vivo gene-editing drug products reportedly have evaluated thousands of candidate off-target sites. The situation is made more challenging by the continued development of methods to nominate candidate off-target sites that has not been paralleled by methods to determine whether any verified off-target site is a source of regulatory concern. In our case of base editing in the human liver, no experimental method exists that would determine whether a verified off-target site poses such a concern due to potential tumorigenicity.

Our objective in advancing k-abe through nonclinical development and regulatory review was to leverage multiple orthogonal methods for candidate off-target site nomination—in silico, in vitro, and in cellulo—in ways that use, wherever possible, the patient's own genome as the substrate. We note that such personalized off-target site nomination is not currently a regulatory standard nor, to the best of our knowledge, has it ever been performed for gene-editing therapies administered to patients. As summarized in **Fig. S12**, we used ONE-seq, CHANGE-seq-BE, and a modified version of GUIDE-seq (UNCOVERseq) as the empirical nomination methods, supplemented with in silico nomination. The union set of nominations provided by these methods—obtained using prioritization methods described below—was used for a verification study using primary human hepatocytes.

Candidate off-target site nomination in silico using the patient's genome sequence

Whole-genome sequencing (WGS) was performed for the patient as part of clinical care. The resulting VCF file was filtered for single-nucleotide variants (SNVs) using bcftools v1.21.¹⁸ SNV calls were prefiltered to retain high-confidence variants (QUAL ≥ 15 , DP ≥ 5). Next, multiallelic sites (i.e., those where the patient was heterozygous for a given SNV) were split into biallelic records. To facilitate downstream analyses, a BED file was generated from the filtered VCF file before generating consensus FASTA sequences from variant alleles with GRhg38.p14. The resulting FASTA file was used to nominate off-target sites using GuideScan2 v2.2.1¹⁹ for sites with (1) up to four mismatches plus up to one RNA or DNA bulge compared to the on-target protospacer and (2) an NGN PAM. Finally, to overcome partial multiallelic variants' alleles lost in the generated consensus sequence, the previously created BED file was merged with the final GuideScan2 report. The nominated sites identified by this approach are provided in **Supplementary Excel File** in the worksheet labeled “In silico”.

Candidate off-target site nomination using ONE-seq, a patient-variant-aware in vitro assay

To maximize the likelihood of nominating bona fide off-target sites, we performed two complementary in vitro assays. In the first such assay, off-target sites nominated in silico using the patient's genome sequence were used as substrates in OligoNucleotide Enrichment and sequencing (ONE-seq),²⁰ a homology-dependent biochemical assay that uses a synthetic human genomic library selected by sequence similarity to the protospacer/PAM sequence specified by the ABE/gRNA (i.e., NGC-ABE8e-V106W and kayjayguran). ONE-seq was performed as previously described.¹ The ONE-seq library for the kayjayguran gRNA was designed based on the same criteria used for the in silico nomination described in the previous section, using the patient's genome as the reference. The oligonucleotide library was synthesized by Twist Biosciences. Recombinant NGC-ABE8e-V106W protein was produced by GenScript. Duplicate ONE-seq experiments were performed. The library was PCR-amplified and subjected to 1.25 $\times$ AMPure XP bead (Beckman Coulter) purification. After incubation at 25°C for 10 minutes in CutSmart buffer (New England Biolabs), ribonucleoprotein (RNP) comprising 769 nM recombinant NGC-ABE8e-V106W protein and 1.54 μ M gRNA was mixed

with 100 ng of the purified library and incubated at 37°C for 8 hours. Proteinase K (New England Biolabs) was added to quench the reaction at 37°C for 45 minutes, followed by 2× AMPure XP bead purification. The reaction was then serially incubated with EndoV (New England Biolabs) at 37°C for 30 minutes, Klenow Fragment (New England Biolabs) at 37°C for 30 minutes, and NEBNext Ultra II End Prep Enzyme Mix (New England Biolabs) at 20°C for 30 minutes followed by 65°C for 30 minutes, with 2× AMPure XP bead purification after each incubation. The reaction was ligated with an annealed adaptor oligonucleotide duplex at 20°C for 1 hour to facilitate PCR amplification of the cleaved library products, followed by 2× AMPure XP bead purification. Size selection of the ligated reaction was performed on a BluePippin system (Sage Science) to isolate DNA of 150-200 bp on a 3% agarose gel cassette, followed by two rounds of PCR amplification to generate a barcoded library, which underwent paired-end sequencing on an Illumina MiSeq System. The analysis pipeline used for processing the data assigned a score quantifying the editing efficiency with respect to the on-target site to each potential off-target site. Sites were ranked based on this ONE-seq score, and the mean ONE-seq score between duplicate experiments was used for site prioritization. The nominated sites identified by this approach are provided in **Supplementary Excel File** in the worksheet labeled “**ONE-seq**”.

Candidate off-target site nomination using CHANGE-seq-BE, an in vitro assay, with the patient's father's genomic DNA

The second in vitro assay we used, Circularization for High-throughput Analysis of Nuclease Genome-wide Effects by sequencing adapted for adenine base editing (CHANGE-seq-BE), involved purified genomic DNA as a substrate for base editing.^{21,22} In light of our inability to collect enough of the patient's genomic DNA due to blood draw limits, we performed CHANGE-seq-BE on genomic DNA from the patient's father, who was heterozygous for the *CPS1* Q335X variant. (Of note, genomic DNA from the patient's mother would not harbor the *CPS1* Q335X variant and so would not have been suitable for CHANGE-seq-BE with the kayjayguran gRNA.) Human genomic DNA was isolated from peripheral blood mononuclear cells (PBMCs) using the PureGene Cell Kit (8 x 108) (Qiagen) and quantified by Qubit fluorimetry (Invitrogen). Purified genomic DNA was tagged with a Tn5-transposase, gap-repaired with HiFi HotStart Uracil+ Ready Mix (Kapa Biosystems), and treated with a mixture of USER enzyme and T4 polynucleotide kinase (New England Biolabs). DNA was circularized at a concentration of 5 ng/μL with T4 DNA ligase (New England Biolabs) and treated with Lambda exonuclease (New England Biolabs), Exonuclease I (New England Biolabs), Exonuclease III (New England Biolabs), and Plasmid-Safe ATP-dependent DNase (Lucigen). Kayjayguran gRNA was re-folded prior to formation of an RNP complex with recombinant NGC-ABE8e-V106W base editor protein. In vitro cleavage reactions were performed in a 50 μL volume with Digenome-seq buffer (50 mM Tris-HCl [pH 8], 25 mM KCl, 2.5 mM MgSO₄, 0.1 mM EDTA, 10% glycerol, 2 mM DTT, 10 μM ZnCl₂), 3 μL of 5 μM protein, 5 μL of 9 μM gRNA, and 125 ng of exonuclease-treated circularized DNA. Deaminated products were treated with EndoV to create double-stranded breaks, end-repaired, A-tailed, ligated with a hairpin adapter (New England Biolabs), treated with USER enzyme, and PCR-amplified using Kapa HiFi HotStart Uracil+ Ready Mix (Kapa Biosystems). Completed libraries were quantified by Qubit High Sensitivity dsDNA fluorimetry and sequenced with 150-bp paired-end reads on an Illumina NextSeq 2000 instrument. Sequence analysis was performed using a modified version of CHANGE-seq-BE analysis software (<https://github.com/tsailabSJ/changeseq/dev>). Briefly, raw FASTQ files were trimmed to remove transposon and Illumina adapter sequences using Cutadapt v3.4.²³ Trimmed reads were then aligned to the human reference genome GRhg38.p14 using BWA v0.7.17. Aligned reads were classified as edited in both RNP-treated and untreated control samples according to the following criteria: (1) paired-end reads had outward-oriented alignments; (2) read pairs overlapped by a minimum of 5 bp and a maximum of 15 bp; (3) alignments were of stringent

quality threshold, MAPQ > 50; (4) the overlapping reads, including +/- 30 bp of flanking region, contained a sequence matching the gRNA and an NGN PAM below a Levenshtein distance of 7. Lastly, to account for variability between replicates, raw read counts of identified sites were normalized using median normalization. Final sites were reported if at least one replicate contained a site with at least 2 reads. The nominated sites identified by this approach are provided in **Supplementary Excel File** in the worksheet labeled “**CHANGE-seq-BE**”.

Candidate off-target site nomination using UNCOVERseq, an in cellulo assay: tissue culture and library preparation

In addition to the in silico and in vitro methods described above, we used Unbiased Nomination of CRISPR Off-target Variants with Enhanced rhPCR (UNCOVERseq), a modified version of an in cellulo assay, genome-wide, unbiased identification of double-strand break (DSBs) enabled by sequencing (GUIDE-seq),²⁴ which relied on capture of synthetic double-strand oligodeoxynucleotide (dsODN) tags into double-strand breaks (whether sporadic or nuclease-induced) in cultured cells. As it was clinically infeasible to obtain the patient's hepatocytes for such a study, we relied on transformed cell lines. We developed a workflow that allowed off-target nomination for the kayjayguran protospacer sequence despite the fact that these cell lines lacked the patient's Q335X variant at the *CPS1* locus. Specifically, we treated the cells with (1) a nuclease editor carrying a gRNA with a spacer sequence that matched the wild-type *CPS1* locus (5'-UGAUUCUGAGCAGUAAUGAA-3') to provide in cellulo evidence of efficient editor delivery, as gauged by on-target cleavage, and (2) a nuclease editor carrying a gRNA with a spacer sequence that matched the variant allele (5'-UGAUUCUAAGCAGUAAUGAA-3'). HuH-7 cells (Japanese Collection of Research Bioresources Cell Bank) were maintained with complete media comprising Dulbecco's Modified Eagle's Medium (American Type Culture Collection) and 10% fetal bovine serum (FBS). U2OS cells (American Type Culture Collection) were maintained in McCoy's 5A Media (American Type Culture Collection) with 10% FBS. gRNAs with the spacer sequences described above were complexed with the nuclease isoform of the NGC-ABE8e-V106W base editor protein (i.e., lacking the TadA adenosine deaminase domain and able to nick both DNA strands), purified employing a custom, proprietary multi-column purification strategy. (Of note, only UNCOVERseq used this nuclease isoform; ONE-seq and CHANGE-seq-BE used the fully functional base editor.) Resulting RNPs (4 μ M) were nucleofected (Lonza) into HuH-7 and U2OS cells (nucleofection code CM-104) in the presence of 4 μ M and 6 μ M dsODN adapter, respectively. Two nucleofections per replicate were performed using Lonza SE buffer with 800,000 cells per nucleofection, and each treatment was performed in triplicate. Following nucleofection, the cells were transferred to 6-well plates for expansion. Genomic DNA from edited and control cells was extracted after 48 hours using the Monarch Genomic DNA Purification Kit (New England Biolabs) according to the manufacturer's instructions, eluted in low-EDTA TE buffer (IDT, 11-05-01-05), and quantified using a NanoDrop 8000 UV-Vis Spectrophotometer (ND-8000-GL). The resulting genomic DNA was enzymatically fragmented and adapter-ligated using the xGenTM DNA Library Prep EZ UNI kit along with the xGen Deceleration Module (IDT, xGen DNA Library Prep EZ UNI 96 rxn, 10009822; xGen Deceleration Module 96 rxn, 10009823) according to the manufacturer's instructions. Five hundred ng of genomic DNA was used as input for each of the samples. Following fragmentation and adapter ligation, rhPCR²⁵ was used to amplify the DNA using a forward primer specific to the P5 adapter and a reverse primer specific to the integrated dsODN tag in the presence of a blocking oligonucleotide meant to prevent amplification of dsODN tag-adapter (so-called “free-floating” adapter-bearing tags) products. In such settings, rhPCR technology allowed the use of primers complementary each to the top strand and the bottom strand of the dsODN without generating primer dimers. Following PCR, samples were diluted 1:20 with nuclease-free H₂O and used in a second PCR that added a unique P7 adapter to each product

from the initial PCR. All resulting libraries were sequenced on an Illumina MiSeq instrument (150-bp paired-end reads).

Candidate off-target site nomination using UNCOVERseq, an in cellulo assay: bioinformatic analysis

Following NGS, Illumina adapters and unique molecular identifiers (UMIs) were identified and annotated using Picard MarkIlluminaAdapters. Tag sequences were identified and trimmed using Cutadapt v4.2. Sequencing reads were aligned to the hg38 (GRCh38.p12) reference genome using BWA mem v0.7.15,²⁶ and UMI consensus reads were generated based on a single-strand consensus (minimum UMI consensus size = 1) using fgbio v0.7.0 (<https://github.com/fulcrumgenomics/fgbio>). The hg38 reference genome was used rather than the patient's genome for this analysis since transformed cell lines were used as the experimental system. Nomination of candidate off-target sites began by using mapped UMI consensus reads to create a flanked search space (+/- 40 bp) to perform alignment between the gRNA and empirical target region using a global implementation of the Needleman–Wunsch alignment.²⁷ After a candidate matched to the gRNA spacer sequence was identified in the sequencing data, nominated off-target sites were identified using a hypergeometric test with multiple testing correction (Benjamini–Hochberg; FDR < 0.05) by comparing individual treatment samples and pooled control samples for significant differences in representation between the two. We used the following criteria to nominate off-target sites from this analysis for verification: (1) at least one sample nominated a given site with NGS evidence on both sides of the cut site; (2) Levenshtein distance < 7 as determined post-alignment; and (3) significant adjusted p-value when comparing the frequency of the event to the pooled control(s). Nominated on/off-target sites had additional meta-data added based on alignment/genomic context and were placed into described Tiers based on this meta-data (**Supplementary Excel File** in the worksheet labeled “**Definitions of Tiers**”). The nominated sites identified by this approach are provided in **Supplementary Excel File** in the worksheets labeled “**UNCOVERseq_CPS1_MUT**” and “**UNCOVERseq_CPS1_WT**”.

Generation of the union set of nominated off-target sites for experimental verification

Candidate off-target sites nominated by different methods were associated with method-specific unique enrichment scores, supporting information, and annotations. With this in mind, the sum total of the above nomination findings was used to generate a union set for experimental prioritization during verification as follows (**Fig. S15** and sections below). First, nominated off-target sites were merged between methods using bedtools²⁸ for coordinates with at least 1-bp overlap between methods. Of note, due to different method-specific alignment and nomination reporting capabilities, off-target sites deriving from the same genomic region may be reported slightly differently or have different estimations of the cut position. In the case of multiple overlaps of different alignments, the coordinate retained was the one with the lowest overall Levenshtein distance from the target gRNA and the meta-data of the highest empirically derived frequency (ONE-seq, CHANGE-seq-BE, and UNCOVERseq) and lowest Levenshtein distance (in silico methods). Second, all sites were annotated using a common hg38 reference genome assembly with the feature that the putative gRNA spacer sequence overlapped (**Supplementary Excel File** in the worksheet labeled “**CHOP_Nominated_Sites_Final_Prop**”). Third, nominated sites aligning to the mitochondrial genome (chrM) were removed from analysis given the biological implausibility of the gRNA entering the mitochondrion and the lack of mitochondrion-targeting sequences in Cas9. Following the above steps, sites were given a priority classification as described in **Supplementary Excel File** in the worksheet labeled “**Priority classification**”. Briefly, empirically derived sites with high frequencies ($\geq 1\%$ UNCOVERseq; ≥ 100 ONE-seq score; ≥ 30 CHANGE-seq-BE score), intra-method

reproducibility, or exonic annotations (all UNCOVERseq; ≥ 10 ONE-seq score; all CHANGE-seq-BE) and the on-target *CPS1* locus were assigned “Priority 1”. Empirically derived sites with lower frequencies (all UNCOVERseq; ≥ 10 ONE-seq score) and lower frequency sites with exonic annotations (≥ 1 ONE-seq score) in addition to any computationally predicted sites with high similarity (Levenshtein distance ≤ 2) or exonic annotations (Levenshtein distance ≤ 3) were assigned “Priority 2”.

Experimental verification of nominated off-target sites: library preparation and bioinformatic analysis

Genomic DNA was extracted from untreated cells and cells treated with k-abe, as described below. Libraries for amplicon NGS were prepared using a previously described rhAmpSeq amplification-based method (IDT) using 100 ng of gDNA input.²⁹ Libraries were purified using AMPure XP beads and quantified by qPCR before being sequenced on the Illumina NextSeq platform (150-bp paired-end reads). Read demultiplexing was performed on the resulting BCL files using Picard v2.18.9 IlluminaBasecallsToFastq.

Analysis of the sequencing data to identify bona fide off-target editing at the nominated sites was performed using CRISPAItRations v1.2.1.³⁰ This analysis comprised two parallel workflows: identification of indels at the position of the base-editor-induced nick, and identification of base-editor-induced A>G transversions in the relevant base-editing window.

For identifying indels, the window for event quantification was centered on the canonical cut site and events quantified utilizing the default window size for Cas9 (8 bp). To determine whether indels found in the sequencing data could result from bona fide off-target cleavage, indels were grouped by location relative to the cut site (prioritizing minimum distance to cut site) followed by fitting counts of events to a negative binomial model with a Wald test for significance in each location bin per off-target using the DESeq2 package³¹ in IDT’s OTEasy tool environment. For classification of indel off-target editing, the tool required (1) sufficient read coverage for the site ($>1000\times$) in all replicates, (2) significant edits to occur at or adjacent to the cut site after optimal alignment, (3) the classified cumulative significant edits to exceed 0.01%, (4) the comparison of treatment/control samples at the site to have a significant p-value ($p < 0.05$), and (5) an average coverage frequency of at least $5\times$ the ascribed cumulative frequency observed (e.g., for 0.1% editing, at least $5,000\times$ coverage).

For identifying adenine base editing off-target effects, the window for event quantification was centered in the middle of canonical base editing window between positions 5 and 6 of the protospacer sequence with a 5-bp window for quantification. To determine whether A>G transitions could result from bona fide off-target editing, all individual events that contained an A>G or T>C transition were grouped according to unique base editing events in the window (“No Collapse”) and fitting counts of events for both approaches to a negative binomial model with a Wald test for significance in each location bin per off-target using the DESeq2 package in IDT’s OTEasy tool environment. For classification of adenine base editing at off-target sites, the tool required (1) sufficient read coverage for the site ($>1000\times$) in all replicates, (2) the classified cumulative significant edits to exceed 0.5%, (3) the comparison of treatment/control samples at the site to have a significant p-value ($p < 0.05$), and (4) an average coverage frequency of at least $5\times$ the ascribed cumulative frequency observed (e.g., for 0.1% editing, at least $5,000\times$ coverage). While we have yet to rigorously establish the lower limit of detection of rhAmpSeq for SNVs, based on previously published validation studies of multiplexed amplicon NGS assays for detecting somatic variants in tumor and cell-free DNA,³¹⁻³⁴ we expect that the sensitivity will likely be below 0.5%.

Translocation analysis

To quantify translocations from editing, the IDT-developed Primer Anchored Statistical Translocation Analysis (PASTA) methodology was used. This analysis was only performed on the amplicon sequencing pools containing the on-target site because multiplexed amplification is a requirement for event detection using the method, and reactions not containing the on-target site are unlikely to have any significant translocation events. To quantify translocations, expected primers were identified in reads using fg-idprimer: (<https://github.com/fulcrumgenomics/fg-idprimer>; -k=6, -K=8, -S=5, --max-mismatch-rate=0.07). Following this, treatment/control pairs had their counts paired and primer count frequencies subjected to a one-tailed hypergeometric test with Benjamini–Hochberg correction (statsmodel v0.15.0; default settings) to calculate an adjusted p-value (p-adj). Unexpected primer pairs with p-adj < 0.01 with no flags were classified as a translocation and had the translocation frequency (P_t) calculated using the following equation:

$$P_t = \frac{n_t}{f_{total}} + \frac{n_t}{r_{total}}$$

where n was equal to the count of the unexpected primer pair of interest, t was the significant translocation being interpreted, f was the total count of the shared forward primer events excluding the count participating in the n translocation event, and r was the total count of shared reverse primer events excluding the count participating in the n translocation event. The translocation frequency was then adjusted by the background level frequency in the control sample by subtracting any translocation frequency observed in the control sample from the treatment frequency. Total translocation burden (B) was calculated using the following equation:

$$B = 1 - \prod_t^{t_n} (1 - P_t)$$

where t was equal to a significant translocation, and t_n was equal to the last significant translocation of all translocations. All translocations for the purposes of this equation were assumed to be occurring independently. Using the method, translocations were quantified if (1) the estimated frequency exceeded 0.1% of editing, (2) if the translocation had a significant p-value ($p < 0.01$), and (3) if the translocation was found to meet these criteria in all replicates.

Initial experimental verification of off-target sites in hepatocytes

We took a **two-stage approach** to verifying candidate sites as bona fide off-target sites, i.e., sites where off-target editing genuinely occurred in hepatocytes. This two-stage approach was necessitated by the urgent need to treat the single patient with k-abe due to the high risk of permanent neurologic damage and death with each hyperammonemic episode. Manufacturing of the **clinical batch** of k-abe was completed only 3 weeks before the submission of single-patient expanded-access IND application to the FDA, providing only a limited amount of time to perform an initial set of verification studies (of note, these studies were performed with an aliquot of the clinical batch of k-abe, while release testing of the k-abe drug product was occurring in parallel).

In the first stage, we completed an evaluation of a high-priority subset of candidate sites with individual targeted amplicon sequencing (PCR followed by NGS). This subset comprised the sites that met either of two criteria:

- Located within exons of genes, regardless of nomination method—the 3rd through 9th sites in **Table S3**, all of which are annotated as “exon” or “3’UTR”
- Higher scores than the on-target site in ONE-seq (>1.0), CHANGE-seq-BE (>10), or both—the 10th through 23rd sites in **Table S3**, all of which are annotated as “intron”, “intergenic”, or “noncoding”

We assessed for off-target editing by the **clinical batch** of k-abe in two cell types:

- HuH-7 cells bearing the Q335X variant (Q335X lentivirus-transduced HuH-7 cells)
- Primary human hepatocytes (PHHs) from three individuals—all male, with ages of 7 weeks (PDV lot), 6 months (YEQ lot), and 13 months (ICH lot), respectively—obtained via a commercial vendor (BioIVT); these individuals were chosen because they approximated the age of the single patient at the time of initial dosing with k-abe (between 6 and 7 months of age)

The **clinical batch** of k-abe was assessed for corrective editing activity in Q335X lentivirus-transduced HuH-7 cells (**Fig. 2C**). The estimated EC₉₀ from that assessment was ≈52 ng/mL. In order to perform off-target analysis in cells subjected to a much higher level of drug exposure than the level that would be experienced by hepatocytes in the single patient to be dosed with the same drug product, we used HuH-7 cells treated with a k-abe dose 20-fold greater than the EC₉₀, drawing on a published precedent (nexiguran ziclumeran, a Cas9 nuclease editor LNP drug product) in which an LNP dose 27-fold greater than the EC₉₀ was used for off-target analysis.¹⁵ Accordingly, HuH-7 cells were treated at a dose level of 1000 ng/mL of k-abe (versus no treatment), and either genomic DNA or RNA was extracted 3 days later.

Individual targeted amplicon sequencing was attempted for 23 genomic sites in the HuH-7 cell-derived DNA (**Fig. 2D, Table S3**): the lentivirus-encoded on-target Q335X site (corrective editing), the endogenous wild-type *CPS1* Q335 site (lacking the Q335X variant and thus mismatched to the kayjayguran gRNA by 1 base), and 21 candidate off-target sites prioritized as described above. Of the successfully sequenced sites, only one displayed off-target editing (**Fig. 2D**, shown in red in **Table S3**), an intronic site in the *ATP7B* gene. We assessed for *ATP7B* off-target editing using the samples from the k-abe dose-response study shown in **Fig. 2C**. Across the dose range, the observed off-target editing was ≤0.5% (**Table S4**); at the dose approximating the EC₅₀ for corrective editing of the on-target site, 15.6 ng/mL, no off-target editing was evident at the site.

Of note, the *ATP7B* intronic site was near the top of the list of candidate sites for each of the three nomination methods: ONE-seq, CHANGE-seq-BE, and UNCOVERseq/GUIDE-seq. The site is 379 nucleotides upstream of the closest coding sequence, a splice acceptor, and thus is unlikely to affect gene function. Although *ATP7B* is expressed in hepatocytes, it encodes a copper-transporting protein. Loss of function of *ATP7B* is linked to Wilson disease, an autosomal recessive disorder; a very low level of off-target editing, in the unlikely scenario that the off-target intronic base edit were to inactivate gene function, would not be expected to significantly perturb copper transport and induce Wilson disease. Increased expression of *ATP7B* in tumor cells has been reported to confer resistance to platinum-based therapies,³⁵ due to increased cellular drug efflux, but there is no reported link between **reduced** *ATP7B* function and cancer. Thus, the oncogenic risk of the intronic off-target editing in *ATP7B* was felt to be negligible.

PHHs from three very young male donors were selected for analysis to best model in vivo hepatocytes in the single patient to be dosed with k-abe. Because these PHHs did not harbor the *CPS1* Q335X variant, it was not possible to assess corrective on-target editing as confirmation that treatment with the k-abe drug product had effectively transduced the cells.

However, despite having a mismatch with the wild-type *CPS1* Q335 site, the kayjayguran gRNA was nonetheless able to edit bystander adenine bases at the site in wild-type HuH-7 cells at low efficiency, $\approx 3\%$ (**Fig. 3D**, black bold in **Table S3**). Thus, editing at the wild-type *CPS1* Q335 site in PHHs could serve as a marker of activity of the k-abe drug product.

PHHs from the three donors were treated at a dose level of 1000 ng/mL of k-abe (versus no treatment), and either genomic DNA or RNA was extracted 3 days later. We measured abengcemeran mRNA levels in HuH-7 cells and PHHs treated with the clinical batch of k-abe via quantitative reverse transcriptase–polymerase chain reaction (qRT-PCR). We observed that the mRNA levels in PHHs treated with a dose of 1000 ng/mL were 3 to 7 times greater than the mRNA levels in Q335X lentivirus-transduced HuH-7 cells treated with a dose of 1000 ng/mL (**Table S5**), supporting the adequacy of the editing condition in the PHHs at that dose.

In PHHs from each of the three donors, individual targeted amplicon sequencing (**Table S6**) was undertaken for the endogenous wild-type *CPS1* Q335 site (lacking the Q335X variant) and all the candidate off-target sites that were successfully sequenced in HuH-7 cells. At the endogenous wild-type *CPS1* Q335 site, there was low-level editing in all three PHH types, confirming the activity of the k-abe drug product in the cells. As with the HuH-7 cells, only one site displayed even minimal evidence of off-target editing, the *ATP7B* intronic site, albeit at negligible levels that would not have been interpreted *a priori* as being indicative of off-target editing.

Integrating off-target site nomination data for more comprehensive experimental verification

The results of the first stage of experimental verification of off-target sites were submitted as part of the single-patient expanded-access IND application to the FDA. A **second stage** of experimental verification in PHHs, entailing a much more comprehensive analysis of the nominated off-target sites, was undertaken in parallel and completed after IND submission.

All off-target nomination methods, whatever their basis, have limitations due to both sensitivity (false negative rate) and specificity (false positive rate). In silico methods do not account for incompletely understood sequence-dependent effects on gene editor enzyme thermodynamics or epigenomic effects on editor action. In vitro methods account for the former to some extent but do not account in any way for the epigenomic effects, nor can they model the actual per-cell dose of the gene editor. Both of these types of methods have well-established high false-positive rates. In cellulo nomination methods use transformed cells that have a different epigenome than the cells targeted therapeutically and cannot model in-liver gene editor pharmacokinetics and thus pose concerns with respect to sensitivity. Further, while the in silico/in vitro methods can account for patient-specific genetic variation, in the present setting the in cellulo nomination method did not account for such variation. To account for the benefits and drawbacks of these different methods, we took an orthogonal approach to nominating off-target sites and used site prioritization based on perceived risk and probability of occurrence to define a benefit-risk appropriate set of candidate off-target sites for interrogation (**Fig. S15**).

The total number of method-specific nominated off-target sites ranged from 87 identified by CHANGE-seq-BE to 7090 sites identified using the combined findings of the more promiscuous in silico models (**Fig. S16A**). Sites nominated by the UNCOVERseq/GUIDE-seq method were obtained from experiments using two distinct gRNAs in two distinct cell types (**Fig. S17**). Robust on-target editing (83-97%) was observed across all conditions, with 3-7% of cells integrating the dsODN tag at the on-target locus (**Supplementary Excel File** in the worksheet labeled “**On-target locus integration**”). Evaluation of a positive control established that the assay had a robust dynamic range, nominating editing events resulting from 0.02% to 96% indels at the

nominated sites (**Supplementary Excel File** in the worksheet labeled “**Nomination metrics**”). Nominated sites shared between conditions (gRNAs and cell lines) accounted for >95-98% of the cumulative frequency of events with conserved rank order correlations between cell lines ($r = 0.81$), indicating a high level of reproducibility for top candidate loci (**Fig. S17**).

In generating the union set for off-target verification, we first examined the Venn diagram of data from three in vitro and in cellulo methods (i.e., those that involved experimentation). As shown in **Fig. S16B**, in addition to the target site, *CPS1*, nine sites were identified by all three methods, showcasing the known sensitivity/specificity challenges associated with using any one given method and highlighting the utility of combining data from orthogonal approaches such as in the present study. Further, we found that 40 candidate off-target sites were nominated by two methods, and 685 were unique to a single empirical method (**Fig. S16B**). Our perspective on the number of nominated off-target sites that should be experimentally verified was based on three considerations. First, given that each assay ranked the nominated off-target sites by likelihood of representing a bona fide off-target site, there were “diminishing returns” from sampling nominated sites further down the list in a way that was agnostic to the specific nominating assay or biological risk. In other words, it was unreasonable to sample a candidate off-target site that was at position #500 from an assay with a known high false-positive rate in favor of such a site nominated with an assay with higher specificity. Second, there were fundamental technology limitations to assessing whether a nominated off-target site was a bona fide one: these stemmed from the inability to sample more than a fixed amount of human genome equivalents per verification PCR ($\approx 30,000$ haploid genomes in this case) as well as the intrinsic sequence noise at lower limits of detection for NGS-based assays. Further, one must be mindful of the fact that definitive de-risking was technically impossible given the discrepancy in the number of cells evaluated versus the number of cells treated in the liver of an infant. Finally, as alluded to above, no current experimental method allowed the de-risking of a verified off-target site even in the exon of a coding gene for cells such as hepatocytes. For all these reasons we did not believe it to be operationally valuable to engage in exhaustive off-target mapping exercise, given that it would have limited utility in guiding clinical decision-making in the setting of a severe disease indication such as a urea cycle disorder.

Based on these considerations, and with the goal of establishing a more generalized framework for generating a union set of sites nominated by various methods, we adopted a workflow prioritizing sites obtained through orthogonal approaches (**Fig. S15** and **Supplementary Excel File** in the worksheet labeled “**Priority classification**”). Based on this ruleset, we generated two pools of nominated off-target sites. The first pool, comprising 122 nominated sites, prioritized nominated sites that (1) had high empirically derived frequencies or (2) had moderate/low empirically derived frequencies but targeted a gene exon. The second pool, comprising 236 sites, expanded the inclusion criteria to (1) sites nominated with moderate/low empirically derived frequencies, (2) sites shared between more than one empirical method using stated thresholds, (3) sites with lower empirically derived frequencies but targeting a gene exon, and (4) sites nominated using in silico methods with high similarity to the kayjayguran gRNA. The full details and criteria used for prioritization can be found in the relevant sections above.

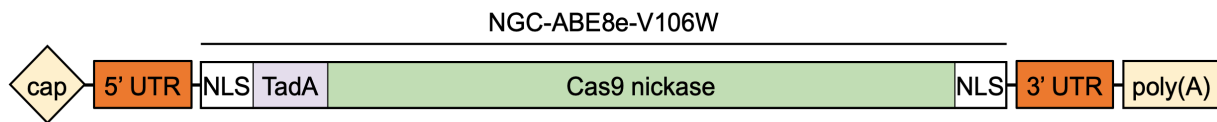
In using our nomination data to assign candidate off-target sites to Priority 1 and 2 pools, we found that 27 and 15 exonic sites (including the *CPS1* on-target site), respectively, met these criteria (**Fig. S16C** and **Supplementary Excel File** in the worksheet labeled “**CHOP_Nominated_Sites_Final_Prop**”). Importantly, 100% of the 10 sites shared among all three of the empirical methods were nominated at the Priority 1 criteria by at least one assay (**Fig. S16D**), with 100% meeting criteria for UNCOVERseq, 70% meeting criteria for CHANGE-seq-BE, and 60% meeting criteria for ONE-seq (**Supplementary Excel File** in the worksheet labeled “**CHOP_Nominated_Sites_Final_Prop**”). While the empirically derived frequencies can

be variable among methods for the reasons described above, the majority of high-frequency empirical nominations were shared between at least two methods (**Fig. S16E**). In sum, in this workflow we prioritized sets of nominated off-target sites of potential regulatory concern for verification. Further, analysis of the patient's genome identified 10 prioritized sites that were nominated empirically and that contained patient-specific SNPs in the region targeted by the gRNA spacer sequence (**Fig. S18** and **Supplementary Excel File** in the worksheet labeled "**CHOP_Nominated_Sites_Final_Prop**").

Verification of Priority 1 and Priority 2 off-target sites was performed using multiplex targeted amplicon sequencing (rhAmpSeq) of genomic DNA from PHHs treated with the k-abe drug product. In this analysis, 97.3%/93.2% of targets exceeded 1,000× coverage, and 65%/44% of targets exceeded 10,000× coverage in the Priority 1/Priority 2 pools, respectively (**Supplementary Excel File** in the worksheets labeled "**Average read depth coverage**" and "**Sensitivity of coverage method**"). As shown in **Fig. S19**, analysis of these data found no verified off-target sites in Priority 1 and Priority 2 panels, i.e., no ABE-induced base editing, no indels from non-homologous end-joining (NHEJ), and no translocations in any of the PHH types at interrogated candidate off-target sites. The only significant ABE-induced base editing event was synonymous bystander editing observed at the endogenous wild-type *CPS1* Q335X site at ranges varying from 0.5% to 3.9% editing, in agreement with the previous findings of the first stage of experimental verification (compare **Fig. 2D** and **Table S6** to **Fig. S19A–C**).

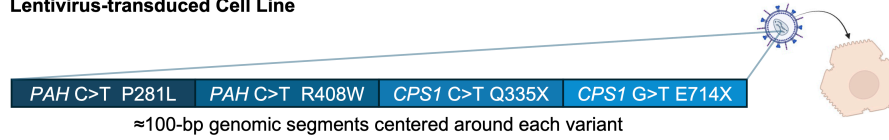
The sum total of the above efforts emerged from work by three teams, distributing the tasks according to optimal levels of expertise given the limited time available, unfolding over ≈2.5 months. Given our focus on establishing a platform approach, and the stated goal of limiting the length of time for such analysis, we believe that all the nomination and verification activities could be completed in 6 to 8 weeks from when the patient's WGS data become available and the protein/mRNA/gRNA for the gene editor to be used clinically become available. Work currently in progress based on the effort described above focuses on establishing a standardized framework for prioritizing candidate off-target sites derived from distinct methods.

Figure S1. Structure of mRNA Drug Substance.

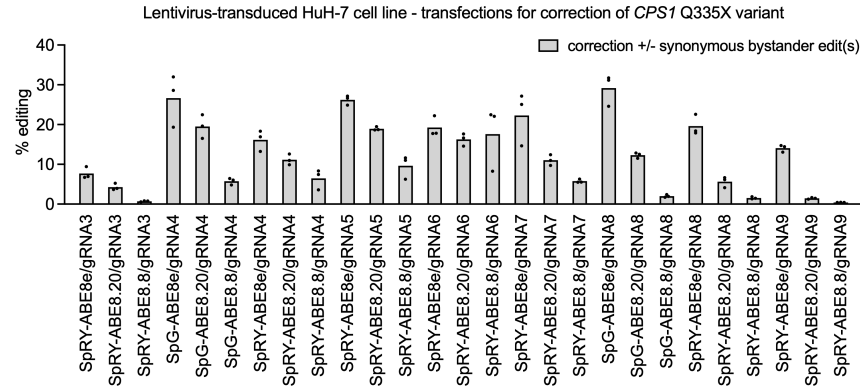


Abbreviations: Cap = methylated 5'-Cap-1; UTR = untranslated region; NLS = nuclear localization signal; TadA = evolved tRNA-specific adenosine deaminase; Cas9 = clustered regularly interspaced short palindromic repeats (CRISPR)-associated protein 9; poly(A) = polyadenylic acid. Not to scale.

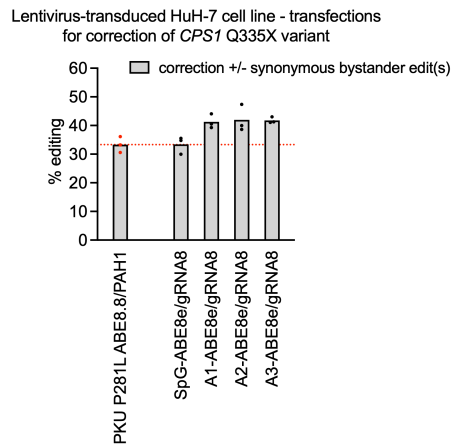
A Lentivirus-transduced Cell Line



B Screening of ABE/gRNA Combinations



C Screening of ABEs with NGC PAM Specificity



D Screening of ABEs with V106W Variant

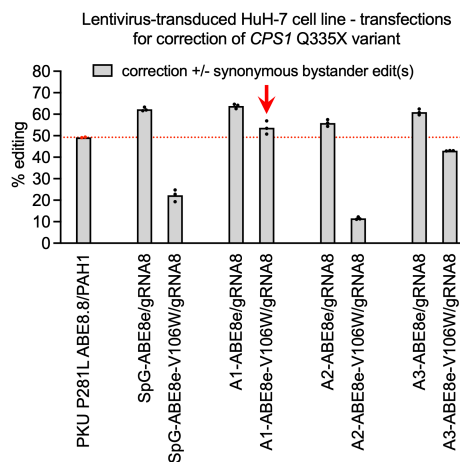


Figure S2. Optimization of Base Editing to Correct *CPS1* Q335X Variant.

Panel A shows how lentiviral vector was used to transduce human HuH-7 hepatoma cells with a cassette comprising four adjacent 100-bp genomic segments with the patient's two *CPS1* variants, including the Q335X variant, and two unrelated *PAH* variants serving as reference controls. Panels B, C, and D show corrective *CPS1* Q335X editing (determined from genomic DNA) following transfection of lentivirus-transduced HuH-7 cells with plasmids encoding adenine base editor (ABE)/guide RNA (gRNA) combinations (N = 3 biological replicates), calculated as the proportion of aligned sequencing reads with the indicated type of edits. "Correction +/- synonymous bystander edit(s)" refers to reads in which the *CPS1* Q335X adenine variant, or the *PAH* P281L variant, was edited to guanine, with or without base editing of one or more nearby synonymous adenines, with no base editing of any other adenines. The red horizontal dotted lines in panel C and panel D indicate the editing level for the validated *PAH* P281L reference control condition, and the red arrow in panel D indicates the ABE/gRNA combination chosen for k-abe. Differing from the PAM-relaxed SpG enzyme, A1 encoded SpCas9-LWKYQS, A2 encoded SpCas9-MQKSER+, and A3 encoded eSpGC. For the purpose of the single-patient expanded-access IND application, A1-ABE8e-V106W was designated NGC-ABE8e-V106W.

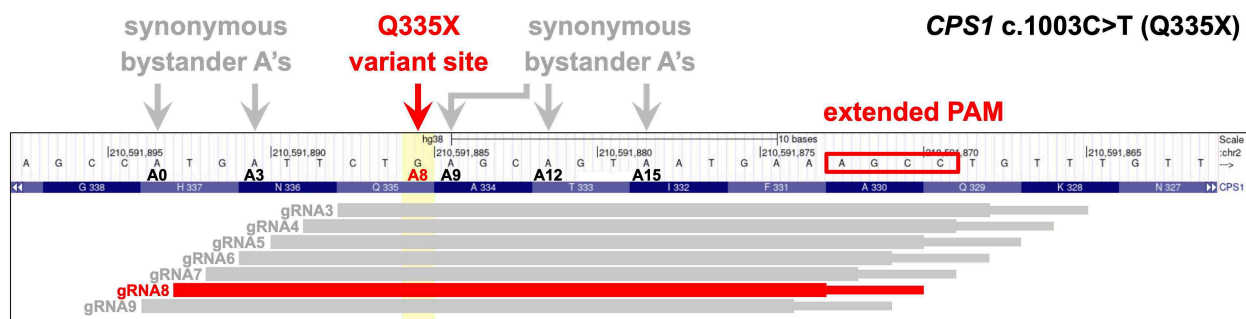


Figure S3. Schematic of Genomic Site of *CPS1* Q335X Variant.

Adapted from the UCSC Genome Browser (GRCh38/hg38). The red arrow and the vertical yellow bar indicate the position of the G altered to A (A8, in red) by the Q335X variant on the antisense strand. The grey arrows indicate the sites of potential bystander editing (A0, A3, A9, A12, and A15, in black). The horizontal bars indicate protospacer (thick) and PAM (thin) sequences targeted by the gRNA3 through gRNA9 guide RNAs; the number in the name indicates the position of the Q335X variant adenine in that guide RNA's protospacer sequence. The red horizontal bar indicates gRNA8, which was chosen for use in the k-abe drug product due to its high editing activity (see **Fig. S2**). The red box indicates the extended PAM sequence for gRNA8 (AGCC).

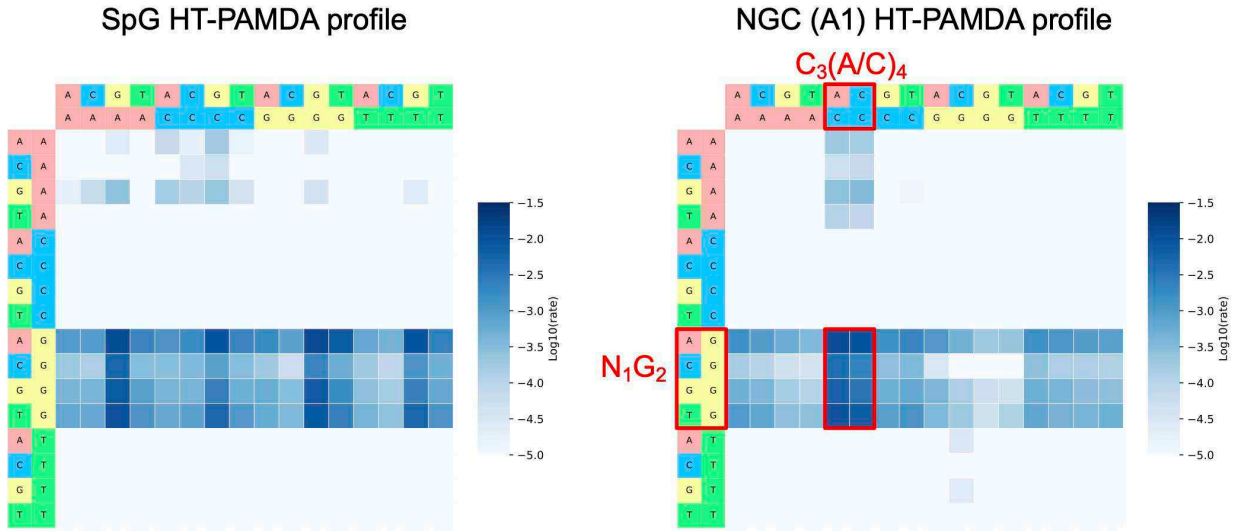


Figure S4. High-Throughput PAM Determination Assay (HT-PAMDA) Profiles of SpG and NGC Cas9 Proteins.

Heatmap representations of the PAM profiles of SpG or NGC (left and right panels, respectively), determined using the HT-PAMDA assay⁸ where the rate constant (k) on a PAM is a measure of targeting efficiency. The NGC Cas9 showed a preference for NGC(A/C) PAMs. HT-PAMDA datasets were the mean of N = 2 biological replicates using different target sites.

Base editing outcomes among edited reads: Amino acid sequence

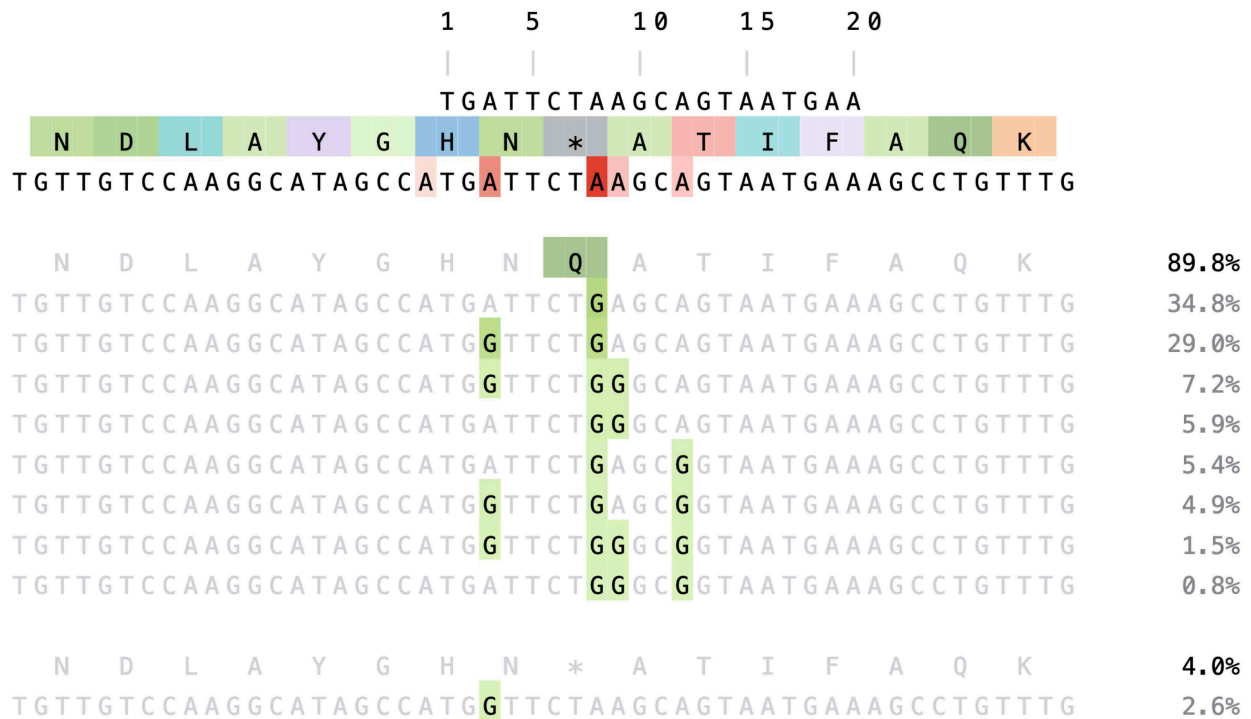


Figure S5. Predicted Corrective Adenine Base Editing of *CPS1* Q335X Variant.

Output of the BE-Hive machine learning model (<https://www.crisprbehive.design/>) showing the predicted editing profile of gRNA8, set for ABE8e in mESCs. All predicted bystander editing results in synonymous changes.

Editing in lentivirus-transduced HuH-7 cells treated with NGC-ABE8e-V106W and gRNA8 plasmids

H337 N336 **335X** A334 T333 I332 baseline/reference identity of *CPS1* codons

H337 N336 **Q335** A334 T333 I332 codons resulting from base editing

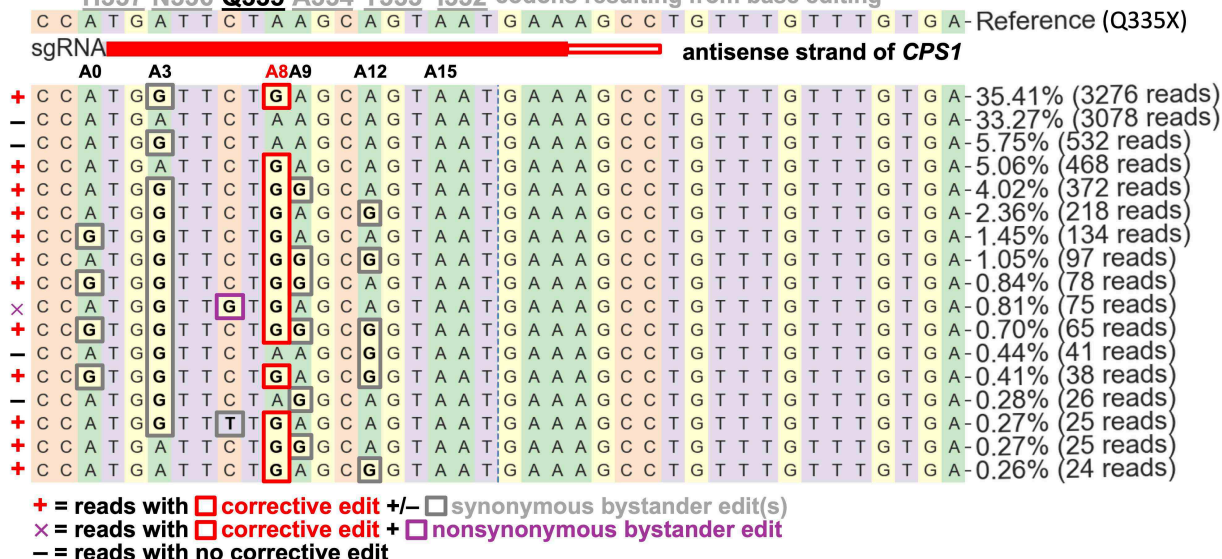


Figure S6. Empirical Corrective Adenine Base Editing of *CPS1* Q335X Variant.

Standard CRISPResso (<http://crispresso2.pinellolab.org/submission>) next-generation sequencing (NGS) output for the editing in the sample from the NGC-ABE8e-V106W/gRNA8 plasmid-treated HuH-7 cells that displayed the highest level of editing (the condition marked by the red arrow in **Fig. S2D**, also designated A1-ABE8e-V106W/gRNA8). The codons in the vicinity of the Q335X site are indicated; the top-listed amino acid is the baseline/reference identity of the codon, and the bottom-listed amino acid is the one that results from base editing of the adenine in the codon. The red horizontal bar indicates the gRNA8 protospacer sequence, and the adjacent thin red box indicates the extended PAM sequence.

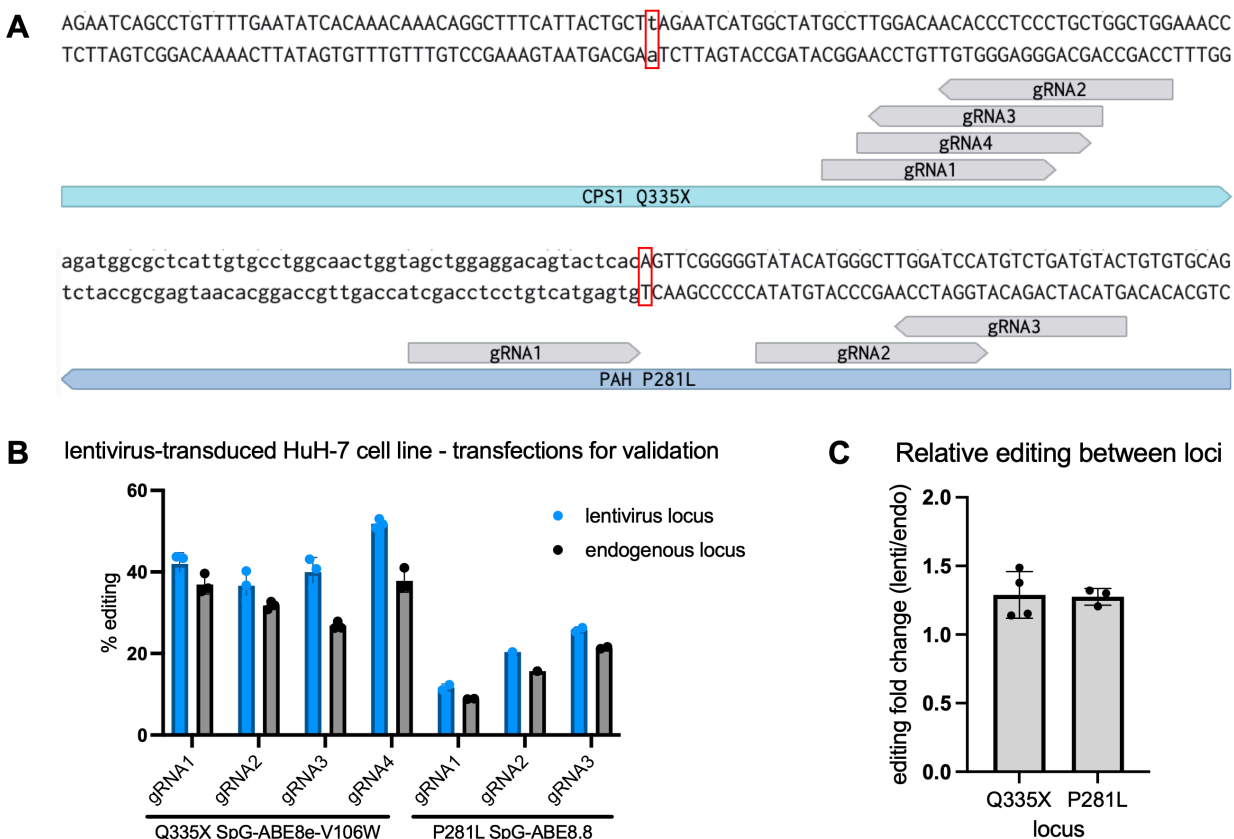


Figure S7. Calibration of Adenine Base Editing Between Lentiviral Cassettes and Endogenous Loci.

Panel A shows the *CPS1* Q335X variant sequence and the *PAH* P281L variant sequence, with the variant adenines indicated by red boxes, and the tested gRNAs targeting adjacent to but not overlapping the variant adenines. Panel B shows the overall editing with each of the gRNAs and the specified ABEs in the lentiviral cassette and in the endogenous locus, measured in the same cells. Panel C shows the ratios of lentivirus cassette editing to endogenous locus editing with the gRNAs across the two loci, averaging ≈ 1.25 in each locus.

Editing in lentivirus-transduced HuH-7 cells treated with clinical batch of k-abe

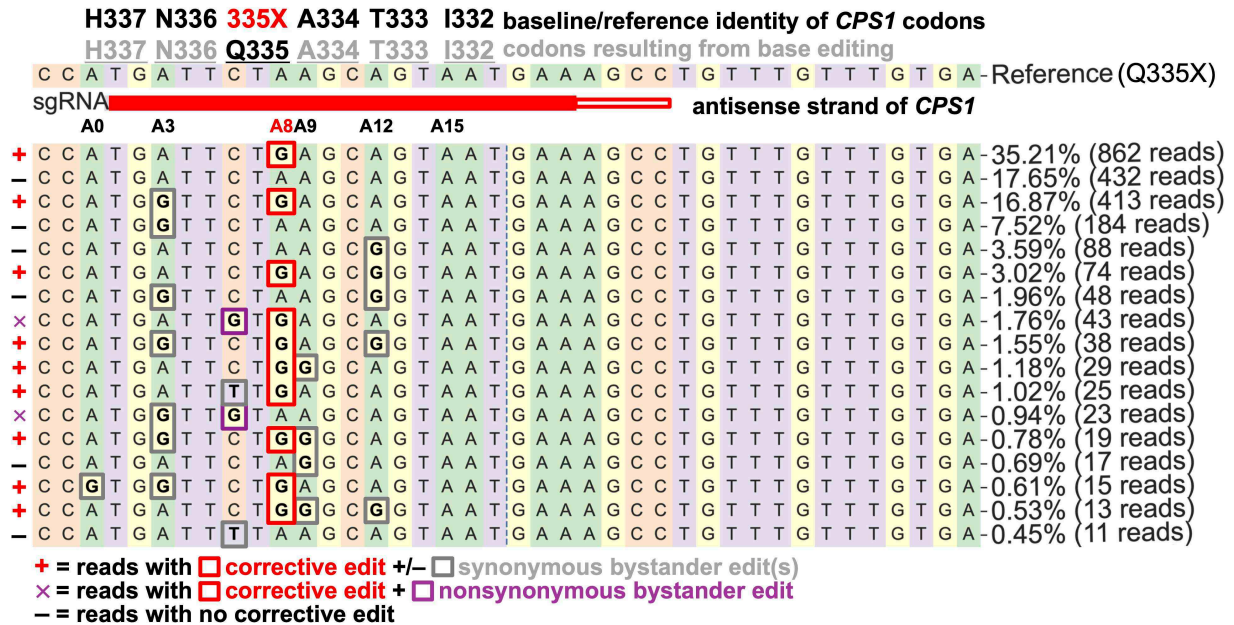


Figure S8. Corrective Editing of *CPS1* Q335X Variant After Treatment of HuH-7 Cells with Clinical Batch of K-abe.

Standard CRISPResso2 NGS output for the editing in the sample from the k-abe-treated Q335X lentivirus-transduced HuH-7 cells that displayed the highest level of editing in **Fig. 2C**. The codons in the vicinity of the Q335X site are indicated; the top-listed amino acid is the baseline/reference identity of the codon, and the bottom-listed amino acid is the one that results from base editing of the adenine in the codon. The red horizontal bar indicates the kayjayguran protospacer sequence, and the adjacent thin red box indicates the extended PAM sequence.

Mosaic alleles in founder *Cps1*-Q335X mouse

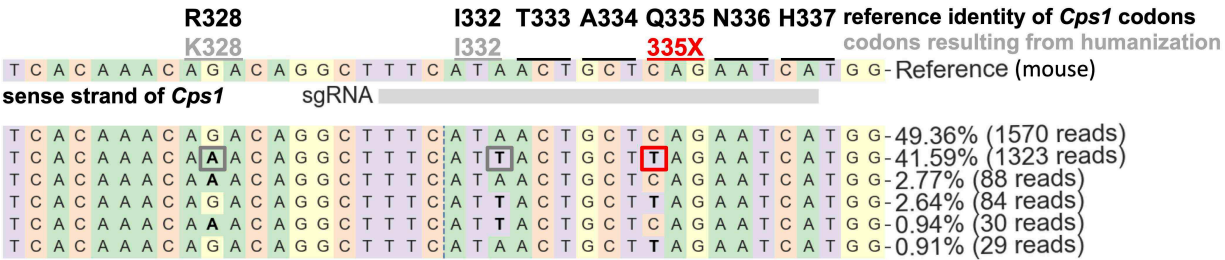


Figure S9. Founder Mouse with Humanized *Cps1* Q335X Allele.

Standard CRISPResso2 NGS output for the editing in a genomic DNA sample from a founder pup derived from a mouse zygote into which CRISPR-Cas9 and a single-strand DNA oligonucleotide with the human Q335X target sequence with homology arms matched to the endogenous *Cps1* gene were injected. The codons in the vicinity of the Q335X site are indicated; the top-listed amino acid is the reference identity of the codon (wild-type mouse ortholog), and the bottom-listed amino acid is the one that results from CRISPR-Cas9-mediated editing (humanized sequence). The grey horizontal bar indicates the span of the humanized sequence targeted by the kayjayguran gRNA, with almost half of the alleles in the mouse sample bearing the humanized sequence in that span. The red square indicates the human pathogenic variant, and the grey squares indicate additional changes that humanize the sequence.

In vivo liver editing in *Rosa26-Q335X* mice treated with toxicology batch of k-abe

H337 N336 **335X** A334 T333 I332 baseline/reference identity of *CPS1* codons

H337 N336 **Q335** A334 T333 I332 codons resulting from base editing

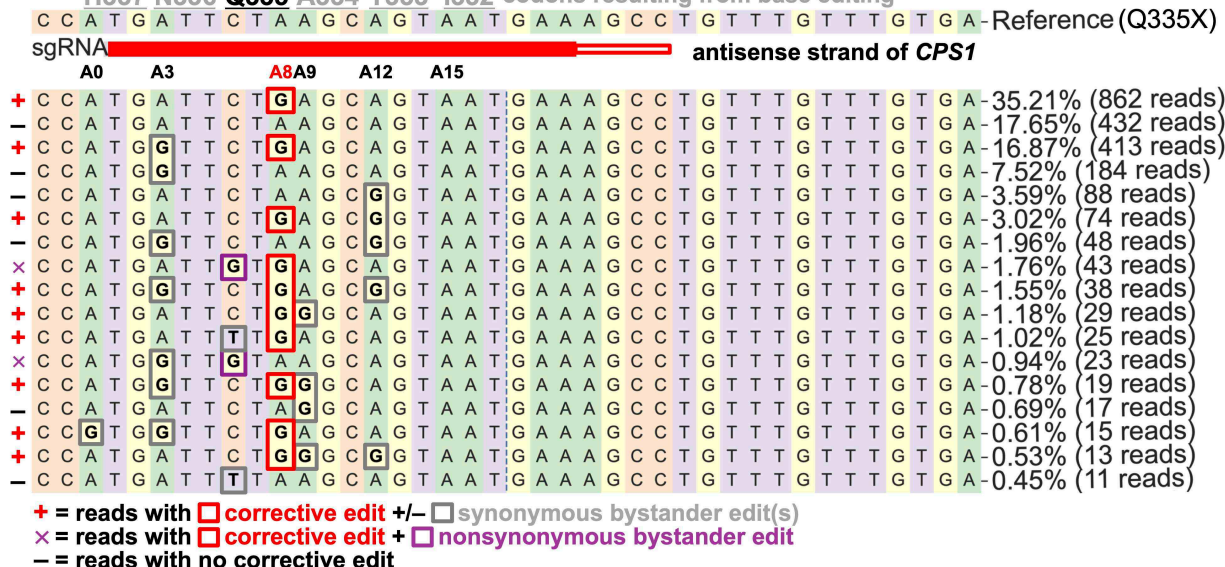


Figure S10. Corrective Editing of *CPS1* Q335X Variant After Treatment of *Rosa26-Q335X* Transgenic Mouse with Toxicology Batch of K-abe.

Standard CRISPResso2 NGS output for the editing in a representative liver sample from a *Rosa26-Q335X* mouse treated with a 3 mg/kg dose of k-abe. The codons in the vicinity of the Q335X site are indicated; the top-listed amino acid is the baseline/reference identity of the codon, and the bottom-listed amino acid is the one that results from base editing of the adenine in the codon. The red horizontal bar indicates the kayjayguran protospacer sequence, and the adjacent thin red box indicates the extended PAM sequence.

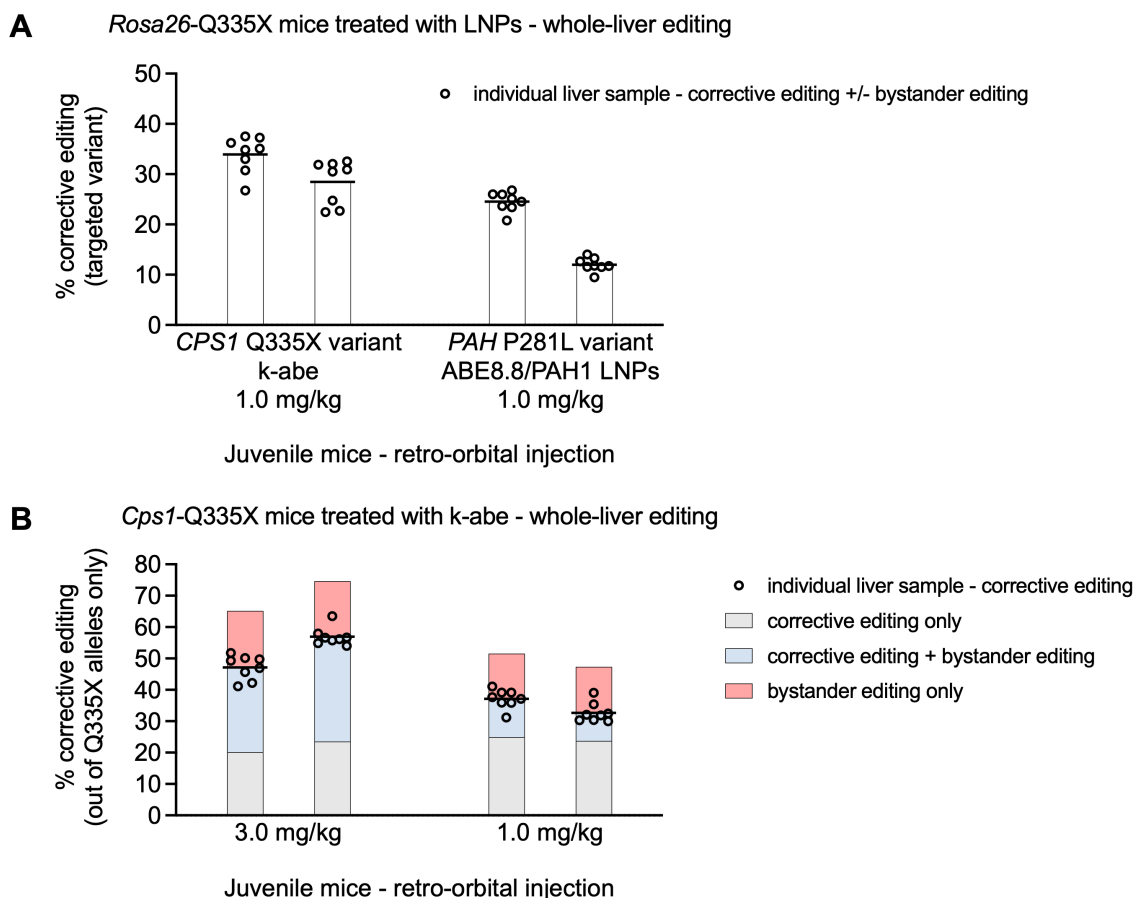


Figure S11. Whole-liver Editing of *Rosa26*-Q335X Transgenic Mice and *Cps1*-Q335X Knock-in Mice After Lipid Nanoparticle Treatment.

Panel A, on the right-hand side of the graph, shows whole-liver corrective editing of the *PAH* P281L variant sequence incorporated into the *Rosa26* locus in F1 *Rosa26*-Q335X mice (**Fig. 2A**), following a single treatment with ABE8.8/PAH1 LNPs at a 1.0 mg/kg dose. Each mouse had multiple liver samples, distributed throughout the liver, collected upon necropsy (N = 8 samples per mouse in juvenile mice treated at 1-2 months of age, with necropsy several days after treatment) and assessed with NGS of the *PAH* P281L variant sequence in the *Rosa26* locus. There was minimal bystander editing. The *PAH* P281L variant served as a positive reference control, as was the case with Q335X lentivirus-transduced HuH-7 cells (**Fig. S2A**); ABE8.8/PAH1 is the optimized ABE/gRNA solution for the P281L variant.² For comparison, on the left-hand side of the graph are the same data shown in **Fig. 2B** for the 1.0 mg/kg dose of the toxicology batch of k-abe, i.e., data from a separate experiment that had previously been performed with F1 *Rosa26*-Q335X mice of roughly the same age. Although in vitro editing of the *CPS1* Q335X variant and the *PAH* P281L variant with plasmid transfections of the lentivirus-transduced HuH-7 cells was of comparable efficiency (**Fig. S2D**), predicting that in vivo editing of the variants would be similar, the discrepancy observed in vivo might have been due to differences in the LNP formulations: k-abe was manufactured to a much higher quality standard (clinical-grade process and scale) in a different facility than the ABE8.8/PAH1 LNPs (research-grade process at a small scale). Panel B shows whole-liver corrective and/or bystander editing of the endogenous Q335X variant sequence in F1 *Cps1*-Q335X mice, following a single treatment with the toxicology batch of k-abe at the indicated dose. Each mouse had multiple liver samples, distributed throughout the liver, collected upon necropsy (N = 8 samples per mouse in juvenile mice treated at 1 month of age, with necropsy several days after treatment) and assessed with NGS of the endogenous *Cps1* locus.

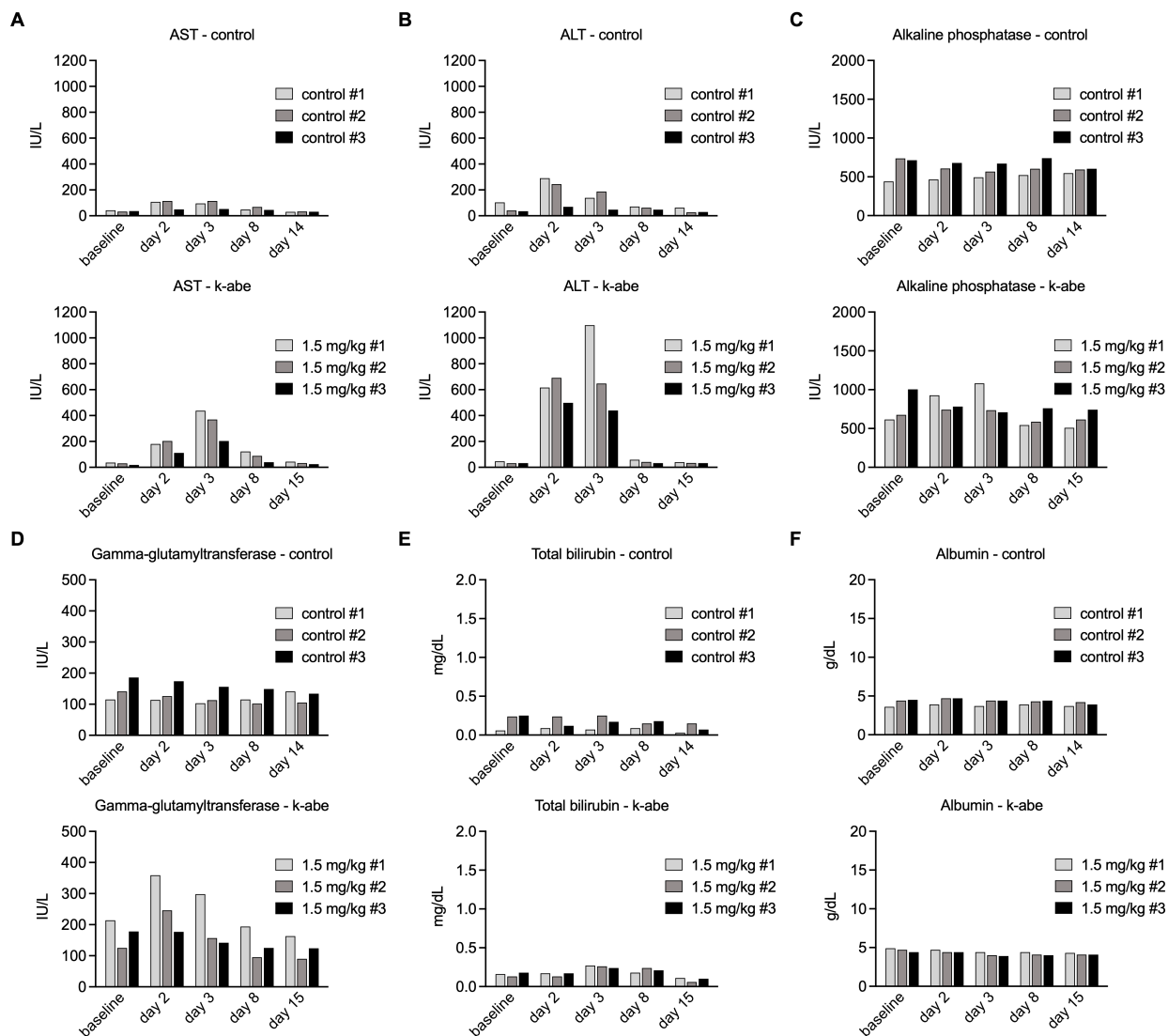


Figure S12. Serum Enzymes/Liver Function Tests in Cynomolgus Monkeys Treated with Vehicle Control or with K-abe.

Following a single treatment, each monkey in Group 1 (PBS vehicle control) or Group 3 (1.5 mg/kg of the toxicology batch of k-abe) had multiple blood collections during the 2-week post-treatment observation period. Aspartate aminotransferase (AST) (panel A), alanine aminotransferase (ALT) (panel B), alkaline phosphatase (panel C), gamma-glutamyltransferase (GGT) (panel D), total bilirubin (panel E), and albumin (panel F) levels were measured.

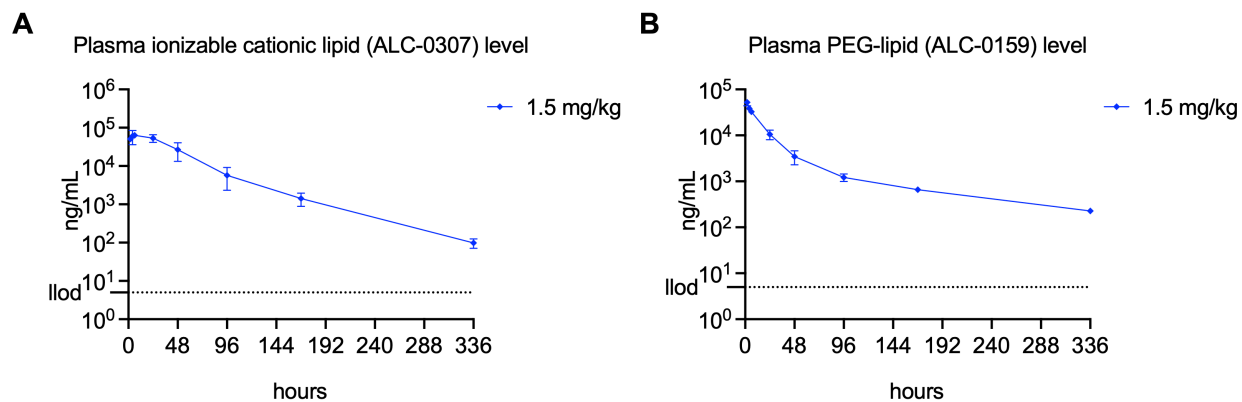


Figure S13. Plasma Lipid Excipients in Cynomolgus Monkeys Treated with K-abe.

Following a single treatment, each monkey in Group 3 (1.5 mg/kg of the toxicology batch of k-abe) had multiple blood collections during the 2-week post-treatment observation period. Ionizable cationic lipid (panel A) and PEG-lipid (panel B) levels were measured.

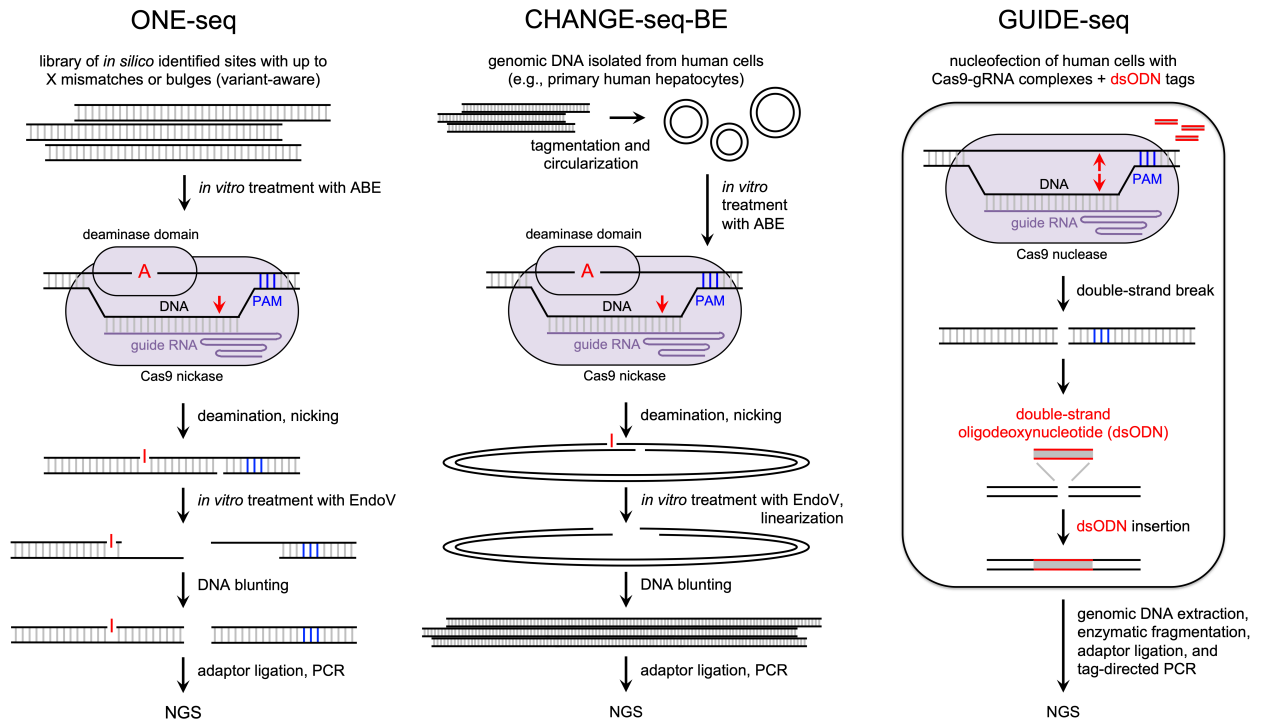


Figure S14. Three Off-target Site Nomination Methods.

These methods nominate candidate off-target sites, which are subsequently evaluated to verify whether off-target editing genuinely occurs at the sites in target cells.

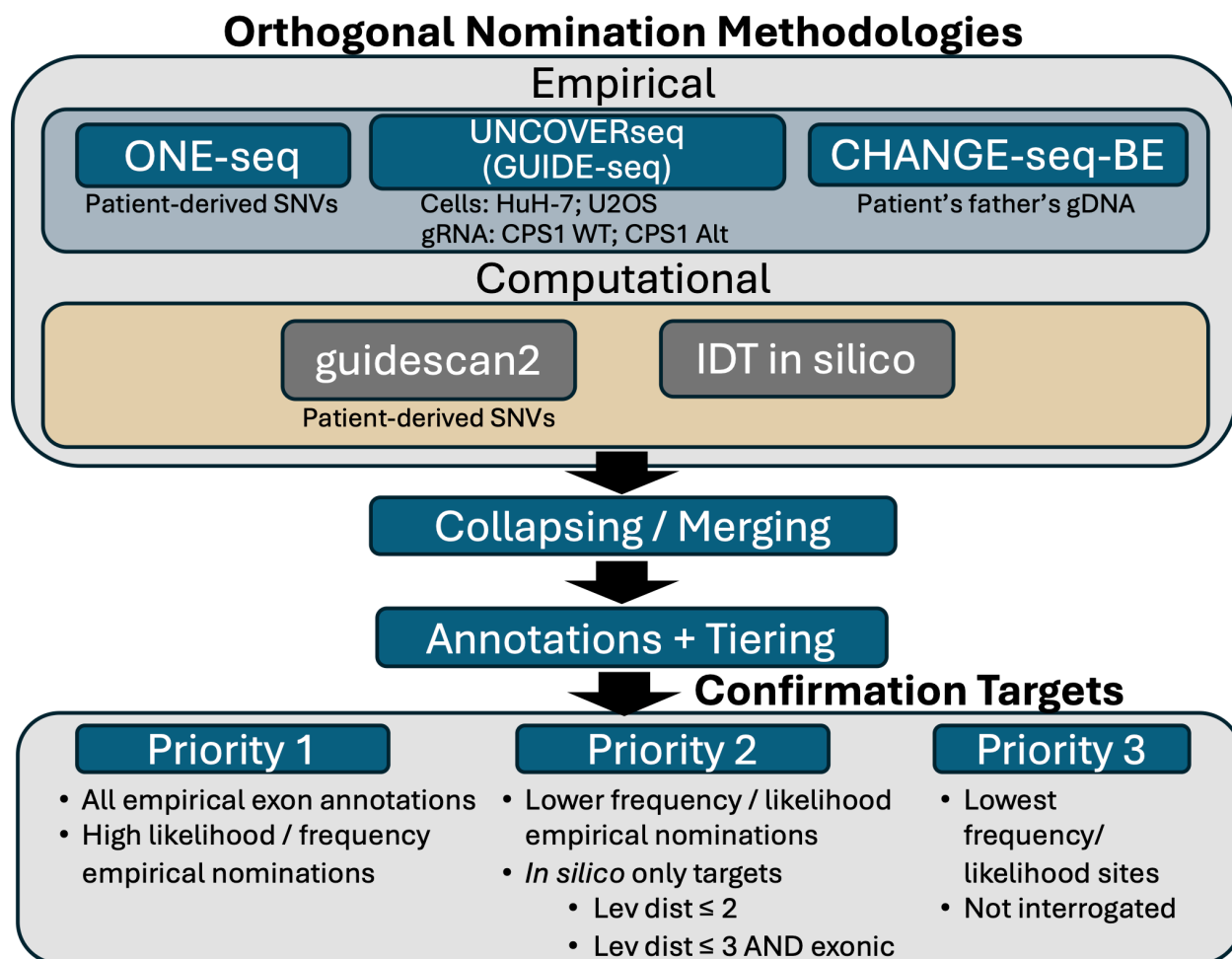


Figure S15. Off-target Nomination Workflow

Overview of the workflow consolidating and prioritizing off-target site lists from three empirical and two computational off-target nomination methodologies based on impact/risk and event likelihood.

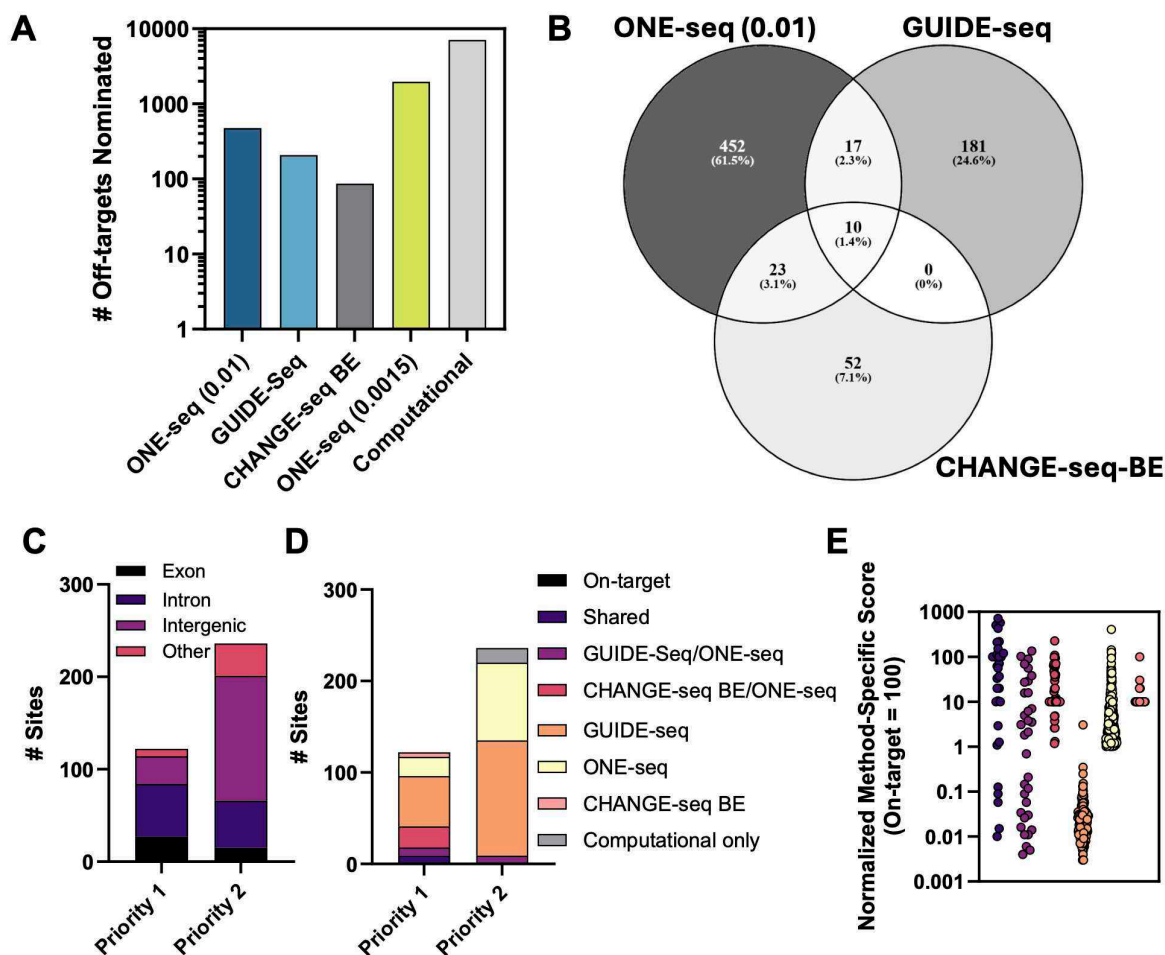


Figure S16. Determination of Candidate Off-target Site List.

Panel A shows the total candidate off-target sites quantified by each methodology at relevant nomination stringency thresholds. Panel B shows the overlap of sites nominated by different empirical methodologies. Following prioritization, the number of candidate off-target sites grouped into the top two prioritized bins had (panel C) the genomic feature annotations, (panel D) assay origin, and (panel E) the normalized frequency of the sites in each unique empirical overlap subset determined. It is important to note that while these frequencies were normalized, they were not necessarily comparable since the sensitivities, read frequencies, and reporting methodologies differed significantly among methods.

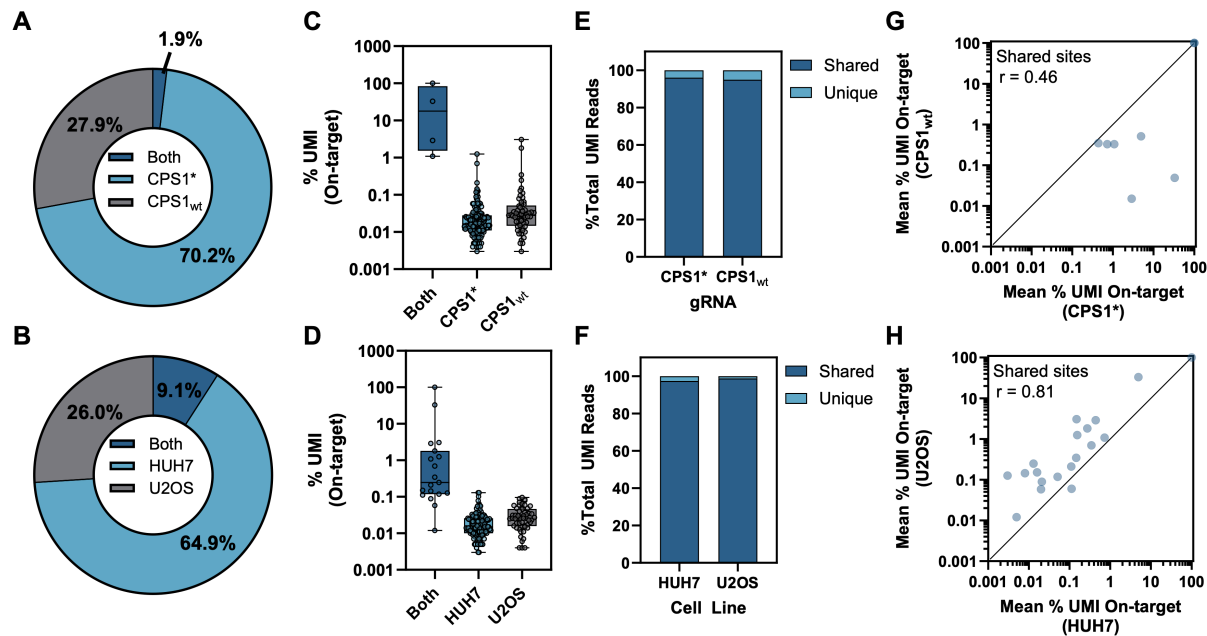


Figure S17. Origin of UNCOVERseq-nominated Sites.

The origin of 208 sites nominated by UNCOVERseq/GUIDE-seq is shown as it pertains to the gRNA (CPS1* versus CPS1_{wt}; panels A, C, E, and G) and cell line (HuH-7 versus U2OS; panels B, D, F, and H) used for the experimental condition. Panels A and B show the fractions of total off-target sites nominated, and panels C and D show the nomination frequencies of the off-target sites, under the different conditions. Panels E and F show the fractions of total UMI reads that were shared or unique between the different conditions, and panels G and H compare the shared site nomination frequencies.

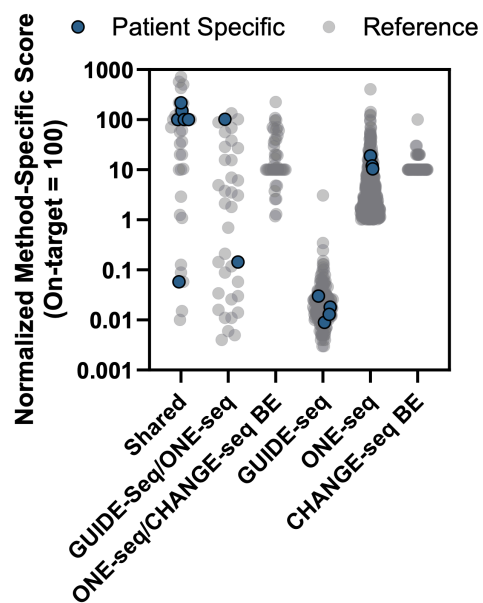


Figure S18. Nomination Frequencies of Sites with Patient-specific Variants.

Nominations from ONE-seq (normalized score > 1), CHANGE-seq-BE (all sites), and UNCOVERseq/GUIDE-seq (all sites) had their frequencies normalized to 100 (on-target frequency = 100) per method, and frequencies were compared between methods. Sites selected in Priority 1 and Priority 2 panels with patient-specific variants are highlighted in blue.

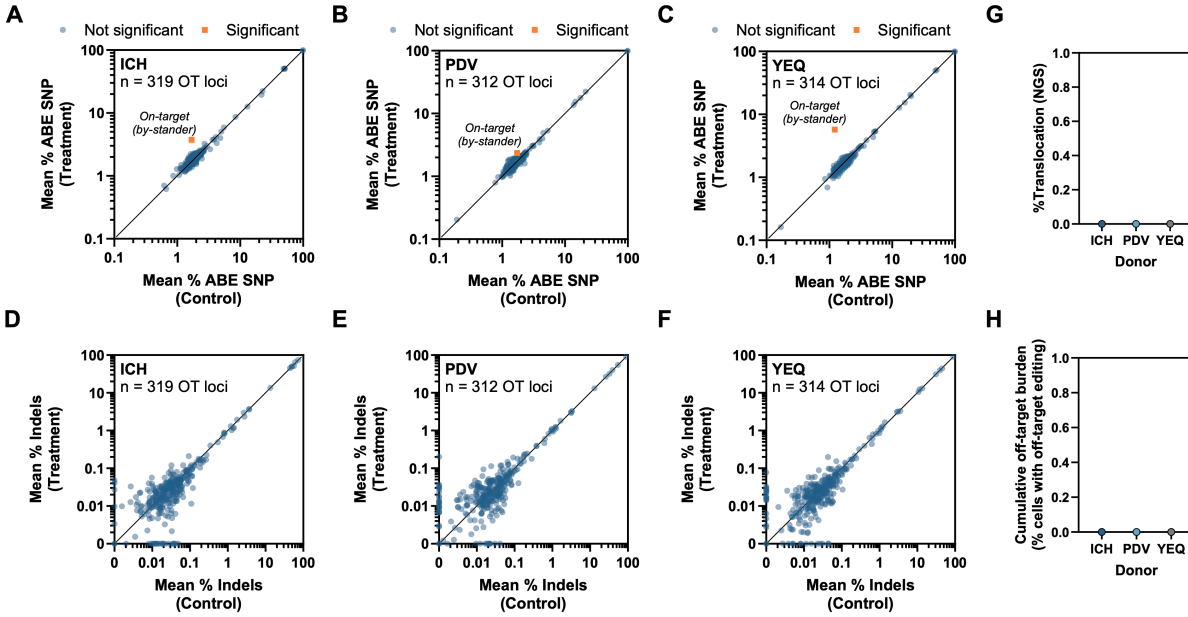


Figure S19. Candidate Off-target Site Verification in Primary Human Hepatocytes.

Evaluation of a prioritized subset of candidate off-target sites with >1000× read depth coverage for (panels A-C) adenine-to-guanine editing, (panels D-F) non-homologous end-joining (NHEJ)-induced indel editing, and (panel G) on-target:off-target/off-target:off-target translocations via multiplexed targeted amplicon sequencing in untreated cells versus cells treated with k-abe, at 1000 ng per milliliter of media, of three different PHH types: donor ICH (13 months of age, male), donor PDV (7 weeks of age, male), and donor YEQ (6 months of age, male). Low-level synonymous bystander editing was evident at the endogenous wild-type *CPS1* Q335 site in all three PHH types due to the kayjayguran gRNA having a 1-base mismatch to the wild-type sequence. Panel H shows cumulative off-target editing for each PHH type, with no significant off-target base editing, indel editing, or translocations observed for target sites meeting classification requirements.

Table S1. Guide RNA Sequence.

kayjayguran	5'- <u>usgsas</u> UUCUAAGCAGUAAUGAAGUUUUAGAgcuagaaaauagcAAGUUAAAAUAAGG CUAGUCCGUUAUCAacuugaaaaaguggcaccgagucggugcusususu-3'

Abbreviations: A = adenosine; a = 2'-O-methyladenosine; C = cytidine; c = 2'-O-methylcytidine; G = guanosine; g = 2'-O-methylguanosine; U = uridine, u = 2'-O-methyluridine; s = phosphorothioate backbone linkage. Underline indicates spacer sequence.

Table S2. Abengcemeran mRNA Sequence, not Including 5' Cap or 3' Polyadenylate Tail, and Protein Sequence.

NGC-ABE8e-V106W mRNA	AGCAΨAAAAGΨCΨCAACACAACAΨAΨACAAAACAAACGAAΨCΨCAAGCAAΨCAAGCA ΨΨCΨACΨΨCΨAΨΨGCAGCAAΨΨΨAAAΨCAΨΨCΨΨΨΨAAAAGCAAAGCAAΨΨΨ ΨCΨGAAAAΨΨΨΨCACCACΨΨΨACGAACGAΨAGCGCΨGCCACCAΨGAAGCGCACCG CCGACGGCΨCCGAGΨΨCGAGΨCCOCCAAGAAGAAGCGCAAGGΨGΨCCGAGGΨGG AGΨΨCΨCCCACGAGΨACΨGGAΨGCGCCACGCCCΨGACCCΨGGCCAAGCGCGCCC GCGACGAGCGCGAGGΨGCCCGΨGGGCGCCGΨGCΨGGΨGCΨGAACAACCGCGΨGA ΨCGGCGAGGGCΨGGAACCGCGCCAΨCGGCCΨGCACGACCCACCGCCCACGCCGA GAΨCAΨGGCCCΨGCGCCAGGGCGGCCΨGGΨGAΨGCAGAACΨACCGCCΨGAΨCGA CGCCACCCΨGΨACGΨGACCΨΨCGAGCCCΨGCGΨGAΨGΨGCGCCGGCGCCAΨGA ΨCCACΨCCCGCAΨCGGCCGCGΨGGΨGΨΨCGGCΨGGCGCAACΨCCAAGCGCGGGC CCGCCGGCΨCCCΨGAΨGAACGΨGCΨGAACΨACCCCGGCAΨGAACCACCGCGΨGG AGAΨCACCGAGGGCAΨCCΨGGCCGACGAGΨGCGCCGCCCΨGCΨGΨGCGACΨΨCΨ ACCGCAΨGCCCCGCCAGGΨGΨΨCAACGCCCAGAAGAAGGCCCAGΨCCΨCCAΨCAA CΨCCGGCGGGCΨCCΨCCGGCGGGCΨCCΨCCGGCΨCCGAGACCCCGGCACCCΨCCGA GΨCCGCCACCCCGAGΨCCΨCCGGCGGGCΨCCΨCCGGCGGGCΨCCGACAAGAAGΨA CΨCCAΨCGGCCΨGGCCAΨCGGCACCAACΨCCGΨGGGCΨGGGCCGΨGAΨCACCGA CGAGΨACAAGGΨGCCCΨCCAAGAAGΨΨCAAGGΨGCΨGGGCAACACCGACCGCCAC ΨCCAΨCAAGAAGAACCΨGAΨCGGCGCCCΨGCΨGΨΨCGACΨCCGGCGAGACCGCC GAGGCCACCCGCCΨGAAGCGCACCGCCCGCCGCCGΨACACCCGCCGCAAGAACC GCAΨCΨGCΨACCΨGCAGGAGAΨCΨΨCΨCCAACGAGAΨGGCCAAGGΨGGACGACΨ CCΨΨCΨΨCCACCGCCΨGGAGGAGΨCCΨΨCCΨGGΨGGAGGAGGACAAGAAGCACG AGCGCCACCCCAΨCΨΨCGGCAACAΨCGΨGGACGAGGΨGGCCΨACCACGAGAAGΨA CCCCACCAΨCΨACCACCΨGCGCAAGAAGCΨGGΨGGACΨCCACCGACAAGGCCGAC CΨGCGCCΨGAΨCΨACCΨGGCCCΨGGCCCACAΨGAΨCAAGΨΨCCGCGGCCACΨΨC CΨGAΨCGAGGGCGACCCΨGAACCCCGACAACΨCCGACGΨGGACAAGCΨGΨΨCAΨC CAGCΨGGΨGCAGACCΨACAACGAGCΨGΨΨCGAGGAGAACCCCAΨCAACGCCΨCCG CGCΨGGACGCCAAGGCCAΨCCΨGΨCCGCCCGCCΨGΨCCAAGΨCCCGCCGCCΨGG AGAACCΨGAΨCGCCAGCΨGCCCGCGAGAAGAAGAACGGCCΨGΨΨCGGCAACCΨ GAΨCGCCCΨGΨCCCΨGGGCCΨGACCCCAACΨΨCAAGΨCCAACΨΨCGACCΨGGC CGAGGACGCCAAGCΨGCAGCΨGΨCCAAGGACACCΨACGACGACGACCΨGGACAAC CΨGCΨGGCCCAGAΨCGGCGACCCAGΨACGCCGACCΨGΨΨCCΨGGCCGCCAAGAAC CΨGΨCCGACGCCAΨCCΨGCΨGΨCCGACAΨCCΨGCGCGΨGAACACCGAGAΨCACC AAGGCCCCCCΨGΨCCGCCΨCCAΨGAΨCAAGCGGΨACGACGAGCACCACCAGGACC ΨGACCCΨGCΨGAAGGCCΨGGΨGCGCCAGCAGCΨGCCCGAGAAGΨACAAGGAGA ΨCΨΨCΨΨCGACCAGΨCCAAGAACGGCΨACGCCGGCΨACAΨCGACGGCGGGCGCCΨ CCCAGGAGGAGΨΨCΨACAAGΨΨCAΨCAAGCCCAΨCCΨGGAGAAGAΨGGACGGCAC CGAGGAGCΨGCΨGGΨGAAGCΨGAACCGCGAGGACCΨGCΨGCGCAAGCAGCGCAC CΨΨCGACAACGGCΨCCAΨCCCCCACCAGAΨCCACCΨGGGCGAGCΨGCACGCCAΨC CΨGCGCCGCCAGGAGGACΨΨCΨACCCΨΨCCΨGAAGGACAACCGCGAGAAGAΨC GAGAAGAΨCCΨGACCΨΨCCGCAΨCCCCΨACΨACGΨGGGCCCCCΨGGCCCGCGGC AACΨCCCGCΨΨCGCCΨGGAΨGACCCGCAAGΨCCGAGGAGACCAΨCACCCCCΨGGA ACΨΨCGAGGAGGΨGGΨGGACAAGGGCGCCΨCCGCCCAGΨCCΨΨCAΨCGAGCGCA ΨGACCAACΨΨCGACAAGAACCΨGCCCAACGAGAAGGΨGCΨGCCCAAGCACΨCCCΨ GCΨGΨACGAGΨACΨΨCACCGΨGΨACAACGAGCΨGACCAAGGΨGAAGΨACGΨGAC CGAGGGCAΨGCGCAAGCCCGCCΨΨCCΨGΨCCGGCGAGCAGAAGAAGGCCAΨCGΨ GGACCΨGCΨGΨΨCAAGACCAACCGCAAGGΨGACCGΨGAAGCAGCΨGAAGGAGGAC ΨACΨΨCAAGAAGAΨCGAGΨGCΨΨCGACΨCCGΨGGAGAΨCΨCCGGCGΨGGAGGAC CGCΨΨCAACGCCΨCCCΨGGGCACCΨACCACGACCΨGCΨGAAGAΨCAΨCAAGGACA AGGACΨΨCCΨGGACAACGAGGAGAACGAGGACAΨCCΨGGAGGACAΨCGΨGCΨGA CCCΨGACCCΨGΨΨCGAGGACCGCGAGAΨGAΨCGAGGAGCGCCΨGAAGACCΨACG CCACCCΨGΨΨCGACGACAAGGΨGAΨGAAGCAGCΨGAAGCGCCCGCCGΨACACCG CΨGGGGCCGCCΨGΨCCCGCAAGCΨGAΨCAACGGCAΨCCGCGACAAGCAGΨCCGG

	CAAGACCAΨCCΨGGACΨΨCCΨGAAGΨCCGACGGCΨΨCGCCAACCGCAACΨΨCAΨ GCAGCΨGAΨCCACGACGACΨCCCΨGACCΨΨCAAGGAGGACAΨCCAGAAGGCCAG GΨGΨCCGGCCAGGGCGACΨCCCΨGCACGAGCACAΨCGCCAACCΨGGCCGGCΨCC CCCGCCAΨCAAGAAGGGCAΨCCΨGCAGACCGΨGAAGGΨGGΨGGACGAGCΨGGΨG AAGGΨGAΨGGGCCGCCACAAGCCCCGAGAACAΨCGΨGAΨCGAGAΨGGCCCGCGAGA ACCAGACCACCCAGAAGGGCCAGAAGAACΨCCCGCGAGCGCAΨGAAGCGCAΨCGAG GAGGGCAΨCAAGGAGCΨGGGCΨCCCAGAΨCCΨGAAGGAGCACCCCGΨGGAGAACA CCCAGCΨGCAGAACGAGAAGCΨGΨACCΨGΨACΨACCΨGCAGAACGGCCCGCGACAΨ GΨACGΨGGACCAGGAGCΨGGACAΨCAACCGCCΨGΨCCGACΨACGACGΨGGACCA CAΨCGΨGCCCCAGΨCCΨΨCCΨGAAGGACGACΨCCAΨCGACAACAAGGΨGCΨGAC CCGCΨCCGACAAGAACCGCGGCAAGΨCCGACAACGΨGCCΨCCGAGGAGGΨGGΨ GAAGAAGAΨGAAGAACΨACΨGGCGCCAGCΨGCΨGAACGCCAAGCΨGAΨCACCCAG CGCAAGΨΨCGACAACCΨGACCAAGGCCGAGCGCGGGCGGCCΨGΨCCGAGCΨGGAC AAGGCCGGCΨΨCAΨCAAGCGCCAGCΨGGΨGGAGACCCGCCAGAΨCACCAGCACG ΨGGCCCAGAΨCCΨGGACΨCCCGCAΨGAACACCAAGΨACGACGAGAACGACAAGCΨ GAΨCCGCGAGGΨGAAGGΨGAΨCACCΨGAAGΨCCAAGCΨGGΨGΨCCGACΨΨCCG CAAGGACΨΨCCAGΨΨCΨACAAGGΨGCGCGAGAΨCAACAACΨACCACCACGCCAC GACGCCΨACCΨGAACGCCGΨGGΨGGGCACCGCCCΨGAΨCAAGAAGΨACCCCAAGC ΨGGAGΨCCGAGΨΨCGΨGΨACGGCGACΨACAAGGΨGΨACGACGΨGCGCAAGAΨGA ΨCGCCAAGΨCCGAGCAGGAGAΨCGGCAAGGCCACCGCCAAGΨACΨΨCΨΨCΨACΨ CCAACAΨCAΨGAACΨΨCΨΨCAAGACCGAGAΨCACCΨGGCCAACGGCGAGAΨCCG CAAGCGCCCCΨGAΨCGAGACCAACGGCGAGACCGGCGAGAΨCGΨGΨGGGACAAG GGCGCGACΨΨCGCCACCGΨGCGCAAGGΨGCΨGΨCCAΨGCCCCAGGΨGAACAΨC GΨGAAGAAGACCGAGGΨGCAGACCGGCGGCΨΨCΨCCAAGGAGΨCCAΨCCΨGCC AAGCGCAACΨCCGACAAGCΨGAΨCGCCCGCAAGAAGGACΨGGGACCCCAAGAAGΨ ACGGCGGCΨΨCCΨGΨGGCCACCGΨGGCCΨACΨCCGΨGCΨGGΨGGΨGGCCAAG GΨGGAGAAGGGCAAGΨCCAAGAAGCΨGAAGΨCCGΨGAAGGAGCΨGCΨGGGCAΨC ACCAΨCAΨGGAGCGGΨCCΨCCΨΨCGAGAAGAACCCCAΨCGACΨΨCCΨGGAGGCC AAGGGCΨACAAGGAGGΨGAAGAAGGACCΨGAΨCAΨCAAGCΨGCCCAAGΨACΨCCC ΨGΨΨCGAGCΨGGAGAACGGCCGCAAGCGCAΨGCΨGGCCΨCCGCCAAGΨACCΨGC AGAAGGGCAACGAGCΨGGCCCΨGCCCΨCCAAGΨACGΨGAACΨΨCCΨGΨACCΨGG CCΨCCCACΨACGAGAAGCΨGAAGGGCΨCCCCCGAGGACAACGAGCAGAAGCAGCΨ GΨΨCGΨGGAGCAGCACAAGCACΨACCΨGGACGAGAΨCAΨCGAGCAGAΨCΨCCGA GΨΨCΨCCAAGCGCGΨGAΨCCΨGGCCGACGCCAACCΨGGACAAGGΨGCΨGΨCCGC CΨACAACAAGCACCGCGACAAGCCCAΨCCGCGAGCAGGCCGAGAACAΨCAΨCCACC ΨGΨΨCACCCΨGACCAACCΨGGGCGCCCCCGCCGCCΨΨCAAGΨACΨΨCGACACCA CCAΨCGACCGCAAGCAGΨACΨCCΨCCACCAAGGAGGΨGCΨGGACGCCACCCΨGAΨ CCACCAGΨCCAΨCACCGGCCΨGΨACGAGACCCGCAΨCGACCΨGΨCCCAGCΨGGG CGGCGACΨCCGGCGGCΨCCAAGCGCACCGCCGACGGCΨCCGAGΨΨCGAGCCCAA GAAGAAGCGCAAGGΨGΨAAΨAAACΨAGΨAGΨGACΨGACΨAGGAΨCΨGGΨΨACCA CΨAAACCAGCCΨCAAGAACACCCGAAΨGGAGΨCΨCΨAAGCΨACAΨAAΨACCAACΨ ΨACACΨΨACAAAAΨGΨΨGΨCCCCAAAAΨGΨAGCCAΨΨCGΨAΨCΨGCΨCCΨAAΨ AAAAAGAAAGΨΨΨCΨΨCACAΨΨCΨ
NGC-ABE8e-V106W protein	MKRTADGSEFESPKKKRKVSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIG EGWNRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVV FGWRNSKRGAAGSLMNVLNYPGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKA QSSINSGGSSGGSSGSETPGTSESATPESSGGSSGSDKKYSIGLAIGTNSVGWAVITDE YKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFS NEMAKVDDSFHRLVESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKA DLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDITYDDDL DNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALV RQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRK QRTFDNGSIPHQIHLGELHAILRRQEDFYPLKDNREKIEKILTRIPYYVGPLARGNSRFAW MTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPHKSHLLYEYFTVYNELT

	KVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF NASLGTYHDLLKIIKD KDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQL KRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDLVKVMGRHKPENIVIAMARENQTTQKG QKNSRERMKRIEEGKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLS DYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKMKMKNYWRQLLNAKLITQR KFDNLTKAERGGELSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITL KSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVR KMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFAT VRKVL SMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSV LVVAKVEKGKSKKLKSVKELLGITIMERSSSFENPIDFLEAKGYKEVKKDLIIKLPKYSLFEE NGRKRMLASAKYLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLD EIIQISEFSKRVLADANLDKVL SAYNKHDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTID RKQYSSTKEVL DATLIHQ SITGLYETRIDLSQLGGDSGGSKRTADGSEFEPKKKRKV*

Ψ = N1-methylpseudouridine

Table S3. Off-target Editing in Q335X Lentivirus-transduced HuH-7 Cells Treated with 1000 ng/mL of Clinical Batch of K-abe.

Protospacer/PAM sequence ^a	Chromosome: location ^b	Closest gene	Genomic location	CHANGE-seq-BE ^c	ONE-seq ^d	GUIDE-seq ^e	Treated sample 1 ^f	Treated sample 2	Treated sample 3	Control sample 1	Control sample 2	Control sample 3	Mean net editing % ^g
TGATTCTAAGCAGTAATGAAAGC	lentiviral insert	—	—	10/10	1.00	—	63.62	58.59	61.40	—	—	—	—
TGATTCTgAGCAGTAATGAAAGC	chr2:210591871	<i>CPS1</i>	exon	—	0.24	100%	2.70	2.74	3.42	0.09	0.10	0.09	+2.86
TctTTCaAAGCAaTAATGAAAGG	chr12:25111833	<i>DNAI7</i>	exon	—	0.02	—	0.05	0.04	0.06	0.03	0.05	0.04	+0.01
gGgTTCTAAaCAGTAATGAAAGT	chr4:140621583	<i>TBC1D9</i>	3'UTR	—	0.02	—	0.05	0.04	0.05	0.04	0.04	0.04	+0.00
TtAagCTAAGCAGTgATG-AAGA	chr2:99672551	<i>AFF3</i>	exon	—	0.01	—	0.07	0.07	0.10	0.08	0.10	0.10	-0.01
TaTTTCaTAAGCAGTAATGAAAGA	chr7:86879345	<i>ELAPOR2</i>	3'UTR	—	0.01	—	0.14	0.11	0.04	0.09	0.00	0.06	+0.05
TGATTaTAAG-AGTAATatATGT	chr13:33065694	<i>KL</i>	3'UTR	—	0.01	—	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
aGATTaTAAGCAGaAATtGAAGGC	chr12:122788878	<i>CCDC62</i>	exon	—	0.01	—	0.04	0.04	0.03	0.05	0.06	0.04	-0.01
aGAcTC-AAGCAGTAATGAAGGT	chr13:77205514	<i>MYCBP2</i>	exon	—	0.01	—	0.02	0.02	0.04	0.03	0.02	0.02	+0.00
TGATTaTAAGCAaTAATGtAAGC	chr17:14085182	<i>COX10</i>	intron	118/43	5.74	0.01%	0.08	0.05	0.03	0.06	0.05	0.09	-0.01
TGATaTcCaAAGCAGTAATGAATGT	chr13:51941585	<i>ATP7B</i>	intron	62/30	5.05	0.73%	0.52	0.60	0.51	0.19	0.14	0.17	+0.38
aGATaCTAAGCAGTAaAg-AAGA	chr10:106941006	<i>SORCS1</i>	intron	—	4.04	—	0.13	0.10	0.11	0.08	0.13	0.09	+0.01
TGATcCTAAG-AGTAATGAAGGA	chr2:7733230	—	intergenic	3/0	2.24	—	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
TaATTaTAAGaAGTAATGAACGC	chr18:2161220	—	intergenic	21/10	2.17	0.02%	0.04	0.07	0.01	0.06	0.06	0.06	-0.02
T-ATaCTAAGCAGTAATaAATGC	chrX:94310326	—	intergenic	—	1.42	—	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
TGATaCTgAGaAGTAATGAAGGA	chr2:88552100	<i>LOC101928371</i>	noncoding	—	1.34	—	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
TGATTtagAAGCAGTAATGAaggG	chr5:102333544	—	intergenic	—	1.25	—	0.11	0.08	0.08	0.07	0.09	0.09	+0.01
T-AcTCTAAGCAcTAATGAATGC	chr12:42377214	<i>PPHLN1</i>	intron	—	1.20	—	0.00	0.06	0.00	0.13	0.04	0.04	-0.05
aGATTaTAAGCAITaATG-AAGG	chr2:198087319	<i>PLCL1</i>	intron	14/10	1.11	0.01%	0.06	0.07	0.08	0.06	0.05	0.07	+0.01
TGATTCTAAGaAGTAATaAAAGA	chr6:28319171	—	intergenic	7/8	1.08	—	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
gacATCTAAGCAGTAATGAaAgAGA	chr22:33548899	<i>LARGE1</i>	intron	—	1.02	0.01%	0.02	0.03	0.05	0.05	0.06	0.06	-0.02
TATTTCTAAGCAGTAATGAAAGA	chr6:71690558	—	intergenic	21/21	—	4.94%	0.03	0.02	0.04	0.06	0.03	0.02	-0.01
AGATTCTAAGCAGTAATAAATCA	chr5:89092433	<i>MEF2C-AS1</i>	noncoding	17/6	—	—	0.05	0.08	0.16	0.10	0.10	0.05	+0.02

^aThe on-target sequence and candidate off-target sequences with mismatched positions and bulges indicated by lower case letters and dashes.

^bCoordinates in the GRCh38/hg38 assembly of the human genome. ^{c,d,e}Scores prior to the normalization shown in Fig. S16. ^fn.d. = PCR was unsuccessful for the genomic site. ^gMean net editing = mean editing in treated samples – mean editing in untreated samples; editing was calculated as (aligned reads with A>G edits in any of the first 10 positions of the protospacer ÷ total aligned reads). The black bold text indicates the endogenous wild-type *CPS1* Q335 site, and the red bold text indicates the site verified as a bona fide off-target site.

Table S4. Off-target Editing at *ATP7B* Intronic Site in Q335X Lentivirus-transduced HuH-7 Cells.

K-abe dose (diluted in cell medium)	Sample 1	Sample 2	Sample 3	Mean net % editing^a
untreated control cells	0.17	0.12	0.17	—
3.9 ng/mL	0.09	0.20	0.22	+0.02
7.8 ng/mL	0.17	0.23	0.14	+0.03
15.6 ng/mL	0.14	0.19	0.13	+0.00
31.3 ng/mL	0.29	0.18	0.28	+0.10
62.5 ng/mL	0.24	0.29	0.25	+0.11
125 ng/mL	0.56	0.24	0.25	+0.20
250 ng/mL	0.44	0.20	0.19	+0.12

^aMean net editing = mean editing in treated samples – mean editing in untreated samples; editing was calculated as (aligned reads with A>G edits in any of the first 10 positions of the protospacer + total aligned reads). The samples used for this analysis were from the k-abe dose-response study shown in **Fig. 2C**.

Table S5. mRNA Levels in Q335X Lentivirus-transduced HuH-7 Cells Versus Primary Human Hepatocytes.*

Two biological replicates for each cell type								
	HuH-7		PHH – ICH lot		PHH – PDV lot		PHH – YEQ lot	
Abengcemeran mRNA (normalized to HuH-7 cells)	1.01	0.99	4.89	7.62	4.47	2.94	7.50	6.29

*HuH-7 cells and PHHs from three donors were treated with the clinical batch of k-abe at a dose of 1000 ng/mL. Upon harvest, for each cell type two biological replicates were used for qRT-PCR analysis, with TaqMan gene expression assays (Thermo Fisher Scientific) specific for the abengcemeran mRNA and for human *GAPDH* (relative mRNA levels calculated with the $2^{-\Delta\Delta C_t}$ method), and three biological replicates were used for genomic DNA extraction and NGS analysis of candidate off-target sites, shown in **Table S3** and **Table S6**.

Table S6. Off-target Editing in Primary Human Hepatocytes Treated with 1000 ng/mL of Clinical Batch of K-abe.

Protospacer/PAM sequence ^a	Chromosome: location ^b	Closest gene	Genomic location	CHANGE-seq-BE ^c	ONE-seq ^d	GUIDE-seq ^e	Treated sample 1	Treated sample 2	Treated sample 3	Control sample 1	Control sample 2	Control sample 3	Mean net editing % ^f
PHH – ICH lot													
TGATTCTgAGCAGTAATGAAAGC	chr2:210591871	<i>CPS1</i>	exon	—	0.24	100%	0.23	0.85	1.04	0.21	0.11	0.08	+0.58
TctTTCaAAGCAaTAATGAAAGG	chr12:25111833	<i>DNAI7</i>	exon	—	0.02	—	0.05	0.05	0.03	0.06	0.04	0.03	+0.00
gGgTTCTAAaCAGTATGAAAGT	chr4:140621583	<i>TBC1D9</i>	3'UTR	—	0.02	—	0.04	0.04	0.04	0.04	0.06	0.04	–0.01
TtAagCTAAGCAGTgATG-AAGA	chr2:99672551	<i>AFF3</i>	exon	—	0.01	—	0.13	0.07	0.09	0.08	0.08	0.10	+0.01
TatTTCaTAAGCAGTATGAAAGA	chr7:86879345	<i>ELAPOR2</i>	3'UTR	—	0.01	—	0.05	0.07	0.05	0.05	0.03	0.10	–0.01
aGATTaTAAGCAGaAATGAAGGC	chr12:122788878	<i>CCDC62</i>	exon	—	0.01	—	0.05	0.02	0.06	0.05	0.04	0.05	+0.00
aGAcTC-AAGCAGTAATGAAGGT	chr13:77205514	<i>MYCBP2</i>	exon	—	0.01	—	0.05	0.05	0.03	0.02	0.04	0.02	+0.02
TGATTaTAAGCAaTAATGtAAGC	chr17:14085182	<i>COX10</i>	intron	118/43	5.74	0.01%	0.03	0.06	0.04	0.06	0.08	0.05	–0.02
TGATaCcAAGCAGTAATGAATGT	chr13:51941585	<i>ATP7B</i>	intron	62/30	5.05	0.73%	0.16	0.15	0.34	0.16	0.17	0.16	+0.05
aGATaCTAAGCAGTAaAaG-AAGA	chr10:106941006	<i>SORCS1</i>	intron	—	4.04	—	0.09	0.10	0.12	0.10	0.12	0.11	–0.01
TaATTaTAAGaAGTAATGAACGC	chr18:2161220	—	intergenic	21/10	2.17	0.02%	0.05	0.07	0.04	0.04	0.09	0.06	–0.01
TGATTtagAAGCAGTAATGAAGGG	chr5:102333544	—	intergenic	—	1.25	—	0.08	0.07	0.09	0.05	0.10	0.08	+0.00
T-AcTCTAAGCAcTAATGAATGC	chr12:42377214	<i>PPHLN1</i>	intron	—	1.20	—	0.03	0.00	0.21	0.14	0.05	0.00	+0.02
aGATTaTAAGCAITaATG-AAGG	chr2:198087319	<i>PLCL1</i>	intron	14/10	1.11	0.01%	0.07	0.07	0.08	0.08	0.09	0.08	–0.01
TGATTCTAAGaAGTAATaAAGA	chr6:28319171	—	intergenic	7/8	1.08	—	0.04	0.04	0.06	0.05	0.04	0.04	+0.01
TATTTCTAAGCAGTAATGAAAGA	chr6:71690558	—	intergenic	21/21	—	4.94%	0.04	0.03	0.07	0.04	0.04	0.05	+0.01
AGATTCTAAGCAGTAATAATCA	chr5:89092433	<i>MEF2C-AS1</i>	noncoding	17/6	—	—	0.07	0.06	0.05	0.07	0.09	0.07	–0.02
PHH – PDV lot													
TGATTCTgAGCAGTAATGAAAGC	chr2:210591871	<i>CPS1</i>	exon	—	0.24	100%	0.31	0.30	0.55	0.07	0.09	0.07	+0.31
TctTTCaAAGCAaTAATGAAAGG	chr12:25111833	<i>DNAI7</i>	exon	—	0.02	—	0.04	0.07	0.06	0.05	0.04	0.04	+0.01
gGgTTCTAAaCAGTATGAAAGT	chr4:140621583	<i>TBC1D9</i>	3'UTR	—	0.02	—	0.03	0.02	0.04	0.03	0.04	0.04	–0.01
TtAagCTAAGCAGTgATG-AAGA	chr2:99672551	<i>AFF3</i>	exon	—	0.01	—	0.08	0.09	0.10	0.08	0.08	0.10	+0.01
TatTTCaTAAGCAGTATGAAAGA	chr7:86879345	<i>ELAPOR2</i>	3'UTR	—	0.01	—	0.08	0.07	0.06	0.05	0.09	0.07	+0.00
aGATTaTAAGCAGaAATGAAGGC	chr12:122788878	<i>CCDC62</i>	exon	—	0.01	—	0.07	0.05	0.03	0.07	0.06	0.07	–0.01
aGAcTC-AAGCAGTAATGAAGGT	chr13:77205514	<i>MYCBP2</i>	exon	—	0.01	—	0.04	0.03	0.03	0.02	0.02	0.03	+0.00
TGATTaTAAGCAaTAATGtAAGC	chr17:14085182	<i>COX10</i>	intron	118/43	5.74	0.01%	0.03	0.02	0.04	0.05	0.03	0.04	–0.01
TGATaCcAAGCAGTAATGAATGT	chr13:51941585	<i>ATP7B</i>	intron	62/30	5.05	0.73%	0.11	0.19	0.21	0.14	0.15	0.17	+0.02
aGATaCTAAGCAGTAaAaG-AAGA	chr10:106941006	<i>SORCS1</i>	intron	—	4.04	—	0.12	0.09	0.11	0.11	0.14	0.11	–0.01
TaATTaTAAGaAGTAATGAACGC	chr18:2161220	—	intergenic	21/10	2.17	0.02%	0.04	0.05	0.07	0.06	0.06	0.05	+0.00
TGATTtagAAGCAGTAATGAAGGG	chr5:102333544	—	intergenic	—	1.25	—	0.11	0.07	0.10	0.09	0.14	0.11	–0.02
T-AcTCTAAGCAcTAATGAATGC	chr12:42377214	<i>PPHLN1</i>	intron	—	1.20	—	0.07	0.00	0.07	0.00	0.13	0.03	–0.01
aGATTaTAAGCAITaATG-AAGG	chr2:198087319	<i>PLCL1</i>	intron	14/10	1.11	0.01%	0.05	0.09	0.07	0.08	0.07	0.08	–0.01
TGATTCTAAGaAGTAATaAAGA	chr6:28319171	—	intergenic	7/8	1.08	—	0.04	0.05	0.05	0.04	0.06	0.06	–0.01
TATTTCTAAGCAGTAATGAAAGA	chr6:71690558	—	intergenic	21/21	—	4.94%	0.03	0.04	0.03	0.02	0.05	0.03	+0.00
AGATTCTAAGCAGTAATAATCA	chr5:89092433	<i>MEF2C-AS1</i>	noncoding	17/6	—	—	0.08	0.04	0.07	0.09	0.06	0.07	–0.01
PHH – YEQ lot													
TGATTCTgAGCAGTAATGAAAGC	chr2:210591871	<i>CPS1</i>	exon	—	0.24	100%	2.24	2.59	2.49	0.09	0.07	0.10	+2.36
TctTTCaAAGCAaTAATGAAAGG	chr12:25111833	<i>DNAI7</i>	exon	—	0.02	—	0.05	0.04	0.05	0.05	0.06	0.04	+0.00
gGgTTCTAAaCAGTATGAAAGT	chr4:140621583	<i>TBC1D9</i>	3'UTR	—	0.02	—	0.03	0.02	0.04	0.04	0.03	0.04	+0.00
TtAagCTAAGCAGTgATG-AAGA	chr2:99672551	<i>AFF3</i>	exon	—	0.01	—	0.07	0.07	0.10	0.08	0.07	0.10	–0.01
TatTTCaTAAGCAGTATGAAAGA	chr7:86879345	<i>ELAPOR2</i>	3'UTR	—	0.01	—	0.03	0.06	0.04	0.11	0.09	0.11	–0.06
aGATTaTAAGCAGaAATGAAGGC	chr12:122788878	<i>CCDC62</i>	exon	—	0.01	—	0.05	0.06	0.07	0.05	0.08	0.06	+0.00
aGAcTC-AAGCAGTAATGAAGGT	chr13:77205514	<i>MYCBP2</i>	exon	—	0.01	—	0.04	0.04	0.02	0.02	0.03	0.01	+0.01
TGATTaTAAGCAaTAATGtAAGC	chr17:14085182	<i>COX10</i>	intron	118/43	5.74	0.01%	0.04	0.03	0.04	0.05	0.03	0.03	+0.00
TGATaCcAAGCAGTAATGAATGT	chr13:51941585	<i>ATP7B</i>	intron	62/30	5.05	0.73%	0.15	0.22	0.15	0.17	0.11	0.12	+0.04
aGATaCTAAGCAGTAaAaG-AAGA	chr10:106941006	<i>SORCS1</i>	intron	—	4.04	—	0.13	0.11	0.11	0.10	0.11	0.10	+0.01
TaATTaTAAGaAGTAATGAACGC	chr18:2161220	—	intergenic	21/10	2.17	0.02%	0.06	0.07	0.06	0.06	0.04	0.05	+0.01
TGATTtagAAGCAGTAATGAAGGG	chr5:102333544	—	intergenic	—	1.25	—	0.09	0.10	0.10	0.07	0.10	0.10	+0.01
T-AcTCTAAGCAcTAATGAATGC	chr12:42377214	<i>PPHLN1</i>	intron	—	1.20	—	0.00	0.00	0.00	0.11	0.15	0.07	–0.11
aGATTaTAAGCAITaATG-AAGG	chr2:198087319	<i>PLCL1</i>	intron	14/10	1.11	0.01%	0.08	0.07	0.06	0.07	0.07	0.07	+0.00
TGATTCTAAGaAGTAATaAAGA	chr6:28319171	—	intergenic	7/8	1.08	—	0.05	0.05	0.05	0.05	0.04	0.06	+0.00
TATTTCTAAGCAGTAATGAAAGA	chr6:71690558	—	intergenic	21/21	—	4.94%	0.04	0.02	0.03	0.02	0.07	0.06	–0.02
AGATTCTAAGCAGTAATAATCA	chr5:89092433	<i>MEF2C-AS1</i>	noncoding	17/6	—	—	0.11	0.07	0.06	0.07	0.05	0.07	+0.02

^aThe candidate off-target sequences with mismatched positions and bulges indicated by lower case letters and dashes. ^bCoordinates in the GRCh38/hg38 assembly of the human genome. ^{c,d,e}Scores prior to the normalization shown in **Fig. S16**. ^fMean net editing = mean editing in treated samples – mean editing in untreated samples; editing was calculated as (aligned reads with A>G edits in any of the first 10 positions of the protospacer + total aligned reads). The black bold text indicates the endogenous wild-type *CPS1* Q335 site, and the red bold text indicates the site verified as an off-target site in HuH-7 cells (**Table S3**).

Legends for Supplementary Excel File

Individual worksheets supporting the off-target analyses are listed below. Please see additional file available at NEJM.org.

In silico. Primary data from in silico nomination.

ONE-seq. Primary data from ONE-seq nomination assay.

CHANGE-seq-BE. Primary data from CHANGE-seq-BE nomination assay.

Definitions of Tiers. Definitions of tiers for prioritization criteria for advancing UNCOVERseq/GUIDE-seq-nominated sites for verification studies.

UNCOVERseq_CPS1_MUT. Primary data from UNCOVERseq/GUIDE-seq nomination assays using the CPS1* guide RNA.

UNCOVERseq_CPS1_WT. Primary data from UNCOVERseq/GUIDE-seq nomination assays using the CPS1_{wt} guide RNA.

Computational. Integration of data from the various nomination assays.

CHOP_Nominated_Sites_Final_Prop. List of candidate off-target sites advanced to verification.

Priority classification. Prioritization criteria for advancing nominated sites for verification studies.

On-target locus integration. Tag counts for on-target sites in UNCOVERseq/GUIDE-seq nomination assays.

Nomination metrics. Quantitative metrics of data from UNCOVERseq/GUIDE-seq nomination assays.

Average read depth coverage. Average read depth coverage for rhAmpSeq verification studies.

Sensitivity of coverage method. Sensitivity of rhAmpSeq confirmation method at variable sequencing depth on known mixture.

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chr	start	stop	strand	Samples	Min_LevDist
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chr10	4848318	4848342	-		2
chr10	23031066	23031091	+		2
chr10	82835931	82835955	+		2
chr13	56306141	56306166	-		2
chr13	94095947	94095971	+		2
chr14	86882702	86882726	+		2
chr15	86580721	86580745	-		2
chr16	47135987	47136012	+		2
chr2	16052332	16052356	+		2
chr1	23294960	23294984	-		3
chr1	62872881	62872906	+		3
chr1	66589068	66589092	-		3
chr1	71437454	71437478	+		3
chr1	76393651	76393675	+		3
chr1	82404787	82404812	-		3
chr1	98723238	98723262	+		3
chr1	98839389	98839413	+		3
chr1	###	###	+		3
chr1	###	###	+		3
chr1	###	###	-		3
chr1	###	###	-		3
chr1	###	###	-		3
chr1	###	###	+		3
chr1	###	###	+		3
chr1	###	###	+		3
chr1	###	###	+		3
chr1	###	###	-		3
chr1	###	###	-		3
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chr10	25890787	25890811	+		3
chr10	42274503	42274528	+		3
chr10	43021833	43021857	-		3
chr10	57637038	57637062	+		3
chr10	63760955	63760979	-		3
chr10	93354541	93354566	-		3
chr10	94743856	94743880	+		3
chr10	95204610	95204634	-		3
chr10	###	###	+		3
chr10	###	###	-		3
chr10	###	###	-		3
chr10	###	###	+		3
chr10	###	###	-		3
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chr17	63470582	63470606 +	3
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chr18	60039260	60039284 +	3
chr19	29167553	29167577 +	3
chr19	34835232	34835256 +	3
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chr2	43672943	43672968 -	3
chr2	54981872	54981896 -	3
chr2	58649920	58649944 +	3

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chr2	###	### +	3
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chr20	42028946	42028970 +	3
chr20	51534630	51534654 -	3
chr20	59203684	59203708 -	3
chr21	9890747	9890771 -	3
chr21	16697981	16698005 -	3
chr21	24922452	24922476 -	3
chr21	26368775	26368799 -	3
chr22	29027997	29028022 +	3
chr22_KI270731v1_random	61686	61711 +	3
chr3	23460917	23460942 -	3
chr3	31923338	31923362 +	3
chr3	42163205	42163229 +	3
chr3	48081775	48081800 +	3
chr3	64195460	64195484 +	3
chr3	65034782	65034806 +	3
chr3	69553205	69553230 +	3
chr3	70369332	70369356 -	3
chr3	75938232	75938256 -	3
chr3	78719782	78719805 -	3
chr3	87433025	87433049 +	3
chr3	90078547	90078571 +	3
chr3	96430288	96430312 +	3
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chr3	###	### +	3
chr3	###	### -	3
chr3	###	### -	3

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chr3	###	### +	3
chr3	###	### -	3
chr3	###	### -	3
chr3	###	### +	3
chr3	###	### -	3
chr3_KI270781v1_alt	108117	108141 +	3
chr4	9074115	9074139 -	3
chr4	28917610	28917634 -	3
chr4	40419575	40419599 +	3
chr4	62983097	62983122 +	3
chr4	65032146	65032171 +	3
chr4	88797082	88797107 -	3
chr4	###	### +	3
chr4	###	### -	3
chr4	###	### +	3
chr4	###	### +	3
chr4	###	### +	3
chr4	###	### +	3
chr4	###	### -	3
chr4	###	### -	3
chr4	###	### -	3
chr4	###	### +	3
chr4	###	### +	3
chr4	###	### -	3
chr4	###	### +	3
chr1	60077	60101 +	4
chr1	1276462	1276486 -	4
chr1	3489706	3489730 +	4
chr1	7827696	7827720 -	4
chr1	8751871	8751895 +	4
chr1	11848002	11848026 -	4
chr1	12770981	12771005 -	4
chr1	14581371	14581396 -	4
chr1	17226254	17226278 -	4
chr1	17751571	17751595 -	4
chr1	18756316	18756341 -	4
chr1	19260842	19260866 -	4
chr1	19595683	19595708 -	4
chr1	20031317	20031341 +	4
chr1	20122138	20122162 -	4
chr1	20878594	20878618 +	4
chr1	22447226	22447250 +	4
chr1	23598049	23598073 +	4
chr1	24007303	24007326 +	4
chr1	24042621	24042646 +	4
chr1	24431290	24431314 +	4
chr1	24870611	24870635 -	4

chr1	25693987	25694011 +	4
chr1	26502435	26502460 +	4
chr1	26797315	26797339 +	4
chr1	29702365	29702389 -	4
chr1	31013952	31013976 -	4
chr1	31405469	31405493 -	4
chr1	32367683	32367707 +	4
chr1	32945624	32945648 +	4
chr1	33480148	33480172 +	4
chr1	33527539	33527563 -	4
chr1	33739804	33739828 +	4
chr1	34156764	34156788 -	4
chr1	34749825	34749850 -	4
chr1	36549575	36549600 -	4
chr1	37399997	37400021 -	4
chr1	37424367	37424391 -	4
chr1	38609824	38609848 -	4
chr1	38720828	38720853 -	4
chr1	39285790	39285814 -	4
chr1	40084129	40084153 +	4
chr1	41956367	41956392 +	4
chr1	42542900	42542924 -	4
chr1	43386258	43386283 +	4
chr1	45786307	45786331 +	4
chr1	47615058	47615082 +	4
chr1	48370187	48370211 -	4
chr1	49300104	49300129 +	4
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chr1	50842445	50842469 -	4
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chr1	52239646	52239670 +	4
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chr1	52993425	52993449 -	4
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chr1	54610731	54610755 +	4
chr1	55654763	55654787 +	4
chr1	55669441	55669465 +	4
chr1	55925451	55925475 -	4
chr1	57415720	57415744 -	4
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chr1	57617495	57617519 -	4
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chr1	60325891	60325915 -	4
chr1	60523209	60523234 -	4
chr1	61239905	61239930 -	4
chr1	62067448	62067472 -	4
chr1	62287562	62287586 -	4

chr1	62820767	62820792 +	4
chr1	63056623	63056647 +	4
chr1	63175359	63175383 -	4
chr1	66587574	66587598 -	4
chr1	66608502	66608526 -	4
chr1	68688292	68688316 +	4
chr1	69248880	69248904 +	4
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chr1	69563085	69563109 +	4
chr1	69645549	69645573 -	4
chr1	69745234	69745258 +	4
chr1	70118600	70118625 +	4
chr1	73404302	73404326 +	4
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chr1	74830371	74830395 -	4
chr1	75394396	75394420 +	4
chr1	75821551	75821575 +	4
chr1	76743564	76743588 +	4
chr1	77214023	77214047 +	4
chr1	77288683	77288708 +	4
chr1	77825910	77825934 -	4
chr1	77866219	77866243 +	4
chr1	79370034	79370058 -	4
chr1	79531946	79531970 +	4
chr1	80019364	80019388 -	4
chr1	81608360	81608384 +	4
chr1	81635500	81635524 +	4
chr1	81776907	81776931 +	4
chr1	82539262	82539286 -	4
chr1	83000657	83000682 +	4
chr1	83005302	83005325 -	4
chr1	83281956	83281981 +	4
chr1	84155552	84155576 +	4
chr1	84273511	84273536 +	4
chr1	84871843	84871867 -	4
chr1	84902563	84902587 +	4
chr1	84915423	84915447 -	4
chr1	85058252	85058276 +	4
chr1	86044142	86044166 +	4
chr1	86321684	86321709 -	4
chr1	86404744	86404768 -	4
chr1	88239186	88239211 +	4
chr1	88720962	88720986 -	4
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chr1	89510395	89510420 -	4
chr1	90658052	90658076 +	4

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chr1	92835919	92835943 -	4
chr1	94323817	94323841 -	4
chr1	95846256	95846281 +	4
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chr1	97031354	97031379 -	4
chr1	97154445	97154469 +	4
chr1	97301756	97301781 +	4
chr1	98041078	98041102 -	4
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chr1	98608391	98608415 -	4
chr1	99351090	99351114 -	4
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chr1	###	### -	4
chr1	###	### -	4
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chr1	###	### -	4
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chr1	###	### -	4
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chr1	###	### +	4
chr1	###	### +	4
chr1	###	### +	4
chr1	###	### -	4
chr1	###	### -	4
chr1	###	### -	4

chr1	###	### -	4
chr1	###	### -	4
chr1	###	### +	4
chr1	###	### -	4
chr1	###	### +	4
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chr1	###	### +	4
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chr1	###	### +	4
chr1	###	### +	4
chr1	###	### -	4
chr1	###	### +	4
chr1	###	### +	4
chr1	###	### -	4

chr1	###	### +	4
chr1	###	### -	4
chr1	###	### +	4
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chr1	###	### +	4
chr1	###	### +	4
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chr1	###	### +	4
chr1	###	### +	4
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chr1	###	### +	4

chr1	###	### -	4
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chr1	###	### -	4
chr1	###	### +	4
chr1	###	### +	4
chr1	###	### -	4
chr1	###	### +	4
chr1	###	### +	4

chr1	###	### +	4
chr1	###	### -	4
chr1	###	### -	4
chr1	###	### +	4
chr1	###	### -	4
chr1_KI270759v1_alt	246214	246238 -	4
chr1_KI270763v1_alt	408551	408575 +	4
chr1_KI270763v1_alt	462162	462186 +	4
chr1_KI270763v1_alt	782948	782972 -	4
chr10	2674549	2674573 -	4
chr10	4536517	4536541 -	4
chr10	4741020	4741044 -	4
chr10	5036566	5036590 +	4
chr10	5792487	5792511 -	4
chr10	5906746	5906770 -	4
chr10	6392276	6392300 +	4
chr10	6984506	6984530 -	4
chr10	7218457	7218482 +	4
chr10	8727518	8727542 +	4
chr10	9891257	9891281 +	4
chr10	11005501	11005525 -	4
chr10	11581127	11581151 +	4
chr10	11605442	11605466 -	4
chr10	13038704	13038728 +	4
chr10	13471913	13471937 -	4
chr10	13472931	13472955 -	4
chr10	13473911	13473935 -	4
chr10	13474406	13474430 -	4
chr10	13640308	13640332 -	4
chr10	13965727	13965751 +	4
chr10	14263374	14263398 -	4
chr10	14427822	14427846 +	4
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chr10	17398737	17398761 -	4
chr10	17610228	17610252 +	4
chr10	18003625	18003649 +	4
chr10	18775550	18775574 +	4
chr10	18909018	18909042 +	4
chr10	19350021	19350046 +	4
chr10	19807529	19807553 -	4
chr10	20950802	20950826 +	4
chr10	21565199	21565223 -	4
chr10	22069486	22069510 +	4
chr10	22168686	22168710 -	4
chr10	23143843	23143867 -	4
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chr10	24623558	24623582 -	4
chr10	25084714	25084738 -	4

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chr10	26048171	26048195 -	4
chr10	26429148	26429173 -	4
chr10	26918968	26918993 +	4
chr10	27355026	27355050 -	4
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chr10	28570743	28570767 +	4
chr10	28942509	28942534 +	4
chr10	29139676	29139700 -	4
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chr10	31121536	31121560 +	4
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chr10	32744430	32744454 +	4
chr10	33078323	33078347 +	4
chr10	33669738	33669762 -	4
chr10	34295928	34295953 -	4
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chr10	34544804	34544828 +	4
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chr10	38199562	38199586 -	4
chr10	38758638	38758662 +	4
chr10	42706833	42706858 -	4
chr10	44725353	44725377 -	4
chr10	45211325	45211349 +	4
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chr10	45780493	45780518 +	4
chr10	46401506	46401530 +	4
chr10	46563794	46563818 -	4
chr10	46669762	46669786 +	4
chr10	46874206	46874230 -	4
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chr10	50243173	50243198 -	4
chr10	50256611	50256635 +	4
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chr10	52678787	52678811 -	4
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chr10	53116602	53116626 -	4
chr10	53981128	53981152 +	4
chr10	55557680	55557704 +	4
chr10	55987737	55987761 +	4
chr10	56275436	56275460 +	4

chr10	57070032	57070057 -	4
chr10	57959314	57959338 +	4
chr10	58584900	58584924 +	4
chr10	59539508	59539532 -	4
chr10	60332715	60332740 +	4
chr10	60342717	60342741 +	4
chr10	60388414	60388438 -	4
chr10	60688426	60688450 -	4
chr10	62496959	62496983 +	4
chr10	62744689	62744713 -	4
chr10	62906708	62906733 -	4
chr10	63413763	63413787 +	4
chr10	64175175	64175199 +	4
chr10	64409953	64409977 -	4
chr10	64441110	64441134 -	4
chr10	65010149	65010173 -	4
chr10	65367353	65367377 -	4
chr10	65471950	65471974 +	4
chr10	65840403	65840427 +	4
chr10	69348077	69348101 +	4
chr10	72195983	72196007 -	4
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chr10	72766927	72766951 -	4
chr10	73018019	73018044 +	4
chr10	73878072	73878096 +	4
chr10	74134152	74134176 -	4
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chr10	75176833	75176857 +	4
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chr10	76857480	76857504 -	4
chr10	78449385	78449409 +	4
chr10	78803705	78803729 -	4
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chr10	79341980	79342005 +	4
chr10	80050272	80050296 -	4
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chr10	81432046	81432071 +	4
chr10	81828006	81828030 +	4
chr10	81969942	81969966 -	4
chr10	82033639	82033663 +	4
chr10	82122512	82122536 +	4
chr10	82141619	82141643 -	4
chr10	82161882	82161906 -	4
chr10	82266797	82266822 +	4
chr10	83907614	83907638 -	4
chr10	85045730	85045754 -	4

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chr10	85311900	85311924 -	4
chr10	85817908	85817932 +	4
chr10	87060117	87060141 +	4
chr10	87133607	87133631 -	4
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chr10	88024718	88024743 +	4
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chr10	88397036	88397060 -	4
chr10	89128922	89128946 -	4
chr10	89783574	89783598 +	4
chr10	90731777	90731801 -	4
chr10	91791235	91791259 -	4
chr10	91988108	91988132 +	4
chr10	93206676	93206700 +	4
chr10	93375279	93375304 -	4
chr10	93675861	93675886 -	4
chr10	95247358	95247382 +	4
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chr10	95557946	95557970 -	4
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chr10	95912411	95912435 +	4
chr10	96683552	96683577 -	4
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chr10	98580232	98580256 -	4
chr10	99364686	99364711 -	4
chr10	99648367	99648392 +	4
chr10	###	### -	4
chr10	###	### +	4
chr10	###	### -	4
chr10	###	### +	4
chr10	###	### +	4
chr10	###	### +	4
chr10	###	### +	4
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chr10	###	### -	4
chr10	###	### -	4
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chr10	###	### -	4
chr10	###	### +	4
chr10	###	### -	4

chr10	###	### -	4
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chr10	###	### +	4
chr10	###	### +	4
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chr10	###	### +	4
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chr10_GL383546v1_alt	64760	64784 +	4
chr10_KI270824v1_alt	108054	108078 -	4
chr10_KI270824v1_alt	157060	157085 +	4
chr11	2735882	2735906 -	4
chr11	4251250	4251275 +	4
chr11	5663594	5663619 +	4
chr11	7357753	7357778 -	4
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chr11	10091488	10091511 +	4
chr11	10092710	10092734 -	4
chr11	11164927	11164952 -	4
chr11	11179763	11179787 +	4
chr11	11701130	11701155 +	4
chr11	12030538	12030562 +	4
chr11	12285781	12285805 +	4
chr11	13265797	13265821 -	4
chr11	13945039	13945063 +	4
chr11	14212321	14212345 -	4
chr11	14950514	14950539 -	4
chr11	15082003	15082027 -	4
chr11	15316864	15316888 +	4
chr11	15849733	15849757 +	4
chr11	16657900	16657924 +	4

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chr11	19806496	19806520 +	4
chr11	21389497	21389521 +	4
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chr11	23042436	23042460 -	4
chr11	23288338	23288362 -	4
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chr11	###	### -	4
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chr11	###	### -	4
chr11	###	### -	4
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chr12	14844722	14844746 -	4
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chr12	84704806	84704830 -	4
chr12	86656943	86656967 +	4
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chr12	###	### -	4
chr12	###	### -	4
chr12	###	### -	4

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chr12_KI270904v1_alt	539399	539424 +	4
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chr13	###	### -	4
chr13	###	### +	4
chr13	###	### -	4
chr13	###	### -	4
chr13	###	### -	4
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chr14	27666054	27666077 -	4
chr14	28046599	28046623 -	4
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chr15	47501006	47501031 +	4
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chr15	48164238	48164262 +	4
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chr15	93263938	93263962 -	4
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chr15	94410707	94410732 -	4
chr15	96234710	96234734 +	4
chr15	96377581	96377605 -	4
chr15	96744347	96744372 -	4
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chr15	97927140	97927164 -	4
chr15	98346978	98347003 -	4
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chr15	###	### -	4
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chr15_KI270852v1_alt	144930	144955 -	4
chr15_KI270905v1_alt	41655	41680 +	4
chr15_KI270905v1_alt	198228	198252 -	4
chr15_KI270905v1_alt	703345	703369 -	4
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chr15_KI270905v1_alt	4746042	4746066 -	4
chr15_KI270906v1_alt	50724	50748 -	4
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chr16	8775688	8775712 +	4
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chr16_KI270728v1_random	1351252	1351276 -	4
chr16_KI270853v1_alt	937349	937373 -	4
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chr16_KI270853v1_alt	1992019	1992043 +	4
chr16_KI270853v1_alt	2377493	2377517 -	4
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chr17_JH159147v1_alt	37935	37959 +	4
chr17_JH159148v1_alt	40302	40327 -	4
chr17_KI270857v1_alt	1088221	1088246 -	4
chr17_KI270857v1_alt	1143624	1143648 +	4
chr17_KI270857v1_alt	1476075	1476100 -	4
chr17_KI270858v1_alt	37178	37202 -	4

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chr18	31631759	31631783 -	4
chr18	31732245	31732270 +	4
chr18	31769870	31769895 -	4
chr18	32632789	32632813 +	4

chr18	33777246	33777270 +	4
chr18	33849993	33850017 +	4
chr18	34113846	34113870 +	4
chr18	34200879	34200903 +	4
chr18	34352307	34352331 -	4
chr18	35525828	35525853 +	4
chr18	37303453	37303477 +	4
chr18	37771508	37771532 -	4
chr18	38217655	38217680 -	4
chr18	38586957	38586981 -	4
chr18	38807453	38807477 +	4
chr18	39141102	39141127 -	4
chr18	40432665	40432689 -	4
chr18	40439435	40439459 -	4
chr18	41287020	41287045 +	4
chr18	42487208	42487232 -	4
chr18	42593172	42593196 -	4
chr18	43411797	43411821 -	4
chr18	43913124	43913148 -	4
chr18	44002944	44002968 +	4
chr18	44857655	44857679 -	4
chr18	45267550	45267574 +	4
chr18	45626524	45626549 -	4
chr18	45883189	45883214 -	4
chr18	45952064	45952088 -	4
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chr18	48739025	48739049 +	4
chr18	49913002	49913026 +	4
chr18	50535986	50536010 +	4
chr18	50663670	50663694 +	4
chr18	50757838	50757862 +	4
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chr18	53289980	53290004 +	4
chr18	54436371	54436395 +	4
chr18	54501821	54501846 +	4
chr18	54896445	54896470 -	4
chr18	54977583	54977607 -	4
chr18	55205609	55205633 -	4
chr18	55342952	55342976 +	4
chr18	55516397	55516421 +	4
chr18	55579916	55579940 +	4
chr18	55593293	55593317 -	4
chr18	55795985	55796009 -	4
chr18	57603426	57603450 -	4
chr18	58105543	58105567 -	4
chr18	58678390	58678414 -	4
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chr18	59200884	59200909 +	4

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chr18	60554618	60554642 +	4
chr18	60838564	60838588 -	4
chr18	62248116	62248140 -	4
chr18	62369992	62370016 +	4
chr18	64050837	64050861 -	4
chr18	64247956	64247980 -	4
chr18	64836007	64836031 +	4
chr18	64862266	64862291 +	4
chr18	64998032	64998056 -	4
chr18	65259839	65259863 +	4
chr18	66571707	66571731 -	4
chr18	66974512	66974536 -	4
chr18	68382577	68382601 -	4
chr18	68675908	68675933 -	4
chr18	69801543	69801567 +	4
chr18	70087222	70087246 +	4
chr18	70939178	70939202 -	4
chr18	71109736	71109760 -	4
chr18	74497315	74497340 +	4
chr18	75603174	75603198 +	4
chr18	76368022	76368046 +	4
chr18	76846380	76846404 +	4
chr18	77713859	77713883 +	4
chr18	77866403	77866427 +	4
chr18	78666242	78666267 -	4
chr18	79014877	79014901 -	4
chr18	79016370	79016394 -	4
chr18	79016424	79016448 -	4
chr18	79017116	79017140 -	4
chr18_GL383567v1_alt	251025	251049 +	4
chr18_GL383571v1_alt	33301	33325 +	4
chr18_GL383572v1_alt	79463	79487 -	4
chr18_GL383572v1_alt	79516	79540 -	4
chr18_GL383572v1_alt	80311	80335 -	4
chr18_GL383572v1_alt	84092	84116 -	4
chr18_GL383572v1_alt	84574	84598 -	4
chr18_GL383572v1_alt	84684	84708 -	4
chr18_GL383572v1_alt	84790	84814 -	4
chr18_GL383572v1_alt	84897	84921 -	4
chr18_GL383572v1_alt	84950	84974 -	4
chr18_GL383572v1_alt	85003	85027 -	4
chr18_GL383572v1_alt	85056	85080 -	4
chr18_GL383572v1_alt	85109	85133 -	4
chr18_GL383572v1_alt	85162	85186 -	4
chr18_GL383572v1_alt	85321	85345 -	4
chr18_GL383572v1_alt	85375	85399 -	4
chr18_GL383572v1_alt	85428	85452 -	4

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chr18_GL383572v1_alt	85534	85558 -	4
chr18_GL383572v1_alt	85587	85611 -	4
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chr18_GL383572v1_alt	85693	85717 -	4
chr18_GL383572v1_alt	85746	85770 -	4
chr18_GL383572v1_alt	85800	85824 -	4
chr18_GL383572v1_alt	85855	85879 -	4
chr18_GL383572v1_alt	85909	85933 -	4
chr18_GL383572v1_alt	85962	85986 -	4
chr18_GL383572v1_alt	86015	86039 -	4
chr18_GL383572v1_alt	86068	86092 -	4
chr18_GL383572v1_alt	86122	86146 -	4
chr18_GL383572v1_alt	86176	86200 -	4
chr18_GL383572v1_alt	86230	86254 -	4
chr18_GL383572v1_alt	86283	86307 -	4
chr18_GL383572v1_alt	86336	86360 -	4
chr18_GL383572v1_alt	86389	86413 -	4
chr18_GL383572v1_alt	86442	86466 -	4
chr18_GL383572v1_alt	86495	86519 -	4
chr18_GL383572v1_alt	86548	86572 -	4
chr18_GL383572v1_alt	86601	86625 -	4
chr18_GL383572v1_alt	86654	86678 -	4
chr18_GL383572v1_alt	86708	86732 -	4
chr18_GL383572v1_alt	86761	86785 -	4
chr18_GL383572v1_alt	86814	86838 -	4
chr18_GL383572v1_alt	86867	86891 -	4
chr18_GL383572v1_alt	86920	86944 -	4
chr18_GL383572v1_alt	87026	87050 -	4
chr18_GL383572v1_alt	87079	87103 -	4
chr18_GL383572v1_alt	87132	87156 -	4
chr18_GL383572v1_alt	87185	87209 -	4
chr18_GL383572v1_alt	87238	87262 -	4
chr18_GL383572v1_alt	87345	87369 -	4
chr18_GL383572v1_alt	87399	87423 -	4
chr18_GL383572v1_alt	87452	87476 -	4
chr18_GL383572v1_alt	87506	87530 -	4
chr18_GL383572v1_alt	87559	87583 -	4
chr18_GL383572v1_alt	87665	87689 -	4
chr18_GL383572v1_alt	131698	131723 +	4
chr18_KI270863v1_alt	164076	164101 +	4
chr18_KI270911v1_alt	80684	80708 -	4
chr18_KI270911v1_alt	80790	80814 -	4
chr18_KI270911v1_alt	81376	81400 -	4
chr18_KI270911v1_alt	81591	81615 -	4
chr18_KI270911v1_alt	81647	81671 -	4
chr18_KI270911v1_alt	81700	81724 -	4
chr18_KI270911v1_alt	81753	81777 -	4

chr18_KI270911v1_alt	81806	81830 -	4
chr18_KI270911v1_alt	81859	81883 -	4
chr18_KI270911v1_alt	81912	81936 -	4
chr18_KI270911v1_alt	81965	81989 -	4
chr18_KI270911v1_alt	82018	82042 -	4
chr18_KI270911v1_alt	82071	82095 -	4
chr18_KI270911v1_alt	82124	82148 -	4
chr18_KI270911v1_alt	82177	82201 -	4
chr18_KI270911v1_alt	82283	82307 -	4
chr18_KI270911v1_alt	82336	82360 -	4
chr18_KI270911v1_alt	82389	82413 -	4
chr18_KI270911v1_alt	82601	82625 -	4
chr18_KI270911v1_alt	82654	82678 -	4
chr18_KI270911v1_alt	82707	82731 -	4
chr18_KI270911v1_alt	82760	82784 -	4
chr18_KI270911v1_alt	82813	82837 -	4
chr18_KI270911v1_alt	82975	82999 -	4
chr18_KI270911v1_alt	83028	83052 -	4
chr18_KI270911v1_alt	83081	83105 -	4
chr18_KI270911v1_alt	83134	83158 -	4
chr18_KI270911v1_alt	83187	83211 -	4
chr18_KI270911v1_alt	83240	83264 -	4
chr18_KI270911v1_alt	83346	83370 -	4
chr18_KI270911v1_alt	84618	84642 -	4
chr18_KI270911v1_alt	84671	84695 -	4
chr18_KI270911v1_alt	84724	84748 -	4
chr18_KI270911v1_alt	84777	84801 -	4
chr18_KI270911v1_alt	84830	84854 -	4
chr18_KI270911v1_alt	84936	84960 -	4
chr18_KI270911v1_alt	85095	85119 -	4
chr18_KI270911v1_alt	85148	85172 -	4
chr18_KI270911v1_alt	85202	85226 -	4
chr18_KI270911v1_alt	85255	85279 -	4
chr18_KI270911v1_alt	85308	85332 -	4
chr18_KI270911v1_alt	85361	85385 -	4
chr18_KI270911v1_alt	85414	85438 -	4
chr18_KI270911v1_alt	85467	85491 -	4
chr18_KI270911v1_alt	85520	85544 -	4
chr18_KI270911v1_alt	85573	85597 -	4
chr18_KI270911v1_alt	85626	85650 -	4
chr18_KI270911v1_alt	85679	85703 -	4
chr18_KI270911v1_alt	85732	85756 -	4
chr18_KI270911v1_alt	85785	85809 -	4
chr18_KI270911v1_alt	85838	85862 -	4
chr18_KI270911v1_alt	85891	85915 -	4
chr18_KI270911v1_alt	85944	85968 -	4
chr18_KI270911v1_alt	85997	86021 -	4
chr18_KI270911v1_alt	86050	86074 -	4

chr18_KI270911v1_alt	86103	86127 -	4
chr18_KI270911v1_alt	86156	86180 -	4
chr18_KI270911v1_alt	86209	86233 -	4
chr18_KI270911v1_alt	129861	129886 +	4
chr18_KI270912v1_alt	43955	43979 +	4
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chr19	2125702	2125726 +	4
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chr19	3853299	3853323 -	4
chr19	4593749	4593773 +	4
chr19	4629739	4629763 -	4
chr19	5171661	5171685 -	4
chr19	5186390	5186414 +	4
chr19	5715266	5715290 -	4
chr19	6140730	6140753 +	4
chr19	6153371	6153395 +	4
chr19	6165573	6165597 -	4
chr19	6649260	6649284 -	4
chr19	7113411	7113435 -	4
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chr19	9175911	9175935 -	4
chr19	9279595	9279620 -	4
chr19	9512657	9512682 -	4
chr19	9698525	9698549 +	4
chr19	9702008	9702032 -	4
chr19	9714206	9714230 -	4
chr19	10180586	10180610 +	4
chr19	10212900	10212924 +	4
chr19	11006744	11006768 +	4
chr19	11309440	11309464 -	4
chr19	11376651	11376675 -	4
chr19	11535556	11535580 +	4
chr19	11664559	11664583 -	4
chr19	11685835	11685859 +	4
chr19	11685956	11685980 -	4
chr19	11869317	11869342 +	4
chr19	11912780	11912805 +	4
chr19	11950615	11950640 +	4
chr19	12062677	12062701 -	4
chr19	12241738	12241763 +	4
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chr19	12424155	12424180 -	4
chr19	12526802	12526826 +	4
chr19	13319319	13319343 -	4
chr19	13553851	13553875 +	4

chr19	13617200	13617224 -	4
chr19	13716284	13716309 -	4
chr19	13782446	13782470 +	4
chr19	14222856	14222880 -	4
chr19	14380400	14380424 +	4
chr19	14424777	14424801 -	4
chr19	14596628	14596652 +	4
chr19	14662105	14662129 -	4
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chr19	14789228	14789252 +	4
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chr19	14972721	14972745 +	4
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chr19	15253005	15253029 -	4
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chr19	15318322	15318346 +	4
chr19	15544234	15544258 +	4
chr19	15577540	15577564 +	4
chr19	15580435	15580459 -	4
chr19	15626496	15626520 -	4
chr19	15947924	15947948 -	4
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chr19	16244391	16244415 +	4
chr19	16387078	16387102 +	4
chr19	16428963	16428987 -	4
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chr19	20179258	20179283 +	4
chr19	20207045	20207069 +	4
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chr19	20319276	20319300 +	4
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chr19	20508183	20508208 +	4
chr19	20721631	20721655 -	4
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chr19	20844595	20844619 +	4
chr19	20869255	20869279 -	4
chr19	20872012	20872036 -	4

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chr19	20984784	20984808 -	4
chr19	21377732	21377756 -	4
chr19	22142540	22142564 -	4
chr19	22617097	22617121 -	4
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chr19	28659791	28659815 +	4
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chr19	42669796	42669820 +	4
chr19	42775299	42775323 +	4
chr19	43667203	43667227 -	4
chr19	44122521	44122545 +	4
chr19	46327532	46327556 -	4
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chr19	53211044	53211068 +	4
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chr19	56318835	56318859 +	4
chr19	56624351	56624375 -	4
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chr19_GL383575v2_alt	164624	164648 -	4
chr19_KI270867v1_alt	26804	26828 -	4
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chr2	6960052	6960076 +	4

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chr2	9397057	9397081 +	4
chr2	10374257	10374281 +	4
chr2	11283794	11283819 -	4
chr2	11315551	11315575 -	4
chr2	12041848	12041872 +	4
chr2	12050669	12050693 +	4
chr2	12271846	12271870 -	4
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chr2	13511748	13511772 +	4
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chr2	23810264	23810288 +	4
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chr2	37829933	37829957 -	4
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chr2	40948607	40948631 -	4
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chr2	45420499	45420523 -	4
chr2	45461806	45461831 -	4
chr2	45816583	45816607 -	4
chr2	45951440	45951464 +	4
chr2	47846529	47846554 +	4
chr2	48018468	48018492 -	4
chr2	49561578	49561603 -	4
chr2	49564942	49564966 +	4
chr2	49568346	49568370 +	4
chr2	49625352	49625376 -	4
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chr2	52851262	52851285 -	4
chr2	53526701	53526726 +	4
chr2	54949855	54949879 -	4
chr2	55130823	55130848 +	4
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chr2	55635618	55635642 -	4
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chr2	56201228	56201252 +	4
chr2	56228443	56228467 -	4
chr2	57367818	57367842 -	4
chr2	57506796	57506820 -	4
chr2	57731193	57731217 +	4
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chr2	62559177	62559202 -	4
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chr2	64083606	64083631 +	4
chr2	64297993	64298017 +	4
chr2	64354132	64354157 -	4
chr2	64409492	64409517 -	4

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chr2	64652010	64652034 +	4
chr2	66609618	66609642 +	4
chr2	66649166	66649191 +	4
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chr2	69023611	69023636 +	4
chr2	69430751	69430775 +	4
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chr2	72418384	72418408 +	4
chr2	72841544	72841568 +	4
chr2	73930029	73930054 +	4
chr2	75546351	75546375 +	4
chr2	75666638	75666662 +	4
chr2	76715391	76715415 -	4
chr2	78041070	78041094 -	4
chr2	78399003	78399027 +	4
chr2	78589833	78589857 +	4
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chr2	80736044	80736068 +	4
chr2	81538050	81538074 -	4
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chr2	82864762	82864786 -	4
chr2	83548552	83548576 -	4
chr2	84395733	84395757 +	4
chr2	84475924	84475948 -	4
chr2	84710236	84710260 -	4
chr2	84757574	84757598 -	4
chr2	84771626	84771650 +	4
chr2	86330949	86330974 +	4
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chr2	###	### +	4
chr2	###	### -	4
chr2	###	### -	4

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chr2	###	### -	4
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chr2_KI270775v1_alt	185	209 +	4
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chr20	8236882	8236906 +	4
chr20	8536235	8536259 +	4
chr20	9629690	9629715 -	4
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chr20	9964952	9964976 +	4
chr20	10247061	10247085 +	4
chr20	10645539	10645563 -	4
chr20	10992484	10992508 -	4
chr20	11437928	11437952 +	4
chr20	11515003	11515027 -	4
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chr20	12169787	12169811 +	4
chr20	12268926	12268950 -	4

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chr20	17095098	17095122 -	4
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chr20	18184092	18184116 -	4
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chr20	19709404	19709428 -	4
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chr20	24087495	24087520 +	4
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chr20	34534165	34534189 +	4
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chr20	42132702	42132727 -	4
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chr20	46168109	46168133 +	4
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chr20	48784352	48784377 +	4
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chr20	52190687	52190711 +	4

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chr20	57905561	57905585 +	4
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chr21	9918851	9918875 +	4
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chr21	16543059	16543084 +	4
chr21	16625943	16625967 +	4
chr21	17133696	17133720 +	4
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chr21	18469606	18469630 +	4
chr21	19057455	19057479 +	4
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chr21	28150092	28150116 +	4
chr21	28170976	28171001 -	4
chr21	28483215	28483240 +	4

chr21	28548696	28548720 +	4
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chr21	29068329	29068353 -	4
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chr21	30116596	30116620 +	4
chr21	31226415	31226439 +	4
chr21	32234597	32234622 -	4
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chr21	34434061	34434085 -	4
chr21	35455026	35455050 +	4
chr21	35528422	35528446 -	4
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chr21	44623752	44623777 -	4
chr21	46240322	46240346 +	4
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chr21_KI270873v1_alt	15960	15985 +	4
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chr22	16236437	16236461 +	4
chr22	16465790	16465814 +	4
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chr22	21858559	21858583 -	4
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chr22_KI270879v1_alt	300933	300957 -	4
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chr3	82453191	82453215 +	4
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chr3	87012640	87012665 -	4
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chr3	89398730	89398754 -	4
chr3	89742031	89742055 +	4
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chr3	###	### +	4
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chr3	###	### -	4
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chr3_KI270784v1_alt	114280	114305 -	4
chr3_KI270924v1_alt	41319	41343 -	4
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chr4	14099249	14099273 -	4
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chr4	14528822	14528846 +	4
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chr4	17197900	17197925 -	4
chr4	17501442	17501466 -	4
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chr4	18522131	18522155 -	4
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chr4	26271826	26271850 -	4
chr4	27280180	27280205 +	4
chr4	27474445	27474469 -	4
chr4	28023820	28023844 -	4
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chr4	30161151	30161176 +	4
chr4	30163711	30163735 +	4
chr4	30340914	30340938 +	4
chr4	30634001	30634025 +	4
chr4	30935561	30935586 +	4
chr4	31352783	31352807 +	4
chr4	31392043	31392068 -	4
chr4	31516829	31516853 -	4
chr4	33548030	33548054 +	4
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chr4	35657098	35657122 +	4
chr4	35805727	35805752 -	4
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chr4	45057115	45057140 -	4
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chr4	57477953	57477978 +	4
chr4	57545122	57545146 +	4
chr4	57848951	57848975 -	4
chr4	59195290	59195314 +	4
chr4	59437035	59437059 +	4
chr4	59439465	59439489 +	4
chr4	59634671	59634695 -	4
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chr4	62705123	62705147 -	4
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chr4	64715067	64715092 +	4
chr4	64754165	64754189 +	4
chr4	65024826	65024850 +	4
chr4	65369404	65369428 +	4
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chr4	66668820	66668844 +	4
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chr4	67360785	67360809 -	4
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chr4	70709162	70709186 +	4
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chr4	72221176	72221200 -	4
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chr4	92310264	92310288 +	4
chr4	92371946	92371970 +	4
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chr4	###	### -	4
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chr1	1738988	1739012 +	5
chr1	1828413	1828437 -	5
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chr1	3218253	3218278 -	5
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chr1	3540106	3540131 +	5
chr1	3815025	3815049 +	5
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chr1	4517148	4517172 +	5
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chr1	6116627	6116651 +	5
chr1	6232175	6232199 -	5
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chr1	6699912	6699937 -	5
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chr1	6756249	6756274 +	5
chr1	6821663	6821687 +	5
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chr1	7029165	7029189 -	5

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chr1	12256577	12256601 +	5
chr1	12307954	12307978 +	5
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chr1	15050590	15050614 +	5
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chr1	16895348	16895372 +	5
chr1	17276385	17276409 +	5
chr1	17284254	17284278 -	5
chr1	17411155	17411179 +	5
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chr1	17833234	17833258 +	5
chr1	17847173	17847197 -	5
chr1	17867686	17867710 +	5
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chr1	18028742	18028766 -	5
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chr1	18121001	18121025 -	5
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chr1	18263301	18263326 -	5
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chr1	18609331	18609355 +	5
chr1	18655131	18655156 -	5
chr1	18749237	18749261 -	5

chr1	18826366	18826390 +	5
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chr1	###	### +	5
chr1	###	### -	5
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chr1	###	### -	5
chr1	###	### -	5
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chr1	###	### +	5
chr1	###	### +	5
chr1	###	### -	5
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chr1	###	### -	5
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chr1	###	### +	5

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chr1	###	### -	5
chr1	###	### +	5
chr1	###	### -	5

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chr1	###	### +	5
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chr1	###	### +	5
chr1	###	### -	5
chr1	###	### -	5

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chr1	###	### -	5

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chr1	###	### +	5

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chr1	###	### -	5

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chr1	###	### -	5
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chr1	###	### -	5
chr1	###	### +	5
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chr1	###	### -	5
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[illegible]

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chr1_GL383518v1_alt	58513	58537+	5
chr1_GL383518v1_alt	125258	125282-	5
chr1_GL383519v1_alt	8803	8827-	5
chr1_GL383519v1_alt	29417	29441-	5
chr1_GL383520v2_alt	17168	17192+	5
chr1_GL383520v2_alt	50292	50316+	5
chr1_GL383520v2_alt	155933	155958-	5

chr1_KI270706v1_random	56567	56591 -	5
chr1_KI270706v1_random	109685	109709 +	5
chr1_KI270706v1_random	140289	140313 +	5
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chr1_KI270708v1_random	11309	11333 +	5
chr1_KI270708v1_random	97092	97116 -	5
chr1_KI270713v1_random	22646	22670 -	5
chr1_KI270759v1_alt	116330	116354 +	5
chr1_KI270759v1_alt	223590	223615 -	5
chr1_KI270759v1_alt	279006	279031 +	5
chr1_KI270759v1_alt	341351	341375 -	5
chr1_KI270759v1_alt	350306	350330 +	5
chr1_KI270761v1_alt	148475	148499 +	5
chr1_KI270763v1_alt	83264	83288 -	5
chr1_KI270763v1_alt	130823	130847 -	5
chr1_KI270763v1_alt	135077	135101 +	5
chr1_KI270763v1_alt	203251	203275 -	5
chr1_KI270763v1_alt	206063	206088 -	5
chr1_KI270763v1_alt	208317	208341 +	5
chr1_KI270763v1_alt	307728	307752 -	5
chr1_KI270763v1_alt	353401	353425 +	5
chr1_KI270763v1_alt	400422	400446 +	5
chr1_KI270763v1_alt	708059	708083 -	5
chr1_KI270763v1_alt	760589	760613 -	5
chr1_KI270765v1_alt	26673	26698 +	5
chr1_KI270765v1_alt	72756	72780 -	5
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chr1_KI270765v1_alt	110839	110863 +	5
chr1_KI270765v1_alt	155071	155096 +	5
chr1_KI270765v1_alt	183415	183439 +	5
chr1_KI270765v1_alt	184938	184962 +	5
chr1_KI270766v1_alt	57252	57276 +	5
chr1_KI270892v1_alt	144853	144877 +	5
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chr10	133164	133188 -	5
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chr10	286439	286464 -	5
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chr10	360799	360823 +	5
chr10	462175	462199 +	5
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chr10	676380	676404 +	5
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chr10	1127356	1127380 +	5
chr10	1164172	1164196 +	5

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chr10	1387059	1387083 +	5
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[illegible]

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[illegible]

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chr12	85632866	85632890 -	5
chr12	85752682	85752706 -	5
chr12	85835528	85835552 -	5
chr12	85912515	85912539 -	5
chr12	85969020	85969044 +	5
chr12	86029090	86029114 +	5
chr12	86108166	86108191 +	5
chr12	86250158	86250183 -	5
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chr12	86934811	86934835 +	5
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chr12	87134577	87134601 -	5
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chr12	87214705	87214729 +	5
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chr12	87438517	87438541 -	5
chr12	87479065	87479089 +	5
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chr12	87747258	87747283 +	5
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chr12	87960078	87960103 +	5
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chr12	88116557	88116581 -	5
chr12	88168967	88168991 +	5
chr12	88169119	88169143 +	5
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chr12	88243881	88243905 +	5
chr12	88259217	88259241 +	5
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chr12	89365562	89365587 -	5
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chr12	93476847	93476871 +	5
chr12	93486777	93486801 -	5
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chr12	###	### -	5
chr12_GL383549v1_alt	34791	34815 +	5
chr12_GL383550v2_alt	113251	113275 -	5
chr12_GL383551v1_alt	113071	113096 -	5
chr12_GL383551v1_alt	147583	147607 +	5
chr12_GL383552v1_alt	44614	44638 +	5
chr12_GL383552v1_alt	90756	90780 +	5
chr12_GL383553v2_alt	94972	94996 +	5
chr12_GL383553v2_alt	133247	133271 +	5

chr12_GL877875v1_alt	10789	10813 -	5
chr12_GL877875v1_alt	52840	52864 +	5
chr12_GL877875v1_alt	138638	138662 +	5
chr12_GL877876v1_alt	209336	209360 +	5
chr12_GL877876v1_alt	252830	252854 -	5
chr12_GL877876v1_alt	265060	265084 -	5
chr12_GL877876v1_alt	300954	300978 +	5
chr12_GL877876v1_alt	319330	319354 -	5
chr12_GL877876v1_alt	335725	335749 +	5
chr12_GL877876v1_alt	367881	367905 +	5
chr12_GL877876v1_alt	376521	376545 +	5
chr12_GL877876v1_alt	376746	376770 +	5
chr12_GL877876v1_alt	386862	386886 -	5
chr12_KI270834v1_alt	87570	87595 -	5
chr12_KI270835v1_alt	24897	24922 -	5
chr12_KI270835v1_alt	116754	116778 +	5
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chr12_KI270836v1_alt	22193	22217 -	5
chr12_KI270837v1_alt	27567	27592 +	5
chr12_KI270837v1_alt	32855	32880 -	5
chr12_KI270904v1_alt	15468	15492 -	5
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chr12_KI270904v1_alt	283701	283725 -	5
chr12_KI270904v1_alt	300087	300111 +	5
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chr13	20048150	20048174 +	5
chr13	20141103	20141127 +	5
chr13	20144219	20144244 +	5
chr13	20170892	20170916 -	5
chr13	20241169	20241193 +	5
chr13	20273938	20273961 +	5
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chr14_KI270846v1_alt	1327	1351 +	5
chr14_KI270846v1_alt	195000	195025 -	5
chr14_KI270846v1_alt	224373	224398 -	5
chr14_KI270846v1_alt	267977	268001 -	5
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chr14_KI270846v1_alt	277792	277816 -	5
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chr14_KI270846v1_alt	663984	664009 -	5
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chr14_KI270846v1_alt	1192247	1192271 +	5
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chr14_KI270847v1_alt	202289	202313 +	5
chr14_KI270847v1_alt	425431	425455 +	5
chr14_KI270847v1_alt	503138	503162 +	5
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chr14_KI270847v1_alt	1179406	1179430 -	5
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chr15	98445642	98445667 -	5
chr15	98454299	98454323 -	5
chr15	98533868	98533893 +	5
chr15	98621110	98621135 +	5
chr15	98803300	98803324 +	5
chr15	98808019	98808043 +	5
chr15	98901517	98901541 -	5
chr15	98985870	98985894 -	5
chr15	99027089	99027113 -	5
chr15	99275969	99275993 -	5
chr15	99357385	99357410 -	5
chr15	99492652	99492677 +	5
chr15	99506506	99506531 -	5
chr15	99858184	99858208 +	5
chr15	99881495	99881519 -	5
chr15	99891312	99891337 -	5
chr15	99902166	99902191 +	5
chr15	99982192	99982217 +	5
chr15	###	### -	5
chr15	###	### -	5
chr15	###	### -	5
chr15	###	### +	5
chr15	###	### -	5
chr15	###	### +	5
chr15	###	### -	5
chr15	###	### +	5
chr15	###	### +	5
chr15	###	### -	5
chr15	###	### +	5
chr15	###	### +	5
chr15	###	### +	5
chr15	###	### +	5
chr15	###	### -	5
chr15	###	### -	5
chr15	###	### +	5
chr15	###	### +	5
chr15	###	### -	5
chr15	###	### -	5
chr15	###	### +	5
chr15_GL383554v1_alt	127000	127024 -	5
chr15_GL383554v1_alt	189156	189180 +	5
chr15_GL383555v2_alt	57564	57588 -	5
chr15_GL383555v2_alt	68427	68451 -	5
chr15_GL383555v2_alt	312943	312967 -	5
chr15_GL383555v2_alt	347025	347049 +	5
chr15_KI270727v1_random	58046	58070 -	5

chr15_KI270727v1_random	109076	109100 -	5
chr15_KI270727v1_random	114179	114204 -	5
chr15_KI270727v1_random	207294	207318 +	5
chr15_KI270727v1_random	244583	244607 -	5
chr15_KI270727v1_random	262969	262993 -	5
chr15_KI270727v1_random	266373	266397 +	5
chr15_KI270727v1_random	273605	273629 +	5
chr15_KI270727v1_random	303470	303494 +	5
chr15_KI270727v1_random	337409	337434 +	5
chr15_KI270727v1_random	432514	432538 +	5
chr15_KI270848v1_alt	120786	120810 +	5
chr15_KI270848v1_alt	181375	181399 -	5
chr15_KI270848v1_alt	195245	195270 -	5
chr15_KI270848v1_alt	252022	252047 -	5
chr15_KI270848v1_alt	299584	299608 -	5
chr15_KI270849v1_alt	24126	24150 -	5
chr15_KI270849v1_alt	69736	69760 +	5
chr15_KI270849v1_alt	103595	103620 -	5
chr15_KI270849v1_alt	210149	210173 -	5
chr15_KI270849v1_alt	225388	225412 -	5
chr15_KI270850v1_alt	17257	17281 +	5
chr15_KI270850v1_alt	416228	416253 -	5
chr15_KI270851v1_alt	28012	28036 +	5
chr15_KI270851v1_alt	58316	58341 +	5
chr15_KI270851v1_alt	88317	88342 +	5
chr15_KI270851v1_alt	220944	220969 -	5
chr15_KI270852v1_alt	88797	88821 -	5
chr15_KI270852v1_alt	139827	139851 -	5
chr15_KI270852v1_alt	238045	238069 +	5
chr15_KI270852v1_alt	275334	275358 -	5
chr15_KI270852v1_alt	293720	293744 -	5
chr15_KI270852v1_alt	297124	297148 +	5
chr15_KI270852v1_alt	334221	334245 +	5
chr15_KI270852v1_alt	339357	339381 -	5
chr15_KI270852v1_alt	368160	368185 +	5
chr15_KI270852v1_alt	463265	463289 +	5
chr15_KI270905v1_alt	220553	220577 +	5
chr15_KI270905v1_alt	729352	729377 -	5
chr15_KI270905v1_alt	765373	765397 +	5
chr15_KI270905v1_alt	814621	814646 +	5
chr15_KI270905v1_alt	946786	946811 -	5
chr15_KI270905v1_alt	1018996	1019020 +	5
chr15_KI270905v1_alt	1370794	1370818 -	5
chr15_KI270905v1_alt	1375239	1375263 +	5
chr15_KI270905v1_alt	1474315	1474339 -	5
chr15_KI270905v1_alt	1505600	1505625 -	5
chr15_KI270905v1_alt	1568491	1568516 -	5
chr15_KI270905v1_alt	1587478	1587502 -	5

chr15_KI270905v1_alt	1769614	1769638 -	5
chr15_KI270905v1_alt	1841903	1841927 +	5
chr15_KI270905v1_alt	1999055	1999079 +	5
chr15_KI270905v1_alt	2245028	2245052 -	5
chr15_KI270905v1_alt	2500212	2500236 +	5
chr15_KI270905v1_alt	2534814	2534838 -	5
chr15_KI270905v1_alt	2799529	2799554 +	5
chr15_KI270905v1_alt	2987047	2987071 +	5
chr15_KI270905v1_alt	3164866	3164890 +	5
chr15_KI270905v1_alt	3234900	3234925 -	5
chr15_KI270905v1_alt	3322498	3322522 +	5
chr15_KI270905v1_alt	3360990	3361014 +	5
chr15_KI270905v1_alt	3421431	3421455 +	5
chr15_KI270905v1_alt	3569496	3569520 -	5
chr15_KI270905v1_alt	3709129	3709153 -	5
chr15_KI270905v1_alt	3736204	3736228 +	5
chr15_KI270905v1_alt	3741060	3741084 -	5
chr15_KI270905v1_alt	3741084	3741108 -	5
chr15_KI270905v1_alt	3801406	3801430 +	5
chr15_KI270905v1_alt	3832232	3832256 +	5
chr15_KI270905v1_alt	3989491	3989515 -	5
chr15_KI270905v1_alt	4027602	4027627 +	5
chr15_KI270905v1_alt	4104135	4104159 +	5
chr15_KI270905v1_alt	4196650	4196674 -	5
chr15_KI270905v1_alt	4227148	4227172 -	5
chr15_KI270905v1_alt	4241831	4241855 -	5
chr15_KI270905v1_alt	4321657	4321682 +	5
chr15_KI270905v1_alt	4354059	4354083 -	5
chr15_KI270905v1_alt	4362527	4362551 +	5
chr15_KI270905v1_alt	4373655	4373680 +	5
chr15_KI270905v1_alt	4375565	4375590 -	5
chr15_KI270905v1_alt	4574493	4574517 +	5
chr15_KI270905v1_alt	4770586	4770611 +	5
chr15_KI270905v1_alt	4980684	4980708 -	5
chr15_KI270905v1_alt	5003175	5003199 +	5
chr15_KI270905v1_alt	5096091	5096115 +	5
chr15_KI270905v1_alt	5133923	5133947 -	5
chr15_KI270906v1_alt	64596	64621 -	5
chr15_KI270906v1_alt	121024	121049 -	5
chr15_KI270906v1_alt	168586	168610 -	5
chr16	37696	37720 +	5
chr16	878249	878273 -	5
chr16	1532798	1532822 +	5
chr16	1836344	1836369 -	5
chr16	2008613	2008637 -	5
chr16	2098765	2098789 -	5
chr16	2217347	2217372 -	5
chr16	2264659	2264683 +	5

chr16	2290230	2290255 -	5
chr16	2950114	2950138 -	5
chr16	3122679	3122703 -	5
chr16	3405153	3405178 +	5
chr16	3431677	3431701 -	5
chr16	3451418	3451442 -	5
chr16	3591080	3591104 -	5
chr16	3621713	3621737 -	5
chr16	3709414	3709438 +	5
chr16	4047081	4047106 +	5
chr16	4430254	4430278 +	5
chr16	4566861	4566885 -	5
chr16	4836465	4836489 +	5
chr16	4842683	4842707 -	5
chr16	5150482	5150506 -	5
chr16	5167431	5167455 +	5
chr16	5353950	5353974 +	5
chr16	5493906	5493931 +	5
chr16	5876714	5876738 -	5
chr16	5999148	5999173 -	5
chr16	6024836	6024860 +	5
chr16	6056334	6056358 +	5
chr16	6081445	6081470 +	5
chr16	6089113	6089137 +	5
chr16	6218098	6218121 -	5
chr16	6220453	6220477 -	5
chr16	6245222	6245246 +	5
chr16	6269742	6269766 +	5
chr16	6290023	6290047 +	5
chr16	6316856	6316880 -	5
chr16	6352637	6352661 -	5
chr16	6354821	6354844 -	5
chr16	6375944	6375968 -	5
chr16	6392953	6392977 -	5
chr16	6428579	6428603 +	5
chr16	6530138	6530162 -	5
chr16	6737025	6737049 +	5
chr16	7142796	7142820 +	5
chr16	7164906	7164930 -	5
chr16	7166918	7166942 -	5
chr16	7210838	7210862 +	5
chr16	7244198	7244223 -	5
chr16	7305818	7305842 -	5
chr16	7312610	7312634 -	5
chr16	7335731	7335756 +	5
chr16	7345704	7345729 -	5
chr16	7447587	7447611 +	5
chr16	7470375	7470399 +	5

chr16	7565540	7565564 -	5
chr16	7594206	7594231 +	5
chr16	7681944	7681969 +	5
chr16	7740266	7740290 +	5
chr16	7793576	7793600 +	5
chr16	7853025	7853050 +	5
chr16	7900263	7900287 +	5
chr16	7928005	7928029 +	5
chr16	8006996	8007021 +	5
chr16	8257959	8257983 +	5
chr16	8461535	8461559 -	5
chr16	8484815	8484838 -	5
chr16	8625264	8625289 +	5
chr16	8932665	8932689 -	5
chr16	9123733	9123757 -	5
chr16	9241651	9241675 -	5
chr16	9246356	9246381 +	5
chr16	9273770	9273794 +	5
chr16	9342270	9342294 +	5
chr16	9455297	9455321 +	5
chr16	9486586	9486611 +	5
chr16	9578669	9578693 +	5
chr16	9664806	9664831 -	5
chr16	9715886	9715911 +	5
chr16	9969278	9969302 -	5
chr16	10024591	10024616 -	5
chr16	10139604	10139628 -	5
chr16	10218196	10218220 +	5
chr16	10357565	10357589 -	5
chr16	10373984	10374008 +	5
chr16	10417456	10417481 +	5
chr16	10837153	10837177 +	5
chr16	10850462	10850487 -	5
chr16	10974740	10974764 +	5
chr16	11277269	11277293 -	5
chr16	11285670	11285694 +	5
chr16	11288315	11288339 -	5
chr16	11353305	11353330 +	5
chr16	11361675	11361699 +	5
chr16	11524511	11524535 +	5
chr16	11526092	11526116 +	5
chr16	11676963	11676987 -	5
chr16	11688023	11688047 -	5
chr16	11766979	11767003 -	5
chr16	11833046	11833070 +	5
chr16	11998676	11998700 +	5
chr16	12056483	12056508 +	5
chr16	12133940	12133964 -	5

chr16	12141083	12141107 +	5
chr16	12144503	12144526 +	5
chr16	12146655	12146679 -	5
chr16	12165875	12165899 -	5
chr16	12201340	12201365 -	5
chr16	12342870	12342894 -	5
chr16	12346081	12346105 +	5
chr16	12484114	12484138 -	5
chr16	12485359	12485383 -	5
chr16	12771807	12771832 -	5
chr16	12836010	12836034 +	5
chr16	13067434	13067458 -	5
chr16	13095538	13095562 -	5
chr16	13174380	13174404 -	5
chr16	13210570	13210594 -	5
chr16	13573643	13573667 -	5
chr16	13607505	13607530 +	5
chr16	13670455	13670479 -	5
chr16	13784428	13784452 +	5
chr16	13870674	13870699 -	5
chr16	13876623	13876648 +	5
chr16	13908208	13908233 -	5
chr16	14005264	14005288 +	5
chr16	14013714	14013738 -	5
chr16	14128667	14128691 -	5
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chr16	14305756	14305780 -	5
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chr16	14361406	14361430 -	5
chr16	14587878	14587903 -	5
chr16	14616053	14616077 -	5
chr16	14646871	14646895 -	5
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chr16	14981344	14981368 -	5
chr16	14983192	14983216 +	5
chr16	14997128	14997152 +	5
chr16	15126591	15126615 -	5
chr16	15168281	15168305 +	5
chr16	15429060	15429084 +	5
chr16	15440589	15440613 +	5
chr16	15445901	15445925 +	5
chr16	15510236	15510261 +	5
chr16	15544416	15544440 -	5
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chr16	15886410	15886434 -	5
chr16	16031472	16031497 -	5
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chr16	16247964	16247988 +	5

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chr16	16542683	16542708 -	5
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chr16	17091267	17091292 -	5
chr16	17179879	17179903 -	5
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chr16	17508572	17508596 +	5
chr16	17523951	17523976 -	5
chr16	17559923	17559947 -	5
chr16	17615190	17615214 +	5
chr16	17647335	17647359 +	5
chr16	17841220	17841244 +	5
chr16	17889607	17889631 -	5
chr16	17917378	17917403 -	5
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chr16	18079987	18080011 +	5
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chr16	18642610	18642634 +	5
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chr16	19066009	19066033 -	5
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chr16	20516777	20516801 +	5
chr16	20563223	20563247 -	5
chr16	20651701	20651725 -	5

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chr16	20822188	20822212 -	5
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chr16	20940755	20940779 -	5
chr16	21466659	21466683 +	5
chr16	21565171	21565195 +	5
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chr16	22082571	22082595 +	5
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chr16	22675390	22675414 -	5
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chr16	26174479	26174503 -	5
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chr16	26360324	26360348 +	5

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chr16	26476655	26476679 +	5
chr16	26516498	26516522 -	5
chr16	26522723	26522747 -	5
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chr16	26889400	26889424 -	5
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chr16	27166924	27166948 -	5
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chr16	28431553	28431578 -	5
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chr16	30363627	30363651 -	5
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chr16	31744146	31744170 -	5
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chr16	31855888	31855912 -	5
chr16	31917280	31917303 +	5
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chr16	32331096	32331120 -	5
chr16	32334507	32334531 -	5
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chr16	32699450	32699474 -	5

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chr16	33170926	33170950 +	5
chr16	33281006	33281030 +	5
chr16	33540523	33540547 -	5
chr16	33657448	33657472 +	5
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chr16	33764947	33764971 +	5
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chr16	34649704	34649728 -	5
chr16	34724947	34724972 -	5
chr16	34972818	34972842 +	5
chr16	35045159	35045183 -	5
chr16	35089293	35089318 -	5
chr16	35178806	35178830 -	5
chr16	35186079	35186103 -	5
chr16	35269816	35269840 +	5
chr16	35407217	35407241 +	5
chr16	35821689	35821714 +	5
chr16	35852362	35852387 +	5
chr16	35880850	35880874 -	5
chr16	35908344	35908369 -	5
chr16	46416082	46416106 -	5
chr16	46501706	46501730 +	5
chr16	46526805	46526829 +	5
chr16	46532250	46532274 -	5
chr16	46629258	46629282 +	5
chr16	46833586	46833610 +	5
chr16	46944804	46944828 -	5
chr16	46960297	46960321 -	5
chr16	47141522	47141547 -	5
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chr16	47565931	47565955 -	5
chr16	47606005	47606029 +	5
chr16	47611555	47611579 +	5
chr16	47624754	47624778 -	5
chr16	47627321	47627345 +	5
chr16	47735997	47736021 +	5
chr16	47749280	47749305 -	5
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chr16	47835602	47835626 +	5
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chr16	48045231	48045255 -	5
chr16	48078262	48078286 +	5
chr16	48130786	48130810 -	5
chr16	48131809	48131833 +	5

chr16	48158173	48158197 -	5
chr16	48164835	48164859 -	5
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chr16_KI270728v1_randorr	1719688	1719712 +	5
chr16_KI270728v1_randorr	1723097	1723121 +	5
chr16_KI270728v1_randorr	1840825	1840849 -	5
chr16_KI270853v1_alt	160735	160760 -	5
chr16_KI270853v1_alt	160774	160799 -	5
chr16_KI270853v1_alt	188909	188933 -	5
chr16_KI270853v1_alt	198627	198652 -	5
chr16_KI270853v1_alt	219727	219751 -	5
chr16_KI270853v1_alt	494205	494229 -	5
chr16_KI270853v1_alt	538643	538667 +	5
chr16_KI270853v1_alt	672533	672557 -	5
chr16_KI270853v1_alt	686461	686485 -	5
chr16_KI270853v1_alt	688309	688333 +	5
chr16_KI270853v1_alt	735365	735389 -	5
chr16_KI270853v1_alt	820693	820717 -	5
chr16_KI270853v1_alt	822541	822565 +	5
chr16_KI270853v1_alt	836474	836498 +	5
chr16_KI270853v1_alt	1054928	1054952 -	5
chr16_KI270853v1_alt	1087032	1087056 +	5
chr16_KI270853v1_alt	1098564	1098588 +	5
chr16_KI270853v1_alt	1103885	1103909 +	5

chr16_KI270853v1_alt	1168228	1168253 +	5
chr16_KI270853v1_alt	1170937	1170962 -	5
chr16_KI270853v1_alt	1202408	1202432 -	5
chr16_KI270853v1_alt	1299800	1299824 -	5
chr16_KI270853v1_alt	1544411	1544435 -	5
chr16_KI270853v1_alt	1689350	1689375 -	5
chr16_KI270853v1_alt	1802213	1802237 +	5
chr16_KI270853v1_alt	1905962	1905986 +	5
chr16_KI270853v1_alt	2037179	2037203 +	5
chr16_KI270853v1_alt	2190451	2190475 +	5
chr16_KI270853v1_alt	2203743	2203768 -	5
chr16_KI270853v1_alt	2519965	2519989 -	5
chr16_KI270853v1_alt	2616951	2616976 -	5
chr16_KI270855v1_alt	132577	132601 +	5
chr17	80820	80844 -	5
chr17	373795	373819 +	5
chr17	607449	607473 -	5
chr17	740593	740617 +	5
chr17	740638	740662 +	5
chr17	740683	740707 +	5
chr17	740727	740751 +	5
chr17	740771	740795 +	5
chr17	1478184	1478208 +	5
chr17	1585033	1585058 +	5
chr17	1808529	1808553 -	5
chr17	1933616	1933640 -	5
chr17	2165112	2165136 -	5
chr17	2241199	2241223 +	5
chr17	2480791	2480815 +	5
chr17	2634607	2634631 -	5
chr17	2729691	2729715 -	5
chr17	2822251	2822275 -	5
chr17	2868442	2868466 +	5
chr17	2884281	2884305 -	5
chr17	2973096	2973121 +	5
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chr17	3096787	3096811 -	5
chr17	3163920	3163944 -	5
chr17	3221425	3221449 +	5
chr17	3401386	3401410 -	5
chr17	3448680	3448705 +	5
chr17	3515212	3515235 +	5
chr17	3617917	3617942 +	5
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chr17	3801777	3801801 -	5
chr17	3956989	3957013 -	5
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chr17	4049677	4049701 +	5

chr17	4072256	4072280 +	5
chr17	4081274	4081298 -	5
chr17	4107859	4107883 +	5
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chr17	4155829	4155853 -	5
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chr17	4561212	4561236 -	5
chr17	4679269	4679293 +	5
chr17	5100725	5100749 -	5
chr17	5269363	5269387 -	5
chr17	5326029	5326054 -	5
chr17	5355547	5355572 -	5
chr17	5480147	5480171 +	5
chr17	5491718	5491742 +	5
chr17	5681431	5681455 +	5
chr17	5726543	5726567 +	5
chr17	5809062	5809086 +	5
chr17	5876657	5876681 -	5
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chr17	5951581	5951605 -	5
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chr17	6353008	6353032 +	5
chr17	6381015	6381039 -	5
chr17	6452798	6452822 -	5
chr17	6494693	6494717 -	5
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chr17	6598887	6598911 +	5
chr17	6653214	6653238 +	5
chr17	6691444	6691469 +	5
chr17	7025297	7025321 -	5
chr17	7058184	7058209 -	5
chr17	7058832	7058856 +	5
chr17	7145201	7145225 +	5
chr17	7152385	7152410 -	5
chr17	7210866	7210891 +	5
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chr17	7761222	7761246 +	5
chr17	7786623	7786647 +	5
chr17	7909639	7909663 -	5
chr17	8038003	8038027 -	5
chr17	8276553	8276577 +	5
chr17	8372228	8372253 +	5

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chr17	8795342	8795366 -	5
chr17	8855721	8855746 -	5
chr17	8904786	8904810 +	5
chr17	8916843	8916867 +	5
chr17	8931052	8931076 -	5
chr17	8941462	8941486 +	5
chr17	8969034	8969058 +	5
chr17	9080755	9080779 +	5
chr17	9120622	9120646 -	5
chr17	9154797	9154822 +	5
chr17	9282489	9282513 -	5
chr17	9308098	9308122 -	5
chr17	9811140	9811164 -	5
chr17	9920138	9920162 +	5
chr17	9935726	9935750 +	5
chr17	10043196	10043220 -	5
chr17	10081963	10081988 -	5
chr17	10241017	10241042 +	5
chr17	10259638	10259663 +	5
chr17	10297933	10297957 +	5
chr17	10318247	10318271 -	5
chr17	10350439	10350463 +	5
chr17	10361202	10361227 +	5
chr17	10395254	10395278 -	5
chr17	10493168	10493192 -	5
chr17	10517518	10517542 -	5
chr17	10681763	10681787 -	5
chr17	10747092	10747116 +	5
chr17	10834270	10834294 +	5
chr17	11084230	11084255 +	5
chr17	11086887	11086911 -	5
chr17	11203997	11204022 +	5
chr17	11215059	11215084 +	5
chr17	11343778	11343802 +	5
chr17	11453454	11453478 +	5
chr17	11472778	11472803 +	5
chr17	11771878	11771902 -	5
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chr17	11944150	11944174 +	5
chr17	11983821	11983845 -	5
chr17	12000993	12001017 -	5
chr17	12131765	12131790 +	5
chr17	12180827	12180851 -	5
chr17	12315723	12315747 -	5
chr17	12344613	12344637 +	5
chr17	12383342	12383366 -	5
chr17	12400039	12400064 -	5

chr17	12614128	12614152 -	5
chr17	12709384	12709409 -	5
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chr17	13004624	13004649 +	5
chr17	13106116	13106140 +	5
chr17	13258454	13258478 -	5
chr17	13299544	13299568 +	5
chr17	13326637	13326661 -	5
chr17	13331479	13331503 -	5
chr17	13351837	13351862 +	5
chr17	13370356	13370381 +	5
chr17	13391719	13391743 +	5
chr17	13541590	13541615 -	5
chr17	13617680	13617705 -	5
chr17	13661080	13661104 -	5
chr17	13687020	13687044 -	5
chr17	13691360	13691385 +	5
chr17	13693507	13693531 -	5
chr17	13747192	13747216 -	5
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chr17	14605322	14605346 +	5
chr17	14614671	14614695 -	5
chr17	14617629	14617654 -	5
chr17	14645723	14645747 -	5
chr17	14678176	14678200 +	5
chr17	14708655	14708679 -	5
chr17	14746138	14746162 +	5
chr17	14821280	14821305 -	5
chr17	14837716	14837741 -	5
chr17	14874993	14875017 -	5
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chr17	14931222	14931246 -	5
chr17	14967124	14967149 +	5
chr17	14983140	14983164 -	5
chr17	15016124	15016148 -	5
chr17	15064386	15064410 +	5
chr17	15131885	15131909 +	5
chr17	15148055	15148079 -	5
chr17	15151588	15151612 +	5
chr17	15238642	15238666 +	5
chr17	15247690	15247715 -	5
chr17	15290369	15290394 +	5
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chr17	15643280	15643304 -	5
chr17	15720828	15720852 +	5
chr17	15884035	15884059 -	5

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chr17	16069768	16069792 +	5
chr17	16070017	16070041 -	5
chr17	16150012	16150037 +	5
chr17	16382895	16382919 -	5
chr17	16668213	16668237 -	5
chr17	16787614	16787638 -	5
chr17	16901120	16901145 +	5
chr17	16942695	16942719 +	5
chr17	17412706	17412730 -	5
chr17	17907204	17907229 +	5
chr17	17930879	17930903 +	5
chr17	17939767	17939791 +	5
chr17	17940345	17940369 -	5
chr17	18528060	18528084 +	5
chr17	18653042	18653066 -	5
chr17	18658367	18658391 -	5
chr17	18721751	18721775 +	5
chr17	18943302	18943327 -	5
chr17	18968259	18968283 +	5
chr17	19050223	19050247 +	5
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chr17	19339234	19339259 -	5
chr17	19559081	19559105 +	5
chr17	19591267	19591291 +	5
chr17	19704313	19704337 -	5
chr17	19794358	19794382 +	5
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chr17	20813910	20813934 +	5
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chr17	20880573	20880597 -	5
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chr17	21217232	21217256 -	5
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chr17	21538005	21538029 +	5
chr17	21568068	21568092 -	5
chr17	21639020	21639044 +	5

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chr17	22508705	22508729 +	5
chr17	22510239	22510263 -	5
chr17	22534415	22534439 +	5
chr17	22657226	22657251 -	5
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chr17	26788984	26789008 +	5
chr17	26960703	26960727 +	5
chr17	27224545	27224569 +	5
chr17	27495709	27495733 -	5
chr17	27516570	27516594 +	5
chr17	27860923	27860947 +	5
chr17	27919279	27919303 -	5
chr17	27930481	27930505 +	5
chr17	28126481	28126505 +	5
chr17	28171734	28171759 -	5
chr17	28577102	28577126 -	5
chr17	28687648	28687672 -	5
chr17	28724359	28724383 -	5
chr17	28927532	28927556 -	5
chr17	28982150	28982174 -	5
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chr17	29441916	29441940 -	5
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chr17	29614724	29614749 +	5
chr17	29660732	29660757 -	5
chr17	29717109	29717133 -	5
chr17	29777524	29777548 -	5
chr17	29980743	29980767 -	5
chr17	29987572	29987596 -	5
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chr17	30777219	30777243 +	5
chr17	30844826	30844850 +	5
chr17	30876183	30876207 -	5
chr17	30921114	30921138 +	5
chr17	31015965	31015989 -	5
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chr17	31330532	31330556 +	5

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chr17	31518022	31518046 +	5
chr17	31705180	31705204 +	5
chr17	31746854	31746878 -	5
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chr17	32224790	32224814 -	5
chr17	32240644	32240668 +	5
chr17	32375056	32375080 +	5
chr17	32464679	32464704 +	5
chr17	32479091	32479116 -	5
chr17	32510463	32510488 +	5
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chr17	32576223	32576247 +	5
chr17	32669619	32669644 +	5
chr17	32746963	32746987 +	5
chr17	32782123	32782147 +	5
chr17	32808533	32808557 +	5
chr17	32857138	32857163 +	5
chr17	32938676	32938700 +	5
chr17	32995321	32995346 +	5
chr17	33003730	33003754 +	5
chr17	33034663	33034687 -	5
chr17	33068829	33068852 -	5
chr17	33076938	33076962 +	5
chr17	33108154	33108178 +	5
chr17	33119682	33119706 +	5
chr17	33125012	33125036 +	5
chr17	33226484	33226508 +	5
chr17	33334899	33334923 +	5
chr17	33345308	33345332 +	5
chr17	33533045	33533069 +	5
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chr17	36682471	36682496 -	5
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chr17	36851892	36851917 -	5
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chr17	37034449	37034473 -	5
chr17	37227149	37227173 +	5
chr17	37230527	37230551 -	5
chr17	37240094	37240119 -	5
chr17	37273267	37273291 -	5
chr17	37360250	37360274 -	5
chr17	37412405	37412429 +	5
chr17	37568520	37568544 +	5
chr17	37588157	37588181 -	5
chr17	37911076	37911100 -	5
chr17	38335812	38335836 -	5
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chr17	38981587	38981612 -	5
chr17	38994333	38994358 -	5
chr17	39046239	39046263 -	5
chr17	39053392	39053415 -	5
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chr17	39098737	39098761 +	5
chr17	39341677	39341702 +	5
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chr17	40818400	40818424 +	5

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chr17	41266785	41266810 +	5
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chr17	44943532	44943556 +	5
chr17	45096436	45096460 -	5
chr17	45099124	45099148 +	5
chr17	45393277	45393301 -	5
chr17	45644647	45644672 +	5
chr17	45864341	45864364 +	5
chr17	45942056	45942080 +	5
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chr17	47577750	47577774 -	5
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chr17	48321050	48321074 +	5
chr17	48340723	48340747 +	5
chr17	48350204	48350228 +	5
chr17	48363176	48363200 -	5
chr17	48474721	48474745 +	5
chr17	48638516	48638540 +	5
chr17	48950913	48950937 -	5
chr17	49050685	49050709 +	5
chr17	49073253	49073277 -	5
chr17	49166060	49166084 +	5
chr17	49323427	49323451 -	5
chr17	49330122	49330146 -	5
chr17	49431467	49431491 -	5
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chr17	49634230	49634254 -	5
chr17	49660993	49661017 -	5
chr17	49881974	49881998 +	5
chr17	49896337	49896361 +	5
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chr17	50251427	50251451 -	5
chr17	50319122	50319146 +	5
chr17	50330630	50330654 -	5
chr17	50381901	50381926 -	5
chr17	50382590	50382615 +	5
chr17	50383670	50383694 +	5
chr17	50800989	50801013 +	5
chr17	50955617	50955641 -	5
chr17	51087328	51087352 +	5
chr17	51152850	51152874 -	5
chr17	51208261	51208285 +	5
chr17	51215562	51215586 +	5
chr17	51291982	51292006 -	5
chr17	51450140	51450164 +	5
chr17	51518567	51518591 -	5

chr17	51521594	51521618 -	5
chr17	51524194	51524218 +	5
chr17	51605054	51605078 +	5
chr17	51606360	51606385 -	5
chr17	51636214	51636238 +	5
chr17	51916679	51916703 +	5
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chr17	61653577	61653601 +	5
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chr17	63138646	63138670 -	5
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chr17	69250147	69250171 -	5
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chr17	70307794	70307818 -	5
chr17	70347813	70347838 +	5
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chr17	70448296	70448321 +	5
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chr17	70566163	70566187 +	5
chr17	70628900	70628924 -	5
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chr17	75065097	75065121 -	5
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chr17_GL000258v2_alt	83798	83822 -	5
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chr17_GL000258v2_alt	289056	289081 -	5
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chr17_GL000258v2_alt	473005	473029 +	5
chr17_GL000258v2_alt	625042	625066 +	5
chr17_GL000258v2_alt	641657	641681 -	5
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chr17_GL000258v2_alt	1665890	1665915 +	5
chr17_GL000258v2_alt	1710618	1710642 -	5
chr17_GL000258v2_alt	1711843	1711868 -	5
chr17_GL000258v2_alt	1807701	1807725 -	5
chr17_GL383563v3_alt	20820	20844 -	5
chr17_GL383563v3_alt	346849	346873 +	5
chr17_GL383564v2_alt	33179	33203 +	5
chr17_GL383564v2_alt	81925	81949 -	5
chr17_GL383565v1_alt	1517	1541 -	5
chr17_GL383565v1_alt	41536	41561 +	5
chr17_GL383565v1_alt	115630	115655 +	5
chr17_GL383565v1_alt	130840	130864 +	5
chr17_GL383565v1_alt	148072	148097 +	5
chr17_GL383565v1_alt	171010	171034 +	5
chr17_JH159146v1_alt	35590	35615 +	5
chr17_JH159146v1_alt	158086	158110 +	5
chr17_JH159146v1_alt	206878	206902 -	5
chr17_JH159148v1_alt	48207	48231 +	5
chr17_JH159148v1_alt	67181	67206 -	5
chr17_JH159148v1_alt	75150	75174 -	5
chr17_KI270729v1_random	51974	51998 +	5
chr17_KI270857v1_alt	129952	129977 +	5
chr17_KI270857v1_alt	168851	168875 +	5
chr17_KI270857v1_alt	636709	636733 +	5
chr17_KI270857v1_alt	729082	729106 -	5
chr17_KI270857v1_alt	917983	918008 -	5
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chr17_KI270857v1_alt	1463135	1463159 +	5
chr17_KI270857v1_alt	1466507	1466531 -	5
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chr17_KI270857v1_alt	1651556	1651580 +	5
chr17_KI270857v1_alt	1807687	1807711 +	5
chr17_KI270857v1_alt	1827330	1827354 -	5
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chr17_KI270857v1_alt	2813623	2813648 -	5
chr17_KI270858v1_alt	36008	36032 +	5
chr17_KI270858v1_alt	47062	47087 +	5
chr17_KI270858v1_alt	69015	69040 +	5
chr17_KI270858v1_alt	163588	163613 -	5
chr17_KI270859v1_alt	26787	26811 -	5
chr17_KI270859v1_alt	86259	86283 +	5
chr17_KI270859v1_alt	92953	92977 -	5
chr17_KI270859v1_alt	108101	108126 -	5
chr17_KI270860v1_alt	19649	19673 -	5
chr17_KI270860v1_alt	21746	21770 -	5
chr17_KI270860v1_alt	146421	146446 +	5
chr17_KI270860v1_alt	167299	167323 -	5
chr17_KI270861v1_alt	15061	15086 +	5
chr17_KI270862v1_alt	125508	125532 +	5
chr17_KI270908v1_alt	83780	83804 -	5
chr17_KI270908v1_alt	346775	346800 +	5
chr17_KI270908v1_alt	644211	644235 +	5
chr17_KI270908v1_alt	847099	847123 +	5
chr17_KI270908v1_alt	864038	864062 -	5
chr17_KI270908v1_alt	1103434	1103459 -	5
chr17_KI270908v1_alt	1173729	1173753 +	5
chr17_KI270908v1_alt	1199423	1199448 +	5
chr17_KI270908v1_alt	1244156	1244180 -	5
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chr17_KI270908v1_alt	1341414	1341438 -	5
chr17_KI270910v1_alt	121978	122002 +	5
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chr18	1435273	1435297 +	5
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chr18_KI270911v1_alt	80949	80973 -	5
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chr19	24113918	24113942 -	5
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chr19	28153025	28153050 +	5
chr19	28231333	28231357 -	5
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chr19_GL949746v1_alt	529608	529632 -	5
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chr19_GL949752v1_alt	341603	341627 +	5
chr19_GL949752v1_alt	528104	528128 -	5
chr19_GL949752v1_alt	593165	593189 +	5
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chr19_KI270867v1_alt	2438	2462 -	5
chr19_KI270867v1_alt	2827	2851 -	5
chr19_KI270867v1_alt	46299	46323 +	5
chr19_KI270867v1_alt	124985	125009 +	5
chr19_KI270938v1_alt	419209	419233 +	5
chr19_KI270938v1_alt	605791	605815 -	5
chr19_KI270938v1_alt	670960	670984 +	5
chr2	25667	25691 +	5
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chr2	178167	178191 +	5
chr2	216733	216758 -	5
chr2	304366	304390 +	5
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chr2	73652240	73652264 +	5
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chr22	50792657	50792681 -	5
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chr22_KI270734v1_randorr	25133	25158 -	5
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chr22_KI270738v1_randorr	95972	95997 -	5
chr22_KI270875v1_alt	19298	19322 +	5
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chr22_KI270875v1_alt	48842	48866 -	5
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chr22_KI270876v1_alt	53090	53114 +	5
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chr22_KI270876v1_alt	95299	95323 -	5
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chr22_KI270876v1_alt	192337	192361 +	5
chr22_KI270876v1_alt	207368	207393 +	5
chr22_KI270878v1_alt	8071	8096 +	5
chr22_KI270879v1_alt	294122	294147 +	5
chr22_KI270928v1_alt	100765	100789 -	5
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[illegible]

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chr3_GL000221v1_random	105261	105285 -	5
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chr3_KI270777v1_alt	34964	34988 +	5
chr3_KI270777v1_alt	42227	42251 -	5
chr3_KI270777v1_alt	104997	105022 +	5
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chr3_KI270778v1_alt	61141	61165 +	5
chr3_KI270778v1_alt	80342	80367 -	5
chr3_KI270778v1_alt	104894	104918 +	5
chr3_KI270778v1_alt	139045	139069 -	5
chr3_KI270778v1_alt	146603	146628 -	5
chr3_KI270778v1_alt	212884	212908 +	5
chr3_KI270778v1_alt	228076	228101 +	5
chr3_KI270780v1_alt	86932	86956 +	5
chr3_KI270780v1_alt	177930	177954 -	5
chr3_KI270782v1_alt	9600	9624 +	5
chr3_KI270783v1_alt	63349	63373 +	5
chr3_KI270784v1_alt	28735	28759 -	5
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chr3_KI270895v1_alt	90592	90616 +	5
chr3_KI270895v1_alt	100810	100834 -	5
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chr3_KI270934v1_alt	101372	101396 -	5
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chr3_KI270936v1_alt	91866	91890 +	5
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chr4	3134150	3134174 +	5
chr4	3416682	3416706 +	5
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chr4	10657882	10657906 -	5

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chr4	24392891	24392915 -	5
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chr4	24703641	24703665 -	5
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chr4	92991557	92991582 +	5
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chr4	93266765	93266789 +	5
chr4	93276872	93276896 -	5
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chr4_GL000008v2_random	58035	58059 +	5
chr4_GL000008v2_random	69605	69629 +	5
chr4_GL000008v2_random	195584	195608 +	5
chr4_GL000257v2_alt	23686	23710 -	5
chr4_GL000257v2_alt	28290	28314 +	5
chr4_GL000257v2_alt	54274	54299 -	5
chr4_GL000257v2_alt	91164	91188 +	5
chr4_GL000257v2_alt	94093	94117 -	5
chr4_GL000257v2_alt	137493	137518 -	5
chr4_GL000257v2_alt	173882	173906 -	5
chr4_GL000257v2_alt	205587	205611 +	5
chr4_GL000257v2_alt	231230	231254 +	5
chr4_GL000257v2_alt	286176	286200 +	5
chr4_GL000257v2_alt	396953	396977 -	5
chr4_GL000257v2_alt	402702	402726 -	5
chr4_GL000257v2_alt	454500	454525 +	5
chr4_GL000257v2_alt	585729	585753 +	5
chr4_GL383527v1_alt	31345	31369 +	5
chr4_GL383527v1_alt	126890	126914 -	5
chr4_GL383527v1_alt	153448	153472 -	5
chr4_GL383527v1_alt	157839	157864 -	5
chr4_GL383528v1_alt	13453	13477 -	5
chr4_GL383528v1_alt	76981	77005 +	5
chr4_GL383528v1_alt	108170	108194 -	5
chr4_GL383528v1_alt	115825	115849 -	5
chr4_GL383528v1_alt	181145	181169 +	5
chr4_GL383528v1_alt	260965	260990 +	5
chr4_GL383528v1_alt	276046	276070 +	5
chr4_GL383528v1_alt	293363	293387 -	5
chr4_GL383528v1_alt	299834	299858 -	5
chr4_KI270785v1_alt	82409	82433 +	5
chr4_KI270786v1_alt	219186	219211 -	5
chr4_KI270787v1_alt	64841	64866 +	5
chr4_KI270787v1_alt	99347	99371 +	5
chr4_KI270788v1_alt	12484	12508 -	5
chr4_KI270788v1_alt	44420	44444 +	5
chr4_KI270788v1_alt	104846	104871 -	5
chr4_KI270788v1_alt	136498	136522 -	5

chr4_KI270789v1_alt	20630	20654 -	5
chr4_KI270789v1_alt	69897	69921 +	5
chr4_KI270790v1_alt	61699	61723 +	5
chr4_KI270790v1_alt	82518	82543 -	5
chr4_KI270790v1_alt	183939	183963 +	5
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[illegible]

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chr6_GL000250v2_alt	809226	809250 +	5
chr6_GL000250v2_alt	850241	850265 +	5
chr6_GL000250v2_alt	1068475	1068500 -	5
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chr6_GL000250v2_alt	1489221	1489245 -	5
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chr6_GL000251v2_alt	3302143	3302167 +	5
chr6_GL000251v2_alt	3756191	3756215 +	5
chr6_GL000251v2_alt	3801996	3802020 -	5
chr6_GL000251v2_alt	3806748	3806773 -	5
chr6_GL000251v2_alt	4212259	4212284 -	5
chr6_GL000251v2_alt	4255391	4255415 +	5
chr6_GL000251v2_alt	4302158	4302182 +	5
chr6_GL000251v2_alt	4329037	4329061 -	5
chr6_GL000251v2_alt	4466564	4466588 +	5
chr6_GL000251v2_alt	4555211	4555235 +	5
chr6_GL000251v2_alt	4601109	4601134 +	5
chr6_GL000252v2_alt	33167	33191 +	5
chr6_GL000252v2_alt	44221	44245 +	5
chr6_GL000252v2_alt	127917	127941 -	5
chr6_GL000252v2_alt	354888	354913 +	5
chr6_GL000252v2_alt	409400	409424 +	5
chr6_GL000252v2_alt	491933	491958 -	5
chr6_GL000252v2_alt	497071	497095 +	5
chr6_GL000252v2_alt	576504	576528 +	5
chr6_GL000252v2_alt	577748	577772 -	5
chr6_GL000252v2_alt	586235	586259 -	5
chr6_GL000252v2_alt	591600	591624 +	5
chr6_GL000252v2_alt	730844	730869 +	5
chr6_GL000252v2_alt	850096	850120 +	5
chr6_GL000252v2_alt	1065668	1065693 -	5

chr6_GL000252v2_alt	1163191	1163215 -	5
chr6_GL000252v2_alt	1406374	1406399 +	5
chr6_GL000252v2_alt	1479586	1479610 +	5
chr6_GL000252v2_alt	1487042	1487066 -	5
chr6_GL000252v2_alt	1488025	1488049 -	5
chr6_GL000252v2_alt	1546440	1546464 -	5
chr6_GL000252v2_alt	1552645	1552669 -	5
chr6_GL000252v2_alt	1575513	1575537 +	5
chr6_GL000252v2_alt	1605194	1605218 +	5
chr6_GL000252v2_alt	1630221	1630245 -	5
chr6_GL000252v2_alt	1658227	1658251 +	5
chr6_GL000252v2_alt	1760717	1760742 +	5
chr6_GL000252v2_alt	1799553	1799578 +	5
chr6_GL000252v2_alt	2094407	2094431 +	5
chr6_GL000252v2_alt	2292575	2292599 -	5
chr6_GL000252v2_alt	2394946	2394970 -	5
chr6_GL000252v2_alt	2509356	2509380 +	5
chr6_GL000252v2_alt	2597615	2597639 +	5
chr6_GL000252v2_alt	2850231	2850255 -	5
chr6_GL000252v2_alt	3072668	3072692 +	5
chr6_GL000252v2_alt	3559180	3559204 +	5
chr6_GL000252v2_alt	3604988	3605012 -	5
chr6_GL000252v2_alt	3609728	3609753 -	5
chr6_GL000252v2_alt	3688038	3688063 +	5
chr6_GL000252v2_alt	3930486	3930510 -	5
chr6_GL000252v2_alt	4043445	4043470 -	5
chr6_GL000252v2_alt	4086762	4086786 +	5
chr6_GL000252v2_alt	4133481	4133505 +	5
chr6_GL000252v2_alt	4160367	4160391 -	5
chr6_GL000252v2_alt	4297983	4298007 +	5
chr6_GL000252v2_alt	4387224	4387248 +	5
chr6_GL000252v2_alt	4433101	4433126 +	5
chr6_GL000253v2_alt	33140	33164 +	5
chr6_GL000253v2_alt	44192	44216 +	5
chr6_GL000253v2_alt	127873	127897 -	5
chr6_GL000253v2_alt	213564	213589 -	5
chr6_GL000253v2_alt	354845	354870 +	5
chr6_GL000253v2_alt	409356	409380 +	5
chr6_GL000253v2_alt	491895	491920 -	5
chr6_GL000253v2_alt	497033	497057 +	5
chr6_GL000253v2_alt	576463	576487 +	5
chr6_GL000253v2_alt	577707	577731 -	5
chr6_GL000253v2_alt	586194	586218 -	5
chr6_GL000253v2_alt	591559	591583 +	5
chr6_GL000253v2_alt	730446	730471 +	5
chr6_GL000253v2_alt	808690	808714 +	5
chr6_GL000253v2_alt	849731	849755 +	5
chr6_GL000253v2_alt	1065352	1065377 -	5

chr6_GL000253v2_alt	1162331	1162355 -	5
chr6_GL000253v2_alt	1461179	1461204 +	5
chr6_GL000253v2_alt	1534354	1534378 +	5
chr6_GL000253v2_alt	1541818	1541842 -	5
chr6_GL000253v2_alt	1542801	1542825 -	5
chr6_GL000253v2_alt	1577625	1577649 +	5
chr6_GL000253v2_alt	1600823	1600847 -	5
chr6_GL000253v2_alt	1607032	1607056 -	5
chr6_GL000253v2_alt	1629901	1629925 +	5
chr6_GL000253v2_alt	1659582	1659606 +	5
chr6_GL000253v2_alt	1684610	1684634 -	5
chr6_GL000253v2_alt	1712614	1712638 +	5
chr6_GL000253v2_alt	1815120	1815145 +	5
chr6_GL000253v2_alt	1853959	1853984 +	5
chr6_GL000253v2_alt	2148390	2148414 +	5
chr6_GL000253v2_alt	2346444	2346468 -	5
chr6_GL000253v2_alt	2446137	2446161 -	5
chr6_GL000253v2_alt	2560614	2560638 +	5
chr6_GL000253v2_alt	2658702	2658726 +	5
chr6_GL000253v2_alt	2671275	2671299 +	5
chr6_GL000253v2_alt	2764215	2764239 +	5
chr6_GL000253v2_alt	2907520	2907544 -	5
chr6_GL000253v2_alt	3622715	3622739 +	5
chr6_GL000253v2_alt	3668874	3668898 -	5
chr6_GL000253v2_alt	3673597	3673622 -	5
chr6_GL000253v2_alt	3751957	3751982 +	5
chr6_GL000253v2_alt	4218344	4218369 -	5
chr6_GL000253v2_alt	4262545	4262569 +	5
chr6_GL000253v2_alt	4309312	4309336 +	5
chr6_GL000253v2_alt	4336197	4336221 -	5
chr6_GL000253v2_alt	4563171	4563195 +	5
chr6_GL000253v2_alt	4609074	4609099 +	5
chr6_GL000254v2_alt	213750	213775 -	5
chr6_GL000254v2_alt	355017	355042 +	5
chr6_GL000254v2_alt	409537	409561 +	5
chr6_GL000254v2_alt	576684	576708 +	5
chr6_GL000254v2_alt	577928	577952 -	5
chr6_GL000254v2_alt	586415	586439 -	5
chr6_GL000254v2_alt	591780	591804 +	5
chr6_GL000254v2_alt	730695	730720 +	5
chr6_GL000254v2_alt	849942	849966 +	5
chr6_GL000254v2_alt	1065325	1065350 -	5
chr6_GL000254v2_alt	1494535	1494560 +	5
chr6_GL000254v2_alt	1746420	1746444 +	5
chr6_GL000254v2_alt	1848939	1848964 +	5
chr6_GL000254v2_alt	1887776	1887801 +	5
chr6_GL000254v2_alt	2380068	2380092 -	5
chr6_GL000254v2_alt	2479749	2479773 -	5

chr6_GL000254v2_alt	2556123	2556147 +	5
chr6_GL000254v2_alt	2594291	2594315 +	5
chr6_GL000254v2_alt	2692063	2692087 +	5
chr6_GL000254v2_alt	2704647	2704671 +	5
chr6_GL000254v2_alt	3659811	3659835 +	5
chr6_GL000254v2_alt	3705624	3705648 -	5
chr6_GL000254v2_alt	3710363	3710388 -	5
chr6_GL000254v2_alt	3788696	3788721 +	5
chr6_GL000254v2_alt	3985121	3985145 -	5
chr6_GL000254v2_alt	4098082	4098107 -	5
chr6_GL000254v2_alt	4142261	4142285 +	5
chr6_GL000254v2_alt	4188989	4189013 +	5
chr6_GL000254v2_alt	4215887	4215911 -	5
chr6_GL000254v2_alt	4353514	4353538 +	5
chr6_GL000254v2_alt	4625558	4625583 +	5
chr6_GL000255v2_alt	213583	213608 -	5
chr6_GL000255v2_alt	354867	354892 +	5
chr6_GL000255v2_alt	409383	409407 +	5
chr6_GL000255v2_alt	491919	491944 -	5
chr6_GL000255v2_alt	497057	497081 +	5
chr6_GL000255v2_alt	730787	730812 +	5
chr6_GL000255v2_alt	809030	809054 +	5
chr6_GL000255v2_alt	850059	850083 +	5
chr6_GL000255v2_alt	1065627	1065652 -	5
chr6_GL000255v2_alt	1162836	1162860 -	5
chr6_GL000255v2_alt	1405586	1405611 +	5
chr6_GL000255v2_alt	1478812	1478836 +	5
chr6_GL000255v2_alt	1486268	1486292 -	5
chr6_GL000255v2_alt	1487251	1487275 -	5
chr6_GL000255v2_alt	1545672	1545696 -	5
chr6_GL000255v2_alt	1551877	1551901 -	5
chr6_GL000255v2_alt	1574749	1574773 +	5
chr6_GL000255v2_alt	1604430	1604454 +	5
chr6_GL000255v2_alt	1629454	1629478 -	5
chr6_GL000255v2_alt	1657463	1657487 +	5
chr6_GL000255v2_alt	1759984	1760009 +	5
chr6_GL000255v2_alt	1798814	1798839 +	5
chr6_GL000255v2_alt	2093239	2093263 +	5
chr6_GL000255v2_alt	2291564	2291588 -	5
chr6_GL000255v2_alt	2393641	2393665 -	5
chr6_GL000255v2_alt	2605786	2605810 +	5
chr6_GL000255v2_alt	2618359	2618383 +	5
chr6_GL000255v2_alt	2858293	2858317 -	5
chr6_GL000255v2_alt	3080720	3080744 +	5
chr6_GL000255v2_alt	3541096	3541120 +	5
chr6_GL000255v2_alt	3586917	3586941 -	5
chr6_GL000255v2_alt	3591653	3591678 -	5
chr6_GL000255v2_alt	3670788	3670813 +	5

chr6_GL000255v2_alt	4037480	4037504 +	5
chr6_GL000255v2_alt	4084246	4084270 +	5
chr6_GL000255v2_alt	4111141	4111165 -	5
chr6_GL000255v2_alt	4248739	4248763 +	5
chr6_GL000255v2_alt	4338102	4338126 +	5
chr6_GL000255v2_alt	4384005	4384030 +	5
chr6_GL000256v2_alt	76931	76955 +	5
chr6_GL000256v2_alt	87980	88004 +	5
chr6_GL000256v2_alt	171563	171587 -	5
chr6_GL000256v2_alt	257391	257416 -	5
chr6_GL000256v2_alt	271062	271086 -	5
chr6_GL000256v2_alt	398650	398675 +	5
chr6_GL000256v2_alt	453161	453185 +	5
chr6_GL000256v2_alt	535705	535730 -	5
chr6_GL000256v2_alt	540843	540867 +	5
chr6_GL000256v2_alt	620294	620318 +	5
chr6_GL000256v2_alt	621538	621562 -	5
chr6_GL000256v2_alt	630036	630060 -	5
chr6_GL000256v2_alt	635396	635420 +	5
chr6_GL000256v2_alt	774334	774359 +	5
chr6_GL000256v2_alt	1108888	1108913 -	5
chr6_GL000256v2_alt	1205724	1205748 -	5
chr6_GL000256v2_alt	1449385	1449410 +	5
chr6_GL000256v2_alt	1522593	1522617 +	5
chr6_GL000256v2_alt	1530057	1530081 -	5
chr6_GL000256v2_alt	1531040	1531064 -	5
chr6_GL000256v2_alt	1589049	1589073 -	5
chr6_GL000256v2_alt	1595255	1595279 -	5
chr6_GL000256v2_alt	1618130	1618154 +	5
chr6_GL000256v2_alt	1647805	1647829 +	5
chr6_GL000256v2_alt	1672820	1672844 -	5
chr6_GL000256v2_alt	1700835	1700859 +	5
chr6_GL000256v2_alt	1805652	1805677 +	5
chr6_GL000256v2_alt	1844486	1844511 +	5
chr6_GL000256v2_alt	2138854	2138878 +	5
chr6_GL000256v2_alt	2336663	2336687 -	5
chr6_GL000256v2_alt	2652327	2652351 +	5
chr6_GL000256v2_alt	2664902	2664926 +	5
chr6_GL000256v2_alt	2758399	2758423 +	5
chr6_GL000256v2_alt	2901760	2901784 -	5
chr6_GL000256v2_alt	3633982	3634006 +	5
chr6_GL000256v2_alt	3679795	3679819 -	5
chr6_GL000256v2_alt	3684533	3684558 -	5
chr6_GL000256v2_alt	3762873	3762898 +	5
chr6_GL000256v2_alt	4129462	4129486 +	5
chr6_GL000256v2_alt	4133798	4133822 +	5
chr6_GL000256v2_alt	4199147	4199172 -	5
chr6_GL000256v2_alt	4242444	4242468 +	5

chr6_GL000256v2_alt	4289170	4289194 +	5
chr6_GL000256v2_alt	4316075	4316099 -	5
chr6_GL000256v2_alt	4503470	4503494 +	5
chr6_GL000256v2_alt	4638246	4638271 +	5
chr6_GL000256v2_alt	4896456	4896480 +	5
chr6_GL000256v2_alt	4920635	4920659 +	5
chr6_GL383533v1_alt	7014	7038 -	5
chr6_GL383533v1_alt	54360	54384 -	5
chr6_GL383533v1_alt	117164	117188 +	5
chr6_KB021644v2_alt	150348	150373 -	5
chr6_KB021644v2_alt	158789	158813 -	5
chr6_KI270797v1_alt	180191	180215 +	5
chr6_KI270798v1_alt	74083	74107 +	5
chr6_KI270798v1_alt	101284	101308 -	5
chr6_KI270798v1_alt	177385	177409 -	5
chr6_KI270798v1_alt	218817	218842 -	5
chr6_KI270798v1_alt	224791	224816 -	5
chr6_KI270799v1_alt	30493	30517 -	5
chr6_KI270799v1_alt	59841	59865 +	5
chr6_KI270799v1_alt	61473	61497 +	5
chr6_KI270799v1_alt	110893	110917 -	5
chr6_KI270800v1_alt	1857	1882 +	5
chr6_KI270800v1_alt	31283	31307 -	5
chr6_KI270800v1_alt	42343	42368 -	5
chr6_KI270800v1_alt	70018	70042 +	5
chr6_KI270800v1_alt	117806	117830 -	5
chr6_KI270800v1_alt	145687	145711 +	5
chr6_KI270801v1_alt	49437	49462 -	5
chr6_KI270801v1_alt	113270	113295 -	5
chr6_KI270801v1_alt	143413	143437 -	5
chr6_KI270801v1_alt	153787	153811 -	5
chr6_KI270801v1_alt	191685	191709 -	5
chr6_KI270801v1_alt	202709	202734 -	5
chr6_KI270801v1_alt	248838	248863 +	5
chr6_KI270801v1_alt	285764	285788 +	5
chr6_KI270801v1_alt	376533	376557 -	5
chr6_KI270801v1_alt	391268	391293 -	5
chr6_KI270801v1_alt	400847	400871 -	5
chr6_KI270801v1_alt	409783	409807 +	5
chr6_KI270801v1_alt	556502	556527 -	5
chr6_KI270801v1_alt	628275	628300 +	5
chr6_KI270801v1_alt	692425	692449 -	5
chr6_KI270801v1_alt	758041	758065 -	5
chr6_KI270801v1_alt	769733	769757 -	5
chr7	22023	22047 -	5
chr7	204176	204200 -	5
chr7	230872	230897 +	5
chr7	398243	398267 +	5

chr7	1112121	1112145 +	5
chr7	1122196	1122220 -	5
chr7	1242034	1242059 -	5
chr7	1298062	1298087 -	5
chr7	1377928	1377952 -	5
chr7	1422893	1422918 -	5
chr7	1436979	1437003 +	5
chr7	1629107	1629131 -	5
chr7	1672660	1672684 +	5
chr7	1706655	1706679 +	5
chr7	1710814	1710838 -	5
chr7	1799846	1799870 +	5
chr7	2045611	2045635 -	5
chr7	2482304	2482329 +	5
chr7	2727540	2727564 +	5
chr7	2785409	2785433 +	5
chr7	3053011	3053035 -	5
chr7	3071864	3071888 -	5
chr7	3106541	3106566 -	5
chr7	3107586	3107611 -	5
chr7	3178284	3178309 +	5
chr7	3306928	3306952 +	5
chr7	3378315	3378339 -	5
chr7	3392129	3392154 +	5
chr7	3430309	3430333 +	5
chr7	3482764	3482788 +	5
chr7	3617816	3617840 -	5
chr7	3625716	3625740 -	5
chr7	3684594	3684618 -	5
chr7	3685468	3685492 +	5
chr7	3754930	3754955 -	5
chr7	3831659	3831683 +	5
chr7	3865435	3865460 +	5
chr7	3923976	3924000 +	5
chr7	4091654	4091678 +	5
chr7	4144878	4144902 -	5
chr7	4527945	4527969 +	5
chr7	4618743	4618767 +	5
chr7	4981853	4981877 +	5
chr7	5008303	5008327 -	5
chr7	5116636	5116660 -	5
chr7	5190900	5190924 -	5
chr7	5715513	5715538 +	5
chr7	5717429	5717454 -	5
chr7	5732612	5732636 -	5
chr7	5784028	5784052 +	5
chr7	5825132	5825156 +	5
chr7	5980180	5980204 -	5

chr7	5981898	5981923 +	5
chr7	6036849	6036873 +	5
chr7	6110755	6110779 +	5
chr7	6139156	6139180 +	5
chr7	6204744	6204768 -	5
chr7	6320222	6320246 +	5
chr7	6742758	6742783 -	5
chr7	6744574	6744598 +	5
chr7	7078722	7078747 +	5
chr7	7120937	7120961 +	5
chr7	7128278	7128303 +	5
chr7	7253146	7253170 +	5
chr7	7267125	7267149 -	5
chr7	7274001	7274024 +	5
chr7	7276996	7277020 +	5
chr7	7283422	7283446 +	5
chr7	7378273	7378297 -	5
chr7	7449513	7449537 +	5
chr7	7510266	7510290 -	5
chr7	7730682	7730706 -	5
chr7	7748668	7748692 -	5
chr7	7829656	7829680 +	5
chr7	7844542	7844566 -	5
chr7	7904348	7904372 +	5
chr7	7906119	7906144 +	5
chr7	7986679	7986703 +	5
chr7	8152523	8152547 -	5
chr7	8213627	8213651 +	5
chr7	8219104	8219129 +	5
chr7	8224929	8224953 -	5
chr7	8248896	8248921 -	5
chr7	8281977	8282001 +	5
chr7	8503574	8503598 -	5
chr7	8510240	8510265 +	5
chr7	8583481	8583506 +	5
chr7	8584893	8584917 -	5
chr7	8614736	8614761 +	5
chr7	8628126	8628150 +	5
chr7	8673171	8673195 +	5
chr7	8690930	8690954 -	5
chr7	8809228	8809252 +	5
chr7	8864800	8864824 -	5
chr7	8883564	8883588 -	5
chr7	8960567	8960591 -	5
chr7	8983009	8983033 +	5
chr7	9014622	9014646 -	5
chr7	9038823	9038847 -	5
chr7	9098041	9098065 +	5

chr7	9118718	9118742 +	5
chr7	9135000	9135025 -	5
chr7	9207293	9207317 -	5
chr7	9239280	9239304 +	5
chr7	9307657	9307681 -	5
chr7	9321418	9321443 +	5
chr7	9455876	9455900 +	5
chr7	9562937	9562962 +	5
chr7	9575754	9575778 +	5
chr7	9648715	9648739 -	5
chr7	9700150	9700174 +	5
chr7	9709075	9709100 -	5
chr7	9731786	9731810 -	5
chr7	9761058	9761082 +	5
chr7	9818709	9818733 -	5
chr7	9869216	9869240 +	5
chr7	9882428	9882452 +	5
chr7	9891079	9891103 -	5
chr7	9955624	9955648 +	5
chr7	10005491	10005515 -	5
chr7	10030979	10031003 -	5
chr7	10051706	10051730 -	5
chr7	10052293	10052316 -	5
chr7	10209400	10209425 +	5
chr7	10216375	10216399 -	5
chr7	10228125	10228149 +	5
chr7	10599150	10599175 +	5
chr7	10634752	10634776 -	5
chr7	10683589	10683614 -	5
chr7	10788542	10788565 +	5
chr7	10865733	10865757 +	5
chr7	10872673	10872697 +	5
chr7	10929088	10929113 -	5
chr7	10945351	10945375 +	5
chr7	11001882	11001906 +	5
chr7	11104004	11104028 +	5
chr7	11150856	11150880 -	5
chr7	11154779	11154803 -	5
chr7	11285224	11285248 +	5
chr7	11311318	11311342 -	5
chr7	11418324	11418348 +	5
chr7	11538003	11538027 -	5
chr7	11612192	11612216 +	5
chr7	11657863	11657887 +	5
chr7	11688284	11688308 +	5
chr7	11788197	11788221 +	5
chr7	11789315	11789339 +	5
chr7	11828348	11828372 -	5

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chr7_KI270803v1_alt	664798	664822 +	5
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chr7_KI270805v1_alt	156455	156479 -	5
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chr7_KI270806v1_alt	128014	128038 -	5
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chr8	6605589	6605613 +	5
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chr9	89757870	89757894 -	5
chr9	89809322	89809346 -	5
chr9	89831572	89831596 +	5
chr9	89833178	89833202 -	5
chr9	89844068	89844092 +	5
chr9	90006093	90006118 +	5
chr9	90342501	90342525 +	5

chr9	90342662	90342685 +	5
chr9	90358387	90358411 +	5
chr9	90393042	90393066 +	5
chr9	90408321	90408345 +	5
chr9	90480833	90480857 -	5
chr9	90589365	90589389 +	5
chr9	90799631	90799656 +	5
chr9	91051701	91051725 -	5
chr9	91059505	91059529 -	5
chr9	91213726	91213750 +	5
chr9	91223560	91223584 -	5
chr9	91261222	91261246 +	5
chr9	91280360	91280385 -	5
chr9	91329800	91329824 -	5
chr9	91343010	91343034 -	5
chr9	91457122	91457147 -	5
chr9	91459830	91459854 +	5
chr9	91475924	91475948 +	5
chr9	91531605	91531630 -	5
chr9	91562516	91562540 -	5
chr9	91577654	91577678 +	5
chr9	91621242	91621266 +	5
chr9	91626490	91626514 +	5
chr9	91712446	91712470 -	5
chr9	91714992	91715017 +	5
chr9	91720603	91720628 -	5
chr9	91823077	91823102 +	5
chr9	91865132	91865156 +	5
chr9	91961522	91961547 +	5
chr9	92049639	92049664 +	5
chr9	92164312	92164336 +	5
chr9	92187446	92187470 +	5
chr9	92230723	92230747 +	5
chr9	92232456	92232480 +	5
chr9	92233064	92233088 -	5
chr9	92268028	92268052 +	5
chr9	92384855	92384879 -	5
chr9	92415159	92415183 +	5
chr9	92498739	92498763 +	5
chr9	92601147	92601171 -	5
chr9	92666152	92666176 -	5
chr9	92707527	92707551 -	5
chr9	92871513	92871537 +	5
chr9	92968445	92968470 +	5
chr9	93368743	93368767 +	5
chr9	93380711	93380735 +	5
chr9	93388476	93388501 +	5
chr9	93416283	93416307 -	5

chr9	93569373	93569398 -	5
chr9	93702934	93702958 -	5
chr9	93716920	93716945 +	5
chr9	93718034	93718058 +	5
chr9	93826286	93826310 +	5
chr9	93831015	93831039 -	5
chr9	93858086	93858109 -	5
chr9	93992675	93992700 -	5
chr9	93992948	93992972 +	5
chr9	94097121	94097145 +	5
chr9	94112935	94112959 -	5
chr9	94152803	94152827 -	5
chr9	94159204	94159229 -	5
chr9	94378660	94378684 -	5
chr9	94407237	94407262 -	5
chr9	94442230	94442254 -	5
chr9	94452055	94452079 -	5
chr9	94504578	94504602 +	5
chr9	94509467	94509491 +	5
chr9	94717238	94717262 -	5
chr9	94978738	94978762 +	5
chr9	95021378	95021402 +	5
chr9	95065256	95065280 +	5
chr9	95078152	95078176 +	5
chr9	95132965	95132989 -	5
chr9	95277719	95277744 +	5
chr9	95509389	95509414 -	5
chr9	95641689	95641713 +	5
chr9	95656646	95656671 +	5
chr9	95676806	95676830 -	5
chr9	95836052	95836076 -	5
chr9	95871988	95872012 +	5
chr9	95893188	95893212 +	5
chr9	95982476	95982500 +	5
chr9	96099627	96099651 +	5
chr9	96195778	96195803 -	5
chr9	96339716	96339740 +	5
chr9	96348648	96348672 +	5
chr9	96386949	96386973 -	5
chr9	96407690	96407714 +	5
chr9	96484745	96484769 +	5
chr9	96518002	96518026 +	5
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chr9	96772322	96772346 +	5
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chr9	96820941	96820965 -	5
chr9	96839635	96839659 -	5
chr9	96980830	96980855 +	5

chr9	97009514	97009538 +	5
chr9	97066730	97066755 +	5
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chr9	97174344	97174368 -	5
chr9	97279418	97279441 +	5
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chr9	97302987	97303011 +	5
chr9	97418589	97418613 +	5
chr9	97468390	97468414 -	5
chr9	97617827	97617851 +	5
chr9	97642982	97643006 -	5
chr9	97680859	97680883 +	5
chr9	97850794	97850818 -	5
chr9	97860179	97860203 +	5
chr9	97915562	97915586 -	5
chr9	97917287	97917311 +	5
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chr9	98412958	98412982 +	5
chr9	98448986	98449011 +	5
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chr9	98969188	98969212 +	5
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chr9	99524119	99524143 +	5
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chr9	99983714	99983738 +	5

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chr9	###	### +	5

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chr9	###	###+	5
chr9_GL383539v1_alt	44952	44976-	5
chr9_GL383539v1_alt	149251	149276+	5
chr9_GL383540v1_alt	5242	5266+	5
chr9_GL383540v1_alt	26252	26276+	5
chr9_GL383540v1_alt	48651	48675-	5
chr9_GL383540v1_alt	61053	61077-	5
chr9_GL383541v1_alt	12435	12459+	5
chr9_GL383541v1_alt	90438	90462-	5
chr9_GL383541v1_alt	115868	115892+	5

chr9_KI270718v1_random	13561	13586 +	5
chr9_KI270719v1_random	17019	17043 -	5
chr9_KI270719v1_random	28823	28847 -	5
chr9_KI270719v1_random	36564	36588 +	5
chr9_KI270719v1_random	134678	134702 +	5
chr9_KI270720v1_random	3317	3341 +	5
chr9_KI270823v1_alt	64348	64372 +	5
chr9_KI270823v1_alt	70441	70465 -	5
chr9_KI270823v1_alt	107757	107782 +	5
chr9_KI270823v1_alt	135922	135946 +	5
chr9_KI270823v1_alt	185427	185452 -	5
chr9_KI270823v1_alt	216319	216343 +	5
chrUn_GL000195v1	83912	83937 -	5
chrUn_GL000213v1	31640	31664 -	5
chrUn_GL000213v1	81486	81510 -	5
chrUn_GL000213v1	86573	86598 -	5
chrUn_GL000214v1	5013	5037 +	5
chrUn_GL000214v1	16663	16687 +	5
chrUn_GL000214v1	89261	89285 +	5
chrUn_GL000216v2	121242	121266 -	5
chrUn_GL000218v1	1959	1983 +	5
chrUn_GL000218v1	2675	2699 -	5
chrUn_GL000218v1	111057	111081 -	5
chrUn_GL000218v1	122689	122713 -	5
chrUn_GL000218v1	156800	156824 -	5
chrUn_GL000219v1	29429	29453 +	5
chrUn_GL000219v1	121299	121323 +	5
chrUn_GL000219v1	155690	155715 +	5
chrUn_GL000220v1	45272	45297 -	5
chrUn_KI270442v1	90289	90313 +	5
chrUn_KI270741v1	148338	148362 +	5
chrUn_KI270742v1	28174	28198 -	5
chrUn_KI270742v1	135286	135310 -	5
chrUn_KI270743v1	42871	42895 +	5
chrUn_KI270743v1	54461	54485 +	5
chrUn_KI270743v1	183589	183613 +	5
chrUn_KI270743v1	184299	184323 -	5
chrUn_KI270744v1	37640	37664 +	5
chrUn_KI270745v1	4283	4307 +	5
chrUn_KI270746v1	10127	10151 -	5
chrUn_KI270749v1	59143	59167 -	5
chrUn_KI270749v1	144587	144611 +	5
chrUn_KI270749v1	157328	157352 +	5
chrUn_KI270750v1	7874	7898 +	5
chrUn_KI270750v1	21023	21047 +	5
chrUn_KI270750v1	129009	129033 +	5
chrUn_KI270750v1	142540	142564 +	5
chrUn_KI270751v1	14803	14827 -	5

chrUn_KI270751v1	99041	99065 -	5
chrUn_KI270753v1	42189	42214 +	5
chrX	2276398	2276421 -	5
chrX	2894654	2894678 +	5
chrX	2972011	2972035 -	5
chrX	3270961	3270986 +	5
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chrX	3374448	3374472 +	5
chrX	3609970	3609994 +	5
chrX	3626032	3626056 +	5
chrX	3736721	3736746 -	5
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chrX	4363275	4363299 +	5
chrX	4492263	4492288 +	5
chrX	4530578	4530602 +	5
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chrX	4676549	4676573 +	5
chrX	4717621	4717645 -	5
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chrX	4780749	4780774 +	5
chrX	4920623	4920647 -	5
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chrX	5068748	5068773 -	5
chrX	5152994	5153019 -	5
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chrX	5262495	5262519 +	5
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chrX	5594935	5594959 -	5
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chrX	5656656	5656680 +	5
chrX	5758615	5758639 +	5
chrX	5762417	5762442 +	5
chrX	5775527	5775551 +	5
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chrX	6032704	6032728 -	5
chrX	6106392	6106416 -	5
chrX	6143018	6143042 -	5
chrX	6192425	6192449 -	5
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chrX	6349601	6349625 -	5
chrX	6359277	6359302 +	5
chrX	6364392	6364416 -	5
chrX	6447480	6447504 +	5
chrX	6512494	6512518 +	5
chrX	6544956	6544980 -	5
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chrX	6644030	6644055 -	5
chrX	6674076	6674101 -	5
chrX	6860863	6860887 +	5
chrX	6889950	6889975 +	5
chrX	6905001	6905025 -	5
chrX	6973204	6973228 -	5
chrX	6984293	6984317 +	5
chrX	6985080	6985105 +	5
chrX	7001428	7001453 +	5
chrX	7120546	7120570 +	5
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chrX	7616834	7616859 +	5
chrX	7667116	7667140 -	5
chrX	7676555	7676579 +	5
chrX	7692958	7692982 +	5
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chrX	8602609	8602634 +	5
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chrX	10526113	10526138 -	5
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chrX	10583080	10583104 -	5
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chrX	11048229	11048253 -	5
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chrX	11783888	11783913 -	5
chrX	11784334	11784358 -	5
chrX	11817975	11817999 -	5
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chrX	11906555	11906580 -	5
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chrX	12172781	12172805 +	5
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chrX	12463624	12463648 -	5
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chrX	12843663	12843687 +	5
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chrX	13059336	13059361 -	5
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chrX	13274557	13274581 +	5
chrX	13281121	13281146 +	5
chrX	13302740	13302764 +	5
chrX	13400807	13400832 -	5
chrX	13442422	13442446 +	5
chrX	13487892	13487916 -	5
chrX	13683822	13683846 +	5
chrX	13695988	13696012 +	5
chrX	13705800	13705824 +	5
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chrX	14384537	14384562 -	5
chrX	14512792	14512816 -	5
chrX	14597414	14597439 -	5
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chrX	14653407	14653431 +	5
chrX	14681281	14681305 -	5
chrX	14713335	14713359 -	5
chrX	14782934	14782958 +	5
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chrX	14845564	14845588 +	5
chrX	14903802	14903826 +	5
chrX	14957534	14957557 +	5
chrX	14963038	14963062 +	5
chrX	14976338	14976362 +	5
chrX	15066032	15066056 +	5
chrX	15086165	15086189 -	5
chrX	15098848	15098872 -	5
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chrX	15194900	15194925 -	5
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chrX	15526087	15526112 +	5
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chrX	15673682	15673706 +	5
chrX	15694412	15694436 +	5
chrX	15695849	15695874 -	5
chrX	15716515	15716539 -	5
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chrX	15832660	15832685 +	5
chrX	15922999	15923023 -	5
chrX	15937684	15937708 -	5
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chrX	16313788	16313812 -	5
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chrX	17081418	17081442 +	5
chrX	17086867	17086891 +	5
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chrX	17535347	17535371 +	5
chrX	17564407	17564432 -	5
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chrX	17743316	17743341 -	5
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chrX	18254978	18255002 -	5
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chrX	19037401	19037425 -	5
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chrX	19167712	19167737 +	5
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chrX	19712574	19712598 +	5
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chrX	20908660	20908684 -	5
chrX	20955981	20956006 +	5
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chrX	23596899	23596923 -	5
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chrX	25474399	25474423 -	5
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chrX	25575570	25575594 +	5
chrX	25576822	25576846 +	5
chrX	25627134	25627159 +	5

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chrX	26293058	26293082 -	5
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chrX	26451221	26451245 +	5
chrX	26459137	26459162 +	5
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chrX	26711238	26711262 +	5
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chrX	27598840	27598864 +	5
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chrX	31392884	31392908 +	5
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chrX	33380152	33380176 -	5
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chrX	33933695	33933719 -	5
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chrX	34136280	34136305 +	5
chrX	34199492	34199516 +	5
chrX	34265222	34265246 +	5
chrX	34293244	34293268 +	5
chrX	34466339	34466364 +	5
chrX	34537641	34537666 -	5
chrX	34562592	34562617 -	5
chrX	34607810	34607834 +	5
chrX	34673327	34673351 +	5

chrX	34748241	34748265 -	5
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chrX	34759200	34759224 -	5
chrX	34889443	34889468 +	5
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chrX	35007735	35007759 +	5
chrX	35020808	35020832 -	5
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chrX	35422785	35422809 +	5
chrX	35448484	35448508 -	5
chrX	35509261	35509285 +	5
chrX	35509806	35509831 +	5
chrX	35548751	35548775 +	5
chrX	35652367	35652391 -	5
chrX	35718345	35718369 -	5
chrX	35744471	35744495 +	5
chrX	35771022	35771046 -	5
chrX	35954082	35954106 -	5
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chrX	36202180	36202204 -	5
chrX	36281989	36282014 +	5
chrX	36320181	36320205 +	5
chrX	36359644	36359668 -	5
chrX	36381407	36381432 +	5
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chrX	36571851	36571875 +	5
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chrX	36808565	36808589 -	5
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chrX	36838200	36838224 +	5
chrX	36844944	36844968 +	5
chrX	36863584	36863608 +	5
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chrX	37314461	37314485 -	5
chrX	37531038	37531062 -	5
chrX	37694959	37694983 +	5
chrX	37713327	37713351 +	5
chrX	37725477	37725502 -	5
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chrX	37999298	37999322 +	5
chrX	38102242	38102267 +	5
chrX	38103842	38103867 -	5
chrX	38177957	38177981 +	5
chrX	38236969	38236993 +	5
chrX	38237701	38237726 +	5
chrX	38263227	38263252 -	5
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chrX	38346334	38346359 -	5
chrX	38378606	38378630 -	5
chrX	38412148	38412172 -	5
chrX	38481049	38481073 +	5
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chrX	39968962	39968986 -	5
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chrX	40596226	40596250 -	5
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chrX	43320242	43320267 -	5
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chrX	43527879	43527903 -	5
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chrX	43657620	43657644 -	5
chrX	43738428	43738452 +	5
chrX	43872072	43872096 -	5
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chrX	44075044	44075068 +	5

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chrX	44454730	44454754 +	5
chrX	44458809	44458834 +	5
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chrX	51643451	51643476 +	5
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chrX	51876300	51876324 -	5
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chrX	54179866	54179890 +	5
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chrX	65782851	65782875 +	5
chrX	65805807	65805832 +	5
chrX	65922482	65922506 -	5
chrX	65941286	65941310 +	5
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chrX	74253531	74253556 -	5
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chrX	74361738	74361762 +	5
chrX	74370319	74370344 +	5
chrX	74492655	74492679 -	5
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chrX	74609000	74609025 -	5
chrX	74612078	74612102 +	5
chrX	74712455	74712479 +	5
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chrX	74958871	74958895 -	5
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chrX	75057827	75057851 +	5
chrX	75064040	75064064 +	5
chrX	75064584	75064608 +	5
chrX	75227736	75227760 +	5
chrX	75266409	75266433 -	5
chrX	75354412	75354436 -	5
chrX	75391303	75391327 +	5
chrX	75397393	75397417 +	5
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chrX	75596449	75596473 +	5
chrX	75675047	75675071 +	5
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chrX	75683514	75683538 -	5
chrX	75742607	75742631 -	5
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chrX	75984963	75984987 -	5
chrX	76023524	76023549 +	5
chrX	76088783	76088807 -	5

chrX	76091777	76091801 -	5
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chrX	76253123	76253148 -	5
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chrX	76649388	76649412 -	5
chrX	76650846	76650869 -	5
chrX	76661445	76661469 +	5
chrX	76782965	76782989 +	5
chrX	76786846	76786870 +	5
chrX	76803553	76803577 +	5
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chrX	76953300	76953324 +	5
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chrX	76970624	76970648 -	5
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chrX	77533508	77533532 +	5
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chrX	77796835	77796860 -	5
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chrX	78324217	78324241 +	5
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chrX	78757411	78757436 -	5
chrX	78758271	78758295 +	5
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chrX	###	### -	5
chrX	###	### -	5
chrX	###	### -	5
chrX	###	### -	5
chrX	###	### +	5
chrX	###	### +	5

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chrX	###	### -	5
chrX	###	### -	5
chrX	###	### +	5
chrX	###	### +	5
chrX	###	### -	5
chrX	###	### -	5
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chrX	###	### +	5
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chrX	###	### +	5
chrX	###	### +	5
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chrX	###	### -	5
chrX	###	### -	5
chrX	###	### +	5
chrX	###	### -	5
chrX	###	### +	5
chrX	###	### -	5
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chrX	###	### +	5
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chrY	1223008	1223033 +	5
chrY	1273978	1274002 -	5
chrY	1395957	1395981 +	5
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chrY	22820621	22820645 +	5
chrY	22954805	22954829 +	5
chrY	23004430	23004454 +	5
chrY	23415452	23415476 -	5
chrY	23487866	23487890 -	5
chrY	23497628	23497653 +	5
chrY	23572472	23572496 -	5
chrY	23690313	23690337 +	5
chrY	23763370	23763394 +	5
chrY	23816794	23816818 +	5
chrY	23821898	23821923 +	5
chrY	23831044	23831068 -	5
chrY	24002252	24002276 -	5
chrY	24050212	24050236 -	5

chrY	24122291	24122315 +	5
chrY	24130806	24130830 -	5
chrY	24356119	24356143 -	5
chrY	24370162	24370186 -	5
chrY	24378584	24378608 -	5
chrY	24394833	24394858 -	5
chrY	24454369	24454393 +	5
chrY	24588549	24588573 +	5
chrY	24638172	24638196 +	5
chrY	25031915	25031939 -	5
chrY	25081521	25081545 -	5
chrY	25215718	25215742 -	5
chrY	25275266	25275291 +	5
chrY	25291534	25291558 +	5
chrY	25299955	25299979 +	5
chrY	25313996	25314020 +	5
chrY	25438607	25438631 +	5
chrY	25539310	25539334 +	5
chrY	25547825	25547849 -	5
chrY	25619898	25619922 +	5
chrY	25667868	25667892 +	5
chrY	25839028	25839052 +	5
chrY	25848172	25848197 -	5
chrY	25853274	25853298 -	5
chrY	25906691	25906715 -	5
chrY	25979742	25979766 -	5
chrY	26098124	26098148 +	5
chrY	26172957	26172982 -	5
chrY	26182721	26182745 +	5
chrY	26255147	26255171 +	5
chrY	26351501	26351525 -	5
chrY	26413452	26413476 +	5
chrY	26436968	26436992 -	5
chrY	56952158	56952182 +	5
chrY	56979738	56979762 +	5
chrY	57071015	57071039 -	5
chrY	57072483	57072507 +	5

Gene	Region
CPS1	exon
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NRG3	intron
ATP7B	intron
LINC01049	non-coding RNA
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SCAPER	intron
HS3ST4	intron
none	intergenic
KDM1A	intron
DOCK7	intron
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RABGAP1L	intron
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RASAL2	intron
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KCNT2	intron
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LINC00582	non-coding RNA
MTR	intron
AKT3	intron
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ARHGAP21	intron
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IDE	intron
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CRTAC1	intron
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SORCS3	intron
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QSER1	intron

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LRRC4C	intron
TTC17	intron
TMX2	intron
PPFIA1	intron
FCHSD2	3utr
TENM4	intron
MTMR2	intron
ARHGAP42	intron
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SLC2A14	intron
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ST8SIA1	intron
PDZRN4	intron
PPHLN1	intron
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MYCBP2	exon
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CFAP97D2	intron

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NOVA1	intron
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MDGA2	intron
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GPR137C	intron
SYNE2	intron
TTLL5	intron
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NRXN3	intron
RCOR1	intron
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DPH6	intron
TMEM62	intron
SHC4	intron
THSD4	intron
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RBFOX1	intron
REXO5	intron
ZNF423	intron
FTO	intron
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CDH1	intron
LINC01228	non-coding RNA
CDH13	intron
COX10	intron
LHX1-DT	non-coding RNA
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MAP2K6	3utr
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GRB2	intron
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DSG2	intron
DCC	intron
MUC16	intron
SLC25A42	intron
LDAH	intron
BIRC6	intron
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LOC730100	non-coding RNA

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NAALADL2	intron
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DGKG	intron
OPA1	intron
LDB2	intron
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CLOCK	intron
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GRID2	intron
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ELOVL6	intron
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UGT8	intron
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MEGF6	3utr
PER3	exon
RERE	intron
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MACO1	intron
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ARID1A	intron
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SDC3	intron
SNRNP40	intron
HDAC1	intron
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ZSCAN20	intron
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CSMD2	exon
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HIVEP3	intron
ZMYND12	intron
MPL	intron
IPP	intron
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AGBL4	intron
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FAF1	intron
EPS15	intron
ZFYVE9	intron
COA7	intron
SCP2	intron
MAGOH	intron
ACOT11	intron
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FGGY	intron
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NFIA	intron
PATJ	intron
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DOCK7	intron
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TNNI3K	intron
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SLC44A5	intron
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PIGK	intron
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AK5	intron
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ADGRL2	intron
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LINC01725	non-coding RNA
TLL7	intron
RPF1	intron
SPATA1	intron
SSX2IP	intron
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COL24A1	intron
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PKN2-AS1	non-coding RNA
KYAT3	intron
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BRDT	intron
EVI5	intron
DNTTIP2	exon
TLCD4-RWDD3	intron
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PTBP2	intron
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DPYD	intron
DPYD	intron
MIR137HG	non-coding RNA
LINC01776	non-coding RNA
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CDC14A	intron
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COL11A1	intron
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SORT1	intron
AHCYL1	intron
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CSDE1	intron
SYCP1	intron
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LOC101928977	non-coding RNA
LINC01525	non-coding RNA
LINC01525	non-coding RNA
SPAG17	intron
WARS2-AS1	non-coding RNA
LINC01780	non-coding RNA
none	intergenic
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H2BP1	non-coding RNA
EMBP1	non-coding RNA

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H3-7	3utr
GPR89B	non-coding RNA
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PDE4DIP	intron
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H2BC18	intron
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CTXND2	intron
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KCNN3	intron
ARHGEF2	intron
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OR6Y1	intron
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DCAF8	intron
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ATF6	intron
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FAM78B	intron
POU2F1	3utr
DCAF6	intron
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NME7	intron
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LINC01681	non-coding RNA
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KLHL20	intron
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ASTN1	intron
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RASAL2	intron

RALGPS2	intron
ANGPTL1	intron
ANGPTL1	5utr
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FAM163A	intron
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ACBD6	intron
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NPL	intron
HMCN1	intron
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BRINP3	intron
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NR5A2	intron
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RABIF	intron
KLHL12	intron
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NFASC	intron
CTSE	intron
PFKFB2	intron
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TRAF3IP3	intron
KCNH1	intron
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INTS7	intron
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PPP2R5A	intron

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USH2A	intron
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SPATA17	intron
TGFB2	intron
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LYPLAL1-AS1	non-coding RNA
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TP53BP2	intron
WDR26	intron
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CDC42BPA	intron
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OBSCN-AS1	non-coding RNA
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CCSAP	3utr
ABCB10	intron
COG2	intron
TTC13	intron
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SLC35F3	intron
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FMN2	intron
RGS7	intron

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PLD5	intron
CATSPERE	intron
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KIF26B	intron
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ADARB2	intron
LINC02669	non-coding RNA
LOC105376360	non-coding RNA
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ITIH5	intron
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CAMK1D	intron
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PTER	intron
RSU1	intron
ST8SIA6	intron
HACD1	intron
CACNB2	intron
ARL5B	3utr
PLXDC2	intron
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NEBL	intron
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KIAA1217	intron

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ARHGAP21	intron
GPR158	intron
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GAD2	intron
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ABI1	intron
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SVIL	intron
ZNF438	intron
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ARHGAP12	intron
CCDC7	intron
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ITGB1-DT	non-coding RNA
PARD3	intron
CCNY	intron
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ZNF37BP	non-coding RNA
ZNF487	intron
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TMEM72-AS1	non-coding RNA
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PTPN20	intron
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TMEM26	intron
CABCOC01	intron
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JMJD1C	intron
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CTNNA3	intron
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ASCC1	intron
MICU1	intron
P4HA1	intron
SEC24C	intron
ADK	intron
KAT6B	intron
LRMDA	intron
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KCNMA1	intron
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TMEM254-AS1	non-coding RNA
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SH2D4B	intron
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NRG3	intron
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LOC105378396	non-coding RNA
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GRID1	intron
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WAPL	intron
PAPSS2	intron
RNLS	intron
ACTA2	intron
PANK1	intron
none	intergenic
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HECTD2-AS1	non-coding RNA
TNKS2-DT	non-coding RNA
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MYOF	intron
FRA10AC1	intron
LGI1	intron
PLCE1	intron
PDLIM1	intron
SORBS1	intron
CC2D2B	intron
TLL2	intron
PIK3AP1	intron
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DNMBP	intron
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BTRC	intron
NT5C2	intron
SH3PXD2A	intron
SORCS3	intron
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SORCS1	intron
SORCS1	intron
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VTI1A	intron

FHIP2A	intron
ATRNL1	intron
ATRNL1	intron
VAX1	3utr
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WDR11-DT	non-coding RNA
TACC2	3utr
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ADAM12	intron
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INSYN2A	intron
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EBF3	intron
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TCERG1L	intron
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INPP5A	intron
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STIM1	intron
OR52R1	exon
MMP26	intron
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PPFIBP2	intron
TRIM66	intron
DENND2B	intron
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TMEM41B	intron
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GALNT18	intron
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TEAD1	intron
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PDE3B	intron

CYP2R1	intron
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SOX6	intron
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ZDHHC13	intron
NAV2	intron
NELL1	intron
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LINC01495	non-coding RNA
CCDC179	intron
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LUZP2	intron
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LINC01499	non-coding RNA
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LINC02745	non-coding RNA
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TSPAN18	intron
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GRM5P1	non-coding RNA
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BTBD18	intron
LPXN	intron
LINC00301	non-coding RNA
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MAJIN	intron
SLC22A20P	non-coding RNA
PACS1	intron
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XNDC1N-ZNF705EP-ALG1L9P	non-coding RNA
FAM168A	intron
RAB6A	intron
UVRAG	intron
EMSY	intron
GDPD4	intron
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PAK1	intron
USP35	intron
GAB2	intron
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MIR4300HG	non-coding RNA
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NOX4	intron
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DISC1FP1	non-coding RNA
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DISC1FP1	non-coding RNA
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C11orf54	intron
ANKRD49	intron
AMOTL1	intron
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MAML2	intron
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CNTN5	intron
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ARHGAP42	intron
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WTAPP1	non-coding RNA
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CASP4LP	non-coding RNA
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GRIA4	intron
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GUCY1A2	intron
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CADM1	intron
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FXD6	intron
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GRIK4	intron
TBCEL-TECTA	intron
SORL1	intron
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GRAMD1B	intron
OR8B2	3utr
OR8B3	3utr
CDON	intron

KIRREL3	intron
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LINC02725	non-coding RNA
ARHGAP32	intron
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BARX2	intron
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ADAMTS15	intron
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LINC02551	non-coding RNA
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SNX19	3utr
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ERC1	intron
TSPAN9	intron
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ANO2	intron
VWF	intron
ZNF705A	intron
DDX12P	non-coding RNA
CLEC1A	intron
LINC02366	non-coding RNA
PRH1	intron
PRH1-TAS2R14	intron
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ETV6	intron
GPRC5A	3utr
HEBP1	intron
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SLC15A5	intron
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PIK3C2G	intron
PDE3A	intron
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SLCO1C1	intron
SLCO1B3-SLCO1B7	intron
ST8SIA1	intron

C2CD5	intron
ETNK1-DT	non-coding RNA
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LRIG3-DT	non-coding RNA
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TAF2	intron
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SRGAP1	intron
LEMD3	intron
LEMD3	intron
HMGA2	intron
GRIP1	intron
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FRS2	intron
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ZFC3H1	intron
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TRHDE	3utr
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KCNC2	intron
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OTOGL	intron
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OTOGL	intron
PTPRQ	intron
PTPRQ	exon
LIN7A	intron
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TMTC2	intron
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MGAT4C	intron
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PLEKHG7	intron
PLEKHG7	exon
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NUDT4	intron
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PLXNC1	exon
RMST	non-coding RNA
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ANKS1B	intron
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UTP20	intron
WASHC3	intron
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NFYB	intron

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ANKRD26P3	non-coding RNA
GJA3	3utr
LATS2	intron
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MIPEP	intron
CDK8	intron
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PLUT	non-coding RNA
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FLT1	intron
MTUS2	intron
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UBL3	intron
HMGB1	intron
HMGB1	intron
B3GLCT	intron
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KL	3utr
STARD13	intron
STARD13	intron
LINC02343	non-coding RNA
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DCLK1	intron
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FREM2	intron
COG6	intron
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NAA16	intron
VWA8	intron
DGKH	intron
EPSTI1	intron
ENOX1	intron
LINC00407	non-coding RNA
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GTF2F2	intron
LCP1	exon
LRRC63	intron
SUCLA2	intron
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RCBTB1	intron
DLEU2	non-coding RNA

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DLEU7	intron
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LINC00355	non-coding RNA
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LINC00383	non-coding RNA
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DACH1	intron
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KLF12	intron
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LMO7	intron
OBI1-AS1	non-coding RNA
OBI1-AS1	non-coding RNA
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LINC00375	non-coding RNA
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CLDN10	intron
HS6ST3	intron
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FARP1	intron
DOCK9	intron
CLYBL	intron
PCCA	intron
NALCN-AS1	non-coding RNA
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RPGRIP1	intron
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AJUBA	intron
STXBP6	intron
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G2E3-AS1	non-coding RNA
G2E3-AS1	non-coding RNA
G2E3-AS1	non-coding RNA
HEATR5A-DT	non-coding RNA
AKAP6	intron
NPAS3	intron
NPAS3	intron
PRORP	intron
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SFTA3	non-coding RNA
SLC25A21	intron
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TTC6	intron
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SEC23A	intron
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CDKL1	intron
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FRMD6	intron
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PRKCH	intron
ZBTB25	3utr
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PALS1	intron
GALNT16-AS1	non-coding RNA
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PCNX1	intron
SIPA1L1-AS1	non-coding RNA
SIPA1L1	intron
RGS6	intron
ZFYVE1	intron
PSEN1	intron
LIN52	intron
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TTLL5	intron
ESRRB	intron
ADCK1	intron
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NRXN3	intron
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DIO2-AS1	non-coding RNA
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CEP128	intron
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DGLUCY	intron
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CLMN	intron
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BDKRB2	intron
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SETD3	intron
EML1	intron
MEG8	non-coding RNA
MOK	intron
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BRF1	intron
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SNHG14	non-coding RNA
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GABRG3	intron
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ENTREP2	intron
TJP1	intron
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MTMR10	intron
TRPM1	intron
KLF13	intron
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CHRNA7	intron
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FMN1	3utr
AQR	intron
DPH6-DT	non-coding RNA
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FSIP1	intron
GPR176	intron
EIF2AK4	intron
RMDN3	intron
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MYEF2	intron
FBN1	intron
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MIR4713HG	non-coding RNA
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WDR72	intron
UNC13C	intron
UNC13C	intron
PRTG	intron
TEX9	intron
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TCF12	intron
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CGNL1	intron
ALDH1A2	intron
ALDH1A2	intron
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MYO1E	intron
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RORA	3utr

TLN2	intron
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DAPK2	intron
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SPG21	intron
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MEGF11	intron
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THSD4	intron
MYO9A	intron
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PTPN9	intron
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SCAPER	intron
PEAK1	intron
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CHRNA3	intron
ANKRD34C-AS1	non-coding RNA
LINC00927	non-coding RNA
TMC3-AS1	non-coding RNA
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AGBL1	intron
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ARPIN-AP3S2	intron
none	intergenic
SV2B	3utr
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SLCO3A1	intron
LINC01581	non-coding RNA
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LOC105369212	non-coding RNA
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LINC02253	non-coding RNA
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IGF1R	intron
PCSK6	intron
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GRIN2A	intron
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SNN	3utr
TXNDC11	intron
SNX29	intron
SHISA9	intron
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MRTFB	3utr
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PARN	intron
PARN	intron
NOMO1	intron
BMERB1	intron
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TANGO6	intron
AP1G1	intron
AP1G1	intron
ZFHX3	intron
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GLG1	intron
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ADAMTS18	intron
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WWOX	intron
MAFTRR	non-coding RNA
DYNLRB2-AS1	non-coding RNA
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SPIRE2	intron
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SMG6	intron

CCDC92B	intron
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ATP2A3	intron
LOC339166	non-coding RNA
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BCL6B	intron
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KRBA2	3utr
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TMEM220-AS1	non-coding RNA
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HS3ST3A1	intron
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TRIM16	intron
ZNF286A-TBC1D26	non-coding RNA
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TRIM16L	non-coding RNA
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CCDC144NL-AS1	non-coding RNA
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TMEM11-DT	non-coding RNA
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LINC01992	non-coding RNA
SEZ6	intron
LOC107984974	non-coding RNA
RAB11FIP4	intron
MYO1D	intron
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CCT6B	intron
SLFN5	3utr
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RARA	intron
SMARCE1	intron
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KRT33B	intron

BRCA1	intron
NBR1	intron
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KANSL1	intron
NSF	intron
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LRR59	intron
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CA10	intron
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ANKFN1	intron
TRIM25	intron
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SMG8	exon
HEATR6	intron
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BRIP1	intron
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METTL2A	intron
MARCHF10-DT	non-coding RNA
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DDX42	intron
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RGS9	intron
NOL11	intron
BPTF	intron
SLC16A6	intron
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ARSG	intron
ABCA5	intron
MAP2K6	intron
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SSTR2	intron
COG1	intron
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CD300H	intron
KCTD2	3utr
SRP68	intron

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LOC100507351	non-coding RNA
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COLEC12	intron
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EMILIN2	intron
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MYOM1	intron
DLGAP1	intron
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EPB41L3	intron
L3MBTL4	intron
PTPRM	intron
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ANKRD12	intron
PIEZO2	intron
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GREB1L	intron
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LOC101927571	non-coding RNA
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ZNF521	intron
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CHST9	intron
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DSC2	3utr
DSG3	exon
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CCDC178	intron
CCDC178	intron
ASXL3	intron
MAPRE2	3utr
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FHOD3	intron
KIAA1328	intron
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LINC00907	non-coding RNA
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SLC14A2	intron
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HAUS1	intron
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LOXHD1	intron
KATNAL2	intron
MIR4527HG	non-coding RNA
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SMAD2	intron
MYO5B	intron
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ME2	intron
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[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

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SMARCA4	intron
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ZNF724	intron
LOC100505851	non-coding RNA
LINC00662	non-coding RNA
LOC100420587	non-coding RNA
VSTM2B	intron
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CHST8	intron
ZNF807P	non-coding RNA
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ZNF146	intron
ZNF568	intron
ZNF540	intron
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CYP2G1P	non-coding RNA
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CEACAM7	intron
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GRIN2D	intron
ZNF610	intron
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ZNF865	intron
NLRP13	intron
ZNF71	3utr
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LINC01250	non-coding RNA
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LINC00487	non-coding RNA
RNF144A	intron
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LINC00299	non-coding RNA
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ASAP2	intron
MIR3681HG	non-coding RNA
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LINC00276	non-coding RNA
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MYCNUT	non-coding RNA
GACAT3	non-coding RNA
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LINC01822	non-coding RNA
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OTOF	intron
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ALK	intron
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YPEL5	intron
XDH	intron
MEMO1	intron
BIRC6	intron
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HEATR5B	intron
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TMEM178A	intron
THUMPD2	intron
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PLEKHH2	intron
CAMKMT	intron
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SRBD1	intron
SRBD1	intron
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LHCGR	intron
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FSHR	intron
NRXN1	intron
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LOC730100	non-coding RNA
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PPP4R3B	intron
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VRK2	intron
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COMMD1	intron
EHBP1	intron
VPS54	intron
AFTPH	intron
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LINC01799	non-coding RNA
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ANXA4	intron
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ZNF638	intron
EXOC6B	intron
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DCTN1-AS1	non-coding RNA
M1AP	3utr
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LRRTM4	intron
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LOC101927967	non-coding RNA
LOC101927967	non-coding RNA
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LOC101928371	non-coding RNA
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ANKRD36C	intron
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KANSL3	intron
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TMEM131	intron
VWA3B	intron
INPP4A	intron
CRACDL	intron
AFF3	intron
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MAP4K4	intron
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TMEM182	intron
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UXS1	intron
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LINC01885	non-coding RNA
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MGAT5	intron
TMEM163	intron
THSD7B	intron
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ACVR2A	intron
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LOC101929319	non-coding RNA
RIF1	intron
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GALNT13	intron
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GPD2	intron
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CCDC148	intron
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TANC1	intron
BAZ2B	intron
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PLA2R1	intron
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SLC4A10	intron
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CSRNP3	intron
SCN1A	intron
SCN1A-AS1	non-coding RNA
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FASTKD1	intron
METTL5	intron
UBR3	intron
ERICH2-DT	non-coding RNA
SLC25A12	intron
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ITGA6	intron
WIPF1	intron
CHN1	intron
ATF2	intron
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OSBPL6	intron
CCDC141	intron
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SCHLAP1	non-coding RNA
LINC01934	non-coding RNA
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PDE1A	intron
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ZNF804A	intron
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CALCRL	3utr
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COL5A2	intron
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MSTN	intron
MFSD6	intron
GLS	intron
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SLC39A10	intron
DNAH7	intron
HECW2	intron
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ANKRD44	intron
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C2CD6	intron
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NBEAL1	intron
PARD3B	intron
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PTH2R	intron
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CPS1	intron
ERBB4	intron
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SPAG16	intron
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VWC2L	intron
FN1	intron

none	intergenic
DIRC3	non-coding RNA
DIRC3	non-coding RNA
USP37	intron
PLCD4	intron
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DNPEP	intron
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DOCK10	exon
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NYAP2	intron
NYAP2	intron
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RHBDD1	intron
COL4A3	intron
MFF	intron
SLC19A3	intron
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LINC01807	non-coding RNA
none	intergenic
DNER	intron
PDE6D	intron
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CAPN10	intron
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CSNK2A1	intron
RSPO4	intron
SDCBP2-AS1	non-coding RNA
SIRPD	intron
ZNF343	intron
ZNF343	intron
PTPRA	intron

FASTKD5	exon
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LINC01428	non-coding RNA
none	intergenic
PLCB1	intron
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PLCB4	intron
SNAP25	intron
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ISM1	intron
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MACROD2	intron
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KIF16B	intron
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NANP	3utr
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BPIFB3	intron
DYNLRB1	intron
PIGU	intron
TRPC4AP	intron
CEP250	intron
EPB41L1	intron
none	intergenic
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RALGAPB	intron
LINC01734	non-coding RNA
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[illegible]

none	intergenic
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LINC00320	non-coding RNA
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NCAM2	intron
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LINC01692	non-coding RNA
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LINC01695	non-coding RNA
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N6AMT1	intron
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LOC101928107	non-coding RNA
ITSN1	intron
LINC00649	non-coding RNA
RCAN1	intron
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HLCS	intron
RIPPLY3	intron
KCNJ6	intron
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BRWD1	intron
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DSCAM	intron
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MX2	intron
LINC00111	non-coding RNA
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ABCG1	intron

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CNTN4	intron
CNTN4	intron
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BHLHE40-AS1	non-coding RNA
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GRM7	intron
GRM7	intron
LOC101927394	non-coding RNA
SSUH2	intron
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SRGAP3	intron
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PPARG	intron
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IQSEC1	intron
RFTN1	intron
TBC1D5	intron
BALR6	non-coding RNA
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KCNH8	intron
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UBE2E2	intron
THRB	intron
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RARB	intron
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LINC00693	non-coding RNA
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RBMS3	intron
RBMS3	intron
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GADL1	intron
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OSBPL10	intron

OSBPL10	intron
DYNC1LI1	intron
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PDCD6IP	3utr
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LRRFIP2	intron
GOLGA4	intron
ITGA9	intron
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EIF1B-AS1	non-coding RNA
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FYCO1	3utr
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COL7A1	intron
ARIH2	intron
BSN	intron
HYAL2	exon
ABHD14A-ACY1	intron
CACNA2D3	intron
CACNA2D3	intron
ERC2	intron
ARHGEF3	intron
DNAH12	intron
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FHIT	intron
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SYNPR	intron
ATXN7	intron
ATXN7	intron
ADAMTS9-AS2	non-coding RNA
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MAGI1	intron
MAGI1	intron

[illegible]

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EPHA6	intron
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SENP7	intron
FAM172BP	non-coding RNA
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ALCAM	intron
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BBX	intron
LINC01205	non-coding RNA
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NECTIN3	intron
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GRAMD1C	intron
CCDC191	intron
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LSAMP	intron
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LOC105374060	non-coding RNA
UPK1B	intron
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CASR	intron
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[illegible]

GYG1	3utr
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CLRN1	intron
MED12L	intron
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MBNL1	intron
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LINC02006	non-coding RNA
LINC02877	non-coding RNA
ARHGEF26	intron
GPR149	intron
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PLCH1	intron
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SCHIP1	intron
SCHIP1	intron
IL12A-AS1	non-coding RNA
PPM1L	intron
B3GALNT1	intron
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LINC01322	non-coding RNA
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LINC01322	non-coding RNA
LOC105374194	non-coding RNA
none	intergenic
WDR49	intron
WDR49	intron
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EGFEM1P	non-coding RNA
FHL1P1	non-coding RNA
TNIK	intron
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ECT2	intron
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NLGN1	intron
NAALADL2	intron
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TBL1XR1	intron
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SOX2-OT	non-coding RNA
SOX2-OT	non-coding RNA
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ATP11B	intron
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LINC02054	non-coding RNA
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RPL39L	intron
LPP	intron
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TPRG1	intron
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P3H2	intron
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FGF12	intron
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LRRC15	intron
ACAP2	intron
MUC4	intron
PAK2	intron
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RNF212	intron
FAM193A	intron
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ADD1	intron
HTT	intron
STK32B	intron
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SORCS2	intron
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CLNK	intron
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C1QTNF7-AS1	non-coding RNA
C1QTNF7	intron
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LDB2	intron
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KCNIP4	intron
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PPARGC1A	intron
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SEPSECS-AS1	non-coding RNA
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ZCCHC4	intron
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RBPJ	intron
LINC02261	non-coding RNA
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LINC02501	non-coding RNA
LINC02501	non-coding RNA
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LOC439933	non-coding RNA

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NWD2	intron
RELL1	intron
LINC01258	non-coding RNA
TMEM156	intron
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RFC1	intron
NSUN7	intron
APBB2	intron
SLC30A9	intron
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ATP8A1	intron
ATP8A1	intron
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SPATA18	intron
SCFD2	intron
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KIT	exon
CLOCK	intron
CRACD	intron
ARL9	intron
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UGT2B11	intron
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RUFY3	intron
SLC4A4	intron
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ANKRD17	intron
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FAM47E-STBD1	intron
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CCNI	intron
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CXCL13	intron
MRPL1	intron
LINC00989	non-coding RNA
ANTXR2	intron
CFAP299	intron
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BMP3	intron
PRKG2	intron
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LINC02994	non-coding RNA
LINC02994	non-coding RNA
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ARHGAP24	intron
MAPK10	intron
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FAM13A	intron
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CCSER1	intron

GRID2	intron
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PDLIM5	intron
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BMPR1B	intron
UNC5C	intron
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LINC02267	non-coding RNA
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LAMTOR3	intron
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PPP3CA	intron
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TACR3	intron
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CXXC4-AS1	non-coding RNA
none	intergenic
TET2	intron
ARHGEF38	3utr
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TBCK	intron
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LEF1	intron
EGF	intron
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LARP7	exon
ARSJ	intron
none	intergenic
NDST4	intron
NDST4	intron
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LINC01378	non-coding RNA
USP53	intron
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ADAD1	intron
CETN4P	non-coding RNA
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SPATA5	intron
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PCDH10-DT	non-coding RNA
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LINC02511	non-coding RNA
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MAML3	intron
TBC1D9	3utr
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INPP4B	intron
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SMAD1	intron
SLC10A7	intron
SLC10A7	3utr
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EDNRA	intron

ARHGAP10	intron
ARHGAP10	intron
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LINC02355	non-coding RNA
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DCLK2	intron
LRBA	intron
FHIP1A	intron
GATB	intron
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ARFIP1	intron
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PDGFC	intron
GRIA2	intron
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ETFDH	intron
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LINC02233	non-coding RNA
LINC02233	non-coding RNA
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FSTL5	intron
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MARCHF1	3utr
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LINC01179	non-coding RNA
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PALLD	intron
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NEK1	intron
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GALNTL6	intron
WASH7P	non-coding RNA

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LOC100288069	non-coding RNA
none	intergenic
SLC35E2B	exon
SLC35E2A	non-coding RNA
GNB1	intron
none	intergenic
PRDM16	intron
PRDM16	intron
PRDM16	intron
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MEGF6	intron
CEP104	3utr
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LINC01777	non-coding RNA
LINC01777	non-coding RNA
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LINC01646	non-coding RNA
AJAP1	intron
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NPHP4	intron
CHD5	intron
ICMT	intron
ICMT-DT	non-coding RNA
PLEKHG5	exon
DNAJC11	intron
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CAMTA1	intron
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SLC25A33	3utr
LZIC	3utr
NMNAT1	intron
UBE4B	intron
UBE4B	intron
PEX14	intron
PEX14	intron
CASZ1	intron
none	intergenic
MTOR	intron
ANGPTL7	intron
UBIAD1	intron
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MAD2L2	intron
none	intergenic
NPPB	intron
MFN2	intron
VPS13D	intron
VPS13D	intron
VPS13D	intron
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PRDM2	intron
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KAZN-AS1	non-coding RNA
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PLEKHM2	intron
SPEN	intron
SPEN	exon
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FBXO42	exon
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PADI3	intron
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RCC2	intron
ARHGEF10L	intron
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ACTL8	intron
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PAX7	intron
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ALDH4A1	intron
UBR4	intron
CAPZB	intron
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PLA2G2D	intron
PLA2G2C	intron
LINC01141	non-coding RNA
PINK1	intron
HP1BP3	3utr
EIF4G3	intron
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ECE1	intron
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RAP1GAP	intron
USP48	intron
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HSPG2	intron
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ZBTB40	intron
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TCEA3	intron
ASAP3	intron
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MDS2	non-coding RNA
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NCMAP-DT	non-coding RN/
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RUNX3	intron
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SYF2	intron
TMEM50A	intron
MAN1C1	intron
AUNIP	intron
PAFAH2	intron
PAFAH2	intron
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TRIM63	intron
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ZNF683	intron
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PIGV	intron
SLC9A1	intron
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SYTL1	3utr
WASF2	intron
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RPA2	intron
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DNAJC8	intron
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YTHDF2	intron
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OPRD1	intron
EPB41	intron
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TINAGL1	intron
PEF1	intron
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TMEM39B	intron
KPNA6	intron
EIF3I	intron
BSDC1	intron
BSDC1	intron
KIAA1522	intron
YARS1	intron
RNF19B	intron
AZIN2	intron
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PHC2	intron
CSMD2	intron
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C1orf94	intron
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DLGAP3	intron
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ZMYM6	intron
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ZMYM1	intron

ZMYM4	intron
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PSMB2	intron
AGO1	intron
AGO3	intron
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GRIK3	intron
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SNIP1	3utr
MTF1	intron
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MACF1	intron
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MYCL-AS1	non-coding RNA
PPT1	intron
RLF	intron
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ZNF684	intron
RIMS3	3utr
NFYC	intron
KCNQ4	intron
SCMH1	intron
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SCMH1	intron
none	intergenic
HIVEP3	3utr
HIVEP3	intron
HIVEP3	non-coding RNA
HIVEP3	non-coding RNA

FOXJ3	intron
none	intergenic
ZMYND12	intron
CCDC30	intron
CCDC30	intron
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P3H1	intron
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CFAP57	intron
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MED8	intron
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ST3GAL3	intron
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DMAP1	intron
ERI3	intron
ERI3	intron
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RNF220	intron
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ARMH1	intron
EIF2B3	intron
ZSWIM5	intron
none	intergenic
TESK2	intron
TESK2	intron
GPBP1L1	intron
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MAST2	intron
MAST2	intron
PIK3R3	intron
RAD54L	intron
UQCRH	intron
NSUN4	intron
ATPAF1	intron
EFCAB14	intron
none	intergenic
CYP4X1	intron
CYP4X1	intron
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TRABD2B	3utr
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SPATA6	intron
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FAF1	intron
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FAF1	intron
FAF1	intron
none	intergenic
EPS15	intron
EPS15	intron
EPS15	intron
EPS15	intron

EPS15	intron
OSBPL9	intron
OSBPL9	intron
OSBPL9	intron
OSBPL9	intron
OSBPL9	intron
OSBPL9	intron
NRDC	intron
NRDC	intron
BTF3L4	intron
none	intergenic
ZFYVE9	intron
ZFYVE9	intron
ZFYVE9	intron
ZFYVE9	intron
CC2D1B	intron
TUT4	intron
none	intergenic
none	intergenic
COA7	3utr
none	intergenic
ZYG11B	intron
ZYG11A	intron
ZYG11A	intron
ECHDC2	intron
SCP2	intron
SCP2	intron
none	intergenic
PODN	intron
none	intergenic
LRP8	3utr
none	intergenic
GLIS1	intron
none	intergenic
IFT25	intron
IFT25	intron
SSBP3	intron
SSBP3	intron
SSBP3	intron
SSBP3	intron
SSBP3	intron
SSBP3	intron
FAM151A	intron
LEXM	intron
DHCR24	intron
none	intergenic
USP24	intron

[illegible]

DAB1	intron
DAB1	intron
DAB1	intron
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DAB1	intron
DAB1	intron
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DAB1	intron
DAB1	intron
DAB1	intron
DAB1	intron
DAB1	intron
OMA1	intron
OMA1	5utr
none	intergenic
none	intergenic
none	intergenic
MYSM1	intron
LINC01135	non-coding RNA
LINC01135	non-coding RNA
LINC01135	non-coding RNA
LINC01135	non-coding RNA
LINC01135	non-coding RNA
none	intergenic
LINC01358	non-coding RNA
none	intergenic
HSD52	non-coding RNA
none	intergenic
none	intergenic
none	intergenic
FGGY	intron
FGGY	intron
FGGY	intron
FGGY	intron
FGGY	intron
FGGY	intron
FGGY	intron
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FGGY	intron
LOC101926944	non-coding RNA
HOOK1	intron
CYP2J2	intron
none	intergenic
none	intergenic
C1orf87	intron
none	intergenic

none	intergenic
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LINC01748	non-coding RNA
LINC01748	non-coding RNA
none	intergenic
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NFIA	intron
NFIA	intron
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NFIA	intron
NFIA	intron
none	intergenic
TM2D1	intron
PATJ	intron
PATJ	intron
PATJ	intron
PATJ	intron
PATJ	intron
KANK4	intron
DOCK7	intron
DOCK7	intron
ATG4C	intron
none	intergenic
none	intergenic
LINC01739	non-coding RNA
none	intergenic
none	intergenic
LINC00466	non-coding RNA
LINC00466	non-coding RNA
ALG6	intron
ITGB3BP	intron
EFCAB7	intron
PGM1	intron
none	intergenic
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ROR1	intron
ROR1	intron
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ROR1	intron
none	intergenic
UBE2U	intron
none	intergenic
none	intergenic

CACHD1	intron
CACHD1	intron
CACHD1	intron
CACHD1	intron
CACHD1	intron
CACHD1	intron
CACHD1	intron
CACHD1	3utr
JAK1	intron
JAK1	intron
JAK1	intron
AK4	intron
none	intergenic
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DNAJC6	intron
DNAJC6	intron
LEPR	intron
LEPR	intron
LEPR	intron
LEPR	intron
LEPR	intron
none	intergenic
none	intergenic
PDE4B	intron
PDE4B	intron
PDE4B	intron
PDE4B	intron
PDE4B	intron
PDE4B	intron
PDE4B	intron
none	intergenic
SGIP1	intron
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SGIP1	intron
SGIP1	intron
DNAI4	intron
SLC35D1	intron
SLC35D1	intron
none	intergenic
IL23R	intron
IL23R	intron
IL12RB2	intron
none	intergenic
SERBP1	intron
none	intergenic
GNG12	intron
GNG12	intron
GNG12	intron

GNG12-AS1	non-coding RNA
WLS	intron
none	intergenic
none	intergenic
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LINC01707	non-coding RNA
LINC02791	non-coding RNA
none	intergenic
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LRRC7	intron
LRRC7	intron
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LRRC7	intron
LRRC7	intron
LRRC7	intron
LRRC7	intron
LRRC7	intron
LRRC40	intron
none	intergenic
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none	intergenic
LINC01788	non-coding RNA
PTGER3	intron
PTGER3	intron
PTGER3	splice site
PTGER3	intron
PTGER3	intron
PTGER3	intron
PTGER3	intron
ZRANB2-AS1	non-coding RNA
none	intergenic
none	intergenic
none	intergenic
none	intergenic
NEGR1	intron
NEGR1	intron

[illegible]

TNNI3K	intron
TNNI3K	intron
TNNI3K	intron
TNNI3K	intron
none	intergenic
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LHX8	intron
SLC44A5	intron
SLC44A5	intron
SLC44A5	intron
SLC44A5	intron
none	intergenic
none	intergenic
RABGGTB	intron
MSH4	intron
MSH4	intron
MSH4	exon
MSH4	intron
MSH4	intron
MSH4	intron
none	intergenic
ST6GALNAC3	intron
ST6GALNAC3	intron
ST6GALNAC3	intron
ST6GALNAC3	intron
ST6GALNAC3	intron
ST6GALNAC3	intron
ST6GALNAC3	intron
ST6GALNAC3	intron
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ST6GALNAC5	intron
ST6GALNAC5	intron
PIGK	intron
PIGK	intron
PIGK	intron

PIGK	intron
AK5	intron
AK5	intron
AK5	intron
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AK5	intron
MIGA1	intron
MIGA1	intron
MIGA1	intron
MIGA1	intron
NEXN	intron
GIPC2	intron
MGC27382	non-coding RNA
MGC27382	non-coding RNA
none	intergenic
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none	intergenic
PTGFR	intron
none	intergenic
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ADGRL4	intron
ADGRL4	intron
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LINC01781	non-coding RNA
LINC01781	non-coding RNA
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ADGRL2	intron
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ADGRL2	intron
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LINC01362	non-coding RNA
LINC01362	non-coding RNA
LINC01362	non-coding RNA
LINC01362	non-coding RNA
LINC01362	non-coding RNA
none	intergenic
none	intergenic
none	intergenic
LINC01712	non-coding RNA
none	intergenic
LINC01725	non-coding RNA
LINC01725	non-coding RNA
LINC01725	non-coding RNA
LINC01725	non-coding RNA
TTLL7	intron
TTLL7	intron
none	intergenic
PRKACB	intron

PRKACB	intron
PRKACB	intron
PRKACB	intron
none	intergenic
none	intergenic
none	intergenic
SAMD13	intron
none	intergenic
UOX	non-coding RNA
none	intergenic
RPF1	intron
none	intergenic
none	intergenic
LPAR3	intron
none	intergenic
none	intergenic
MCOLN3	intron
none	intergenic
DNAI3	intron
DNAI3	intron
none	intergenic
BCL10	intron
none	intergenic
DDAH1	intron
DDAH1	intron
DDAH1	intron
CCN1	intron
none	intergenic
ZNHIT6	intron
COL24A1	intron
COL24A1	intron
COL24A1	intron
COL24A1	intron
COL24A1	intron
COL24A1	intron
COL24A1	intron
COL24A1	intron
none	intergenic
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none	intergenic
ODF2L	intron
ODF2L	intron
none	intergenic
CLCA1	intron
none	intergenic
CLCA4	intron
CLCA4	intron
CLCA4-AS1	non-coding RNA

none	intergenic
HS2ST1	intron
HS2ST1	intron
HS2ST1	intron
none	intergenic
LINC01140	non-coding RNA
LINC01140	non-coding RNA
LINC02801	non-coding RNA
none	intergenic
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none	intergenic
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none	intergenic
none	intergenic
PKN2-AS1	non-coding RNA
PKN2-AS1	non-coding RNA
PKN2-AS1	non-coding RNA
PKN2	intron
PKN2	intron
PKN2	intron
PKN2	intron
PKN2	intron
KYAT3	non-coding RNA
KYAT3	intron
none	intergenic
GBP1	intron
none	intergenic
none	intergenic
GBP1P1	non-coding RNA
none	intergenic
none	intergenic
none	intergenic
none	intergenic
LRR8B	intron
none	intergenic

none	intergenic
none	intergenic
LRRC8D	intron
none	intergenic
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LINC02609	non-coding RNA
ZNF644	intron
none	intergenic
none	intergenic
HFM1	intron
HFM1	intron
CDC7	intron
none	intergenic
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none	intergenic
TGFBR3	intron
TGFBR3	intron
TGFBR3	intron
TGFBR3	intron
TGFBR3	intron
TGFBR3	intron
none	intergenic
BRDT	intron
C1orf146	intron
RPAP2	intron
RPAP2	intron
EVI5	exon
EVI5	intron
EVI5	intron
EVI5	intron
EVI5	intron
EVI5	intron
DIPK1A	intron
DIPK1A	3utr
DIPK1A	intron
DIPK1A	intron

[illegible]

none	intergenic
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PTBP2	intron
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DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	exon
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
DPYD	intron
none	intergenic
MIR137HG	non-coding RNA
MIR137HG	non-coding RNA
MIR137HG	non-coding RNA
none	intergenic
none	intergenic
LINC01776	non-coding RNA
none	intergenic
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none	intergenic
SNX7	exon
SNX7	intron
none	intergenic
none	intergenic
PLPPR5	intron

PLPPR5	intron
PLPPR5-AS1	non-coding RNA
PLPPR5-AS1	non-coding RNA
none	intergenic
PLPPR4	intron
none	intergenic
none	intergenic
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PALMD	intron
PALMD	intron
FRRS1	intron
FRRS1	intron
none	intergenic
AGL	intron
SLC35A3	intron
MFSD14A	intron
SASS6	intron
LRRC39	intron
DBT	intron
none	intergenic
none	intergenic
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CDC14A	intron
CDC14A	intron
CDC14A	intron
CDC14A	intron
CDC14A	intron
CDC14A	intron
CDC14A	intron
LINC01349	non-coding RNA
VCAM1	intron
VCAM1	intron
SLC30A7	intron
SLC30A7	3utr
DPH5-DT	non-coding RNA
DPH5-DT	non-coding RNA
none	intergenic
none	intergenic
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none	intergenic
LINC01307	non-coding RNA
LINC01307	non-coding RNA
none	intergenic
none	intergenic
none	intergenic

[illegible]

[illegible]

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none	intergenic
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	intron
NTNG1	3utr
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VAV3	intron
VAV3	intron
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VAV3	intron
VAV3	intron
VAV3	intron
VAV3	intron
VAV3	intron
VAV3	intron
VAV3	intron
VAV3	intron
VAV3-AS1	non-coding RNA
none	intergenic
none	intergenic
SLC25A24	intron
SLC25A24	intron
SLC25A24	intron
SLC25A24	intron
SLC25A24	intron
NBPF4	intron
NBPF4	intron
none	intergenic
NBPF6	intron
NBPF6	intron
EEIG2	intron
EEIG2	intron
none	intergenic
STXBP3	intron
STXBP3	intron
AKNAD1	intron
AKNAD1	intron

AKNAD1	intron
GPSM2	intron
CLCC1	intron
CLCC1	exon
CLCC1	intron
WDR47	intron
none	intergenic
MYBPHL	intron
SORT1	intron
none	intergenic
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none	intergenic
AHCYL1	intron
AHCYL1	intron
AHCYL1	intron
STRIP1	exon
none	intergenic
none	intergenic
KCNA3	non-coding RNA
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LRIF1	intron
LRIF1	intron
none	intergenic
none	intergenic
CEPT1	exon
CHIA	intron
none	intergenic
none	intergenic
TMIGD3	intron
TMIGD3	intron
TMIGD3	intron
TMIGD3	intron
RAP1A	intron
RAP1A	intron
LINC01750	non-coding RNA
none	intergenic
none	intergenic
LINC02884	non-coding RNA
CTTNBP2NL	intron
ST7L	3utr
CAPZA1	intron
none	intergenic
SLC16A1	intron
SLC16A1	intron
none	intergenic

LRIG2-DT	non-coding RNA
none	intergenic
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MAGI3	intron
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MAGI3	intron
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MAGI3	intron
PHTF1	intron
RSBN1	intron
AP4B1-AS1	non-coding RNA
none	intergenic
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SYT6	intron
SYT6	intron
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DENND2C	intron
DENND2C	intron
DENND2C	intron
CSDE1	intron
none	intergenic
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SYCP1	intron
SYCP1	intron
SYCP1	intron
SYCP1	intron
TSPAN2	intron
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NGF	intron
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CASQ2	intron
CASQ2	intron

none	intergenic
LOC101928977	non-coding RNA
none	intergenic
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ATP1A1	intron
LINC01762	non-coding RNA
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VTCN1	intron
VTCN1	intron
none	intergenic
MAN1A2	intron
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GDAP2	intron
GDAP2	intron
GDAP2	intron
SPAG17	intron
SPAG17	intron
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SPAG17	intron
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TBX15	intron
TBX15	intron
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none	intergenic
NOTCH2	intron
none	intergenic

none	intergenic
none	intergenic
NBPF8	intron
PDE4DIPP2	non-coding RNA
PDE4DIPP2	non-coding RNA
PDE4DIPP2	non-coding RNA
NBPF26	intron
none	intergenic
none	intergenic
LOC105369199	non-coding RNA
PDE4DIPP4	non-coding RNA
H3P4	non-coding RNA
SRGAP2C	intron
SRGAP2C	intron
SRGAP2-AS1	non-coding RNA
EMBP1	non-coding RNA
none	intergenic
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none	intergenic
H2BP2	non-coding RNA
SRGAP2D	non-coding RNA
SRGAP2D	non-coding RNA
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KMT2CP1	non-coding RNA
KMT2CP1	non-coding RNA
SRGAP2B	intron
SRGAP2B	intron
SRGAP2B	intron
none	intergenic
none	intergenic
none	intergenic
NBPF20	intron
none	intergenic
none	intergenic
GPR89A	intron

[illegible]

NOTCH2NLC	intron
none	intergenic
none	intergenic
LINC00869	non-coding RNA
none	intergenic
none	intergenic
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none	intergenic
SV2A	intron
OTUD7B	3utr
VPS45	intron
VPS45	intron
VPS45	intron
RPRD2	intron
TARS2	intron
ADAMTSL4-AS1	non-coding RNA
GOLPH3L	intron
none	intergenic
SETDB1	intron
PRUNE1	intron
none	intergenic
POGZ	3utr
POGZ	intron
SNX27	intron
SNX27	intron
SNX27	intron
none	intergenic
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FLG-AS1	non-coding RNA
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INTS3	intron
GATAD2B	3utr
CRTC2	3utr
NUP210L	intron

[illegible]

none	intergenic
OR6P1	intron
none	intergenic
SPTA1	intron
none	intergenic
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PYHIN1	intron
IFI16	intron
none	intergenic
CADM3	intron
FCER1A	intron
none	intergenic
none	intergenic
OR10J1	intron
OR10J1	exon
none	intergenic
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LINC01133	non-coding RNA
ATP1A2	intron
PEA15	3utr
DCAF8	intron
DCAF8	intron
SLAMF6	intron
none	intergenic
CD48	intron
none	intergenic
none	intergenic
none	intergenic
USF1	intron
none	intergenic
none	intergenic
ATF6	intron
ATF6	intron
ATF6	intron
none	intergenic
NOS1AP	intron
NOS1AP	intron
NOS1AP	intron

NOS1AP	intron
NOS1AP	3utr
none	intergenic
SH2D1B	intron
none	intergenic
UAP1	intron
DDR2	intron
DDR2	intron
DDR2	intron
CCDC190	3utr
CCDC190	intron
CCDC190	intron
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RGS5	intron
RGS5	intron
RGS5	intron
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PBX1	intron
PBX1	intron
PBX1	intron
PBX1	intron
PBX1	intron
none	intergenic
none	intergenic
none	intergenic

LMX1A	intron
LMX1A	intron
LMX1A	intron
LMX1A	intron
none	intergenic
none	intergenic
TMCO1	intron
TMCO1	splice site
none	intergenic
UCK2	intron
UCK2	intron
UCK2	intron
none	intergenic
none	intergenic
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none	intergenic
none	intergenic
none	intergenic
LINC01675	non-coding RNA
LINC01675	non-coding RNA
none	intergenic
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none	intergenic
POGK	intron
MAEL	intron
MAEL	intron
MAEL	intron
GPA33	intron
none	intergenic
POU2F1	intron
POU2F1	intron
POU2F1	intron
POU2F1	intron
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ADCY10	intron
ADCY10	intron
MPC2	intron
DCAF6	intron
DCAF6	intron
DCAF6	intron
none	intergenic
TBX19	intron
none	intergenic
none	intergenic
XCL1	3utr
none	intergenic

[illegible]

DNM3	intron
DNM3	intron
none	intergenic
SUCO	intron
SUCO	intron
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TNFSF18	intron
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TNFSF4	3utr
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SLC9C2	intron
SLC9C2	intron
ANKRD45	intron
KLHL20	intron
DARS2	intron
RC3H1	intron
RC3H1	intron
none	intergenic
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RABGAP1L-DT	non-coding RNA
RABGAP1L-DT	non-coding RNA
RABGAP1L	intron
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RABGAP1L	intron
none	intergenic
TNN	intron
TNN	intron

TNR	exon
TNR	intron
TNR	intron
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TNR	intron
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COP1	intron
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PAPPA2	intron
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ASTN1	intron
ASTN1	intron
BRINP2	intron
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RASAL2	intron
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RALGPS2	intron
RALGPS2	intron
RALGPS2	exon
RALGPS2	intron

RALGPS2	3utr
none	intergenic
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FAM20B	intron
TOR3A	intron
ABL2	intron
none	intergenic
AXDND1	intron
AXDND1	intron
AXDND1	intron
TDRD5	intron
TDRD5	intron
TDRD5	intron
FAM163A	intron
FAM163A	intron
FAM163A	intron
none	intergenic
none	intergenic
TOR1AIP2	intron
TOR1AIP1	intron
none	intergenic
CEP350	intron
CEP350	3utr
LHX4	3utr
ACBD6	intron
ACBD6	intron
none	intergenic
XPR1	intron
XPR1	intron
STX6	intron
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CACNA1E	intron
CACNA1E	intron
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LINC01344	non-coding RNA
none	intergenic

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RGSL1	intron
RGSL1	intron
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RGS8	3utr
RGS8	intron
RGS8	intron
DHX9	intron
SHCBP1L	intron
SHCBP1L	intron
none	intergenic
LAMC1	intron
LAMC2	intron
NMNAT2	intron
NMNAT2	intron
NMNAT2	intron
ARPC5	3utr
RGL1	intron
RGL1	intron
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RGL1	intron
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RGL1	intron
COLGALT2	intron
TSEN15	intron
TSEN15	intron
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C1orf21	intron
C1orf21	intron
C1orf21	intron
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EDEM3	3utr
EDEM3	intron
NIBAN1	intron
NIBAN1	intron
NIBAN1	intron
NIBAN1	intron
RNF2	intron
RNF2	intron
none	intergenic
TRMT1L	intron

[illegible]

[illegible]

[illegible]

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KCNT2	intron
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KCNT2	intron
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CFH	exon
CFH	intron
CFH	intron
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CFHR5	intron
ZBTB41	3utr
CRB1	intron
CRB1	intron
CRB1	intron
CRB1	intron
CRB1	intron
DENND1B	intron
DENND1B	intron
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DENND1B	intron
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NEK7	intron
NEK7	intron
NEK7	intron
NEK7	3utr
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LINC01221	non-coding RNA
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LINC02789	non-coding RNA
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LINC02789	non-coding RNA
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NR5A2	intron
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KIF14	intron
CAMSAP2	intron
CAMSAP2	intron
CAMSAP2	exon
MROH3P	non-coding RNA
MROH3P	non-coding RNA
none	intergenic
CSRP1	intron
NAV1	intron
NAV1	intron
none	intergenic
LGR6	intron
PPP1R12B	intron
PPP1R12B	intron
PPP1R12B	intron
PPP1R12B	intron
PPP1R12B	3utr
none	intergenic
ADIPOR1	intron
PPFIA4	intron
ADORA1	intron
none	intergenic
none	intergenic

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ATP2B4	intron
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SOX13	intron
REN	intron
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PIK3C2B	intron
LRRN2	intron
none	intergenic
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NFASC	intron
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TMCC2	intron
NUAK2	intron
none	intergenic
NUCKS1	3utr
none	intergenic
PM20D1-AS1	non-coding RNA
SLC26A9	intron
RHEX	intron
SRGAP2	intron
SRGAP2	intron
SRGAP2	intron
SRGAP2	intron
SRGAP2	intron
IKBKE-AS1	non-coding RNA
IKBKE-AS1	non-coding RNA
RASSF5	intron
none	intergenic
PIGR	intron
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C1orf116	intron
none	intergenic
C4BPA	intron
C4BPA	intron
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CD55	intron
CR1	intron
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CR1	intron
CR1L	intron
CR1L	intron
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PLXNA2	intron
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CAMK1G	intron
CAMK1G	intron
LAMB3	intron
none	intergenic
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SYT14	intron
SYT14	intron
SERTAD4-AS1	non-coding RNA
LINC02602	non-coding RNA
HHAT	intron
KCNH1	intron
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RCOR3	intron
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NEK2	intron
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LPGAT1	intron
LPGAT1	intron
LPGAT1	intron
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INTS7	intron
INTS7	intron
DTL	intron
DTL	intron
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LINC02608	non-coding RNA
PPP2R5A	intron
PPP2R5A	intron
NENF	intron
LINC02771	non-coding RNA
none	intergenic
NSL1	intron
RPS6KC1	intron
RPS6KC1	intron
RPS6KC1	intron
RPS6KC1	intron
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PROX1-AS1	non-coding RNA
PROX1-AS1	non-coding RNA
PROX1-AS1	non-coding RNA
PROX1-AS1	non-coding RNA
PROX1-AS1	non-coding RNA
PROX1	intron
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SMYD2	intron
SMYD2	intron
PTPN14	intron
PTPN14	intron

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KCNK2	intron
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USH2A	intron
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ESRRG	intron
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GPATCH2	intron

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GPATCH2	intron
SPATA17	intron
SPATA17	intron
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LINC01653	non-coding RNA
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TGFB2	intron
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LYPLAL1-DT	non-coding RNA
LYPLAL1-DT	non-coding RNA
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LYPLAL1-AS1	non-coding RNA
LYPLAL1-AS1	non-coding RNA
LYPLAL1-AS1	non-coding RNA
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EPRS1	intron
EPRS1	intron
BPNT1	intron
BPNT1	intron
RAB3GAP2	intron
RAB3GAP2	intron
RAB3GAP2	intron
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MARK1	intron

MARK1	intron
MARK1	intron
none	intergenic
HLX-AS1	non-coding RNA
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BROX	intron
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DISP1	intron
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TLR5	intron
TLR5	intron
none	intergenic
SUSD4	intron
none	intergenic
CAPN8	intron
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CAPN2	intron
TP53BP2	exon
TP53BP2	splice site
none	intergenic
GTF2IP20	non-coding RNA
none	intergenic
CNIH4	intron
CNIH4	intron
WDR26	intron
CNIH3	intron
CNIH3	intron
CNIH3	intron
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[illegible]

[illegible]

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SLC35F3	intron
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TARBP1	intron
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TOMM20	intron
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ARID4B	intron
B3GALNT2	intron
GNG4	intron
GNG4	intron
none	intergenic
LYST	intron
LYST	intron
LYST	exon
LYST	intron
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LINC02768	non-coding RNA
LINC02768	non-coding RNA
NID1	intron
none	intergenic
ERO1B	intron
HEATR1	intron
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MTR	intron
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RYR2	intron

[illegible]

CHRM3	intron
CHRM3	intron
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FMN2	intron
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GREM2	intron
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RGS7	intron
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none	intergenic
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FH	intron
KMO	intron
KMO	exon
KMO	intron
OPN3	intron
WDR64	exon
WDR64	intron
WDR64	intron
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PLD5	intron
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LINC01347	non-coding RNA
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CEP170	exon
CEP170	intron
CEP170	intron
SDCCAG8	intron
SDCCAG8	intron
SDCCAG8	intron
SDCCAG8	intron
SDCCAG8	intron
SDCCAG8	intron
AKT3	intron
AKT3	intron
AKT3	intron
none	intergenic
LINC02774	non-coding RNA
LINC02774	non-coding RNA
LINC02774	non-coding RNA
LINC02774	non-coding RNA
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ADSS2	intron
ADSS2	intron
CATSPERE	intron
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DESI2	intron
DESI2	intron
none	intergenic
none	intergenic
EFCAB2	intron

none	intergenic
KIF26B	intron
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none	intergenic
SMYD3	intron
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CNST	intron
CNST	intron
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SCCPDH	intron
SCCPDH	intron
AHCTF1	exon
none	intergenic
ZNF670	intron
ZNF124	intron
ZNF124	3utr
ZNF124	intron
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ZNF496	intron
OR2B11	3utr
GCSAML	intron
GCSAML	intron
GCSAML	intron
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OR2T8	3utr
OR2L5	intron

intron

intergenic

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intragenic

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intragenic

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Intergenic

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ZMYND11	intron
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DIP2C	intron
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LARP4B-DT	non-coding RNA
WDR37	intron
LINC00200	non-coding RNA
ADARB2	intron
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LINC02645	non-coding RNA
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PFKF	intron
LOC105376360	non-coding RNA
LINC02669	non-coding RNA
LINC02669	non-coding RNA

LINC02669	non-coding RNA
LOC105376360	non-coding RNA
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AKR1E2	intron
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AKR1C4	intron
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NET1	intron
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TASOR2	exon
GDI2	intron
none	intergenic
none	intergenic
ANKRD16	intron
FBH1	intron
FBH1	intron
IL2RA	intron
none	intergenic
PFKFB3	intron
PFKFB3	intron
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PRKCQ	intron
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SFMBT2	intron
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LINC02642	non-coding RNA
LINC02642	non-coding RNA
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ITIH5	intron
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ITIH5	intron
ITIH2	intron
KIN	3utr
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TAF3	intron
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LOC101928272	non-coding RNA
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CELF2	intron
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CELF2	intron
none	intergenic
USP6NL	intron
USP6NL	intron
USP6NL	intron
USP6NL	intron
none	intergenic
UPF2	intron
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UPF2	intron
CAMK1D	intron
CAMK1D	intron
CAMK1D	intron
CAMK1D	intron
none	intergenic
CCDC3	intron
CCDC3	intron
PHYH	intron
BEND7	intron
BEND7	intron

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PRPF18	non-coding RNA
FRMD4A	intron
FRMD4A	intron
FRMD4A	intron
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FRMD4A	intron
none	intergenic
none	intergenic
FAM107B	intron
FAM107B	intron
FAM107B	intron
CDNF	3utr
HSPA14	exon
DCLRE1C	intron
DCLRE1C	intron
ACBD7-DCLRE1CP1	non-coding RNA
FAM171A1	intron
none	intergenic
ITGA8	intron
MINDY3	intron
MINDY3	intron
MINDY3	intron
none	intergenic
none	intergenic
none	intergenic
PTER	intron
PTER	3utr
RSU1	intron

RSU1	intron
RSU1	intron
RSU1	intron
CUBN	intron
CUBN	intron
CUBN	intron
CUBN	intron
CUBN	intron
CUBN	exon
none	intergenic
ST8SIA6	3utr
ST8SIA6	intron
ST8SIA6	intron
ST8SIA6	intron
none	intergenic
none	intergenic
MRC1	intron
MRC1	intron
MRC1	intron
SLC39A12	intron
SLC39A12	intron
none	intergenic
CACNB2	intron
CACNB2	intron
CACNB2	intron
NSUN6	intron
NSUN6	intron
none	intergenic
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MALRD1	intron
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MALRD1	intron
MALRD1	intron
MALRD1	intron
MALRD1	3utr
none	intergenic

PLXDC2	intron
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PLXDC2	intron
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NEBL	intron
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NEBL	intron
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MLLT10	intron
MLLT10	intron
DNAJC1	intron
DNAJC1	intron
none	intergenic
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LOC100130992	non-coding RNA
none	intergenic
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ARMC3	intron
ARMC3	intron

none	intergenic
C10orf67	intron
C10orf67	intron
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KIAA1217	intron
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ARHGAP21	intron
none	intergenic
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PRTFDC1	intron
ENKUR	intron
ENKUR	intron
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ENKUR	intron
none	intergenic
GPR158	intron
GPR158	intron
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none	intergenic
none	intergenic
LINC00836	non-coding RNA
MYO3A	intron
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MYO3A	intron
MYO3A	intron

MYO3A	intron
MYO3A	intron
GAD2	intron
none	intergenic
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none	intergenic
APBB1IP	intron
none	intergenic
FAM238B	non-coding RNA
ABI1	intron
ABI1	intron
none	intergenic
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ANKRD26	intron
none	intergenic
ODAD2P1	non-coding RNA
none	intergenic
none	intergenic
PTCHD3	intron
ODAD2	intron
none	intergenic
MPP7	intron
none	intergenic
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WAC	intron
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none	intergenic
SVIL-AS1	non-coding RNA
SVIL	intron
SVIL	intron
SVIL	intron
SVIL	intron
none	intergenic
none	intergenic
JCAD	intron
MAP3K8	intron
MAP3K8	3utr
ZNF438	intron
ZNF438	intron
none	intergenic

none	intergenic
none	intergenic
LINC02664	non-coding RNA
LINC02664	non-coding RNA
LINC02664	non-coding RNA
LINC02664	non-coding RNA
none	intergenic
ZEB1	intron
ZEB1	intron
ZEB1	intron
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EPC1	intron
CCDC7	intron
CCDC7	intron
CCDC7	intron
ITGB1	intron
none	intergenic
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NRP1	intron
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PAR3	intron
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PAR3	intron
PAR3	intron
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PAR3	intron
PAR3	intron
PAR3	intron
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none	intergenic
none	intergenic

[illegible]

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ZNF33B	intron
none	intergenic
BMS1	intron
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HNRNPF	intron
ZNF487	intron
none	intergenic
LINC00841	non-coding RNA
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TMEM72-AS1	non-coding RNA
TMEM72-AS1	non-coding RNA
TMEM72-AS1	non-coding RNA
none	intergenic
none	intergenic
ANKRD30BP3	non-coding RNA
ANKRD30BP3	non-coding RNA
none	intergenic
none	intergenic
ALOX5	intron
ZFAND4	intron
ZFAND4	intron
none	intergenic
WASHC2C	intron
none	intergenic
PARGP1-AGAP4	non-coding RNA
PARGP1-AGAP4	non-coding RNA
none	intergenic
LINC00842	non-coding RNA
none	intergenic
none	intergenic
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FRMPD2B	non-coding RNA
none	intergenic

[illegible]

[illegible]

[illegible]

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BICC1	intron
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FAM13C	intron
FAM13C	intron
none	intergenic
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CCDC6	intron
CCDC6	intron
ANK3	intron
ANK3	intron
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ANK3	intron
none	intergenic
none	intergenic
RHOBTB1	intron
RHOBTB1	intron

[illegible]

[illegible]

CTNNA3	intron
CTNNA3	intron
LRRTM3	intron
LRRTM3	intron
LRRTM3	intron
CTNNA3	intron
CTNNA3	intron
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CTNNA3	intron
none	intergenic
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HERC4	intron
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HERC4	intron
MYPN	intron
none	intergenic
none	intergenic
PBLD	intron
RUFY2	intron
none	intergenic
DDX50	intron
VPS26A	intron
HK1	intron
HK1	intron
TACR2	intron
none	intergenic
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MACROH2A2	intron
NPFFR1	intron
LRRC20	intron
LRRC20	intron
EIF4EBP2	3utr
SGPL1	3utr
none	intergenic
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UNC5B	intron
UNC5B	intron
none	intergenic
CDH23	intron
CDH23	intron

none	intergenic
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MICU1	intron
MICU1	intron
MICU1	intron
MCU	intron
MCU	intron
MCU	intron
MCU	intron
MCU	intron
MCU	intron
PLA2G12B	intron
P4HA1	intron
FAM149B1	intron
FAM149B1	intron
DNAJC9	intron
CFAP70	intron
ANXA7	intron
MSS51	3utr
USP54	intron
USP54	intron
SEC24C	intron
ZSWIM8	intron
none	intergenic
C10orf55	non-coding RNA
VCL	intron
VCL	intron
VCL	intron
AP3M1	exon
ADK	intron
ADK	intron
ADK	intron
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ADK	intron
none	intergenic
KAT6B	intron
KAT6B	intron
none	intergenic
DUSP29	intron
SAMD8	exon
SAMD8	3utr
ZNF503	non-coding RNA

ZNF503	non-coding RNA
ZNF503	non-coding RNA
LRMDA	intron
LRMDA	intron
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LRMDA	intron
none	intergenic
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KCNMA1	intron
KCNMA1	intron
KCNMA1	intron
KCNMA1	intron
KCNMA1	intron
none	intergenic
DLG5	intron
DLG5	intron
POLR3A	intron
none	intergenic
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ZMIZ1-AS1	non-coding RNA
ZMIZ1-AS1	non-coding RNA
ZMIZ1	intron
ZMIZ1	intron
ZMIZ1	3utr
none	intergenic
none	intergenic
none	intergenic
none	intergenic
none	intergenic
NUTM2B-AS1	non-coding RNA
NUTM2B-AS1	non-coding RNA

[illegible]

[illegible]

GRID1	intron
GRID1	intron
WAPL	3utr
WAPL	intron
WAPL	intron
BMPR1A	intron
BMPR1A	intron
BMPR1A	intron
none	intergenic
GLUD1	intron
GLUD1	intron
GLUD1	intron
SHLD2	intron
none	intergenic
NUTM2A-AS1	non-coding RNA
none	intergenic
none	intergenic
none	intergenic
PAPSS2	intron
ATAD1	intron
PTEN	intron
none	intergenic
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RNLS	intron
RNLS	intron
RNLS	intron
RNLS	intron
RNLS	intron
RNLS	intron
ANKRD22	intron
STAMBPL1	intron
STAMBPL1	intron
STAMBPL1	intron
ACTA2	intron
none	intergenic
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LIPA	intron
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SLC16A12	intron
none	intergenic
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LINC02653	non-coding RNA
LINC02653	non-coding RNA
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none	intergenic
HTR7	intron
HTR7	intron
ANKRD1	intron
none	intergenic
none	intergenic
HECTD2-AS1	non-coding RNA
HECTD2-AS1	non-coding RNA
HECTD2	intron
HECTD2-AS1	non-coding RNA
none	intergenic
TNKS2	intron
none	intergenic
BTAF1	intron
BTAF1	intron
BTAF1	intron
BTAF1	intron
CPEB3	intron
CPEB3	intron
CPEB3	intron
none	intergenic
none	intergenic
KIF11	intron
EXOC6	intron
EXOC6	intron
EXOC6	3utr
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MYOF	intron
MYOF	intron
MYOF	intron
MYOF	intron
FFAR4	intron
PDE6C	intron
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PLCE1	intron
PLCE1	intron
PLCE1	intron
HELLS	intron
none	intergenic
CYP2C18	intron
none	intergenic
CYP2C19	intron
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CYP2C9	intron
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ACSM6	intron
PDLIM1	intron
PDLIM1	intron
SORBS1	intron
SORBS1	exon
SORBS1	intron
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SORBS1	intron
ALDH18A1	intron
ENTPD1	intron
ENTPD1	intron
ENTPD1-AS1	non-coding RNA
CC2D2B	intron
CC2D2B	intron
none	intergenic
none	intergenic
ZNF518A	intron
none	intergenic
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DNTT	intron
TLL2	intron
TLL2	intron
TM9SF3	intron
TM9SF3	intron
PIK3AP1	intron
LCOR	intron
LCOR	intron
SLIT1	intron
ARHGAP19	intron
ARHGAP19	intron
RRP12	intron
EXOSC1	intron

ZDHC16	intron
UBTD1	intron
HOGA1	3utr
CRTAC1	intron
none	intergenic
HPSE2	intron
HPSE2	intron
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HPSE2	intron
CNNM1	intron
none	intergenic
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ENTPD7	3utr
DNMBP	intron
CPN1	intron
ERLIN1	intron
WNT8B	intron
HIF1AN	3utr
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SLF2	intron
SLF2	intron
none	intergenic
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BTRC	intron
BTRC	intron
BTRC	intron
DPCD	intron
FBXW4	intron
ARMH3	intron
ARMH3	intron
ARMH3	intron
GBF1	intron
GBF1	intron
GBF1	intron
ARL3	intron

WBP1L	intron
CNNM2	intron
CNNM2	intron
CNNM2	intron
NT5C2	exon
INA	intron
SH3PXD2A	exon
none	intergenic
none	intergenic
CFAP43	intron
CFAP43	intron
CFAP43	intron
CFAP58	intron
CFAP58	intron
none	intergenic
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SORCS3	intron
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LINC02627	non-coding RNA
LINC02627	non-coding RNA
LINC02627	non-coding RNA
LINC02627	non-coding RNA
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LINC02624	non-coding RNA
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SORCS1	intron

SORCS1	intron
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SORCS1	intron
none	intergenic
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LINC01435	non-coding RNA
LINC01435	non-coding RNA
LINC01435	non-coding RNA
LINC01435	non-coding RNA
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ADD3	intron
MXI1	exon
none	intergenic
none	intergenic
none	intergenic
SMC3	intron
SMC3	intron
RBM20	intron
RBM20	intron
RBM20	intron
PDCD4	intron
SHOC2	intron

SHOC2	intron
none	intergenic
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GUCY2GP	non-coding RNA
VTI1A	intron
VTI1A	intron
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VTI1A	intron
VTI1A	intron
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VTI1A	intron
none	intergenic
none	intergenic
TCF7L2	intron
TCF7L2	intron
TCF7L2	intron
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HABP2	intron
PLEKHS1	intron
none	intergenic
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none	intergenic
ADRB1	3utr
AFAP1L2	intron
ABLIM1	intron
ABLIM1	intron

ABLIM1	intron
ABLIM1	intron
ABLIM1	intron
ABLIM1	intron
FHIP2A	intron
FHIP2A	intron
TRUB1	intron
none	intergenic
ATRNL1	intron
ATRNL1	intron
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ATRNL1	intron
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GFRA1	intron
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GFRA1	intron
none	intergenic
CCDC172	intron
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HSPA12A	intron
HSPA12A	intron
HSPA12A	intron
ENO4	intron
SHTN1	intron
SHTN1	intron
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none	intergenic
none	intergenic
SLC18A2	intron
PDZD8	intron
PDZD8	exon

[illegible]

none	intergenic
none	intergenic
FGFR2	intron
FGFR2	intron
FGFR2	intron
ATE1	intron
ATE1	intron
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ATE1	intron
TACC2	intron
TACC2	intron
TACC2	intron
TACC2	intron
PLEKHA1	intron
DMBT1	intron
DMBT1	intron
DMBT1	intron
none	intergenic
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none	intergenic
DMBT1L1	non-coding RNA
DMBT1L1	non-coding RNA
DMBT1L1	non-coding RNA
none	intergenic
CUZD1	intron
C10orf88B	non-coding RNA
none	intergenic
ACADSB	intron
none	intergenic
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none	intergenic
CPXM2	intron
CPXM2	intron
CPXM2	intron
none	intergenic
none	intergenic
FAM53B	intron
EEF1AKMT2	intron
EEF1AKMT2	intron
none	intergenic
none	intergenic
CTBP2	3utr
none	intergenic
none	intergenic
none	intergenic

none	intergenic
none	intergenic
EDRF1	intron
DHX32	intron
DHX32	intron
none	intergenic
ADAM12	intron
ADAM12	intron
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C10orf90	intron
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INSYN2A	intron
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PTPRE	intron
none	intergenic
LINC01163	non-coding RNA
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MGMT	intron
MGMT	intron

[illegible]

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DEAF1	intron
none	intergenic
DUSP8	intron
none	intergenic
none	intergenic
CD81-AS1	non-coding RNA
CD81-AS1	non-coding RNA
KCNQ1	intron
KCNQ1	intron
KCNQ1	intron
KCNQ1	intron
none	intergenic
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none	intergenic
ZNF195	intron
NUP98	intron
STIM1	intron
STIM1	intron
STIM1	intron
RRM1	intron
RRM1	intron
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TRIM21	5utr
OR52K2	exon
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MMP26	intron
MMP26	intron
MMP26	intron
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none	intergenic
OR52A1	3utr
none	intergenic
none	intergenic
OR51B5	intron

OR51B5	intron
none	intergenic
TRIM34	intron
TRIM5	3utr
TRIM5	intron
TRIM22	exon
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DNHD1	exon
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NLRP14	intron
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SYT9	intron
SYT9	intron
OLFML1	intron
PPFIBP2	intron
PPFIBP2	intron
none	intergenic
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TUB	intron
TUB	intron
LMO1	intron
none	intergenic
STK33	intron
STK33	intron
STK33	intron
DENND2B	intron
DENND2B	intron
none	intergenic
NRIP3	intron
NRIP3	intron
none	intergenic
DENND5A	intron
DENND5A	intron

DENND5A	intron
ZNF143	exon
SBF2-AS1	non-coding RNA
SBF2	intron
SBF2	intron
SBF2	intron
SBF2	intron
SBF2	intron
SBF2	intron
SBF2	intron
SBF2	intron
AMPD3	intron
AMPD3	intron
AMPD3	exon
RNF141	intron
IRAG1-AS1	non-coding RNA
ZBED5	intron
ZBED5-AS1	non-coding RNA
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none	intergenic
GALNT18	intron
GALNT18	intron
GALNT18	intron
GALNT18	intron
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USP47	intron
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MICAL2	intron
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PARVA	intron
PARVA	intron
PARVA	intron
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TEAD1	intron
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BTBD10	intron

[illegible]

SOX6	intron
SOX6	intron
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SOX6	intron
PLEKHA7	intron
PLEKHA7	intron
PIK3C2A	intron
PIK3C2A	intron
PIK3C2A	intron
none	intergenic
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NCR3LG1	3utr
ABCC8	intron
none	intergenic
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SERGEF	intron
SERGEF	intron
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LDHC	intron
TSG101	intron
UEVLD	intron
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NAV2	intron
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HTATIP2	intron
none	intergenic

[illegible]

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LUZP2	intron
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LINC02699	non-coding RNA
LINC02699	non-coding RNA
LINC02699	non-coding RNA
LINC02699	non-coding RNA
LINC02699	non-coding RNA
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ANO3	intron
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ANO3	intron
MUC15	intron
ANO3	intron
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[illegible]

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MPPED2	intron
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DCDC1	intron
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DCDC1	intron
DCDC1	intron
IMMP1L	intron
IMMP1L	intron
ELP4	intron
ELP4	intron
PAX6	intron
PAX6-AS1	non-coding RNA
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CCDC73	intron
CCDC73	exon
CCDC73	intron
QSER1	intron
none	intergenic
CSTF3	exon
CSTF3	intron
CSTF3-DT	non-coding RNA
none	intergenic
KIAA1549L	intron

KIAA1549L	intron
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KIAA1549L	intron
CD59	intron
FBXO3	intron
FBXO3	intron
FBXO3	exon
FBXO3	intron
none	intergenic
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LMO2	intron
CAPRIN1	intron
ABTB2	intron
ABTB2	intron
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CAT	intron
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APIP	intron
PDHX	intron
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CD44	intron
SLC1A2	intron
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SLC1A2	intron
PAMR1	intron
PAMR1	intron
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TRIM44	intron
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LDLRAD3	intron
LDLRAD3	intron
PRR5L	intron
PRR5L	intron
PRR5L	intron
PRR5L	intron
RAG1	intron

[illegible]

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LINC01499	non-coding RNA
LINC01499	non-coding RNA
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LINC02745	non-coding RNA
LINC02745	non-coding RNA
none	intergenic

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TTC17	intron
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HSD17B12	intron
HSD17B12	intron
ALKBH3	intron
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EXT2	intron
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EXT2	intron
EXT2	intron
EXT2	intron
EXT2	intron
EXT2	3utr
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TSPAN18	intron
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TP53I11	intron
SYT13	intron

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LINC02687	non-coding RNA
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PHF21A	intron
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AMBRA1	intron
AMBRA1	intron
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none	intergenic
CKAP5	intron
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CKAP5	intron
LRP4-AS1	non-coding RNA
CSTPP1	intron
NR1H3	intron
MADD	exon
MADD	intron
CELF1	intron
NUP160	intron
NUP160	3utr
PTPRJ	intron
none	intergenic
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TRIM51G	intron
none	intergenic
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TRIM49B	exon
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FOLH1	intron

[illegible]

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SMTNL1	intron
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OR9Q1	intron
OR9Q1	intron
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ZFP91	intron
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GLYATL1	intron
GLYATL1	intron
LOC283194	non-coding RNA
none	intergenic
MPEG1	3utr
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OSBP	intron
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PATL1	intron
PATL1	intron
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STX3	intron
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MS4A6A	intron
MS4A4E	intron
MS4A4A	intron
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MS4A5	intron
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LINC00301	non-coding RNA
MS4A8	intron
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CD6	intron
VPS37C	intron
VPS37C	intron
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CYB561A3	3utr
SDHAF2	intron
RPLP0P2	non-coding RNA
none	intergenic
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AHNAK	intron
WDR74	intron
none	intergenic
SLC22A24	intron
SLC22A25	intron
none	intergenic
ATL3	3utr
FLRT1	intron
none	intergenic
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NRXN2	intron
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MRPL49	intron
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POLA2	intron
NEAT1	non-coding RNA
TALAM1	non-coding RNA
SCYL1	intron
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PACS1	intron
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PACS1	intron
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RBM4	intron
C11orf80	intron
C11orf80	intron
LOC107984341	non-coding RNA
KDM2A	intron
KDM2A	intron
KDM2A	intron
LOC100130987	non-coding RNA
ALDH3B1	intron
KMT5B	intron
KMT5B	intron
none	intergenic
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PPP6R3	intron
PPP6R3	intron
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CPT1A	intron
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ANO1	intron
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SHANK2	intron
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RNF121	intron
CLPB	intron
CLPB	intron
none	intergenic
FCHSD2	intron
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ARHGEF17	intron
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FAM168A	intron
FAM168A	intron
RAB6A	intron
RAB6A	intron

RAB6A	intron
MRPL48	intron
PAAF1	intron
PAAF1	intron
DNAJB13	intron
UCP2	intron
C2CD3	intron
C2CD3	intron
PPME1	intron
PPME1	intron
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PPME1	intron
P4HA3	intron
P4HA3-AS1	non-coding RNA
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RNF169	intron
XRRA1	intron
XRRA1	intron
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SPCS2	intron
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MAP6	intron
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DGAT2	intron
UVRAG	intron
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EMSY	exon
EMSY	intron
EMSY	intron
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ACER3	intron

[illegible]

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MIR4300HG	non-coding RNA
MIR4300HG	non-coding RNA
MIR4300HG	non-coding RNA
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MIR4300HG	non-coding RNA
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LINC02734	non-coding RNA
PRCP	intron
PRCP	intron
RAB30	intron
PCF11	exon
none	intergenic
DLG2	intron
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CREBZF	non-coding RNA
SYTL2	intron
SYTL2	intron
SYTL2	intron
CCDC83	intron
none	intergenic
PICALM	intron
none	intergenic
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CCDC81	intron
CCDC81	intron
ME3	intron
ME3	intron
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none	intergenic
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PRSS23	intron
PRSS23	non-coding RNA
PRSS23	non-coding RNA

none	intergenic
TMEM135	intron
TMEM135	intron
TMEM135	intron
TMEM135	3utr
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RAB38	intron
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CTSC	3utr
none	intergenic
GRM5	intron
GRM5	intron
GRM5	intron
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GRM5	intron
none	intergenic
TYR	intron
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NOX4	intron
NOX4	intron
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NOX4	intron
none	intergenic
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TRIM77	exon
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TRIM49	exon
none	intergenic
TRIM53AP	non-coding RNA
TRIM49C	exon
none	intergenic
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NAALAD2	intron
NAALAD2	intron

NAALAD2	intron
DISC1FP1	non-coding RNA
DISC1FP1	non-coding RNA
DISC1FP1	non-coding RNA
DISC1FP1	non-coding RNA
DISC1FP1	non-coding RNA
DISC1FP1	non-coding RNA
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DISC1FP1	non-coding RNA
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LINC02748	non-coding RNA
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FAT3	intron
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FAT3	intron
none	3utr
none	intergenic
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SLC36A4	3utr

SLC36A4	intron
SLC36A4	intron
SLC36A4	intron
SLC36A4	intron
none	intergenic
DEUP1	intron
DEUP1	intron
SMCO4	intron
SMCO4	intron
none	intergenic
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MED17	intron
none	intergenic
HEPHL1	intron
PANX1	intron
none	intergenic
GPR83	3utr
MRE11	intron
MRE11	intron
PIWIL4	intron
PIWIL4	intron
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none	intergenic
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AMOTL1	intron
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MAML2	intron
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MAML2	intron

[illegible]

CNTN5	intron
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TRPC6	intron
TRPC6	intron
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CEP126	intron
CEP126	intron
CEP126	exon
YAP1	intron
YAP1	intron
YAP1	intron
YAP1	intron
none	intergenic
TMEM123	intron
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MMP20	intron
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MMP27	intron
MMP12	intron
DYNC2H1	intron
DYNC2H1	intron
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PDGFD	intron
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LINC02552	non-coding RNA
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GRIA4	intron
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GRIA4	intron
LINC02719	non-coding RNA
LINC02719	non-coding RNA

[illegible]

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ZC3H12C	intron
RDX	intron
RDX	intron
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ARHGAP20	intron
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POU2AF2	intron
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HOATZ	intron
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SIK2	intron
ALG9	intron
ALG9	intron
ALG9	intron
none	intergenic
C11orf52	exon
DIXDC1	intron
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DIXDC1	intron
TIMM8B	3utr
none	intergenic
IL18	intron
BCO2	intron
PLET1	intron

[illegible]

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BUD13	intron
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SIK3	intron
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SIK3	intron
RNF214	intron
DSCAML1	intron
DSCAML1	intron
FXVD6-FXVD2	intron
FXVD6-FXVD2	intron
FXVD6	intron
none	intergenic
SMIM35	intron
TMPRSS4	intron
JAML	intron
CD3E	intron
none	intergenic
KMT2A	intron
ARCN1	intron
PHLDB1	intron
none	intergenic
DDX6	intron
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USP2-AS1	non-coding RNA
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GRIK4	intron
GRIK4	intron
GRIK4	exon
TBCEL-TECTA	intron
TBCEL-TECTA	intron

TBCEL-TECTA	intron
TBCEL-TECTA	intron
TBCEL-TECTA	intron
TECTA	intron
none	intergenic
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SORL1-AS1	non-coding RNA
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UBASH3B	intron
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SAE1P1	non-coding RNA
CLMP	intron
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GRAMD1B	intron
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GRAMD1B	intron
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GRAMD1B	intron
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VWA5A	intron
OR8G1	intron
OR8G1	3utr
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OR8D1	intron
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SIAE	intron
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CCDC15	intron
CCDC15	intron
FEZ1	intron
STT3A	intron
CHEK1	intron
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FAM118B	intron
KIRREL3	intron
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none	intergenic

[illegible]

[illegible]

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WASH8P	non-coding RNA
none	intergenic
IQSEC3	intron
IQSEC3	intron
KDM5A	intron
KDM5A	intron
B4GALNT3	intron
NINJ2	intron
NINJ2	intron
none	intergenic
ERC1	intron
ERC1	intron
ERC1	intron
ERC1	3utr
none	intergenic
none	intergenic
ADIPOR2	intron
ADIPOR2	intron
ADIPOR2	intron
LRTM2	intron
none	intergenic
CACNA1C	intron
CACNA1C	intron
CACNA1C	intron

CACNA1C	intron
CACNA1C	intron
CACNA1C	intron
CACNA1C	intron
CACNA1C	intron
CACNA1C	intron
CACNA1C	3utr
ITFG2-AS1	non-coding RNA
NRIP2	intron
ITFG2	non-coding RNA
TULP3	intron
TULP3	intron
none	intergenic
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PRMT8	intron
CRACR2A	intron
CRACR2A	intron
CRACR2A	intron
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TIGAR	intron
TIGAR	intron
TIGAR	3utr
none	intergenic
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C12orf4	intron
GAU1	non-coding RNA
GALNT8	intron
none	intergenic
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LINC02443	non-coding RNA
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NTF3	intron
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ANO2	intron
ANO2	intron
ANO2	intron
ANO2	intron
ANO2	intron
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TAPBPL	intron
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P3H3	intron
USP5	intron
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ATN1	intron
LPCAT3	intron
ACSM4	intron
CD163L1	intron
CD163L1	intron
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CLEC4C	intron
NANOG	intron
SLC2A14	intron
SLC2A14	intron
SLC2A14	intron
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KLRG1	intron
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KLRG1	intron
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PZP	intron
LINC00987	non-coding RNA
LINC00987	non-coding RNA
none	intergenic
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LOC408186	non-coding RNA
none	intergenic
CLECL1P	non-coding RNA
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CLEC12A	intron
CLEC9A	intron
CLEC7A	intron
CLEC7A	intron
none	intergenic
none	intergenic
TMEM52B	intron
KLRD1	intron
KLRD1	intron

[illegible]

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GRIN2B	intron
GRIN2B	intron
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GRIN2B	intron
GRIN2B	intron
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ATF7IP	intron
ATF7IP	intron
PLBD1	intron
PLBD1-AS1	non-coding RNA
none	intergenic
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ERP27	intron
none	intergenic
LINC01489	non-coding RNA
none	intergenic
RERG	3utr
RERG	intron
RERG	intron
RERG	intron
PTPRO	intron
PTPRO	intron
EPS8	intron
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EPS8	intron
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DERA	intron
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SLC15A5	intron
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PIK3C2G	intron
PIK3C2G	intron
PIK3C2G	intron
PIK3C2G	intron
PIK3C2G	intron
PIK3C2G	intron
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PLCZ1	intron
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PLEKHA5	intron
PLEKHA5	intron
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LINC02398	non-coding RNA
LINC02398	non-coding RNA
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PDE3A	intron
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PDE3A	intron
SLCO1B3-SLCO1B7	intron
SLCO1A2	intron
SLCO1A2	intron
RECQL	intron
SPX	3utr
GYS2	intron
GYS2	intron
none	intergenic
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KCNJ8	intron
ABCC9	intron
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ST8SIA1	3utr
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C2CD5	3utr
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ETNK1-DT	non-coding RNA
ETNK1	3utr
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none	intergenic

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SOX5	intron
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BCAT1	intron
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LINC02909	non-coding RNA
IRAG2	intron
IRAG2	intron
DNAI7	exon
DNAI7	intron
KRAS	intron
none	intergenic
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LMNTD1	intron
LMNTD1	intron
LMNTD1	intron

[illegible]

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FAR2	intron
FAR2	intron
FAR2	intron
ERGIC2	3utr
ERGIC2	intron
OVCH1	intron
TMTC1	intron
TMTC1	intron
TMTC1	intron
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IPO8	intron
IPO8	intron
LINC00941	non-coding RNA
none	intergenic
OVOS2	non-coding RNA
SINHCAF	intron
none	intergenic
DENND5B	intron
DENND5B	intron
DENND5B	intron
DENND5B	intron
DENND5B	intron
DENND5B	intron
DENND5B-AS1	non-coding RNA
none	intergenic
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BICD1	intron
BICD1	intron
BICD1	intron
BICD1	intron
FGD4	intron
FGD4	intron
FGD4	intron
FGD4	intron
FGD4	intron
FGD4	3utr
DNM1L	intron
none	intergenic

[illegible]

none	intergenic
ABCD2	intron
C12orf40	intron
SLC2A13	intron
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LINC02471	non-coding RNA
none	intergenic
LRRK2	intron
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LRRK2	intron
none	intergenic
MUC19	intron
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CNTN1	intron
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PDZRN4	intron
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GXYLT1	intron
GXYLT1	intron
YAF2	intron
none	intergenic
ZCRB1	exon
ZCRB1	intron
PPHLN1	intron

PPHLN1	intron
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PRICKLE1	intron
PRICKLE1	intron
LINC02451	non-coding RNA
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ADAMTS20	intron
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TMEM117	intron
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PLEKHA8P1	non-coding RNA
ANO6	intron
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ARID2	intron
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ARID2	intron
ARID2	intron
ARID2	intron
ARID2	intron
ARID2	intron
ARID2	3utr
SCAF11	intron
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SLC38A1	intron
SLC38A2	intron
SLC38A4-AS1	non-coding RNA
SLC38A4-AS1	non-coding RNA
SLC38A4-AS1	non-coding RNA
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SLC38A4	intron
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PCED1B	intron
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RPAP3	intron
VDR	intron
VDR	intron
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SENP1	intron
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DDX23	intron
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WNT10B	intron
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TROAP-AS1	non-coding RNA
SPATS2	intron
none	intergenic
CERS5	intron
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FAM186A	intron
FAM186A	intron
DIP2B	intron
none	intergenic
ATF1	intron
TFCP2	intron
TFCP2	intron
SMAGP	intron
BIN2	intron
SLC4A8	intron
SLC4A8	intron
none	intergenic
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SCN8A	intron
SCN8A	intron
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SCN8A	intron
ACVR1B	intron
none	intergenic
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EIF4B	exon
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CSAD	intron
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ATF7	intron
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FLJ12825	non-coding RNA
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CBX5	intron
GPR84-AS1	non-coding RNA

GTSF1	intron
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OR6C74	3utr
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BLOC1S1	intron
SARNP	intron
SARNP	intron
PMEL	intron
IKZF4	intron
ESYT1	intron
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TAC3	intron
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R3HDM2	intron
R3HDM2	intron
DTX3	intron
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LINC02388	non-coding RNA
LOC100506869	non-coding RNA
LOC100506869	non-coding RNA
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LOC100506869	non-coding RNA
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LRIG3	intron
LRIG3-DT	non-coding RNA
LRIG3-DT	non-coding RNA
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SLC16A7	intron
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TAFA2	intron
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TAFA2	intron
none	intergenic
USP15	intron

USP15	intron
USP15	intron
none	intergenic
MON2	intron
MON2	intron
MON2	intron
MON2	3utr
PPM1H	intron
PPM1H	intron
PPM1H	intron
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RXYLT1-AS1	non-coding RNA
none	intergenic
SRGAP1	intron
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SRGAP1	intron
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C12orf56	intron
C12orf56	intron
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RASSF3	intron
RASSF3	intron
TBC1D30	intron
none	intergenic
WIF1	intron
LEMD3	intron
MSRB3	intron
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MSRB3	intron
MSRB3-AS1	non-coding RNA
MSRB3-AS1	non-coding RNA
MSRB3-AS1	non-coding RNA
MSRB3-AS1	non-coding RNA
MSRB3-AS1	non-coding RNA
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RPSAP52	non-coding RNA
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TMBIM4	intron
IRAK3	intron
GRIP1	intron
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none	intergenic
CAND1	intron
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LINC02408	non-coding RNA
LINC02408	non-coding RNA
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DYRK2	3utr
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LINC01479	non-coding RNA
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IL26	intron
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RAP1B	3utr
NUP107	intron
NUP107	intron
SLC35E3	intron
CPM	intron
CPM	intron
CPM	intron
CPSF6	3utr
CPSF6	3utr
FRS2	intron
BEST3	intron
none	intergenic
LOC101928002	non-coding RNA
RAB3IP	intron
MYRFL	intron
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[illegible]

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LINC02882	non-coding RNA
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LINC02882	non-coding RNA
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LINC02882	non-coding RNA
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KCNC2	exon
KCNC2	intron
KCNC2	intron
KCNC2	intron
KCNC2	intron
CAPS2	intron

GLIPR1L1	intron
GLIPR1L2	intron
none	intergenic
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NAP1L1	intron
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OSBPL8	intron
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OSBPL8	intron
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ZDHHHC17	intron
CSRP2	intron
E2F7	intron
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SYT1	intron
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PAWR	intron
PPP1R12A	intron
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PPP1R12A	intron
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OTOGL	intron
OTOGL	intron
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OTOGL	intron
PTPRQ	intron
PTPRQ	intron
none	intergenic
MYF5	3utr
LIN7A	intron
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ACSS3	intron
PPFIA2	intron
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[illegible]

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LRRIQ1	intron
LINC02820	non-coding RNA
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RASSF9	intron
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MGAT4C	3utr
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RLIG1	intron
CEP290	intron
CEP290	intron
CEP290	intron
TMTC3	intron
TMTC3	intron
none	intergenic

[illegible]

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LUM	5utr
LINC02823	non-coding RNA
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LINC01619	non-coding RNA
LINC01619	non-coding RNA
BTG1-DT	non-coding RNA
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CLLU1-AS1	non-coding RNA
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PLEKHG7	intron
PLEKHG7	intron
PLEKHG7	intron
EEA1	intron
EEA1	intron
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EEA1	intron
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LOC643339	non-coding RNA
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MRPL42	intron
MRPL42	intron

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CRADD	intron
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LOC105369911	non-coding RNA
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PLXNC1	intron
PLXNC1	intron
CEP83	3utr
CEP83	intron
none	intergenic
none	intergenic
NR2C1	intron
NR2C1	intron
FGD6	3utr
VEZT	3utr
METAP2	intron
PGAM1P5	non-coding RNA
NTN4	3utr
LINC02410	non-coding RNA
CCDC38	intron
CCDC38	intron
CCDC38	intron
none	intergenic
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ELK3	intron
CDK17	intron
none	intergenic
CFAP54	intron
CFAP54	intron
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CFAP54	intron
NEDD1	intron
none	intergenic
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RMST	non-coding RNA
RMST	non-coding RNA
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PAFAH1B2P2	non-coding RNA
none	intergenic

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TMPO	intron
SLC25A3	3utr
IKBIP	3utr
IKBIP	intron
ANKS1B	intron
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ANKS1B	intron
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BLTP3B	intron
none	intergenic
ACTR6	3utr
SCYL2	intron
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ANO4	intron
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SLC5A8	intron
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MYBPC1	intron
GNPTAB	intron
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WASHC3	intron
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PARPBP	intron
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IGF1	intron
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PAH	intron
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C12orf42	intron
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C12orf42	intron
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STAB2	intron
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STAB2	intron
TTC41P	non-coding RNA
TTC41P	non-coding RNA
TTC41P	non-coding RNA
GLT8D2	intron
HCFC2	intron

HCFC2	exon
none	intergenic
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CHST11	intron
CHST11	intron
SLC41A2	intron
SLC41A2	intron
ALDH1L2	intron
WASHC4	intron
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APPL2	intron
none	intergenic
C12orf75	intron
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TCP11L2	intron
POLR3B	intron
POLR3B	intron
LOC100287944	non-coding RNA
RFX4	intron
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RFX4	intron
RFX4	intron
RIC8B	intron
RIC8B	intron
RIC8B	3utr
CRY1	intron
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ABTB3	intron
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SART3	intron
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TMEM119	3utr
CORO1C	intron
USP30	intron
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ACACB	intron
ACACB	intron
ACACB	intron
MYO1H	intron
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KCTD10	intron
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TRPV4	intron
GIT2	intron
ANAPC7	intron
RAD9B	intron
PPTC7	intron
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CUX2	intron
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ATXN2	intron
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BRAP	intron
MAPKAPK5	intron
ERP29	intron
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TRAFD1	intron
PTPN11	intron
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RPH3A	intron
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TPCN1	intron
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RBM19	intron

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MED13L	intron
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MED13L	intron
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MAP1LC3B2	intron
none	intergenic
SPRING1	3utr
SPRING1	intron
FBXW8	intron
TESC	intron
TESC-AS1	non-coding RNA
NOS1	intron
NOS1	intron
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NOS1	intron
KSR2	intron
KSR2	intron
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TAOK3	intron
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LINC02423	non-coding RNA
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SRRM4	intron
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LINC00934	non-coding RNA
CIT	intron
CIT	intron
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BICDL1	intron
BICDL1	intron
GCN1	intron
PXN	intron
PXN	intron
DYNLL1	intron
RNF10	intron
SPPL3	intron
SPPL3	intron
HNF1A	intron
P2RX7	intron
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CAMKK2	intron
ANAPC5	intron
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KDM2B	intron
KDM2B	intron
MLXIP	intron
none	intergenic
CLIP1	intron
CLIP1	intron
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KNTC1	intron
DENR	intron
MPHOSPH9	intron
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DDX55	intron

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TMEM132C	intron
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LOC100128276	non-coding RNA
TMEM132D	intron
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RIMBP2	intron
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ADGRD1	intron
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EP400	intron
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POLE	intron
ZNF605	intron

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[illegible]

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LINC00540	non-coding RNA
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SGCG	intron
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SACS	exon
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LINC00327	non-coding RNA
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TNFRSF19	intron
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MIPEP	intron
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SPATA13	intron
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ATP12A	intron
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RNF17	intron
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MTMR6	intron

NUP58	intron
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ATP8A2	intron
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RNF6	intron
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CDK8	intron
CDK8	exon
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WASF3	intron
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USP12	intron
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MTIF3	intron
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LNK2	3utr
LNK2	intron
POLR1D	intron
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FLT3	intron
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PAN3	intron
FLT1	intron
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MTUS2	intron
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SLC7A1	intron
SLC7A1	intron
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UBL3	intron
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LINC00297	non-coding RNA
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LINC00365	non-coding RNA
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KATNAL1	intron
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HMGB1	intron
USPL1	3utr
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TEX26	intron
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B3GLCT	intron
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RXFP2	exon
EEF1DP3	non-coding RNA
FRY	intron
FRY	intron
FRY	intron
ZAR1L	intron
BRCA2	intron
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N4BP2L2	intron
N4BP2L2	intron

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PDS5B	intron
PDS5B	intron
LINC00423	non-coding RNA
LINC00423	non-coding RNA
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KL	intron
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STARD13	intron
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RFC3	intron
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LINC02343	non-coding RNA
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DCLK1	intron
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FREM2	intron
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STOML3	intron
NHLRC3	intron
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LHFPL6	intron
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COG6	intron
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LINC00548	non-coding RNA
LINC00548	non-coding RNA
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TPTE2P5	non-coding RNA
ELF1	intron
ELF1	intron
ELF1	intron
LOC101929140	non-coding RNA
VWA8	intron
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DGKH	intron
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LINC02341	non-coding RNA
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TNFSF11	intron

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LINC00428	non-coding RNA
LINC00428	non-coding RNA
EPSTI1	intron
DNAJC15	intron
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ENOX1	intron
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LINC00390	non-coding RNA
SMIM2	intron
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TSC22D1	intron
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NUFIP1	3utr
GPALPP1	intron
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GTF2F2	intron
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GTF2F2	intron
ERICH6B	intron

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ZC3H13	intron
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LRRC63	intron
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RUBCNL	intron
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LRCH1	intron
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HTR2A	intron
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SUCLA2	intron
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MED4	intron
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RB1	intron
RCBTB2	intron
RCBTB2	intron
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LINC01077	non-coding RNA
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CYSLTR2	intron
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LOC105370203	non-coding RNA
CAB39L	intron
PHF11	exon
KPNA3	exon
KPNA3	intron
SPRYD7	intron
DLEU2	non-coding RNA
DLEU1	non-coding RNA
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C13orf42	intron
C13orf42	non-coding RNA
C13orf42	non-coding RNA
FAM124A	intron
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INTS6	intron
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WDFY2	intron
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TMEM272	intron
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ATP7B	intron
ATP7B	intron
NEK5	intron
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LINC00345	non-coding RNA
LINC00345	non-coding RNA
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CNMD	intron
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OLFM4	intron
OLFM4	intron
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[illegible]

[illegible]

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LINC00434	non-coding RNA
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TDRD3	intron
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LINC01442	non-coding RNA
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LINC01075	non-coding RNA
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[illegible]

[illegible]

[illegible]

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LINC00348	non-coding RNA
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BORA	intron
BORA	intron
DIS3	intron
PIBF1	intron
PIBF1	intron
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LINC00393	non-coding RNA
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KLF12	intron
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TBC1D4	intron
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LMO7	intron
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FBXL3	intron
MYCBP2	intron
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SCEL	intron
SCEL	intron
SLAIN1	intron
EDNRB-AS1	non-coding RNA
EDNRB-AS1	non-coding RNA
EDNRB	intron
EDNRB	intron
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OBI1-AS1	non-coding RNA
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OBI1	intron
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LINC00331	non-coding RNA
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RBM26	intron
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RBM26-AS1	non-coding RNA
NDFIP2	intron
NDFIP2	intron
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LINC01068	non-coding RNA

[illegible]

[illegible]

[illegible]

[illegible]

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[illegible]

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IPO5	intron
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FARP1	intron
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STK24	intron
DOCK9	intron
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TM9SF2	exon
CLYBL	intron
CLYBL	intron
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CLYBL	intron
none	intergenic
PCCA	intron
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GGACT	intron
GGACT	intron
TMTC4	intron
NALCN-AS1	non-coding RNA
NALCN-AS1	non-coding RNA
NALCN-AS1	non-coding RNA
NALCN-AS1	non-coding RNA
NALCN-AS1	non-coding RNA
NALCN	intron
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ITGBL1	intron
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[illegible]

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DAOA-AS1	non-coding RNA
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LINC00343	non-coding RNA
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LINC00460	non-coding RNA
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NALF1	intron

[illegible]

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COL4A1	intron
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RAB20	intron
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NAXD	intron
NAXD	intron
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ARHGEF7	intron
ARHGEF7	intron
TEX29	intron
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LINC02337	non-coding RNA
LOC101928730	non-coding RNA
SPACA7	intron
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TUBGCP3	intron
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ATP11A	intron
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ATP11A	intron
MCF2L	intron
none	intergenic
LAMP1	intron
ADPRHL1	intron
TMCO3	intron
TFDP1	intron
GAS6-AS1	non-coding RNA
none	intergenic
RASA3	intron
RASA3	intron

CFAP97D2	intron
CFAP97D2	intron
CFAP97D2	intron
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UPF3A	intron
CHAMP1	intron
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POTEM	intron
POTEM	intron
none	intergenic
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LINC01297-DUXAP10-NBEAP	non-coding RNA
LINC01297-DUXAP10-NBEAP	non-coding RNA
POTEG	intron
POTEG	intron
none	intergenic
OR4K2	3utr
none	intergenic
OR4K1	intron
none	intergenic
none	intergenic
OR4N5	3utr
none	intergenic
CCNB1IP1	intron
none	intergenic
RNASE10	exon
none	intergenic
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TPPP2	3utr
NDRG2	intron
none	intergenic

HNRNPC	intron
RPGRIP1	intron
SUPT16H	exon
CHD8	intron
TOX4	intron
TOX4	3utr
none	intergenic
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DAD1	intron
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OR6J1	intron
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SLC7A7	intron
SLC7A7	intron
ACIN1	intron
SLC7A8	intron
SLC7A8	intron
RNF212B	intron
none	intergenic
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DHRS2	exon
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DHRS4L2	intron
DHRS4L2	intron
DHRS4L1	non-coding RNA
DHRS4L1	non-coding RNA
NEDD8	intron
none	intergenic
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LOC101927045	non-coding RNA
none	intergenic
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STXBP6	intron
STXBP6	intron
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NOVA1	intron
NOVA1	intron
NOVA1-DT	non-coding RNA
NOVA1-DT	non-coding RNA
LINC02293	non-coding RNA
none	intergenic
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MIR3171HG	non-coding RNA
MIR3171HG	non-coding RNA
MIR3171HG	non-coding RNA

MIR3171HG	non-coding RNA
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LINC01551	non-coding RNA
LINC02327	non-coding RNA
LINC02326	non-coding RNA
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PRKD1	intron
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SCFD1	intron
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NPAS3	intron
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EAPP	intron
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BAZ1A	intron
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PRORP	intron
PRORP	intron
PRORP	3utr
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RALGAPA1	intron
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RALGAPA1	intron
BRMS1L	3utr
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SFTA3	non-coding RNA
SFTA3	non-coding RNA

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[illegible]

[illegible]

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LINC02302	non-coding RNA
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KLHL28	intron
TOGARAM1	intron
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PRPF39	intron
PRPF39	intron
FANCM	intron
MIS18BP1	intron
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LINC00871	non-coding RNA
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LINC00871	non-coding RNA
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MDGA2	intron
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MDGA2	intron

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LINC00648	non-coding RNA
LINC00648	non-coding RNA
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LRR1	intron
POLE2	intron
POLE2	intron
NEMF	intron
MAP4K5	intron
MAP4K5	intron
MAP4K5	intron
MAP4K5	intron

ATL1	intron
ATL1	intron
ATL1	intron
SAV1	intron
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NIN	intron
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ABHD12B	intron
ABHD12B	intron
PYGL	intron
TRIM9	intron
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LINC00519	non-coding RNA
LINC00519	non-coding RNA
FRMD6	intron
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GNG2	intron
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PTGER2	intron
TXNDC16	intron
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GPR137C	intron
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FERMT2	intron
FERMT2	intron
FERMT2	intron
DDHD1	intron
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LINC02331	non-coding RNA
LINC02331	non-coding RNA

LINC02331	non-coding RNA
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SAMD4A	intron
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SOCS4	intron
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LGALS3	intron
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FBXO34	intron
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KTN1	intron
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PELI2	intron
PELI2	intron
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LOC101927690	non-coding RNA
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TMEM260	intron
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OTX2-AS1	non-coding RNA
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NAA30	intron
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SLC35F4	intron
SLC35F4	3utr
SLC35F4	intron

ARMH4	3utr
ARMH4	intron
ARMH4	intron
ACTR10	intron
none	intergenic
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KIAA0586	exon
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LINC01500	non-coding RNA
DAAM1	intron
DAAM1	intron
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JKAMP	intron
CCDC175	intron
RTN1	intron
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RTN1	intron
none	intergenic
PCNX4	intron
PCNX4	intron
PCNX4	3utr
none	intergenic
PPM1A	3utr
none	intergenic
C14orf39	intron
C14orf39	exon
none	intergenic
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MNAT1	intron
MNAT1	intron
SLC38A6	intron
SLC38A6	intron
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PRKCH	intron
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LINC01303	non-coding RNA
LINC03033	non-coding RNA
LINC03033	non-coding RNA
HIF1A	intron
SNAPC1	intron
SYT16	intron
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none	intergenic
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KCNH5	3utr
KCNH5	intron
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RHOJ	intron
PPP2R5E	intron
PPP2R5E	intron
none	intergenic
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SYNE2	intron
SYNE2	intron
ESR2	3utr
ESR2	intron
ZBTB25	3utr
none	intergenic
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CHURC1-FNTB	intron
RAB15	intron
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FUT8	intron
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GPHN	intron
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PALS1	intron
EIF2S1	intron
PLEK2	intron
ARG2	intron
VTI1B	intron
VTI1B	intron
ZFYVE26	intron
RAD51B	intron
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ACTN1	intron
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DCAF5	3utr
GALNT16-AS1	non-coding RNA
EXD2	intron
GALNT16	intron
ERH	intron
SLC39A9	intron
PLEKHD1	intron
PLEKHD1	3utr

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SUSD6	intron
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SMOC1	intron
SLC8A3	intron
SLC8A3	intron
LOC646548	non-coding RNA
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COX16	intron
ADAM21	3utr
none	intergenic
MED6	intron
TTC9	intron
MAP3K9	intron
PCNX1	intron
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SIPA1L1	intron
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DPF3	intron
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ZFYVE1	intron

RBM25	intron
NUMB	intron
none	intergenic
RIOX1	3utr
PTGR2	intron
LIN52	intron
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LTBP2	intron
LTBP2	intron
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YLPM1	intron
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MLH3	intron
ZC2HC1C	intron
TMED10	intron
TTLL5	intron
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IFT43	intron
IFT43	intron
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GPATCH2L	intron
ESRRB	intron
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TMEM63C	intron
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TMED8	intron
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ISM2	intron
SPTLC2	intron
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SNW1	intron
ADCK1	intron
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NRXN3	intron
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DIO2-AS1	non-coding RNA
DIO2-AS1	non-coding RNA
DIO2-AS1	non-coding RNA
DIO2-AS1	non-coding RNA
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CEP128	intron
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CEP128	intron
TSHR	intron
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TSHR	intron
STON2	intron
STON2	intron
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STON2	intron
SEL1L	intron
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[illegible]

[illegible]

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GALC	3utr
GALC	intron
GALC	intron
LINC01147	non-coding RNA
HISLA	non-coding RNA
none	intergenic
KCNK10	intron
KCNK10	intron
none	intergenic
none	intergenic
SPATA7	intron
SPATA7	exon
PTPN21	intron
PTPN21	intron
PTPN21	intron
EML5	intron
EML5	intron
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EML5	intron
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FOXN3	intron
FOXN3	intron
FOXN3	intron
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EFCAB11	intron
EFCAB11	intron
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PSMC1	intron
PSMC1	intron
NRDE2	intron
none	intergenic
TTC7B	intron
TTC7B	intron
TTC7B	intron
RPS6KA5	intron
RPS6KA5	intron
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RPS6KA5	intron
DGLUCY	intron
DGLUCY	intron
GPR68	intron
CCDC88C	intron
PPP4R3A	exon
CATSPERB	intron
CATSPERB	intron
TC2N	intron
TC2N	intron
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TRIP11	intron
TRIP11	intron
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SLC24A4	intron
RIN3	intron
RIN3	intron
none	intergenic
GOLGA5	intron
LINC02287	non-coding RNA
ITPK1	intron
BTBD7	intron
UNC79	intron
UNC79	intron
UNC79	splice site
UNC79	intron
UNC79	exon
UNC79	intron
UNC79	intron
OTUB2	intron
DDX24	3utr
DDX24	intron
PPP4R4	intron
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SERPINA11	intron
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DICER1	intron
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LOC107984703	non-coding RNA
LOC107984703	non-coding RNA
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C14orf132	intron
C14orf132	intron
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GSKIP	intron
AK7	intron
AK7	intron
PAPOLA	intron
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LINC02299	non-coding RNA
LINC02299	non-coding RNA
VRK1	intron
VRK1	intron
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LINC02291	non-coding RNA
LINC02291	non-coding RNA
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BCL11B	intron
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EML1	intron
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EML1	intron
YY1	intron
WDR25	intron
WDR25	intron
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MEG8	non-coding RNA
MEG8	non-coding RNA
MEG8	non-coding RNA
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LINC02320	non-coding RNA
none	intergenic
PPP2R5C	intron
none	intergenic
none	intergenic
MOK	intron
MOK	intron
ZNF839	intron
CINP	3utr
TECPR2	intron
TECPR2	intron
RCOR1	intron
TRAF3	intron
TRAF3	exon
CDC42BPB	intron
LBHD2	3utr
MARK3	intron
none	intergenic
COA8	intron
none	intergenic
none	intergenic

intron

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intronic

intergenic
intragenic

intergenic

[illegible]

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OR4M2-OT1	non-coding RNA
OR4M2-OT1	non-coding RNA
OR4M2-OT1	non-coding RNA
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none	intergenic
none	intergenic
HERC2P2	non-coding RNA
none	intergenic
WHAMMP3	non-coding RNA
TUBGCP5	intron
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PWRN2	non-coding RNA
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PWRN3	non-coding RNA
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SNRPN	intron
SNRPN	intron
SNHG14	non-coding RNA

SNHG14	non-coding RNA
UBE3A	intron
UBE3A	intron
UBE3A	intron
none	intergenic
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ATP10A	intron
ATP10A	intron
LINC02346	non-coding RNA
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OCA2	intron
OCA2	intron
OCA2	intron
HERC2	intron
none	intergenic
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none	intergenic
HERC2P9	non-coding RNA

WHAMMP2	non-coding RNA
APBA2	intron
APBA2	intron
ENTREP2	intron
ENTREP2	intron
ENTREP2	intron
ENTREP2	intron
TJP1	intron
TJP1	intron
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WHAMMP4	non-coding RNA
LOC100288637	non-coding RNA
none	intergenic
TRPM1	intron
TRPM1	intron
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OTUD7A	intron
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CHRNA7	intron
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CHRNA7	intron
WHAMMP1	non-coding RNA
LINC02256	non-coding RNA
FMN1	intron
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FMN1	intron
RYR3	intron
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AVEN	intron

AVEN	intron
CHRM5	intron
CHRM5	intron
EMC7	intron
KATNBL1	intron
KATNBL1	intron
none	intergenic
SLC12A6	intron
none	intergenic
none	intergenic
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none	intergenic
GJD2-DT	non-coding RNA
GJD2-DT	non-coding RNA
AQR	intron
ZNF770	3utr
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DPH6	intron
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DPH6-DT	non-coding RNA
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CDIN1	intron
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MEIS2	intron
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SPRED1	intron
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RASGRP1	intron
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FSIP1	intron
GPR176	intron
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EIF2AK4	intron
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PLCB2	intron
IVD	intron
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RAD51	intron
RMDN3	intron

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INO80	intron
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EXD1	intron
RTF1	intron
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PLA2G4E-AS1	non-coding RNA
PLA2G4E	intron
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GANC	intron
STARD9	intron
STARD9	exon
STARD9	intron
CDAN1	exon
TTBK2	intron
TTBK2	intron
UBR1	intron
UBR1	intron
UBR1	intron
TMEM62	intron
CCNDBP1	intron
ADAL	intron
TP53BP1	intron
TP53BP1	intron
none	intergenic
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PDIA3	intron
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PDIA3	intron
FRMD5	3utr
FRMD5	intron
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GOLM2	intron
GOLM2	intron
CTDSPL2	intron
SPG11	intron
PATL2	intron
TRIM69	intron
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SORD2P	non-coding RNA
SORD2P	non-coding RNA
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TERB2	intron
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DUOX1	intron

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SLC30A4	intron
HMGN2P46	non-coding RNA
SQOR	intron
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SLC24A5	intron

MYEF2	intron
CTXN2	intron
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SLC12A1	intron
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FBN1	intron
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SHC4	intron
EID1	3utr
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COPS2	intron
GALK2	intron
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FAM227B	intron
FGF7	intron
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ATP8B4	intron
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SLC27A2	intron
none	intergenic
USP8	intron
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TRPM7	intron
LOC128092252	intron
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AP4E1	intron

MIR4713HG	non-coding RNA
MIR4713HG	non-coding RNA
CYP19A1	intron
DMXL2	intron
DMXL2	intron
TMOD2	intron
TMOD3	intron
TMOD3	intron
GNB5	3utr
MYO5C	intron
MYO5C	intron
MYO5A	intron
MYO5A	intron
MYO5A	intron
ARPP19	intron
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ONECUT1	3utr
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LINC02490	non-coding RNA
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WDR72	intron
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UNC13C	intron
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RSL24D1	intron
RAB27A	intron
DNAAF4	intron
PYGO1	intron
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PRTG	intron
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NEDD4	intron
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MNS1	intron
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ZNF280D	intron
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TCF12	intron
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LINC00926	non-coding RNA
CGNL1	intron

GCOM1	intron
GCOM1	intron
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ALDH1A2	intron
ALDH1A2	intron
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ALDH1A2	intron
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AQP9	intron
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LIPC	intron
ADAM10	3utr
ADAM10	intron
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RNF111	intron
RNF111	intron
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MYO1E	intron
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MYO1E	intron
none	intergenic
FAM81A	intron
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ICE2	intron
ICE2	intron
RORA	intron
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VPS13C	intron
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LOC107984784	non-coding RNA
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MIR8067	non-coding RNA
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TLN2	intron
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RAB8B	intron
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CA12	intron
USP3	intron
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HERC1	intron
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DAPK2	intron
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CIAO2A	intron
SNX1	intron
SNX1	intron
CSNK1G1	intron

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CSNK1G1	intron
ZNF609	intron
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none	intergenic
SLC51B	intron
CLPX	exon
PARP16	intron
none	intergenic
HACD3	intron
INTS14	intron
SLC24A1	intron
DENND4A	intron
DENND4A	intron
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DENND4A	intron
none	intergenic
MEGF11	intron
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MAP2K1	intron
ZWILCH	intron
SMAD6	intron
none	intergenic
IQCH	intron
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IQCH	intron
IQCH	exon
MAP2K5	intron
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PIAS1	intron
PIAS1	intron
ITGA11	intron
ITGA11	intron

CORO2B	intron
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NOX5	exon
GLCE	intron
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PCAT29	non-coding RNA
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UACA	intron
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LRRC49	intron
THSD4	intron
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ARIH1	intron
ARIH1	3utr
ADPGK	intron
ADPGK-AS1	non-coding RNA
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NEO1	intron
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REC114	intron
NPTN	intron
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PML	intron
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UBL7-DT	non-coding RNA
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ARID3B	intron
EDC3	intron
CPLX3	intron
SCAMP2	intron
FAM219B	intron
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PTPN9	intron
SNX33	3utr
NRG4	intron
ETFA	intron
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SCAPER	intron
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PEAK1	intron

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HMG20A	intron
HMG20A	intron
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LINGO1	intron
TBC1D2B	intron
none	intergenic
IREB2	intron
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CHRNA5	intron
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MORF4L1	3utr
RASGRF1	intron
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TMED3	intron
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ST20-MTHFS	intron
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ZFAND6	intron
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LINC00927	non-coding RNA
ARNT2-DT	non-coding RNA
ARNT2	intron
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CEMIP	intron
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MESD	intron
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TMC3-AS1	non-coding RNA
TMC3-AS1	non-coding RNA
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EFL1	exon
ADAMTS7P1	non-coding RNA
CPEB1	intron
SNHG21	non-coding RNA
FSD2	intron
none	intergenic
C15orf40	intron
HDGFL3	intron
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SH3GL3	intron
SH3GL3	intron
ADAMTSL3	intron
EFL1P1	non-coding RNA
SEC11A	intron
ZNF592	intron
ZNF592	intron
SLC28A1	intron
PDE8A	exon
PDE8A	3utr
AKAP13	intron
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KLHL25	intron
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AGBL1	intron
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NTRK3	intron
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ACAN	intron
ABHD2	intron
ABHD2	3utr
FANCI	intron
MIR9-3HG	non-coding RNA
PEX11A	intron
WDR93	intron
ARPIN-AP3S2	intron
ARPIN-AP3S2	intron
ARPIN-AP3S2	intron
none	intergenic
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CIB1	3utr
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IQGAP1	intron
IQGAP1	intron
CRTC3	intron
BLM	intron
BLM	intron
MAN2A2	3utr
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VPS33B	intron
SV2B	intron
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CRAT37	non-coding RNA
CRAT37	non-coding RNA

[illegible]

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NR2F2-AS1	non-coding RNA
NR2F2-AS1	non-coding RNA
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LINC02253	non-coding RNA
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LINC00923	non-coding RNA
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ARRDC4	intron
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LINC02351	non-coding RNA
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LINC02351	non-coding RNA
FAM169BP	non-coding RNA
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FAM169BP	non-coding RNA
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[illegible]

[illegible]

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LMF1	intron
LMF1	intron
TMEM204	intron
MEIOB	intron
ZNF598	intron
PKD1	intron
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RNPS1	intron
ABCA3	intron
FLYWCH1	3utr
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ZNF174	intron
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[illegible]

SNX29	intron
CPPED1	intron
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SHISA9	intron
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LINC02185	non-coding RNA
MRTFB	intron
MRTFB	intron
MIR193BHG	non-coding RNA
MIR193BHG	non-coding RNA
MIR193BHG	non-coding RNA
PARN	intron
PARN	intron
BFAR	intron
PKD1P3-NPIPA1	non-coding RNA
PDXDC1	intron
PDXDC1	intron
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PDXDC1	intron
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MPV17L-BMERB1	intron
MPV17L-BMERB1	intron
BMERB1	intron
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BMERB1	intron
MARF1	intron
CEP20	intron
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ABCC1	intron
PKD1P1	non-coding RNA
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XYLT1	intron
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NPIPA9	intron
SMG1	intron
SMG1	intron
TMC7	intron
TMC7	intron
COQ7-DT	non-coding RNA
SYT17	intron
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TMC5	intron
VPS35L	intron
VPS35L	intron
IQCK	intron
GPR139	intron
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GP2	intron
ACSM5	intron
none	intergenic
ACSM2B	intron
ACSM1	intron
REXO5	intron
LYRM1	intron
DNAH3	intron
SMG1P3	non-coding RNA
none	intergenic
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METTL9	intron
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UQCRC2	intron
MOSMO	intron
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MOSMO	3utr

[illegible]

[illegible]

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ANKRD26P1	non-coding RNA
ANKRD26P1	non-coding RNA
ANKRD26P1	non-coding RNA
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DNAJA2	intron
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NETO2	intron
NETO2	intron
ITFG1	intron
PHKB	intron
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ABCC12	exon
ABCC12	intron
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ABCC11	intron
LONP2	intron
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ZNF423	intron
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HEATR3	intron
HEATR3	exon
HEATR3	intron
TENT4B	intron
TENT4B	intron
TENT4B	intron
BRD7	exon
NKD1	intron
CYLD	intron
LINC02128	non-coding RNA
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LINC02127	non-coding RNA
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SALL1	3utr
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LINC01571	non-coding RNA
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LINC02180	non-coding RNA
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CASC22	non-coding RNA
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TOX3	intron
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CHD9NB	non-coding RNA
CHD9	intron
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RBL2	3utr
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RPGRIP1L	intron
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FTO	intron
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LPCAT2	intron
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CES5A	intron
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GNAO1	intron
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MT1IP	non-coding RNA
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NUP93	intron
NLRC5	intron
CPNE2	intron
PSME3IP1	intron
RSPRY1	intron
DOK4	intron
none	intergenic
DRC7	intron
none	intergenic

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[illegible]

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CDH11	intron
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LINC00922	non-coding RNA
LINC00922	non-coding RNA
LINC00922	non-coding RNA
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LINC00922	non-coding RNA
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CMTM4	intron
NAE1	exon
FBXL9P	non-coding RNA
ZDHH1	intron
RANBP10	intron
RANBP10	intron
RANBP10	intron
EDC4	intron
none	intergenic
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CDH1	intron
TANGO6	intron
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TANGO6	intron
UTP4	intron
SNTB2	intron
SNTB2	intron
SNTB2	intron
NFAT5	intron
none	intergenic
WWP2	intron
CLEC18A	intron

[illegible]

ZFHX3	intron
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PSMD7-DT	non-coding RNA
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CLEC18B	intron
GLG1	intron
GLG1	intron
ZFP1	intron
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CFDP1	intron
GABARAPL2	intron
KARS1	intron
TERF2IP	intron
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CNTNAP4	intron
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CNTNAP4	intron
CNTNAP4	exon
CNTNAP4	intron
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ADAMTS18	intron
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WVOX	intron
WVOX	intron

[illegible]

[illegible]

[illegible]

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VPS53	intron
TLCD3A	intron
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MYO1C	intron
SLC43A2	intron
SMYD4	intron
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SMG6	intron
SMG6	intron
METTL16	intron
PAFAH1B1	intron
PAFAH1B1	intron
PAFAH1B1	intron
RAP1GAP2	intron
RAP1GAP2	intron
RAP1GAP2	intron
RAP1GAP2	intron
OR1D2	3utr
OR1D2	intron
LOC100288728	non-coding RNA
none	intergenic
SPATA22	intron
TRPV3	intron
TRPV3	intron
SHPK	intron
ITGAE	intron
none	intergenic

ZZEF1	intron
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CYB5D2	intron
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PELP1	intron
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USP6	intron
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RABEP1	intron
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DERL2	intron
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PITPNM3	3utr
PITPNM3	intron
KIAA0753	exon
KIAA0753	intron
C17orf100	3utr
SLC13A5	intron
TEKT1	intron
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DLG4	intron
FXR2	intron
DNAH2	intron
DNAH2	exon
CHD3	intron
none	intergenic
MYH10	intron

MYH10	intron
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PIK3R6	intron
PIK3R5	intron
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PIK3R5-DT	non-coding RNA
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STX8	intron
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GSG1L2	intron
GAS7	intron
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MYH13	intron
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MYH13	intron
MYH8	exon
MYH1	intron
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SCO1	intron
ADPRM	intron
PIRT	intron
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SHISA6	intron
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ZNF18	intron
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MAP2K4	intron
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LINC00670	non-coding RNA
MYOCD	intron
ELAC2	intron
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LINC02093	non-coding RNA
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PMP22	intron
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TVP23C-CDRT4	intron
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NCOR1	intron
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USP32P1	non-coding RNA
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TNFRSF13B	intron
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TOM1L2	intron
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SLC5A10	intron
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B9D1	intron
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SLC47A1	intron
SLC47A2	intron
ULK2	intron
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ULK2	intron
AKAP10	intron
SPECC1	intron
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USP32P3	non-coding RNA
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LINC02088	non-coding RNA
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CCDC144NL	non-coding RNA
TMEM11-DT	non-coding RNA
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LINC02693	non-coding RNA
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LINC01992	non-coding RNA
NLK	intron
NLK	intron
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SUPT6H	intron
TLCD1	3utr
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PHF12	intron
PHF12	intron
SEZ6	intron
MYO18A	3utr
MYO18A	intron
NUFIP2	intron
TAOK1	intron
TAOK1	intron
TP53I13	intron
ANKRD13B	3utr
SSH2	intron
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EFCAB5	intron
EFCAB5	intron
NSRP1	intron
SLC6A4	intron
BLMH	intron
none	intergenic
CPD	intron
SUZ12P1	non-coding RNA
ATAD5	exon
ATAD5	intron
none	intergenic

[illegible]

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RAD51L3-RFFL	non-coding RNA
SLFN11	3utr
SLFN12L	3utr
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TADA2A	intron
SYNRG	intron
SYNRG	intron
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GPR179	intron
PIP4K2B	intron
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LRRC37A11P	non-coding RNA
none	intergenic
PLXDC1	intron
FBXL20	intron
MED1	intron
PGAP3	intron
GRB7	intron
GRB7	intron
IKZF3	intron
IGFBP4	intron
SMARCE1	intron

SMARCE1	intron
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KRT10	3utr
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KRTAP3-1	3utr
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ACLY	intron
RAB5C	intron
STAT5B	intron
STAT5B	intron
STAT3	intron
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VPS25	intron
AARSD1	intron
BRCA1	intron
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PYY	intron
HROB	intron
GPATCH8	intron
LINC01180	non-coding RNA
DBF4B	exon
KIF18B	intron
NMT1	intron
NMT1	intron
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LINC02210-CRHR1	intron
MAPT-AS1	non-coding RNA
MAPT	intron
KANSL1	intron
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NSF	intron
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CDC27	3utr

MYL4	intron
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EFCAB13	intron
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NPEPPS	intron
TBKBP1	intron
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IGF2BP1	3utr
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B4GALNT2	intron
ZNF652	intron
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NGFR-AS1	non-coding RNA
SPOP	intron
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LRR59	3utr
LRR59	3utr
MYCBPAP	intron
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SPAG9	intron
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MBTD1	intron
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[illegible]

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ANKFN1	intron
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ANKFN1	3utr
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SRSF1	non-coding RNA
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DYNLL2-DT	non-coding RNA
DYNLL2	intron
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PPM1E	intron
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TRIM37	intron
TRIM37	intron
SKA2	intron
YPEL2	intron
LINC01476	non-coding RNA
LINC01476	non-coding RNA
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CLTC	intron
CLTC	intron
VMP1	intron
TUBD1	intron
RPS6KB1	intron
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LOC653653	non-coding RNA
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USP32	intron
USP32	intron
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APPBP2	3utr
APPBP2	intron
LINC01999	non-coding RNA
PPM1D	intron
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BCAS3	intron
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INTS2	intron
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EFCAB3	intron
EFCAB3	intron
EFCAB3	3utr
MRC2	intron
MARCHF10	intron
MARCHF10-DT	non-coding RNA
MARCHF10-DT	non-coding RNA
TANC2	intron
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DCAF7	intron
STRADA	intron
STRADA	intron
DDX42	exon
DDX42	intron
DDX42	intron
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SMURF2	intron
SMURF2	intron
LRRC37A3	intron
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PRKCA	intron
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[illegible]

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CASC17	non-coding RNA
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SOX9-AS1	non-coding RNA
SOX9	3utr
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SLC39A11	intron
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SDK2	intron
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GPRC5C	3utr
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CD300LD	intron
RAB37	intron
OTOP2	intron
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GRB2	intron
GRB2	intron
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RECQL5	intron
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UNC13D	intron
ACOX1	intron
SRP68	intron
SRP68	intron
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RNF157	intron
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QRICH2	intron
QRICH2	intron
PRPSAP1	intron
PRPSAP1	intron
ST6GALNAC1	intron
MXRA7	3utr
MXRA7	intron
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SEC14L1	intron
SEC14L1	intron
SEPTIN9	intron
SEPTIN9	intron
SEPTIN9	intron
LOC400622	non-coding RNA
LOC400622	non-coding RNA
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TNRC6C	intron
TNRC6C	intron
TNRC6C	intron
DNAH17	intron
SCAT1	non-coding RNA
CYTH1	intron
CYTH1	intron
USP36	intron
TIMP2	intron
none	intergenic
ENGASE	intron
RBFOX3	intron
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[illegible]

[illegible]

[illegible]

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METTL4	intron
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SMCHD1	intron
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EMILIN2	intron
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DLGAP1	intron
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MIR3976HG	non-coding RNA
LOC121725015	non-coding RNA
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LOC121725015	non-coding RNA
L3MBTL4	intron
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LINC01387	non-coding RNA
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ARHGAP28	intron
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LAMA1	intron
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MTCL1	intron
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NDUFV2	intron
ANKRD12	intron
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TWSG1	intron
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RALBP1	intron
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RAB31	intron
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LINC01887	non-coding RNA
PIEZO2	intron
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CHMP1B	3utr
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C18orf61	non-coding RNA
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SPIRE1	intron
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CEP76	intron
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MC2R	intron
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ZNF519	non-coding RNA
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ANKRD20A5P	non-coding RNA
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CXADRP3	non-coding RNA
CXADRP3	non-coding RNA
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ANKRD30B	intron
ANKRD30B	intron
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LINC01443	non-coding RNA
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LOC644669	non-coding RNA
ROCK1	3utr
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GREB1L	intron
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ABHD3	intron
MIB1	intron
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[illegible]

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TAF4B	intron
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TAF4B	intron
KCTD1	intron
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PCAT18	non-coding RNA
PCAT18	non-coding RNA
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AQP4	intron
CHST9	3utr
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DSC1	intron
DSC1	intron

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DSG1-AS1	non-coding RNA
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KLHL14	3utr
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CCDC178	intron
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ASXL3	intron
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ASXL3	exon
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NOL4	intron
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MAPRE2	intron
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ZNF397	intron
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ZSCAN30	3utr
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RPRD1A	intron
SLC39A6	intron
FHOD3	intron
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CELF4	intron
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KC6	non-coding RNA
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PIK3C3	intron
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LINC00907	non-coding RNA
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SETBP1	intron
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SLC14A2	intron
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SIGLEC15	intron
EPG5	intron
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ARK2C	intron
LOXHD1	intron

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ST8SIA5	intron
ST8SIA5	intron
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IER3IP1	intron
SKOR2	intron
MIR4527HG	non-coding RNA
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SMAD2	intron
ZBTB7C	intron
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DYM	intron
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MYO5B	intron
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CFAP53	intron
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MAPK4	intron
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MEX3C	intron

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STAR6	intron
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DYNAP	intron

RAB27B	intron
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RAB27B	intron
RAB27B	3utr
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CCDC68	intron
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TCF4	intron
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LINC01416	non-coding RNA
LINC03069	non-coding RNA
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ONECUT2	intron
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NARS1	intron

ATP8B1	intron
ATP8B1	intron
NEDD4L	intron
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ALPK2	intron
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ALPK2	intron
MALT1	intron
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[illegible]

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CDH7	intron
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DSEL-AS1	non-coding RNA
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[illegible]

[illegible]

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FBXO15	intron
FBXO15	intron
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CYB5A	intron
C18orf63	exon
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CNDP2	intron
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ZNF407	intron
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LOC339298	non-coding RNA
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LINC01927	non-coding RNA
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ZNF236	intron
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MBP	intron
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GALR1	3utr
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ATP9B	intron
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CTDP1	intron
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KCNG2	intron
KCNG2	intron
SLC66A2	intron
SLC66A2	intron
TXNL4A	intron
PARD6G	intron
none	intergenic

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WASH5P	non-coding RNA
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MIER2	intron
PWWP3A	intron
AP3D1	intron
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ZFR2	intron
SH3GL1	intron
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LONP1	intron
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ACSBG2	intron
ACSBG2	intron
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ADGRE1	intron
ADGRE1	intron
ADGRE4P	non-coding RNA
INSR	3utr
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PEX11G	intron
PNPLA6	intron
HNRNPM	intron
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MUC16	intron
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ZNF317	intron
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OR7D4	intron
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ZNF812P	non-coding RNA
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DNMT1	intron
TSPAN16	intron
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ZNF833P	non-coding RNA
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ZNF440	3utr
ZNF439	3utr

ZNF69	intron
ZNF700	3utr
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ZNF442	exon
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ZNF564	exon
CACNA1A	intron
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CLEC17A	intron
ADGRE3	intron
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OR7C1	intron
SLC1A6	exon
BRD4	intron
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CYP4F22	exon
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CYP4F8	intron
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HSH2D	intron
AP1M1	3utr
EPS15L1	intron
EPS15L1	intron
CPAMD8	intron
COLGALT1	intron
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FKBP8	intron
SUGP2	3utr
SUGP2	intron
SUGP1	intron
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GATAD2A	intron
GMIP	intron
ZNF682	3utr
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ZNF486	intron
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ZNF714	3utr
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ZNF738	intron
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ZNF208	intron
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LINC01785	non-coding RNA
ZNF492	intron
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RPSA2	non-coding RNA
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LINC02987	non-coding RNA
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LOC100420587	non-coding RNA

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VSTM2B-DT	non-coding RNA
VSTM2B-DT	non-coding RNA
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ZNF536	intron
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LINC01791	non-coding RNA
TSHZ3	intron
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LINC02841	non-coding RNA
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NUDT19	intron
TDRD12	intron
CEP89	intron
FAAP24	intron
FAAP24	3utr
GPATCH1	intron
none	intergenic
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PEPD	intron
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CHST8	intron
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GARRE1	intron
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PDCD2L	intron
UBA2	intron
ZNF599	intron
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HPN-AS1	non-coding RNA
FXD1	intron
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MAG	intron
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TBCB	intron
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ZNF790-AS1	non-coding RNA
ZNF790	intron
ZNF790	intron
ZNF568	intron
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ZNF420	intron
ZNF585A	intron
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ZNF527	3utr
ZNF569	intron
ZNF540	intron
ZFP30	exon
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LOC644554	non-coding RNA
SIPA1L3	intron
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RYR1	exon
ACTN4	intron
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SELENOV	intron

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ZNF780B	exon
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SPTBN4	intron
SHKBP1	intron
LTBP4	intron
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CYP2B7P	non-coding RNA
CYP2B6	intron
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CYP2F1	intron
AXL	intron
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CEACAM21	intron
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CEACAM7	intron
POU2F2	intron
LIPE-AS1	non-coding RNA
LIPE-AS1	non-coding RNA
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PSG9	intron
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TEX101	3utr
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PLAUR	intron
ZNF404	exon
ZNF225	intron
ZNF227	intron
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CEACAM20	intron
PPP1R37	intron
EXOC3L2	intron
PPP1R13L	intron
PPP1R13L	intron
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EML2	intron
IGFL4	non-coding RNA
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HIF3A	intron
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CALM3	3utr
PRKD2	intron
STRN4	intron
ARHGAP35	intron
SAE1	intron
SAE1	intron
C5AR1	intron
NAPA-AS1	non-coding RNA
BICRA	intron
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GRIN2D	intron
LMTK3	intron
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MED25	intron
ZNF473	intron
ZNF473	intron
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MYH14	intron
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EMC10	3utr
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FPR3	intron
ZNF841	exon
ZNF610	intron
ZNF534	intron
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ZNF468	3utr
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ZNF347	intron
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ZNF677	intron
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[illegible]

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TPO	intron
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MYT1L	intron
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LINC01250	non-coding RNA
EIPR1	intron
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EIPR1	intron
TRAPPC12	intron
RNASEH1-DT	non-coding RNA
COLEC11	intron
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DCDC2C	intron
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LINC01249	non-coding RNA
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SILC1	non-coding RNA
LOC400940	non-coding RNA
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LINC00487	non-coding RNA
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RNF144A	intron
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LINC00298	non-coding RNA
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LINC00299	non-coding RNA
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ID2-AS1	non-coding RNA
KIDINS220	intron
MBOAT2	intron
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ASAP2	intron

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ADAM17	intron
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TAF1B	intron
TAF1B	intron
TAF1B	exon
GRHL1	intron
GRHL1	intron
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GRHL1	intron
RRM2	non-coding RNA
HPCAL1	intron
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NOL10	intron
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SLC66A3	intron
ROCK2	intron
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GREB1	intron
GREB1	intron
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LPIN1	intron
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MIR3681HG	non-coding RNA
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LOC100506474	non-coding RNA
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[illegible]

[illegible]

[illegible]

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KLHL29	intron
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ATAD2B	exon
ATAD2B	intron
ATAD2B	intron
ATAD2B	intron
ATAD2B	intron
ATAD2B	intron
UBXN2A	3utr
ITSN2	intron
NCOA1	intron
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DNAJC27	exon
EFR3B	intron
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DNMT3A	intron
DNMT3A	intron
none	intergenic
DTNB	intron
DTNB	intron
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DTNB	intron
ASXL2	intron
none	intergenic
RAB10	intron
HADHA	exon
HADHA	intron
HADHB	intron

[illegible]

[illegible]

LINC01317	non-coding RNA
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LINC01320	non-coding RNA
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CRIM1	intron
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CRIM1	intron
FEZ2	intron
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VIT	intron
HEATR5B	intron
HEATR5B	intron
NDUFAF7	intron
PRKD3	3utr
none	intergenic
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[illegible]

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LINC02898	non-coding RNA
none	intergenic
EML4-AS1	non-coding RNA
EML4	intron
EML4	intron
EML4	intron
KCNG3	intron
MTA3	intron
MTA3	intron
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THADA	intron
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PLEKHH2	intron
PLEKHH2	intron
PLEKHH2	intron
none	intergenic
LRPPRC	intron
LRPPRC	intron
LRPPRC	intron
LRPPRC	intron
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PPM1B	intron
none	intergenic
none	intergenic
PREPL	exon

CAMKMT	intron
CAMKMT	intron
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LINC01121	non-coding RNA
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SRBD1	intron
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SRBD1	intron
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PRKCE	intron
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EPAS1	intron
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EPAS1	intron
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ATP6V1E2	intron
ATP6V1E2	intron
none	intergenic
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TTC7A	intron
STPG4	intron
STPG4	intron
EPCAM	exon
none	intergenic
KCNK12	intron
MSH2	intron
MSH2	intron
FBXO11	intron

[illegible]

[illegible]

[illegible]

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VRK2	intron
VRK2	intron
VRK2	intron
VRK2	intron
FANCL	intron
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LINC01795	non-coding RNA
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LINC01122	non-coding RNA
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MIR4432HG	non-coding RNA
BCL11A	intron
none	intergenic
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PUS10	intron
SANBR	intron
USP34	intron
USP34	intron
USP34	intron
USP34	intron
USP34	exon
USP34	intron
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COMMD1	exon
COMMD1	intron
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COMMD1	intron
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TMEM17	3utr
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EHBP1	intron
EHBP1	intron
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EHBP1	intron
EHBP1	intron

[illegible]

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MEIS1	intron
MEIS1	intron
LINC01798	non-coding RNA
LINC01798	non-coding RNA
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LINC01799	non-coding RNA
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LINC01828	non-coding RNA
LINC01828	non-coding RNA
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DNAAF10	intron
PPP3R1	intron
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BMP10	intron
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ANTXR1	intron
ANTXR1	intron
ANTXR1	intron
NFU1	intron
AAK1	intron
AAK1	intron
AAK1	intron
ANXA4	intron
MXD1	intron
PCBP1-AS1	non-coding RNA
TIA1	intron
PCYOX1	intron
none	intergenic
TGFA	intron
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ADD2	3utr
ADD2	intron
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FIGLA	intron
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PAIP2B	intron
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ZNF638	intron
DYSF	intron
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EXOC6B	intron
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SFXN5	intron
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PRADC1	intron
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ALMS1	intron
ALMS1	intron
ALMS1	exon
ALMS1	intron
ALMS1P1	non-coding RNA
DGUOK	intron
DGUOK	intron
TET3	intron

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MTHFD2	intron
M1AP	intron
SEMA4F	intron
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HK2	intron
LINC01291	non-coding RNA
TACR1	intron
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EVA1A	intron
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GCFC2	intron
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LOC101927967	non-coding RNA
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LOC101927967	non-coding RNA
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CTNNA2	intron
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[illegible]

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DNAH6	intron
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TRABD2A	intron
KCMF1	intron
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KCMF1	3utr
LINC01964	non-coding RNA
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ST3GAL5	intron
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POLR1A	intron
REEP1	intron
none	intergenic
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KDM3A	intron
RNF103-CHMP3	intron
RMND5A	intron
ANAPC1P1	non-coding RNA
RGPD1	intron
ANAPC1P2	non-coding RNA
none	intergenic
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LOC102724642	non-coding RNA
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CYTOR	non-coding RNA
CYTOR	non-coding RNA
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RGPD2	intron
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ANKRD36BP2	non-coding RNA
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KMT2CP4	non-coding RNA
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KMT2CP5	non-coding RNA
KMT2CP5	non-coding RNA
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GGT8P	non-coding RNA
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ANKRD20A8P	non-coding RNA
LOC442028	non-coding RNA
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ZNF2	intron
PROM2	intron
PROM2	intron
KCNIP3	intron
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ANKRD36C	intron
ASTL	intron
ITPRIPL1	exon
ARID5A	intron
FAM178B	intron
FAM178B	intron
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ANKRD36	intron
ANKRD36	intron
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ANKRD36B	intron
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TMEM131	intron
TMEM131	intron
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TMEM131	intron
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CNGA3	intron
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INPP4A	intron
INPP4A	intron
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MGAT4A	intron
CRACDL	intron
CRACDL	intron
none	intergenic
TSGA10	intron
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TSGA10	intron
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EIF5B	intron
none	intergenic
none	intergenic

AFF3	exon
AFF3	intron
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AFF3	intron
LINC01104	non-coding RNA
LINC01104	non-coding RNA
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NPAS2	intron
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NPAS2	intron
TBC1D8	intron
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TBC1D8	intron
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RNF149	intron
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RFX8	exon
RFX8	intron
RFX8	intron
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IL1RL2	intron
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IL18R1	intron
IL18RAP	intron
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SLC9A2	intron
SLC9A2	intron
SLC9A2	intron
TMEM182	intron
TMEM182	intron
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LINC01935	non-coding RNA
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MRPS9-AS2	non-coding RNA
MRPS9-AS2	non-coding RNA
FHL2	intron
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ECRG4	intron
UXS1	intron
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RGPD3	intron
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ST6GAL2	intron
ST6GAL2	intron
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[illegible]

MIR4435-2HG	non-coding RNA
MIR4435-2HG	non-coding RNA
MIR4435-2HG	non-coding RNA
MIR4435-2HG	non-coding RNA
MIR4435-2HG	non-coding RNA
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ANAPC1	intron
MERTK	intron
MERTK	intron
none	intergenic
FBLN7	intron
FBLN7	intron
none	intergenic
ZC3H8	intron
ZC3H6	intron
RGPD8	intron
none	intergenic
TTL	intron
TTL	intron
CKAP2L	intron
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PSD4	intron
LINC02966	non-coding RNA
LINC02966	non-coding RNA
ZNG1B	intron
none	intergenic
none	intergenic
WASH2P	non-coding RNA
RPL23AP7	non-coding RNA
none	intergenic
ACTR3-AS1	non-coding RNA
ACTR3-AS1	non-coding RNA
ACTR3	intron
ACTR3	intron
LINC01191	non-coding RNA
LINC01191	non-coding RNA
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[illegible]

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DDX18	3utr
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CCDC93	intron
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C2orf76	intron
CFAP221	intron
CFAP221	intron
CFAP221	exon
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[illegible]

[illegible]

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ERCC3	intron
MAP3K2	intron
MAP3K2	intron
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MYO7B	intron
WDR33	exon
WDR33	intron
AMMECR1L	3utr
SAP130	intron
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UGGT1	intron
HS6ST1	intron
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POTEF	intron
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POTEI	intron
POTEI	intron
POTEJ	intron
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ARHGEF4	intron
ARHGEF4	intron
FAM168B	intron
PLEKHB2	intron
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POTEE	intron
POTEE	intron

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LINC01087	non-coding RNA
C2orf27A	non-coding RNA
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LINC01945	non-coding RNA
LINC01945	non-coding RNA
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GPR39	intron
LYPD1	intron
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NCKAP5	intron
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MGAT5	intron
MGAT5	3utr
TMEM163	intron
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[illegible]

THSD7B	intron
THSD7B	intron
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LOC101928273	non-coding RNA
HNMT	intron
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SPOPL	intron
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NXPH2	intron
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NXPH2	intron
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LINC01853	non-coding RNA
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LRP1B	intron
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LRP1B	intron
LRP1B	intron

[illegible]

[illegible]

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ACVR2A	intron
ACVR2A	intron
ORC4	intron
ORC4	intron
MBD5	intron
MBD5	intron
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MBD5	intron
none	intergenic
KIF5C	intron
KIF5C	intron
KIF5C	intron

[illegible]

[illegible]

[illegible]

GALNT5	intron
GALNT5	intron
GALNT5	3utr
none	intergenic
CYTIP	intron
none	intergenic
ACVR1C	intron
ACVR1C	intron
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ACVR1	intron
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UPP2	intron
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CCDC148	intron
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PKP4	intron
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DAPL1	intron
TANC1	intron
TANC1	intron
WDSUB1	intron
BAZ2B	intron
BAZ2B	intron
BAZ2B	intron
BAZ2B	intron
BAZ2B	non-coding RN/
MARCHF7	intron
CD302	3utr
CD302	intron

CD302	intron
LY75	intron
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PLA2R1	intron
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PLA2R1	intron
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ITGB6	intron
ITGB6	intron
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LINC02478	non-coding RNA
RBMS1	intron
RBMS1	intron
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TANK	intron
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PSMD14	intron
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AHCTF1P1	non-coding RNA
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SLC4A10	intron
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SLC4A10	intron
DPP4	intron

LOC101929532	non-coding RNA
none	intergenic
IFIH1	intron
KCNH7	intron
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FIGN	exon
FIGN	intron
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GRB14	intron
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COBLL1	intron
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SCN3A	intron
SCN3A	intron

SCN2A	intron
CSRNP3	intron
CSRNP3	intron
none	intergenic
LOC100506124	non-coding RNA
TTC21B	intron
SCN1A	intron
SCN1A	intron
SCN1A	intron
SCN1A	intron
SCN1A	intron
SCN1A-AS1	non-coding RNA
SCN9A	intron
SCN9A	intron
SCN7A	intron
SCN7A	intron
none	intergenic
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XIRP2	intron
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XIRP2	intron
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B3GALT1	intron
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B3GALT1	intron
B3GALT1-AS1	non-coding RNA
STK39	intron
STK39	intron
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STK39	intron
CERS6	intron
CERS6	intron
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CERS6	intron
CERS6	intron

CERS6	intron
CERS6-AS1	non-coding RNA
NOSTRIN	intron
SPC25	intron
none	intergenic
ABCB11	intron
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LRP2	intron
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BBS5	intron
PPIG	intron
CFAP210	intron
CFAP210	intron
UBR3	intron
UBR3	exon
UBR3	intron
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MYO3B	intron
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ERICH2-DT	non-coding RNA
none	intergenic
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TLK1	3utr
TLK1	intron
TLK1	intron
TLK1	intron
METTL8	intron
METAP1D	intron
METAP1D	intron

[illegible]

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MTX2	intron
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NFE2L2	intron
LOC100130691	non-coding RNA
AGPS	intron
PDE11A	intron
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OSBPL6	intron
FKBP7	exon
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TTN	exon
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CCDC141	intron
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CCDC141	intron
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SESTD1	intron
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ZNF385B	intron
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CWC22	exon
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SCHLAP1	non-coding RNA
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UBE2E3	intron
UBE2E3	intron
LINC01934	non-coding RNA
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ITGA4	intron
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PPP1R1C	non-coding RNA
PPP1R1C	intron
PPP1R1C	intron
PPP1R1C	intron
PDE1A	3utr
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none	intergenic
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FRZB	intron
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NCKAP1	3utr
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NCKAP1	intron
none	intergenic
DUSP19	3utr
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ZNF804A	intron

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FSIP2-AS2	non-coding RNA
FSIP2-AS2	non-coding RNA
FSIP2	intron
FSIP2	intron
FSIP2	intron
FSIP2	exon
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ITGAV	intron
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FAM171B	intron
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TFPI	intron
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LINC01090	non-coding RNA
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GULP1	intron
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DIRC1	non-coding RNA
DIRC1	non-coding RNA
DIRC1	non-coding RNA
none	intergenic
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COL3A1	intron
COL5A2	intron
COL5A2	intron
COL5A2	intron
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WDR75	exon
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SLC40A1	intron
SLC40A1	intron
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ANKAR	intron
ANKAR	intron
ORMDL1	intron
ORMDL1	intron
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MSTN	3utr
none	intergenic

[illegible]

[illegible]

[illegible]

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SATB2	intron
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LINC01877	non-coding RNA
FTCDNL1	intron
none	intergenic
TYW5	intron
SPATS2L	intron
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SPATS2L	intron
SGO2	intron
AOX1	intron
AOX1	intron
AOX1	intron
none	intergenic
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AOX3P-AOX2P	non-coding RNA
AOX3P-AOX2P	non-coding RNA
none	intergenic
ORC2	intron
HYCC2	3utr
HYCC2	intron
HYCC2	intron
HYCC2	intron
NDUFB3	intron
CASP8	3utr
FLACC1	intron
STRADB	intron
C2CD6	intron
C2CD6	intron
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MPP4	intron
MPP4	intron
MPP4	intron
CDK15	intron
CDK15	intron
none	intergenic
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KIAA2012	intron
NOP58	intron
BMPR2	exon
BMPR2	3utr
FAM117B	intron
FAM117B	intron
FAM117B	intron
FAM117B	intron
WDR12	3utr
NBEAL1	intron
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CYP20A1	intron
ABI2	intron
ABI2	intron
RAPH1	3utr
RAPH1	3utr
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ICOS	intron
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PAR3D3B	intron
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PAR3D3B	intron
PAR3D3B	intron

PARD3B	intron
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NRP2	intron
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INO80D	intron
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ADAM23	intron
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DYTN	intron
MDH1B	intron
FASTKD2	intron
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CPO	intron
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KLF7	intron
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MYOSLID-AS1	non-coding RNA
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CREB1	intron
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PLEKHM3	intron
PLEKHM3	intron

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PIKFYVE	intron
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LOC101927960	non-coding RNA
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MAP2	intron
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UNC80	intron
UNC80	intron
UNC80	intron
KANSL1L	intron
KANSL1L	intron
KANSL1L	intron
LANCL1-AS1	non-coding RNA
LANCL1-AS1	non-coding RNA
CPS1	intron
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ERBB4	intron
ERBB4	intron

[illegible]

SPAG16	intron
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BARD1	3utr
SNHG31	non-coding RNA
ABCA12	intron
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ABCA12	intron
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LINC02862	non-coding RNA
FN1	intron
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LINC00607	non-coding RNA
LINC00607	non-coding RNA
LINC00607	non-coding RNA
LINC00607	non-coding RNA
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LINC00607	non-coding RNA
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MREG	intron
XRCC5	intron
XRCC5	3utr
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MARCHF4	intron
MARCHF4	intron
SMARCA1	intron
none	intergenic
IGFBP5	intron
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DIRC3-AS1	non-coding RNA
DIRC3-AS1	non-coding RNA
DIRC3	non-coding RNA
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DIRC3	non-coding RNA
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TNS1	intron
TNS1	intron
CXCR2	5utr
none	intergenic
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PNKD	intron
CATIP-AS2	non-coding RNA
SLC11A1	intron
VIL1	3utr
RNF25	intron
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NHEJ1	intron
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DNPEP	intron
STK11IP	intron
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CUL3	intron
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DOCK10	intron
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NYAP2	intron
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IRS1	intron
COL4A4	intron
COL4A4	intron
COL4A4	intron
COL4A3	intron
COL4A3	intron
COL4A3	3utr
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AGFG1	intron
AGFG1	intron
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C2orf83	non-coding RNA
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CCL20	intron
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SPHKAP	intron
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LINC01807	non-coding RNA
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TRIP12	exon
TRIP12	exon
SLC16A14	intron
none	intergenic
SP140	intron
SP140L	intron
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CAB39	intron
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DIS3L2	intron
DIS3L2	intron
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DIS3L2	intron
EIF4E2	intron
GIGYF2	intron
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NGEF	intron
ATG16L1	intron
ATG16L1	intron
ATG16L1	3utr
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DGKD	3utr
USP40	intron
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HJURP	intron
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SH3BP4	intron
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ASB18	intron
IQCA1	intron

IQCA1	intron
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COL6A3	intron
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MLPH	intron
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LRRFIP1	intron
RBM44	intron
RBM44	exon
UBE2F	intron
UBE2F	intron
TRAF3IP1	intron
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HDAC4	intron
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NDUFA10	non-coding RNA
NDUFA10	intron
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GPR35	intron
KIF1A	intron
CROCC2	intron
SNED1	intron
PPP1R7	exon
HDLBP	intron
FARP2	intron
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ZCCHC3	3utr
NRSN2-AS1	non-coding RNA
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RBCK1	intron
TBC1D20	intron
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CSNK2A1	intron
CSNK2A1	intron
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SLC52A3	intron
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FAM110A	intron
RSPO4	intron
PSMF1	intron
PSMF1	intron
SNPH	intron
SDCBP2	intron
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SIRPB3P	non-coding RNA
SIRPB3P	non-coding RNA
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TGM3	intron
ZNF343	3utr
ZNF343	intron
ZNF343	intron
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EBF4	intron

PTPRA	intron
PTPRA	exon
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DNAAF9	intron
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ATRN	intron
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SLC23A2	intron
GPCPD1	intron
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SHLD1	intron
FERMT1	intron
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CASC20	non-coding RNA
CASC20	non-coding RNA
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LINC01706	non-coding RNA
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[illegible]

PAK5	intron
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SNAP25-AS1	non-coding RNA
SNAP25	intron
SNAP25	3utr
MKKS	intron
LOC128706666	intron
LOC128706666	intron
SLX4IP	intron
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JAG1	intron
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LOC101929413	non-coding RNA
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LINC00687	non-coding RNA
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BTBD3	intron
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LINC01722	non-coding RNA
LINC01722	non-coding RNA

[illegible]

MACROD2	intron
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KIF16B	intron
KIF16B	intron
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SNRPB2	intron
OTOR	intron
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PCSK2	intron
PCSK2	intron
BFSP1	intron
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SNX5	intron
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KAT14	intron
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ZNF133	intron
DZANK1	intron
DZANK1	intron
POLR3F	intron
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DTD1	intron
DTD1	intron
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SLC24A3	intron
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SLC24A3	intron
RIN2	intron
RIN2	intron

[illegible]

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SYNDIG1	intron
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ABHD12	intron
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GINS1	intron
GINS1	intron
NINL	intron
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LINC01733	non-coding RNA
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NCOR1P1	non-coding RNA
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DEFB123	intron
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BCL2L1	intron
TPX2	intron
DUSP15	intron
PDRG1	intron
none	intergenic
NOL4L	intron
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BPIFB1	intron
ZNF341-AS1	non-coding RNA
CHMP4B	intron
none	intergenic
AHCY	intron
DYNLRB1	intron
PIGU	intron
NCOA6	intron
NCOA6	intron
ACSS2	intron
GSS	intron
TRPC4AP	intron
none	intergenic
MMP24-AS1-EDEM2	intron
UQCC1	intron
UQCC1	intron
RBM12	3utr
PHF20	intron
PHF20	intron
DLGAP4	intron
DLGAP4	intron
DLGAP4-AS1	non-coding RNA
TGIF2-RAB5IF	intron
NDRG3	intron
SAMHD1	3utr
none	intergenic
RBL1	intron
MROH8	intron
RPN2	intron
none	intergenic
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TTI1	intron
KIAA1755	intron
LOC149684	non-coding RNA
none	intergenic
BPI	intron
RALGAPB	intron
RALGAPB	intron
ARHGAP40	intron
ARHGAP40	intron
ARHGAP40	intron
none	intergenic
PPP1R16B	intron
DHX35	intron
DHX35	intron
none	intergenic

[illegible]

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JPH2	intron
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HNF4A	intron
PKIG	intron
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STK4	intron
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MATN4	intron
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WFDC8	intron
WFDC10B	intron
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SLC12A5	intron
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CDH22	intron
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ELMO2	intron
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EYA2	intron
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NCOA3	intron
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SULF2	intron
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PREX1	intron
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CSE1L	intron
STAU1	intron
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B4GALT5	intron
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UBE2V1	intron
LINC01271	non-coding RNA
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PTPN1	intron
PAR6B	intron
PAR6B	intron
DPM1	intron
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CBLN4	intron
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FAM210B	intron
CSTF1	3utr
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PCK1	intron
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PMEPA1	intron
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ANKRD60	3utr
PPP4R1L	non-coding RN/
RAB22A	3utr
APCDD1L-DT	non-coding RN/
NPEPL1	intron
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PHACTR3	intron
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CDH26	intron
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MIR646HG	non-coding RNA
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LSM14B	intron
SS18L1	intron
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SLCO4A1	intron
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NTSR1	intron
TCFL5	3utr
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LINC01749	non-coding RNA
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ARFGAP1	intron
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OPRL1	intron
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LOC102723996	3utr
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LOC102724219	non-coding RNA
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LOC102724652	intron
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LOC102724843	non-coding RNA
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LOC102724951	non-coding RNA
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LOC105379514	non-coding RNA
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BAGE2	non-coding RNA
BAGE2	non-coding RNA
ANKRD30BP2	non-coding RNA
ANKRD30BP2	non-coding RNA

[illegible]

MIR99AHG	non-coding RNA
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CXADR	intron
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BTG3	intron
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CHODL	intron
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TMPRSS15	intron
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MIR548XHG	non-coding RNA
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[illegible]

[illegible]

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LINC01684	non-coding RNA
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LINC01692	non-coding RNA
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LINC00158	non-coding RNA
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JAM2	intron
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GABPA	3utr
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APP	intron
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CYYR1-AS1	non-coding RNA
CYYR1-AS1	non-coding RNA
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ADAMTS5	intron
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LINC01673	non-coding RNA
LINC00113	non-coding RNA
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LINC01697	non-coding RNA
LINC01697	non-coding RNA
LINC01695	non-coding RNA
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CCT8	intron
CCT8	intron
CCT8	intron
MAP3K7CL	intron
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LINC00189	non-coding RNA
BACH1	intron

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GRIK1	intron
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LINC00307	non-coding RNA
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TIAM1	intron
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SCAF4	exon
SCAF4	intron
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HUNK	intron
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URB1	intron
EVA1C	intron
EVA1C	intron
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CFAP298-TCP10L	intron

SYNJ1	intron
PAXBP1	intron
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LOC101928107	non-coding RNA
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IL10RB	3utr
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IFNAR1	intron
SON	intron
DONSON	intron
ITSN1	intron
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LOC100506403	non-coding RNA
LOC100506403	non-coding RNA
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MORC3	intron
CHAF1B	intron
CLDN14	intron

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HLCS	intron
HLCS	intron
TTC3	intron
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DYRK1A	intron
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KCNJ6	intron
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DSCR8	non-coding RNA
DSCR8	non-coding RNA
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KCNJ15	intron
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ERG	intron
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ETS2	intron
ETS2-AS1	non-coding RNA
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LINC01700	non-coding RNA
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BRWD1	3utr
BRWD1	intron
BRWD1	intron
LCA5L	intron
SH3BGR	intron
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PCP4	intron
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DSCAM	intron
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BACE2	intron
FAM3B	intron
FAM3B	3utr
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UMODL1	intron
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RSPH1	intron
SLC37A1	intron
PDE9A	intron
PDE9A	intron
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WDR4	intron
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HSF2BP	intron
HSF2BP	intron
RRP1B	intron
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TRAPPC10	intron
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ICOSLG	3utr
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TSPEAR	intron

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ADARB1	intron
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SLC19A1	intron
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LSS	3utr
MCM3AP	intron
PCNT	intron
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POTEH	intron
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TPTEP1	non-coding RNA
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XKR3	intron
LINC01664	non-coding RNA
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CECR2	intron
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CECR2	intron
BCL2L13	intron
BCL2L13	intron
MICAL3	intron
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DGCR5	non-coding RNA
DGCR2	intron
DGCR2	intron
CLTCL1	intron
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CDC45	intron
DGCR8	intron
SERPIND1	intron
PI4KA	intron
CRKL	intron
CRKL	intron
none	intergenic
LRRC74B	intron
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GGT2P	non-coding RNA
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UBE2L3	intron
PPIL2	3utr
MAPK1	intron
PRAMENP	non-coding RNA
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CES5AP1	non-coding RNA
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DRICH1	intron
RGL4	5utr
GUSBP11	non-coding RNA
GSTT4	intron
none	intergenic
SPECC1L	intron
SPECC1L	exon
SPECC1L	intron
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SPECC1L	intron
ADORA2A-AS1	non-coding RNA
ADORA2A-AS1	non-coding RNA
GGT1	intron
PIWIL3	intron
SGSM1	intron
KIAA1671	intron
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GRK3	intron
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MYO18B	intron
MYO18B	intron
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SEZ6L	intron
SEZ6L	intron
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LINC01422	non-coding RNA
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PITPNB	intron
TTC28-AS1	non-coding RNA
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CHEK2	intron
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XBP1	intron
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ZNRF3	intron
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EMID1	intron
EMID1	intron
EWSR1	intron
THOC5	intron
none	intergenic
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NF2	intron
ZMAT5	intron
MTMR3	intron
HORMAD2-AS1	non-coding RNA
HORMAD2	intron
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OSBP2	intron
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LIMK2	intron
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SFI1	intron
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DEPDC5	intron
DEPDC5	intron
YWHAH	intron
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SLC5A4	intron
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BPIFC	intron
BPIFC	intron
FBXO7	exon
SYN3	intron
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SYN3	intron
TIMP3	3utr
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LARGE1	intron
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LINC02885	non-coding RNA
LINC02885	non-coding RNA
LINC01399	non-coding RNA
LINC01399	non-coding RNA
LINC01399	non-coding RNA
HMGXB4	intron

TOM1	intron
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RBFOX2	intron
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APOL3	intron
APOL4	intron
MYH9	intron
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CACNG2	intron
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MICALL1	intron
POLR2F	intron
PLA2G6	intron
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TMEM184B	intron
DMC1	intron
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CBY1	intron
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PDGFB	intron
MIEF1	3utr
CACNA1I	intron
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ENTHD1	intron
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GRAP2	intron
GRAP2	intron
TNRC6B	intron
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ADSL	intron
SGSM3	intron
SGSM3	intron
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ST13	intron
XPNPEP3	intron

EP300	intron
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EP300	intron
EP300-AS1	non-coding RNA
ZC3H7B	intron
DESI1	intron
XRCC6	3utr
CCDC134	intron
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ARFGAP3	intron
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MPPED1	intron
MPPED1	intron
EFCAB6	exon
EFCAB6	intron
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none	intergenic
SHISAL1	intron
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ARHGAP8	intron
none	intergenic
NUP50-DT	non-coding RNA
NUP50	3utr
KIAA0930	intron
ATXN10	intron
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PRR34	non-coding RNA
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MIRLET7BHG	non-coding RNA
PPARA	intron
PPARA	intron
GTSE1	intron
GTSE1	intron
CERK	intron
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TBC1D22A	intron
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LINC01644	non-coding RNA
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LINC01310	non-coding RNA
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MIR3667HG	non-coding RNA
MIR3667HG	non-coding RNA
MIR3667HG	non-coding RNA
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MLC1	3utr
DENND6B	intron
PPP6R2	intron
PPP6R2	intron
SBF1	intron
SBF1	intron
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SHANK3	intron
RPL23AP82	non-coding RNA
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CHL1	intron
CHL1	intron

[illegible]

CNTN4	intron
CNTN4	intron
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LRRN1	intron
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SUMF1	intron
SUMF1	intron
ITPR1	intron
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ITPR1	intron
ITPR1	exon
ITPR1	intron
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BHLHE40-AS1	non-coding RNA
BHLHE40-AS1	non-coding RNA
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GRM7-AS3	non-coding RNA
GRM7-AS3	non-coding RNA

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LOC101927394	non-coding RNA
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LMCD1-AS1	non-coding RNA
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LMCD1-AS1	non-coding RNA
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LMCD1-AS1	non-coding RNA
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SSUH2	intron
SSUH2	intron
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SRGAP3	intron
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LHFPL4	intron
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TATDN2	intron
SEC13	intron
ATP2B2	intron
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ATP2B2	intron
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SLC6A11	intron
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HRH1	intron
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ATG7	intron
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VGLL4	intron
TAMM41	intron
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SYN2	intron
SYN2	intron
PPARG	intron
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TSEN2	intron
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CAND2	intron
CAND2	intron
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IQSEC1	intron
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WNT7A	intron
WNT7A	intron
none	intergenic
CHCHD4	intron
XPC	intron
none	intergenic
SLC6A6	intron
GRIP2	intron
none	intergenic
C3orf20	intron
C3orf20	exon
FGD5	intron

NR2C2	intron
NR2C2	intron
none	intergenic
CAPN7	intron
SH3BP5	3utr
METTL6	intron
none	intergenic
HACL1	intron
HACL1	intron
HACL1	intron
BTD	intron
ANKRD28	intron
ANKRD28	intron
ANKRD28	intron
ANKRD28	intron
none	intergenic
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none	intergenic
RFTN1	intron
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PLCL2	intron
PLCL2	intron
TBC1D5	3utr
TBC1D5	intron
TBC1D5	intron
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TBC1D5	intron
none	intergenic
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BALR6	non-coding RNA
BALR6	non-coding RNA
BALR6	non-coding RNA
BALR6	non-coding RNA
none	intergenic
none	intergenic
SATB1	intron
SATB1	intron
SATB1-AS1	non-coding RNA

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KCNH8	intron
KCNH8	intron
KCNH8	intron
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KAT2B	intron
KAT2B	intron
KAT2B	intron
KAT2B	intron
KAT2B	intron
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ZNF385D	intron
ZNF385D	intron
ZNF385D	intron
none	intergenic
ZNF385D-AS2	non-coding RNA
none	intergenic
none	intergenic
none	intergenic
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none	intergenic

[illegible]

RARB	intron
RARB	intron
RARB	intron
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RARB	intron
RARB	intron
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OXSM	intron
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LRRC3B	intron
none	intergenic
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NEK10	intron
NEK10	intron
NEK10	intron
SLC4A7	exon
SLC4A7	intron
none	intergenic
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CMC1	intron
ZCWPW2	intron
LINC00693	non-coding RNA
LINC00693	non-coding RNA
LINC00693	non-coding RNA
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RBMS3	intron
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GADL1	exon
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STT3B	intron
STT3B	intron
STT3B	intron
STT3B	intron
none	intergenic
OSBPL10	intron
OSBPL10	intron
none	intergenic
none	intergenic
DYNC1LI1	intron
DYNC1LI1	intron
none	intergenic

[illegible]

[illegible]

none	intergenic
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CTNNB1	3utr
ULK4	intron
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TRAK1	intron
TRAK1	intron
TRAK1	intron
none	intergenic
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none	intergenic
SEC22C	intron
SS18L2	intron
ZBTB47-AS1	non-coding RNA
none	intergenic
none	intergenic
ACKR2	intron
none	intergenic
KRBOX1	intron
KRBOX1	exon
GASK1A	intron
none	intergenic
none	intergenic
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none	intergenic
none	intergenic
SNRK	intron
ANO10	intron
ANO10	intron
ANO10	intron
ABHD5	intron
none	intergenic
none	intergenic

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TOPAZ1	intron
TCAIM	intron
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TCAIM	intron
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KIF15	exon
KIF15	intron
CLEC3B	intron
CLEC3B	intron
CDCP1	intron
none	intergenic
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LARS2	intron
LARS2	intron
LIMD1	3utr
LZTFL1	intron
XCR1	intron
none	intergenic
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CCR3	intron
none	intergenic
LTF	intron
none	intergenic
PRSS43P	non-coding RNA
none	intergenic
none	intergenic
CSPG5	intron
SMARCC1	intron
SMARCC1	intron
SMARCC1	intron
SMARCC1	intron
MAP4	intron
MAP4	intron
MAP4	intron
MAP4	intron
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NME6	intron
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SHISA5	intron
PFKFB4	intron
none	intergenic
PRKAR2A	intron
PRKAR2A	intron
SLC25A20	intron
P4HTM	intron
IMPDH2	intron
USP4	intron
RHOA	intron
none	intergenic
RBM6	intron
RBM6	intron
SEMA3B	intron
CACNA2D2	intron
MAPKAPK3	intron
DOCK3	intron
DOCK3	intron
DOCK3	intron
DOCK3	intron
DOCK3	intron
DOCK3	intron
RAD54L2	intron
none	intergenic
PBRM1	3utr
PBRM1	intron
NEK4	intron
none	intergenic
SFMBT1	intron
none	intergenic
none	intergenic
CACNA1D	intron
CACNA1D	intron
CACNA1D	intron
none	intergenic
none	intergenic
CACNA2D3	intron
CACNA2D3	intron
CACNA2D3	intron
CACNA2D3	intron
CACNA2D3	intron
CACNA2D3	intron
none	intergenic
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none	intergenic

LINC02030	non-coding RNA
LINC02030	non-coding RNA
none	intergenic
none	intergenic
WNT5A	intron
ERC2	intron
ERC2	intron
ERC2	intron
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ERC2	intron
none	intergenic
CCDC66	intron
TASOR	exon
ARHGEF3	intron
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ARHGEF3	intron
ARHGEF3	intron
IL17RD	intron
IL17RD	intron
IL17RD	intron
DNAH12	exon
DNAH12	intron
DNAH12	intron
DNAH12	intron
DNAH12	intron
DNAH12	intron
PDE12	intron
none	intergenic
SLMAP	intron
SLMAP	intron
SLMAP	intron
FLNB	intron
ABHD6	exon
PXK	intron
PXK	intron
FAM3D-AS1	non-coding RNA
FAM3D	intron
CFAP20DC	intron
CFAP20DC	intron
CFAP20DC	intron

[illegible]

PTPRG	intron
PTPRG	intron
PTPRG	intron
PTPRG	intron
CADPS	intron
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SYNPR	intron
SYNPR	intron
none	intergenic
ATXN7	intron
ATXN7	intron
ATXN7	intron
PSMD6-AS2	non-coding RNA
PRICKLE2	intron
PRICKLE2	intron
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PRICKLE2	intron
none	intergenic
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ADAMTS9	intron
ADAMTS9	intron
ADAMTS9	intron

ADAMTS9-AS2	non-coding RNA
ADAMTS9-AS2	non-coding RNA
ADAMTS9-AS2	non-coding RNA
none	intergenic
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none	intergenic
LINC02040	non-coding RNA
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MAGI1	intron
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none	intergenic
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SLC25A26	intron
SLC25A26	intron
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SLC25A26	intron
LRIG1	intron
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SUCLG2	intron
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SUCLG2	intron
SUCLG2-DT	non-coding RNA
SUCLG2-DT	non-coding RNA
SUCLG2-DT	non-coding RNA
SUCLG2-DT	non-coding RNA
SUCLG2-DT	non-coding RNA
TAF1	intron
TAF1	intron

TAF4	intron
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TAF4	intron
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UBA3	intron
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FRMD4B	intron
FRMD4B	intron
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MITF	intron
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MDFIC2	intron
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FOXP1	intron
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EIF4E3	3utr
EIF4E3	intron
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RYBP	intron
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SHQ1	intron
GXYLT2	intron
GXYLT2	intron
PPP4R2	intron
EBLN2	exon
PDZRN3	intron
PDZRN3	intron
PDZRN3	intron
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LINC02005	non-coding RNA
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LINC02047	non-coding RNA
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CNTN3	intron
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[illegible]

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ROBO1	intron
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[illegible]

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LINC00971	non-coding RNA
LINC00971	non-coding RNA
LINC00971	non-coding RNA
LINC00971	non-coding RNA
LINC00971	non-coding RNA
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none	intergenic
CADM2	intron
CADM2	intron
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CADM2	intron
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none	intergenic

[illegible]

[illegible]

[illegible]

EPHA6	intron
EPHA6	intron
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ARL6	intron
none	intergenic
CRYBG3	intron
CRYBG3	intron
none	intergenic
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ST3GAL6-AS1	non-coding RNA
DCBLD2	intron
none	intergenic
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none	intergenic
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COL8A1	intron
COL8A1	intron
COL8A1	intron
COL8A1	intron
FILIP1L	intron
FILIP1L	intron
FILIP1L	intron
FILIP1L	intron
FILIP1L	intron
FILIP1L	intron
CMSS1	intron
none	intergenic
NIT2	3utr
TMEM45A	intron
ABI3BP	3utr

[illegible]

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ALCAM	intron
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CBLB	intron
CBLB	intron
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LINC00882	non-coding RNA

[illegible]

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NECTIN3	intron
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NECTIN3	intron
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CD96	intron
CD96	non-coding RNA
PLCXD2	exon
PLCXD2	intron
PHLDB2	intron
PHLDB2	intron
TBILA	non-coding RNA
SLC9C1	intron
SLC9C1	intron
none	intergenic
none	intergenic
none	intergenic
CCDC80	intron
none	intergenic
none	intergenic
none	intergenic
CD200R1L-AS1	non-coding RNA
CD200R1L	intron
none	intergenic
CD200R1	intron
none	intergenic
none	intergenic
LINC02044	non-coding RNA

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none	intergenic
SPICE1	intron
SPICE1	intron
SPICE1	intron
SPICE1	intron
SPICE1	intron
SIDT1	intron
SIDT1	intron
SIDT1	intron
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SIDT1	intron
SIDT1	intron
USF3	intron
NAA50	3utr
GRAMD1C	intron
CCDC191	intron
CCDC191	intron
none	intergenic
DRD3	intron
DRD3	intron
TIGIT	intron
ZBTB20	3utr
ZBTB20	intron
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ZBTB20	intron
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none	intergenic
GAP43	intron

[illegible]

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IGSF11	intron
IGSF11	intron
none	intergenic
ARHGAP31	intron
ARHGAP31	intron
ARHGAP31	intron
ARHGAP31	intron
CD80	intron
none	intergenic
NR1I2	intron
GSK3B	intron
GSK3B	intron
none	intergenic
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FSTL1	intron
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HGD	intron
RABL3	intron
none	intergenic
none	intergenic
none	intergenic
STXBP5L	intron
STXBP5L	intron
STXBP5L	intron
STXBP5L	intron
STXBP5L	intron
STXBP5L	intron
none	intergenic
EAF2	intron
none	intergenic
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CD86	intron
none	intergenic
none	intergenic
CASR	intron
WDR5B-DT	non-coding RNA
KPNA1	intron
PARP9	intron
PARP15	intron
PARP15	intron
PARP15	intron

none	intergenic
HSPBAP1	intron
none	intergenic
SEMA5B	intron
PDIA5	intron
ADCY5	intron
ADCY5	intron
ADCY5	intron
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none	intergenic
MYLK	intron
MYLK	intron
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MYLK	intron
CCDC14	intron
KALRN	intron
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KALRN	intron
UMPS	intron
ITGB5	intron
ITGB5	intron
ITGB5	intron
MUC13	intron
none	intergenic
HEG1	intron
HEG1	intron
SLC12A8	intron
ZNF148	intron
OSBPL11	intron
OSBPL11	intron
none	intergenic
LINC02614	non-coding RNA
none	intergenic
SLC41A3	intron
SLC41A3	intron
SLC41A3	intron
none	intergenic
ALDH1L1-AS2	non-coding RNA
none	intergenic
CHCHD6	intron
CHCHD6	intron
CHCHD6	intron

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MGLL	intron
MGLL	intron
KBTBD12	intron
KBTBD12	intron
none	intergenic
SEC61A1	intron
RUVBL1	intron
EEFSEC	intron
EEFSEC	intron
none	intergenic
none	intergenic
RPN1	intron
CFAP92	intron
CFAP92	intron
ISY1	intron
none	intergenic
none	intergenic
IFT122	intron
IFT122	intron
TMCC1	intron
TMCC1	intron
LINC02021	non-coding RNA
none	intergenic
none	intergenic
COL6A4P2	non-coding RNA
COL6A5	intron
COL6A5	intron
COL6A5	intron
COL6A6	intron
COL6A6	intron
PIK3R4	intron
ATP2C1	intron
ASTE1	intron
NEK11	intron
NEK11	intron
NUDT16-DT	non-coding RNA
none	intergenic
none	intergenic
CPNE4	intron
CPNE4	intron
CPNE4	intron
CPNE4	intron
CPNE4	intron

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CPNE4	intron
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DNAJC13	intron
ACAD11	intron
ACKR4	intron
ACAD11	intron
UBA5	intron
NPHP3	intron
NPHP3-AS1	non-coding RNA
NPHP3-AS1	non-coding RNA
NPHP3-AS1	non-coding RNA
NPHP3-AS1	non-coding RNA
none	intergenic
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TMEM108	intron
TMEM108	intron
none	intergenic
none	intergenic
TOPBP1	intron
TF	intron
SRPRB	intron
SRPRB	intron
SRPRB	non-coding RNA
RAB6B	intron
RAB6B	intron
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none	intergenic
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CEP63	intron
KY	intron
KY	intron
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EPHB1	intron
EPHB1	intron
EPHB1	intron

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EPHB1	intron
EPHB1	intron
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PPP2R3A	intron
PPP2R3A	intron
PPP2R3A	intron
MSL2	intron
MSL2	intron
PCCB	intron
PCCB	intron
STAG1	intron
STAG1	intron
STAG1	intron
NCK1	intron
IL20RB-AS1	non-coding RNA
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DZIP1L	intron
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ARMC8	intron
NME9	intron
MRAS	intron
CEP70	intron
none	intergenic
PIK3CB	intron
PIK3CB	intron
PIK3CB	intron
PIK3CB	intron

PIK3CB	intron
PRR23A	3utr
none	intergenic
BPESC1	non-coding RNA
none	intergenic
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COPB2	intron
COPB2-DT	non-coding RNA
NMNAT3	intron
NMNAT3	intron
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CLSTN2	intron
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SLC25A36	intron
PXYLP1	intron
ZBTB38	intron
none	intergenic
RASA2	intron
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RASA2	intron
LINC02618	non-coding RNA
none	intergenic
TFDP2	intron
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none	intergenic
GK5	intron
GK5	intron
none	intergenic

[illegible]

[illegible]

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LINC02046	non-coding RNA
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HPS3	intron
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WWTR1	intron
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RNF13	intron
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LINC01214	non-coding RNA
LINC01214	non-coding RNA
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EIF2A	intron
EIF2A	intron
SELENOT	intron
SELENOT	intron
none	intergenic
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CLRN1-AS1	non-coding RNA
MED12L	intron
MED12L	intron
GPR171	intron

IGSF10	intron
IGSF10	intron
none	intergenic
none	intergenic
AADACL2-AS1	non-coding RNA
AADACL2-AS1	non-coding RNA
AADACL2-AS1	non-coding RNA
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LOC101928166	non-coding RNA
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MBNL1	intron
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LINC02006	non-coding RNA
LINC02006	non-coding RNA
LINC02006	non-coding RNA
LINC02006	non-coding RNA
none	intergenic
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ARHGEF26	intron
ARHGEF26	intron
GPR149	3utr
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MME	intron
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PLCH1	intron
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C3orf33	3utr
C3orf33	intron
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GMPS	intron
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KCNAB1	intron
KCNAB1	intron
SSR3	intron
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LEKR1	intron
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VEPH1	intron
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RSRC1	intron
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MLF1	intron
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none	intergenic
GFM1	intron
GFM1	intron
LOC100287290	non-coding RNA
LOC100287290	non-coding RNA
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IQCJ-SCHIP1	intron
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IL12A-AS1	non-coding RNA
IL12A-AS1	non-coding RNA
IL12A-AS1	non-coding RNA
IL12A-AS1	non-coding RNA
IL12A-AS1	non-coding RNA
IFT80	intron
SMC4	intron
KPNA4	3utr
none	intergenic
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PPM1L	intron
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[illegible]

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SI	intron
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SLITRK3	intron
LINC01322	non-coding RNA
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ZBBX	intron
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SERPINI2	intron
WDR49	intron
WDR49	intron
WDR49	intron
PDCD10	intron
SERPINI1	intron
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GOLIM4	intron
GOLIM4	intron
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EGFEM1P	non-coding RNA
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MECOM	intron
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FHL1P1	non-coding RNA
FHL1P1	non-coding RNA
PHC3	intron
PHC3	intron
PHC3	intron
none	intergenic
SKIL	exon
none	intergenic
SLC7A14-AS1	non-coding RNA

SLC7A14-AS1	non-coding RNA
SLC7A14-AS1	non-coding RNA
SLC7A14-AS1	non-coding RNA
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SLC2A2	intron
TNIK	intron
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none	intergenic
PLD1	intron
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PLD1	intron
TMEM212-AS1	non-coding RNA
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FNDC3B	intron
FNDC3B	intron
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NCEH1	3utr
SPATA16	intron
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NLGN1	intron
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NLGN1	3utr
NLGN1	3utr

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TBL1XR1	intron
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LINC00501	non-coding RNA
none	intergenic

LINC00578	non-coding RNA
LINC00578	non-coding RNA
LINC00578	non-coding RNA
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LINC02015	non-coding RNA
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LINC01014	non-coding RNA
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KCNMB2	intron
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ZMAT3	intron
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PIK3CA-DT	non-coding RNA
none	intergenic
ZNF639	exon
GNB4	3utr
none	intergenic
USP13	intron
USP13	intron
PEX5L	intron
PEX5L	intron
PEX5L	intron
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TTC14-DT	non-coding RNA

LOC101928882	non-coding RNA
none	intergenic
SOX2-OT	non-coding RNA
SOX2-OT	non-coding RNA
SOX2-OT	non-coding RNA
LOC102724604	non-coding RNA
SOX2-OT	non-coding RNA
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LINC01206	non-coding RNA
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LINC01994	non-coding RNA
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ATP11B	intron
DCUN1D1	intron
MCF2L2	intron
MCF2L2	intron
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KLHL6	intron
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YEATS2	intron
YEATS2	intron
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PARL	intron
ABCC5	intron
EIF2B5-DT	non-coding RNA
EIF4G1	intron
none	intergenic
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VPS8	intron
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EHHADH-AS1	non-coding RNA
EHHADH-AS1	non-coding RNA
MAP3K13	intron
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MAP3K13	intron
LIPH	intron
none	intergenic
IGF2BP2	intron
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IGF2BP2	intron
none	intergenic
NMRAL2P	non-coding RNA
none	intergenic
DGKG	intron
LINC02052	non-coding RNA
TBCCD1	intron
FETUB	intron
KNG1	3utr
none	intergenic
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RTP1	3utr
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LINC01991	non-coding RNA
none	intergenic
LPP-AS2	non-coding RNA
LPP	intron
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[illegible]

FGF12	intron
FGF12	intron
MB21D2	intron
MB21D2	intron
MB21D2	intron
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ATP13A5	intron
ATP13A5	intron
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ATP13A5	intron
ATP13A4	intron
ATP13A4	intron
none	intergenic
OPA1	intron
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LINC02026	non-coding RNA
LINC02026	non-coding RNA
CPN2	intron
ATP13A3	intron
ATP13A3	intron
ATP13A3	intron
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TMEM44	intron
LINC01968	non-coding RNA
LINC01968	non-coding RNA
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SDHAP2	non-coding RNA
MIR570HG	non-coding RNA
MIR570HG	non-coding RNA
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TFRC	exon
SLC51A	intron
PCYT1A	intron
UBXN7	intron
UBXN7	intron
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[illegible]

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ZNF876P	non-coding RNA
ZNF876P	non-coding RNA
ZNF732	intron
ZNF141	intron
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UVSSA	intron
NSD2	intron
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POLN	intron
POLN	intron
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FAM193A	intron
FAM193A	intron
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HTT	intron
HTT	intron
RGS12	intron
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ZBTB49	intron
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STX18	intron
STX18-AS1	non-coding RNA
STX18-AS1	non-coding RNA
STX18-AS1	non-coding RNA
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[illegible]

[illegible]

LINC02360	non-coding RNA
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LINC02270	non-coding RNA
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RAB28	intron
RAB28	intron
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BOD1L1	exon
LINC01182	non-coding RNA
LINC01182	non-coding RNA
LINC01182	non-coding RNA
LINC01182	non-coding RNA
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[illegible]

[illegible]

SLIT2	intron
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KCNIP4	intron
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LOC100505912	non-coding RNA
GBA3	non-coding RNA
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PPARGC1A	3utr
PPARGC1A	intron
PPARGC1A	intron

[illegible]

[illegible]

[illegible]

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LOC101928622	non-coding RNA
LOC101928622	non-coding RNA
LOC101928622	non-coding RNA
LOC101928622	non-coding RNA
LOC101928622	non-coding RNA
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LINC02484	non-coding RNA
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DTHD1	intron
DTHD1	intron
LINC02505	non-coding RNA

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LINC02505	non-coding RNA
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NWD2	intron
NWD2	intron
C4orf19	intron
C4orf19	intron
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RELL1	intron
RELL1	intron
none	intergenic
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PGM2	intron
PGM2	intron
PGM2	exon
none	intergenic
TBC1D1	intron
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KLF3	intron
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FAM114A1	intron
TMEM156	intron
TMEM156	intron
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WDR19	intron
RFC1	intron

[illegible]

[illegible]

[illegible]

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SCFD2	intron
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SCFD2	intron
FIP1L1	intron
FIP1L1	intron
LNX1	intron
LNX1	intron
none	intergenic
LOC100506444	non-coding RNA
none	intergenic
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CHIC2	intron
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PDGFRA	intron
PDGFRA	intron
LINC02283	non-coding RNA
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EXOC1	exon
none	intergenic
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CRACD	intron
CRACD	intron
CRACD	intron
CRACD	intron
CRACD	3utr
AASDH	intron

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

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JCHAIN	intron
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RUFY3	intron
RUFY3	intron
RUFY3	intron
GRSF1	exon
GRSF1	exon
MOB1B	intron
none	intergenic
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SLC4A4	intron
SLC4A4	intron
SLC4A4	intron
SLC4A4	intron
SLC4A4	intron
SLC4A4	intron
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ADAMTS3	intron
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BTC	intron
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PARM1	intron
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G3BP2	intron
USO1	intron
NAAA	intron
ART3	intron
ART3	intron
ART3	intron
NUP54	exon
SCARB2	intron
CCDC158	intron
SHROOM3	intron
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SHROOM3	intron
SEPTIN11	intron
SEPTIN11	3utr
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FRAS1	intron
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BMP2K	intron

BMP2K	intron
LINC01088	non-coding RNA
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NAA11	intron
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PCAT4	non-coding RNA
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ANTXR2	intron
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CFAP299	intron
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CFAP299	intron
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CFAP299	intron
CFAP299	intron
CFAP299	intron
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RASGEF1B	intron
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TMEM150C	intron
TMEM150C	intron
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SCD5	intron
LIN54	intron
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HELQ	intron
HELQ	intron
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LINC02994	non-coding RNA
LINC02994	non-coding RNA
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CDS1	intron
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WDFY3	3utr
WDFY3	intron
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ARHGAP24	intron
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MAPK10	intron
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MAPK10	intron
PTPN13	intron
PTPN13	intron
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PTPN13	intron
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C4orf36	intron
C4orf36	intron
AFF1	intron
AFF1	intron
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KLHL8	intron
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HSD17B11	intron
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SPARCL1	intron
SPARCL1	exon
SPARCL1	intron
none	intergenic
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none	intergenic

[illegible]

[illegible]

GRID2	intron
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SMARCAD1-DT	non-coding RNA
SMARCAD1	intron
HPGDS	intron
none	intergenic
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PDLIM5	intron
PDLIM5	intron
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BMPR1B-DT	non-coding RNA
BMPR1B	intron
BMPR1B	intron
BMPR1B	intron
BMPR1B	intron
UNC5C	3utr
UNC5C	intron
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UNC5C	intron
UNC5C-AS1	non-coding RNA
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LINC02267	non-coding RNA

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STPG2-AS1	non-coding RNA
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RAP1GDS1	intron
RAP1GDS1	intron
RAP1GDS1	intron
TSPAN5	intron
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EIF4E	intron
METAP1	intron
ADH6	intron
LOC100507053	non-coding RNA
LOC100507053	non-coding RNA
LOC100507053	non-coding RNA
ADH1A	intron
ADH1C	intron
ADH7	intron
C4orf17	exon
C4orf17	intron
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DAPP1	intron

DAPP1	intron
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DNAJB14	intron
H2AZ1-DT	non-coding RNA
H2AZ1-DT	non-coding RNA
none	intergenic
DDIT4L	intron
DDIT4L	intron
DDIT4L-AS1	non-coding RNA
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EMCN	intron
EMCN	intron
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PPP3CA	intron
PPP3CA	intron
PPP3CA	intron
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BANK1	intron
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BANK1	intron
BANK1	3utr
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SLC39A8	intron
SLC39A8	intron
LOC105377621	non-coding RNA
NFKB1	intron
MANBA	intron
LOC102723704	non-coding RNA
SLC9B1	intron
SLC9B1	intron
SLC9B1	intron

SLC9B2	intron
CENPE	intron
CENPE	intron
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TACR3	3utr
TACR3	intron
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CXXC4	3utr
CXXC4-AS1	non-coding RNA
CXXC4-AS1	non-coding RNA
CXXC4-AS1	non-coding RNA
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TET2	intron
TET2-AS1	non-coding RNA
PPA2	intron
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ARHGEF38	intron
GSTCD	intron

[illegible]

COL25A1	intron
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SEC24B	intron
MCUB	intron
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EGF	intron
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ELOVL6	intron
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ENPEP	intron
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PANCR	non-coding RNA
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FAM241A	intron
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[illegible]

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LINC01378	non-coding RNA
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LINC02264	non-coding RNA
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NDST3	intron
NDST3	intron
PRSS12	intron

PRSS12	intron
PRSS12	intron
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LOC729218	non-coding RNA
SEC24D	intron
SEC24D	intron
SYNPO2	intron
SYNPO2	intron
SYNPO2	intron
SYNPO2	intron
SYNPO2	intron
SYNPO2	3utr
SYNPO2	intron
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MYOZ2	intron
MYOZ2	intron
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SEPTIN7P14	non-coding RNA
PDE5A	intron
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PRDM5	intron
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NDNF	intron
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TNIP3	intron
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QRFPR	intron
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ANXA5	intron
ANXA5	intron
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TRPC3	intron
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BLTP1	intron
IL21	3utr
IL21-AS1	non-coding RNA
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SPATA5	intron
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LINC01091	non-coding RNA
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LINC01091	non-coding RNA
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LINC02516	non-coding RNA
LINC02516	non-coding RNA

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FAT4	intron
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INTU	intron
INTU	3utr
SLC25A31	intron
SLC25A31	intron
HSPA4L	intron
none	intergenic
MFSD8	intron

[illegible]

[illegible]

[illegible]

none	intergenic
LINC02511	non-coding RNA
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LINC02172	non-coding RNA
LINC02172	non-coding RNA
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SLC7A11-AS1	non-coding RNA
SLC7A11	intron
LINC00499	non-coding RNA
LINC00499	non-coding RNA
LINC00499	non-coding RNA
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LOC105377448	non-coding RNA
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LOC105377448	non-coding RNA
ELF2	intron
ELF2	intron
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RAB33B	intron
SETD7	intron
MAML3	intron
MAML3	intron
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SCOC	intron

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SCOC	intron
CLGN	intron
MGAT4D	intron
TBC1D9	intron
TBC1D9	intron
RNF150	intron
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IL15	intron
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INPP4B	intron
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USP38	intron
USP38	intron
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GAB1	intron

FREM3	intron
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LOC101927636	non-coding RNA
LOC101927636	non-coding RNA
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HHIP	intron
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ABCE1	intron
OTUD4	intron
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SMAD1	intron
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C4orf51	intron
ZNF827	intron
ZNF827	intron
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LINC01095	non-coding RNA
none	intergenic
REELD1	intron

[illegible]

LINC02355	non-coding RNA
IQCM	intron
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IQCM	intron
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DCLK2	intron
LRBA	intron
LRBA	exon
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SH3D19	intron
SH3D19	intron
SH3D19	intron
PRSS48	intron
SH3D19	intron
SH3D19	intron
none	intergenic
FHIP1A	intron
FHIP1A	intron
LOC127898557	non-coding RNA
none	intergenic
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LINC02273	non-coding RNA
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FBXW7	intron
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FBXW7	intron
none	intergenic
TMEM154	3utr

TMEM154	intron
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ARFIP1	intron
ARFIP1	intron
FHDC1	intron
none	intergenic
TRIM2	intron
TRIM2	intron
TRIM2	intron
none	intergenic
TMEM131L	intron
TMEM131L	intron
TMEM131L	intron
TMEM131L	intron
LOC100419170	non-coding RNA
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DCHS2	intron
DCHS2	intron
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DCHS2	intron
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PLRG1	intron
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PLRG1	intron
FGG	intron
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GUCY1B1	intron
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PDGFC	intron
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GLRB	intron
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GLRB	intron
GRIA2	intron
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GASK1B	intron
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GASK1B	intron

GASK1B-AS1	non-coding RNA
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RXFP1	intron
PPID	intron
PPID	intron
none	intergenic
FNIP2	intron
C4orf45	intron
C4orf45	intron
RAPGEF2	intron
none	intergenic
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LINC02233	non-coding RNA
LINC02233	non-coding RNA
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FSTL5	intron
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[illegible]

[illegible]

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GALNTL6	intron
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GALNT7-DT	non-coding RN/
GALNT7-DT	non-coding RN/
GALNT7	intron
GALNT7	intron

[illegible]

[illegible]

[illegible]

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LINC00290	non-coding RNA
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TENM3	intron
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WWC2	intron
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TRAPPC11	intron
STOX2	non-coding RNA
STOX2	non-coding RNA
ENPP6	intron
ENPP6	intron
ENPP6	intron
none	intergenic
IRF2	intron
IRF2	intron
LINC02427	non-coding RNA
CENPU	intron
ACSL1	intron
ACSL1	intron
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[illegible]

[illegible]

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PLEKHG4B	intron
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AHRR	intron
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AHRR	intron
SLC9A3	intron
SLC9A3	intron
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ZDHHC11B	intron
ZDHHC11	intron
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[illegible]

LINC01020	non-coding RNA
LINC01020	non-coding RNA
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ADAMTS16	intron
ICE1	intron
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LINC02145	non-coding RNA
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UBE2QL1	intron
NSUN2	intron
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LINC02236	non-coding RNA
LINC02236	non-coding RNA
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LINC02199	non-coding RNA
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SEMA5A	intron
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SEMA5A	intron
none	intergenic
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TAS2R1	intron
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CTNND2	intron
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LINC01194	non-coding RNA
LINC01194	non-coding RNA
LINC01194	non-coding RNA
LINC01194	non-coding RNA
LINC01194	non-coding RNA
LINC01194	non-coding RNA
none	intergenic
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DNAH5	intron
DNAH5	intron
DNAH5	intron
DNAH5	intron
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TRIO	intron
TRIO	intron
ANKH	intron
none	intergenic
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none	intergenic
LINC02149	non-coding RNA
LINC02149	non-coding RNA

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

ADAMTS12	intron
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ADAMTS12	intron
AMACR	intron
C1QTNF3	non-coding RNA
none	intergenic
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TTC23L-AS1	non-coding RNA
RAD1	intron
PRLR	intron
PRLR	intron
PRLR	intron
PRLR	intron
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SPEF2	intron
SPEF2	intron
SPEF2	intron
SPEF2	intron
SPEF2	intron
SPEF2	intron
CAPSL	exon
CAPSL	intron
UGT3A1	intron
UGT3A1	intron
NADK2	intron
none	intergenic
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SLC1A3	intron
SLC1A3	intron
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NIPBL	intron
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NIPBL	intron
NIPBL	intron

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CPLANE1	intron
NUP155	intron
NUP155	intron
WDR70	intron
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LINC02107	non-coding RNA
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EGFLAM	intron
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EGFLAM	intron
LIFR	intron
LIFR	intron
LIFR	intron
none	intergenic
OSMR-DT	non-coding RNA
OSMR	intron
none	intergenic
FYB1	exon
FYB1	exon
FYB1	intron
C9	intron
C9	intron
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TTC33	intron

TTC33	intron
C7	intron
C7	intron
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MROH2B	intron
PLCXD3	intron
PLCXD3	intron
PLCXD3	intron
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OXCT1	intron
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GHR	intron
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SELENOP	intron
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ZNF131	intron
NIM1K	intron
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C5orf34	intron
PAIP1	intron
none	intergenic
NNT-AS1	non-coding RNA
NNT	intron
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FGF10	intron
LINC02224	non-coding RNA
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HCN1	intron
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EMB	intron
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PARP8	intron
PARP8	intron
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PARP8	intron
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[illegible]

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LINC02998	non-coding RNA
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CDC20B	3utr
CDC20B	intron
CDC20B	intron
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MTREX	intron
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MTREX	intron
SLC38A9	intron
SLC38A9	intron
DDX4	intron
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DDX4	intron
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C5orf67	non-coding RNA
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MAP3K1	intron
MAP3K1	intron
MAP3K1	3utr
MIER3	intron
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GPBP1	intron
GPBP1	intron
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LOC101928505	non-coding RNA
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LINC02101	non-coding RNA
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RAB3C	intron
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RAB3C	intron
RAB3C	intron
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RAB3C	intron
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PDE4D	intron

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PART1	non-coding RNA
DEPDC1B	intron
DEPDC1B	intron
DEPDC1B	intron
none	intergenic
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ELOVL7	intron
ELOVL7	intron
ERCC8	intron
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ERCC8	intron
NDUFAF2	intron
NDUFAF2	intron
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PIK3R1	intron
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LINC02198	non-coding RNA
CCNB1	intron
RAD17	intron
OCLN	intron
OCLN	intron
GUSBP3	non-coding RNA
none	intergenic
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GUSBP14	non-coding RNA
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GUSBP15	non-coding RNA
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GUSBP16	non-coding RNA
GUSBP16	non-coding RNA
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GUSBP17	non-coding RNA
LINC02197	non-coding RNA

LINC02197	non-coding RNA
LINC02197	non-coding RNA
MCCC2	intron
none	intergenic
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MRPS27	intron
MRPS27	intron
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LINC02056	non-coding RNA
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TNPO1	intron
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FCHO2	intron
FCHO2	intron
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ARHGEF28	intron
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LINC02122	non-coding RNA
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LINC01333	non-coding RNA
LINC01331	non-coding RNA
LINC01331	non-coding RNA

LINC01331	non-coding RNA
LINC01331	non-coding RNA
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HEXB	intron
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POLK	intron
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SV2C	intron
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SV2C	intron
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IQGAP2	intron
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PDE8B	intron
PDE8B	intron
PDE8B	intron
OTP	intron
TBCA	intron
TBCA	intron
none	intergenic
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LOC101929154	non-coding RNA
AP3B1	intron
none	intergenic
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SCAMP1	intron
SCAMP1	intron
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LHFPL2	intron
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ARSB	intron
ARSB	intron
ARSB	intron
ARSB	intron
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DMGDH	intron
BHMT2	3utr
HOMER1	intron
HOMER1	intron
HOMER1	intron
CMYA5	intron
THBS4	intron
THBS4	intron
THBS4	intron
THBS4	intron
SERINC5	intron
SERINC5	intron
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FAM151B	intron
FAM151B	intron
MSH3	intron
MSH3	intron
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RASGRF2	intron

[illegible]

[illegible]

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NBPF22P	non-coding RNA
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COX7C	intron
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LINC01949	non-coding RNA
CCNH	intron
CCNH	intron
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TMEM161B	intron
TMEM161B-DT	non-coding RNA
none	intergenic
none	intergenic
LINC00461	non-coding RNA

[illegible]

[illegible]

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NR2F1-AS1	non-coding RNA
NR2F1-AS1	non-coding RNA
NR2F1-AS1	non-coding RNA
NR2F1-AS1	non-coding RNA
NR2F1-AS1	non-coding RNA
NR2F1	intron
none	intergenic
FAM172A	3utr
FAM172A	intron
FAM172A	intron
FAM172A	intron
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FAM172A	intron
none	intergenic
KIAA0825	intron
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MCTP1	intron
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SKIC3	intron
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SKIC3	intron

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ELL2	intron
ELL2	intron
LOC101929710	non-coding RNA
LOC101929710	non-coding RNA
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LOC101929710	non-coding RNA
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LOC101929710	non-coding RNA
CAST	intron
ERAP1	intron
ERAP2	intron
none	intergenic
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RIOK2	3utr
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LINC01340	non-coding RNA
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LINC02234	non-coding RNA
LINC02234	non-coding RNA
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none	intergenic
CHD1	3utr
CHD1	3utr
CHD1-DT	non-coding RNA
CHD1-DT	non-coding RNA
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none	intergenic

[illegible]

[illegible]

[illegible]

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EFNA5	intron
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FBXL17	intron
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FER	intron
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LOC285638	non-coding RNA
PJA2	intron
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MAN2A1	intron
MAN2A1	intron
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MAN2A1	intron
MAN2A1	intron

MAN2A1	3utr
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WDR36	exon
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CAMK4	intron
CAMK4	intron
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CAMK4	intron
STARD4-AS1	non-coding RNA
STARD4-AS1	non-coding RNA
STARD4-AS1	non-coding RNA
NREP	intron
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NREP-AS1	non-coding RNA
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EPB41L4A	intron

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APC	intron
APC	intron
REEP5	intron
MCC	intron
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YTHDC2	intron
YTHDC2	intron
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KCNN2	intron
KCNN2	intron
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LOC101927078	non-coding RNA
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TRIM36	intron
PGGT1B	intron
PGGT1B	intron
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FEM1C	intron
none	intergenic
TMED7-TICAM2	3utr

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AP3S1	intron
AP3S1	intron
AP3S1	intron
LVRN	intron
LVRN	intron
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COMMD10	intron
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SEMA6A	intron
SEMA6A	intron
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LINC00992	non-coding RNA
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LINC02147	non-coding RNA
LINC02147	non-coding RNA
LINC02147	non-coding RNA
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LINC02147	non-coding RNA
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LINC02208	non-coding RNA
LINC02208	non-coding RNA
LINC02208	non-coding RNA

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LINC02215	non-coding RNA
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DTWD2	intron
DTWD2	intron
DTWD2	intron
DTWD2	intron
DMXL1-DT	non-coding RNA
DMXL1	intron
DMXL1	intron
DMXL1	intron
none	intergenic
TNFAIP8	3utr
HSD17B4	intron
HSD17B4	intron
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PRR16	intron
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SRFBP1	intron
SRFBP1	intron
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LOC100505841	intron
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LINC02201	non-coding RNA
LINC02201	non-coding RNA
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LINC02201	non-coding RNA
SNX24	intron
SNX24	intron
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PRDM6	intron
PRDM6	intron
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CEP120	intron
CEP120	intron
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CSNK1G3	intron
CSNK1G3	intron
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[illegible]

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LINC02039	non-coding RNA
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GRAMD2B	intron
GRAMD2B	intron
GRAMD2B	3utr
LMNB1-DT	non-coding RNA
LMNB1	intron
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MARCHF3	intron
MARCHF3	intron
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MARCHF3	intron
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CCDC192	intron
SLC12A2-DT	non-coding RNA
SLC12A2-DT	non-coding RNA
SLC12A2-DT	non-coding RNA
SLC12A2	intron
none	intergenic
FBN2	intron
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ISOC1	intron
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ADAMTS19	intron
ADAMTS19	intron
CHSY3	intron
CHSY3	intron
CHSY3	intron
CHSY3	intron
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LYRM7	3utr
CDC42SE2	intron
RAPGEF6	intron
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FNIP1	intron
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MEIKIN	intron
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none	intergenic
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P4HA2	3utr
MIR3936HG	non-coding RNA
IRF1-AS1	non-coding RNA
IRF1-AS1	non-coding RNA
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RAD50	intron
SEPTIN8	exon
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AFF4	intron
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FSTL4	intron
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VDAC1	intron
PPP2CA	intron
CDKL3	intron
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CDKN2AIPNL	intron
JADE2	intron
CAMLG	exon
DDX46	intron
TXNDC15	intron
PITX1-AS1	non-coding RNA
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SLC25A48	intron

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KLHL3	intron
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PKD2L2	intron
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FAM13B	intron
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BRD8	intron
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CTNNA1	intron
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SIL1	intron
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MATR3	intron
MATR3	exon
SLC23A1	intron
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UBE2D2	intron
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NRG2	intron
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CYSTM1	intron
PFDN1	intron
ANKHD1-EIF4EBP3	intron
ANKHD1-EIF4EBP3	intron
EIF4EBP3	intron
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HARS2	intron
PCDHA11	intron
PCDHAC2	intron
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PCDHB7	5utr
PCDHB10	exon
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PCDHGA11	intron
DIAPH1	intron
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ARAP3	intron

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RNF14	intron
NDFIP1	intron
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SPRY4-AS1	non-coding RNA
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FGF1	intron
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ARHGAP26	intron
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PRELID2	intron
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PRELID2	intron
GRXCR2	intron
SH3RF2	intron
PLAC8L1	5utr
LARS1	intron
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PPP2R2B	intron
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STK32A	intron
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DPYSL3	intron
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JAKMIP2	intron
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SPINK1	intron
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C5orf46	intron
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FBXO38-DT	non-coding RNA
HTR4	intron
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SH3TC2	intron
SH3TC2-DT	non-coding RNA
ABLIM3	intron
AFAP1L1	intron
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CSF1R	intron
CAMK2A	intron
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SYNPO	intron
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ANXA6	intron
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CCDC69	intron
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SLC36A2	5utr
FAT2	intron
SPARC	intron
G3BP1	intron
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LINC01933	non-coding RNA
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LINC01470	non-coding RNA
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GRIA1	intron
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FAM114A2	intron
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GALNT10	intron
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LARP1	intron
CNOT8	intron
GEMIN5	intron
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SGCD	intron
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TIMD4	intron
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HAVCR1	intron
HAVCR2	intron
MED7	exon
ITK	intron
FNDC9	3utr
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ADAM19	intron

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SOX30	intron
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LSM11	intron
CLINT1	intron
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LINC02227	non-coding RNA
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EBF1	intron
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LINC01932	non-coding RNA
IL12B	intron
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LINC01847	non-coding RNA
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PWWP2A	intron

[illegible]

[illegible]

[illegible]

SLIT3	intron
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DOCK2	intron
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INSYN2B	intron
INSYN2B	intron
none	intergenic
LCP2	intron
KCNMB1	intron
KCNIP1	intron
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GABRP	intron
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RANBP17	intron
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FBXW11	intron
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STK10	intron
UBTD2	intron
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SH3PXD2B	intron
SH3PXD2B	intron
SH3PXD2B	intron
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DUSP1	3utr
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CPEB4	intron
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C5orf47	intron
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NSG2	intron
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LINC01411	non-coding RNA
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LINC01951	non-coding RNA
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SFXN1	intron
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CPLX2	intron

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DUSP22	3utr
EXOC2	intron
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GMDS	intron
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GMDS-DT	non-coding RNA
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WRNIP1	intron
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SERPINB6	intron
RIPK1	intron
PSMG4	3utr
SLC22A23	intron
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PXDC1	intron
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PRPF4B	exon
TEX56P	non-coding RNA
ECI2-DT	non-coding RNA
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CDYL	intron
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RPP40	intron

LYRM4-AS1	non-coding RNA
LYRM4	intron
FARS2	intron
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F13A1	intron
LY86-AS1	non-coding RNA
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LY86	intron
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RREB1	intron
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CAGE1	intron
CAGE1	intron
CAGE1	intron
none	intergenic
DSP	intron
BMP6	intron
BMP6	intron
BMP6	intron
BLOC1S5-TXNDC5	non-coding RNA
BLOC1S5-TXNDC5	non-coding RNA
EEF1E1	exon
none	intergenic
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SLC35B3	intron
SLC35B3	intron
LOC100506207	non-coding RNA
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OFCC1	non-coding RNA
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OFCC1	non-coding RNA
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GCNT2	3utr
SYCP2L	intron
SYCP2L	intron
SYCP2L	intron
SYCP2L	intron
none	intergenic
ELOVL2	3utr
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[illegible]

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JARID2	intron
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DTNBP1	intron
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ATXN1	intron
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STMND1	intron
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CAP2	intron
CAP2	intron
NUP153	intron
NUP153	intron
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DCDC2	intron
DCDC2	intron
GPLD1	intron
KIAA0319	intron
ACOT13	intron
RIPOR2	intron
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CMAHP	non-coding RNA
CMAHP	non-coding RNA
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CARMIL1	intron
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SLC17A4	3utr
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SLC17A3	intron
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SLC17A2	intron
TRIM38	3utr
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HFE	intron
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BTN3A2	intron
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GUSBP2	non-coding RNA
LINC00240	non-coding RNA
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PRSS16	intron
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HCG18	non-coding RNA
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TSBP1	intron
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PSMB8	intron
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HCG24	non-coding RNA
COL11A2	intron
SYNGAP1	intron
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IP6K3	intron
LEMD2	intron
LEMD2	exon
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HMGA1	intron
RPS10-NUDT3	intron
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SPDEF	intron
ILRUN	intron
ILRUN	intron
BLTP3A	intron
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ANKS1A	intron
ANKS1A	intron
ANKS1A	3utr
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TCP11	intron
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ZNF76	intron
PPARD	intron
FKBP5	3utr
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SLC26A8	intron
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BRPF3	intron
PNPLA1	intron
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RAB44	intron
CPNE5	intron
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PPIL1	intron
PI16	intron
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TMEM217B	intron
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CMTR1	intron
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GLO1	3utr
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DNAH8	intron
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GLP1R	intron
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KCNK16	exon
KIF6	intron
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DAAM2	intron
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LRFN2	intron
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LOC101929555	non-coding RNA
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USP49	exon
BYSL	intron
CCND3	intron
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TRERF1	intron
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LOC107986596	non-coding RNA

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PTCRA	intron
CNPY3	non-coding RNA
PPP2R5D	intron
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PTK7	intron
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ZNF318	intron
ABCC10	intron
MRPS18A	intron
POLR1C	intron
POLR1C	intron
POLR1C	intron
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POLR1C	intron
SPATS1	intron
CDC5L	intron
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SUPT3H	intron
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[illegible]

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EFHC1	intron
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TRAM2	3utr
TRAM2	intron
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CILK1	intron
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GCM1	intron
ELOVL5	intron
GCLC-AS1	non-coding RNA
GCLC	intron
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KLHL31	intron
LRRC1	intron
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MLIP	intron
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TINAG	intron

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KHDRBS2	non-coding RNA
KHDRBS2	non-coding RNA
KHDRBS2	non-coding RNA
KHDRBS2	intron
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KHDRBS2	intron
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LGSN	3utr
none	intergenic
none	intergenic

[illegible]

[illegible]

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LINC02549	non-coding RNA
LINC02549	non-coding RNA
LINC02549	non-coding RNA
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ADGRB3	intron
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LMBRD1	intron
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COL19A1	intron
COL19A1	intron
COL19A1	intron
COL19A1	intron
COL19A1	intron
COL19A1	intron
COL9A1	intron
FAM135A	intron
FAM135A	intron
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SMAP1	intron
B3GAT2	intron
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RIMS1	intron
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KCNQ5	intron
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KCNQ5	intron
MTO1	3utr
none	intergenic
CD109	intron
CD109	intron
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none	intergenic

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LOC101928516	non-coding RNA
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COL12A1	intron
COL12A1	intron
COL12A1	exon
COL12A1	intron
COL12A1	intron
COL12A1	intron
COL12A1	intron
none	intergenic
FILIP1	intron
none	intergenic
SENP6	intron
SENP6	intron
SENP6	intron
MYO6	intron
MYO6	intron
MYO6	3utr
IMPG1	intron
IMPG1	intron
IMPG1	intron
IMPG1	exon
IMPG1	intron
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LINC02540	non-coding RNA
LINC02540	non-coding RNA
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MEI4	intron
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IRAK1BP1	intron

IRAK1BP1	intron
IRAK1BP1	intron
PHIP	intron
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PHIP	intron
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LCA5	intron
SH3BGRL2	non-coding RNA
SH3BGRL2	non-coding RNA
SH3BGRL2	non-coding RNA
none	intergenic
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TTK	intron
TTK	intron
BCKDHB	intron
BCKDHB	intron
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LINC02542	non-coding RNA
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LINC02542	non-coding RNA
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UBE3D	intron
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UBE3D	intron
DOP1A	intron
DOP1A	intron
DOP1A	intron
ME1	intron
ME1	intron
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ME1	intron
none	intergenic
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PRSS35	intron
SNAP91	intron
none	intergenic
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CYB5R4	intron
CYB5R4	intron
CYB5R4	intron
CEP162	intron
CEP162	intron
none	intergenic
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LINC01611	non-coding RNA
LINC01611	non-coding RNA
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TBX18-AS1	non-coding RNA
TBX18	intron
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none	intergenic

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NT5E	intron
SNX14	intron
SNX14	intron
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SYNCRIP	intron
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ZNF292	intron
ZNF292	intron
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CFAP206	intron
CFAP206	intron
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RARS2	intron
ORC3	intron
ORC3	intron
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LOC101928911	non-coding RNA
LOC101928911	non-coding RNA
LOC101928911	non-coding RNA
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CNR1	3utr
none	intergenic
none	intergenic

[illegible]

[illegible]

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EPHA7	intron
EPHA7	intron
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TSG1	non-coding RNA
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MANEA-DT	non-coding RNA
MANEA	intron
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FUT9	intron
FUT9	intron
FUT9	intron
FUT9	intron
FUT9	3utr
FUT9	3utr
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[illegible]

[illegible]

GRIK2	intron
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HACE1	intron
HACE1	intron
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LIN28B	intron
LIN28B	intron
BVES	intron
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PREP	intron
PREP	intron
PREP	intron

PREP	intron
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ATG5	intron
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CRYBG1	intron
CRYBG1	intron
CRYBG1	intron
CRYBG1	intron
CRYBG1	exon
CRYBG1	intron
CRYBG1	intron
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CRYBG1	intron
RTN4IP1	intron
none	intergenic
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LINC02532	non-coding RNA
LINC02532	non-coding RNA
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BEND3	intron
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PDSS2	intron
PDSS2	intron
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SOBP	intron
SOBP	intron
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SCML4	intron
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OSTM1	3utr
OSTM1	intron
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NR2E1	intron
AFG1L	intron

AFG1L	intron
AFG1L	intron
AFG1L	intron
none	intergenic
FOXO3	intron
FOXO3	intron
none	intergenic
ARMC2	intron
ARMC2	intron
CEP57L1	intron
CCDC162P	non-coding RNA
PPIL6	intron
ZBTB24	3utr
AK9	intron
AK9	intron
FIG4	intron
FIG4	intron
FIG4	intron
none	intergenic
WASF1	3utr
none	intergenic
SLC22A16	intron
SLC22A16	intron
SLC22A16	intron
none	intergenic
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CDK19	intron
AMD1	3utr
none	intergenic
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SLC16A10	intron
SLC16A10	intron
SLC16A10	intron
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REV3L	intron
REV3L	intron
REV3L	intron
FYN	intron
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FYN	intron
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LAMA4	intron
LAMA4	intron

[illegible]

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FRK	3utr
FRK	intron
NT5DC1	intron
NT5DC1	intron
NT5DC1	3utr
DSE	intron
DSE	intron
DSE	3utr
none	intergenic
RWDD1	intron
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KPNA5	intron
KPNA5	intron
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GPRC6A	intron
RFX6	intron
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ROS1	intron
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NUS1	intron
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SLC35F1	intron
SLC35F1	3utr
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CEP85L	intron
CEP85L	exon
CEP85L	intron
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[illegible]

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TBC1D32	intron
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PKIB	intron
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FABP7	intron
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TRDN	intron
TRDN	intron
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TRDN	intron

[illegible]

[illegible]

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LAMA2	intron
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ARHGAP18	3utr
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L3MBTL3	intron
L3MBTL3	intron
SAMD3	intron
SAMD3	intron
SAMD3	intron
TMEM200A	intron
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EPB41L2	intron
EPB41L2	intron
EPB41L2	intron
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AKAP7	intron
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MED23	intron
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ENPP1	intron
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LINC01013	non-coding RNA
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MOXD1	intron
MOXD1	intron
STX7	intron
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VNN1	intron
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VNN2	intron
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EYA4	intron
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TARID	non-coding RNA
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TARID	non-coding RNA
TBPL1	intron
SLC2A12	intron
SLC2A12	intron
SGK1	intron
SGK1	intron

[illegible]

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WAKMAR2	non-coding RNA
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LINC02865	non-coding RNA
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ARFGEF3	intron
PBOV1	exon
ARFGEF3	intron
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NHSL1	intron
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CCDC28A-AS1	non-coding RNA
CCDC28A-AS1	non-coding RNA
ECT2L	intron
ECT2L	intron
REPS1	intron
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HECA	intron
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FILNC1	non-coding RNA
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LOC103352541	non-coding RNA
LOC103352541	non-coding RNA
LINC02941	non-coding RNA
LINC02941	non-coding RNA

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NMBR	intron
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NMBR	intron
VTA1	intron
VTA1	intron
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ADGRG6	intron
ADGRG6	intron

LOC153910	non-coding RNA
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HIVEP2	intron
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HIVEP2	intron
none	intergenic
LINC01277	non-coding RNA
LINC01277	non-coding RNA
AIG1	intron
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none	intergenic
ADAT2	intron
PHACTR2	intron
PHACTR2	intron
PHACTR2	intron
PHACTR2	intron
PHACTR2	intron
LTV1	intron
LTV1	intron
ZC2HC1B	intron
ZC2HC1B	intron
PLAGL1	intron
PLAGL1	intron
none	intergenic
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UTRN	intron
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[illegible]

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SASH1	intron
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UST	intron
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PPIL4	intron
GINM1	intron
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PCMT1	intron
PCMT1	intron
RAET1E-LRP11	non-coding RNA
RAET1E-LRP11	non-coding RNA
RAET1E	3utr
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IYD	intron
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PLEKHG1	intron
PLEKHG1	intron
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MTHFD1L	intron
MTHFD1L	intron
MTHFD1L	intron
MTHFD1L	intron
none	intergenic
AKAP12	intron
ZBTB2	intron
ARMT1	intron
none	intergenic
ESR1	intron

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ESR1	intron
SYNE1	intron
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LINC02840	non-coding RNA
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FBXO5	intron
FBXO5	intron
RGS17	intron
RGS17	intron
RGS17	intron
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OPRM1	intron
OPRM1	intron

[illegible]

[illegible]

[illegible]

PACRG	intron
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PDE10A	intron
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[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

SDK1	intron
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SDK1	intron
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RNF216P1	non-coding RNA
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none	intergenic
WIPI2	intron
RNF216	intron
RNF216	intron
RNF216	intron
none	intergenic
ZNF815P	non-coding RNA
PMS2	intron
PMS2	intron
EIF2AK1	intron
USP42	intron
USP42	exon
CYTH3	intron
none	intergenic
PMS2CL	non-coding RNA
PMS2CL	non-coding RNA
LOC100131257	non-coding RNA
none	intergenic
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none	intergenic
LINC03016	non-coding RNA
LINC03016	non-coding RNA
LINC03016	non-coding RNA
none	intergenic
COL28A1	intron
COL28A1	intron
COL28A1	intron
UMAD1	intron
UMAD1	intron
UMAD1	intron
UMAD1	intron
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GLCCI1	intron
ICA1	intron
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ICA1	intron
ICA1-AS1	non-coding RNA
NXPH1	intron

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MGC4859	non-coding RNA
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none	intergenic

[illegible]

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ETV1	intron
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DGKB	intron
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AGMO	intron
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MEOX2	intron
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CRPPA	intron
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[illegible]

HDAC9	intron
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TMEM196	intron
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LOC101927668	non-coding RNA
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MACC1	intron
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ITGB8	intron
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ABCB5	intron
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LINC01162	non-coding RNA
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DNAH11	intron
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CDCA7L	intron
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RAPGEF5	3utr
STEAP1B	intron
none	intergenic
HYCC1	3utr
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KLHL7-DT	non-coding RNA
IGF2BP3	3utr
IGF2BP3	intron
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TRA2A	intron
CCDC126	intron
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STK31	intron
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PALS2	intron
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[illegible]

JAZF1	intron
JAZF1-AS1	non-coding RNA
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CREB5	intron
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CPVL	intron
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CHN2	intron
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WIPF3	intron
SCRN1	intron
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PLEKHA8	intron
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LOC105375218	non-coding RNA
ZNRF2	intron
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NOD1	intron
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MINDY4	intron
AQP1	intron
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ITPRID1	intron
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PPP1R17	intron
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PDE1C	intron
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LOC100130673	non-coding RNA
AVL9	intron
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DPY19L1P1	non-coding RNA
DPY19L1P1	non-coding RNA
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NT5C3A	intron
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BBS9	intron
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BMPER	3utr
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NPSR1-AS1	non-coding RNA
NPSR1-AS1	non-coding RNA

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GPR141	intron
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SFRP4	intron
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EPDR1	intron
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STARD3NL	intron
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AMPH	intron
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VPS41	intron
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POU6F2	intron
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RALA	intron
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CDK13	intron
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INHBA	3utr
INHBA-AS1	non-coding RNA
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GLI3	intron
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LINC01448	non-coding RNA
LINC01448	non-coding RNA
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[illegible]

[illegible]

[illegible]

[illegible]

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VOPP1	intron
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ZNF713	intron
ZNF713	intron
NIPSNAP2	intron
PSPH	intron
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LOC650226	non-coding RNA
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ZNF479	3utr
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ZNF736	intron
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INTS4P1	non-coding RNA
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ZNF92	intron
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LINC03006	non-coding RNA
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LINC03006	non-coding RNA

[illegible]

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GALNT17	intron
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CALN1	intron
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TYW1B	intron
TYW1B	intron
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GTF2IP4	non-coding RNA

[illegible]

MAGI2	intron
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GNAI1	intron
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SEMA3C	intron
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LOC105369146	non-coding RNA
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LOC100128317	non-coding RNA
LOC100128317	non-coding RNA
LOC100128317	non-coding RNA
LOC100128317	non-coding RNA
HGF	intron
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CACNA2D1	intron
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PCLO	3utr
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SEMA3E	intron
SEMA3E	intron

[illegible]

[illegible]

ZNF804B	intron
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STEAP2-AS1	non-coding RNA
STEAP2-AS1	non-coding RNA
STEAP2-AS1	non-coding RNA
STEAP2-AS1	non-coding RNA
STEAP2-AS1	non-coding RNA
CFAP69	intron
FAM237B	intron
GTPBP10	intron
PTTG1IP2	intron
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CDK14	intron
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AKAP9	exon
AKAP9	intron
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AKAP9	intron
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KRIT1	intron
none	intergenic
TMBIM7P	non-coding RNA
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PEX1	intron
PEX1	intron
CDK6	intron
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SAMD9L	intron
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HEPACAM2	intron
VPS50	intron
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CALCR	intron
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CASD1	intron
SGCE	intron
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PPP1R9A	intron
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PON2	intron
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DYNC1I1	intron
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SLC25A13	intron
SLC25A13	intron
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SEM1	non-coding RNA

SEM1	non-coding RN/
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ASNS	exon
LMTK2	intron
LMTK2	intron
BAIAP2L1	intron
BAIAP2L1	intron
none	intergenic
TRRAP	exon
TRRAP	intron
SMURF1	intron
SMURF1	intron
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SMURF1	intron
KPNA7	intron
BUD31	intron
ATP5MF-PTCD1	intron
ZKSCAN5	intron
none	intergenic
ZNF655	exon
CYP3A5	intron
CYP3A5	intron
none	intergenic
none	intergenic
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ZNF3	intron
TAF6	intron
STAG3	intron
STAG3L5P-PVRIG2P-PILRB	non-coding RN/
AGFG2	3utr

[illegible]

LHFPL3	intron
LHFPL3	intron
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LHFPL3-AS2	non-coding RNA
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KMT2E	intron
SRPK2	intron
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ATXN7L1	intron
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CDHR3	intron
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NAMPT	intron
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LINC02577	non-coding RNA
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[illegible]

[illegible]

[illegible]

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TES	intron
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CAV1	intron
MET	intron
MET	intron
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CAPZA2	intron
ST7	intron
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ASZ1	intron
ASZ1	intron
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CFTR	intron
CFTR	exon
CFTR	intron
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CTTNBP2	intron
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LINC02476	non-coding RNA
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CPED1	intron
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PTPRZ1	intron
AASS	intron
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CADPS2	intron
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SLC13A1	intron
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IQUB	intron
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LMOD2	intron
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WASL	intron
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GPR37	intron
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POT1	intron
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POT1-AS1	non-coding RNA
POT1-AS1	non-coding RNA

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LOC101928283	non-coding RNA
LOC101928283	non-coding RNA
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METTL2B	intron
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[illegible]

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LOC101928782	non-coding RNA
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PLXNA4	intron
PLXNA4	intron
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FLJ40288	non-coding RNA
FLJ40288	non-coding RNA
CHCHD3	intron
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none	intergenic
EXOC4	intron
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EXOC4	intron
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LRGUK	intron
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SLC35B4	intron
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AKR1B15	intron
BPGM	intron
BPGM	intron
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AGBL3	intron
AGBL3	intron
CYREN	intron
CYREN	intron
WDR91	intron
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CNOT4	intron
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NUP205	intron
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MTPN	3utr
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CHRM2	intron
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LOC349160	non-coding RNA
none	intergenic
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DGKI	3utr
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CREB3L2	intron
AKR1D1	intron
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TRIM24	intron
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KIAA1549	intron
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ZC3HAV1	intron
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UBN2	intron
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FMC1	intron
HIPK2	intron
HIPK2	intron
TBXAS1	intron
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KDM7A	intron
RAB19	intron
DENND2A	intron
BRAF	3utr
BRAF	intron
BRAF	intron
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TMEM178B	intron

TMEM178B	intron
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AGK-DT	non-coding RNA
DENND11	3utr
WEE2	intron
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OR9A4	intron
MGAM	intron
MGAM	intron
MGAM	intron
MGAM2	exon
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CASP2	intron
EPHA1-AS1	non-coding RNA
EPHA1-AS1	non-coding RNA
TCAF2	intron
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TCAF2P1	non-coding RNA
none	intergenic
TCAF1	intron
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TCAF1	intron
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OR2A25	intron
OR2A12	intron
ARHGEF35	intron
OR2A1-AS1	non-coding RNA
ARHGEF5	intron
TPK1	intron
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TPK1	intron

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CNTNAP2	intron
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CUL1	intron
EZH2	intron
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ZNF777	intron
ACTR3C	intron
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AOC1	intron
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NUB1	intron
PRKAG2	intron
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GALNTL5	intron
GALNT11	intron
GALNT11	exon
KMT2C	intron
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XRCC2	intron
ACTR3B	intron
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ACTR3B	3utr
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PAXIP1	exon
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INSIG1-DT	non-coding RN/
INSIG1	intron
LINC03010	non-coding RN/
CNPY1	intron
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RBM33	intron
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[illegible]

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FBXO25	intron
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FBXO25	intron
FBXO25	3utr
ERICH1	intron
ERICH1	intron
DLGAP2	intron
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ARHGEF10	exon
MYOM2	intron
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LINC03021	non-coding RNA
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LINC03021	non-coding RNA
LOC105377785	non-coding RNA

LOC105377785	non-coding RNA
LOC105377785	non-coding RNA
CSMD1	intron
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TNKS	intron
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MSRA	intron
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RP1L1	exon
RP1L1	intron
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LOC102723313	non-coding RNA
PINX1	intron
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PINX1	intron
XKR6	intron
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none	intergenic
MTMR9	intron
TDH	non-coding RNA
FAM167A-AS1	non-coding RNA
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CTSB	intron
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DEFB134	intron
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FAM66D	non-coding RNA
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[illegible]

SGCZ	intron
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MSR1	intron
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VPS37A	intron
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MTMR7	intron
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SLC7A2	intron
SLC7A2	intron

[illegible]

[illegible]

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KCTD9	intron
CDCA2	intron
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EBF2	intron
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PPP2R2A	intron
PPP2R2A	intron
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DPYSL2	intron
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PTK2B	intron
SCARA3	intron
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CCDC25	intron
ESCO2	intron
SCARA5	intron
NUGGC	intron
NUGGC	intron

ELP3	intron
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ZNF395	intron
FBXO16	intron
FZD3	intron
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EXTL3	intron
HMBOX1	intron
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KIF13B	intron
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LINC00589	non-coding RNA
LINC02099	non-coding RNA
LEPROTL1	intron
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RBPMS	intron
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GTF2E2	intron
GTF2E2	intron
GSR	intron
none	intergenic
TEX15	exon
TEX15	intron
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WRN	intron
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FUT10	intron
TTI2	intron
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LINC01288	non-coding RNA
LINC01288	non-coding RNA
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KCNU1	intron

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LINC01605	non-coding RNA
LINC01605	non-coding RNA
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LOC102723701	non-coding RNA
ADRB3	3utr
none	intergenic
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BAG4	intron
BAG4	intron
NSD3	intron
LETM2	intron
TACC1	intron
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TACC1	intron
none	intergenic
PLEKHA2	intron
ADAM9	intron
ADAM9	intron
ADAM9	intron
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ADAM5	non-coding RNA
ADAM5	non-coding RNA
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ADAM3A	non-coding RNA
LOC100130964	non-coding RNA
none	intergenic
ADAM18	intron
ADAM2	intron
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IDO2	intron

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ZMAT4	intron
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SFRP1	intron
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GOLGA7	3utr
GPAT4-AS1	non-coding RNA
GPAT4	intron
GPAT4	intron
ANK1	intron
ANK1	intron
KAT6A	intron
KAT6A	intron
KAT6A-AS1	non-coding RNA
none	intergenic
IKBKB-DT	non-coding RNA
IKBKB	intron
IKBKB	intron
POLB	intron
SLC20A2	intron
none	intergenic
none	intergenic
CHRNA3	exon
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RNF170	intron
HOOK3	intron
HOOK3	intron
HOOK3	intron
HOOK3	exon
FNTA	intron
none	intergenic
POTEA	intron

[illegible]

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PXDNL	intron
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PCMTD1	intron
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ST18	intron
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ALKAL1	intron
RB1CC1	intron
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ATP6V1H	intron
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RGS20	intron
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LYPLA1	intron
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RP1	intron
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RP1	intron

[illegible]

[illegible]

[illegible]

NKAIN3	intron
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GGH	intron
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CYP7B1	intron
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MTFR1	intron
PDE7A	intron
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DNAJC5B	5utr
DNAJC5B	intron
TRIM55	intron
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LINC00967	non-coding RNA
RRS1-DT	non-coding RNA
ADHFE1	intron
MYBL1	intron
MYBL1	intron
VCPIP1	3utr
SGK3	intron
SGK3	intron
SGK3	intron
none	intergenic
PPP1R42	intron
CSPP1	intron
CSPP1	intron
ARFGEF1	intron
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ARFGEF1-DT	non-coding RNA
CPA6	intron
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PREX2	intron

[illegible]

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LACTB2	intron
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MSC-AS1	non-coding RNA
TRPA1	intron
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LOC392232	non-coding RNA
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[illegible]

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LINC01111	non-coding RNA
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PEX2	intron
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LOC102724874	non-coding RNA
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IL7	intron

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STMN2	intron
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LOC101927040	non-coding RNA
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TPD52-MRPS28	intron
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PAG1	3utr
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FABP5	intron
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IMPA1	intron
CHMP4C	intron
LINC02235	non-coding RNA
LINC02235	non-coding RNA

[illegible]

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CA2	intron
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ATP6V0D2	intron
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WWP1	intron
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WWP1	intron
CPNE3	intron
CPNE3	intron
CNGB3	intron
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RIPK2	intron
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NBN	intron
DECR1	intron
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LINC00534	non-coding RNA
LINC00534	non-coding RNA
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TMEM64	intron
NECAB1	intron
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PIP4P2	intron
OTUD6B	intron
SLC26A7	intron
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RUNX1T1	intron
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LOC102724710	non-coding RNA
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TRIQK	intron
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LINC02906	non-coding RNA
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CIBAR1-DT	non-coding RNA
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CIBAR1-DT	non-coding RNA
CIBAR1	intron
TMEM67	intron
TMEM67	intron
TMEM67	intron
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CDH17	intron
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RAD54B	intron
RAD54B	intron
RAD54B	intron
ESRP1	intron
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INTS8	intron
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NDUFAF6	intron
NDUFAF6	intron
NDUFAF6	intron
PLEKHF2	intron
CFAP418-AS1	non-coding RNA
CFAP418-AS1	non-coding RNA
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GDF6	intron
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UQCRB	3utr
MTERF3	intron
PTDSS1	intron

PTDSS1	intron
PTDSS1	intron
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SDC2	intron
CPQ	intron
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LOC101927066	non-coding RNA
LOC101927066	non-coding RNA
none	intergenic
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MTDH	exon
MATN2	intron
MATN2	intron
MATN2	intron
MATN2	3utr
NIPAL2	intron
none	intergenic
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STK3	intron
STK3	intron
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VPS13B	intron
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VPS13B	intron
RGS22	intron
FBXO43	intron
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SPAG1	intron
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SNX31	intron
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YWHAZ	exon
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GRHL2	intron
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NCALD	intron
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RRM2B	intron
UBR5	intron
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LOC101927245	non-coding RNA
AZIN1	intron
MAILR	non-coding RNA
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BAALC	intron
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NUDCD1	intron
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PKHD1L1	intron
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EBAG9	3utr
SYBU	intron
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LINC01608	non-coding RNA
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[illegible]

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AARD	intron
SLC30A8	intron
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SAMD12	non-coding RNA
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SAMD12-AS1	non-coding RNA
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TNFRSF11B	3utr
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ZHX2	intron
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TBC1D31	intron
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FAM83A	3utr
ZHX1-C8orf76	intron
ZHX1	intron
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NTAQ1	intron
NTAQ1	non-coding RNA
FBXO32	intron
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ANXA13	intron
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FAM91A1	intron
FER1L6	intron
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FER1L6-AS2	non-coding RNA
FER1L6-AS2	non-coding RNA
FER1L6-AS2	non-coding RNA
LOC101927588	non-coding RNA
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TMEM65	3utr
TMEM65	intron
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RNF139	intron
MTSS1	intron
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SQLE	intron
NSMCE2	intron
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CCAT1	non-coding RNA
CASC8	non-coding RNA
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CASC11	non-coding RNA
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PVT1	non-coding RNA
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LINC00976	non-coding RNA
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CCDC26	non-coding RNA
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GSDMC	intron
CYRIB	intron
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ASAP1	intron
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EFR3A	intron

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LOC101927845	non-coding RNA
LOC101927845	non-coding RNA
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LINC01591	non-coding RNA
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KHDRBS3	intron
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LINC02055	non-coding RNA
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LINC02055	non-coding RNA

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LOC401478	non-coding RNA
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FAM135B	intron
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COL22A1	intron
COL22A1	intron
COL22A1	intron
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AGO2	intron
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AGO2	intron

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WASHC1	intron
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ZNG1A	intron
DOCK8	intron
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KANK1	intron

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SPATA6L	intron
CDC37L1-DT	non-coding RNA
CDC37L1	intron
CDC37L1	intron
AK3	3utr
AK3	intron
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JAK2	intron
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PDCD1LG2	intron
ERMP1	intron
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KIAA2026	intron
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IL33	intron
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UHRF2	intron
GLDC	intron
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[illegible]

[illegible]

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TYRP1	splice site
LURAP1L-AS1	non-coding RNA
LURAP1L-AS1	non-coding RNA
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MPDZ	intron
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NFIB	intron
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ZDHHC21	3utr
ZDHHC21	intron
FREM1	intron
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LOC389705	non-coding RNA
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TTC39B	intron
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SNAPC3	intron
PSIP1	intron
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CCDC171	intron
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CCDC171	exon
CCDC171	intron
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LINC03041	non-coding RNA
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BNC2	intron
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CNTLN	intron

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SH3GL2	intron
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SH3GL2	intron
SH3GL2	exon
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ADAMTSL1	intron
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SAXO1	intron
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DENND4C	intron
DENND4C	intron
DENND4C	intron
SLC24A2	intron
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MLLT3	intron
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MTAP	intron
CDKN2B-AS1	non-coding RNA
CDKN2B-AS1	non-coding RNA
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LINC01239	non-coding RNA
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CAAP1	exon
CAAP1	intron
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PLAA	intron
IFT74	exon
IFT74	intron
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TEK	intron
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LINC00032	non-coding RNA
MOB3B	intron
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[illegible]

[illegible]

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ACO1	intron
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B4GALT1	intron
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CHMP5	intron
NFX1	intron
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SUGT1P1	non-coding RNA
ANKRD18B	intron
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UBE2R2-AS1	non-coding RNA
UBE2R2	intron
UBAP1	intron
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FAM219A	intron
DNAI1	intron
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UNC13B	intron

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ATP8B5P	non-coding RNA
RUSC2	intron
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TMEM8B	3utr
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GLIPR2	intron
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RNF38	intron
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MELK	intron
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PAX5	intron
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ZCCHC7	intron
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FRMPD1	intron
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EXOSC3	3utr
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ANKRD18A	intron
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FGF7P3	non-coding RNA
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LOC102724580	non-coding RNA
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FGF7P6	non-coding RNA
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LINC01189	non-coding RNA
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FLJ43315	non-coding RNA
FLJ43315	non-coding RNA

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LOC101929583	non-coding RNA
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LOC105379443	non-coding RNA
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ZNF658	non-coding RNA
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CNTNAP3P2	non-coding RNA
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CNTNAP3P2	non-coding RNA
CNTNAP3P2	non-coding RNA
CNTNAP3P2	non-coding RNA
CNTNAP3P2	non-coding RNA
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none	intergenic

[illegible]

[illegible]

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RORB	intron
RORB	intron
TRPM6	intron
TRPM6	intron
TRPM6	intron
TRPM6	exon
TRPM6	intron
NMRK1	intron
none	intergenic
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PCSK5	intron
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GCNT1	intron
PRUNE2	intron
PRUNE2	intron
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PRUNE2	intron
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VPS13A	intron
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VPS13A	intron
VPS13A	intron
GNA14	intron
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GNAQ	intron
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LNCARSR	non-coding RNA
TLE4	intron
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LINC01507	non-coding RNA
LINC01507	non-coding RNA

LINC01507	non-coding RNA
LINC01507	non-coding RNA
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TLE1-DT	non-coding RNA
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RASEF	intron
RASEF	intron

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FRMD3	intron
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GKAP1	intron
KIF27	intron
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SLC28A3	intron
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NTRK2	intron
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NTRK2	intron
NTRK2	intron
NTRK2	3utr
NTRK2	intron
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AGTPBP1	intron
AGTPBP1	intron
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none	intergenic

[illegible]

SHC3	intron
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SHC3	intron
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LINC03062	non-coding RNA
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LINC01508	non-coding RNA
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LINC01508	non-coding RNA
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LINC01508	non-coding RNA
LINC01501	non-coding RNA
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AUH	intron
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ROR2	intron
ROR2	intron
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SPTLC1	intron
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IARS1	intron

IARS1	intron
IARS1	intron
IARS1	intron
OGN	3utr
OMD	exon
ECM2	intron
CENPP	intron
IPPK	intron
none	intergenic
ZNF484	intron
FGD3	intron
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PTPDC1	intron
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LOC107987099	non-coding RNA
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MFSD14B	intron
MFSD14B	intron
MFSD14B	intron
MFSD14B	intron
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AOPEP	intron
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AOPEP	intron
FANCC	intron
FANCC	intron
PTCH1	intron
none	intergenic
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ERCC6L2-AS1	non-coding RNA
ERCC6L2-AS1	non-coding RNA
ERCC6L2	intron

ERCC6L2	intron
LOC158435	non-coding RNA
none	intergenic
SLC35D2	intron
SLC35D2	intron
ZNF367	3utr
ZNF367	intron
HABP4	intron
CDC14B	intron
none	intergenic
ZNF510	intron
ZNF782	exon
ZNF782	intron
ZNF782	intron
MFSD14CP	non-coding RNA
MFSD14CP	non-coding RNA
none	intergenic
GAS2L1P2	non-coding RNA
ANKRD18CP	non-coding RNA
SUGT1P4-STRA6LP-CCDC180	non-coding RNA
SUGT1P4-STRA6LP-CCDC180	non-coding RNA
SUGT1P4-STRA6LP-CCDC180	non-coding RNA
TDRD7	intron
TDRD7	intron
TSTD2	exon
NCBP1	intron
XPA	intron
PTCSC2	non-coding RNA
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TRMO	intron
TRMO	intron
ANP32B	intron
GABBR2	intron
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ANKS6	intron
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COL15A1	intron
COL15A1	intron

COL15A1	intron
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LOC101928438	non-coding RNA
NR4A3	intron
NR4A3	exon
ERP44	intron
ERP44	intron
INVS	intron
INVS	intron
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INVS	intron
TMEFF1	intron
TMEFF1	intron
CAVIN4	intron
CAVIN4	3utr
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PLPPR1	intron
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PLPPR1	intron
GRIN3A	intron
GRIN3A	intron
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LINC00587	non-coding RNA

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CYLC2	intron
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LINC01492	non-coding RNA
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ABCA1	intron
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ELP1	intron
TMEM245	intron
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FRRS1L	3utr
FRRS1L	intron
EPB41L4B	intron
EPB41L4B	intron
EPB41L4B	intron
PTPN3	intron
PTPN3	intron
PALM2AKAP2	intron
PALM2AKAP2	intron
PALM2AKAP2	intron
PALM2AKAP2	intron
TXNDC8	intron
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SVEP1	intron
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MUSK	intron
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ECPAS	intron
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ZNF483	intron
SHOC1	intron
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SHOC1	intron

SHOC1	intron
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UGCG	intron
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PTBP3	intron
PTBP3	intron
KIAA1958	intron
KIAA1958	intron
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SLC46A2	intron
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SLC31A1	intron
RGS3	intron
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ZNF618	intron
ZNF618	intron
ZNF618	intron
ZNF618	intron
ZNF618	3utr
none	intergenic
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COL27A1	intron
COL27A1	intron
WHRN	intron
WHRN	intron
TEX48	intron
TNFSF15	intron
TNFSF15	intron
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DELEC1	non-coding RNA
DELEC1	non-coding RNA
DELEC1	non-coding RNA
DELEC1	non-coding RNA
DELEC1	non-coding RNA

[illegible]

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CDK5RAP2	intron
CDK5RAP2	intron
CDK5RAP2	intron
MEGF9	intron
MEGF9	intron
none	intergenic
FBXW2	intron
PHF19	intron
TRAF1	intron
none	intergenic
C5	intron
C5	intron
C5	exon
C5	intron
C5	intron
CNTRL	intron
CNTRL	intron

GSN	intron
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TTLL11	intron
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OR1L8	intron
OR1B1	intron
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PDCL	3utr
ZBTB26	3utr
RABGAP1	intron
STRBP	intron
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DENND1A	intron
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PSMB7	intron
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NR6A1	intron
NR6A1	intron
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NR6A1	intron
OLFML2A	intron
SCAI	intron
SCAI	intron
PPP6C	intron
PPP6C	intron
GAPVD1	intron

GAPVD1	intron
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MAPKAP1	intron
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PBX3	intron
PBX3	intron
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MVB12B	intron
MVB12B	intron
none	intergenic
LMX1B	intron
none	intergenic
ZBTB43	intron
ZBTB43	3utr
none	intergenic
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RALGPS1	intron
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GARNL3	intron
STXBP1	intron
CIZ1	intron
GOLGA2	intron
ODF2	intron
ZER1	intron
none	intergenic
PRRX2	intron
C9orf78	intron
FNBP1	intron
FNBP1	intron
HMCN2	intron
PRDM12	intron
EXOSC2	intron
ABL1	intron
ABL1	intron
LAMC3	intron
NUP214	intron
NUP214	intron

FAM78A	intron
PRRC2B	intron
PRRC2B	intron
none	intergenic
RAPGEF1	intron
MED27	intron
MED27	intron
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MED27	intron
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SETX	intron
SETX	exon
TTF1	intron
TTF1	intron
DDX31	intron
DDX31	intron
DDX31	exon
none	intergenic
RALGDS	intron
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VAV2	intron
VAV2	intron
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OLFM1	intron
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GLT6D1	intron
GLT6D1	intron
CAMSAP1	intron
none	intergenic
none	intergenic
CCDC183	intron
FAM166A	intron
EXD3	intron
PNPLA7	intron
EHMT1	intron
EHMT1	intron
CACNA1B	intron

[illegible]

[illegible]

[illegible]

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PNPLA4	intron
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ANOS1	intron
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TBL1X	intron
TBL1X	intron
GPR143	intron
SHROOM2	intron
SHROOM2	intron
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WWC3	intron
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CLCN4	intron
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MID1	intron

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TLR7	intron
LOC105373133	non-coding RNA
LOC105373133	non-coding RNA
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LINC02154	non-coding RNA
LINC02154	non-coding RNA

LINC02154	non-coding RNA
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RAB9A	intron
RAB9A	intron
GPM6B	intron
GPM6B	intron
GPM6B	intron
GEMIN8	3utr
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GEMIN8	intron
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GLRA2	intron
GLRA2	intron
GLRA2	intron
GLRA2	intron
GLRA2	intron
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FANCB	intron
FANCB	intron
MOSPD2	intron
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PIR	intron
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ACE2	intron
CLTRN	intron
none	intergenic
CA5BP1-CA5B	non-coding RNA
CA5BP1-CA5B	non-coding RNA
CA5BP1-CA5B	non-coding RNA

CA5BP1-CA5B	non-coding RNA
AP1S2	3utr
AP1S2	3utr
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REPS2	intron
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REPS2	intron
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NHS	intron
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SCML1	intron
RAI2	intron
LINC01456	non-coding RNA
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SCML2	intron
CDKL5	intron
CDKL5	intron
CDKL5	intron
PPEF1	intron
PPEF1	intron
PHKA2	intron
ADGRG2	intron
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ADGRG2	intron
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MAP3K15	intron

SH3KBP1	intron
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SH3KBP1	intron
BCLAF3	intron
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MAP7D2	intron
MAP7D2	intron
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SMPX	intron
SMPX	intron
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MBTPS2	intron
MBTPS2	intron
MBTPS2	intron

MBTPS2	intron
none	intergenic
SMS	intron
none	intergenic
PHEX	intron
PHEX	intron
PTCHD1-AS	non-coding RNA
PTCHD1-AS	non-coding RNA
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ZFX	intron
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PDK3	intron
PCYT1B	intron
POLA1	intron
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[illegible]

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IL1RAPL1	intron
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[illegible]

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LOC101928627	non-coding RNA
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[illegible]

[illegible]

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MAOA	intron
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MAOB	intron
NDP	intron
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EFHC2	intron
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KDM6A	intron
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ZNF674	intron
SLC9A7	intron
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LINC01545	non-coding RNA
JADE3	intron
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ZNF157	intron
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SYN1	intron
UXT	intron
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CXXC1P1	non-coding RNA
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ZNF81	intron
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SSX1	intron
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FTSJ1	intron
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ERAS	intron
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USP27X	3utr
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CLCN5	intron
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CCNB3	intron
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DGKK	exon
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SHROOM4	3utr
SHROOM4	intron
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MAGED1	intron
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SSX8P	non-coding RNA
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XAGE3	intron
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KANTR	non-coding RNA
KDM5C	intron
KDM5C	intron
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IQSEC2	intron
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HUWE1	intron
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FAM120C	intron
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WNK3	intron
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FGD1	intron
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PFKFB1	intron
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LINC01278	non-coding RNA
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ASB12	intron
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MTMR8	intron
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ZC4H2	intron
ZC3H12B	intron
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EDA	intron
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DGAT2L6	intron
KIF4A	intron
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GDPD2	intron
DLG3	intron
TEX11	intron
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MED12	intron
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TAF1	intron
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TAF1	non-coding RNA
OGT	intron
NHSL2	intron
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HDAC8	intron
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PHKA1	3utr
DMRTC1B	intron

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DMRTC1	intron
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CHIC1	intron
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TSIX	non-coding RNA
XIST	non-coding RNA
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JPX	non-coding RNA
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FTX	non-coding RNA
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SLC16A2	intron
RLIM	exon
RLIM	intron
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NEXMIF	intron
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ABCB7	intron
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UPRT	intron
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ZDHC15	intron
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TTC3P1	non-coding RNA
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MIR325HG	non-coding RNA
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FGF16	intron
ATRX	intron
ATRX	exon
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ATP7A	intron
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CYSLTR1	intron
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LPAR4	3utr
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GPR174	intron
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CHMP1B2P	non-coding RNA
CHMP1B2P	non-coding RNA
TENT5D	intron
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SATL1	intron
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POF1B	intron
POF1B	intron
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[illegible]

[illegible]

[illegible]

[illegible]

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PCDH19	intron
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SRPX2	intron
SYTL4	intron
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XKRX	intron
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TRMT2B	intron
TRMT2B	intron
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DRP2	intron
DRP2	intron
TAF7L	3utr
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GLA	intron
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ZMAT1	intron
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NXF2	intron
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NXF2B	intron
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ARMCX5-GPRASP2	intron
GPRASP3	3utr
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LINC00630	non-coding RNA
LINC00630	non-coding RNA
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NXF3	intron
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RAB40A	3utr
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PLP1	3utr
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FAM199X	intron
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IL1RAPL2	intron
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NRK	intron
NRK	intron
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PWWP3B	intron
PWWP3B	exon
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RADX	intron
CLDN2	intron
MORC4	intron
MORC4	intron
RBM41	intron
RBM41	intron
RBM41	intron
DNAAF6	intron
DNAAF6	intron
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FRMPD3	intron
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MID2	intron
VSIG1	intron
VSIG1	intron
VSIG1	intron
ATG4A	intron
COL4A6	intron
COL4A6	intron
COL4A6	intron

COL4A6	intron
COL4A5	intron
COL4A5	intron
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ACSL4	3utr
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TMEM164	intron
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AMMECR1	intron
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RTL9	intron
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CHRD1	intron
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PAK3	intron

[illegible]

[illegible]

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KLHL13	exon
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DOCK11	intron
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DOCK11	3utr
LINC01285	non-coding RNA
LONRF3	intron
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SLC25A43	intron
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NKAP	intron
RHOXF1-AS1	non-coding RNA
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TMEM255A	intron

[illegible]

[illegible]

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ELF4	intron
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ENOX2	intron
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FIRRE	non-coding RNA
FRMD7	intron
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RAP2C-AS1	non-coding RNA
MBNL3	intron
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HS6ST2	intron
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USP26	intron
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GPC4	intron
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GPC3	intron
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PHF6	intron
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PLAC1	intron
PLAC1	intron
PABIR3	intron
PABIR3	intron
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FGF13	intron
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F9	intron
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ATP11C	intron
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[illegible]

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IDS	intron
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MAGEA8-AS1	non-coding RNA
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MAMLD1	intron
MAMLD1	exon
MAMLD1	intron
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CD99L2	intron
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PASD1	intron
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GABRA3	intron

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DHRSX	intron
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RPS4Y1	intron
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ZFY	intron
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LINC00278	non-coding RNA
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PCDH11Y	intron
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[illegible]

[illegible]

[illegible]

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FAM41AY1	non-coding RNA
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FAM41AY2	non-coding RNA
TTY14	non-coding RNA
TTY14	non-coding RNA

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BCORP1	non-coding RNA
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TXLNGY	non-coding RNA
KDM5D	intron
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TTTY10	non-coding RNA
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RPS4Y2	intron
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TTTY4B	non-coding RNA
BPY2B	intron
BPY2C	intron
TTTY4C	non-coding RNA
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SPRY3	intron
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VAMP7	intron
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Patient Variant

chr2:210591885C>T

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chr1:207493876G>T

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chr1:243753175A>T

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chr18:2161222G>T

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chr1:78895991C>T

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chr1:109392882C>T

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chr1:193108170C>T
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chr1:223671528G>A

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chr10:30923920A>G

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chr10:127903029G>A

chr11:7596040T>C

chr11:13253692C>T

chr11:19987715A>G

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chr11:26059669A>G

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chr11:44850246G>C

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chr11:55409231A>G

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chr11:90479249A>G

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chr11:114323619C>G

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chr12:5548232T>G

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rs12393411
rs181368382

rs7876668

chromosome	location	aligned_sequence	orientation	distance
chr17	14085182	TGATTaTAAGCAaTAATGtAAGC	+	3
chr13	51941585	TGATaCcAAGCAGTAATGAATGT	-	2
chr10	106941006	aGATaCTAAGCAGTAAaG.AAGA	-	4
chr10	106941004	aGATaCTAAGCAGTAAaGAaGAG-	-	4
chr2	7733230	TGATcCTAAG.AGTAATGAAGGA	-	2
chr18	2161220	TaATTaTAAGaAGTAATGAACGC	+	3
chrX	94310326	T.ATaCTAAGCAGTAATaAATGC	+	3
chr2	88552100	TGATaCTgAGaAGTAATGAAGGA-	-	3
chr5	102333544	TGATTaGAAAGCAGTAATGAaGGG-	-	3
chr12	42377214	T.AcTCTAAGCAcTAATGAATGC	+	3
chr2	198087319	aGATTaTAAGCAtTAATG.AAGG	-	4
chr6	28319171	TGATTCTAAGaAGTAATaAAAGA	+	2
chr22	33548899	gacaTCTAAGCAGTAATGAaGAG/+	-	5
chr2	210591871	TGATTCTAAGCAGTAATGAAAGC-	-	0
chr21	39362120	acATTCTAAGCAGTAAaAAAGC	-	4
chr18	76326706	aGATTacAAGCAGTAATGtAtAGA	-	5
chr3	69014319	TaATTaTAAGCAGTAAT.AAAGT	-	3
chr5	29153508	aaAaTCTAAGCAGTAATGAtATGC-	-	4
chr15	76599707	TGATTCTAAtCAGTgATGAAAGA	+	2
chr16	46526806	gaATTCTAAGCAGTAATatAtGGA	+	5
chr8	122636882	TGATTC.AAGCAGTAAgGAAGGA	+	2
chr13	105960510	TGATTCTAAtgAGTAATGAAGGC	-	2
chr9	8207017	TctTTCTAAGCAGTAAaGAAAGC	+	3
chr3	96019253	TctTTCTAAGCAGTAATGgAAGA	+	3
chr4	29910267	TGATTaaAAGCAGTAATGAtgTGA-	-	4
chr5	68439834	T.ATTCTAAGCAGTAATGtgAGG	+	3
chr6	71690558	TatTTCTAAGCAGTAATGAAAGA	+	2
chr15	71407311	TGATcCTAAGCAGcAATaAAAGC	-	3
chr20	13784114	TGATTCT.AcCAGTgATGAAGGC	+	3
chrX	143455206	acATTCTAAGCAGTtAATaAATGC	+	4
chr10	24349863	gaAaTCTAAGCAGTAATGAAaAG(+	-	4
chr8	119822680	cagTTCTAAGCAGTgATGAAgTGC-	-	5
chr4	56229948	TaATTCTAAGCAGTAATattTGC	-	4
chr2	88552101	TGATaCTgAGaAGTAATG.AAGG	-	4
chr5	102333543	TGATTaGAAAGCAGTAATGAaGGG-	-	4
chr4	168790775	TGATaaTAAaCAGTAATaAAAGA	-	4
chr9	98969188	caATTCTAAGCAGTAATttATGG	+	4
chr5	68439835	ctATTCTAAGCAGTAATGtgAGGT	+	4
chr12	14009531	TGATTtaAAGCAGTAATGgAGGA	+	3
chr2	198087318	aGATTaTAAGCAtTAATGAAGGA	-	3
chr16	46526805	gaATTCTAAGCAGTAATatATGG	+	4
chr5	102333545	TGATTaGAAAGCAGTAATG.AGGG	-	3
chr22	33548897	gacaTCTAAGCAGTAATG.AAGA	+	5
chr5	92964369	TGATaaTAAGCAtTAATaAAAGC	-	4
chr10	62298418	TGATTCTAAtCAGTAAatAAAGA	+	3
chr10	24703809	TGAagCTAAGCAGTAAT.cAAGG	-	4
chr12	60336187	TGATTCTAAttAGTAATaAAAGA	-	3
chr6	139651459	aGATTacAAaCAGTAATG.AAGA	+	5
chr13	105960511	TGATTCTAAtgAGTAATG.AAGG	-	3
chr11	104272431	acATTCTAAcCAGTAATGtATGA	+	4

chr3	103377338 a.AcaCTAAGCAGTgATGAAGGA +	5
chr2	132665289 TGAcatTAAGCAGTAATGAAAGG -	3
chr2	196584625 gGATgCTAAGCAGcAATGgAATG(-	4
chr8	33172351 TGATcCTAAtCAGTAATaAAGGA +	3
chr9	72624464 gGcTTCTAAGCAGTAgtGAATGG -	3
chr6	138770135 TGATTcCTAAGCAGcAATGAATG(-	2
chr8	33172350 TGATcCTAAtCAGTAAT.AAAGG +	3
chr10	24703808 TGAagCTAAGCAGTAATcAAGGA -	3
chr10	128590290 aGAaTCTAAGCAGTAAT.AATGA -	3
chrX	12101653 TGATTc.cAGaAGTAATGAATGT +	3
chr11	23310308 TaATaCTAtGCAGTAATGAAAGA +	3
chr7	131268504 TGATTCTAtGCAGTAATtcAAGC +	3
chr20	46262546 TtAcTCTAAaCAGTAATGAATGA -	3
chr5	159669115 TtATTCTAAGtAGTgATGAAAGA -	3
chr13	47975528 T.tcTCTAAaCAGTAATGAATGC -	4
chr16	71935132 atA.cCTAAGCAcTAATGAAGGC +	5
chr2	210591871 TGATTCTgAGCAGTAATGAAAGC -	0
chr13	94810697 TGcTTaCTAAGCAGTAATGAgtGT(-	3
chr18	31525121 TGA.gCTAAGCAGTAATGAtGGT -	3
chr4	183698555 TGAcTCTAAGaAGTgATGAAaGG(-	4
chr4	105489466 T.tccCTAAGaAGTAATGAAGGA -	5
chr5	93612876 TGcTgTCTAAGCAGTAATGAcTGT(-	3
chr12	14009530 TGATTtaAAGCAGTAATG.gAGG +	4
chr8	89001651 TacTaCTAAGCAGTAATcAAGGC +	4
chr14	75771561 TccTTCTAAGCAGTAcATGAAGGT(-	3
chr9	114797502 TGATaggAAGCAGTAATGAATGA +	3
chr7	95815050 TGAagCTAAGCAGTAATGAcACG(-	3
chr9	69177156 TGAcTCTAAGCAGTAAT.cAGGG +	3
chr1	198803213 accTTtTAAGCAGTAATGAaAgAGT -	5
chr9	13154688 TGATT.actGCAGTAATGAAAGC +	4
chr20	531898 attTTCTAAGCAGTAATGtgAGGC -	5
chrX	5844979 TatcTCTAAGCAGTAaGAaAGGT(-	5
chr2	2481322 TGAcTCaAAGCAGTAATaAAgTGT+	4
chr10	98353396 TGATT.aAAGCAGaAATGAAAGA +	3
chr7	95118627 TGgTTaTAAGtAGTAATGtATGA +	4
chr5	71257683 TcA.TCTAAGCAGgAATGAATGC +	3
chr2	132665288 TGAcatTAAGCAGTAATGAAaGGT(-	4
chr11	38405975 gcATTCTAAaCAcTAATGAAGGC -	4
chr8	103195894 TGATaCcAA.CAGTgATGAATGC +	4
chr3	35964693 TGATTaTAtaCAGTAATaAAGGG +	4
chr10	3903015 TGATTcCTAAGCAGaAATGAAGG +	2
chr14	71303380 aGtTTCTAAGaAGTAATGAgtAGG(+	4
chr2	56536807 TGAaTCTAAGCAGTgATtAatGGA+	4
chr8	91428678 TGATaaTAAaGCAGTAATGAtTGT -	4
chr13	59092808 gtAcTCTAAGCAGgTAATGAAAGT(-	4
chr3	35964694 TGATTaTAtaCAGTAATaAAgGGG+	5
chr6	26923611 TGccaTCTAAGCAGgAATGAATGC(+	4
chr10	128590288 aGAaTCTAAGCAGTAATaAtgAGC(-	5
chr2	50480856 aGATTCaAAGCAGTAA.GgAAGA -	4
chrX	90582651 TaATTacAAGCAGTAATGAgtGGA -	4
chr14	99778818 gatTTCTAAaCAGTAATGAtAGGA -	5

chr18	28430785 TaATTCTAAcCAGTAAT.AAAGG -	3
chr10	37410204 T.ATTCaAAGCAaTAATGAATGA +	3
chr5	70553711 TcA.TCTAAGCAGgAATGAATGC +	3
chrY	4160398 TaATTacAAGCAGTAATGAgGGA -	4
chr3	35964692 TGATTaTataCAGTAAT.AAAGG +	4
chr18	28430784 TaATTCTAAcCAGTAATaAAGGA -	3
chr3	28647017 TtAaTCTAAGCAGTgATG.AAGA -	4
chrX	74492655 TGATT.agAGCAGTAATGAATGA -	3
chr10	82028855 TGATTCTcAGCAGTtATGAAAGT -	2
chr5	38430473 TGtTaCTAAGCAGTAATtAgTGT +	4
chr5	70257375 TcA.TCTAAGCAGgAATGAATGC +	3
chr16	49741759 TcA.gCTAAGCAGTgATGAAAGT +	4
chr7	130096728 TaAcaTaTAAGCAGTgATGAAGGT-	5
chr8	89001650 TacTaCTAAGCAGTAAT.caAGG +	5
chr19	31131287 aG.gcCTAAGCAGTAATGAATGG -	4
chr9	69177157 TGAcTCTAAGCAGTAATcAgGGG +	3
chr20	54569344 TaATTCTAAGtCAGTAATtAATGG +	3
chr11	23819014 gtATTCTAAGaAGTAAT.AAAGA +	4
chr9	10481625 TGATT.aAAGaAGTAATGAcAGC +	4
chr14	26538248 TGAaTCTAAGtAGTAATcAAAGA +	3
chr18	71192166 TGATTaaAAaCAGTAATcAAGGC -	4
chr1	173744099 TcATTCTAAcCAGTAATatATGA +	4
chr14	47343292 aagTTCTAAGtAGTAATGAgACGC+	5
chrX	90582652 TaATTacAAGCAGTAATG.AGGG -	4
chr14	78582297 c.AacCTAAGCAGTAATGgAGGA -	5
chr8	35134229 TGATTCatAGCAGcTAATGAAAGA+	3
chr9	69177158 TGAcTCTAAGCAGTAATcAggGG(+	4
chr5	69677638 TcA.TCTAAGCAGgAATGAATGC +	3
chrX	99977466 TagaTaTAAG.AGTAATGAAAGA -	5
chr3	116794546 catTTCTAAG.AGTAATGAATGT +	4
chr14	91205120 TGATTCTAAagAGTAATaAgAGC +	4
chr17	52735306 TaAcTCTAAaCAGTAATGtATGT -	4
chr14	99778819 gGATTtCTAAaCAGTAATGAtAGG-	4
chr5	34216789 TcA.TCTAAGCAGgAATGAATGC +	3
chr1	232678835 T.tcTaTAAGCAGTAATGAATGC -	4
chr10	21381244 aGATTCTAAGCAGTAA.GAAAGC -	2
chr9	72624463 gGcTTCTAAGCAGTAgtGAAtGG(-	4
chr13	58498225 gGA.TCTAAaCAGTAATGAAAGA +	3
chr21	20131792 aGtTTCTAAGaAGTAATGAtAAGT +	4
chr10	56324290 TGATgCcAAGCAGTAATGAAGGA-	2
chr6	160766287 TGATTtaAAGaAGTAATaAAGGA -	4
chr16	61032968 ctATTCTAAGCAGTAAGaAtATGC +	5
chr2	2481320 TGAcTCaAAGCAGTAAT.AAAGT +	3
chr10	96683552 gGATTCTAAGtAGcAATGgAATGA-	4
chr13	59089343 atcTTCTAAG.AGTAATGAATGA -	4
chr5	55692828 TaAaTaTAAGCAcTAATGAATGC -	4
chr5	69876804 TcA.TCTAAGCAGgAATGAATGC -	3
chrY	4160399 TaATTacAAGCAGTAATG.AGGG -	4
chr2	56300994 TtA.TaTAAGCAGTgATGAATGG +	4
chr4	29910269 TGATTaaAAGCAGTAATG.ATGT -	3
chr2	76472633 TGATagTAAGCAGTAAT.AtTGG +	4

chr12	89074645 TGATTaTAAGCAaTcATG.AAGG -	4
chr4	183698556 TGAcTCTAAGaAGTgATGAAAGG -	3
chr3	60110417 TGATTCTAAGgAGTgATtAAAGC +	3
chr5	55411614 TGATTCTAAAtCAGTAATcAgGGA -	3
chr7	133338228 T.ATTCaAAGCAGTgATGAATGA -	3
chr6	160521284 TGATTtaAAGaAGTAATaAAGGA +	4
chr12	92630949 T.cTTCTAAcCAGTAATcAATGC +	4
chr8	66973038 TGATTaaAtGCAGTAATGtATGT +	4
chr7	16000188 TGATTaTAAG.AGTAATaAATGC -	3
chr16	85790536 TtgTTCTAAGCAGcAATaGAAAGC-	4
chr3	78011514 T.ATTCTAAGCAGaAAgGAAAGC -	3
chr4	158509742 gaAaTCTAAGCAGTAATG.AGGC -	4
chrX	127326066 gGATTCaAAaCAGTAATGAAGTG/+	4
chr9	2523608 TGgTTCTAAGCAGTtATGAgAGG +	3
chrX	5844980 TtATcTCTAAGCAGTAAaGAAAGG-	3
chr6	144389901 TtATTaTAAG.AGTAATGAAGGA -	3
chr1	24022747 aGATTaTAtGCAGTAATGAgGGG -	4
chr5	145132491 acAcTCTAAGCAGgTtATGAATGC -	5
chr15	94410707 TtATcCTAAGCAGTAAGGAtATGC -	4
chr6	163645654 TGATTCaAtGCAGTAATtAACGT +	3
chrX	83324803 TaATTtTAAGCAGTAATaAgTGT -	4
chr5	70752717 TcA.TCTAAGCAGgAATGAATGC -	3
chr3	188324604 aGATTCaAAaGaAGTAATGAtAGC-	5
chr5	18991974 aaATgCTAAGaAGTAATGAAAGC -	4
chr12	68339096 aGATTCaTAAGCAaTAATaAATGC-	4
chr11	98721934 aGA.TCTAAGCAGTtATaAAAGC +	4
chr5	125680622 aGATTaTAAaCAGTAAGGAAGGG/+	5
chr1	24022748 aGATTaTAtGCAGTAATG.AGGG -	4
chr15	40747766 TacTctTAAGCAGTAATGAAGGA +	4
chr4	139286223 TGATTCT.ttCAGTAATGAAAGA -	3
chr10	56324291 TGATgCcAAGCAGTAATG.AAGG -	3
chrX	63259188 TaATTtTAAGaAGTAATGAATGC -	3
chr8	24653755 T.ATTCaAAGCAGTAATGAtTGT +	3
chr11	106436351 TaATaTCTAAGCAGcAATGAATGC+	3
chr3	116167665 aGAaTaTAAGCAGTAATcAAGGC +	4
chr1	159129699 TGATaaT.AGtAGTAATGAAAGT -	4
chr8	33681794 TGATTCTAA.tAGTAATaAgAGC -	4
chr9	34456813 c.tgTCTAAGCAGTcATGAAAGG +	5
chr2	37998054 a.AcTCTAAGCAGTAATatATGT +	5
chr5	28867713 TacATTCTAAGCAGTgATcAtTGC +	5
chr5	55411615 TGATTCTAAAtCAGTAAT.cAGGG -	3
chr12	89074644 TGATTaTAAGCAaTcATGAAGGG -	3
chr15	80583544 TGATaaTAA.tAGTAATGAtAGC +	5
chrX	79459162 TaAaTCTAAaCAGTAATGtATGT -	4
chr1	103807329 aGcTTCTAAGaAGTAATaAATGA +	4
chr14	52567619 TGAaTgTAAGCAGTgATGAACGC -	3
chr7	120928494 c.tTaCTAAaCAGTAATGAATGA -	5
chr2	184617623 aaATTCTAAaCAGTgATGAAAGT -	4
chr14	38007078 aaATTaTAAGaAGTAATGAATGC +	4
chr1	24022746 aGATTaTAtGCAGTAATGAggGGC-	5
chr16	69616350 atAacCTAAGCAGTAATG.AGGA -	5

chr1	73675952 aaATcTCTAAGCAGTAATtAAAGG-	4
chr2	123150227 T.tTaaTAAGCAGTgATGAAGGA -	5
chr3	30966851 caATTcCaaAGCAGTAAGGAAGGA +	4
chr6	62978683 TGccTTCTAAGtAGTAATaAAAGT +	4
chr1	198803215 accTTtTAAGCAGTAATG.AAGA -	5
chr1	62684618 TGATaCTcAGCAGTAATG.ATGA -	3
chr3	64616861 caATTtCTAAGCAGTgATGAgTGA-	5
chr9	98969189 caATTCTAAGCAGTAATttAtGGG +	5
chr18	27363813 TtATTCaTAAGCAGatATGAATGC -	4
chr11	38405976 gcATTCTAAaCAcTAATG.AAGG -	5
chr4	81002878 TcAcTaTAAGCAGTtATGAAGGC +	4
chr5	137707031 TGATgCTtAAGCAGTAATGAAGG/+	2
chr7	33042480 TatcTCTAAtCAGTAATG.AAGA +	5
chr10	1731371 TGATaCTAAGaCAGTAAtATGC +	5
chr5	89944441 TGcaTaTAAGaAGTAATGAATGG -	4
chrX	148981098 TGATTC.ActCAaTAATGAAAGA +	4
chr4	160590690 TaAaTaCTAAGtAGTAATaAAAGA +	5
chr20	16331864 T.AaTaTAAGCAcTAATGAgAGC +	5
chr6	160766288 TGATTtaAAGaAGTAAT.AAAGG -	4
chr13	85349177 TtAgaaTAAGCAGTAATGAAtAGT -	5
chr8	55994344 aGATTcCAaCAGTAATtAAAGC -	4
chr10	127903012 TGATaaTAAGCAaTAAaGAATGA +	4
chr11	19987704 aGcTTCTAAGaAGTAATaAATGA +	4
chr10	96466784 TtA.TCTAAtCAGTAATGtATGC +	4
chr10	14207849 TGATT.acAGaAGTAATGtATGC -	5
chr3	54521200 TGATTCTcAcCAGTAATGtATGT +	3
chr10	126121709 atA.TgTAAGCAGTAATGAATGA -	4
chr5	23002823 T.ATataAAGCAGTAATGtAGGT +	5
chr13	71570261 cGATTCTAAGCAGTtATagATGC -	4
chr5	155857439 aaATaCTAAGCAGcAATGAAaGG/+	5
chr6	21546527 TGATTgcAAGCAGTAATGctATGC-	4
chr2	28761512 TG.TaCTAAGCAaTAATGAcGGC -	4
chr9	107046975 TtAaT.aAAGCAGTAATGAgTGC +	5
chr4	89729108 TtcTcaCTAAGCAcTAATGAAAGA +	5
chr11	57726497 TaATTtTAAGaAGTAATGAATGC +	3
chr3	81518412 aGATTaTAgGCAGTAATGAAtAGT-	4
chr2	56536806 TGAaTCTAAGCAGTgATtAATGG +	3
chr12	37841516 TGATaCTAAGCAGTgAgaAAAGG-	4
chr5	125680621 aGATTaTAAaCAGTAAGGAAGGG+	4
chr16	71068014 TGgagtTAAGCAGTAATGAAtTGC+	5
chr5	29462621 aGtTaCTAAGCAGTtAATGAAAGT+	4
chr10	132678338 TaGATTaTAAaCAaTAATaAATGA -	5
chr1	76029167 TGtTTCTAAttAGTAATGAAAGT +	3
chr2	17253827 aGATTCTAAGCAGcAATtAAAGG +	3
chr6	92638542 TGATagaAAGCAGTAATcAAAGA -	4
chr8	113351437 TGATaCTAAGgAaTAATGAAaAG/+	4
chr9	74783103 TttgTtTAAGCAGTAATGAAtTGT +	5
chr5	125680620 aGATTaTAAaCAGTAA.GgAAGG +	5
chr9	3942121 T.ATTCaAAGCAGTAATaAcAGC +	4
chr18	38681955 T.cTatTAAGCAcTAATGAAAGA +	5
chr6	121364352 TGATTCT.AGtAcTAATGAAGGT +	3

chr2	98814249 TGtTTCaAAGCAGTAATttAAGC	-	4
chr4	28326943 TGAgaataAAGCAGTAATGAaGAG/-		5
chr9	18299467 ctgTTCTAAGCAaTAAT.AAAGA	-	5
chr12	115168669 TGATTgcAAGCAtTAATGAATGC	-	3
chr3	115758510 TcAgTCTAAGtAGTAATaAATGG	-	4
chr17	8916843 gGtTTCTAAatAGTAATGAAAGG	+	4
chr4	13091088 aGATaCTAAGCA.TAATaAAAGA	+	4
chr6	160521283 TGATTtaAAGaAGTAAT.AAAGG	+	4
chr1	172608153 atATcaCTAAGCAaTAATGAATGA	-	5
chr15	49676664 atATcaTAAGCAGTAATG.AAGT	-	5
chr2	194778492 TaAaTTaTAAGCAaTAATaAAAGC	+	5
chr10	105639992 TaATTCaAAGCAGTgAT.AAAGA	-	4
chr10	104896552 TGATTC.AAGaAGTAATGAaGAGA	+	3
chr13	91359595 a.AcTCTAAGCAGTtATGtATGC	-	5
chr6	140273726 TGtTTCTAAGCAGaAATtAAGGC	-	3
chr5	36418781 TGATTC.AAaCAaTAATGAtGGC	-	4
chr11	89409112 a.ATaCTAAGaAGTAATGgATGC	-	5
chr8	112959313 atATTCTAAGaCAaTAATGAAGGT	+	4
chr6	23969180 TGATTCTAAattAGTAATGAcTGC	+	4
chr20	531899 T.tTTCTAAGCAGTAATGtgAGG	-	4
chr4	73221089 T.tTTCTAAGtAGTAATaAAAGA	-	4
chr9	9145345 TaATTaTAAGCAaTAATcAAAGG	-	4
chr21	20707788 T.ccTCTAAGaAGTAATGAtAGA	-	5
chr7	49502145 caATTCTAAGCAaTAATtGAATGC	-	4
chr12	60820228 TGATaCTAAG.AGaAATGAATGA	+	3
chr6	33054452 aGA.TgTAAGCAGTAATGtATGG	+	4
chr3	103143984 gcAcTCTAAGCAGTAgtTG.AAGA	-	5
chr5	42803367 aaATaCTAAG.AGTAATGAAAGA	-	4
chr18	8592181 TGATaCTAAtCAGcAATGAtAGC	+	4
chr5	85914607 TGAcaCTAAGCAGTAATttgAAGC	-	5
chr1	166138815 ctATTCTAAGCAaTAATG.ATGC	-	4
chr13	58641008 TtA.TaTtAGCAGTAATGAtAGT	-	5
chr8	138201089 TGtgaCTAAGCAGaAATGAAAGC	+	4
chr15	29292945 TaATaCTAAGCAGTAAtTGAaAAGC	-	4
chr18	6402899 TGATTaTttGCAGTgATGAAAGA	-	4
chr3	115758509 TcAgTCTAAGtAGTAATaAAtGGG	-	5
chr2	107701687 T.tTTCaAAGCAGTAATGAATGC	+	3
chr11	100693293 TGATTaTAAGaAGTAaAaTGAATGC	-	3
chr14	71303379 aGtTTCTAAGaAGTAATGAaAGG	+	4
chr5	75737801 TGATTaTAA.aAGTAATaAATGC	+	4
chr10	105043144 TtA.TCTAAGaAGTAATGAgtGT	-	4
chr3	180119078 TatTTCTAAGCAGTAaAaGgATGC	-	4
chr3	116167664 aGAaTaTAAGCAGTAAT.cAAGG	+	5
chr21	18061347 atA.TaTAAGCAGTAATGtAAGG	+	5
chr21	18061348 TataTaTAAGCAGTAATGtAAGGG	+	5
chr1	216922386 gcAgT.TAAGCAGTAATGAaGGA	+	5
chr15	40747765 TacTctTAAGCAGTAATG.AAGG	+	5
chr10	16955659 c.ATagTAAGCAcTAATGAATGG	-	5
chr1	99525354 TaATTCTAAtCAaTAATGAtATGA	+	4
chr1	82895852 aGATTCTAAaCcAGTAATGtATGA	-	4
chr1	168658192 TGATaaTAAGCAaTAATaAAtAGC	-	5

chr6	119080098 cG.TTCTAAGCAGaAATGtATGC +	4
chr10	72870145 aGATTaTAAGgAGTAA.GgAAGG +	5
chr10	93209355 aGATTaTAAGCAGTAA.GAAAGA -	3
chr8	17959893 aGATT.aAAGCAGTAAaGAAAGC -	4
chr5	92045469 TtATcCTAAGCAaGTAATGAAGGA-	3
chr14	38228862 TGATagTAAatAGTAATG.AAGA -	5
chr2	51546416 TttTTCTAAGCAGaAATaAAAGC +	4
chr11	8796203 gGATTCT.AtCAGTAgtGAAGGC -	4
chr6	55567907 gGtTTCTAAaCAaTAATGAAGGG -	4
chr5	150638144 c.ATTCTAAGCAaTgATGAtAGC -	5
chr9	86880734 T.AacaTAAGaAGTAATGAAAGT +	5
chr2	17253828 aGATTCTAAGCAGcAATtAAaGGT+	4
chrY	13512008 TGAaaCTAAGCAGTAATtAcAGGA+	4
chr14	41452496 aGA.TaTAAGaAGTAATaAATGC +	5
chr12	37841515 TGATaCTAAGCAGTgAgaAAaGG(-	5
chr15	49761284 TcA.aaTAAGCAGTAATGAcAGC +	5
chr6	22552869 TtgTTCTAAGCAcTAATG.AAGC -	4
chr2	36833720 TGATTaTAAaaAGTAATaAATGT -	4
chr8	59708548 TGATTgCaAAGCAGaAATGAAAG-	3
chr1	194793130 T.AagCTAAaCAGTAATGAATGT -	4
chr12	127250445 TGATTCTAAtCcAaTAATGAAGGT-	3
chr8	65709174 TGgaT.TAAGCAaTAATGAAAGC +	4
chr6	2119493 TtATTCTAAGaAcTAATGAAAGC +	3
chr17	8916844 gGtTTCTAAatAGTAATGAAaGGA+	5
chr4	92711231 T.tTaaTAAGCAGTAAGGAATGA -	5
chr18	55010794 TGATTCTAcaCAGTAgtGtATGC +	4
chr8	92672487 TcAgTgCTAAGCAGTAAGGAAGG-	4
chr5	123104159 TtAagCTAAGCAGTAATG.ATGA -	4
chr8	93197076 TcATgaTAAGCAcTAATGAATGT -	4
chr18	32984099 TacaTCTAAGCAGTtAATaAAAGC -	5
chrY	19601192 TaAgTCTAAaaAGTAATGAAGGT -	4
chr18	71192167 TGATTaaAAaCAGTAAT.cAAGG -	5
chr1	211674689 cagTTCTAAGCAGTAAaTgtATGT +	5
chr7	142653998 aaAcTCTAAGCAGTAgtTG.AAGA +	5
chr9	24489062 TcAaatTAAGCAGTAATGAATGC -	4
chrX	7277659 TGATTCTAtaaAGTAATGAgtAGT +	4
chr5	146647213 TGcTTCTAAGCAaTAgtGAATGT -	3
chr2	63159812 TGATTCTAAcCAGTAAtaTaAAAGA-	3
chr15	29819065 TGATaCTAAaGaAGTAATaAAGG(-	4
chr10	80905064 TGATaCTAAtCAGTAAT.AtTGG +	4
chr4	96821215 gtATgCaTAAGCAGTAATGAAAGT-	4
chr3	118129059 TtATTCTAAGaAGTAAT.AAAGC -	3
chr5	155857438 aaATaCTAAGCAGcAATGAAAGG +	4
chr10	61790928 TGATTCaAgGaAGTAATtAAAGC -	4
chr9	9145344 TaATTaTAAGCAaTAATcAAaGGA-	5
chr10	72870147 aGATTaTAAGgAGTAAGGAAGGG+	5
chr2	95993162 aaATTCTAAGgAGTAAGGAATGC +	4
chr21	19827585 TtAaTaTAAaGCAGTAAGGAATGC+	5
chr5	22467604 TtATTCTAAGCAcTgATGAATGG -	3
chr4	134194889 TGATTtTAAG.AGTAATGgAAGG +	3
chr2	83152573 TcATgTCTAAGCAGTtATaAAGGT +	4

chr3	180302024 TG.ggCTAAGCAGTAATGgAGGA -	4
chr17	69291492 cGA.TaTAAaCAGTAATGAAAGT +	4
chr1	146642927 TGgagtTAAGCAGTAATGAAtTGC-	5
chr10	72870146 aGATTaTAAGgAGTAAGGAAGGG+	4
chr7	15752517 TGATaCTAAG.AaTAATaAATGC +	4
chr9	29597727 TGATaaTAAGCtGTAATaAATGA -	4
chrX	135859974 atcTTCTAAGCAGTAATG.gTGC +	5
chrX	5656655 aG.TgaTAAGCAaTAATGAATGC +	5
chr5	127874962 gGtTTtTAAGCAGTAATGAACAGG-	4
chr2	22630248 TccTTCTAAGaAGgTAATGAtAGC -	5
chr9	2523609 TGgTTCTAAGCAGTtATGAgAGG(+	3
chr1	91034672 gaATaCTAAaCAGTAAT.AAAGA +	5
chrY	13512007 TGAaaCTAAGCAGTAATtAcAGG +	4
chr4	80882182 TGATTtaAAGCAaTAATGAtGGA +	4
chr18	48913991 aGA.TCccAGCAGTAATGAgTGA -	5
chr3	103145276 TaATTCaAAGCAGTAAtTaAAAGC -	4
chr5	89944440 TGcaTaTAAGaAGTAATGAAtGGA-	5
chr10	103679776 ctATgCTAAGCAGTgATGAcAGGC-	5
chr2	68938444 TGATaacAA.CAGTAATGAATGC -	4
chrX	135825437 atcTTCTAAGCAGTAATG.gTGC +	5
chr4	28326945 TGAgataAAGCAGTAATG.AAGA -	5
chrX	118646782 TaATTCTAtGCAGaTAATGAATGC-	3
chr2	97591168 aaATTCTAAGgAGTAAGGAATGC +	4
chr3	132220586 aGcTaCTAAG.AGTAATGAAAGA +	4
chrX	74325664 TGATT.agAGCAGTAaGAATGC +	4
chr5	22467603 TtATTCTAAGCAcTgATGAAtGGT -	4
chr7	88409482 TcATTtTAAGCAtTAATGAAAGC -	3
chr2	72456140 acATTaCTAAGtAaTAATGAATGC +	5
chr2	4365632 aGATT.aAAGCAGTAATaAATGA -	4
chr1	208049898 aG.gTCaAAGCAGTAATGAtAGT +	5
chr13	103331266 TGcTTCTAgGCAGTAATGAAtAGA-	3
chr9	5828919 ccATTtCaAAGCAGTAATaAATGT -	5
chr4	81002877 TcAcTaTAAGCAGTtATG.AAGG +	5
chr5	100031084 aGA.TaTtAGCAGaAATGAATGA +	5
chr9	122557256 atATTCaAAaGCAGTAATGAgGGC+	5
chr9	69431798 TGATTgatAGCAGTgATGAATGA +	4
chr16	79803968 T.ATTCTtAGCAGTAATGtATGA +	3
chr22	34061590 T.ATTtTAAGCAGTAATGgATGT -	3
chr16	67058735 aGAacCTAAGgAGTAATGAATGA +	4
chr1	196214341 TtATTCTAAG.AGTAATaAAAGG +	3
chr9	118970081 aGATTaCaAAGaAGTAATGAgGG,-	5
chr12	25111833 TctTTCaAAGCAaTAATGAAAGG +	4
chr12	114950635 TGA.TaacAGCAaTAATGAAAGT -	5
chr15	89838339 T.AaTCTAAGCAGTAAGaAATGA -	4
chr5	96344850 T.tgTgTAAGCAaTAATGAAAGA -	5
chr2	97112265 aaATTCTAAGgAGTAAGGAATGC -	4
chr1	194817761 aGAaTCTAAaCAGTAATGAgtAGT+	5
chrX	97042145 aaATTCTAAGCAGTgATtAAtGGA -	5
chr19	11006744 TacTTCTAAttAGTAATGAAAGT +	4
chr16	51659549 TGA.TaagAGaAGTAATGAAGGA +	5
chr4	20350515 TGcAaaaTAAGCAGTAATGAtAGC-	5

chr4	59434504	TagaTCaAAGCAGTAAT.AAAGA	-	5
chr7	43908039	TGATTCaAgGgAGTAATGAAaTG/+		4
chr2	214708775	caATcCTAAGCAGcTAATaAAGGC-		5
chr1	51400864	TtATTaTtAAGCAGaAATGAATGA	+	4
chr1	66457973	TGcaTCTAAaGCAGTAATGAAGG(-		3
chr1	161868703	TGA.TCTAAGaAGTAATatAAGC	+	4
chr6	55567906	gGtTTCTAAaCAaTAATGAAgGGA-		5
chrX	135935484	atcTTCTAAGCAGTAATG.gTGC	+	5
chr4	140621583	gGgTTCTAAaCAGTtATGAAAGT	-	4
chr12	13959398	TGcTaaTAAGCAGTAATGgAgAG(+		5
chr14	22737279	TGATTaagAAGCAGTtATGgAGGC	-	4
chr13	56893207	T.ATTaaAAGaAGTAATGAATGC	+	4
chr19	19076144	TGA.TCTtAGCAGTgATGAAAGC	-	3
chrX	135877253	atcTTCTAAGCAGTAATG.gTGC	+	5
chr7	83055756	TGATTCTAcaCAGTAAGGAAaAGC+		4
chr2	50532613	TcATgCaAAGCAGTAATGAtgTGC+		5
chr15	71969840	TGA.TaTgAGCAaTAATGAATGA	-	4
chr5	101192025	TcA.aCTAAGCAGaAATGAAAGA	+	4
chr3	65174813	TGtTaCTAAGCAGgAAaTGAAAG(-		4
chr13	57044243	TGATTaTAAaCAGT.ATGAAAGG	+	3
chr1	216922385	TGcagtTAAGCAGTAATG.AGGG	+	5
chr14	26082058	TtAcTaTAAaGCAGTAATGAtCGA	+	5
chr1	60304542	aGATTCTAA.agGTAATGAAAGC	-	4
chr3	30232839	TGATaCTAAGCAGTAgtGgtAAG/-		4
chr17	14645722	TGATTCTAAtCAGTAgtTatAGGT	-	4
chr16	25745362	TGATTCTAAGCAtTAcTGAATGC	+	2
chr13	46268409	aGATTCTtAGaAGTAATaAAAGA	+	4
chr18	79182938	TGATTCTAA.tAGTAATGtgTGC	+	4
chr14	48064241	TG.TTCTAgGCAGTAATGtAAGC	+	3
chr6	55567908	gGtTTCTAAaCAaTAATG.AAGG	-	5
chr8	24586985	TGgaTCcAAGCAtTAATGAAAGC	-	4
chr13	102669082	aGA.TaTAAaCAGTAATGtATGG	-	5
chrX	135842691	atcTTCTAAGCAGTAATG.gTGC	+	5
chr2	163595695	a.AcTCTAAaCAcTAATGAATGT	+	5
chr9	88761404	aGA.TCaAAGCAGaAATGAATGA	+	4
chr1	33476807	TGcTTaT.AGCAGTAATGtAGGT	+	4
chr4	77290314	TGATTCTAAG.AaTAATGAgtAGA	+	3
chr12	20416667	gGcTT.TAAGaAGTAATGAAGGC	-	4
chr2	6665239	gGA.gCTAAGaAGTAATGAgtAGC	-	5
chrX	64753702	aGATTaaAAGCAaGTAATaAAAG(-		5
chr17	80433988	TGgaaCTAAaCAGTAATG.ATGG	-	5
chr4	151501089	TGA.TaTcAGCAGTAATaAAGGC	+	4
chr10	120815637	TGAaTagAAGCAGTgATGAAAGC+		4
chr2	151114249	c.cTcCTAAGCAGTAATcAAAGG	-	5
chr6	110556867	acAgT.TAAGtAGTAATGAATGT	+	5
chrX	129896814	TtATTCTAAGCAGTAATatAcTGA	+	4
chr4	139245123	gGATaCTAAGaAGTAATG.ATGC	+	4
chr7	50834958	gGATTCaAAcCAGTAATGAtAGA	+	4
chr16	83158939	TaATaTaTAtGCAGTAATGAAGGT-		4
chr5	158378998	TG.TTCTAAGaAGTAATGAcTGA	+	3
chr3	52168774	TaATTtTAAGgAGTAATGAATGC	+	3

chr15	93262852 TGATTaTAAGgAGgAATGAAAGA -	3
chr6	38710556 TtATT.aAAGCAaTAATGAAGGA +	4
chr13	64034150 aGATgCTAAGCAGTAAGaAAAGT +	4
chr2	161826799 TGATTaTAA.CAGTAATaAATGT +	3
chr14	64023789 TGATTCT.AtCAGTAAaGAATGG -	3
chr3	131795527 TcA.aCTAAcCAGTAATGAcTGC +	5
chr3	191113383 TtccTC.AAGCAGTAATGAATGA +	4
chr10	88979487 TGATTtTAAaCAGTAATaAgTGT +	4
chr8	56912043 TtAcT.TAAGCAaTAATGAAGGA -	4
chr7	11538003 acAgTaTAAG.AGTAATGAAGGT -	5
chr12	89074643 TGATTaTAAGCAaTcATGAAgGG(-	4
chr5	123474872 T.ATTaaAAGCAaTAATGAAAGC +	4
chr2	170039445 gGATTCatAGCAtTAATG.AAGG +	5
chr4	35278587 TttaTCTAAGgAGTAAT.AAAGG +	5
chr4	103717840 T.ATaCatAGtAGTAATGAAGGG +	5
chr1	51868508 gG.TaCTAAGCAGTAATtAgAGT -	5
chr9	79271628 gG.TaaTAAGCAGaAATGAATGA +	5
chr11	12446686 caATaCTAtAGCAGTAATGAtTGT +	5
chr21	33810805 aGAgTCTAAGCAGTAATG.cTGA -	4
chr1	23039527 TGATT.TtAGtAGTAATGAAGGA -	3
chr11	70308964 TGATTCcAA.CAGaAATGAAAGC -	3
chr2	114459342 TGA.TaTAAtCAGTgATGAAGGT -	4
chr2	215759236 TaAacCTAAGCAcTAATG.AAGA +	5
chr11	102516991 TtcTTtTAAGCAGTAgtGAAGGA -	4
chr4	151972909 TGATTCaTAAGaAcTAATGAgAGC+	4
chr12	7888287 TGAcaC.AAGCAGTAATGAAAGA +	3
chr8	124317416 aG.TTtTAAGaAGTAATGAATGA -	4
chr5	158600635 gtATTC.AAGaAGTAATGAAGGA -	4
chr13	22992999 gG.TaCaAAGCAGTAATGAtTGT -	5
chrX	152850564 TcATTCTAAGCAGTAAGaAtgTGG-	5
chr3	186203168 cGATTCTAAGCAtTAgtGAAGGA +	3
chr5	64462369 aGATT.aAAGCAGTAATaAAAGA +	4
chr12	87438517 TGATTacAtGCAGgAATGAATGC -	4
chr2	236996410 TGATTaTAA.aAGTAATaAATGC +	4
chr8	81282064 TGATaCT.AtCAGTAAaGAAGGC +	4
chr7	17238559 T.ATTCaAAGtAGTAATaAAAGC -	4
chrX	55551028 T.ATTtatAGCAGTAATGAgtGGC +	5
chrX	135808171 atcTTCTAAGCAGTAATG.gTGC +	5
chr2	170039446 gGATTCatAGCAtTAATGAAGGG +	4
chrX	135773637 atcTTCTAAGCAGTAATG.gTGC +	5
chr16	77369332 aGA.TCcAAGCAGTAATaAATGA -	4
chrX	110795033 TcAgTCaTAAGCAGcAATGAAAGC-	4
chrX	128242819 TGATTCTtAgTAgTAATGttATGC -	4
chr11	5329449 ccA.TCTAtGCAGTAATGAtAGT -	5
chrY	19601193 TaAgTCTAAaaAGTAATG.AAGG -	5
chr14	105294496 TGATaacAA.CAGTAATGAAAGC -	4
chr17	80433987 gGA.aCTAAaCAGTAATGAtGGT -	5
chr12	114081736 aGcTTgTAAGCAGTAATGAAAGA +	3
chr3	115884381 gaATTCTAAGgAaGTAAaAAAGC+	5
chr1	149324067 TacTTCatAGCAGTAATGAATGC -	4
chr12	118745964 TtATTCTAAG.AGTAAaGAAAGC +	3

chr3	127263159 gGcTTCTAAGgAaGTAATGAAGG-	4
chr11	13945623 gGATTCTAtGgAGTAATaAAGGT +	4
chrX	70836705 aGATTCTtAcCAGTAATGtATGA -	4
chr19	44213874 TagTTaT.AGaAGTAATGAATGC +	5
chr15	77208895 T.ATaCaAAGCAGTAATGgAGGT -	4
chr2	199359085 TttTcCTAAGCAGTAATGttAAGT -	5
chr16	6818294 TGATTCTcA.tAGTAATGAAAGA -	3
chr2	139354771 gtATTCaAAGCAGTAaAaGAaGTGC+	5
chr13	65823444 aGtTTCTAAGCAtTAATG.AAGA -	4
chrX	36202180 TtATTCTAAGCtGTAATGAtAGA -	3
chr2	99672551 TtAagCTAAGCAGTgATG.AAGA -	5
chr17	34236701 TtgTgaTAAGCAGTAATG.AGGA -	5
chr5	157805400 TGATaCTgAtCAGTAATGAcTGT +	4
chr6	74656341 TGATT.acAGaAGTAATGAaAGT +	5
chr4	92777625 ccATT.aAGaAGTAATGAAGGT +	5
chr1	71350543 TGATTaTAtGCAGTAATGAAAGA+	3
chr5	60248242 T.ATTCTAAAtCAGaAATGAAGGT +	3
chr13	89352273 ctATTaCaAAGtAGTAATGAAAGA +	5
chr19	20319275 TGATTtaAAGCAGTAAT.AgAGA +	4
chr3	84822323 TGtcTaTAtAGCAtTAATGAAAGC -	5
chr7	86879345 TatTTCaTAAGCAGTtATGAAAGA -	4
chr13	33065694 TGATTaTAAG.AGTAATatATGT +	4
chr13	39724779 TaATcCTAAaCAGTAATGAtgAGA -	5
chr12	122788878 aGATTaTAAGCAGaAATtGAAGG(+	4
chr10	31257508 aGcaT.TAAaCAGTAATGAATGT -	5
chr5	60248241 atATTCTAAAtCAGaAATG.AAGG +	5
chr13	82584822 TaATaCTAAGCA.TAATGAATGT -	3
chr4	80882181 TGATTtaAAGCAaTAATG.ATGG +	4
chr5	35668042 cctTTCTcAGCAGTAATGAAtAGT -	5
chr4	137938422 aGA.TCaAAGCAGTAATaAATGT +	4
chr12	25111834 TctTTCaAAGCAaTAATGAAaGGA+	5
chr4	137601282 ctAgT.TAAGCAGTAATGcAAGC +	5
chr2	81254335 TGAgaTCaAAGCAGTAATaAAAG(-	4
chr13	66842768 ctATTcCaAGCAcTAATG.AAGA +	5
chrX	135790898 atcTTCTAAGCAGTAATG.gTGC +	5
chr15	57960989 TGgaTCTAAGCAGTAaGAgTGT +	4
chr6	157872422 aGATTcCTAAGCAGTAaCaAATGC-	4
chr2	12547787 TtcTTCaAAGCAGTgATGAAAGT -	4
chr12	82172618 TaAaTaTAAaCAGTAATGAAtGGC+	5
chr5	102587054 TGATTCaAAaCAGTAAtTGAgAGC +	4
chr2	116876533 TctcTCTAAAtCAGTAATGAAaAGG -	5
chr12	115524644 TccTTCTAAG.AGTAATGgAAGC +	4
chrX	97522573 TaATT.aAAGCAcTAATGAAAGC -	4
chr2	175076576 TtcTgaTcAAGCAGTAATGAATGT +	5
chr9	33153504 TtATTaTAAtCAGTAATGAAAGA +	3
chr5	131624117 TGATaaTAAaCAGTAaATGAtAGC-	5
chr21	35176496 T.AaTaTAAGCAGcAATGgAAGG -	5
chr13	60049655 TaAaTaaTAAGtAGTAATGAAAGT-	5
chr4	80076889 T.tTcCTAAGCAaTAATGAaGGA +	5
chr4	34030094 TcAcT.aAAGCAaTAATGAATGC -	5
chr7	16838182 TGATTCTAAaCAAtTAATcAAAGT -	3

chr22	21799365 TtgTgCTAAGCAGaTAATGAAAGC-	4
chr3	30966850 caATTcCAGCAGTAA.GgAAGG +	5
chr19	32242623 TaATTaCcAAGCAGTAATGAcAGT+	4
chr9	87427610 gtATTCTAAGCAGaAAaTGAATGA-	4
chr6	125285390 TaGAaaCTAAGCAaTAAGGAACG(+	5
chr6	126295674 TaATaTaTAAGCAGTAATaAtTGA +	5
chr4	183817238 aGATTaCTAAGCAGTttTGAAAGC-	4
chr4	141985163 aGATTtTAAaCAGTtATGAATGC +	4
chr5	166868127 aGtTTCTAAaCAGTAATtAATGG +	4
chr6	96268783 TaATTCTAAGtAGTAtTGAAAGA +	3
chrY	22708302 aGA.TgTAAaCAGTAATGAATGG +	4
chr11	61633212 gcAcTC.AAGCAGTAATGAgAGT -	5
chr13	20293321 atATaC.AAGaAGTAATGAATGT -	5
chr6	41392473 gGtTTCTAAGtAGTgATGAATGT +	4
chr17	62815551 TGA.TgTAAGCAaTAATGAAtAGC -	4
chr4	146616216 TacAcTCTAAGCAaTAATGAcAGT -	5
chr3	186203167 cGATTCTAAGCAtTAgtTG.AAGG +	4
chr16	6245222 TGAaTaTAAGCAGaAATGAtGGC +	4
chr1	205859267 acAaT.TAAGCAGTAATGgAGGA +	5
chr4	158134444 TcA.gCTAAGCAaTAATGAgtTGT +	5
chr7	45093423 TGATT.aAAGaAGTAATGgAAGG +	4
chr1	86135720 aGATaCTAAGgCAGaAATGAAAG-	4
chrX	55551027 TtATTtatAGCAGTAATG.AGGG +	5
chr21	17497271 TtcTaCTAAtCAGTAATG.AAGA -	5
chr17	50330630 gGA.caTAAGCAGaAATGAATGA -	5
chr1	104797678 TtA.cCaAAGCAGTAAGGAATGC +	5
chr13	77205514 aGAcTC.AAGCAGTAATGAAGGT -	3
chr2	204605749 TGATTaTAAGagtTAATG.AAGA +	5
chr13	41313814 T.ATaCTAAGCAGaAATGAAtAGA -	4
chr15	98581563 TGgATatcAtGCAGTAATGAATGC -	5
chr21	18819497 TcATTCaAAaCAGTAATGAAAGA +	3
chr10	78449384 TGAaT.aAAGaAGTAATGAAGGA +	4
chr4	38472502 TctTTCTAAGgAGTAAGGAAAGT -	4
chr1	148806156 TacTTCatAGCAGTAATGAATGC +	4
chr9	72482417 TtcTTaTAgtAGCAcTAATGAATGT +	5
chr3	113972068 TaAaTCTAAGCAGaAATaAATGA -	4
chr17	11203998 TaGATTtaAAGCAGaAATGAgtAGC+	5
chr10	130032620 aGATTtaAAGaAGTAATG.AAGA -	5
chr13	30993590 TGATTCTAAGCAGTAaAG.gAGA +	3
chr3	104934836 TGA.TCTAAGaAGTgATGAAAGT +	3
chr3	39532936 aGATTaCcAAGCAGaAATGAAAG(+	4
chr10	72591374 TGATT.agAGCAGaAATGAATGA +	4
chr7	78866181 TGcTTCTAAGCAGTAAGGttAGC -	4
chr9	10265922 TtATTCTAttCAGTgATGAAAGC -	4
chr1	158971358 TtcTcTCTAAGCAcTAAGGAAAGC -	5
chr2	169958903 TGATTtTAAGaAaTAATGAAGGGA-	4
chr5	93480523 TGATaCTAAaCAGTAACtTAAAGC +	4
chr5	85308277 TtATTCTAgGaAGTAATGAAtATGC +	4
chr5	11969731 aGATTCTAAGCAGTAaAGttAGA -	4
chr2	224360168 T.ccTCTAAGgAGTAATGAgtGGG -	5
chr4	59634671 TGATTaTAAGCAcTAATGAgtTGG-	4

chr17	42272306 T.ATatTAAGtAGTAATGAtAGC	-	5
chr2	219382555 gGAaTgTAAGCAGTgATGAATGT	+	4
chrX	97042146 aaATTCTAAGCAGTgATtAATGG	-	4
chr12	68759296 aGATTCaAAtaAGgTAATGAATGT	-	5
chr10	93209389 aGATcaTAAGCAGTAA.GAAAGA	-	4
chr13	26077172 T.tTaCTAAGCAGTgATGAgGGG	+	5
chr19	9215705 TaATagT.AGCAGTAATGAtAGC	-	5
chr5	162364358 T.ATTtTAAGaAGTAATGAAAGA	-	3
chr1	76381946 a.AaTCTAAGCAGaAATGtAAGC	+	5
chr13	34542779 TcATTtaTAAGCAGTAgtGAAAGA-		4
chr12	114425132 gGgTTaTtAAGCAaTAATGAAAGA+		5
chr11	98248035 TGAgATCaAAGCAGTAATaAAAG/-		4
chr12	10605446 gGtTaCTAA.aAGTAATGAAAGA	+	5
chr15	48919799 TG.TTCTAAGCAGTtATGgAAGC	-	3
chr4	35278588 TtA.TCTAAGgAGTAATaAAGGG	+	4
chr4	147267014 TGcTaCTAAaCAGTAATG.AGGA	-	4
chr17	53861544 TccTTCTAAaCAaTAATG.AAGA	-	5
chrX	147856764 T.tcTCaAAGCAaTAATGAAAGT	-	5
chr12	110078825 TGATT.TAAaaAGTAATGAACGC	-	3
chr1	61892314 acATaCTAAGCAGT.ATGAAGGT	-	4
chrX	33155044 aGATTaTAAGCAGaAAT.cAAGG	-	5
chr1	170765256 aGcTaaTAAGCAGTAATG.ATGA	+	5
chr12	99264504 c.AgaCTAAGCAGTcATGAAGGG	-	5
chr11	102516992 TtcTTtTAAGCAGTAgtTG.AAGG	-	5
chr1	93876585 TagTTCTcAGCAGTgATGAAAGC	-	4
chr9	31527885 gGtTcCTAAGtAGTAATGgAAAGA-		5
chr20	11136784 TcAcTaaAAGCAGTAATG.AAGT	+	5
chr15	71734643 gaAcTCTAAGCAaTAATGAcATGT	+	5
chr11	62253400 aGATTacAAGCAGTAgtTG.AAGC	+	5
chr12	122319053 TGATcCTAAtaAGTAATGAAgtTGA+		4
chr12	84609764 gtATTtTAAGCAGTAATG.tAGA	+	5
chr20	17203383 ccA.aCTAAaCAGTAATGAATGG	+	5
chr16	6352637 TatTTCTAA.aAGTAATGAATGA	-	4
chr18	44270222 T.AggaTtAGCAGTAATGAATGA	+	5
chr9	26360017 TGAaT.aAAGCAGTgATGAACGT	+	4
chr5	55112965 cGATTC.AAaCAGTAATaAAAGA	+	4
chr5	18965935 TttTTCTAAGCAGTAATtAgAGA	-	4
chr18	38544135 aGccTCTAAGgAaGTAATGAAGG -		5
chr2	81416788 aGATTCTAA.CAGTAATGtgTGA	+	4
chr10	59302772 T.cTTaTAACcAGTAATGAtTGC	+	5
chr13	55162581 TGtcTtTAAGCAaTAATGgAATGT	+	5
chr4	106183151 TGATTCTAAGCAGTAgaAgtAGA	-	4
chr11	56113010 aGATT.agAGCAGaAATGAATGA	+	5
chr9	106848263 TtATTaTAA.aAGTAATGAATGC	-	4
chrY	7622785 aGA.TgTAAaCAGTAATGAATGG	-	4
chr8	117394125 TacATTtaAAGCAGTAATaAAAGG+		5
chr3	122632378 TtATTCaTtAGCAGTAATGAAGGA+		3
chr4	65824521 gGtTTaTAAGCAGTAATaAtATGT	-	5
chr3	137998049 TGcTTCTAAaCAGTAATcAgTGC	-	4
chr3	175725542 cGATTCTAAGgAaTAATcAAGGG	-	4
chr16	49647264 TGATgCcAAGCAcTAATGAATGT	+	3

chr6	9078109 TaATTCTAAGaAGTAAaGtATGC +	4
chr14	82199323 TGATTCaAAGCAG.AATGAAGGA -	2
chr13	30595368 TcAaTCTAAGaAGTAATtGAAGGC+	4
chr2	167283795 aGtTTacAAGCAGTAATGAAAGA +	4
chr1	78256670 ccATaTCTAAtCAGTAATaAATGA +	5
chr4	33353708 T.ATatTAAGCAaTAATGAtTGC +	5
chr10	83887598 TGATTCTAAaCAG.AtgaAAGGA +	5
chr4	94648155 aGATT.acAGCAGaAATGAATGA +	5
chr8	88680935 TGATTtTAAGaAGTAATGAAtTGA +	3
chr18	411180 TccacCTAAGCAGTAATG.AGGT +	5
chr11	105566875 TGAaTaaAAGaAGTAATG.AAGG +	5
chr4	100881360 gGAgTTCTAAGCAGTAgtTtAATGA+	4
chrX	152850566 TcATTCTAAGCAGTAA.GAATGT -	2
chr1	147097101 TGATcaaAAcCAGTAATG.AAGA -	5
chr3	30725337 T.tcTCTAAGCAGTAATcAgTGT +	5
chr1	191993355 TG.TTCTAAGCAGTAatgatAGGC +	5
chr18	40246683 TtA.TaaAAGCAcTAATGAAAGG +	5
chr4	173915524 TtAccTCTAAGaAaTAATGAAGGC +	5
chr14	54681331 TaGATaCTAAtCAGacATGAAAGC+	5
chrX	38614794 TGATatTgtGCAGTAATG.AAGG +	5
chr9	118823989 TGATcaaAAGCAGTAATaAtAAGA+	5
chr3	120110282 c.ATTaTAAGCAGTAATttATGT -	5
chr20	43169458 TG.TaaaAAGCAGTgATGAAAGC -	5
chr19	8931281 TGAcTTaaAAGCAGTAATGAATGC(-	3
chr10	44688444 TcATTCTAgGgAGTAATaAAAGC -	4
chr9	29854752 TttTcCTAAGCAGTAgtATGAATGA -	4
chr2	54764550 gaATTaCTAAGCAtTAATGtAAGC -	5
chr13	95556480 gGATTCTAAGCAGaAATtAgAGC -	4
chr5	173916346 TGAaTgTAAGCAaTAATGAtTGC +	4
chr18	3115581 TcATTCTAAGtAGTAAGtAATGC +	4
chrX	121195094 cctTTCTAAGCAGTAAT.tATGA -	5
chr11	62253402 aGATTacAAGCAGTAgtGAAGCGl+	5
chr8	109733166 gGcTTaTAAaGCAtTAATGAACGC+	5
chr5	123198203 TGATTaaAAaaAGTAATGAATGG -	4
chrX	96766795 TGATTagAAGCAGaAATGgAGGC+	4
chr11	55409220 aGA.TCaAAGCAGaAATGAAGGA -	4
chr16	67880462 T.AgTaTtAGCAGTAATGAgAGA -	5
chr5	92742898 TaATTCTAAaCAGTAA.GAAAGC +	3
chr17	50383669 T.ATTgTAAGCAGTgATGAtTGC +	4
chrX	13442421 aGATTC.AtaCAGTAAGGAAAGG +	5
chr3	137632736 TG.TctTAAaCAGTAATGAtTGC -	5
chrY	21758904 gGA.TgTAAaCAGTAATGAATGG -	4
chr6	120896541 TtAaTC.AAGCAaTAATGAAAGT -	4
chr4	167702998 aGATaCTAAGCAaaAATG.AAGA +	5
chr4	133639879 aGATTCTtAGCAGTAATtAtAAGT +	4
chr8	79314312 aaATaC.AAGCAGTAATGAACGG -	4
chr13	92188102 aGATTC.ctGCAGTAATGAtTGA -	5
chr2	6737776 aG.TgCTtAGCAGTAATGAAAGT +	4
chr5	37091685 aGA.TgTAAaCAGTAATGAATGG +	4
chr1	146376157 TGA.TaaAAcCAGTAAGgAAAGGC +	5
chr13	61063000 TGATaCTAAatAGgTAATGAATGG-	4

chr7	79292940 TG.TTtaAAGCAGTAATGtAGGT	-	4
chr14	106747007 aGA.TgTAAaCAGTAATGAATGG	+	4
chr2	172477308 TGATTccAGCAGTgATGAAAGC	-	4
chr15	60491344 TccTTCTAAGaAcTAATGAAAGA	-	4
chr8	82480363 TGA.TaaAtGtAGTAATGAATGA	-	5
chr4	171470248 cG.TTaTAtGaAGTAATGAAAGT	+	5
chr8	119822682 cagTTCTAAGCAGTgATG.AAGT	-	5
chr1	154557478 T.ATTCTAAGCAGTAacagtTGC	-	5
chr17	62446125 TttTTCT.AcCAGTAATGAAGGA	-	4
chr12	117241243 TttTTCT.AGCACtAATGAAGGT	+	4
chr4	14373929 TtATTCaTAAtaAGTAATGAATGG	-	4
chr3	109441320 cccTTCTAgGCAGTAATGAAAGT	+	4
chr20	46395338 T.ATTCcAAGCAGTAAcTAAAGC	+	4
chrY	19276682 gtATTCaTAAGCAaTAATaAAGGA	+	5
chr1	233914785 TGgTTCaAAGCAGTggTGAATGT	+	4
chr14	52441865 T.AaTaTtAGCAGTAATGAcTGT	+	5
chr7	91019771 aG.ccCTAAGCAGTAAaGAAAGG	-	5
chr8	77986703 TaAcT.aAAGCAaTAATGAAGGC	+	5
chr14	46532402 aGA.TCaAAGCAGaAATGAAGGA	-	4
chr11	23402475 T.ATcaTAAGCAGTAATaAgAGC	-	5
chr6	95854478 atATTC.AAGCAGTAATaAATGA	-	4
chr4	25657757 TtATTaTtAGCAGTAATGtAGGG	+	4
chr4	15692067 aGtTTCcAAGCAGTgATGAAGGT	-	4
chrX	33155043 aGATTaTAAGCAGaAATcAAGGT	-	4
chr16	19978372 TGAgTaTAAGCAGTAA.GAtAGG	+	4
chr6	14737489 acA.TCTAAGgAGTAgTGAATGC	-	5
chr11	78822006 TGAcTCaAAGCAGgTAATGAATG	+	3
chr1	90211235 aGAgTCTAAGgCAGTAAaGAATG	+	4
chr17	53007348 gGATTaTAAGCAaTAAT.AtAGG	-	5
chr10	106363426 aGATTCT.gGaAGTAATGAAGGC	+	4
chr1	16514908 TGA.TaaAAcCAGTAAGaGAAGGC	-	5
chr5	166868128 aGtTTCTAAaCAGTAATtAAtGGC	+	5
chr19	35217275 aGAcTTgTAAGCAaTAATGAATGC	+	4
chr3	159339823 gGA.caaAAGCAGTAATGAAAGA	-	5
chr14	79116388 ccATcTCTAAGCtGTAATGgATGC	+	5
chr8	9809826 aGA.TgTAAaCAGTAATGtATGC	+	5
chr11	38659031 T.AgaaTAtGCAGTAATGAAAGA	-	5
chr18	52395603 TGATTCTAAGCAGatATG.AAGT	+	3
chr13	50807275 gGATTCTAAGaAaTAATaGAAAGC	-	4
chr4	82608439 atcTTCTAAGgAGTAAaTGAAAGC	+	5
chr13	26095784 TacTagTAAGCAGTtAATGAATGC	+	5
chr6	8104478 aGtaTCTAAG.AGTAATGAgGGG	+	5
chr7	152855204 TGAacaCTAAaCAGTAATGtATGA	+	5
chr13	38071594 T.tTTaatAGCAGTAATGAAAGC	-	5
chr1	33480147 TGcTTaT.AGCAGTAATGtAGGT	+	4
chr8	106197043 aGA.cCaAGaAGTAATGAATGC	+	5
chr1	165447147 aGtgTCTAAGgCAcTAATGAATGG	-	5
chr15	41235574 ccATTC.AAGtAGTAATGAATGC	+	4
chr5	144711445 TcccaC.AAGCAGTAATGAAGGT	+	5
chr4	121053752 TGATTCTtAG.AaTAATGAAAGC	+	3
chr3	111459732 aG.TTtTAAGCAGTAATGgATGT	+	4

chr12	13959396 TGcTaaTAAGCAGTAATG.gAGA	+	5
chr4	103930753 TG.TcCatAGCAGTgATGAAGGT	+	5
chr10	130032618 aGATTtaAAGaAGTAATGAAgAGT-		5
chr11	14212321 ctATT.aAAGCAGTAATGgAGGT	-	5
chr7	85009355 caATT.aAAGCAaTAATGAAAGA	+	5
chr7	11311318 gG.TTaaAAGCAaTAATGAAGGT	-	5
chr10	4741020 TGATTCTAAttAGTgATaAATGA	-	4
chrY	26182720 aGA.TgTAAaCAGTAATGAATGG	+	4
chr7	148984765 T.cTgCaAAGCAaTAATGAATGC	-	5
chr6	65806096 TGA.TaaAAGCAGTAAGtAAGGC	-	5
chrX	41883340 TGATTaTAAGCAGTAA.ctcAGA	+	5
chr17	75373699 TGATaCTAAGCAG.AATtAAAGA	-	3
chr12	117241634 TttTTCT.AGCACtAATGAAAGT	-	4
chr4	15385864 TaATaTaTAAGCcGTAATGAAGGT-		4
chr11	72838756 TGATTgT.AGCAGTAATGgATGG	+	3
chr18	4083373 TtATTaTAA.aAGTAATGAATGT	+	4
chr7	128499323 TttTTCT.AcCAGTAATGAAGGA	-	4
chr7	57508463 TGATcaTAAGCcAGTAATGtAAGT-		4
chr13	64541584 TtATTCTAAGCAG.AATaAATGT	+	3
chr1	120194734 TacTTCatAGCAGTAATGAATGC	+	4
chr6	17128216 cagTTCaAAGCAGTAATG.ATGA	-	5
chr9	93831014 TGcTTCTAAGgAtTAATGAAGGC	-	3
chrX	97662194 TGtTaCcAAGCAGTAA.GgAAGG	+	5
chr2	169958904 TGATTtTAAGaAaTAATGAAGGG	-	3
chr5	77227080 TG.cTCTAAGCtcTAATGAAGGC	-	4
chr9	71297190 aGATaCTgAGaAGTAATGAAaAG/-		5
chr2	162012693 TGATTaacAAGCAGaAATGAgAG(-		5
chr1	147097099 TGATcaaAAcCAGTAATGAAgAGA-		5
chr4	31243704 aGATTCTAAGttGTAgTGAATGC	+	4
chrY	21746714 gGA.TgTAAaCAGTAATGAATGG	+	4
chr3	61363623 ctATTaCTtAGCAaTAATGAATGA	+	5
chr12	76127978 TGAaaCaAAGCAGTAATGgATGT	+	4
chr19	36436007 T.tcTCatAGCAGTAATGAAAGT	+	5
chr15	51515652 TaAacTgTAAGCAaTAATGAATGA-		5
chr6	45497252 TttTTCTAAGCAGTcAATGAAAGT	+	3
chr8	116798265 TGcaTCTAAcCAGTAAT.AAAGA	-	4
chr5	82231967 ccATTCTAAaaAGTAATGAtAGGT	+	5
chr9	104462633 TGATTaTtAGCAGaAATG.AAGA	-	4
chr19	31043654 T.ATTaaAAGCAtTAATGAATGC	-	4
chrY	21638119 TaAaT.aAAGaAGTAATGAAAGA	-	5
chr10	49316502 TcATTCTAAaCAGTggTGAAGGA	-	4
chr13	85323695 caAcTTCTAAGCAGaAATaAAAGA-		5
chr1	84536173 aGATTCagAGCAGgAATGAAAGA+		4
chr1	50789425 TGATaCT.AGgAGTAATGgAGGA	-	4
chr17	14645723 TGATTCTAAtCAGTAgtT.AtAGG	-	4
chr6	55912467 TccTTCTAA.aAGTAATGAAAGA	-	4
chr7	138235235 caAgTCTAAGCAGcAATtGAAGGT+		5
chr2	193986338 TtATTCaAAGtAGTAATaAAAGA	+	4
chr8	25240644 gaATaCTAtGCAGTAATGAAaAGA-		5
chrX	27219165 TGATaTCTAAGCAGTttTGAAAGG-		3
chr5	55771447 gaATaCTAAaCAGTAAT.AATGA	-	5

chr3	193620675 TGAcT.TAAcCAGTAATGAAAGT -	3
chr14	27776484 gGATTaaAAGCAGTAATtAAAGG +	4
chr3	77080830 TaATgCTtAAGCAaTAATGtAAGC -	5
chr4	132860827 TcATTcCaaAcCAGTAATGAATGA +	3
chr12	82172617 TaAaTaTAAaCAGTAATGAATGG +	4
chr1	12770981 TG.TcaTcAGCAGTAATGAAGGA -	4
chr7	15264451 TGATaCTAAcTAgTAtGAATGC +	4
chr2	189437921 aGATaCTAAGCAGTAA.aAATGT +	4
chr8	120246700 TGA.TCTAAGCAGTgATtAAGGA +	3
chr1	174303553 TgTgCTAAGCtGTAATGAATGC +	3
chr11	22458583 TaAaaTaTAAGCAGTAgtGAAGG/-	5
chr21	25096128 aaATaaT.AGCAGTAATGAAAGA +	5
chr8	68010579 aGATTacAtGCAGgTAATGAAAGC-	5
chrY	21654802 aGA.TgTAAaCAGTAATGAATGG +	4
chr15	89279538 gGAgTTaTAAaCAGTgATGAATG/-	5
chr18	77713858 T.AcaCTAAGCAGaAATGAcAGC +	5
chr5	87505183 TtA.TCTAAaCAGTAATtAAGGA -	4
chr21	19280692 TcA.TaTtAGCAaTAATGAATGC -	5
chr3	63494171 TctTTCTAAG.AGTAATGtATGT -	4
chr3	82757357 caATTCTAAGCAGTcATGAAaTGG+	4
chr5	60502755 TcccTTCaAAGCAGTAATaAAAGT +	5
chrX	128290431 aGAcTaTAAaGCacTAATGAAAGA+	5
chr14	27776485 gGATTaaAAGCAGTAATtAAaGGA+	5
chr2	115415188 TGATaCTAAGCAG.AAaGAAAGA -	3
chr12	41477421 aGATTCTcAGCAGTAtTG.AAGG +	4
chr1	81584829 aGtTTaTAAGCAGcAATGAATGA -	4
chr1	57347702 TaATTaTcAGCAcTAATGAAAGA +	4
chr4	15692068 aGtTTCcAAGCAGTgATG.AAGG -	5
chr5	151171602 TG.gTgTtAGCAGTAATGAtGGA +	5
chr10	34121666 TgTgTaTAAGCAGTAATG.AAGC +	4
chr5	55218281 TGgAcTCTAAcCAGTgATGAgTGC-	5
chr2	98074120 TGATTCatAtCAGTAAaTGgAGGC+	5
chr5	178877620 TGATTCaAAGCAGTAATttgcAGT +	5
chr4	180825602 TGATTaTAAGgAGT.ATGAAGGC +	3
chr6	98902830 TGATTtTAAtgAGTAATGAtATGC +	4
chr2	223854032 TGATaCT.AGtAGTAATaAtAGC -	5
chr12	111868095 T.AgaCTAAGCAaTAATaAAGGC -	5
chr4	142756136 aGATTCTAAaCAGagATG.AAGA +	5
chr11	21375388 gGAaTaCTAAaCAGTAATaAAAGA-	5
chr2	95507830 gGtaTCTAAaCAGcTAATGAATGT -	5
chr13	38878811 TccTT.TAAGCAGTAAGGAAAGT -	4
chr6	67400268 TGcTaTaTAAatAGTAATGAAAGC -	5
chr3	25990008 aGAaTC.AAGCAGTAATGAgAGA +	4
chrY	23487866 aGA.TgTAAaCAGTAATGAATGG -	4
chr2	103730651 TctTTCT.AGCAaTAATGAATGG -	4
chr2	190060698 aGgTTCTAtGaAGTAATGAACGC +	4
chr14	38228860 TGATagTAAatAGTAATGAAGAGC-	5
chr11	13945622 gGATTCTAtGgAGTAAT.AAAGG +	4
chr4	27225055 TaGATTaTAAGgAGTAAGaAAGG/-	5
chr2	61937548 TaATTaTAAGggGTAATGAATGC -	4
chr8	94310025 TtATT.agAGCAGTAATGAAAGG +	4

chr15	87729318 gtATTCTAAG.AGTAATGggAGC -	5
chr14	20053502 T.ATTCTAAaCAGTAgaGAAAGC +	4
chrX	10846483 atATTCTAAGCAGTAAtTGAAAGC -	4
chr9	129693646 TG.TatTAACcAGTAATGAtGGC -	5
chr11	105566876 TGAaTaaAAGaAGTAATGAAGGT +	4
chr9	118232718 TGATcCTAAGaAaTAATGAtGGC -	4
chr5	142183155 TG.TaaTAAaaAGTAATGAATGC -	5
chr10	93675861 TGAaTCTAAaCAGTAATatAATGT -	4
chr2	114840847 aGATTCTAAcCA.TAATGAAAGG -	3
chr3	57039498 TGATT.acAGCAGcAATGAAAGA -	4
chr11	26629368 T.AaTagAtGCAGTAATGAAAGG -	5
chr5	162301975 T.tTTCTAAaCAtTAATGAAAGC -	4
chr12	1030305 TGATaCTAAGaAGTAAaG.AAGC +	4
chr7	99437614 TaATTtCaAAGCAGTAATaAATGT +	4
chr13	90518592 TGcATTCTcAGCAGTAATGAATGA-	2
chr5	13767437 TaATaCT.AGCAGTtATGAAAGC +	4
chr1	62554038 aGA.TgTtAGCAGTAATGAAGGT -	4
chrX	127326064 gGATTCaAAaCAGTAATG.AAGT +	4
chr6	64811323 TaAcTtTAtAGCAGTAATGAATGC +	4
chr4	77560668 aGATaCTAAGCAGTAA.aAATGT -	4
chr20	24387939 TGAcTCTgAGCAGTAATGAttTGT -	4
chr3	80794189 TGgTTCTAAG.AGTAATaAATGT +	3
chr14	78775490 atATaCTAA.CAGTAATGAtAGT -	5
chr12	74045663 TGAaTgaTAAGCAaTAATGgAAG(+	5
chr6	28862315 T.ATTtagAGCAcTAATGAAGGA -	5
chr1	60477573 T.ATaCTAtGaAGTAATGAATGA +	4
chr1	74078166 TctaTCTAA.aAGTAATGAAAGA -	5
chr1	37424367 aGATTCTAAGCAGggATGtAtTGC-	5
chr4	108518772 atATTcCaAGCAGTtAATaAAAGT +	5
chr7	120366940 TGATTCTAgGaAGTAAaGAAGGG-	3
chr18	41291611 T.tTaCTAAaCAGaAATGAAAGC +	5
chr15	80125855 ctcTTtTAAG.AGTAATGAAAGT -	5
chr12	41477422 aGATTCTcAGCAGTAtTGAAGGT +	3
chr11	131567954 aaATTCaTAAaCAGTAATGAtGGC+	5
chr2	18722140 TtAcTCTAgGCAGTAATG.AAGA -	4
chr13	39724781 TaATcCTAAaCAGTAATG.ATGA -	4
chrX	149409843 a.ATaCaAAGCAGTAATGgAGGA -	5
chr2	134935901 TaAcTaT.AGCAaTAATGAAAGC -	5
chr1	185051456 aGA.TaTAAGaAGTAATGtACGT +	5
chrX	41663831 TaATaCT.AGCAaTAATGAtAGC -	5
chr1	174976284 TGATgTtaAAGCAGTAATGtAAGT+	4
chr4	7200637 TctTTC.AAGtAGTAATGAAGGA +	4
chr14	92905909 TG.gcaTAAGtAGTAATGAAAGA +	5
chr3	105544363 gGtTTCaAAGCAGTAAT.AAAGG -	4
chr1	236320476 TGATTcCaAG.AaTAATGAgAGC -	4
chr6	128060448 T.ATTaTAAGaAGTAATaAtAGC +	5
chr7	89759987 TtATgaCTAAGaAGTAATaAAGGA+	5
chr4	92783006 TaATaCTAAG.AGTAATaAAAGT -	4
chr2	71216121 TtATTtTAAaCAGTAATGtAGGA -	4
chrY	9211729 aGA.TgTAAaCAGTAATGAATGG -	4
chr20	11344611 TttTTCcAAGCAGTAATGAAAGA +	3

chr22	17676775 TaATTaTAAaCAGTAATG.gAGA	+	5
chr2	118604528 TcA.gCTAAtCAGTAATGAgAGA	+	5
chr18	31461372 TGATcCT.AGAcTAATGAAGGC	+	4
chr15	83164806 c.ATTCTAAGgAaTAATGtATGT	-	5
chr4	25657756 TtATTaTtAGCAGTAATG.tAGG	+	5
chr3	80617502 caAacCTAAG.AGTAATGAAAGA	-	5
chr10	85995910 gGATTCTAAtCAGTAAtTaAAAGC	+	4
chr8	109565709 TGATTCTAgGCAGTAActtAAGA	-	4
chr2	149824168 a.ATTaTAAGCAGTAAGaAATGA	-	5
chr20	52975898 TaATTtTAAGCAGTgATaAAAGT	-	4
chr2	99672549 TtAagCTAAGCAGTgATGAAGAGC-	5	
chr6	69917794 atATaCTAA.CAGTAATGAtAGC	+	5
chr5	109495412 TtcTTCaAAaGCAGTAATGAAAGA+	4	
chr16	50084158 gctTTCT.AGCAGTgATGAAAGT	+	5
chr8	72823120 TGA.TaaAAGCAGagATGAAGGA	-	5
chr3	101391577 aGA.TCaAAGCAGTAATaAAAGG	+	4
chr5	128868658 TGAcTCTAAaCA.TAATGAAAGG	+	3
chr4	33819550 caAgTCTAtAGCAGTAATGAgtGG-	5	
chr9	89809322 TGATTCTAttCAGTAAaGAcTGC	-	4
chr6	11627035 TccTTCTAAGCAGgAATGAgtGGC	+	4
chr2	184931902 a.tTTCTAAGCAGTAAaGcATGC	-	5
chr3	20123331 attTTCTAAG.AGTAATGAcTGC	-	5
chr15	92115920 TaATTCTAAGaAaTAATGAtAGT	-	4
chr7	136969757 a.ATgaTAAGCAaTAATGAAAGC	-	5
chr1	190002536 aaAgaC.AAGCAGTAATGAATGC	-	5
chr7	22758912 caAagCTAAaGCAGTAATGAAAGC-	5	
chr4	76866040 TGATTCT.tcCAcTAATGAAAGT	+	4
chr6	92563158 aGA.TCTAAGCAGaAATaAATGA	-	4
chr3	72442326 TGtgatTAAGCAGTAgtATGAAAGT+	5	
chr10	92572038 aGATTCaAAGCA.TAATGAATGA	-	3
chr13	92318677 TctTaaTAAGCAGTAATG.AGGT	+	5
chr7	47724812 TGAaaTCTAAGCAGTAAtTGAAAGA-	3	
chr12	115803219 cGgTgtTAAGCAaGTAATGAAGGC-	5	
chrX	49881804 ctAgTCTAAGCAGTgtATGAAAGG+	5	
chr2	168628194 T.cTaCTAAGtAGTAATaAATGT	-	5
chr9	17021182 TctcTtTAAGCAGcTAATGAAGGC	-	5
chr3	20661525 TGATTaCcAAtCAGTAATaAAAGG-	4	
chr12	60190370 T.cTTtTAAGCAGaAATGAAAGA	+	4
chr3	175725543 cGATTCTAAGgAaTAAT.cAAGG	-	5
chr18	39317610 T.ATaaTcAGCAaTAATGAATGA	+	5
chr5	36585403 TGATcCTAAGtAtTAATaAAAGC	-	4
chr10	21432946 aGAaTCTAAGCAGgTcATGAAGG+	4	
chr1	75014319 TGcTcCaAAGCAGTAATG.AAGT	+	4
chr5	123198202 TGATTaaAAaaAGTAATGAAtGGC-	5	
chr7	81303569 TaGATTCTgAttAGTAATaAATGA	-	5
chr5	117897188 TGtTcaaAAGCAGTAATGAgtAGGA-	5	
chr19	52451153 a.ATTaTAAaCAGTgATGAAAGA	-	5
chr10	10330380 T.ATTCTAAGagaTAATGAAGGT	-	4
chr1	189975422 aaAgaC.AAGCAGTAATGAATGC	-	5
chr20	9486803 acAcTCTAAG.AGTAATGAgtTGT	+	5
chr20	8897858 a.cTTgTAAGCAtTAATGAATGA	+	5

chrX	92046798 TatTTCTAA.tAGTAATGAAGGA -	4
chr6	36025678 c.tTTCTAAGaAGTAATGgAGGG -	5
chr8	80078169 TGtTcCTAAGaAGTAATtAAAGC -	4
chr6	62752109 TGAcTCTtAGCAGcAATGAATGA -	3
chr7	120366939 TGATTCTAgGaAGTAAaGAAgGG-	4
chr5	160555930 TGATaCTgAGCAGTAAaTaAgAG(-	5
chr15	26331245 T.AgaCaAAGCAaTAATGAAAGA +	5
chr4	170016094 TaATaaTAA.aAGTAATGAATGC -	5
chr18	77879183 TGATTaatAGCAaTAAT.AAAGG -	5
chr9	120932396 ccATTCTAAGCAG.AATGAATGG +	3
chr3	88327031 TaATTCTAgGCAaTAATaAATGT -	4
chr1	69865871 aGATTCaccAGCAGTAATGAgTGA+	5
chr2	85570336 TG.TcaTAAGCAGTgATGAgTGA +	5
chr3	34865479 TG.TgtTAAGCAGTAATaAAAGA +	4
chrX	38614795 TGATatTgtGCAGTAATGAAGGA +	4
chr4	14250590 aGgTTCT.AcCAGTAATGAgAGA -	5
chr13	91512729 TGATTC.cAcCAtTAATGAAGGC -	4
chr9	38518241 TaATaaTAA.tAGTAATGAATGC +	5
chr6	43966707 TGATgtTAAGCAGTAAGGgAATG(+	4
chr1	16895347 TGA.TaaAAcCAGTAAGGAAGGC +	5
chr7	32649628 aaATTCTAAGaAGTAACGAAGGA +	4
chr16	11361674 TGATTaTAAGCAG.AgTGttGGG +	5
chr8	123116021 TtATaTtTAAaCAGTAATGAAAGG +	4
chr1	89215866 TtATTggTAAGCAGTAATGAtTGC +	4
chr7	92403900 TGATTC.AgcCAGTAATGAgGGC +	4
chr1	104892129 TGATT.aAAGaAGTAATGgAAGG +	4
chr18	26003456 TGAaTaCTAtGCAGTAAGGAAAG(+	4
chr6	167001206 TtcTTCTAAaGCAGTAAGGAAAGA-	4
chr4	23119411 TtATTc.AcaCAGTAATGAgAGT +	5
chr2	204605751 TGATTaTAAGagtTAATGAAGgAGG+	5
chr14	47886939 gGccTCTAAGgAaGTAATGAAAGT-	5
chr1	77416519 TaAgTTCTAAGCAGTAATGccAGT-	4
chr6	16776093 TcAgT.agAGCAGTAATGAAGGC +	5
chr3	105544362 gGtTTCaAAGCAGTAATaAAGGC -	4
chr16	90017565 TGgTTCaAAcCAcTAATGAAGgGA+	5
chr6	126818961 cGtTTCTAAGCAGaAATGAAcAGT+	4
chr1	104526243 TagTTaT.AGCAGaAATGAAAGC +	5
chr10	25890786 aGAaTCTAAG.AGTAAaGAAAGA +	4
chrX	29185148 gtA.TCaAAGCAaTAATGAAAGC +	5
chr5	137434915 TGATTaTAA.aAGTAATaAATGT +	4
chr5	37941587 TGATT.aAtaCAGTgATGAAAGA +	5
chrX	127438568 TGATTCatAGgAtTAATGAATGG -	4
chr6	103498383 cGAaTaTAAGCAGTgATGAtATGT+	5
chr11	22476281 aGAgTCTAAGgAGTAAaGAAAGA-	4
chr2	176808412 TGtcTCTAtGCAGTAATGtAAGT -	4
chr21	18976016 aGAaaCcAAGCAGTAATG.AAGG +	5
chr2	169958905 TGATTtTAAGaAaTAATG.AAGG -	4
chr8	71748700 aGAaaC.AAGaAGTAATGAAAGC +	5
chr14	31878811 TtATT.TAAGCAGTAAtgAAGG +	5
chr9	36627295 TtATgTtaAGaAGTAATGAAAGT +	5
chr4	60933491 aG.TTCTAAcCAGTAATttAAGC +	5

chr16	59971629 TtcaT.TAAGCAGTAAaGAAGGT +	5
chr4	165716611 T.AcTCTAAGCAGTAgtTGgAGGA -	4
chr5	51214950 TGAcTtaAAaCAGTAATGAaAcTGC -	5
chr5	124334352 TGATTaTAAGCAaTAAGaAgAGG(+	5
chr4	25696319 TGATTCTAAGaAGTAA.GAATGG +	2
chrX	14015974 TtcTTC.AAGCgGTAATGAATGA -	4
chr4	25657758 TtATTaTtAGCAGTAATGtAgGGA +	5
chr20	58104865 cGATTCTAA.aAGTAATatAGGT -	5
chrX	141468794 gcAcTCcAAaGCAGTAATGAAAGA-	5
chr9	30085548 TaGAgTCTAAGgAGTAATcAtTGC +	5
chr17	54628892 TGAaTCTAAG.AGaAATGAATGC -	3
chr9	93992948 TGATTCTAAaacaTAATGAAAGG +	4
chr1	51750447 TG.TTCTAAGCAGTgATaAtGGA -	4
chr2	32593145 aaATTCTAAGCAGTAgtTGtAAAGA+	4
chr11	33837703 TGA.TagcAGaAGTAATGAATGA +	5
chr1	92745859 aGATTCaTgAagAGTAATGAATGC-	5
chr2	149605148 gagTaCTAAGCA.TAATGAAGGA -	5
chr2	117328608 TaATTaTAAGCAGaAgTGAAaGG/-	5
chr8	106627299 acATT.TAAaaAGTAATGAATGC -	5
chr13	23360198 TtATaaTAA.CAGTAATGAtAGC -	5
chr20	60121129 aGATTCagAaCAGTAAT.AAAGG +	5
chr8	48730318 TGATTCTgAGgAGTAATttATGC -	4
chr2	178999949 TGATTaTAA.aAGTAATGtAAGT +	4
chr14	97164896 TGATTaTAAGgAGaAATaAATGG -	4
chrX	13487892 TG.cTgTcAGCAGTAATGAATGC -	4
chr3	118017519 TGATTc.AtGCAaTAAaGAAGGC +	4
chr14	25845097 TGATTCTAAagAGTAtTaAATGC +	4
chr3	44000317 aG.TggTAAGaAGTAATGAATGG -	5
chr5	163195922 TGATTtTAAGCAGTAAT.AtGGC -	3
chr15	25777989 gGgTTaTAAGaAGTAATGAtATGT-	5
chr5	160555932 TGATaCTgAGCAGTAA.atAAGA -	5
chr15	23081214 T.ATTcCaaAGCAGTAAcTAAAGC -	4
chrX	50375038 aGAcTCTAAGCAGaAATG.ATGC -	4
chr14	67790093 aacTTC.AAGaAGTAATGAAAGG +	5
chr2	234219236 TtcaTC.AAGCAGTAATGgATGC +	5
chr1	55834785 TGATTaTAAGtAGTAATccAAGT +	4
chr3	153494051 TccTT.TAAGCAGTAATaAACGG -	4
chr11	28442877 TtATTaTAA.aAGTAATGAATGT +	4
chr15	85608467 TGATTCTAAGCAaaTAATaAtTGC -	4
chr12	80542229 TaATTaTcAGaAGTAATGAAAGA -	4
chr6	116941644 TGtccCTAAGCAGTtATG.AAGA -	5
chr3	114498227 TtcTgCTAAaCAGTAATGgAATGG+	5
chr2	237827236 TttcTCTAAGCAGaAATG.AAGA +	5
chr12	111868096 TtAgaCTAAGCAaTAAT.AAAGG -	5
chrX	71920761 TaATTgTAAGCAGTAAT.AATGC +	3
chr13	57949316 TG.TatTAAGCAtTAATGAAAGT -	4
chr6	115525284 TctaTCTAAGCAaGTgATGAAAGT +	5
chr17	5876655 aGATTCTgAGCAGTAATaGAgTG]-	4
chr1	120703597 TacTTCatAGCAGTAATGAATGC -	4
chr2	28761513 TtgTaCTAAGCAaTAATG.ACGG -	5
chr3	89827459 TtATTCTAgGCAGTAAT.AAAGC -	3

chr1	207493863 TGATTCTAAcCAGTAATG.tTGT	+	3
chr2	170039447 gGATTCatAGCAtTAATGAAgGGT	+	5
chr6	119331501 T.AcctTAAGCAtTAATGAAAGT	-	5
chr17	46724727 TGtaTC.AAGCAtTAATGAAGGC	-	4
chr4	32609798 T.ATTCagAGaAGTAATGAATGC	-	4
chr3	64512986 TGccTaTAAGaAGgTAATGAAGGT	+	5
chr1	225517168 TG.TTagtAGCAaTAATGAAAGC	+	5
chrX	151750878 TtATTaTAAG.AGTAATGgAAGA	-	4
chr1	144561459 TGA.TaaAAcCAGTAAGGAAGGC	-	5
chr15	78375862 TGATTgTAAG.AGTAATatATGC	+	4
chr10	101406162 aaAgTaTAAGCAGTAAT.AAAGA	-	5
chr2	152741516 T.tTaCTAAaCAGTAATaAATGT	-	5
chr13	30576975 TGAccTCTAAGgAGTAATtAAGGT	+	4
chr5	156836988 TGATTcCAGCAGaAATaGAAAG/-		3
chr8	135142311 TccTcCTcAGCAGTAATGAAGTGA	-	5
chrX	73377810 aGATT.agAGCAGaAATGAAGGA	+	5
chr1	23947960 aGATT.aAAGCAGagATGAATGA	-	5
chr11	38952333 TGA.TaTAAaCAaTgATGAATGC	-	5
chr12	29357945 TGATTc.cAtCAGTAATGgATGT	+	4
chr2	184472037 atATTcCAGCAGTAA.GAAGGA	+	4
chr11	16246345 aGATTtTAAaaAGTAATGAAGGT	-	4
chr2	117328609 TaATTaTAAGCAGaAgTGAAAGG	-	4
chrX	144929059 TtATTCTAAGCA.TAATGgAAGC	-	3
chr2	145923685 TG.gTaTAtGCAGTAATGAAAGG	+	4
chr11	94809715 TGAaTCTAAaCAaTAATGtATGT	+	4
chr1	237611482 TGcATTCTAgGCAGTAATaAtAGT	+	4
chr4	166326963 TGATTtTAAGtCAGTAATaAAAGC	-	3
chr5	91376611 caATTCTtAcCAGTAATGAAGGA	+	4
chrX	79574457 T.AgTCTAAGCAGTcATGAtGGC	+	4
chr14	106700567 aGA.TgTAAaCAGTAATGAATGG	+	4
chr1	56948556 gG.TTagAAGCAGTgATGAAGGC	+	5
chr1	207523500 aGATTaaAAGCAaaTAATGAATGT	+	5
chrX	95149154 TtATTCaAAtCAGTAATGAAAGA	-	3
chr9	106269792 aaATTCTAAGaAGTAATtAAaTGA	-	5
chr3	138563841 aGATT.acAGCAGaAATGAAGGA	+	5
chr4	62523678 TGATTaaAAcCAGTAAGGAAAGA	-	4
chr9	28787777 TtA.TaTAAGCAaTgATGAATGT	-	5
chr5	170905230 TGgTTCTAAaCAG.AATGAAAGC	+	3
chr3	103408177 TGATTCTAccaAaTAATGAATGC	-	4
chr8	78730981 acATTCTAAGCAGTAA.GAACGT	+	3
chr6	3740023 gtATTCT.AGcTgTAATGAAAGT	-	4
chr5	99745367 aGA.TCagAGCAGaAATGAATGC	-	5
chr10	83765970 acATTcCAGCAGcAATGAATGG	+	4
chr4	109090647 TGAaaCTAAGtAGTAAaGAAGGT	-	4
chr14	53327733 ccATTCTAAGCAGTcAATaAAAGG-		4
chr1	201278286 TtgTTCTAAG.AGTAATGAcAGA	-	4
chr4	27225056 aGATTaTAAGgAGTAA.GAAAGG	-	4
chr2	186380554 TGcTTtgAcAGCAGTAATGAtGGT	-	5
chr5	160589763 TGATTaTAAaGCAtcAATGAAGGC	+	4
chr12	107677730 aGgTTaT.tGCAGTAATGAAGGG	-	5
chr10	108807524 aGATatTAAG.AGTAATtAATGC	-	5

chr9	84347720 TGATTC.cAcCAGaAATGAATGC	+	4
chr14	59382214 aaATaC.AtGCAGTAATGAATGC	-	5
chr1	71741122 TtcTT.agAGCAGTAATGAATGC	-	5
chr14	55029194 aGATgaTAgtGCAGTAATGAAAG/	+	5
chr4	109875105 aGA.aCTAAGCAGTAATGgcTGC	-	5
chr18	50910800 gGATTCcTAAaCAGTAATGAcAGC	+	4
chr2	132659195 atATTaT.AGCAGaAATGAAGGA	-	5
chr7	20119222 aG.TgaTAAcCAGTAATGAAGGT	+	5
chr12	62350947 acATcTCTAAcCAGTAgtGAATGT	-	5
chr6	156076352 T.AgTaTcAGCAaTAATGAAGGA	+	5
chr13	50593807 TG.TaCTAtGCACaTAATGAAAGT	-	4
chr5	85470184 TaATaCTAAGCAG.gATGAATGC	+	4
chrX	35020808 TtATTaTtAGaAGTAATGAAAGA	-	4
chr7	54584206 TatcTCT.AGCAGTAATGtAGGC	+	5
chr8	40053247 TG.TaCTtAGaAGTAATGAtAGC	-	5
chr6	10054865 T.ATTCatAaCAGTAATGAgAGT	-	5
chr18	57458664 T.tTgCTAAGCAGTgATGAgTGA	+	5
chr14	75806959 TG.TTaTAAaaAGTAATGAAGGA	-	4
chr20	54089073 atATTCTAAGCAGTcAgTGAATGC	+	4
chr3	54754646 TGAcTCTAAGtAcTAATaAAGGA	+	4
chr18	55235784 TGATTCatAGCAGT.ATaAATGT	-	4
chr1	116365293 aaATTaT.AGCAGTAATGAtTGG	-	5
chrX	14832061 aatTTCTAA.aAGTAATGAATGT	+	5
chr2	34289431 ccATTCaAtAGCAGTAATGgAGGC	+	5
chrY	15943974 aGA.TCatAGCAGaAATGAAGGA	-	5
chr3	37495575 TGATTgTAA.tAGTAATaAAAGC	-	4
chr2	101061437 TatTTCaTAAGgAaTAATGAAAGT	+	5
chr4	106452938 T.ATTaaAAGCAcTAATGAcAGC	+	5
chr22	32463582 cGATT.aAgGgAGTAATGAATGA	+	5
chr2	48412400 T.ATTCTAAGCAaTAATaAcAGA	-	4
chr6	24572522 aGATT.aAAGCAGaAATGAtAGC	-	5
chr6	81186321 TtATTCacAGCAaTAATGAAAGC	+	4
chr9	126627345 TGATTCTAtGCAGTgAtaGAATGC	+	3
chr10	95398183 TGgTTCTAAGtAGTAAT.AtAGA	-	4
chr2	224360169 TtccTCTAAGgAGTAATG.AGGG	-	5
chr2	20740872 TGATTCccAcCAGTAATGAATGA	+	3
chr12	115490834 TGATTCcAAGCAG.AATGcAAGC	+	3
chr1	8456290 TGATaacAAG.AGTAATGAcTGC	+	5
chr16	54353871 TGcTTaTAA.CAGTAATGAtAGT	-	4
chr7	131295925 TttTTCTAAGCAcTAATG.AAGC	-	4
chrX	127438567 TGATTCatAGgAtTAATGAAtGGA	-	5
chr8	15441740 gtATT.gAAGCAGTgATGAAAGC	+	5
chr4	46706612 catTTCTAA.tAGTAATGAAGGA	+	5
chr1	51750448 ctgTTCTAAGCAGTgAT.AATGG	-	5
chr8	33403373 TcAcTaCTAAcCAGTAATGAgAGA	-	5
chr3	86153600 TcAgTCT.AcCAGTAATGAAAGT	+	4
chrX	67441896 gatcTCTAAGCAG.AATGAAGGA	-	5
chr13	55370396 aaAaTCaAAGCAGTAATGAAtTGT	+	5
chr4	60459532 TatTTCTAAGCAGTAaCaGAATGG	+	4
chr9	90006094 TcATaCTAAaCAGTAATGtcATGC	+	5
chr2	65713709 TGATcaTAAGCAaTAATGcAAGA	-	4

chr1	151864209 TaGtaTCTAAGgAGTAAaGAAAGT+	5
chrY	15401814 aGAaTC.AAGCAGTAATGgAGGA +	4
chr12	48848370 gGATTtTAAatAGTAATGAATGC +	4
chr10	67987351 TaAgaTAAGCAGaTAATGAAAG(+	5
chr14	33209367 TttTaCTAA.aAGTAATGAAGGA +	5
chr7	122742661 TGATTaTAAGCA.cAATGtAAGT -	4
chr5	24311889 aGAaTC.AAGCAGTAATGgAGGA -	4
chr21	44931000 TGATTaTAA.aAtTAATGcATGG -	5
chr9	2072345 TGAaTaTAAtCAGTAAcGAATGA -	4
chrX	17535346 T.AcTagAAGCAGTAAGGAAGGC +	5
chr19	38178021 TGATTaTAAaCAGTAcT.AcAGA +	5
chr6	155979135 TcAgTC.AAaCAcTAATGAAGGC +	5
chrX	95747168 ctA.TaTAAtCAGTAATGAAAGG -	5
chr1	68332352 cttTTCTAAG.AGTAATGtATGT -	5
chr4	167703000 aGATaCTAAGCAaaAATGAAGgAG/+	5
chr12	9871994 TtA.cCaAAGCAGTAAGGAAGGC +	5
chr12	44905979 T.ATTCTAAaCAGTAATacgTGC +	5
chr13	23551617 TccATcCTAAGCAaTAATaAAAGT -	5
chr12	78131649 TGtTcCTAAGgAaTAATGAAGGT -	4
chr6	101497393 TGATTtaAtGCAaTAATGAATGA +	4
chrX	95356921 aGATaCcAA.CAtTAATGAATGC -	5
chr21	24782672 c.ATTaTtAGaAGTAATGAATGT -	5
chr3	135836036 TGATTtTtAGaAGTAATGAAtGGT +	4
chr1	189544524 TGATTaTAAtCAGTtATaAATGG -	4
chr2	170325146 TaGATaCTAAGgAGTAAaGAgAG-	5
chr7	104639942 aGATTaTAAGCAG.AATGAtGGC +	4
chr7	32649627 aaATTCTAAGaAGTAACg.AAGG +	5
chr10	83765971 acATTcCaaAGCAGcAATGAAtGGG+	5
chr18	9343126 aGATaCcAAaCAG.AATGAATGA -	5
chr5	76590602 T.AaTaaAAaCAGTAATGAATGT +	5
chr3	83775809 gGAcaTaTAAGCAGTAATaAATGT+	5
chr1	217821071 gcATTCT.AGCAGTAgTGAATGA -	4
chr1	61170879 TtgTTtTAAaCAGTAATGAACtGT +	5
chr9	133241093 TGATTaaAAG.AGTAATaAATGG -	4
chr3	179512663 TGAgcaCaAAGCAGaAATGAATG(-	5
chr1	52726139 TGAcaaT.AGtAGTAATGAATGA +	5
chr3	6233737 TcATaaTAtGCAGTAATGAgaAGA+	5
chr14	97164895 TGATTaTAAGgAGaAATaAAtGGC-	5
chr2	84313506 aGcTT.TAAGCAtTAATGAAAGA -	4
chr2	170277681 TGATTaTAA.aAGTAATatATGC +	5
chr1	212113005 TGA.TCcAtGCAGTAAGGAAGGT +	4
chr2	228307209 TtcTT.TtAGCAGTAATGAcAGG -	5
chr2	32441484 TtATTCTtA.CAGTAATGAAAGT +	3
chr12	27556264 TcATTaacAtGCAGTAATGAATGT -	5
chr11	31188179 TaAaaCTAAGCAGaAATG.AAGA +	5
chr7	90362129 aGA.TCagAGCAGaAATGAAGGA -	5
chr2	45119104 TtATTCTtAAGtAGTAATGAtTGC +	4
chr2	103908747 TGcATaCTtAcCAGTAATGAAGGA+	4
chr3	155700716 TGATTCTtAAcCAaTAATGAgtGT -	4
chr2	62974367 TGATTaTAAG.AGTAgTacATGT +	5
chr6	166362797 TGATTAgAAGCAGTAaggGAAAGG-	4

chr8	131046190 TaATgaaAAGCAGTAATGAAAGC +	4
chr19	55880732 TGATTCaAAGCAaTgATacAACGT+	5
chrX	98471388 TaATaaTAA.CAGTAATGAAAGT -	4
chr4	97831517 aGA.TCagAGCAGaAATGAAGGA +	5
chr2	435681 TGAaTC.AAaaAGTAATaAAGGA -	5
chr12	64309938 TGATaCTAAG.AcaAATcAATGG +	5
chr5	25139885 aGA.TgTAAGCAGTcATGAAGGT +	4
chr3	187122717 ccATcCTtAGCAGTAATGAAGGA +	4
chr4	123199401 gGA.aCatAGCAGTAATGAAAGA +	5
chr4	113240365 TaATaTaTAAGCAaTAATaAATGC -	5
chr5	79088566 aGAcTTCTAAGgAGTAgtGAAAG/+	4
chr7	133953258 gG.TgCTAAGaAGTAATGAtTGA -	5
chr7	115515766 gGATTaTAAtCAGTAAGGAAGGA -	4
chr5	121796709 TGATTC.AtGCAGTtATGgAGGC +	4
chr4	68360632 aGcTTCTAAGCAGTAAaTgtTGC -	5
chr1	62182379 aGAaTC.AAGCAGTAATGgAGGA -	4
chr13	86156963 TGtaTCTAAG.AGaAATGAAAGC +	4
chr5	65638215 TcATTaacAAGCAcTAATGAATGC +	5
chr16	69910981 TGATTaCagAGCAGaAATGAgAG(-	5
chr2	222045980 cccTTCT.AGCAGTAgtTGAATGA +	5
chr3	39815458 a.cTTCTAAGgAcTAATGAAGGG -	5
chr5	5453018 TcA.gaTtAGCAGTAATGAATGC +	5
chr6	71173812 TcAcTCctAGCAGTAATGAgAAGC -	5
chr4	142756138 aGATTCTAAaCAGagATGAAGAG(+	5
chr10	24763244 TGATcTaatAGaAGTAATGAATGT -	5
chr11	16246346 aGATTtTAAaaAGTAATG.AAGG -	5
chr9	32705021 TGATTcCaaAGCAtTAATatAAGA -	4
chr4	100592890 TGATTCTgAGCAGTAAT.cAAGC +	3
chr5	18483193 T.AgTaTAAaCAGTAATGAcTGA +	5
chr13	66842770 ctATTcCaaAGCAcTAATGAAGAGG +	5
chr4	45162264 gGATTacAAG.AGTAATGAgTGC -	5
chr12	83919555 gttTTaTAAtGCAGTAATGAAGGA -	5
chrX	88842767 TGAcTCT.AGCAaTAATGAtAGC -	4
chr21	40449591 atATTCTAAaCAGTAAT.cAAGC +	5
chr13	112523019 TGAcTCTAAGCAGTAA.cAtAGC +	4
chr3	191311711 TcATT.aAgGCAcTAATGAATGC -	5
chr12	18499067 TGATTaTAAatAGaAATGAgATGA-	5
chr2	117218000 TG.TTCTAAaCAGTgcTGAtAGT -	5
chr1	76573815 TacTTCTAgGaAGTAATGAAtGGT +	5
chr5	169644087 aGATgCaAAGCAGTAAGGAAtGG,+	5
chr7	88352208 aG.TTCTAAGCAGcAATcAAGGC -	4
chr7	42315756 acAgTC.AAGCAGcAATGAAAGC -	5
chr15	85571608 aGATT.aAAGCAGgAATGAAGGT -	4
chr4	58257597 TGATTCTAAaC.GTAATatAAGG +	4
chr1	182841751 TGAgtCTAAaCtGTAA.GcAAGA -	5
chr2	237573793 ccATcCT.AGCAGTAATGAtGGA +	5
chrX	67741951 TG.TTaTtAttAGTAATGAATGT +	5
chr6	85613519 TacTTCTAA.CAGTAATGAtGGG -	4
chr5	55334953 T.ATTCctAcCAGTAATGtATGA +	5
chr2	39688686 TttTTCTAAGCAaTAATcAAAGT -	4
chr21	18337775 TtgTT.TAAGCAGTAATaAAAGG -	4

chr14	73108850 acATTCTgAGaAGTAATGAAcTGC+	5
chr7	79562731 aGATTcCaaGCAGTAATGttAGA-	5
chr21	18169358 TtAcT.aAAcCAGTAATGAAAGA -	5
chr8	142050227 gGATTCTttaCAGTAATGAAgAGT -	5
chr3	29250288 TcAgTTgaAAGCAGTAAcGAAGG(+	5
chr7	83944341 TGtTagTAAGtAGTAATGAcAGGC+	5
chr3	180044948 T.tcTCTAtGaAGTAATGAAAGT +	5
chr3	159875655 gttTTCT.AGCAGcAATGAATGC -	5
chr1	188587128 TaGAaTaTAAaCAaTAATGAAGGT-	5
chr9	120131574 TcAgTCcAAaGCAGTAATGAAAG^+	4
chrY	9978533 aGA.TgTAAaCAGTAATGAATGG +	4
chr4	173137759 ctATTCTAAGCAGTAA.GgATGT +	4
chr10	8568706 TGcTTCTAAaCAGTgATcAAGGC -	4
chr18	33352649 TGAgtCaAAGCAGTAATcAcAGG -	4
chr3	124450388 aaAaT.TAAGtAGTAATGAAAGC +	5
chrX	16072368 atA.TCaAAGCAGaAATGAATGA -	5
chr6	67101936 TtAcT.TAtGCAGTAATGAATGA -	4
chr4	26824694 TaATaCTAAGaAGTAAaTGAAtAGC-	5
chr5	80152066 TcAgTTCaAAGCAGaAATGAAAGT-	4
chr8	56192333 TaAaT.aAtGCAGTAATGAATGA -	5
chr3	189282603 TtATT.aAAGCAGTtATGAAAGA -	4
chr10	101519646 TtATTc.AAaCAGTAATGtAGGT -	4
chr18	64163203 TGcTTtTAAGCAGagATGAAGGC -	4
chr10	1164173 gGATTaaAAaCAGTAATGAAaAGT+	5
chr12	78131650 TGtTcCTAAGgAaTAATG.AAGG -	5
chr9	102458067 TGATTaTAAaCA.TAATtcATGT +	5
chr20	43226751 aGtTTCTAAGCAaTtAATtAATGC -	5
chrX	71920763 TaATTgTAAGCAGTAATaAtgCGA+	5
chr11	104866644 acATTaTAA.tAGTAATGAATGC +	5
chr9	15683264 TGATTaTAtAatAGTAATGAtTGC +	5
chr18	45952064 TGATTaTAA.aAGTAATcAtCGG -	5
chr12	24492679 TaGAcTCTAAGaAGTAATtcAGGC-	5
chr13	74922546 a.ATTCTAAaCAGTgATaAAAGG -	5
chr4	170340562 TGATcCTAAGCAGTAgtAtAtAGT -	5
chr10	75942427 TGATTaTAAGCcAtaAATGtAAGT -	5
chr3	76531171 acATTaTAA.aAGTAATGAAAGA +	5
chr1	179745640 TGATTaTtAaCatTAATGAAAGT +	4
chr6	83757592 aGATTCTAAGCAG.AcTGAcTGT +	4
chr2	239977180 TctTcCTAA.CAGTAAcGAAGGC +	5
chr3	177064955 TGAgtTaAAGCAGTgATG.AGGT -	4
chr7	16452986 TcATTaTcAGtAGTAATGAAAGG -	4
chr2	234097266 TGAcT.TAAatAGTAATGAATGC -	4
chr11	39258888 TGATTCTgAGCAGTAcT.AAAGT -	3
chr11	134648775 TGATTaTAAaCgGTAATGcATGT +	4
chr14	38225690 TtcTgCTAtAGCAGTAATGtATGG +	5
chr6	154331967 aGtTTCagAGCAGTAATGAAaGG/-	5
chr2	44342440 TGATaacAAaC.GTAATGAACGC -	5
chr11	42652494 TaATTCTAAtCAGTAATaAAcTGG +	4
chr3	94679862 aGATT.agAGCAGaAATGAAGGA +	5
chr8	132244043 aGATTc.AAcCAcTgATGAAGGA +	5
chr2	61788298 aaATTaTAAGgAGTAATGAAcTGA+	5

chr11	134263650 caATTCcAAG.AGTAATGgAAGG -	5
chr6	166362796 TGATTgAAGCAGTAaggGAAaGG-	5
chr13	83067001 T.cTTCaAAGCAGTAATtAAAGC +	4
chrX	142523707 T.AagggAAGCAGTAATGAATGT +	5
chr7	26605212 TGATTCTAAaCttTAAaTGgAGGA +	5
chr1	172483406 aGATTC.AAGaAGTcATGAtTGT +	5
chr10	13473148 TGAgtCTAAG.AGagATGAcAGG -	5
chr10	46983377 TGATTCTgAGtAGTAAgGAgAGG +	4
chr8	142050229 gGATTCTttaCAGTAATG.AAGA -	5
chr16	90017564 TGgTTCaAAcCAcTAATGAAGGG +	4
chrY	12793244 cG.TTCcAAGCAGaAATGAATGA +	4
chr16	60712105 TGATTCTAAagcaTAA.GAAAGT -	5
chr2	192839279 acATTCTAAGCAGgAAgGAAAGA -	4
chr17	52706886 gGAaTCTAAGCA.TAATtcatGA +	5
chr4	21943678 TGATTCT.AtaAGTAATGgAGGG +	4
chr7	87586801 TGgTTaTtAcCAGTAATGAAtGGC +	5
chrX	80549813 aG.cTCTAAGCAGcAATaAACGC -	5
chr11	16772740 TGATaCaTAAGCAGcAATaAAGG]+	4
chr7	138340637 aGAaTC.AAGCAGTAATGgAGGA +	4
chr20	62371146 TGAcACTAAcCAGgAATG.AAGG +	5
chr16	66038672 atATaCTAAGCAcTcAATGAATGT +	5
chr13	84919472 TtATTCatAtCAGTAATGAAaGGA +	5
chrX	75683514 aGA.TCatAGCAGaAATGAAGGA -	5
chr6	55903880 T.ATTacAtGCACtAATGAAGGG +	5
chr3	164076571 TGATTaggA.aAGTAATGAAGGC -	5
chr2	8283998 TGATTCctActAGTAATGAgAAGC -	5
chr20	8513325 TG.TgtTAtGCAGTAATGAAGGG +	4
chr4	176105850 TaATaTCTAAGCAGagATaAATGA+	5
chr20	35046297 aGATTtTAAGgAGTAATGAgTGA -	4
chr4	189816541 TGATTC.AtGgAcTAATGAAAGT +	4
chr9	1970633 TtcaTCTAAGaAGTAATG.AAGT -	5
chr6	104998587 gGATTCTAAGagGaAATGAAtGG/-	5
chr3	175061291 TGATTtTAAGCAGcAAgGAAAGC +	3
chr5	122650392 TGcTTCTAAGCAGTtATcAATGG +	3
chr10	97973154 TGATTCTAA.aAGTAATGcAAGC -	3
chr7	41072891 T.AaaCTAAaaAGTAATGAATGA +	5
chr5	50995276 TGgTTCTgAGCAGTAgtGAATGT +	3
chr2	211699038 TGATTtaAAaCAGTAATG.ACGA -	4
chr15	75553006 gGATTCTAAaCAGTgAgTGAtAGA-	5
chr2	135946156 TtcTTCTActGCAGTAATGtACGC -	5
chr21	30213487 TGATTCTAttgAGTAATcAATGA +	4
chr12	65006273 aGATTCaAAGCAGaAATaAAcAGC-	5
chr13	23828807 TGATTCTAAaatGTAtATGAAAGA +	4
chr13	92322485 gcATTCTAAaCAG.AATGAAAGA +	4
chr3	189140793 TaATTCaAAGgAGaAATGAAAGG -	4
chr8	116592318 TGA.TCTAAGaAGaAATGAAAGA -	3
chr4	172685436 TcAcTaTAAGCAGTAgtGAACAGA-	5
chr6	19685746 TGATTCTAAaatGTAcgTGAAAGA +	5
chr4	176726370 TGATaCTAA.aAGaAATGAtAGC +	5
chr2	213565854 TGATTCaAAGCAaTgAT.AACGA +	4
chr6	157151825 gcATTCaTAACAGTAgtGAAAGC-	5

chrX	13070340 TGATTC.AAaaAGgAATGgAGGG	+	5
chr1	205940515 gGAgTCatAGCAGTAATG.ATGA	-	5
chr12	71326993 ctATTCTAA.aAGTAATGtATGT	-	5
chr5	92419011 a.ATTtaAAGCAGTAATGgAGGA	-	5
chr1	98413164 TGATcCTAAGCA.aAATGAATGA	-	3
chr8	140561402 TGATTaTAA.aAtTAATGtAAGT	+	5
chrX	101878460 TGATaCT.AGtAGaAATGAATGT	-	4
chr5	163453071 aGATagTAAtCAGTAATG.AGGA	+	5
chr5	25374371 aGA.TCTAAaCAGTAATaAtGGT	-	5
chr12	71032404 T.ATTaaAtGaAGTAATGAATGC	+	5
chr2	217758953 gGcTTCaAAaCAGTAATG.AAGT	-	5
chr18	67979540 TaATTc.AAaaAGaAATGAATGA	+	5
chr1	219600316 ctA.TCTtAGaAGTAATGAATGC	+	5
chr14	52316617 TG.TaagAAGCAGTAATGgAGGC	-	5
chr2	167962136 TccTT.TAAaaAGTAATGAAAGG	+	5
chr14	87215594 TG.TTtTAAGCAGTAATaAtAGT	+	4
chr11	95145818 TGtcTCTAAGCAGaAATG.AAGC	-	4
chr2	174419752 TctTaaTAA.CAGTAATGAATGT	-	5
chr10	18817906 T.ATTCTAAGCAGTAAGatcAGT	+	5
chr6	2955764 T.cTTtTAAGCAGTAATaAgGGT	-	5
chr3	59722497 TtAgTCTAA.aAGTAATGAACGG	-	4
chr5	67531582 TGgTTaTAAGCAaaTcATGAAAGC-		5
chr19	27826980 c.ATTaTatGCAGTgATGAAAGA	-	5
chr15	85599086 aGATT.TcAGCAcTAATGAAGGA	-	4
chr11	12378234 TGATTtTAAGgAccAATGAAGGC	-	4
chr1	215489226 TGgTTaTAAGCAGTAtaGAaAcTGA+		5
chrX	78201883 TGgTTaTAAaCAGTAtGtAATGA	-	5
chr12	10295960 TGATTCaAAGCAGT.tTaAtTGG	-	5
chrY	20972319 aGA.TgTAAatAGTAATGAATGG	+	5
chrY	1551459 TtATTcccAtGCAGTAATGAgtGA	-	5
chr10	133246584 TGATTacAA.aAGTAATaAAGGT	+	5
chr9	88762798 TtATTc.AAGaAGTAATagATGG	+	5
chr1	242633870 T.cTTCTAAGCAGTAAatAgTGC	-	5
chrX	153173222 TGcATTtctAcCAGTAATGAATGA	-	5
chr10	31121852 TtATT.TAAGCAaTAATGAcTGC	+	4
chr7	135926938 TctTTCTAAGCgGTAATGgAGGA	-	4
chr8	90815994 TGcTTtTctAcCAGTAATGAATGT	+	5
chr4	66688511 TaAgcCTAAGCAGTgATGAgATG/+		5
chr9	93992949 TGATTCTAAaacaTAATGAAaGGC+		5
chr3	11740209 gGATTtTcAGCAGTAATGAcACGC-		4
chr14	50793427 acATTCTAAGCAaTtAATGAcAGC	+	5
chr13	78905226 TaAaT.aAAGCAGTAgtGAATGA	-	5
chr13	56550666 T.tTTaaAAGCAGTgATGAATGT	-	5
chr9	85539802 TctcTCT.AGtAGTAATGAAGGA	-	5
chr9	100930036 T.tTTaaAAGaAGTAATGAAGGG	+	5
chrX	121934349 ccATTCTAAGgAaTAATG.AGGG	-	5
chr1	90098976 aGA.caTAAaCAGTAATGAAAGG	+	5
chr3	131420544 T.ATgagAAGCAGTAATGAgaGA	-	5
chr1	216415354 TG.TTaTAAGaAGTAATGgAAGC	-	4
chr12	67830057 TGAaTCTActCAGTAATGAATGC	+	3
chr14	24362496 T.ATgtTatGaAGTAATGAATGA	+	5

chr4	55512191 TGcATTCTAAcCAGcAATGAATGA+	3
chr3	60529546 T.ATaaTtAGaAGTAATGAATGG -	5
chr7	88104642 TtAaaCTAAGaAGTAATG.AAGC -	5
chr17	8711662 TaATaTaTAAaCAaTAATGAATGA +	5
chr4	109090648 TGAaaCTAAGtAGTAAaG.AAGG -	5
chr18	43921450 TGATaCTAAaCAtTAA.GAcAGA +	5
chr10	82771593 TtccTCTAAGCAGTAA.GAATGT -	4
chr9	20813300 TGAaT.aAAGCAGaAATGAATGT +	4
chr3	32734655 T.AaTaTAAGCAGTtATaAAAGC -	5
chr22	12203090 aGAaTC.AAGCAGTAATGgAAGA -	4
chr3	127953169 T.AcTaTAAGCAaTAATGAtTGT -	5
chr18	24873614 TGATTcAcAGCAtTAAgGAAAGA -	4
chr1	200595244 cacTTCTAAGCAGTAA.GtATGC +	5
chr8	2578139 TGATaCTAAGCAG.AcTGAACGT +	3
chr13	73153253 TGATTCTAAGgAcTAgAgGAgGG(-	5
chr15	68005383 TGATaCTAAGgAGTAAGGtAtTGC+	5
chr15	54890437 aGA.TgTAAaCAGTAATGtATGG +	5
chr3	180082484 TGcATTCTtAcCAGTAATGAATGA -	3
chrX	102951177 T.ATTCTAcagAGTAATGAATGT +	4
chr13	92692852 TGATTaTAAGCAcTAAT.AtGGT +	4
chr3	75810909 aGAaTC.AAGCAGTAATGgAAGA -	4
chr4	126948936 aG.TTCTAAGCAaTAATaAtAGT +	5
chr6	58043575 T.ATTCTAAGCAGTtATGtgAGA +	4
chr2	106958217 TGATTaTAA.aAGTAATatATGT +	5
chr17	62068336 TGATT.TAAagAGTAATGgAGGC +	4
chr15	71321679 T.ATTaaAAGCAGTtATGAATGT +	4
chr1	83966443 TGATcCTAtGgAaTAATGAATGT -	4
chr7	146160337 aGA.TCagAGCAGaAATGAAGGT +	5
chr6	95401114 TtATTCaAAG.AGTAATGAtTGA +	4
chr18	5071102 aGATTCTAAGaAGTcAcG.ATGT -	5
chr6	133004488 gatTTCTAAG.AGTgATGAAAGT +	5
chrX	22480026 TtA.aaTAAcCAGTAATGAATGG -	5
chr4	163081266 TGATTCTAAaactTAtATGAAAGT +	5
chr2	40105462 TaATTCTAAaCAGTgAT.tAAGC +	5
chr2	223897292 aGATgCTAAGCtGTAATGgAtTGC-	5
chr21	22131008 TGATTCaAAGCAcTgATtCAAAGC -	5
chrX	36281990 TGATTCTAAaaAaTAATaAtAAGA +	5
chr20	38418935 TaAgTCTAAGCAGTAAT.AcAGT -	4
chr18	38217655 TGcTTtCTAAcCAGcAATGAATGA -	4
chr8	100862283 TGATaCTAAGaAGTAAT.AcAGC -	4
chr2	3899914 TGATTcAcAGCAcTcATGAAAGG -	4
chr4	23774430 TtAcT.aAAGCAGaAATGAAAGA +	5
chr10	78803705 TtcaTCTAA.CAGTgATGAAGGT -	5
chr18	65814639 TaATTCTAAGCAGcAAacAAaTGA-	5
chr2	35134671 TGgTTCTcAGCAGTAATtAgAGC -	4
chr7	119892715 TGATTCTAAaGtAGTAgctAAAGG +	5
chr4	119044779 TGtTTCTAAGC.tTAtTaAATGG -	5
chr12	11742225 ccATTCTAAaaAGTAAaTGAATGA -	5
chr18	57119026 T.ATTtaAAaCAaTAATGAAGGC +	5
chr6	147053153 TGATTCTAAaCAGcAAgaGgATGC+	5
chr18	74521921 TGAacCTcAGCAGTAATGAcACGT+	4

chr1	103892123 TGgTTCTAAGaAcTAAaTGAAAGA-	4
chr3	36841699 gaATTCcAAGCAGgAATGAAGTG(-	5
chr1	57050930 gGATTacAA.aAGTAATGAAGGT +	5
chr11	95355308 TGATaTagAAaCAGTAATGAtGGA+	5
chr15	27299446 caAaTC.AAGaAGTAATGAAGGA -	5
chr8	141312080 TGgAacCTAAGCAGTgATGgAGG(-	5
chr7	87586800 TGgTTaTtAcCAGTAATGAATGG +	4
chr6	146079691 TctTcCTAAGCAGTcAATGAAAGA +	4
chr5	61866835 TtgTTCaAAGCAGTAATG.AGGT -	4
chr1	54327047 TGgTTtCTAAGCAGTAActcAGGC +	5
chr22	11789146 aGAaTC.AAGCAGTAATGgAAGA +	4
chr2	132617859 TGATaCTtAGaAGTAATGAaAAGC+	4
chr8	104570280 TGATTCTAAaatGTAtATGgAAGA +	5
chr2	78041070 TGATTCTAA.aAGTAATatATGG -	4
chr2	209926159 aGATagTAAGCAGTAAT.AtGGG -	5
chrX	97662195 TGtTaCcAAGCAGTAAGGAAGGG +	4
chr4	94550508 TtATTCTgAGaAGTAATGAtAAGC -	4
chr2	132845546 TaATagT.AGCAGTAAGGAATGA -	5
chr6	137690696 TGcTT.acAGaAGTAATGAAAGC +	5
chr2	14237528 TtATTc.AAGCAaTgATGAAAGC -	4
chr3	98202447 TcA.TgTAAaCAGTAATGAtGGA -	5
chr4	135299001 TGAgaagAAGCAGTAATGAAaGG-	5
chr11	13265797 TtATTCT.AcCAaTAATGAAAGG -	4
chr4	110104549 TG.TTCTAAGCAGaAATGgATGT -	3
chr3	135836035 TGATTtTtAGaAGTAATGAATGG +	3
chr1	52170120 TaATTCTAAGCtGTAATaAtTGT +	4
chr4	176504324 TGATTaTgAGCAGTgATGtAATGC-	4
chr4	144886898 TGAgtTtTtAGCAGTAATGAcAGT +	4
chrX	124336829 TGATcCTAAActAGTAAT.AAAGA +	4
chr1	191993354 gtgTTCTAAGCAGT.ATGAtAGG +	5
chr7	135137468 atATT.gAAGCAGTAATGAcGGA +	5
chr1	210152314 TGgcTgT.AGaAGTAATGAAGGA -	5
chr2	228000993 T.ATTCcAAtCAGTAATGAATGA +	3
chr18	42282738 aGATTCTAAGtA.TAATaAATGC -	4
chr4	112148998 TGATTaTAA.aAGTAATGtgTGC +	5
chr12	130238323 TGcATTCTtAcCAGTAATGAATGA -	3
chr5	159232678 TGATTCTAAaCAaTgATaAcACGC +	5
chr16	20324622 TtAaT.aAAGCAGaAATGAAAGT +	5
chr18	77522781 TGATTCaAAGCAtTtATcAAgTGT +	5
chr2	61220049 gGcATgaTcAGCAGTAATGAAGG(-	5
chr4	62847041 aGAaTaTAAaCAGgTAATGAAAG(+	5
chr11	37798921 gGATTCaAAG.tGTAgTGAAAGA -	5
chr7	15125977 T.ATatTAAttAGTAATGAATGC +	5
chr2	48307482 aGATTCTAAGCAG.ccTGAAGGC +	4
chr20	62863240 c.ATTtTAAGaAGTAATGAtTGC +	5
chr5	130288434 TGATTaTAAaCAaTtAT.AATGG +	5
chr8	98025850 TcGATagTAAGCAGaAATaAAAGC-	5
chr10	67152436 TGAcaCTAAaC.GTAATGtATGC -	5
chr20	59113033 gtAaTCTAA.CAGTAATGAtGGT +	5
chr11	99451349 TGATTCTAAGaAcT.AgGgAGGG +	5
chr6	66820026 T.ATTtTAAatAGTAATGAATGA -	4

chr13	78197985 TGATaCT.AGaAaTAATGtAAGC	+	5
chr4	38913207 TGATTCTAAGCA.TctTttATGT	-	5
chrX	104263412 TaATcaTAA.aAGTAATGAATGA	+	5
chr6	135285534 aGATaCTAAGgAGgAA.GAAAGG	-	5
chr4	102137245 TGgTTCTAAaCAGTcA.GgAAGG	-	5
chr1	83395041 aGATTCaAAGCAGgAgATGgATG(-		5
chr20	3070919 TGAaTCTAAaCAGTAtATagAGGC+		5
chr17	63253118 aGAgaC.AAGCAaTAATGAATGC	-	5
chr6	82530603 TGATTCTAAaaAGTAAaGAaCGC+		4
chr10	76746615 TaATTCTAAGtAcTAAaGAAAGC	+	4
chr3	135159801 TGATTCagAAGCAGTtgTGAAGG/-		5
chr11	24953763 gGATTCTAAatCAGTAtTGgATGA	-	5
chr6	77527529 TGATTCaAAG.AaaAcTGAATGC	+	5
chr13	55642592 TGATTtagAAGCAGTgA.GgAAGG	-	5
chr15	36105460 TGATTCTAAaatGTAtATtAAAGG	+	5
chr18	14628355 TGATTaTAAaCtGTAAT.cAAGA	+	5
chr14	46448119 T.tTTaTAAaCAaTAATGAATGT	-	5
chrX	136340326 TGATTCTAAaaAGcTAcTGAATGT	+	5
chr11	27635479 TG.TTCTAAGCAtTAAatgAAGA	+	5
chr11	121511009 TGATTaTAAGatGTAtTgTAAGGC	-	5
chr3	120360986 TGATTC.AtGCAGcAATaAAAGT	+	4
chr2	192945234 TGtgTtcAAG.AGTAATGAAAGG	-	5
chr5	68880185 TGATTgTAAaCA.TAATatATGC	-	5
chrX	74755084 atATTCTAAGCAGTgAaGAaCAGC+		5
chr2	123287949 TtcTaCaAAGCAGcTAATGAATGA	+	5
chr5	30522598 gtAcTCTAAaCAG.AATGAAAGC	+	5
chr10	93975 TaATTCaAAGaCAaaAATGAAGGT+		5
chr10	20439188 aGA.TCagAGCAGaAATGAAGGA	-	5
chr1	236847570 aGATTCTAAGCAGcAA.GAAGGA	-	3
chr15	35180963 TGcaTtTAAGCAaaTAATGAATGT	+	5
chr17	51291982 TGATcCaAAGCA.TcAgGAAAGC	-	5
chr4	102958981 TGA.aagAAGCAGTAATGtAAGA	+	5
chr18	47173219 TGAgt.TAAaCAGTAtTGgAGGA	-	5
chr5	21875811 aaATTtagAAGCAGTAATGAtAAGC-		5
chr5	110910016 TG.TaaaAAGCAGTAAGGAATGC	-	5
chrX	111400602 gGgTaTCTAAaaAGTAATGAATGC+		5
chr2	18292925 TGATaCTAAGCAtTAA.cAATGA	+	4
chr5	67872213 TGtgTCTtAGaAGTAATGAATGA	-	4
chr7	103051257 TGATagTAAGCAGTAAT.AtTGC	-	4
chr6	21286706 aGATTCTAAGaAGT.ATGAAAGA	-	3
chr13	64090735 TGAgtCaAAGCAGTAAGTaAtAGC-		5
chr16	60490357 TGAgtTaActGCACtAATGAAAGT	+	5
chr3	168425672 T.AcTaTAAGCAGTAAGGAgGGC	-	5
chr1	103329864 aGAagCTAAGCAGTAAaTaAAAG(+		5
chr7	73355054 c.ATaaTAAGCAGTAATcAAAGA	-	5
chr12	11527355 TtcTTCTAAGCAGTtAAaGAAGGA-		4
chr6	140273727 TGtTTCTAAGCAGaAAT.taAGG	-	4
chr1	239450269 TGATTC.AAGCAGTtAcGAtTGA	-	4
chr7	15610606 T.ATTCTAAGCAGaAATGctTGG	-	4
chr5	111272046 TGATTCatAcCAGTAA.cAAAGG	-	5
chr7	7276995 TGATTCTtAG.AGTAATatATGA	+	4

chr4	167945328 TaGATTaTAAGCAGaAATcAgGG(+	5
chr2	207679592 aGATTaTAAGCA.aAtTGAAAGT -	5
chr16	6245221 TGAaTaTAAGCAGaAATG.ATGG +	4
chr3	137093566 caATTCTAttCAGTAATGAAaTGA -	5
chr3	62535554 TGATTCTAAaCAcTAAaG.tTGA -	5
chr5	176545581 ctgTTCTAAGgAGTAATG.ATGT -	5
chr5	5254719 TGATTCatAGCAGgAATGtAAGGA-	4
chr7	109162471 aGATTCTAA.attTAATGAATGC -	5
chr22	21996446 TcAgaCTAcAGCAGTAATGAAAGC-	4
chr12	72225653 TGATTaTAAaCAG.AAgGAAAGA -	4
chr3	35436627 TGgTTCT.AcCAGTAATGAcTGA -	4
chrX	67367286 aG.TaCTAAGCAGggATGAATGT +	5
chrX	151936704 aGA.TCTAAGCAaTAATctAAGC -	5
chr11	28528337 TaATaCTAAGCAaTtATGtAAGGA +	5
chr3	72476082 TGATTCTAAatAGTAtTGAAtATGG -	4
chr1	177849696 acATTCaAAGCtGTAATG.AAGG +	5
chr1	101784853 gcATcCTAA.aAGTAATGAAAGC -	5
chr6	13003566 T.AaaagAAGCAGTAATGAAGGC -	5
chr14	105727231 TGATTCTAAatCAAtTcATGAgGGA -	5
chrX	45289618 TGATTCTgAGCAGTAAactATGA +	4
chr12	46896764 TcAaaCTAAtCAGTAATGAATGC +	4
chr11	31166853 atATTCcAAGCAGTAA.GAAGGA -	4
chr18	23574883 TGATTCTAAGgAaaAAaGAAaCG1+	5
chr4	44463640 TcAaTCTAA.aAGTAATGAAAGT -	4
chr2	84995907 TtATTtaAAGaAGTAATG.AAGA +	5
chr5	12751216 TaATTCTAAatAGTAAT.AAAGT +	4
chr3	10883721 TGATTCTAAGCAaGgAcccAAAGA+	5
chr6	160895326 TGgTTtagAAGCAcTAATGAAAGA+	5
chr17	60624250 TGATTC.AAaCttaAATGAAAGA +	5
chr1	91847301 TGATTaTAAG.AaTAAaGtAGGG +	5
chr1	221735065 caATTCTAAGgAGTgATG.AAGT +	5
chr6	6655296 T.AaTgaAtGCAGTAATGAACGC -	5
chr20	4366484 aG.TggTAAGCAGTAATaAATGG +	5
chr2	86635593 TtATTCTAAGaAGTAATttAAGT -	4
chr4	42459709 caAaTCT.AGCAGTAATGAACGA +	4
chr3	133801006 aaAcTC.AAGCAaTAATGAAAGC -	5
chr16	18546709 TGtaTgTcAGCAGTAATGAATGA -	4
chr3	32564830 TGATTaTAA.aAaTAATGAgAGT -	5
chr6	29802853 TGgTTCTAAaCcGTtcATGAAGGA -	5
chr19	30551287 T.cTTCctAtCAGTAATGAAGGA +	5
chr1	215321624 TaATTtTAAGCAcTAATaAATGA +	4
chr3	62939320 TGATTCTAAaatGTAtATaAAAGA -	5
chr3	75501947 TGAaTCTAAGCAGgAATG.cCGT +	4
chr13	68276782 ctATTCT.AtCAGTAAGGAAGGA +	5
chr8	39445256 TGATTCTAAGCAcTAcTG.AAGA +	3
chr8	76579997 TaATTCTAAGCAGTggTG.ATGG +	4
chr8	115540521 TGAaT.TctGCAGTAATGgAAGA -	5
chr3	113886692 aGATTaTAA.CAGaAATGAATGA +	4
chr8	49026957 TtA.TCTAAGgAGTAATGttTGC +	5
chr10	8568707 TGcTTCTAAaCAGTgAT.cAAGG -	5
chr4	135299002 TGAgagAAGCAGTAATGAAAGG-	4

chr14	37252278 TGATTCTAAatCAGgAATcAtTGT +	5
chr19	101652 TGATcCTAAGCAGTAA.acATGA +	4
chr2	223253424 a.ATaCTAAaCAGaAATGAAAGA -	5
chr6	98542993 TtATTaTAAaCcAGTAATGAtAGA +	5
chr10	50058068 TGATTCTAAatCAGTtcTcAAAGA +	5
chr1	88217203 TGATTCTAAagtGTAATtGtATGG +	5
chr5	84191636 TGATTaTAAGCAGTcAT.tATGT -	4
chr20	40039271 TGATgTCCaAGCAGTAACGAATG/+	3
chr1	176057216 TGATTCTAAaCatTtAT.AtAGT +	5
chr4	81585152 TaATTaTAAGgCAGTAATcAgAGA+	5
chr15	40584687 gtgTTCTAAGCAG.AATGAgtGTC -	5
chr9	16371783 TGATTCaAAGtAGTAAGAAtGGC+	5
chr1	88593228 aaAgTC.AAGCAaTAATGAATGC +	5
chr2	106573996 a.AaTCTAAGCAtTAATGAgtAGA +	5
chr9	1070331 TGAaaCTAAGgCAGTAATGttTGT +	5
chrX	29011030 T.ATTCTAAaCAaTgATaAAAGT -	5
chr2	51330520 TGATTgTAAGCA.TAATGtAGGC -	3
chr11	111522187 gttTTaTAAGCAGaTAATGAATGT -	5
chr1	114956818 TGATTCTAAGaAGT.cTGgtTGT -	5
chr22	32316420 aagaTCTAA.CAGTAATGAATGT +	5
chr12	18991466 TGATTaTAA.aAGTAaccAATGT -	5
chr2	211762064 TG.TaaTAAGCAGTAATcAATGT +	4
chr4	39341843 ctgTTtTAAG.AGTAATGAAAGT -	5
chr8	82305121 TGATTCTAAaCAGTcAAgGAAAG(+	3
chr5	57178580 TtAaTCTAAGCAGTAgtTGttAGGA +	5
chr4	129150637 aGtTTCagAGCAGTAATGAAAGG -	4
chr12	58749602 TGATTCTAAatAG.AAaGgAAGA -	5
chr11	63444037 TGATTCTtAtCAGTAATGttTGA +	4
chr15	74221388 TGATTCaAAGCcAGTcgTGgAAGT-	5
chr18	58247067 TGATaCTAAaGCacagATGAAAG(-	5
chr7	111027874 TGATTaTAAaCAaTAAT.AcCGC -	5
chr4	43271562 TGATgTCTAAagtGTAATGgATGA-	5
chr7	41156889 TGATTggAA.CAcTAATGAAGGA +	4
chr1	210728155 TG.cTCTAAGCcaTAATGAATGT +	4
chr3	187191973 TcATTCTAgGaAG.AATaAATGG -	5
chr5	129385570 TGATTCTcAcCAGTgATaAtAAGG -	5
chr15	58000641 TGATTCTAtaCAGTAA.GcAAGT -	4
chr4	90119615 gcAgTCTAAGCA.TAATGgAGGA -	5
chr3	3852714 TGATTaTAA.CAGTAgtTatATGT +	5
chr8	42270710 TGATTCcAAGCAGgAAgGAgtAG,+	4
chr4	108362005 TGATTCcAAAtCAGTAtATaAgAGG +	5
chr2	108743941 TGATTaTAAGCAtaAAaTGtAGGT +	5
chr7	105178429 TtccTaTAA.CAGTAATGAATGG +	5
chr1	167909578 TaATaCTAA.CAaTAATGAtAGC -	5
chr2	216745780 TGATTCacAGCAGagAAgGAAAG/-	5
chr12	74120340 TtATTCTAAAtCAGTAATtAtAGGT +	4
chr2	239232181 TGATTaTAA.aAGcAATGtATGT -	5
chr6	93422947 TGATTaTAAGCAGaAAaG.AAGC +	4
chr10	128324457 TcATTCTAAG.AGTAATatATGT +	4
chr11	111574100 TcAaTgTtAAGCAGcAATGAAGGG-	5
chr3	37098247 TGtTTCaAAGCAGgTAATGAcAGC+	4

chr5	145796622 TGATTaTAAGtgGTAAT.tATGC	-	5
chr11	101600578 TGgaT.aAAGCAtTAATGAATGA	+	5
chr2	202656298 aGATTtCaAAAtCAGTAATGtAAGC	-	5
chr1	98771024 TGATTaTAAGaAaTgAATaAAGGC-		5
chr2	211049386 TGATaCTAAGgAGTcAgGgAAAG(+		5
chrX	7941005 TGgTcCT.AGCAGTgATGAATGG	+	4
chr1	76573814 TacTTCTAgGaAGTAATGAATGG	+	4
chrX	117172335 atATTaTAAGCAGcAAaTGAAAGG+		5
chr4	72442525 ccATTgT.AGCAGTAATGAgtGA	-	5
chr2	111511730 TGATTaTAA.aAGTtATaAATGC	+	5
chr5	168229956 TGATTaTAAGtAGTAAT.cgTGC	+	5
chr5	131740451 TGATTCTAAaCAaggAT.AAAGT	-	5
chr11	109703127 atATTCTgAGCAtTAATGAAaGGA-		5
chr11	10949263 aGA.TCagAGCAGaAATGAAGGC	-	5
chr14	48713519 TGATTaTAA.aAGTAATatATGC	+	5
chr15	73894957 aGATTCacAAcCAGaAATGAAGG/+		5
chr21	23019022 gaATaCTAAGaAGTAATG.ATGT	+	5
chr15	35040235 TGATTaTAA.aAGTAATatACGG	-	5
chr10	37036576 TGATaCTAA.aAGTAATGgcAGC	-	5
chr9	23770954 TGAgtCTAAGagGTAATG.AGGC	+	4
chr18	31626560 TGgagCTcAAGCAGTAATGAtCGC-		5
chr10	35751666 TGATT.acAGaAcTAATGAAAGC	-	5
chr18	78931035 TatTTCTAAaCAGTAATGcAAAGA-		4
chr20	42902888 TtgaTCT.AGCAtTAATGAATGA	-	5
chr3	152299540 TGATTaTAAGtAGaAATG.gGGG	-	5
chr11	14751335 TGATTCaAAaCAGaAAaGAATGA	-	4
chr21	9299763 aGAaTC.AAGCAGTAATGgAAGA	+	4
chr4	96165874 TGATTCTAAaaAtaTAATGAAAGA+		4
chr2	199580372 TaATTCTAAGCAGTAgtAgaAAAG/+		4
chr21	18976017 aGAaaCcAAGCAGTAATGAAGGC+		4
chr6	60694790 TacTTCTtAAGCAGTAATatATGT	+	5
chr3	32556933 TatTTaTatG.AGTAATGAATGA	-	5
chr12	86882585 gGtTTaT.tGCAGTAATGAATGA	-	5
chr8	17602527 aGATTCaAAaCAGaAATGAAaAG(+		5
chrX	41883342 TGATTaTAAGCAGTAACtCgAGA+		4
chr3	187122716 ccATcCTtAGCAGTAATG.AAGG	+	5
chrX	57779691 TtATTCTAAGCcAGTtATGAATGA	+	3
chr9	93831015 TGcTTCTAAGgAtTAATG.AAGG	-	4
chr7	24253616 TtATTtaAAGCAtTAATGAAAGA	-	4
chr3	48081776 TGATaCcctAGCAGTAATGAgtTGC+		5
chr2	64557184 TGA.TaaAAGagGTAATGAATGT	+	5
chr1	166998155 TGATTCTAAatAGTgtATGgAAGA-		5
chr3	82453190 T.cTTgaAAGCAGTgATGAAGGT	+	5
chr2	2802763 TGtTgTgTtAGCAGTAATGAAAGC+		4
chr5	60784185 aGATTCcAAGtAcTAATGAAaTGA	+	5
chr1	38432948 aGATTtTAAG.AGTAATGAtGGA	-	4
chrY	20803862 aGA.TgTAAaCAGTAATGtATGG	+	5
chr12	51578798 TGATTaTAAaCAG.AAgGAAAGA	-	4
chr6	157246204 TGATTCcAgcCAGaAATGAAAGC	+	4
chr15	92681650 TGATTaTAAGCAG.gAgGAtAGT	+	5
chr4	95501813 atATTCTtA.CAGTgATGAATGA	+	5

chr12	46081346 T.ATTgTtAGCAGTAATGtAGGC	-	4
chrX	110471117 TaATTCaAAG.AcTAgtTGAATGA	-	5
chr6	63433711 T.ATTCTAAGCAGaAcTGgtAGA	-	5
chr3	125752449 TGgTTCTAAaCAaT.gTGAATGT	+	5
chr9	71480243 aGATT.TAAaCAGTAATaAtGGC	-	5
chrX	105864184 TGATaCTAAGCAGcAcTGAgtAGC	-	4
chr4	112512785 T.cTcCaAAGCAGaAATGAATGA	-	5
chr4	59499918 T.tTTgTAtaCAGTAATGAATGG	+	5
chr2	213869664 TaATTCTAA.aAGTAATaAAGGA	+	4
chr15	77127669 TtATTaTAAGCAGTcA.GgAGGA	-	5
chr4	189120780 TtATTCaAtGtAGTAATGAAAGT	+	4
chr21	40939130 TtATTgaAAtGCAGTAATGAATGT	+	4
chr13	84198866 TGATTCTAAGagGTAAgGAtAGG	+	4
chr2	48206019 TGATTCTAAGCAGaAATagtGGA	-	4
chr14	50530048 TGATTCTAAaCA.TccTtAAGGC	-	5
chr4	141215543 T.ATTaaAtGtAGTAATGAATGT	+	5
chr11	1494491 aGATTC.AccCAGTAATGtAAGC	+	5
chr15	86163798 T.tTcCTAtGtAGTAATGAATGA	+	5
chr12	9966156 TacTTaTAA.CAGTtATGAAGGC	+	5
chr4	158362099 aaATTCT.AGaAGTAATGAtAGC	-	5
chr6	72566208 TGgTTCTAA.aAtaAATGAAAGG	+	5
chr17	14395599 TG.cTggAAGCAGTAATGAtGGA	+	5
chr4	44078440 TaGtTTaaAAGCAGaAATGAATGA-		5
chr10	83711053 TGATTCTAAaatGT.ATGtAGGT	+	5
chr2	14311407 TatTTCTtA.CAGTgATGAAGGC	+	5
chr18	55906970 cagTaCTAAGCAGTAA.GAAAGT	-	5
chr21	26263406 TGATTCTAAaCAacAtATcAACGA	+	5
chr1	209758316 TGATTCCaAGCAGaAATGtgAGG	-	4
chrX	39026470 gGAgT.gAAGCAaTAATGAAGGC	-	5
chrY	1273978 aGATTCaAAGCAagAATG.ATGG	-	5
chr11	34681779 aGATTgTAAG.AtTAATGAcAGG	-	5
chr8	116093596 TGATTCTgAGCAtcAgTtGAATGA	+	5
chr1	188676156 TGATTC.AtaaAGcAATGAAAGC	+	5
chr6	87843138 TtATaaTAA.CAGTAATGtAGGT	-	5
chrX	80633724 aGA.TCagAGCAGaAATGAATGA	-	5
chr18	64585864 aGgTTgT.AGCAGTAAgGAATGC	+	5
chr15	59016837 gaAcTC.AAGCAGTAATGtAAGT	-	5
chr9	99298743 TGcTTCTAAGCAtaAATGAAAGT	-	3
chr16	52685804 TtATT.aAtGCAaTAATGAATGA	-	5
chr13	59266995 TGATTCTAAtatGTAATG.AAGA	-	4
chr5	154013145 caATTCTAAaCAGTAgtATGAcAGT-		5
chr2	26242286 TGAgtCTAAatAGTAATatAAGGG+		5
chr19	29556254 TaATTCTAAaCAG.AAcGAAAGA	+	4
chr15	23593583 aGATTaTAAaaCAGTAAaGAAAGT+		5
chr1	26476917 TGAcT.TcAGCAaTAATGAAAGT	-	4
chr12	67299303 T.ATTaacAGCAtTAATGAATGA	-	5
chr17	36902202 TGATTtgAtGCAGTAATGAAAGT	+	3
chr6	143254257 TGATTCTcAGttGTAcTG.AAGC	+	5
chr11	56627540 TGATTC.AAGCAtTAgtTccAGGT	+	5
chr9	19682792 TtATTCTAAGCAaGTtATGgAAGA	+	4
chr6	161495778 aGATTCT.AGaAaTgATGAAAGT	-	5

chr5	87648924 aGATTCaAAGgAG.AATGAgAGG +	5
chr3	24262244 aGATgaTAA.CAGTAATGAtGGA -	5
chr5	26573534 TGATTCTAA.aAtatATGAAGGG -	5
chr4	14435014 TGgTTaTAAGCAGaAcTG.AAGA +	5
chr11	130861542 TGATTCTAgGCAGTctTaAAAGG -	4
chr3	192650933 TaATTCTAAaCAGTgAT.cAAGA +	5
chr6	37078550 TG.TTaTAtaCAGTgATGAAAGG +	5
chr20	62371147 TGAcaCTAAcCAGgAATGAAGGA +	4
chr4	53431325 gaATcaTAAGCAGcTAATGAAAGA+	5
chr18	52567654 aGATTCTAAaGCAGggATGAAAG +	4
chr12	32176322 TatTTCT.AGCAGTAATGtATGA +	4
chr1	78895978 gGATTtCTAAGCAGTttTGAATGA +	4
chr6	87403726 TaATTaCTgAGaAGTAATGAATGT-	4
chr11	114885323 TGtTTaTAAaCAG.AATGAATGA -	4
chr7	5715514 TGATTaTAAaCAGcAAgGAtAAGG+	5
chr12	20599080 T.tTTaTtAGCAGaAATGAAGGT -	5
chr13	99810623 gtATTCTAAG.gGTAATGgAAGG +	5
chr5	90482109 gtgTTC.AAGCAGTtATGAAGGA +	5
chr8	113945500 TtATaTaTtAGCtGTAATGAATGT -	5
chr5	58996508 aGATTCT.AGCAaTggTGAAAGC -	5
chr16	22082570 TcAcaC.AAGCAGaAATGAACGC +	5
chr6	154331968 aGtTTCagAGCAGTAATGAAAGG -	4
chr5	5081162 TGcATgaTAAGCAGTgATGgATG(-	5
chr5	121835080 aGATTCagAGCAGgAATGAAAGG-	4
chr16	20824595 TGAgtCTAAtGCACtAATGAACGA+	3
chr9	113879131 TGAgtT.TtAGCAGTgATGAAGGA +	4
chrX	41816698 atATaCTAAG.AaTAATGAATGT +	5
chr2	144806656 TtATaCTAAaCAGTAgtTG.ACGA +	5
chr1	189544523 TGATTaTAAtCAGTtATaAAtGGC -	5
chr16	51721881 TaGATTCTAAGCAaTAAaGttAGA -	5
chr4	40760172 T.AgTCaAAGCAGTAATaAAAGG -	4
chr6	140349137 aG.TgaTAAGCAtTAATGAAAGA +	5
chr16	59245164 TaATcaaTtAGCAGTAATGAATGC +	5
chr3	174240125 aGAaT.TAAaCAGTAATGAtAGA +	5
chr4	162312673 TGAgtTCaAAGtAGTAAT.AAAGA +	4
chr4	178335092 TcATTaCTAAtCAGTAATtAATGA +	4
chr1	200848115 TcgTTCT.AttAGTAATGAAGGA +	5
chr5	5254720 TGATTCatAGCAGgAATGtAAGG -	4
chr3	73684269 TGA.gaTtAGCAGTAATGAAGGA +	4
chr3	7144429 TacTTtgAAaGCAGTAATGAAAGG+	5
chr14	31275063 TGATTCaAAGC.tTAtTtAAAGG +	5
chr2	6765798 TGATaCTAAaCAGgAAaGgAAAG -	5
chr11	46449670 TGATTCTAAagttTAtATGAAAGG +	5
chr4	89477293 gaATaCTAAGCAGTtAT.AAAGA +	5
chr3	125064855 TGATTaTAA.CAGTAATacATGC -	4
chr4	184134945 TGATTCaAAGaAGTAAT.tgTGA -	5
chrX	148722544 atgTTCcAAGCAGTAATG.ATGC -	5
chr4	167945327 aGATTaTAAGCAGaAAT.cAGGG +	5
chr5	4813708 TGATTCTAAGtCtaTAtgGAAAGG -	5
chr10	3446001 TtAgTtTAAGCAtTAATGAAAGG -	4
chr2	28851032 TtATgC.AtGCAGTAATGAATGG -	4

chr2	83167620 T.AaTaTAAGCAGTgATGtAAGA	+	5
chr1	170253587 aGATTCTAAGCAaaAATG.ATGC	+	4
chr4	72501706 aGATaCTAAGCAGTcAaGAACtGC-		5
chr8	67189927 TGATTaTAAGCA.aAAAGAcCGA	+	5
chr7	81525511 TGATTtTAAGCAGaAATGgAAAGT-		3
chr5	123594514 TGATTCTAAGgA.TAATatgAGA	-	5
chr2	115947569 TGATTaTAAGtAaTAAaGAAaGGC+		5
chr3	80304007 TGATTaTAAGtAaTAAT.AATGT	-	4
chr17	31518021 aGATTCTAAGCAG.AcTaAATGC	+	4
chr6	145092419 TGgTTaTAAGCAtTAAaTGAgtGA+		5
chr1	207508424 TGgTTCacAGCAaTAATGAACAGA-		5
chr17	66415091 TGATTaTAA.aAGTAATccAAGC	-	5
chr4	77700278 TGATTCTAAaCA.TtAgcAAAGT	+	5
chr4	11157311 TGcTT.TAAGCAcTAATaAAGGC	+	4
chr2	180104629 TGAcTCTAttaAGTAATGAATGT	-	4
chr2	14364104 gtATTaT.AGCAGaAATGAAAGG	+	5
chr1	178812674 TtATTacAAG.AGTAATGAATGA	-	4
chr11	25930256 TGATagTAAGtAGTAATtGAAGGA-		4
chr5	161376115 TGATTaT.ttCAGTgATGAATGC	-	5
chrX	78214466 TGA.TgTAAatAGTAATGAATGG	-	4
chr2	158009910 TGATTaatAGCAaTAATGtAAGGT	-	5
chr20	14809579 aGA.TCagAGCAGaAATGAAGGA	+	5
chr11	124382383 TaATTaagAAGCAGTAATG.ATGT	-	4
chr2	137235567 TGATTCaAAGtAaTAATG.ACGA	-	4
chr15	89725351 TGATTCTAAaCtGTAcTaAgGGG-		5
chr20	42058895 TGATTCTAAaatGTAcTGAAGgAGT	-	5
chr21	20765669 TGATTgCaAAGtAGTgATGAATGT+		4
chr2	122878236 TtATaagAAGCAGTAATGAgaAAGC+		5
chr10	33078322 T.cTTCTAAtCAGTAATtAATGT	+	4
chr9	102844842 TaATTCTAtGCAGcAATaAATGC	-	4
chr18	70781622 TaATTCTAAGCAaTAgtGAtTGA	-	4
chr15	67281178 aGATTaTAAGC.tTAATGAgtGGC	+	5
chrY	5271373 TatTTCTAA.tAGTAATGAAGGA	-	4
chr8	70282250 TGATTaTAAagAtTAAT.AAAGA	+	5
chr13	88985123 T.ATTtcAtaCAGTAATGAAAGA	+	5
chr14	40745132 TGATTaTAAGgAaGTAgGAAGG,+		5
chr18	57345524 TGATTaTAA.CAGTataaAATGG	-	5
chr4	182241304 TGATTC.AttCAaTAATGAgtAGG	+	5
chr3	45129081 TGATTCaAAGCA.TAAgcAcTGC	-	5
chr12	90847358 cG.cTCagAGCAGTAATGAAAGG	+	5
chr18	8069275 a.ATTCaAAGCAaTgATGAAGGA	-	5
chr7	84959877 TGATTCTAAGaAGggAT.tAAGA	+	5
chr15	60141058 TGATTCTAAG.AcTgATcAgTGG	+	5
chrX	31968240 aGATTaTAAGCAG.ggTGAAGG	-	5
chr2	109816927 TGATTaTAAGCAtaAAaTGtAGGT	+	5
chr4	9208994 TGATTtTAAGgAGT.ATGAtGGA	-	4
chr3	171690158 TGATTCTAAGatAtTAcTGtAAGT	-	5
chr4	42338712 aGATTCTAA.aAGTcATGAgtGA	+	5
chr14	88373014 aGA.TCagAGCAGaAATGAAGGC	+	5
chr4	68556646 aGATTaTAAaC.GTtATGAAAGG	+	5
chr4	118809942 aGcaTCTAAGCAG.AATaAAGGC	+	5

chr3	194350347 TGcTaCTAAGCAG.gATGAgAGT -	5
chr7	55140963 TGATTCTAAagAGT.ATcAtTGG -	5
chr5	164134106 TGATTCTAAaCatGaAgTaAATGC +	5
chrX	8255287 T.tTcCTAAGCAGTAAGGtATGA +	5
chr4	136017844 aGAaT.TAAGCAAtAATGAATGA -	4
chr1	20836574 TG.ccgTAAGCAGTAATaAAGGT +	5
chr3	117531653 a.ATaCTAAGCAGTAATtcAAGA +	5
chr6	148042696 TGAaaCaAAGCAGTAACGAaaAG(-	5
chr11	42691146 aGA.TCagAGCAGaAATGAAGGA +	5
chr3	183233891 TGATTaTAAGaAagAAT.AATGA -	5
chr21	21998858 TaAgTCaAAGCAGTAaAG.AAGA +	5
chr15	24974909 TGATTc.cAcCAGTggTGAAGGA +	5
chr12	12975704 TG.TTaaAAGCAGTAATGgACGT +	4
chr7	49329729 TtAgTaTtAG.AGTAATGAAGGC +	5
chr20	54608221 TGgTTC.cAGaAGTAATGAAGGT -	4
chr11	38121302 TGATTCTAAGCAacTgtTAAAGT +	5
chr17	10241018 TacATTCTtAcCAGTAATGtATGA +	5
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chr2	170640064 TGA.TCTAAGCtcTtAgGAAAGG +	5
chr17	55428936 ccAggC.AAGCAGTAATGAAGGC +	5
chr8	96724227 TGATTCTgAGCAGTAaAatAcTGA -	5
chr14	56029142 TGAaTCTAAG.AGctATGAtTGT -	5
chr5	121835079 aGATTcagAGCAGgAATGAAaGG-	5
chr6	6129985 TGATTgTAAGCAGTgcTGcAATGA+	4
chrX	47858247 TGATTtTAAaaAGT.ATcAAAAGT +	5
chr2	143625937 TGATTCTAAaGatGTtAgGAAAGT +	5
chr6	141870252 TGAaT.TAAagAGgAATGAAGGA +	5
chr20	40066949 TcATTCaAAGaAGTAATaAcAGGG+	5
chr4	63325637 aGATTCaAAatCAGaAATGAAAGA+	5
chr6	50213196 TaATTCTAAGCAG.AgTtcATGA +	5
chr13	66853258 TGATTCTAAG.AGgAtctAAAGA +	5
chr7	40784383 TGA.cCTAAGCAGTtcTGAgtGG -	5
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chr4	65622163 TGATTCTAAaCAacAA.aAAAAGT -	5
chr11	6723392 atAaTCTgAAGCAaTAATGAATGA+	5
chr1	207068645 TGA.TCTAAGCAGaAAgcAAAGA -	4
chr6	51118877 TGAaTTCTAAGttacAATGAAAGT -	5
chr1	182656085 TcATTaTAAGCAGTcAATaAgTGT +	5
chr9	92601147 TGATaC.AAGCAGaAAgGAATGC -	4
chr15	90770767 T.ATTaTAAGCAGTAaGaAtAGC +	5
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chr12	38479185 aacTTCTcAAGCAGTAAGGAAGG/+	5
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chr6	146347937 TGgTTCTAAatAGTAAT.cATGT -	5
chr1	234322714 TGATTaaAAcaAGTgAATGAAGGC-	5
chr1	60168696 TcATTCTAAGCAGTtTaAAAGG -	4
chr11	38625304 TGATTCaAAGaAGTAgcTGAtTGC+	5
chr12	111504057 TaAgTC.AAGCAAtAATGAAGGT +	4
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chrX	99663767 TGgATTCTAAGtgGTAATaAgTGA+	5
chr12	105784128 TaAaTaTAAaCAGTAAT.AATGC -	5

chr2	97343685 aaATTaaAAG.AGTAATGAATGA	+	5
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chr7	42940560 aGATTCTAAGtAtaTAATGAAGGT	-	5
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chr2	173517192 atATTCTAAaCA.TtATGAATGT	-	5
chr10	124785961 T.tcTCTAAtgAGTAATGAATGA	-	5
chr7	117853436 TGATTaTAAG.AGgAAacAAGGG	-	5
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chr17	16150013 TccAcTCTAAGaAGTAATGgAGGC+		5
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chr13	62717897 TGATTgTAAaGCAGTAATattAGC	+	5
chr17	62141298 TGtTTCTAAagAGTAAaGAAAGC	-	4
chrX	155623285 TGATTCTAAGaAGcAATG.AAGT	-	3
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chrX	26028985 TtA.TggAAGCAGTAATGAAGGA	-	4
chr8	73548607 TGATTaTgAtCAaTAATGAAaTGC	+	5
chr3	181839878 TGATTCaAAGCAcTAATcAAaCGT-		4
chrX	32345709 TttTTCTAAGtAGTAATtGAAAGA	-	4
chr11	115611906 TG.TgaTAtGCAGTAATGAgtGA	-	5
chr3	122822279 TGcTTtCTAAGCAcTtATGAAAGA	-	4
chr7	147694680 TacTaCT.AGCAGaAATGAAAGA	-	5
chr10	49316503 TcATTCTAAaCAGTggTG.AAGG	-	5
chr10	26694318 TtATTCaAAtCAGTAATaAAAGC	+	4
chr10	50847539 TcATTCTAAGCAGTAAGTcttAGC	+	5
chr3	61005171 TaATTaTAAGCAaTAATtAtAGGC	-	5

closest_gene	genomic_location	patient_specific	ONE_seq_score
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ATP7B	intron	0	5.048108912
SORCS1	intron	0	4.042746159
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LOC101928371	non-coding	1	1.341129545
.	intergenic	0	1.251672418
PPHLN1	intron	0	1.204710503
PLCL1	intron	0	1.111771749
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LARGE1	intron	1	1.021746961
CPS1	exon	1	1
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SCAPER	intron	0	0.890029975
ANKRD26P1	non-coding	0	0.714139744
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THSD4	intron	0	0.604130687
ESF1	intron	0	0.575666784
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KIAA1217	intron	0	0.562660919
TAF2	intron	0	0.540894442
CRACD	intron	0	0.524221234
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PALLD	intron	0	0.490617544
COL15A1	intron	0	0.487915583
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PLCL1	intron	0	0.482780607
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LARGE1	intron	1	0.472640319
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TMC1	intron	0	0.341119653
CCDC28A-AS1	non-coding	1	0.319938839
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ARHGAP21	intron	0	0.309506789
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FRMPD4	intron	0	0.305570764
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MKLN1	intron	0	0.292247918
CDH22	intron	0	0.287024987
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SUCLA2	intron	0	0.27178127
PKD1L3	intron	0	0.250620863
CPS1	exon	1	0.241664822
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DSG2	intron	0	0.239867019
TRAPPC11	intron	0	0.23052823
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TTLL5	intron	0	0.205395173
TNFSF15	intron	0	0.205267293
DYNC1I1	intron	0	0.198303592
TJP2	intron	0	0.197490687
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MPDZ	intron	0	0.194479229
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GUSBP17	non-coding	1	0.178915501
LYPD1	intron	0	0.177207437
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BAALC	intron	0	0.173721086
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GUSBP2	non-coding	1	0.16056934
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NRXN1	intron	0	0.159474565
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EML1	intron	0	0.158263316

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NRG3	intron	0	0.135679745
EGFLAM	intron	0	0.134653409
GUSBP14	non-coding	1	0.134337319
ZNF423	intron	0	0.13280187
KLHDC10	intron	0	0.129416665
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TJP2	intron	0	0.123721247
DOK5	intron	0	0.123255354
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PTPRD	intron	1	0.12001906
NOVA1	intron	0	0.119996246
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KLHL20	intron	0	0.119709564
MDGA2	intron	0	0.11969486
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NRXN3	intron	0	0.118170818
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C1QTNF3	non-coding	1	0.112473885
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TMC1	intron	0	0.107233843
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TRAPPC11	intron	0	0.091664412
FHIT	intron	0	0.087225869
MTREX	intron	0	0.087023846
EXOC4	intron	0	0.085138978
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EMC8	intron	0	0.083390991
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UTRN	intron	0	0.079088437
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FAM219A	intron	0	0.065563568
RMDN2	intron	0	0.065319215
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MTREX	intron	0	0.064142186
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ARNT2	intron	0	0.064107966
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ADAMTS9	intron	0	0.058072129
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AFF2	intron	0	0.054219249
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KIF16B	intron	1	0.053818499
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LYN	intron	0	0.052971374
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NAV2	intron	1	0.052843494
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SUCO	intron	0	0.041922738
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NOX4	intron	0	0.039639527
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NEK2	intron	0	0.026578144
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WDPCP	intron	0	0.026288164
TJP1	intron	0	0.026020998
.	intergenic	0	0.026009591
.	intergenic	0	0.025998184
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.	intergenic	0	0.025418225
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PTPRD	intron	0	0.025355488
MCU	intron	0	0.025233312
.	intergenic	0	0.025088322
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CDH12	intron	0	0.025071212
.	intergenic	0	0.024926222
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ABCA5	intron	0	0.024619132
HYDIN2	non-coding	0	0.024312042
MCU	intron	0	0.024306339
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.	intergenic	0	0.024132832
.	intergenic	0	0.024004953
.	intergenic	0	0.02388848
CCDC192	intron	0	0.023703566
.	intergenic	0	0.023644127
.	intergenic	1	0.02358139
.	intergenic	0	0.023464917
.	intergenic	0	0.023396477
CFAP299	intron	0	0.023280003
.	intergenic	0	0.023123607
.	intergenic	0	0.023106497
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SH3PXD2A	intron	0	0.022705747
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DOCK11	intron	0	0.022253668
.	intergenic	0	0.022236558
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CDH12	intron	0	0.021929468
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EXOC6B	intron	0	0.021767368
.	intergenic	0	0.021755962
PLXNA2	intron	0	0.021650895
.	intergenic	0	0.021360915
ERMP1	intron	0	0.021233036
.	intergenic	0	0.021088046
.	intergenic	0	0.021042419
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APBA1	intron	0	0.020880319
LINC01228	non-coding	1	0.020706813
LINC01643	non-coding	1	0.020683999
CBFB	intron	0	0.020596043
.	intergenic	0	0.020567526
.	intergenic	0	0.02018959
DNAI7	exon	1	0.020016083
.	intergenic	0	0.019970457
ARPIN-AP3S2	intron	0	0.019947643
LOC101929710	non-coding	1	0.019919127
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.	intergenic	0	0.019802653
DIAPH2	intron	0	0.01970329
SMARCA4	intron	0	0.019680477
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SLIT2	intron	0	0.019657664

.	intergenic	0	0.019569707
URGCP	intron	0	0.019419014
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EPS15	intron	0	0.019401904
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ATF6	intron	0	0.019350574
HMGCLL1	intron	0	0.019234101
.	intergenic	0	0.019199881
TBC1D9	3utr	0	0.019032077
GRIN2B	intron	0	0.018984045
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.	intergenic	0	0.018938418
SLC25A42	intron	0	0.018921308
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PCLO	intron	0	0.018369865
NRXN1	intron	0	0.018358458
MYO9A	intron	0	0.018202062
.	intergenic	0	0.018184952
.	intergenic	0	0.018068479
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ESRRG	intron	0	0.017929192
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.	intergenic	0	0.017698652
.	intergenic	0	0.017639213
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HS3ST4	intron	0	0.017482816
LRRC63	intron	0	0.017337826
ATP9B	intron	0	0.017275089
.	intergenic	0	0.017269386
HMGCLL1	intron	0	0.017263683
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TPP2	intron	0	0.017158616
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ZSCAN20	intron	0	0.016973703
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PDE3A	intron	0	0.016735053
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ENDOV	intron	0	0.016544437
FHIP1A	intron	0	0.016137984
WDR11-DT	non-coding	1	0.016137984
.	intergenic	0	0.015941664
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CDH13	intron	0	0.015674498
LINC02227	non-coding	1	0.015668794
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.	intergenic	0	0.015512398
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LINC00355	non-coding	1	0.015228122
SLC4A10	intron	0	0.015211011
SYNE2	intron	0	0.015088835
CPNE4	intron	0	0.015048912
.	intergenic	0	0.015031802
ACTA2	intron	0	0.014793152
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THSD7A	intron	0	0.014608239
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.	intergenic	0	0.014585425
UBR3	intron	0	0.014486062
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TACR3	intron	0	0.014411919
NRDC	intron	0	0.014295446
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PARVA	intron	1	0.014033983
ITSN1	intron	0	0.014028279
KDM1A	intron	0	0.014005466
PPFIA1	intron	0	0.013994059
DPP10	intron	0	0.013894696
LINC00607	non-coding	1	0.013894696
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SLC2A14	intron	0	0.013854773
TMEM65	intron	0	0.013849069
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NSDHL	intron	0	0.013726893
DGKG	intron	0	0.013604717
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FABP5	intron	0	0.013553386
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UBR3	intron	0	0.01339699
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ADAMTS18	intron	0	0.013297627
CHRD1	intron	0	0.013146934
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TXLNGY	non-coding	1	0.012990537
BRF1	intron	0	0.012990537
ENDOV	intron	0	0.01297913
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LSAMP	intron	0	0.012839844
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TEX11	intron	0	0.012532754
ZNF227	intron	0	0.012515644
PEAK1	intron	0	0.012393468
SATB2	intron	0	0.012376358
RBFOX1	intron	0	0.012370654
.	intergenic	0	0.012254181
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CFAP47	intron	0	0.012248478
AFF3	exon	1	0.012231368
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CLINT1	intron	0	0.012097785
LOC101928516	non-coding	1	0.012074971
GRID2	intron	0	0.012063565
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PDE4D	intron	0	0.011935685
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LINC00971	non-coding	0	0.011645705
ELAPOR2	3utr	0	0.011640002
KL	3utr	0	0.011622892
COG6	intron	0	0.011500715
CCDC62	exon	1	0.011495012
LINC02664	non-coding	0	0.011495012
PDE4D	intron	0	0.011483605
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CFAP299	intron	0	0.011460792
SPEF2	intron	0	0.011367132
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DNAI7	exon	1	0.011315802
LINC02172	non-coding	0	0.011292989
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PCDH9	intron	0	0.011182219
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ALDH1A2	intron	0	0.011165109
SNX9	intron	0	0.011105669
MIR3681HG	non-coding	1	0.011071449
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LINC00492	non-coding	1	0.011060042
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DIAPH2	intron	0	0.011020119
ATF2	intron	0	0.010909349
B4GALT1	intron	0	0.010909349
RAPGEF6	intron	0	0.010747249
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DIAPH3	intron	0	0.010741546
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LOC101928622	non-coding	1	0.010724436
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MAPK1	intron	0	0.01061937
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HDDC2	intron	0	0.01045727
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STOX2	non-coding	1	0.01032939
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RPLP0P2	non-coding	0	0.010266653
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MARCHF10-DT	non-coding	1	0.01015018
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DGKG	intron	0	0.01015018
RBFOX1	intron	0	0.010144477
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GASK1B	intron	0	0.00998808
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COL24A1	intron	0	0.00998808
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.	intergenic	0	0.009976673
MYCBP2	exon	1	0.009976673
PARD3B	intron	0	0.00997097
NAA16	intron	0	0.00995386
.	intergenic	0	0.009871607
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LINC01258	non-coding	1	0.00982598
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CCDC191	intron	0	0.0096981
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.	intergenic	0	0.00968099
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MICU1	intron	0	0.00955311
MAGI2	intron	0	0.00955311
PTPRD	intron	0	0.009547407
PYHIN1	intron	0	0.009430934
UBR3	intron	0	0.009425231
NR2F1-AS1	non-coding	1	0.009413824
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STAT5B	intron	0	0.009368197
DNPEP	intron	0	0.009263131
DIAPH2	intron	0	0.009263131
SLC35E3	intron	0	0.009240317
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OR7D4	intron	0	0.009106734
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ST6GALNAC3	intron	0	0.008938931
LINC02343	non-coding	1	0.008938931
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MAGOHB	3utr	0	0.008805348
SHC4	intron	0	0.008782534
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PATJ	intron	0	0.008620435
DMD	intron	0	0.008521072
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ANKS1B	intron	0	0.008503962
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DNTTIP2	exon	1	0.008503962
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THSD4	intron	0	0.008381785
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CLIP1	intron	0	0.008347565
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RBFOX1	intron	0	0.008341862
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CDC20B	flanking-downstream	0	0.008330455
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FAM13C	intron	0	0.008202575
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TBCK	intron	0	0.008202575
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PARP15	intron	0	0.008068992
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NAALADL2	intron	0	0.008046179
ZNF423	intron	0	0.008040475

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HMGB1	intron	0	0.007912595
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MGC27382	non-coding	1	0.007901189
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PDLIM5	intron	0	0.007784716
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COLEC12	intron	0	0.007761902
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NSDHL	intron	0	0.007750496
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LINC02269	non-coding	0	0.007739089
SAMD4A	intron	0	0.007634022
TSPAN7	intron	0	0.007628319
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PTPRT	intron	0	0.007622616
MUC16	intron	0	0.007616912
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EML6	intron	0	0.007599802
CLDN10	intron	0	0.007594099
CPEB4	intron	0	0.007582692
MYOM1	intron	0	0.007489033
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DIAPH2	intron	0	0.007449109
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EDC4	intron	0	0.007304119
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LRRC59	intron	0	0.007298416
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GPC5	intron	0	0.00715913
LINC00487	non-coding	1	0.007147723
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MAGI2	intron	0	0.007025546
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ITGA6	intron	0	0.007008436
RORA	3utr	0	0.007008436
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TAF2	intron	0	0.006880557
UBE2Q1	intron	0	0.00685204
METTL2A	intron	0	0.00685204
NOS1	intron	0	0.006846336
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LINC01205	non-coding	1	0.006729863
ELMO2	intron	0	0.006729863
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SLC35F3	intron	0	0.00672416
TXNDC16	intron	0	0.006712753
CDK14	intron	0	0.006701347
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SLC34A2	intron	0	0.006584874
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DMD	intron	0	0.00657917
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TENM4	intron	0	0.006573467
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SCHIP1	intron	0	0.006556357
NRXN3	intron	0	0.006556357
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DCC	intron	0	0.006439884
DLEU7	intron	0	0.006439884
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ACTR3B	3utr	0	0.006411367
LINC00571	non-coding	1	0.006411367
ZSCAN20	intron	0	0.006411367
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CHP1	intron	0	0.006405664
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NDNF	intron	0	0.006283487
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GRIN2B	intron	0	0.00627208
.	intergenic	0	0.006266377
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SPON1	intron	0	0.006266377
SEMA3D	intron	0	0.006260674
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CASK	intron	0	0.006127091
GRB2	intron	0	0.006115684
NOS1	intron	0	0.006115684
C1QTNF7	intron	0	0.006109981
FCHSD2	3utr	0	0.006109981
DLGAP1	intron	0	0.006104277
METTL2B	intron	0	0.006104277
.	intergenic	0	0.006098574
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STMND1	intron	0	0.005982101
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UBR3	intron	0	0.005964991
PDE8B	intron	0	0.005964991
TRPM3	intron	0	0.005964991
DPP4	intron	1	0.005959287
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DMXL2	intron	0	0.005837111
RUNX2	intron	0	0.005837111
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ATG10	intron	0	0.005825704
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C10orf71	intron	0	0.005814298
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SPATA1	intron	0	0.005814298
FAF1	intron	0	0.005814298
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DOCK5	intron	1	0.005686418
.	intergenic	0	0.005675011
DDX4	intron	0	0.005675011

OPA1	intron	0	0.005669308
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ROBO2	intron	0	0.005663604
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AGMO	intron	0	0.005547131
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COL14A1	intron	0	0.005535725
RABGAP1L	intron	0	0.005535725
LINC01495	non-coding	1	0.005518614
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PREX2	intron	0	0.005518614
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FANCI	intron	0	0.005512911
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SYNPR	intron	0	0.005490098
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PART1	non-coding	1	0.005385031
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DPP10	intron	0	0.005379328
PDZRN4	intron	0	0.005373625
ADGRL2	intron	0	0.005367921
DAB1	intron	0	0.005367921
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PARD3	intron	0	0.005362218
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ZNF354B	intron	0	0.005350811
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FBXL4	intron	0	0.005350811
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MAPKAPK5	intron	0	0.005234338
INPP4B	intron	0	0.005234338
NELL1	intron	0	0.005228635
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FREM2	intron	0	0.005228635
.	intergenic	0	0.005222931
.	intergenic	0	0.005217228
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.	intergenic	0	0.005211525
MSTN	intron	0	0.005211525
.	intergenic	0	0.005205821
.	intergenic	0	0.005100755
LINC02261	non-coding	0	0.005095052
COMMD1	intron	0	0.005089348
.	intergenic	0	0.005077942

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.	intergenic	0	0.005072238
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PRRX2	intron	0	0.005066535
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.	intergenic	0	0.005060832
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FRA10AC1	intron	0	0.005055128
DPP10	intron	0	0.005055128
ARHGEF3	intron	0	0.005055128
ANO3	intron	0	0.005049425
.	intergenic	0	0.005049425
ERC1	intron	0	0.005049425
ATP5MF-PTCD1	intron	0	0.004944358
LINC01049	non-coding	1	0.004944358
DNAH5	intron	0	0.004932952
DOCK7	intron	0	0.004932952
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EYS	intron	0	0.004927248
CXCL13	intron	0	0.004927248
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.	intergenic	0	0.004921545
NRXN3	intron	0	0.004921545
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LINC01623	non-coding	0	0.004915842
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LRRIQ3	intron	0	0.004910138
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.	intergenic	0	0.004904435
KCND2	intron	0	0.004904435
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ZFAND6	intron	0	0.004898732
PDZRN4	intron	0	0.004799369
NTM	intron	0	0.004782259
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COG6	intron	0	0.004782259
.	intergenic	0	0.004776555
CCNT2	intron	0	0.004776555
RNF2	intron	0	0.004770852
CASK	intron	0	0.004770852
RABGAP1L	intron	0	0.004770852
SORCS2	intron	0	0.004765149
LINC02287	non-coding	1	0.004765149
ALCAM	intron	0	0.004759445
.	intergenic	0	0.004748038
PTPRK	intron	0	0.004736632
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GRID2	intron	0	0.004631565
PAIP2B	intron	0	0.004631565
.	intergenic	0	0.004625862
.	intergenic	0	0.004620159

BCL2L13	intron	0	0.004620159
.	intergenic	0	0.004620159
DSG3	exon	1	0.004614455
HDGFL3	intron	0	0.004614455
SLC34A2	intron	0	0.004614455
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GRID1	intron	0	0.004608752
EBAG9	3utr	0	0.004608752
LINC01931	non-coding	1	0.004603049
TSHZ2	intron	0	0.004497982
AFF3	exon	0	0.004492279
COL19A1	intron	0	0.004492279
.	intergenic	0	0.004486576
HEATR3	exon	1	0.004486576
KCNB2	intron	0	0.004486576
SENP7	intron	0	0.004486576
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.	intergenic	0	0.004480872
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ZNF804A	intron	0	0.004469466
KAT2B	intron	0	0.004463762
SLCO3A1	intron	0	0.004458059
CHRM2	intron	0	0.004341586
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.	intergenic	1	0.004341586
.	intergenic	0	0.004335882
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RYBP	intron	1	0.004330179
IDE	intron	0	0.004330179
GPC5	intron	0	0.004330179
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USP27X	3utr	0	0.004324476
CERS6	intron	0	0.004324476
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NAALADL2	intron	0	0.004313069
MIR924HG	non-coding	0	0.004307366
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LINC02147	non-coding	0	0.004190893
ZNF534	intron	0	0.004185189
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PCDH11X	intron	0	0.004179486
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TPD52	intron	0	0.004179486
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KCND2	intron	0	0.004179486
.	intergenic	0	0.004173782
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MFAP3L	intron	0	0.004173782
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LRRC7	intron	0	0.004168079
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TSPAN7	intron	0	0.004168079
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GPC5	intron	0	0.004168079
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POLR1C	intron	0	0.004162376
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DPY19L1P1	non-coding	1	0.004156672
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TBC1D31	intron	0	0.004051606
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CEP43	intron	0	0.004040199
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PARD3B	intron	0	0.004034496
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AK5	intron	0	0.004028793
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ALCAM	intron	0	0.004023089
DBNDD1	intron	0	0.004017386
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IL1RAPL1	intron	0	0.00389521
SPOCK1	intron	0	0.00389521
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LINC01495	non-coding	1	0.003883803
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UBR3	intron	0	0.003883803
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.	intergenic	0	0.003878099
MELK	intron	0	0.003878099
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LINC02141	non-coding	0	0.003872396
LINC01179	non-coding	1	0.003872396
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LINC01170	non-coding	0	0.003866693
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GEMIN8	intron	0	0.003860989
SLC34A2	intron	0	0.00375022
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OSBPL9	intron	0	0.003727406
BIRC6	intron	0	0.003727406
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EVI5	intron	0	0.003727406
MMADHC-DT	non-coding	0	0.003727406
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OXR1	intron	0	0.003721703
SACS	intron	0	0.003721703
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CLXN	intron	0	0.003716
CCDC141	intron	0	0.003716
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ATP10A	intron	0	0.00358812
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DGKK	exon	1	0.003582416
ZFYVE26	intron	0	0.003582416
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LINC02877	non-coding	1	0.003582416
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AKAP13	intron	0	0.003582416
PTPRQ	exon	1	0.003582416
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ZBTB20	intron	0	0.003576713
RBM44	intron	0	0.003576713
MAPKAPK5	intron	0	0.003576713
NHSL2	intron	0	0.00357101
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PPP1CB	intron	0	0.003559603
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UBR3	intron	0	0.00344313
MAN1A1	intron	0	0.003437427
NSF	intron	0	0.003437427
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ENAH	intron	0	0.003431723
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BTRC	intron	0	0.00342602
ARL6IP6	intron	0	0.00342602
HMGB1	intron	0	0.003420317
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ERGIC2	intron	0	0.003414613
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SOX6	intron	0	0.00340891
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AMOTL1	intron	0	0.00329814
RYR2	intron	0	0.00329814
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ARRDC3	intron	0	0.003292437
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C8B	intron	0	0.003292437
CR1	intron	0	0.003286733
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CEP70	intron	0	0.003286733
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LINGO2	intron	0	0.00328103
RANBP17	intron	0	0.00328103
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PXDC1	intron	0	0.003275327
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COL25A1	intron	0	0.003275327
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LINC02261	non-coding	1	0.003275327
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ATP10B	intron	0	0.00326392
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SLC28A3	intron	0	0.00315315
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NEGR1	intron	0	0.00315315
SOCS4	intron	0	0.00315315
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ME2	intron	0	0.003147447
LYPD1	intron	0	0.003147447
LOC101927668	non-coding	0	0.003147447
USP15	intron	1	0.003147447
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ONECUT2	intron	0	0.00313604
TTLL5	intron	0	0.00313604
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CACNA2D3	intron	0	0.00313604
TCF4	intron	0	0.00313604
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FANCB	intron	0	0.003124634
LINC01317	non-coding	0	0.003124634
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ITGA9	intron	1	0.00311893
TBC1D8	intron	0	0.00311893
LINC02173	non-coding	0	0.003113227
BPIFC	intron	0	0.003113227
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KIAA0319	intron	0	0.003002457
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LMX1B	intron	0	0.002996754
SORBS1	intron	0	0.002996754
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LDAH	intron	0	0.00299105
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RERE	intron	0	0.00299105
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MKLN1	intron	0	0.002985347
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TUSC3	intron	0	0.002979644
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OSBPL9	intron	0	0.002979644
FUT10	intron	0	0.002979644
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DDX23	intron	0	0.00297394
HERC4	intron	0	0.00297394
NPAS3	intron	0	0.002968237
CADPS2	intron	0	0.002968237
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SMARCA2	intron	0	0.002968237
NHS	intron	0	0.002968237
SIPA1L3	intron	0	0.002968237
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NELL2	intron	0	0.002846061
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NAV3	intron	0	0.002846061
GRIK2	intron	0	0.002846061
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MYO3B	intron	0	0.002840357
LHFPL3	intron	0	0.002840357
DPY19L1P1	non-coding	1	0.002840357
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TWSG1	intron	0	0.002840357
IQGAP2	intron	0	0.002834654
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SPATA17	intron	0	0.002834654
NFIA	intron	0	0.002834654
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MYO3B	intron	0	0.00282895
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BIRC6	intron	0	0.00282895
PPFIBP1	intron	0	0.002823247
DCDC1	intron	1	0.002823247
GTPBP10	intron	0	0.002823247
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PLCH1	intron	0	0.002823247
EHBP1	intron	0	0.002823247
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NLRP4	intron	0	0.002823247
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STPG2	intron	0	0.002817544
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C12orf56	intron	0	0.00281184
LINC02228	non-coding	1	0.002701071
RPL39L	intron	0	0.002695367
SPATA5	intron	0	0.002695367
ANK2	intron	0	0.002695367
BHMT2	exon	1	0.002695367
EXOC4	intron	0	0.002695367
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TRAPPC13	intron	0	0.002689664
WWP2	intron	0	0.002689664
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MYRIP	intron	0	0.002689664
ICE1	intron	0	0.002689664
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INPP4B	intron	0	0.002683961
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SOX6	intron	0	0.002683961
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PCDH9	intron	0	0.002683961
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DSCAM	intron	0	0.002678257
TUBGCP3	intron	0	0.002678257
UTS2B	intron	0	0.002678257
PIK3C2G	intron	0	0.002678257
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ST6GALNAC3	intron	0	0.002678257
DOCK2	intron	0	0.002678257
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AKAP13	intron	0	0.002672554
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DHX9	intron	0	0.002672554
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SYNCRIP	intron	0	0.002672554
MTREX	intron	0	0.002672554
TMEM178A	intron	0	0.002666851
TMPRSS15	intron	0	0.002666851

RBM25	intron	0	0.002661147
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CHODL	intron	0	0.002550378
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SCHIP1	intron	0	0.002544674
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GALNT7-DT	non-coding	1	0.002544674
.	intergenic	0	0.002538971
CCDC178	intron	0	0.002538971
KALRN	intron	0	0.002538971
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SERINC5	intron	0	0.002538971
PLAG1	intron	0	0.002538971
TPRG1	intron	0	0.002538971
BTRC	intron	0	0.002538971
LINC01924	non-coding	0	0.002538971
LINC00200	non-coding	1	0.002538971
NAV3	intron	0	0.002538971
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NHSL2	intron	0	0.002533267
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CCDC171	intron	0	0.002533267
EPG5	intron	0	0.002533267
SOX5	intron	0	0.002533267
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LRMDA	intron	0	0.002533267
ROBO2	intron	0	0.002533267
FAM163A	intron	0	0.002533267
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NDUFA10	intron	0	0.002533267
TBL1XR1	intron	0	0.002533267
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IPCEF1	intron	0	0.002527564
PREPL	exon	0	0.002527564
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KCNQ3	intron	0	0.002527564
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ACAD8	intron	0	0.002521861
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BEND7	intron	0	0.002521861
PTPN20	intron	0	0.002521861
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DBNDD1	intron	0	0.002516157
USP9Y	intron	0	0.002516157
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KCNIP4	intron	0	0.002405388
ABCB1	intron	0	0.002405388
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LINC00299	non-coding	0	0.002393981
PLCB1	intron	0	0.002393981
WDR17	intron	0	0.002393981
TRPC4AP	intron	0	0.002388278
FRG1-DT	non-coding	1	0.002388278
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LIN28B	intron	0	0.002388278
NAALADL2	intron	0	0.002388278
LINC02201	non-coding	1	0.002388278
CRTAC1	intron	0	0.002388278
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ERBB4	intron	0	0.002388278
PTPN9	intron	0	0.002388278
DARS1	intron	0	0.002388278
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MIPEP	intron	0	0.002388278
GPC5	intron	0	0.002382574
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GALNTL6	intron	0	0.002382574
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VEGFC	intron	0	0.002382574
SPAG16	intron	0	0.002382574
ARID1B	intron	0	0.002382574

LOC105373133	non-coding	1	0.002382574
SLC26A9	intron	0	0.002382574
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AGO2	intron	0	0.002376871
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NUDCD2	3utr	0	0.002376871
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PTGER2	intron	0	0.002376871
STK39	intron	0	0.002376871
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SCRN3	intron	0	0.002376871
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SERPINB6	intron	0	0.002376871
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LINC02987	non-coding	0	0.002371168
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PARVA	intron	0	0.002371168
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KLRD1	intron	0	0.002371168
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MIR202HG	non-coding	1	0.002371168
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NECAB1	intron	0	0.002248991
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USH2A	intron	0	0.002243288
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CLOCK	intron	0	0.002237584
FHIT	intron	0	0.002237584
ADAM22	intron	0	0.002237584
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COL25A1	intron	0	0.002237584
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NRG3	intron	0	0.002237584
FOCAD	intron	0	0.002237584
CNOT10	intron	0	0.002237584
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KBTBD12	intron	0	0.002237584
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KIF14	intron	0	0.002231881
LINC03021	non-coding	1	0.002231881
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LINC00630	non-coding	1	0.002231881
GPC5	intron	0	0.002231881
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THSD4	intron	0	0.002231881
TTLL7	intron	0	0.002231881
CNTNAP2	intron	0	0.002231881
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PTCHD1-AS	non-coding	1	0.002226178
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SLC8A1	3utr	0	0.002226178
WDFY1	intron	0	0.002226178
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CFAP47	intron	0	0.002226178
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CDH7	intron	0	0.002220474
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LINC02476	non-coding	1	0.002220474
SYNPO2	intron	0	0.002220474
ETV6	intron	0	0.002220474
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STXBP5-AS1	non-coding	0	0.002220474
CNDP2	3utr	0	0.002220474

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TRANK1	intron	0	0.002109705
DAB1	intron	0	0.002109705
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GABRG3	intron	0	0.002098298
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ABCB1	intron	0	0.002098298
GRM1	intron	0	0.002098298
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SSBP3	intron	0	0.002098298
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GPR39	intron	0	0.002092595
LRP12	intron	0	0.002092595
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UNC80	intron	0	0.002092595
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PDLIM5	intron	0	0.002092595
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LINC00276	non-coding	1	0.002092595
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ELOVL6	intron	0	0.002092595
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ZFYVE9	intron	0	0.002086891
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TEX13D	3utr	0	0.002086891
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CYREN	intron	0	0.002086891
SYT14	intron	0	0.002086891
SPHKAP	intron	0	0.002086891
LINC00907	non-coding	1	0.002086891
FAM241A	intron	0	0.002086891
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LINC01932	non-coding	0	0.002086891
GP2	intron	0	0.002081188
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USP34	intron	0	0.002081188
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MATN2	intron	0	0.002081188
CTNNA3	intron	0	0.002081188
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CNTN5	intron	1	0.002081188
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OBI1-AS1	non-coding	1	0.002081188
FAM114A1	intron	0	0.002081188
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AHI1	3utr	0	0.002081188
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TANC2	intron	0	0.002081188
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EPHB1	intron	0	0.002081188
LUZP2	intron	0	0.002081188
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LINC00871	non-coding	1	0.002075485
ADGRG4	intron	0	0.002075485
BDNF-AS	non-coding	0	0.002075485
SORL1	intron	0	0.002075485
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NEXMIF	intron	0	0.002075485
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MTR	intron	0	0.002075485
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UTP18	intron	0	0.002069781
SLC9B1	intron	0	0.002069781
IER3IP1	intron	0	0.002069781
CDH12	intron	0	0.001959011
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DCX	intron	0	0.001953308
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FBXL13	intron	0	0.001947605
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EGFEM1P	non-coding	0	0.001947605
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FKBP6	intron	0	0.001947605
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CHRM3	intron	0	0.001947605
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CAMK4	intron	0	0.001947605
LINC03016	non-coding	1	0.001941901

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RBFOX1	intron	0	0.001941901
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CADPS	intron	0	0.001941901
CDHR2	intron	0	0.001941901
ADAMTS16	intron	0	0.001941901
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PRAMENP	non-coding	1	0.001941901
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LINC01709	non-coding	1	0.001941901
PHACTR1	intron	0	0.001936198
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DCDC1	intron	0	0.001936198
NPC1	intron	0	0.001936198
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KCMF1	intron	0	0.001936198
LINC01194	non-coding	1	0.001936198
SLC6A11	intron	0	0.001936198
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PPM1D	intron	0	0.001936198
TGFBR3	intron	0	0.001936198
DUSP10	intron	0	0.001936198
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RNF103-CHMP3	intron	0	0.001936198
ATP8A1	intron	0	0.001936198
SRPRB	intron	0	0.001936198
NOMO2	intron	0	0.001936198
DYNC1LI1	intron	0	0.001936198
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ZNF536	intron	0	0.001936198
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LINC02018	non-coding	1	0.001936198
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TRPS1	intron	0	0.001936198
GRAMD1C	intron	0	0.001936198
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EDIL3	intron	0	0.001930495
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COP1	intron	0	0.001930495
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PKN2-AS1	non-coding	0	0.001930495
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IL1RAPL1	intron	0	0.001930495
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HOATZ	intron	0	0.001930495
SYCP1	intron	0	0.001930495
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ERBB4	intron	0	0.001930495
RFC1	intron	0	0.001930495
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GPBP1	intron	0	0.001930495
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IMMP2L	intron	0	0.001930495
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KCNH1	intron	0	0.001924791
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ALDH1A2	intron	0	0.001924791
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IKBKB-DT	non-coding	1	0.001924791
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RANBP2	intron	0	0.001924791
SRPK2	intron	0	0.001924791
ADCY10	intron	0	0.001924791
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HDAC4	intron	0	0.001924791
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LRRFIP2	intron	0	0.001802615

PRELID2	intron	0	0.001796912
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FAM117B	intron	0	0.001796912
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ST6GALNAC3	intron	0	0.001796912
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ADAMTS3	intron	0	0.001796912
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TENM2	intron	0	0.001796912
FNIP1	intron	0	0.001796912
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PTPRT	intron	0	0.001791208
MBNL1	intron	0	0.001791208
PDE3B	intron	0	0.001791208
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DYNC1LI1	intron	0	0.001791208
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PDGFRL	intron	0	0.001791208
CASK	intron	0	0.001791208
RPL39L	intron	0	0.001791208
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MAP4	intron	0	0.001791208
AFTPH	intron	0	0.001791208
MAEL	intron	0	0.001791208
LINC02008	non-coding	1	0.001791208
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ELOVL7	intron	0	0.001785505
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UNC5C	intron	0	0.001785505

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NRK	intron	0	0.001785505
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SPAG16	intron	1	0.001785505
PEAK1	intron	0	0.001785505
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LINC00333	non-coding	0	0.001785505
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MAP4K5	intron	0	0.001785505
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AGBL1	intron	0	0.001785505
CLEC12A	intron	1	0.001785505
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LINC00276	non-coding	0	0.001779802
LINC01416	non-coding	0	0.001779802
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TRAF3IP3	intron	0	0.001779802
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CSF2RA	intron	0	0.001779802
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LINC00536	non-coding	1	0.001779802
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LOC101928911	non-coding	0	0.001779802
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RNF111	intron	0	0.001779802
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FAM114A2	intron	0	0.001779802
HADHA	intron	0	0.001779802
VSTM2B	intron	0	0.001779802
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CAND1	intron	0	0.001779802
LHX1-DT	non-coding	1	0.001774098
AIG1	intron	0	0.001774098
.	intergenic	0	0.001774098
SLC24A2	intron	0	0.001774098
PRKN	intron	0	0.001774098

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THRB	intron	0	0.001774098
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LINC02551	non-coding	0	0.001774098
FGF12	intron	0	0.001657625
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FIP1L1	intron	0	0.001657625
DCC	intron	0	0.001651922
BICD1	intron	0	0.001651922
ADGRL4	intron	1	0.001651922
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RNF216	intron	0	0.001651922
PDE3A	intron	0	0.001646218
CLYBL	intron	0	0.001646218
POLR3G	intron	0	0.001646218
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PDE4D	intron	0	0.001646218
MOSMO	3utr	0	0.001646218
IPCEF1	intron	0	0.001646218
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REXO5	intron	0	0.001646218
ZNF618	intron	0	0.001646218
CASK	intron	0	0.001646218
TEX41	non-coding	1	0.001646218
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NSUN7	intron	0	0.001646218
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NLGN1	intron	0	0.001646218
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CAMSAP2	exon	1	0.001646218
ADAMTS16	intron	0	0.001646218
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GRM7	intron	0	0.001640515
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LINC00487	non-coding	1	0.001640515
AMBRA1	intron	0	0.001640515
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ENPP6	intron	0	0.001640515
AFF2	intron	0	0.001640515
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LINC02669	non-coding	1	0.001640515
TRMT61B	intron	0	0.001640515

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ADAMTS3	intron	1	0.001640515
CSPP1	intron	0	0.001640515
LOC105369146	non-coding	1	0.001640515
CSNK1G3	intron	0	0.001640515
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RAB11FIP4	intron	0	0.001640515
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CR1	intron	0	0.001640515
PRKCA	intron	0	0.001640515
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LINC00276	non-coding	1	0.001640515
RALGPS2	intron	0	0.001640515
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GABRB2	intron	0	0.001634812
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UPP2	intron	0	0.001634812
MACROD2	intron	0	0.001634812
OR8B2	flanking-downstream	0	0.001634812
THSD7B	intron	0	0.001634812
WDR93	intron	0	0.001634812
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LINC00320	non-coding	1	0.001634812
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ITGB1-DT	non-coding	1	0.001634812
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IQCH	intron	0	0.001634812
PCDH11Y	intron	0	0.001634812
NCOA2	intron	0	0.001634812
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TENM3	intron	0	0.001634812
CDCP1	intron	0	0.001634812
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PTPRM	intron	0	0.001634812
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DMD	intron	0	0.001634812
RGPD5	intron	0	0.001634812
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PLD1	intron	1	0.001634812
LOC105374428	non-coding	1	0.001634812
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UGT2B17	intron	0	0.001634812
SEC24D	intron	0	0.001634812

CPN2	intron	0	0.001634812
EGFR	intron	0	0.001634812
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EIF4G3	intron	0	0.001634812
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.	intergenic	0	0.001634812
MCF2L2	intron	0	0.001634812
.	intergenic	0	0.001634812
SNRPN	intron	0	0.001634812
HEBP1	intron	0	0.001634812
.	intergenic	0	0.001634812
DOK5	intron	0	0.001634812
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.	intergenic	0	0.001634812
.	intergenic	0	0.001634812
MYO3B	intron	0	0.001629108
.	intergenic	0	0.001629108
CPQ	intron	0	0.001629108
.	intergenic	0	0.001629108
.	intergenic	0	0.001629108
.	intergenic	0	0.001629108
ZNF81	intron	0	0.001629108
ARHGAP15	intron	0	0.001629108
.	intergenic	0	0.001629108
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.	intergenic	0	0.001629108
PCDH9	intron	0	0.001629108
SUGCT	intron	0	0.001629108
.	intergenic	0	0.001629108
EPHA5	intron	0	0.001629108
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PFKFB2	intron	0	0.001629108
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RGS8	intron	0	0.001629108
CENPP	intron	0	0.001629108
BLM	intron	0	0.001629108
STRADB	intron	0	0.001629108
.	intergenic	0	0.001629108
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GRM1	intron	0	0.001629108
SLC35F3	intron	0	0.001629108
.	intergenic	0	0.001629108
LINC02759	non-coding	0	0.001629108
ATXN2	intron	0	0.001629108
.	intergenic	0	0.001629108
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.	intergenic	0	0.001629108

.	intergenic	0	0.001629108
TTC27	intron	0	0.001629108
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PDZRN3	intron	0	0.001629108
CIB1	3utr	0	0.001629108
.	intergenic	0	0.001629108
.	intergenic	0	0.001629108
EEF1AKMT2	intron	0	0.001629108
CTTNBP2	intron	0	0.001629108
AMMECR1	intron	0	0.001629108
.	intergenic	0	0.001506932
NCOR1	intron	0	0.001506932
CADPS	intron	0	0.001501229
RAB33B	intron	0	0.001501229
LINC00448	non-coding	1	0.001501229
.	intergenic	0	0.001501229
SPRY3	intron	0	0.001501229
.	intergenic	0	0.001501229
CSMD1	intron	0	0.001501229
.	intergenic	0	0.001501229
STAU2	intron	0	0.001501229
.	intergenic	0	0.001501229
DMD	intron	0	0.001501229
.	intergenic	0	0.001501229
SLC49A4	intron	0	0.001501229
CNTNAP2	intron	0	0.001501229
C10orf71	intron	0	0.001501229
.	intergenic	0	0.001501229
A1CF	intron	0	0.001501229
FHIT	intron	0	0.001501229

chr	start	stop	strand	Lev Dist
chr17	14085172	14085192	+	3
chr13	51941575	51941595	-	2
chr6	71690548	71690568	+	2
chr18	2161210	2161230	+	4
chr2	198087308	198087328	-	3
chr2	210591861	210591881	-	1
chr5	89092422	89092442	-	3
chr6	28319161	28319181	+	2
chr10	21381234	21381254	-	2
chr4	96821205	96821225	-	4
chr5	153089661	153089681	-	6
chr9	72906365	72906385	-	6
chr1	79729332	79729352	-	6
chr1	223541124	223541144	-	6
chr10	24349853	24349873	+	4
chr10	56324280	56324300	-	2
chr18	22207200	22207220	-	2
chr2	52080116	52080136	-	6
chr2	61288516	61288536	-	6
chr2	130235534	130235554	-	5
chr3	69014309	69014329	-	3
chr4	29910257	29910277	-	3
chr8	117292906	117292926	-	4
chr1	61170869	61170889	+	3
chr1	63945814	63945834	+	6
chr1	232678825	232678845	-	4
chr1_KI270708v1_random	11298	11318	+	4
chr10	3903005	3903025	+	2
chr10	80905054	80905074	+	4
chr10	88545892	88545912	+	6
chr12	14009520	14009540	+	3
chr12	54068671	54068691	-	6
chr12	86196997	86197017	+	5
chr12	106685264	106685284	+	4
chr12	114081726	114081746	+	3
chr13	93207959	93207979	+	4
chr13	105960500	105960520	-	2
chr14	26538238	26538258	+	3
chr14	40774460	40774480	-	6
chr15	53663423	53663443	-	6
chr15	71407301	71407321	-	3
chr16	24194579	24194599	+	5
chr16	86217584	86217604	+	6
chr17	27847846	27847866	+	6
chr18	30253647	30253667	-	6
chr18	54737076	54737096	-	6
chr18	76326696	76326716	-	5

chr19	20319265	20319285 +	4
chr2	7733220	7733240 -	2
chr2	17253817	17253837 +	3
chr2	95541686	95541706 +	6
chr2	132665278	132665298 -	3
chr2	172467658	172467678 +	5
chr2	196584615	196584635 -	4
chr2	230142279	230142299 +	6
chr3	36496558	36496578 -	6
chr3	63605937	63605957 -	6
chr3	103143974	103143994 -	3
chr3	188539771	188539791 +	6
chr3	197582322	197582342 +	5
chr4	21943668	21943688 +	4
chr4	33624125	33624145 -	5
chr4	59287520	59287540 -	6
chr4	172313900	172313920 +	6
chr5	29462611	29462631 +	4
chr5	68439824	68439844 +	3
chr5	94172433	94172453 -	6
chr5	96663993	96664013 -	6
chr5	99031947	99031967 +	6
chr5	133207966	133207986 -	5
chr6	6655286	6655306 -	5
chr6	105754999	105755019 -	6
chr6	137465470	137465490 +	5
chr6	158133945	158133965 +	3
chr6	159571315	159571335 -	6
chr7	36730992	36731012 -	3
chr7	72005015	72005035 -	6
chr7	113149774	113149794 +	6
chr7	131268494	131268514 +	3
chr7	136969747	136969767 -	5
chr8	122636872	122636892 +	2
chr9	13154678	13154698 +	4
chr9	75995880	75995900 -	6
chr9	120131564	120131584 +	4
chr9	125552068	125552088 -	6
chrX	###	### -	6
chrX	###	### +	6

Score/On-Target_Ratio_CPS1_CHANGEseq_BE

[illegible]

[illegible]

Samples

CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CTLseq_U2OS_CPS1_WT|CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_WT|CTLseq_U2OS_CPS1_WT|CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CTLseq_HUH7_CPS1_DiseaseAllele|CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_WT|CTLseq_U2OS_CPS1_WT|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_WT|CTLseq_U2OS_CPS1_WT|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CTLseq_U2OS_CPS1_DiseaseAllele|CTLseq_HUH7_CPS1_DiseaseAllele|CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_CHANGEseq_BE
CPS1_ONEseq_0.01|CPS1_CHANGEseq_BE

[illegible]

Replicate	Gene	Region	Patient Variant	dbSNP ID
	2 COX10	intron		
	2 ATP7B	intron		
	2 none	intergenic		
	2 none	intergenic	chr18:2161222G>T	rs588515
	2 PLCL1	intron		
	2 CPS1	exon	chr2:210591885C>T	.
	2 MEF2C-AS1	non-coding RNA		
	2 none	intergenic		
	2 none	intergenic		
	1 none	intergenic		
	1 none	intergenic		
	1 ALDH1A1	intron		
	1 none	intergenic		
	1 none	intergenic		
	1 KIAA1217	intron		
	1 none	intergenic		
	1 none	intergenic		
	1 NRXN1-DT	non-coding RNA		
	1 USP34	intron		
	1 none	intergenic		
	1 EOGT-DT	non-coding RNA		
	1 none	intergenic		
	1 none	intergenic		
	1 NFIA	intron		
	1 ROR1	intron		
	1 none	intergenic		
	1 .	Not Found		
	1 none	intergenic		
	1 none	intergenic		
	1 RNLS	intron		
	1 none	intergenic		
	1 FLJ12825	non-coding RNA		
	1 MGAT4C	intron		
	1 RFX4	intron		
	1 LOC105369995	non-coding RNA		
	1 none	intergenic		
	1 none	intergenic		
	1 NOVA1	intron		
	1 none	intergenic		
	1 WDR72	intron		
	1 THSD4	intron		
	1 PRKCB	intron		
	1 none	intergenic		
	1 none	intergenic		
	1 none	intergenic		
	1 RAB27B	intron		
	1 none	intergenic		

1 none	intergenic
1 none	intergenic
1 none	intergenic
1 none	intergenic
1 LYPD1	intron
1 ITGA6	intron
1 HECW2	intron
1 none	intergenic
1 STAC	intron
1 SYNPR	intron
1 none	intergenic
1 LPP	intron
1 none	intergenic
1 KCNIP4	intron
1 none	intergenic
1 none	intergenic
1 GALNTL6	intron
1 none	intergenic
1 none	intergenic
1 KIAA0825	intron
1 CAST	intron
1 none	intergenic
1 FSTL4	intron
1 none	intergenic
1 none	intergenic
1 none	intergenic
1 SERAC1	intron
1 none	intergenic
1 none	intergenic
1 CALN1	intron
1 none	intergenic
1 MKLN1	intron
1 CHRM2	intron
1 none	intergenic
1 MPDZ	intron
1 PCSK5	intron
1 none	intergenic
1 MAPKAP1	intron
1 none	intergenic
1 none	intergenic

Tier

Tier1

Tier2

Tier3

Tier4

Tier5

Tier6

Definitions: Tiers below include consensus between positive- and negative-strand libraries and a significant p-value for
Consensus between at least 2 biological replicates, MAR of at least "likely pathogenic, annotation includes
Consensus between at least 2 biological replicates and Annotation includes "exon"
Annotation includes "exon", MAR of at least "likely pathogenic" or >1% Avg_%OnTargetUMI_Reads or cons
Annotation includes "intron" or "intergenic", <1% Avg_%OnTargetUMI_Reads, LD <5
0.1-1% Avg_%OnTargetUMI_Reads or LD<5
<0.1% Avg_%OnTargetUMI_Reads, LD>4

chr	start	stop	strand	Lev. Dist.	Tier
chr2	210591873	210591893	-	1	1
chr6	71690557	71690577	+	2	3
chr10	56324292	56324312	-	2	3
chr13	51941587	51941607	-	2	3
chr13	105960512	105960532	-	2	3
chr11	57726496	57726516	+	3	3
chr18	28430786	28430806	-	3	3
chr20	46262548	46262568	-	3	3
chr22	33548897	33548917	+	4	3
chr2	210591749	210591767	-	6	3
chr17	14085181	14085201	+	3	3
chr2	107701686	107701706	+	4	3
chr16	34588127	34588147	+	6	3
chr10	24349861	24349881	+	3	3
chr18	2161219	2161239	+	4	5
chr16	46389076	46389096	+	6	3
chr17	43472085	43472104	-	6	6
chr19	52675206	52675225	-	6	3
chr4	150673751	150673769	-	6	3
chr9	5828921	5828941	-	5	6
chr16	46400236	46400256	-	6	3
chr4	49103973	49103991	-	6	3
chr1	117371225	117371245	-	6	6
chr12	16700502	16700522	+	3	5
chr19	35923620	35923639	-	6	6
chr20	31213821	31213839	+	6	6
chr16	34581387	34581407	+	6	6
chr4	42524439	42524458	+	6	6
chr13	102978390	102978410	-	6	6
chr15	71560451	71560470	-	6	3
chr16	46401181	46401201	-	6	6
chrX	143455204	143455224	+	4	5
chr11	122891474	122891494	+	6	6
chr3	112911040	112911060	-	6	6
chr10	45987007	45987026	+	6	3
chr17	7602883	7602903	+	6	6
chrM	10324	10344	-	6	6
chr7	121141099	121141119	+	6	3
chr7	49502148	49502168	-	5	6
chr8	2040223	2040243	-	6	6
chr11	55052344	55052362	-	6	6
chr10	114296211	114296231	-	4	3
chr7	86536385	86536405	+	6	6
chr1	231540617	231540637	+	6	3
chr4	49147625	49147643	+	6	6
chr14	38007077	38007097	+	4	5
chrUn_KI270438v1	104376	104396	+	6	6
chr16	46398553	46398573	-	6	3
chr13	103687143	103687163	-	6	6
chr10	63501384	63501403	-	6	3

chr4	64420581	64420601 -	6	6
chr9	121177557	121177577 -	6	3
chr1	148055972	148055992 +	5	6
chr16	34586133	34586153 -	5	6
chr13	100666619	100666638 +	6	3
chr8	123614246	123614266 +	6	6
chrY	11643825	11643844 -	6	6
chr15	25963477	25963497 -	6	3
chr6	41668217	41668235 -	6	6
chr2	190032040	190032060 +	6	3
chr11	85448979	85448997 +	6	3
chr4	52735305	52735323 +	6	6
chr4	149238470	149238488 -	6	6
chr3	125726766	125726786 -	6	6
chr6	137610990	137611008 -	6	6
chr11	106109726	106109744 +	6	6
chr17_KI270729v1_random	59740	59759 +	6	6
chr3	173691237	173691256 -	6	3
chr10	42079675	42079695 -	6	6
chr18	50910799	50910819 +	4	5
chr2	51700372	51700394 -	6	6
chr14	49505304	49505323 -	6	6
chr7	3448464	3448485 -	6	3
chr3	107194685	107194705 +	6	6
chrM	10589	10608 -	6	6
chr2	62015628	62015649 +	6	6
chr3	109441319	109441339 +	4	5
chr2	210590916	210590936 -	6	3
chr5	19552938	19552958 +	5	3
chr22	16269967	16269987 +	6	6
chr11	104272430	104272450 +	4	5
chr11	35453141	35453161 +	6	6
chr20	31068519	31068537 +	4	5
chr16	46386493	46386513 -	6	6
chr6	61383664	61383682 +	5	6
chr2	132665291	132665311 -	3	3
chr5	39966526	39966546 -	5	6
chr15	68647164	68647185 +	6	6
chr11	109138384	109138404 -	6	6
chr3	40277530	40277550 +	6	6
chrUn_KI270517v1	2631	2649 -	5	6
chr14	99778821	99778841 -	4	3
chr3	143788738	143788758 +	6	3
chr12	3124373	3124392 +	6	3
chr3	25248348	25248367 -	6	3
chr11	99844369	99844389 +	6	3
chr2	135947775	135947796 +	6	3
chr16	82705551	82705571 +	6	3
chr1	187763236	187763256 -	6	6
chr12	90832411	90832431 -	6	6
chr11	63335538	63335557 -	6	6

chr3	67097709	67097728 +	6	6
chr14	36880675	36880695 -	6	3
chr1	155614892	155614912 -	6	3
chr3	18286238	18286257 +	5	6
chr10	39392442	39392461 +	6	6
chr2	78933334	78933355 -	6	6
chr7	122094836	122094856 +	6	3
chr1	32334556	32334577 -	6	3
chr11	98349120	98349138 -	6	6
chr9	117808527	117808547 -	6	6
chrX	63259190	63259210 -	3	5
chr3	184821674	184821695 -	6	3
chr7	81628563	81628583 +	6	3
chr13	47975530	47975550 -	4	3
chr11	27616919	27616940 +	5	3
chr21	7255330	7255348 -	4	5
chr6	68587058	68587079 +	6	6
chr2	198087320	198087340 -	3	3
chr3	108858616	108858636 -	6	6
chr1_KI270709v1_random	10583	10603 +	6	6
chr1	101885582	101885601 +	6	6
chr2	91586559	91586578 -	6	6
chr16	34594949	34594969 -	6	6
chrM	7956	7975 -	6	6
chr15	72575185	72575205 +	6	6
chr19	57579217	57579235 +	6	6
chr9	73747216	73747236 +	4	5
chr16	46391230	46391250 +	6	6
chr2	179715527	179715545 +	6	6
chr2	204916812	204916832 +	6	3
chr3	39964863	39964885 -	5	6
chr16	76814991	76815011 +	5	6
chr18	6641253	6641274 -	6	6
chr5	33299687	33299705 +	5	6
chr4	174877223	174877243 +	6	6
chr8	110396641	110396661 +	6	6
chr4	63161261	63161281 +	6	6
chr3	96019252	96019272 +	3	5
chr13	69970655	69970676 -	6	3
chrX	115223463	115223483 +	6	3
chr2	89826531	89826551 -	6	6
chr6	113966592	113966612 -	6	3
chr15	25433727	25433746 -	4	3
chr5	92045471	92045492 -	3	5
chr18	20922197	20922217 +	6	6
chr21	24770731	24770751 +	6	6
chr21	7919637	7919656 -	6	6
chr15	76599706	76599726 +	2	3
chr21	10691030	10691049 -	6	6
chr14	25620214	25620235 -	6	6
chr20	18004086	18004106 +	6	6

chr2

97548295 97548315 -

6

3

Gene	Region	Cell Line	Avg. UMI Reads (U2OS)	Avg. UMI Reads (HuH-7)
CPS1	Exon	both	37842.670	34450.330
none	Intergenic	both	12446.670	1693.670
none	Intergenic	both	1099.670	150.670
ATP7B	Intron	both	414.670	251.330
none	Intergenic	both	473.000	52.330
TMX2	Intron	both	257.330	118.000
none	Intergenic	both	78.670	37.330
CDH22	Intron	both	43.670	17.670
LARGE1	Intron	both	54.330	2.670
CPS1	Intron	HUH7	0.000	47.000
COX10	Intron	both	48.330	1.000
none	Intergenic	both	34.000	7.330
none	Intergenic	HUH7	0.000	36.670
KIAA1217	Intron	U2OS	31.330	0.000
none	Intergenic	both	24.670	6.670
none	Intergenic	HUH7	0.000	26.330
none	Intergenic	U2OS	25.330	0.000
ZNF83	Intron	U2OS	21.000	0.000
LRBA	Intron	U2OS	21.000	0.000
ERMP1	Intron	U2OS	24.670	0.000
none	Intergenic	HUH7	0.000	19.330
none	Intergenic	HUH7	0.000	19.000
MAN1A2	Intron	U2OS	22.330	0.000
none	Intergenic	U2OS	17.000	0.000
none	Intergenic	U2OS	16.670	0.000
none	Intergenic	HUH7	0.000	15.670
none	Intergenic	HUH7	0.000	16.330
ATP8A1	Intron	U2OS	17.000	0.000
none	Intergenic	U2OS	13.000	0.000
THSD4	Intron	HUH7	0.000	12.330
none	Intergenic	HUH7	0.000	13.000
none	Intergenic	U2OS	12.000	0.000
JHY	Intron	HUH7	0.000	11.330
none	Intergenic	U2OS	11.330	0.000
TIMM23	Intron	U2OS	11.000	0.000
FXR2	Intron	U2OS	13.330	0.000
none	Intergenic	U2OS	11.000	0.000
CPED1	Intron	HUH7	0.000	10.000
none	Intergenic	U2OS	10.670	0.000
none	Intergenic	HUH7	0.000	10.330
none	Intergenic	U2OS	12.000	0.000
AFAP1L2	Intron	HUH7	0.000	9.000
none	Intergenic	HUH7	0.000	10.330
TSNAX	Intron	HUH7	0.000	10.000
none	Intergenic	HUH7	0.000	9.670
LOC105370456	Other	U2OS	9.330	0.000
none	Intergenic	U2OS	9.330	0.000
none	Intergenic	HUH7	0.000	8.670
none	Intergenic	HUH7	0.000	9.330
JMJD1C	Intron	U2OS	8.670	0.000

none	Intergenic	U2OS	10.670	0.000
CNTRL	Exon	HUH7	0.000	9.000
PDE4DIPP1	Other	HUH7	0.000	8.330
none	Intergenic	HUH7	0.000	9.000
TMTC4	Intron	HUH7	0.000	8.670
none	Intergenic	HUH7	0.000	8.000
none	Intergenic	HUH7	0.000	8.670
LINC02346	Other	U2OS	9.670	0.000
none	Intergenic	U2OS	10.000	0.000
C2orf88	Other	HUH7	0.000	8.330
DLG2	Intron	HUH7	0.000	7.330
none	Intergenic	HUH7	0.000	8.000
LINC02355	Other	HUH7	0.000	7.000
none	Intergenic	HUH7	0.000	7.000
none	Intergenic	HUH7	0.000	7.000
none	Intergenic	HUH7	0.000	7.000
none	Intergenic	HUH7	0.000	7.330
NLGN1	Intron	U2OS	7.000	0.000
none	Intergenic	HUH7	0.000	7.330
ME2	Intron	U2OS	8.330	0.000
LOC730100	Other	HUH7	0.000	6.330
none	Intergenic	HUH7	0.000	7.000
SDK1	Intron	HUH7	0.000	6.330
LINC00882	Other	HUH7	0.000	6.000
none	Intergenic	HUH7	0.000	6.000
COMMD1	Intron	HUH7	0.000	6.000
LINC01205	Other	both	4.330	1.670
CPS1	Intron	U2OS	6.000	0.000
CDH18	Intron	HUH7	0.000	5.670
none	Intergenic	HUH7	0.000	5.670
none	Intergenic	U2OS	5.670	0.000
PAMR1	Intron	U2OS	7.000	0.000
none	Intergenic	HUH7	0.000	6.000
none	Intergenic	HUH7	0.000	5.330
none	Intergenic	HUH7	0.000	5.330
LYPD1	Exon	U2OS	6.330	0.000
none	Intergenic	U2OS	5.330	0.000
CORO2B	Intron	HUH7	0.000	5.000
none	Intergenic	HUH7	0.000	5.000
EIF1B-AS1	Other	HUH7	0.000	5.330
none	Intergenic	HUH7	0.000	5.330
EML1	Intron	U2OS	6.000	0.000
SLC9A9	Intron	U2OS	5.000	0.000
TSPAN9	Intron	HUH7	0.000	4.670
RARB	Intron	HUH7	0.000	4.670
CNTN5	Intron	HUH7	0.000	5.000
DARS1	Intron	HUH7	0.000	5.000
CDH13	Intron	HUH7	0.000	5.000
none	Intergenic	HUH7	0.000	4.670
none	Intergenic	HUH7	0.000	4.670
none	Intergenic	HUH7	0.000	4.670

none	Intergenic	U2OS	5.670	0.000
SLC25A21	Intron	HUH7	0.000	4.670
MSTO1	Exon	HUH7	0.000	4.670
none	Intergenic	HUH7	0.000	4.330
none	Intergenic	HUH7	0.000	4.330
none	Intergenic	HUH7	0.000	4.670
AASS	Intron	HUH7	0.000	4.000
MARCKSL1	Exon	HUH7	0.000	4.330
none	Intergenic	HUH7	0.000	4.000
LOC105376244	Other	HUH7	0.000	4.000
LOC105377212	Other	U2OS	4.670	0.000
VPS8	Intron	HUH7	0.000	3.670
LOC100128317	Other	HUH7	0.000	3.670
SUCLA2	Intron	HUH7	0.000	4.000
BDNF-AS	Other	HUH7	0.000	4.000
none	Intergenic	HUH7	0.000	4.000
none	Intergenic	HUH7	0.000	3.670
PLCL1	Intron	HUH7	0.000	3.670
none	Intergenic	HUH7	0.000	3.330
none	Intergenic	HUH7	0.000	3.330
OLFM3	Intron	HUH7	0.000	3.330
none	Intergenic	HUH7	0.000	3.330
none	Intergenic	HUH7	0.000	3.670
none	Intergenic	HUH7	0.000	3.670
ARIH1	Intron	HUH7	0.000	3.670
none	Intergenic	HUH7	0.000	3.670
none	Intergenic	HUH7	0.000	3.000
none	Intergenic	HUH7	0.000	3.000
ZNF385B	Intron	HUH7	0.000	3.000
PARD3B	Intron	U2OS	3.000	0.000
MYRIP	Intron	HUH7	0.000	2.670
none	Intergenic	HUH7	0.000	2.670
LOC107985176	Other	HUH7	0.000	2.670
none	Intergenic	U2OS	3.000	0.000
none	Intergenic	HUH7	0.000	2.330
none	Intergenic	HUH7	0.000	2.330
none	Intergenic	HUH7	0.000	2.670
none	Intergenic	U2OS	2.000	0.000
KLHL1	Exon	HUH7	0.000	2.000
LRCH2	Intron	HUH7	0.000	2.000
none	Intergenic	HUH7	0.000	2.330
HDAC2	Intron	HUH7	0.000	2.000
UBE3A	Intron	HUH7	0.000	1.670
none	Intergenic	HUH7	0.000	2.000
none	Intergenic	HUH7	0.000	1.670
none	Intergenic	HUH7	0.000	1.670
none	Intergenic	HUH7	0.000	1.670
SCAPER	Intron	U2OS	1.330	0.000
none	Intergenic	U2OS	1.670	0.000
none	Intergenic	U2OS	1.330	0.000
none	Intergenic	HUH7	0.000	1.330

ANKRD36B	Intron	HUH7	0.000	1.000

Avg. UMI Reads	Avg. % On-Target UMI (U2OS)	Avg. % On-Target UMI (HuH-7)
36146.500	100.000	100.000
7070.170	33.009	4.938
625.170	2.901	0.437
333.000	1.084	0.727
262.665	1.253	0.155
187.665	0.695	0.344
58.000	0.210	0.110
30.670	0.118	0.051
28.500	0.144	0.008
23.500	0.000	0.130
24.665	0.126	0.003
20.665	0.089	0.021
18.335	0.000	0.102
15.665	0.089	0.000
15.670	0.058	0.020
13.165	0.000	0.078
12.665	0.071	0.000
10.500	0.060	0.000
10.500	0.059	0.000
12.335	0.058	0.000
9.665	0.000	0.058
9.500	0.000	0.055
11.165	0.052	0.000
8.500	0.048	0.000
8.335	0.048	0.000
7.835	0.000	0.048
8.165	0.000	0.045
8.500	0.040	0.000
6.500	0.037	0.000
6.165	0.000	0.036
6.500	0.000	0.036
6.000	0.034	0.000
5.665	0.000	0.033
5.665	0.032	0.000
5.500	0.031	0.000
6.665	0.031	0.000
5.500	0.031	0.000
5.000	0.000	0.031
5.335	0.030	0.000
5.165	0.000	0.030
6.000	0.028	0.000
4.500	0.000	0.028
5.165	0.000	0.028
5.000	0.000	0.027
4.835	0.000	0.027
4.665	0.026	0.000
4.665	0.026	0.000
4.335	0.000	0.026
4.665	0.000	0.026
4.335	0.025	0.000

5.335	0.025	0.000
4.500	0.000	0.025
4.165	0.000	0.025
4.500	0.000	0.025
4.335	0.000	0.024
4.000	0.000	0.024
4.335	0.000	0.024
4.835	0.023	0.000
5.000	0.023	0.000
4.165	0.000	0.023
3.665	0.000	0.022
4.000	0.000	0.022
3.500	0.000	0.021
3.500	0.000	0.021
3.500	0.000	0.021
3.500	0.000	0.021
3.665	0.000	0.021
3.500	0.020	0.000
3.665	0.000	0.020
4.165	0.019	0.000
3.165	0.000	0.019
3.500	0.000	0.019
3.165	0.000	0.018
3.000	0.000	0.018
3.000	0.000	0.018
3.000	0.000	0.018
3.000	0.012	0.005
3.000	0.017	0.000
2.835	0.000	0.017
2.835	0.000	0.017
2.835	0.016	0.000
3.500	0.016	0.000
3.000	0.000	0.016
2.665	0.000	0.016
2.665	0.000	0.016
3.165	0.015	0.000
2.665	0.015	0.000
2.500	0.000	0.015
2.500	0.000	0.015
2.665	0.000	0.015
2.665	0.000	0.015
3.000	0.014	0.000
2.500	0.014	0.000
2.335	0.000	0.014
2.335	0.000	0.014
2.500	0.000	0.014
2.500	0.000	0.014
2.500	0.000	0.014
2.335	0.000	0.014
2.335	0.000	0.014
2.335	0.000	0.014

2.835	0.013	0.000
2.335	0.000	0.013
2.335	0.000	0.013
2.165	0.000	0.013
2.165	0.000	0.013
2.335	0.000	0.013
2.000	0.000	0.012
2.165	0.000	0.012
2.000	0.000	0.012
2.000	0.000	0.012
2.335	0.011	0.000
1.835	0.000	0.011
1.835	0.000	0.011
2.000	0.000	0.011
2.000	0.000	0.011
2.000	0.000	0.011
1.835	0.000	0.011
1.835	0.000	0.010
1.665	0.000	0.010
1.665	0.000	0.010
1.665	0.000	0.010
1.665	0.000	0.010
1.835	0.000	0.010
1.835	0.000	0.010
1.835	0.000	0.010
1.835	0.000	0.010
1.500	0.000	0.009
1.500	0.000	0.009
1.500	0.000	0.009
1.500	0.008	0.000
1.335	0.000	0.008
1.335	0.000	0.008
1.335	0.000	0.008
1.500	0.007	0.000
1.165	0.000	0.007
1.165	0.000	0.007
1.335	0.000	0.007
1.000	0.006	0.000
1.000	0.000	0.006
1.000	0.000	0.006
1.165	0.000	0.006
1.000	0.000	0.005
0.835	0.000	0.005
1.000	0.000	0.005
0.835	0.000	0.005
0.835	0.000	0.005
0.835	0.000	0.005
0.665	0.004	0.000
0.835	0.004	0.000
0.665	0.004	0.000
0.665	0.000	0.004

0.500

0.000

0.003

Avg. % On-Target UMI Rep. (U2OS)	Rep. (HuH-7)	
100.000	3	3
18.974	3	3
1.669	3	3
0.906	3	3
0.704	3	3
0.520	3	3
0.160	2	2
0.084	2	3
0.076	2	1
0.065	0	2
0.065	2	1
0.055	2	1
0.051	0	2
0.045	2	0
0.039	1	2
0.039	0	2
0.036	1	0
0.030	1	0
0.030	1	0
0.029	1	0
0.029	0	2
0.028	0	2
0.026	1	0
0.024	1	0
0.024	1	0
0.024	0	1
0.023	0	1
0.020	1	0
0.019	1	0
0.018	0	1
0.018	0	1
0.017	1	0
0.017	0	1
0.016	1	0
0.016	1	0
0.016	1	0
0.016	1	0
0.016	0	1
0.015	1	0
0.015	0	1
0.014	1	0
0.014	0	1
0.014	0	1
0.014	0	1
0.014	0	1
0.013	1	0
0.013	1	0
0.013	0	2
0.013	0	1
0.013	1	0

0.013	1	0
0.013	0	1
0.013	0	1
0.013	0	1
0.012	0	1
0.012	0	1
0.012	0	1
0.012	1	0
0.012	1	0
0.012	0	1
0.011	0	1
0.011	0	1
0.011	0	1
0.011	0	1
0.011	0	1
0.011	0	1
0.011	0	1
0.010	1	0
0.010	0	1
0.010	1	0
0.010	0	1
0.010	0	1
0.009	0	1
0.009	0	1
0.009	0	1
0.009	0	1
0.009	1	1
0.009	1	0
0.009	0	1
0.009	0	1
0.008	1	0
0.008	1	0
0.008	0	1
0.008	0	1
0.008	0	1
0.008	1	0
0.008	1	0
0.008	0	1
0.008	0	1
0.008	0	1
0.008	0	1
0.008	0	1
0.007	1	0
0.007	1	0
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1

0.007	1	0
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1
0.007	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.006	1	0
0.006	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.006	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.005	0	1
0.004	1	0
0.004	0	1
0.004	0	1
0.004	0	1
0.004	1	0
0.004	0	1
0.004	0	1
0.004	0	1
0.003	1	0
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.003	0	1
0.002	1	0
0.002	1	0
0.002	1	0
0.002	0	1

0.002

0

1

chr	start	stop	strand	Lev. Dist.	Tier	Gene
chr2	210591873	210591893	-		0	1 CPS1
chr13	28478362	28478382	-		3	3 FLT1
chr2	88552102	88552122	-		2	3 LOC101928371
chr6	71690557	71690577	+		3	3 none
chr10	56324292	56324312	-		3	3 none
chr6	96750602	96750622	-		4	3 none
chr13	51941587	51941607	-		3	3 ATP7B
chr20	42667000	42667020	+		3	3 PTPRT
chr8	99794486	99794506	-		5	3 VPS13B
chr5	32045171	32045191	+		6	3 PDZD2
chr3	60384958	60384978	-		6	3 FHIT
chr4	129150639	129150659	-		3	5 none
chr7	68154122	68154142	+		2	5 LOC105375341
chr2	191905587	191905607	-		4	5 none
chr6	32368599	32368619	-		3	5 TSBP1
chr11	108029419	108029439	+		4	5 CUL5
chr8	70547400	70547420	+		3	5 none
chr2	21395450	21395470	+		6	6 none
chr13	79419346	79419365	-		6	6 RBM26-AS1
chr2	93754951	93754969	+		5	6 none
chr16	19129826	19129846	-		6	6 none
chr5	146593816	146593836	+		6	6 PPP2R2B
chr1	94757676	94757696	-		6	6 SLC44A3-AS1
chr5	77742179	77742199	+		6	6 TBCA
chr4	159914856	159914876	+		6	6 LOC107986324
chr2	161811106	161811126	+		6	3 SLC4A10
chr20	42970387	42970407	+		6	3 PTPRT
chr6	154331970	154331990	-		3	3 IPCEF1
chr8	107998731	107998751	-		6	3 RSPO2
chr21	40397747	40397766	-		6	3 DSCAM
chr13	105730448	105730466	+		6	3 LINC00343
chr2	218254089	218254109	-		6	3 ARPC2
chrUn_KI270438v1	102368	102386	+		6	5 none
chr7	37590233	37590253	+		2	5 none
chr5	50995275	50995295	+		2	5 none
chr11	74601439	74601458	+		6	6 POLD3
chr2	79046372	79046392	+		6	6 none
chr1	45988663	45988682	+		6	6 MAST2
chr12	114850684	114850705	+		6	6 none
chr16	46401311	46401330	+		5	6 none
chr4	34238119	34238139	-		6	6 LINC02484
chr5	49601725	49601745	+		6	6 none
chr5	49601750	49601770	+		6	6 none
chr4	52575886	52575906	-		6	6 none
chr5	49602115	49602135	+		6	6 none
chr2	89833404	89833424	-		6	6 none
chr3	145538143	145538162	+		6	6 none
chr14	43408726	43408745	+		6	6 none
chr5	49660745	49660765	-		6	6 none
chr19	37732208	37732227	-		6	6 none

chr11	37842595	37842615 -	6	6 none
chr17	26619568	26619587 +	6	6 none
chr3	103265928	103265948 -	6	6 none
chr17	21014472	21014493 -	6	6 USP22
chr20	47912906	47912926 -	6	6 none
chr3	122159469	122159488 -	5	6 none
chr2	131812122	131812141 -	5	6 none
chr17	37868538	37868558 -	6	6 YWHAEP7
chr4	78956535	78956555 -	6	6 none
chr20	29885813	29885831 -	6	6 none
chr5	49657003	49657023 -	6	6 none
chr6	91554457	91554476 -	6	6 none

[illegible]

Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intron HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Other HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000
Intergenic HUH7	0.000	0.000

Avg. UMI Reads (HuH-7)	Avg. % On-Target UMI (HuH-7)	Rep. (U2OS)	Rep. (HuH-7)
32266.000	100.000	3	3
47.000	0.149	3	3
87.670	0.273	3	3
16.000	0.049	3	1
4.330	0.015	3	1
48.670	0.146	3	2
0.000	0.000	3	0
4.330	0.013	2	1
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
5.330	0.016	1	1
0.000	0.000	1	0
33.330	0.112	1	1
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
0.000	0.000	1	0
11.330	0.033	0	1
9.670	0.029	0	1
8.670	0.026	0	1
7.670	0.022	0	1
3.670	0.011	0	1
3.000	0.010	0	1
1.000	0.003	0	1
38.670	0.130	0	1
12.330	0.036	0	1
4.670	0.014	0	1
22.000	0.064	0	1
16.670	0.056	0	1
15.000	0.050	0	1
11.670	0.039	0	1
13.000	0.038	0	1
10.000	0.034	0	1
10.670	0.032	0	1
9.670	0.032	0	1
9.000	0.030	0	1
9.670	0.029	0	1
9.330	0.028	0	1
9.670	0.028	0	1
7.670	0.026	0	1
8.670	0.025	0	1
6.330	0.019	0	1

5.330	0.018	0	1
5.670	0.017	0	1
4.330	0.015	0	1
4.670	0.014	0	1
4.330	0.013	0	1
3.330	0.010	0	1
3.000	0.009	0	1
2.670	0.009	0	1
2.330	0.007	0	1
1.670	0.006	0	1
1.670	0.005	0	1
1.670	0.005	0	1

Rep. (U2OS)

chr	start	stop	strand	Reproducibility
chr2	210591861	210591881	-	5
chrX	152850556	152850576	-	4
chr16	25745352	25745372	+	5
chr8	122636872	122636892	+	5
chr14	82199313	82199333	-	5
chr10	56324281	56324301	-	5
chr10	3903005	3903025	+	5
chr13	105960500	105960520	-	5
chr13	105960501	105960521	-	5
chr5	137707021	137707041	+	5
chr2	7733220	7733240	-	5
chr6	71690548	71690568	+	5
chr15	76599697	76599717	+	5
chr10	21381234	21381254	-	5
chr10	82028845	82028865	-	5
chr13	51941575	51941595	-	5
chr10	56324280	56324300	-	5
chr6	138770125	138770145	-	5
chr6	28319161	28319181	+	5
chr4	25696310	25696330	+	5
chr4	25696309	25696329	+	5
chr13	90518582	90518602	-	5
chr1_KI270763v1_alt	765254	765274	+	1
chr5_GL339449v2_alt	679797	679817	+	1
chr5_GL339449v2_alt	879980	880000	-	1
chr5_GL339449v2_alt	1256203	1256223	+	1
chr5_KI270897v1_alt	82230	82250	-	1
chr5_KI270897v1_alt	786906	786926	+	1
chr2_KI270775v1_alt	56237	56257	+	1
chr21_KI270874v1_alt	119147	119167	+	1
chr17_JH159146v1_alt	52673	52693	-	1
chr17_KI270857v1_alt	1138543	1138563	+	1
chr8_KI270822v1_alt	198050	198070	-	1
chr8_KI270821v1_alt	745789	745809	+	1
chr14	78253995	78254015	+	2
chr1	207493853	207493873	+	2
chr4	77290304	77290324	+	3
chr4	160786597	160786617	-	3
chrX	22753176	22753196	-	3
chrX	16624510	16624530	-	3
chr4	114017374	114017394	-	3
chr4	110765401	110765421	-	3
chr4	93583130	93583150	-	3
chrX	152962496	152962516	-	3
chrX	155623275	155623295	-	3
chr21	37013201	37013221	-	3
chrX	103027137	103027157	-	3
chr4	16704826	16704846	+	3
chr7	16838172	16838192	-	3
chr9	20843954	20843974	+	3

chr8	82305111	82305131 +	3
chr8	39445246	39445266 +	3
chr7	120366931	120366951 -	3
chr7	120366930	120366950 -	3
chr7	120366929	120366949 -	3
chr9	108452738	108452758 -	3
chr9	108452739	108452759 -	3
chr5	55411605	55411625 -	3
chr5	55411604	55411624 -	3
chr6	87620733	87620753 +	3
chr13	30993580	30993600 +	3
chr12	127250435	127250455 -	3
chr13	83100205	83100225 -	3
chr12	60336177	60336197 -	3
chr15	43174945	43174965 -	3
chr1	178295982	178296002 +	3
chr1	231594142	231594162 +	3
chr1	101259536	101259556 -	3
chr1	98575093	98575113 -	3
chr11	32960650	32960670 -	3
chr11	33223038	33223058 -	3
chr10	38577723	38577743 +	3
chr10	62298408	62298428 +	3
chr2	63159802	63159822 -	3
chr2	48206010	48206030 -	3
chr2	34912934	34912954 +	3
chr20	16224613	16224633 -	3
chr17	53960280	53960300 +	3
chr17	72156065	72156085 -	3
chr3	188648620	188648641 -	3
chr2	123046674	123046695 +	3
chr12	88589555	88589576 +	3
chr10	38341106	38341127 -	3
chr5	53888126	53888149 +	3
chr3	111203314	111203335 -	3
chr17	41179659	41179680 +	3
chr9	17791020	17791041 +	3
chr4	27622710	27622731 +	3
chr10	10300229	10300249 +	3
chr10	4463528	4463549 -	3
chr2	205651158	205651179 -	3
chr2	200169847	200169868 +	3
chr5	117081051	117081072 +	3
chr16	26582404	26582427 +	3
chr3	145032189	145032212 +	3
chr2	174446383	174446404 +	3
chr1	217669467	217669488 +	3
chr16	61718244	61718265 +	3
chr1	240296337	240296359 +	3
chr5	87387933	87387955 -	3
chr18	10382058	10382079 -	3

chr5	3843409	3843434 -	3
chr18	22207210	22207235 -	3
chr11	24299881	24299902 +	3
chr4	103820314	103820339 -	3
chr4	167364113	167364134 +	3
chr11	115739376	115739396 +	3
chr8	4718429	4718450 +	3
chr4	121161335	121161357 +	3
chr4	148257315	148257336 -	3
chr8	23681832	23681853 -	3
chr2	48597982	48598003 -	3
chr4	32968663	32968684 +	3
chr10	74367828	74367849 +	3
chr17	65777360	65777382 +	3
chr10	86371480	86371502 -	3
chr2	51457658	51457679 -	3
chr3	27877886	27877906 +	3
chr1	78975267	78975290 -	3
chr1	96035971	96035992 +	3
chr6	138235435	138235455 +	3
chr3	99421709	99421730 +	3
chrX	30399577	30399599 +	3
chr6	97001770	97001791 +	3
chr3	17040386	17040407 +	3
chr22	34737687	34737708 -	3
chr14	72977021	72977041 +	4
chr6	27313497	27313517 -	4
chr14	76533436	76533456 +	4
chr14	75771551	75771571 -	4
chr14	64023779	64023799 -	4
chr6	45497242	45497262 +	4
chr14	103879509	103879529 +	4
chr14	102690732	102690752 -	4
chr6	62752099	62752119 -	4
chr6	54388992	54389012 -	4
chr6	83909225	83909245 -	4
chr6	121364342	121364362 +	4
chr14	23871618	23871638 -	4
chr13	94421881	94421901 -	4
chr13	94810687	94810707 -	4
chr13	103331256	103331276 -	4
chr14	46888117	46888137 +	4
chr14	31532877	31532897 +	4
chr14	26538238	26538258 +	4
chr6	96268773	96268793 +	4
chr5	122650383	122650403 +	4
chr5	122650382	122650402 +	4
chr16	20824585	20824605 +	4
chr5	131142014	131142034 -	4
chr16	6818284	6818304 -	4
chr5	128868648	128868668 +	4

chr5	102333534	102333554 -	4
chr5	102333533	102333553 -	4
chr5	92045459	92045479 -	4
chr5	94965074	94965094 -	4
chr16	68804026	68804046 +	4
chr5	93612866	93612886 -	4
chr5	102333535	102333555 -	4
chr16	49647254	49647274 +	4
chr5	114301332	114301352 -	4
chr16	58771346	58771366 -	4
chr6	4998773	4998793 -	4
chr6	21286696	21286716 -	4
chr15	35414138	35414158 -	4
chr5	156836978	156836998 -	4
chr5	146647203	146647223 -	4
chr15	93262842	93262862 -	4
chr5	162364348	162364368 -	4
chr15	75470949	75470969 +	4
chr5	159669105	159669125 -	4
chr5	158378988	158379008 +	4
chr15	73423484	73423504 -	4
chr7	133338218	133338238 -	4
chr12	41477412	41477432 +	4
chr12	22308939	22308959 +	4
chr7	139343302	139343322 +	4
chr12	73956205	73956225 +	4
chr12	71782832	71782852 +	4
chr7	95761717	95761737 -	4
chr12	78790153	78790173 +	4
chr12	60820218	60820238 +	4
chr11	106436341	106436361 +	4
chr8	40363736	40363756 +	4
chr8	39292339	39292359 -	4
chr11	109703118	109703138 -	4
chr8	33172341	33172361 +	4
chr8	33172340	33172360 +	4
chr8	35134219	35134239 +	4
chr11	100693283	100693303 -	4
chr8	55018889	55018909 -	4
chr11	95881871	95881891 +	4
chr12	7888277	7888297 +	4
chr12	714864	714884 +	4
chr8	10387517	10387537 +	4
chr12	14009520	14009540 +	4
chr12	14009521	14009541 +	4
chr8	2578129	2578149 +	4
chr8	24653745	24653765 +	4
chr13	57044233	57044253 +	4
chr7	8213616	8213636 +	4
chr13	58498215	58498235 +	4
chr13	47252784	47252804 -	4

chr13	76655555	76655575 +	4
chr13	77205504	77205524 -	4
chr6	144389891	144389911 -	4
chr13	82584812	82584832 -	4
chr6	163645644	163645664 +	4
chr13	64541574	64541594 +	4
chr13	71260290	71260310 +	4
chr7	66409482	66409502 +	4
chr12	114081726	114081746 +	4
chr12	88982080	88982100 -	4
chr12	89074634	89074654 -	4
chr7	80790435	80790455 -	4
chr7	81525501	81525521 -	4
chr7	46020632	46020652 -	4
chr12	121334875	121334895 +	4
chr12	130238313	130238333 -	4
chr7	47724802	47724822 -	4
chr12	129974541	129974561 -	4
chr3	135836025	135836045 +	4
chr3	122632368	122632388 +	4
chr2	138532321	138532341 -	4
chr3	146174282	146174302 +	4
chr3	144950698	144950718 +	4
chr3	104934826	104934846 +	4
chr3	96019243	96019263 +	4
chr2	165919377	165919397 +	4
chr2	167119015	167119035 +	4
chr2	161826789	161826809 +	4
chr3	117494125	117494145 +	4
chr2	172209745	172209765 +	4
chr2	173369988	173370008 +	4
chr2	169958894	169958914 -	4
chr2	88552090	88552110 -	4
chr2	88552091	88552111 -	4
chr3	186203158	186203178 +	4
chr3	186203157	186203177 +	4
chr3	193620665	193620685 -	4
chr3	180082474	180082494 -	4
chr2	65782059	65782079 +	4
chr2	123575238	123575258 +	4
chr2	132665278	132665298 -	4
chr2	132665279	132665299 -	4
chr2	115958935	115958955 +	4
chr2	114840837	114840857 -	4
chr2	115415178	115415198 -	4
chr20	40039261	40039281 +	4
chr20	54569334	54569354 +	4
chr20	46262536	46262556 -	4
chr20	18234739	18234759 -	4
chr20	24172109	24172129 -	4
chr3	21732485	21732505 +	4

chr20	22741102	22741122 -	4
chr22	34061580	34061600 -	4
chr20	59691000	59691020 +	4
chr21	17262837	17262857 +	4
chr21	18819487	18819507 +	4
chr3	69014309	69014329 -	4
chr3	65194983	65195003 +	4
chr3	65194971	65194991 -	4
chr3	84259007	84259027 -	4
chr2	198087308	198087328 -	4
chr3	80794179	80794199 +	4
chr3	30329027	30329047 +	4
chr20	11344601	11344621 +	4
chr3	54521190	54521210 +	4
chr2	228000983	228001003 +	4
chr3	59459941	59459961 -	4
chr2	239697036	239697056 -	4
chr18	2161210	2161230 +	4
chr4	183698546	183698566 -	4
chr5	22467594	22467614 -	4
chr5	22467593	22467613 -	4
chr17	75373689	75373709 -	4
chr17	69548520	69548540 -	4
chr5	18895038	18895058 +	4
chr4	152615183	152615203 -	4
chr4	152615181	152615201 -	4
chr18	28430774	28430794 -	4
chr18	28430775	28430795 -	4
chr4	177421215	177421235 +	4
chr18	31525111	31525131 -	4
chr5	68439824	68439844 +	4
chr5	68439825	68439845 +	4
chr5	61963193	61963213 +	4
chr16	83211531	83211551 -	4
chr16	79803958	79803978 +	4
chr17	57074271	57074291 -	4
chr5	60248232	60248252 +	4
chr17	36902192	36902212 +	4
chr5	60248231	60248251 +	4
chr5	52804453	52804473 -	4
chr5	50995266	50995286 +	4
chr17	40903405	40903425 -	4
chr2	20740862	20740882 +	4
chr2	29631974	29631994 +	4
chr2	32441474	32441494 +	4
chr4	52387668	52387688 -	4
chr4	55512181	55512201 +	4
chr2	2481310	2481330 +	4
chr2	17253817	17253837 +	4
chr2	17253818	17253838 +	4
chr2	56536796	56536816 +	4

chr2	60501178	60501198 -	4
chr4	29910259	29910279 -	4
chr4	132860817	132860837 +	4
chr4	134194879	134194899 +	4
chr4	114631547	114631567 -	4
chr4	110104539	110104559 -	4
chr4	139286213	139286233 -	4
chr19	8931271	8931291 -	4
chr4	100592880	100592900 +	4
chr1	82125964	82125984 -	4
chrX	130326345	130326365 +	4
chr1	76029157	76029177 +	4
chrX	57779681	57779701 +	4
chr8	138342034	138342054 -	4
chr9	81873580	81873600 -	4
chr10	120268008	120268028 -	4
chr10	128590280	128590300 -	4
chr10	128590278	128590298 -	4
chr10	24666535	24666555 -	4
chr10	24703798	24703818 -	4
chr9	87991771	87991791 +	4
chrX	123597111	123597131 -	4
chr1	177526053	177526073 -	4
chrX	123674133	123674153 +	4
chr8	108320075	108320095 +	4
chr1	62684608	62684628 -	4
chr11	23310298	23310318 +	4
chr10	9020383	9020403 +	4
chr9	114267834	114267854 -	4
chr9	114797492	114797512 +	4
chrX	148582616	148582636 -	4
chr9	99298733	99298753 -	4
chr1	71350533	71350553 +	4
chr8	120167873	120167893 +	4
chr8	120246690	120246710 +	4
chr1	66457963	66457983 -	4
chr8	116592308	116592328 -	4
chr9	28119334	28119354 +	4
chrX	80943387	80943407 -	4
chrX	95149144	95149164 -	4
chr10	90319237	90319257 +	4
chr10	90319236	90319256 +	4
chr1	160241903	160241923 +	4
chr9	33153494	33153514 +	4
chrX	113748671	113748691 +	4
chr1	98413154	98413174 -	4
chr9	2523599	2523619 +	4
chrX	115635016	115635036 +	4
chr9	2523598	2523618 +	4
chr10	37410194	37410214 +	4
chr1	172947996	172948016 -	4

chrX	114677986	114678006 -	4
chrX	74492645	74492665 -	4
chr10	91131347	91131367 -	4
chr9	69177148	69177168 +	4
chr10	93209345	93209365 -	4
chr9	69177147	69177167 +	4
chr10	92572028	92572048 -	4
chr9	69177146	69177166 +	4
chr9	72624454	72624474 -	4
chr10	104896542	104896562 +	4
chr9	72624453	72624473 -	4
chr10	98353386	98353406 +	4
chrX	107069755	107069775 -	4
chr8	102639794	102639814 +	4
chrX	27219155	27219175 -	4
chr8	78730971	78730991 +	4
chr1	236847560	236847580 -	4
chr8	91421676	91421696 -	4
chr11	43490059	43490079 +	4
chr1	243753146	243753166 +	4
chr11	43490058	43490078 +	4
chr8	91421677	91421697 -	4
chr11	41394964	41394984 -	4
chr8	88680925	88680945 +	4
chrX	12101643	12101663 +	4
chr11	78821996	78822016 +	4
chr11	72838746	72838766 +	4
chr1	23039517	23039537 -	4
chrX	5844970	5844990 -	4
chrX	24825426	24825446 +	4
chr9	120932386	120932406 +	4
chr1	196397897	196397917 -	4
chr11	39258878	39258898 -	4
chrX	36202170	36202190 -	4
chrX	152076512	152076532 +	4
chr1	196214331	196214351 +	4
chr3	89827447	89827467 -	5
chr18	70412136	70412156 +	5
chr3	78011504	78011524 -	5
chr6	2119483	2119503 +	5
chr12	68041554	68041574 -	5
chr12	67830047	67830067 +	5
chr13	114201085	114201105 -	5
chrX	144929049	144929069 -	5
chr12	110078815	110078835 -	5
chr3	118129049	118129069 -	5
chr4	121053742	121053762 +	5
chr12	115168659	115168679 -	5
chr12	115490824	115490844 +	5
chr11	70308954	70308974 -	5
chr12	118745954	118745974 +	5

chr7	3831648	3831668 +	5
chr4	106183141	106183161 -	5
chr17	14085172	14085192 +	5
chr4	166326953	166326973 -	5
chr5	70752707	70752727 -	5
chr15	48919789	48919809 -	5
chr9	8207007	8207027 +	5
chr5	71257673	71257693 +	5
chr16	53997843	53997863 +	5
chr5	69677628	69677648 +	5
chr5	70553701	70553721 +	5
chr5	70257365	70257385 +	5
chr5	69876794	69876814 -	5
chr4	180825592	180825612 +	5
chr6	103373279	103373299 +	5
chr3	175061281	175061301 +	5
chrX	118646772	118646792 -	5
chr1	174303543	174303563 +	5
chr5	34836664	34836684 -	5
chr5	34216779	34216799 +	5
chr20	13784104	13784124 +	5
chr6	87582590	87582610 +	5
chrX	71920753	71920773 +	5
chrX	71920751	71920771 +	5
chr14	48064231	48064251 +	5
chrX	71178318	71178338 +	5
chr14	52567609	52567629 -	5
chr9	93831004	93831024 -	5
chr9	93831005	93831025 -	5
chr5	146893239	146893259 +	5
chr11	57726487	57726507 +	5
chr17	54628882	54628902 -	5
chr2	107701677	107701697 +	5
chr3	11125026	11125046 -	5
chr5	163195912	163195932 -	5
chr3	60110407	60110427 +	5
chr15	71407301	71407321 -	5
chrX	148722534	148722554 -	5
chr19	19076134	19076154 -	5
chr11	7130575	7130595 +	5
chr3	52168764	52168784 +	5
chr12	42377204	42377224 +	5
chr7	16000178	16000198 -	5
chrX	63259178	63259198 -	5
chr8	138201079	138201099 +	5
chr7	131268494	131268514 +	5
chr5	170905220	170905240 +	5
chr3	35706024	35706044 +	5
chr18	52395593	52395613 +	5
chr2	51330510	51330530 -	5
chr10	97973144	97973164 -	5

chrX	94310316	94310336 +	5
chr6	140273717	140273737 -	5
chr9	126627335	126627355 +	5
chr8	59708538	59708558 -	5
chr7	88409472	88409492 -	5
chr6	140273716	140273736 -	5
chr3	89827449	89827469 -	5
chr5	92742888	92742908 +	5
chr7	95815040	95815060 -	5
chr9	72455478	72455498 +	5
chr15	40584677	40584697 -	5
chr18_KI270911v1_alt	83972	83992 -	1
chr18_KI270911v1_alt	86146	86166 -	1
chr18_KI270911v1_alt	85987	86007 -	1
chr18_KI270911v1_alt	85934	85954 -	1
chr18_KI270911v1_alt	85881	85901 -	1
chr19_GL383573v1_alt	222889	222909 -	1
chr19_GL949746v1_alt	343428	343448 +	1
chr19_GL949752v1_alt	341592	341612 +	1
chr18_KI270911v1_alt	85828	85848 -	1
chr18_KI270911v1_alt	85775	85795 -	1
chr18_KI270911v1_alt	85722	85742 -	1
chr18_KI270911v1_alt	84820	84840 -	1
chr18_KI270911v1_alt	84078	84098 -	1
chr18_KI270911v1_alt	84131	84151 -	1
chr18_KI270911v1_alt	84184	84204 -	1
chr18_KI270911v1_alt	84237	84257 -	1
chr18_KI270911v1_alt	84290	84310 -	1
chr18_KI270911v1_alt	84343	84363 -	1
chr18_KI270911v1_alt	84396	84416 -	1
chr18_KI270911v1_alt	84449	84469 -	1
chr18_KI270911v1_alt	84502	84522 -	1
chr18_KI270911v1_alt	84555	84575 -	1
chr18_KI270911v1_alt	84608	84628 -	1
chr18_KI270911v1_alt	84661	84681 -	1
chr18_KI270911v1_alt	84714	84734 -	1
chr18_KI270911v1_alt	84767	84787 -	1
chr18_KI270911v1_alt	84873	84893 -	1
chr18_KI270911v1_alt	85669	85689 -	1
chr18_KI270911v1_alt	84926	84946 -	1
chr18_KI270911v1_alt	84979	84999 -	1
chr18_KI270911v1_alt	85032	85052 -	1
chr18_KI270911v1_alt	85085	85105 -	1
chr18_KI270911v1_alt	85138	85158 -	1
chr18_KI270911v1_alt	85192	85212 -	1
chr18_KI270911v1_alt	85245	85265 -	1
chr18_KI270911v1_alt	85298	85318 -	1
chr18_KI270911v1_alt	85351	85371 -	1
chr18_KI270911v1_alt	85404	85424 -	1
chr18_KI270911v1_alt	85457	85477 -	1
chr18_KI270911v1_alt	85510	85530 -	1

chr18_KI270911v1_alt	85563	85583 -	1
chr18_KI270911v1_alt	85616	85636 -	1
chr2	198489820	198489840 -	1
chr20_GL383577v2_alt	121879	121899 +	1
chr19_KI270867v1_alt	2428	2448 -	1
chr19_KI270938v1_alt	419198	419218 +	1
chr1_KI270708v1_random	11298	11318 +	1
chr1_KI270708v1_random	97082	97102 -	1
chr1_KI270759v1_alt	223580	223600 -	1
chr18_KI270911v1_alt	84025	84045 -	1
chr18_KI270911v1_alt	83919	83939 -	1
chr18_GL383572v1_alt	85418	85438 -	1
chr18_KI270911v1_alt	83866	83886 -	1
chr18_GL383572v1_alt	87708	87728 -	1
chr18_GL383572v1_alt	87549	87569 -	1
chr18_KI270864v1_alt	63176	63196 +	1
chr18_KI270911v1_alt	79452	79472 -	1
chr18_KI270911v1_alt	79505	79525 -	1
chr18_KI270911v1_alt	79558	79578 -	1
chr18_KI270911v1_alt	79611	79631 -	1
chr18_KI270911v1_alt	79664	79684 -	1
chr18_KI270911v1_alt	79717	79737 -	1
chr18_KI270911v1_alt	79770	79790 -	1
chr18_KI270911v1_alt	79823	79843 -	1
chr18_KI270911v1_alt	79876	79896 -	1
chr18_KI270911v1_alt	79929	79949 -	1
chr18_KI270911v1_alt	79982	80002 -	1
chr18_KI270911v1_alt	80035	80055 -	1
chr18_KI270911v1_alt	80088	80108 -	1
chr18_KI270911v1_alt	80141	80161 -	1
chr18_KI270911v1_alt	80194	80214 -	1
chr18_GL383572v1_alt	87335	87355 -	1
chr18_GL383572v1_alt	87228	87248 -	1
chr18_GL383572v1_alt	87175	87195 -	1
chr18_GL383572v1_alt	85524	85544 -	1
chr18_GL383572v1_alt	85577	85597 -	1
chr18_GL383572v1_alt	85630	85650 -	1
chr18_GL383572v1_alt	85683	85703 -	1
chr18_GL383572v1_alt	85736	85756 -	1
chr18_GL383572v1_alt	85790	85810 -	1
chr18_GL383572v1_alt	85845	85865 -	1
chr18_GL383572v1_alt	85899	85919 -	1
chr18_GL383572v1_alt	85952	85972 -	1
chr18_GL383572v1_alt	86058	86078 -	1
chr18_GL383572v1_alt	86326	86346 -	1
chr18_GL383572v1_alt	87122	87142 -	1
chr18_GL383572v1_alt	86379	86399 -	1
chr18_GL383572v1_alt	86432	86452 -	1
chr18_GL383572v1_alt	86485	86505 -	1
chr18_GL383572v1_alt	86591	86611 -	1
chr18_GL383572v1_alt	86644	86664 -	1

chr18_GL383572v1_alt	86751	86771 -	1
chr18_GL383572v1_alt	86804	86824 -	1
chr18_GL383572v1_alt	86857	86877 -	1
chr18_GL383572v1_alt	86910	86930 -	1
chr18_GL383572v1_alt	86963	86983 -	1
chr18_GL383572v1_alt	87016	87036 -	1
chr18_KI270911v1_alt	80247	80267 -	1
chr18_KI270911v1_alt	80300	80320 -	1
chr18_KI270911v1_alt	80356	80376 -	1
chr18_KI270911v1_alt	83018	83038 -	1
chr18_KI270911v1_alt	82273	82293 -	1
chr18_KI270911v1_alt	82326	82346 -	1
chr18_KI270911v1_alt	82379	82399 -	1
chr18_KI270911v1_alt	82432	82452 -	1
chr18_KI270911v1_alt	82485	82505 -	1
chr18_KI270911v1_alt	82538	82558 -	1
chr18_KI270911v1_alt	82591	82611 -	1
chr18_KI270911v1_alt	82644	82664 -	1
chr18_KI270911v1_alt	82697	82717 -	1
chr18_KI270911v1_alt	82750	82770 -	1
chr18_KI270911v1_alt	82803	82823 -	1
chr18_KI270911v1_alt	82859	82879 -	1
chr18_KI270911v1_alt	82912	82932 -	1
chr18_KI270911v1_alt	82965	82985 -	1
chr18_KI270911v1_alt	83071	83091 -	1
chr18_KI270911v1_alt	82167	82187 -	1
chr18_KI270911v1_alt	83124	83144 -	1
chr18_KI270911v1_alt	83177	83197 -	1
chr18_KI270911v1_alt	83230	83250 -	1
chr18_KI270911v1_alt	83283	83303 -	1
chr18_KI270911v1_alt	83336	83356 -	1
chr18_KI270911v1_alt	83389	83409 -	1
chr18_KI270911v1_alt	83442	83462 -	1
chr18_KI270911v1_alt	83495	83515 -	1
chr18_KI270911v1_alt	83548	83568 -	1
chr18_KI270911v1_alt	83601	83621 -	1
chr18_KI270911v1_alt	83654	83674 -	1
chr18_KI270911v1_alt	83707	83727 -	1
chr18_KI270911v1_alt	83760	83780 -	1
chr18_KI270911v1_alt	83813	83833 -	1
chr18_KI270911v1_alt	82220	82240 -	1
chr18_KI270911v1_alt	82114	82134 -	1
chr18_KI270911v1_alt	80409	80429 -	1
chr18_KI270911v1_alt	81204	81224 -	1
chr18_KI270911v1_alt	80462	80482 -	1
chr18_KI270911v1_alt	80515	80535 -	1
chr18_KI270911v1_alt	80568	80588 -	1
chr18_KI270911v1_alt	80621	80641 -	1
chr18_KI270911v1_alt	80674	80694 -	1
chr18_KI270911v1_alt	80727	80747 -	1
chr18_KI270911v1_alt	80780	80800 -	1

chr18_KI270911v1_alt	80833	80853 -	1
chr18_KI270911v1_alt	80886	80906 -	1
chr18_KI270911v1_alt	80939	80959 -	1
chr18_KI270911v1_alt	80992	81012 -	1
chr18_KI270911v1_alt	81045	81065 -	1
chr18_KI270911v1_alt	81098	81118 -	1
chr18_KI270911v1_alt	81151	81171 -	1
chr18_KI270911v1_alt	81257	81277 -	1
chr18_KI270911v1_alt	82061	82081 -	1
chr18_KI270911v1_alt	81313	81333 -	1
chr18_KI270911v1_alt	81366	81386 -	1
chr18_KI270911v1_alt	81419	81439 -	1
chr18_KI270911v1_alt	81475	81495 -	1
chr18_KI270911v1_alt	81528	81548 -	1
chr18_KI270911v1_alt	81581	81601 -	1
chr18_KI270911v1_alt	81637	81657 -	1
chr18_KI270911v1_alt	81690	81710 -	1
chr18_KI270911v1_alt	81743	81763 -	1
chr18_KI270911v1_alt	81796	81816 -	1
chr18_KI270911v1_alt	81849	81869 -	1
chr18_KI270911v1_alt	81902	81922 -	1
chr18_KI270911v1_alt	81955	81975 -	1
chr18_KI270911v1_alt	82008	82028 -	1
chr4_KI270925v1_alt	465260	465280 +	1
chr4_KI270786v1_alt	150084	150104 +	1
chr4_GL383528v1_alt	276036	276056 +	1
chr4_KI270785v1_alt	82398	82418 +	1
chr4_KI270896v1_alt	150087	150107 +	1
chr5_GL949742v1_alt	125881	125901 -	1
chr6_GL000250v2_alt	1165696	1165716 -	1
chr6_GL000250v2_alt	1649152	1649172 +	1
chr6_GL000250v2_alt	3700840	3700860 -	1
chr6_GL000250v2_alt	4359117	4359137 +	1
chr6_GL000251v2_alt	151720	151740 +	1
chr5_KI270791v1_alt	6422	6442 +	1
chr5_KI270796v1_alt	62581	62601 -	1
chr5_KI270796v1_alt	166714	166734 -	1
chr2_KI270775v1_alt	44860	44880 +	1
chr2_KI270773v1_alt	41936	41956 +	1
chr2_KI270774v1_alt	199510	199530 -	1
chr2_KI270775v1_alt	83613	83633 -	1
chr3_GL000221v1_random	105251	105271 -	1
chr3_GL383526v1_alt	70421	70441 +	1
chr22_KI270875v1_alt	48832	48852 -	1
chr22_KI270736v1_random	15872	15892 +	1
chr22_KI270875v1_alt	19287	19307 +	1
chr22_KI270876v1_alt	207359	207379 +	1
chr22_KI270879v1_alt	274679	274699 -	1
chr3_JH636055v2_alt	111085	111105 -	1
chr4_GL000257v2_alt	497016	497036 +	1
chr3_KI270935v1_alt	125188	125208 +	1

chr3_KI270936v1_alt	40003	40023 -	1
chr3_KI270937v1_alt	40003	40023 -	1
chr4_GL000257v2_alt	286165	286185 +	1
chr3_KI270934v1_alt	40003	40023 -	1
chr3_KI270777v1_alt	42216	42236 -	1
chr3_KI270779v1_alt	125188	125208 +	1
chr3_KI270777v1_alt	104988	105008 +	1
chr3_KI270781v1_alt	108106	108126 +	1
chr3_KI270895v1_alt	40003	40023 -	1
chr3_KI270924v1_alt	41309	41329 -	1
chr18_GL383572v1_alt	85471	85491 -	1
chr18_GL383572v1_alt	85365	85385 -	1
chr15_KI270848v1_alt	181365	181385 -	1
chr15_GL383555v2_alt	68417	68437 -	1
chr15_KI270905v1_alt	4104125	4104145 +	1
chr15_KI270905v1_alt	4373646	4373666 +	1
chr15_KI270905v1_alt	4574482	4574502 +	1
chr15_KI270905v1_alt	4980674	4980694 -	1
chr15_KI270906v1_alt	50714	50734 -	1
chr15_KI270905v1_alt	2103175	2103195 -	1
chr15_KI270905v1_alt	1568481	1568501 -	1
chr15_KI270905v1_alt	2534804	2534824 -	1
chr15_KI270905v1_alt	3234890	3234910 -	1
chr15_KI270905v1_alt	3360979	3360999 +	1
chr15_KI270905v1_alt	3709119	3709139 -	1
chr15_KI270905v1_alt	3741050	3741070 -	1
chr18_GL383572v1_alt	85311	85331 -	1
chr12_GL383552v1_alt	44603	44623 +	1
chr14_KI270846v1_alt	1317122	1317142 +	1
chr12_GL877876v1_alt	124104	124124 -	1
chr12_GL877876v1_alt	376735	376755 +	1
chr10_GL383546v1_alt	64750	64770 +	1
chr11_JH159136v1_alt	83245	83265 +	1
chr14_KI270722v1_random	42290	42310 +	1
chr14_KI270722v1_random	130290	130310 -	1
chr14_KI270725v1_random	100682	100702 -	1
chr14_KI270846v1_alt	1192236	1192256 +	1
chr14_KI270846v1_alt	1238681	1238701 +	1
chr12_KI270837v1_alt	27558	27578 +	1
chr12_KI270904v1_alt	124104	124124 -	1
chr12_KI270904v1_alt	341042	341062 +	1
chr12_KI270904v1_alt	544677	544697 -	1
chr13_KI270843v1_alt	61103	61123 +	1
chr13_KI270843v1_alt	61104	61124 +	1
chr18_GL383572v1_alt	80195	80215 -	1
chr18_GL383572v1_alt	80513	80533 -	1
chr18_GL383572v1_alt	80460	80480 -	1
chr18_GL383572v1_alt	80407	80427 -	1
chr18_GL383572v1_alt	80354	80374 -	1
chr18_GL383572v1_alt	80142	80162 -	1
chr18_GL383572v1_alt	80089	80109 -	1

chr18_GL383572v1_alt	80036	80056 -	1
chr18_GL383572v1_alt	79983	80003 -	1
chr18_GL383572v1_alt	79930	79950 -	1
chr18_GL383572v1_alt	79877	79897 -	1
chr18_GL383572v1_alt	79824	79844 -	1
chr18_GL383572v1_alt	80566	80586 -	1
chr18_GL383572v1_alt	80725	80745 -	1
chr18_GL383572v1_alt	80833	80853 -	1
chr18_GL383572v1_alt	80886	80906 -	1
chr18_GL383572v1_alt	80939	80959 -	1
chr18_GL383572v1_alt	80992	81012 -	1
chr18_GL383572v1_alt	81045	81065 -	1
chr18_GL383572v1_alt	81151	81171 -	1
chr18_GL383572v1_alt	81204	81224 -	1
chr18_GL383572v1_alt	81257	81277 -	1
chr18_GL383572v1_alt	81310	81330 -	1
chr18_GL383572v1_alt	81363	81383 -	1
chr18_GL383572v1_alt	79771	79791 -	1
chr18_GL383572v1_alt	79718	79738 -	1
chr18_GL383572v1_alt	79665	79685 -	1
chr17_KI270908v1_alt	1244146	1244166 -	1
chr17_KI270908v1_alt	1341404	1341424 -	1
chr17_KI270910v1_alt	121967	121987 +	1
chr18_GL383567v1_alt	114949	114969 -	1
chr18_GL383567v1_alt	114950	114970 -	1
chr18_GL383572v1_alt	79612	79632 -	1
chr18_GL383571v1_alt	33290	33310 +	1
chr18_GL383572v1_alt	79453	79473 -	1
chr18_GL383572v1_alt	79506	79526 -	1
chr18_GL383572v1_alt	79559	79579 -	1
chr18_GL383572v1_alt	81469	81489 -	1
chr18_GL383572v1_alt	84400	84420 -	1
chr18_GL383572v1_alt	83657	83677 -	1
chr18_GL383572v1_alt	83870	83890 -	1
chr18_GL383572v1_alt	83923	83943 -	1
chr18_GL383572v1_alt	83976	83996 -	1
chr18_GL383572v1_alt	84029	84049 -	1
chr18_GL383572v1_alt	84082	84102 -	1
chr18_GL383572v1_alt	84135	84155 -	1
chr18_GL383572v1_alt	84188	84208 -	1
chr18_GL383572v1_alt	84241	84261 -	1
chr18_GL383572v1_alt	84294	84314 -	1
chr18_GL383572v1_alt	84347	84367 -	1
chr18_GL383572v1_alt	84454	84474 -	1
chr18_GL383572v1_alt	83550	83570 -	1
chr18_GL383572v1_alt	84564	84584 -	1
chr18_GL383572v1_alt	84674	84694 -	1
chr18_GL383572v1_alt	84727	84747 -	1
chr18_GL383572v1_alt	84780	84800 -	1
chr18_GL383572v1_alt	84887	84907 -	1
chr18_GL383572v1_alt	84940	84960 -	1

chr18_GL383572v1_alt	84993	85013 -	1
chr18_GL383572v1_alt	85046	85066 -	1
chr18_GL383572v1_alt	85099	85119 -	1
chr18_GL383572v1_alt	85152	85172 -	1
chr18_GL383572v1_alt	85205	85225 -	1
chr18_GL383572v1_alt	85258	85278 -	1
chr18_GL383572v1_alt	83603	83623 -	1
chr18_GL383572v1_alt	83497	83517 -	1
chr18_GL383572v1_alt	82427	82447 -	1
chr18_GL383572v1_alt	81684	81704 -	1
chr18_GL383572v1_alt	81737	81757 -	1
chr18_GL383572v1_alt	81790	81810 -	1
chr18_GL383572v1_alt	81843	81863 -	1
chr18_GL383572v1_alt	81896	81916 -	1
chr18_GL383572v1_alt	81949	81969 -	1
chr18_GL383572v1_alt	82002	82022 -	1
chr18_GL383572v1_alt	82055	82075 -	1
chr18_GL383572v1_alt	82161	82181 -	1
chr18_GL383572v1_alt	82214	82234 -	1
chr18_GL383572v1_alt	82267	82287 -	1
chr18_GL383572v1_alt	82320	82340 -	1
chr18_GL383572v1_alt	83444	83464 -	1
chr18_GL383572v1_alt	82588	82608 -	1
chr18_GL383572v1_alt	82641	82661 -	1
chr18_GL383572v1_alt	82695	82715 -	1
chr18_GL383572v1_alt	82964	82984 -	1
chr18_GL383572v1_alt	83017	83037 -	1
chr18_GL383572v1_alt	83070	83090 -	1
chr18_GL383572v1_alt	83391	83411 -	1
chr16_KI270853v1_alt	1802203	1802223 +	1
chr16_KI270853v1_alt	1905952	1905972 +	1
chr16_KI270853v1_alt	2377483	2377503 -	1
chr17_GL000258v2_alt	641647	641667 -	1
chr17_GL000258v2_alt	1424085	1424105 -	1
chr17_GL000258v2_alt	1710608	1710628 -	1
chr16_KI270853v1_alt	160725	160745 -	1
chr16_KI270853v1_alt	160764	160784 -	1
chr16_KI270853v1_alt	937339	937359 -	1
chr16_KI270853v1_alt	1098553	1098573 +	1
chr16_KI270853v1_alt	1103874	1103894 +	1
chr17_GL000258v2_alt	1807691	1807711 -	1
chr17_KI270908v1_alt	847088	847108 +	1
chr17_KI270857v1_alt	2305206	2305226 +	1
chr17_KI270862v1_alt	125497	125517 +	1
chr17_GL383564v2_alt	75830	75850 -	1
chr17_GL383564v2_alt	81915	81935 -	1
chr17_JH159147v1_alt	37924	37944 +	1
chr17_JH159148v1_alt	48196	48216 +	1
chr6_GL000254v2_alt	4353503	4353523 +	1
chr6_GL000254v2_alt	3710353	3710373 -	1
chr6_GL000255v2_alt	1162826	1162846 -	1

chr6_GL000255v2_alt	1574738	1574758 +	1
chr6_GL000254v2_alt	1162818	1162838 -	1
chr6_GL000254v2_alt	2594281	2594301 +	1
chr6_GL000256v2_alt	1205714	1205734 -	1
chr6_GL000256v2_alt	1618119	1618139 +	1
chr6_GL000256v2_alt	3684523	3684543 -	1
chr6_GL000256v2_alt	4503459	4503479 +	1
chr6_GL000255v2_alt	3591643	3591663 -	1
chr6_GL000255v2_alt	4248728	4248748 +	1
chr6_GL000253v2_alt	3673587	3673607 -	1
chr6_GL000251v2_alt	3806738	3806758 -	1
chr6_GL000251v2_alt	4466553	4466573 +	1
chr6_GL000252v2_alt	1163181	1163201 -	1
chr6_GL000251v2_alt	1387370	1387390 -	1
chr6_GL000251v2_alt	2732472	2732492 +	1
chr6_GL000251v2_alt	1799340	1799360 +	1
chr6_GL000253v2_alt	1162321	1162341 -	1
chr6_GL000253v2_alt	1629890	1629910 +	1
chr6_GL000253v2_alt	2560604	2560624 +	1
chr6_GL000252v2_alt	1575502	1575522 +	1
chr6_GL000252v2_alt	2509346	2509366 +	1
chr6_GL000252v2_alt	3609718	3609738 -	1
chr6_GL000252v2_alt	4297972	4297992 +	1
chrUn_KI270751v1	99031	99051 -	1
chr6_GL383533v1_alt	7004	7024 -	1
chr9_KI270823v1_alt	216309	216329 +	1
chrUn_GL000214v1	5002	5022 +	1
chrUn_KI270742v1	135276	135296 -	1
chr6_GL383533v1_alt	54350	54370 -	1
chr6_KI270798v1_alt	74073	74093 +	1
chr9_GL383540v1_alt	5232	5252 +	1
chr9_GL383540v1_alt	26242	26262 +	1
chr9_GL383541v1_alt	12424	12444 +	1
chr9_KI270719v1_random	17009	17029 -	1
chr8_KI270810v1_alt	303063	303083 -	1
chr8_KI270821v1_alt	489988	490008 +	1
chr2	226039369	226039389 -	1
chr11	26551524	26551544 +	1
chr2	184425872	184425893 -	1
chr17	63767227	63767253 -	1
chr18	59779878	59779897 +	1
chr19	5763653	5763673 +	1
chr2	9587960	9587981 -	1
chr4	154959957	154959979 +	1
chr5	50514458	50514479 -	1
chr5	29206251	29206275 +	1
chr5	39373864	39373885 -	1
chr4	188764981	188765002 -	1
chr4	186790631	186790653 -	1
chr4	188262974	188262996 -	1
chr5	5398881	5398902 -	1

chr4	180341240	180341263 -	1
chr4	176084828	176084849 -	1
chr4	184620618	184620641 +	1
chr4	162338876	162338897 -	1
chr5	14657981	14658005 +	1
chr5	156288777	156288798 +	1
chr5	155554074	155554094 -	1
chr5	124462378	124462398 -	1
chr5	125938137	125938159 -	1
chr5	138363494	138363515 +	1
chr5	160825925	160825946 -	1
chr5	165866512	165866532 +	1
chr5	92767119	92767138 -	1
chr5	68956116	68956141 +	1
chr5	72671712	72671733 -	1
chr5	94750371	94750392 -	1
chr6	48883803	48883825 +	1
chr3	108976775	108976797 +	1
chr3	81370528	81370549 +	1
chr3	151353831	151353852 -	1
chr3	126957635	126957655 -	1
chr3	118651891	118651912 +	1
chr3	118755098	118755119 -	1
chr3	18651228	18651248 -	1
chr22	46810760	46810781 -	1
chr3	63229965	63229989 -	1
chr3	63686878	63686898 +	1
chr3	73547858	73547880 +	1
chr4	85971132	85971151 -	1
chr4	96959301	96959325 +	1
chr4	89668008	89668029 +	1
chr4	65619462	65619483 -	1
chr4	75765481	75765500 +	1
chr4	135118004	135118026 +	1
chr3	191506157	191506183 -	1
chr3	183410709	183410729 +	1
chr3	175679425	175679445 +	1
chr4	55897956	55897976 +	1
chr4	14251575	14251597 -	1
chr4	28865539	28865559 -	1
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chr9	67475475	67475495 +	1
chr9	62112891	62112911 -	1
chr9	29705276	29705300 -	1
chr9	23693999	23694019 -	1
chr9	115883742	115883763 +	1
chr9	108612613	108612634 +	1
chr9	82902070	82902093 +	1
chr8	98686085	98686105 +	1
chr8	85327784	85327807 +	1
chr9	9658925	9658945 +	1

chr9	3262226	3262247 -	1
chr8	115565720	115565739 +	1
chrX	111830703	111830725 +	1
chrX	135348058	135348081 -	1
chrX	103331330	103331351 +	1
chrY	8083660	8083683 -	1
chrX	142159579	142159599 +	1
chrX	148272499	148272519 +	1
chrX	147356168	147356190 +	1
chrX	20213802	20213821 +	1
chrX	18316063	18316086 +	1
chr9	137129026	137129046 -	1
chr9	132037481	132037501 +	1
chr9	122254123	122254145 -	1
chrX	50473789	50473810 +	1
chr6	166014815	166014836 -	1
chr6	152322665	152322686 -	1
chr6	158133955	158133977 +	1
chr7	55092955	55092975 +	1
chr7	24137045	24137067 +	1
chr6	98587213	98587234 +	1
chr6	94055083	94055103 -	1
chr6	66817230	66817251 -	1
chr6	76596978	76596999 +	1
chr6	130964527	130964552 +	1
chr6	141261879	141261900 +	1
chr6	117276234	117276256 -	1
chr6	114866261	114866283 +	1
chr6	114730656	114730678 +	1
chr7	153599892	153599914 +	1
chr7	146862157	146862179 -	1
chr8	55406127	55406147 +	1
chr8	55234641	55234662 +	1
chr8	29437105	29437126 -	1
chr7	80801900	80801922 -	1
chr7	77314780	77314800 +	1
chr7	78065726	78065747 -	1
chr7	115048837	115048858 +	1
chr7	118486729	118486752 -	1
chr7	90200501	90200521 +	1
chr12	15801835	15801855 +	1
chr11	113426785	113426805 +	1
chr11	128448245	128448266 +	1
chr11	128574735	128574756 -	1
chr12	68024334	68024355 -	1
chr12	64279582	64279605 -	1
chr12	67061942	67061965 +	1
chr12	45725150	45725173 -	1
chr12	39441619	39441641 +	1
chr11	45287738	45287760 +	1
chr11	43984257	43984279 -	1

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chr11	106475014	106475035 -	1
chr11	85360524	85360546 -	1
chr11	84465514	84465536 -	1
chr13	88710237	88710258 -	1
chr13	66809552	66809575 -	1
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chr13	101648788	101648808 +	1
chr13	99962738	99962759 -	1
chr13	94093727	94093747 +	1
chr12	96222168	96222190 -	1
chr12	89783040	89783066 +	1
chr12	84476315	84476337 +	1
chr13	32546702	32546722 +	1
chr12	126795130	126795151 -	1
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chr1	186114202	186114224 -	1
chr1	201117104	201117126 +	1
chr1	167023986	167024009 -	1
chr1	158774890	158774913 -	1
chr1	160149413	160149434 +	1
chr1	174924450	174924471 -	1
chr1	170776538	170776561 +	1
chr1	42280015	42280035 +	1
chr1	31882567	31882588 +	1
chr1	33011231	33011252 +	1
chr1	2573877	2573902 +	1
chr1	4484762	4484782 +	1
chr1	71690772	71690792 -	1
chr1	84576807	84576828 -	1
chr1	45742091	45742112 +	1
chr1	64206949	64206970 +	1
chr1	60141405	60141428 -	1
chr10	58314641	58314663 +	1
chr10	64775278	64775299 +	1
chr10	106169334	106169355 -	1
chr10	113157517	113157537 -	1
chr1	227860420	227860443 -	1
chr1	222370162	222370181 -	1
chr1	221940456	221940477 -	1
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chr10	51077903	51077923 -	1
chr10	18022513	18022533 -	1
chr2	109286021	109286044 -	1
chr2	83794735	83794756 +	1
chr2	84239807	84239829 -	1
chr2	148037343	148037365 -	1
chr2	149266893	149266916 -	1
chr2	162440852	162440873 +	1
chr2	158196947	158196972 -	1
chr2	158900321	158900345 -	1

chr2	141823331	141823356 +	1
chr2	141704165	141704187 -	1
chr2	6510664	6510685 -	1
chr2	22851399	22851420 +	1
chr2	225392	225414 +	1
chr2	50902258	50902280 -	1
chr2	45784706	45784727 +	1
chr2	43716103	43716124 -	1
chr2	44459930	44459951 +	1
chr2	38851103	38851123 -	1
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chr20	32276676	32276697 +	1
chr22	10751287	10751312 +	1
chr21	20189457	20189481 -	1
chr21	16139004	16139024 +	1
chr21	31451477	31451498 +	1
chr21	25598014	25598033 -	1
chr2	197363127	197363148 +	1
chr2	188771168	188771192 +	1
chr2	176657657	176657677 +	1
chr20	3244761	3244784 +	1
chr2	238220660	238220681 -	1
chr20	10516420	10516440 +	1
chr20	9377390	9377410 -	1
chr2	232308408	232308429 -	1
chr2	225455941	225455960 -	1
chr15	76573734	76573758 +	1
chr15	83355419	83355441 +	1
chr16	27155560	27155581 +	1
chr16	22388625	22388644 -	1
chr16	8605389	8605409 +	1
chr14	42430102	42430122 +	1
chr15	35579705	35579727 +	1
chr18	35753207	35753231 +	1
chr18	36993198	36993219 +	1
chr18	39035654	39035676 -	1
chr18	34324772	34324793 -	1
chr18	8222216	8222236 +	1
chr18	24661536	24661558 +	1
chr18	24755010	24755032 -	1
chr18	57910594	57910619 +	1
chr17	8335093	8335113 +	1
chr16	58517056	58517075 -	1
chr16	71719078	71719098 -	1
chr16	72499136	72499158 +	1
chr17	65944424	65944447 -	1
chr17	57033277	57033299 +	1
chr17	78047465	78047486 -	1
chr17	72721499	72721519 +	1
chr17	35733984	35734004 -	1
chr17	39980193	39980214 +	1

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chr15	65156508	65156528 -	2
chr5	148533967	148533987 +	2
chr15	48615475	48615495 -	2
chr15	37787028	37787048 -	2
chr15	57452114	57452134 -	2
chr5	145131215	145131235 +	2
chr5	121731717	121731737 -	2
chr16	54473766	54473786 +	2
chr16	61354147	61354167 -	2
chr16	60453439	60453459 +	2
chr5	109771393	109771413 -	2
chr16	52749138	52749158 -	2
chr15	97927130	97927150 -	2
chr16	9664796	9664816 -	2
chr5	133752981	133753001 +	2
chrX	136806829	136806849 +	2
chrX	136806828	136806848 +	2
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chr14	80463060	80463080 -	2
chr14	80255899	80255919 +	2
chr1	59604022	59604042 -	2
chr1	57445447	57445467 -	2
chr6	65913901	65913921 +	2
chr1	88953577	88953597 -	2
chr6	83732470	83732490 -	2
chr6	82530593	82530613 +	2
chrX	132142844	132142864 +	2
chr1	75552743	75552763 -	2
chr1	75552741	75552761 -	2
chr6	21137047	21137067 -	2
chr6	18929897	18929917 -	2
chr15	25433715	25433735 -	2
chr15	27713651	27713671 -	2
chr6	22849696	22849716 +	2
chr6	24831780	24831800 -	2
chr1	24836275	24836295 -	2
chr14	85076069	85076089 -	2
chr6	47027420	47027440 -	2
chr6	62100104	62100124 +	2
chrY	8333333	8333353 +	2
chr1	8751861	8751881 +	2
chr6	53503438	53503458 -	2
chr18	55579906	55579926 +	2
chr4	150062422	150062442 -	2
chr4	150214338	150214358 +	2
chr4	159728688	159728708 +	2
chr18	46127834	46127854 -	2
chr18	9190119	9190139 +	2
chr18	60036695	60036715 -	2

chr4	115896880	115896900 +	2
chr4	114869069	114869089 -	2
chr4	139976512	139976532 -	2
chr4	138416815	138416835 -	2
chr4	125844524	125844544 +	2
chr17	8372219	8372239 +	2
chr17	7025287	7025307 -	2
chr17	14645713	14645733 -	2
chr17	14645712	14645732 -	2
chr17	14266118	14266138 -	2
chr16	74600215	74600235 -	2
chr16	65137908	65137928 +	2
chr5	19098910	19098930 +	2
chr17	72230561	72230581 -	2
chr17	41364389	41364409 +	2
chr17	70297367	70297387 +	2
chr17	70297366	70297386 +	2
chr11	37623271	37623291 +	2
chr11	39655603	39655623 +	2
chr11	21134183	21134203 +	2
chr13	23828797	23828817 +	2
chr7	45629283	45629303 -	2
chr8	90345583	90345603 +	2
chr8	77962803	77962823 +	2
chr8	73874523	73874543 -	2
chr11	73567660	73567680 +	2
chr8	88206585	88206605 +	2
chr8	88206584	88206604 +	2
chr12	119098827	119098847 -	2
chr11	57749426	57749446 -	2
chr13	57729048	57729068 +	2
chr10	128348388	128348408 -	2
chr13	59266985	59267005 -	2
chr9	4907667	4907687 -	2
chr10	110198787	110198807 -	2
chr13	61770675	61770695 -	2
chr11	14878959	14878979 -	2
chr7	37228631	37228651 -	2
chr8	115764623	115764643 +	2
chr13	40212833	40212853 +	2
chr13	40212832	40212852 +	2
chr7	23416620	23416640 +	2
chr7	19800524	19800544 -	2
chr11	7596026	7596046 -	2
chr11	78344599	78344619 -	2
chr12	5548206	5548226 +	2
chr12	68603462	68603482 +	2
chr12	68603463	68603483 +	2
chr7	143505651	143505671 -	2
chr7	143505650	143505670 -	2
chr7	141456006	141456026 -	2

chr7	130886692	130886712 -	2
chr12	25776774	25776794 +	2
chr7	136760731	136760751 +	2
chr7	138370064	138370084 -	2
chr12	30515888	30515908 +	2
chr7	145739298	145739318 +	2
chr12	47299311	47299331 -	2
chr12	45131305	45131325 +	2
chr7	148626338	148626358 +	2
chr8	51257830	51257850 -	2
chr7	80178033	80178053 +	2
chr11	96192500	96192520 +	2
chr8	65447786	65447806 -	2
chr12	106520367	106520387 -	2
chr8	62468112	62468132 +	2
chr8	61649844	61649864 -	2
chr12	82746093	82746113 -	2
chr8	27107709	27107729 +	2
chr11	122264516	122264536 +	2
chr7	100198007	100198027 +	2
chr12	80104342	80104362 -	2
chr7	89139786	89139806 -	2
chr7	90051237	90051257 +	2
chr13	84198856	84198876 +	2
chr1	223671500	223671520 +	2
chr13	92050090	92050110 +	2
chr1	214041561	214041581 +	2
chr13	97030431	97030451 +	2
chr13	97097358	97097378 -	2
chr1	217319842	217319862 -	2
chr1	112171384	112171404 -	2
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chr1	115923429	115923449 -	2
chrX	94392866	94392886 -	2
chrX	94566218	94566238 -	2
chr6	96801171	96801191 -	2
chrX	104694630	104694650 +	2
chrX	55107298	55107318 +	2
chrX	64063889	64063909 -	2
chr14	22975528	22975548 +	2
chr13	84198857	84198877 +	2
chr10	58733353	58733373 +	2
chr9	76282888	76282908 +	2
chr9	38152226	38152246 +	2
chr10	85311890	85311910 -	2
chr10	80735136	80735156 +	2
chr9	27847382	27847402 -	2
chr10	30923894	30923914 +	2
chr13	70400148	70400168 +	2
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chr1	244624982	244625002 -	2

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chr10	29211234	29211254 +	2
chr9	99103199	99103219 -	2
chr10	26641464	26641484 +	2
chr10	4741010	4741030 -	2
chr6	170011884	170011904 +	2
chr3	72476072	72476092 -	2
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chr2	18330617	18330637 +	2
chr4	58257587	58257607 +	2
chr2	213869654	213869674 +	2
chr2	22231767	22231787 -	2
chr3	82667375	82667395 -	2
chr2	50032151	50032171 +	2
chr4	41999387	41999407 +	2
chr4	35297480	35297500 +	2
chr20	148792	148812 -	2
chr20	18997131	18997151 +	2
chr3	24178315	24178335 +	2
chr4	79944014	79944034 -	2
chr3	30587319	30587339 -	2
chr3	30744309	30744329 +	2
chr4	71605203	71605223 -	2
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chr3	146551580	146551600 -	2
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chr2	84295203	84295223 -	2
chr3	137517085	137517105 +	2
chr2	78041060	78041080 -	2
chr3	173144870	173144890 -	2
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chr2	98126711	98126731 -	2
chr2	180046655	180046675 -	2
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chr2	63910016	63910036 -	2
chr2	52469272	52469292 +	2
chr2	56487911	56487931 +	2
chr2	76832207	76832227 +	2
chr3	130728043	130728063 +	2
chr2	74558470	74558490 +	2
chr2	70326491	70326511 +	2
chr20	48784343	48784363 +	2
chr4	85908632	85908652 +	2
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chr4	85317451	85317471 -	2
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chr21	40904053	40904073 -	2

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chr21	19213932	19213952 +	2
chr3	5040131	5040151 +	2
chr22	46988248	46988268 -	2
chr3	19870080	19870100 +	2
chr20	13926521	13926541 -	2
chr20	13789046	13789065 -	2
chr15	60802787	60802811 -	2
chr16	60407448	60407470 -	2
chr8	29240962	29240984 +	2
chr7	37661989	37662010 +	2
chr1	91990498	91990519 +	2
chr6	123872721	123872742 -	2
chr13	102062666	102062686 +	2
chr4	139250909	139250931 -	2
chr20	25669144	25669167 -	2
chr1	90538777	90538799 -	2
chr1	103426689	103426715 +	2
chr1	90464681	90464702 -	2
chr3	79989805	79989826 -	2
chrX	78706222	78706245 -	2
chr13	92491933	92491954 -	2
chr5	161529103	161529124 +	2
chr2	163755010	163755036 +	2
chr3	153093949	153093971 +	2
chr1	225421710	225421731 +	2
chr18	77837987	77838007 -	2
chr20	24629058	24629080 +	2
chr3	152778404	152778424 +	2
chr4	144426637	144426658 -	2
chr9	109913517	109913537 +	2
chr20	24833902	24833923 +	2
chr5	96453749	96453771 +	2
chr1	103060601	103060622 -	2
chr5	162207832	162207853 -	2
chr8	30154579	30154599 +	2
chr6	128814476	128814496 +	2
chr20	16186092	16186117 -	2
chr4	142982962	142982984 -	2
chr5	94882565	94882586 +	2
chr6	126280459	126280483 -	2
chr15	67407599	67407620 -	2
chr1	96749013	96749033 +	2
chr8	27165057	27165078 +	2
chr4	137317260	137317282 -	2
chr20	20038306	20038327 +	2
chr6	127961307	127961328 -	2
chr1	97771627	97771652 +	2
chr18	79023325	79023347 +	2

chrX	85783414	85783435 +	2
chr15	64636623	64636648 -	2
chrX	85257439	85257459 -	2
chr15	66057606	66057626 +	2
chr20	17959807	17959827 -	2
chr15	66584195	66584216 +	2
chr1	97111299	97111320 -	2
chr7	36227204	36227224 +	2
chr20	18888080	18888101 +	2
chrX	89653820	89653845 -	2
chrX	81738935	81738956 +	2
chr13	22095400	22095421 -	2
chr13	94485937	94485958 +	2
chr15	62063110	62063134 -	2
chr1	93658350	93658373 +	2
chr1	93572894	93572918 -	2
chr3	77745458	77745479 -	2
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chrX	88818086	88818106 -	2
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chr15	63152859	63152880 +	2
chr15	63474323	63474342 -	2
chr5	164165627	164165650 +	2
chr8	21038618	21038639 -	2
chr7	35350803	35350824 +	2
chr3	155186390	155186410 -	2
chr3	77270125	77270147 -	2
chr3	77268586	77268609 +	2
chr15	68909152	68909172 +	2
chr1	94936525	94936547 -	2
chr15	62603587	62603608 -	2
chr1	95152818	95152840 +	2
chrX	88103906	88103927 -	2
chr1	73760943	73760964 -	2
chrX	109001267	109001288 +	2
chr20	44528464	44528486 +	2
chr16	68973981	68974004 +	2
chr1	73529009	73529032 -	2
chr11	78519378	78519400 +	2
chr1	75130013	75130034 +	2
chrX	108313865	108313886 +	2
chr6	4990123	4990143 +	2
chr5	89092432	89092456 -	2
chr9	97187912	97187932 -	2
chr18	68822744	68822765 -	2
chr15	45684441	45684462 -	2
chr8	15444016	15444038 +	2
chr1	73107280	73107301 +	2
chr6	1197351	1197373 +	2
chr4	131882729	131882750 +	2
chrX	104021891	104021912 +	2

chr3	58253850	58253871 -	2
chr14	19838996	19839018 +	2
chr6	2676172	2676194 +	2
chr11	97157955	97157976 -	2
chr3	55590403	55590424 +	2
chr3	55326211	55326232 -	2
chr16	68285184	68285204 -	2
chrX	106419070	106419091 -	2
chr20	51572762	51572784 +	2
chr11	74738880	74738903 +	2
chr1	68252133	68252155 +	2
chr1	241513612	241513637 -	2
chr7	45409817	45409839 +	2
chr8	14478403	14478424 +	2
chr3	47016495	47016518 +	2
chr11	99094346	99094369 +	2
chr11	98001497	98001519 +	2
chrX	116426035	116426058 +	2
chr16	71446361	71446384 -	2
chr3	45163934	45163955 +	2
chr1	242313224	242313245 -	2
chr1	242298209	242298229 +	2
chr1	242257367	242257388 +	2
chr9	94807616	94807638 -	2
chr6	104550465	104550486 +	2
chr4	149448302	149448323 +	2
chr3	164443843	164443864 -	2
chr7	46004589	46004609 +	2
chr9	94845106	94845127 +	2
chr1	67622087	67622107 -	2
chr6	104448218	104448239 +	2
chr20	50896858	50896882 +	2
chr9	96639508	96639528 +	2
chr14	25174963	25174984 -	2
chr3	163630167	163630188 -	2
chr3	163590716	163590736 -	2
chr4	130741763	130741784 -	2
chr3	51602240	51602260 -	2
chr12	127044759	127044782 -	2
chr12	127073580	127073601 -	2
chr6	8127101	8127121 -	2
chrX	113144005	113144026 -	2
chrX	96372882	96372904 +	2
chr1	86318361	86318382 -	2
chr2	161681303	161681324 -	2
chr5	174670542	174670563 +	2
chr5	173895381	173895402 -	2
chrX	97712391	97712412 +	2
chr6	117913313	117913338 +	2
chr1	83711199	83711220 +	2
chr3	63519720	63519741 +	2

chr3	63552416	63552437 +	2
chr1	83848202	83848224 -	2
chr1	83888864	83888885 +	2
chr4	134083595	134083615 +	2
chr16	64643177	64643201 -	2
chr1	85150857	85150879 +	2
chr13	107476534	107476555 +	2
chr20	38546450	38546471 -	2
chr8	19244917	19244939 +	2
chr15	58232753	58232774 +	2
chr18	72313464	72313485 +	2
chr5	92808666	92808686 +	2
chr7	39078502	39078523 +	2
chr6	120758492	120758513 +	2
chr1	234427877	234427898 -	2
chr3	66564550	66564571 -	2
chr3	66270660	66270682 +	2
chr11	94183846	94183866 -	2
chr3	67217747	67217768 -	2
chr1	87617144	87617165 +	2
chr2	159565467	159565492 +	2
chr13	111445272	111445293 +	2
chr3	161396588	161396608 +	2
chr3	161250016	161250039 +	2
chr15	51956502	51956523 +	2
chr11	79692188	79692209 -	2
chr8	34755967	34755988 +	2
chr3	59831451	59831473 +	2
chr5	90079914	90079935 -	2
chr5	180850524	180850546 +	2
chr15	53857887	53857910 +	2
chr19	10046120	10046141 +	2
chr13	108301023	108301045 -	2
chr5	91309997	91310017 -	2
chr1	81349667	81349687 -	2
chr3	160875318	160875339 -	2
chr11	95449914	95449935 -	2
chr20	33648789	33648810 -	2
chr11	95583046	95583066 -	2
chrX	23588238	23588262 +	2
chr2	205257950	205257973 -	2
chr5	124223576	124223599 -	2
chr1	177415450	177415474 -	2
chr1	181878797	181878818 -	2
chr13	56052430	56052451 +	2
chr3	115526673	115526694 -	2
chr1	180019860	180019882 -	2
chr5	122292051	122292073 -	2
chr1	180793604	180793625 -	2
chr2	210191741	210191762 -	2
chr13	61466080	61466101 +	2

chr3	110581712	110581732 -	2
chr6	166962469	166962489 -	2
chr1	172611383	172611404 +	2
chr1	177118033	177118055 -	2
chr5	124506345	124506367 +	2
chr16	12129360	12129381 +	2
chr1	175840180	175840202 -	2
chr2	208757192	208757213 -	2
chr6	167988891	167988912 +	2
chr13	81003730	81003751 -	2
chr3	121828083	121828105 -	2
chr13	50779193	50779214 -	2
chr5	149165944	149165965 -	2
chr13	50307042	50307063 -	2
chr2	197336592	197336613 +	2
chrX	14252929	14252949 +	2
chr2	196879894	196879914 -	2
chr6	143123344	143123364 +	2
chr1	190786494	190786515 +	2
chr15	85599455	85599477 +	2
chr15	86196191	86196212 +	2
chr13	49340753	49340773 -	2
chr3	123223652	123223672 -	2
chr1	190123214	190123235 +	2
chr1	184887762	184887787 +	2
chr16	17547943	17547965 +	2
chr13	54725106	54725127 -	2
chr1	183874559	183874580 -	2
chrX	18935352	18935373 -	2
chr3	117571535	117571556 -	2
chr6	145547913	145547936 +	2
chr2	198406673	198406694 +	2
chr13	71114348	71114369 -	2
chr5	137266214	137266236 +	2
chr6	155464319	155464340 -	2
chr5	137506236	137506257 +	2
chr6	155069427	155069448 +	2
chr13	71403394	71403415 -	2
chr2	225015269	225015291 -	2
chr3	96971827	96971848 -	2
chr3	96831288	96831309 +	2
chrX	43630373	43630395 +	2
chr1	156952193	156952214 -	2
chr6	157462644	157462665 -	2
chr1	159626459	159626481 +	2
chr2	222786252	222786272 -	2
chr13	69547467	69547488 +	2
chrX	39194416	39194439 -	2
chr6	156459267	156459288 +	2
chr1	154382970	154382992 -	2
chr2	228962509	228962529 -	2

chr15	95014083	95014104 -	2
chr13	73148605	73148626 +	2
chr13	73267131	73267153 -	2
chr15	95606244	95606265 -	2
chr1	153260723	153260745 +	2
chr5	141913480	141913503 -	2
chr1	152149800	152149820 -	2
chr15	94798640	94798663 +	2
chr15	91232974	91232995 -	2
chr1	169386319	169386344 +	2
chrX	31792127	31792149 -	2
chr13	78902766	78902787 +	2
chr3	106757883	106757904 +	2
chr3	105668288	105668310 -	2
chr15	89626563	89626583 -	2
chr16	7420341	7420363 +	2
chr3	108166609	108166629 -	2
chr13	62636783	62636804 -	2
chr2	212183955	212183976 -	2
chr3	108303053	108303072 -	2
chr5	128658023	128658043 +	2
chr5	128975908	128975930 -	2
chr5	147458533	147458554 -	2
chr13	63352088	63352110 +	2
chr15	88400830	88400851 +	2
chr5	147342179	147342200 -	2
chr6	145966737	145966758 +	2
chr1	164830397	164830418 -	2
chrX	35517815	35517837 -	2
chrX	36428863	36428884 -	2
chr1	163637201	163637224 +	2
chr16	208338	208361 -	2
chr6	147394307	147394329 -	2
chr6	161676328	161676348 +	2
chr6	161494676	161494697 +	2
chr6	147246702	147246723 +	2
chr16	220257	220279 +	2
chr13	66125115	66125135 -	2
chr6	160938824	160938846 +	2
chr2	174969831	174969853 -	2
chr16	53310225	53310246 -	2
chr20	6448734	6448755 +	2
chr1	216142804	216142825 -	2
chr1	110846881	110846900 -	2
chr13	88282584	88282606 -	2
chr3	84128979	84128999 -	2
chrX	71423566	71423586 +	2
chr20	7141441	7141462 +	2
chr1	215524817	215524838 -	2
chr7	25420603	25420628 +	2
chr2	178876024	178876048 -	2

chr1	212769573	212769595 -	2
chr5	103959859	103959883 +	2
chr3	142237903	142237924 -	2
chr5	104567694	104567717 -	2
chr2	179341981	179342002 -	2
chr13	31204072	31204092 +	2
chr9	119574683	119574706 -	2
chr9	121164302	121164323 +	2
chr3	85888493	85888516 +	2
chr2	177934858	177934879 +	2
chr6	137977399	137977419 -	2
chr2	177572300	177572322 +	2
chr5	102830129	102830149 -	2
chr1	106216692	106216713 -	2
chr7	33749921	33749942 -	2
chr13	23946551	23946572 -	2
chr20	10240307	10240327 -	2
chr5	159254239	159254259 -	2
chr16	58931585	58931606 +	2
chr9	111782415	111782437 -	2
chr13	90138334	90138355 -	2
chr2	168190117	168190138 -	2
chr1	224459180	224459201 -	2
chr6	132996160	132996182 -	2
chr13	91940261	91940282 -	2
chr1	104535305	104535326 -	2
chr1	223708202	223708223 +	2
chr8	25179497	25179518 -	2
chrX	72420245	72420267 -	2
chr5	99267184	99267205 +	2
chr1	221171259	221171285 +	2
chr7	31745135	31745156 +	2
chrX	71629784	71629805 -	2
chr9	115654289	115654311 +	2
chr1	108733139	108733161 +	2
chr20	8087966	8087987 -	2
chr13	27074552	27074578 +	2
chr1	107595439	107595461 +	2
chr3	83075413	83075434 +	2
chr1	221894975	221894996 +	2
chr3	151183852	151183873 -	2
chrX	73732803	73732824 -	2
chr5	98686761	98686783 +	2
chr9	113634782	113634804 -	2
chr6	135370919	135370941 +	2
chr2	188671935	188671956 -	2
chrX	4372001	4372022 +	2
chr2	242106773	242106794 -	2
chr16	32037325	32037348 +	2
chr1	198223956	198223977 +	2
chr20	109332	109353 +	2

chr3	125697945	125697969 -	2
chr7	12771015	12771036 -	2
chr7	12712345	12712367 +	2
chr5	114982459	114982479 +	2
chr3	125720178	125720202 -	2
chr1	191531964	191531985 -	2
chr2	240091267	240091288 +	2
chrX	7320686	7320706 -	2
chr16	26910239	26910260 +	2
chr16	25988436	25988457 -	2
chr1	200090999	200091021 -	2
chr7	22360160	22360180 +	2
chr5	155081633	155081654 -	2
chr5	154270370	154270391 -	2
chr7	21500736	21500756 +	2
chr16	48544762	48544786 +	2
chr9	125366775	125366796 -	2
chr7	23670315	23670337 +	2
chr7	24110785	24110807 +	2
chr16	47487712	47487732 -	2
chr7	23485382	23485403 +	2
chr3	88468542	88468564 -	2
chr1	202543132	202543154 +	2
chr3	133880875	133880896 +	2
chr16	32980888	32980911 +	2
chr16	32853560	32853581 +	2
chr13	83792312	83792334 -	2
chr2	186163525	186163546 +	2
chr16	34007957	34007978 -	2
chr16	33873018	33873041 -	2
chr13	85098130	85098152 +	2
chr9	131703728	131703752 +	2
chr3	87945625	87945646 +	2
chr5	108326974	108326995 +	2
chr9	132559895	132559916 +	2
chr2	184630069	184630091 -	2
chr12	61613087	61613108 -	2
chr11	15608347	15608369 -	2
chr7	127580307	127580328 +	2
chr8	86562168	86562188 +	2
chr12	9085886	9085907 +	2
chr7	80902445	80902466 +	2
chr7	80791631	80791654 +	2
chr5	34408030	34408051 +	2
chr2	21894809	21894831 -	2
chr17	58567973	58567996 -	2
chr4	87038718	87038740 +	2
chr7	82475911	82475931 +	2
chr4	182739631	182739654 -	2
chr11	14267038	14267059 -	2
chr11	14381783	14381804 +	2

chr4	35700160	35700181 -	2
chr2	79169598	79169619 +	2
chr12	9818227	9818249 -	2
chr12	9561958	9561979 -	2
chr17	60111705	60111726 -	2
chr17	60034808	60034829 +	2
chr11	14928849	14928871 +	2
chr10	69099761	69099781 -	2
chr9	8873710	8873730 +	2
chr5	38230305	38230325 +	2
chr12	66400543	66400565 +	2
chr9	8485284	8485307 -	2
chr17	54329650	54329670 -	2
chr5	37962831	37962853 -	2
chr9	4518576	4518597 -	2
chr2	82991082	82991103 -	2
chr4	33115339	33115361 +	2
chr4	33032933	33032954 -	2
chr2	83171988	83172011 -	2
chr12	64669554	64669575 -	2
chr2	25813189	25813209 -	2
chr4	39335011	39335033 -	2
chr12	55206895	55206917 +	2
chr5	29812797	29812822 +	2
chr17	64199718	64199740 -	2
chr4	85372501	85372522 -	2
chr10	82926793	82926814 +	2
chr17	64257091	64257111 -	2
chr12	11860990	11861012 -	2
chr18	29303935	29303955 +	2
chr10	83687943	83687963 -	2
chr17	67219361	67219380 +	2
chr4	40712234	40712256 +	2
chr17	66298242	66298262 +	2
chr4	182931820	182931842 -	2
chr2	23706116	23706137 +	2
chr2	23465420	23465440 -	2
chr4	86057318	86057338 +	2
chr11	13385419	13385440 +	2
chr2	76742615	76742635 -	2
chr12	57861712	57861734 +	2
chr4	184050548	184050569 -	2
chr12	11590289	11590309 +	2
chr11	13202462	13202483 +	2
chr4	37020923	37020943 -	2
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chr4	22660213	22660234 +	2
chr7	68255852	68255874 -	2
chr4	22424739	22424759 -	2
chr9	16759015	16759038 +	2
chr12	2152267	2152291 -	2

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chr5	45074278	45074299 +	2
chr17	45901595	45901616 -	2
chr8	79279092	79279113 +	2
chr8	79630969	79630994 -	2
chr7	133290448	133290469 +	2
chr2	16852917	16852938 +	2
chr7	133155896	133155917 +	2
chr12	72160742	72160764 +	2
chr12	2224429	2224449 +	2
chr2	15739207	15739228 -	2
chr9	15777083	15777105 +	2
chr18	39699859	39699884 -	2
chr4	177171870	177171891 +	2
chr11	134598121	134598143 +	2
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chr12	75348632	75348654 -	2
chr2	14154856	14154877 -	2
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chr7	136000530	136000551 +	2
chr4	176425136	176425157 -	2
chr18	38819164	38819185 +	2
chr5	40627068	40627089 -	2
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chr2	20060164	20060186 +	2
chr17	51935707	51935727 -	2
chr18	32930855	32930875 +	2
chr7	71708828	71708849 -	2
chr2	20197721	20197742 -	2
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chr10	66156405	66156427 -	2
chr4	28698063	28698083 -	2
chr10	66021541	66021561 -	2
chr4	28930830	28930851 -	2
chr4	28030697	28030719 +	2
chr12	68292196	68292217 -	2
chr17	52791369	52791393 +	2
chr17	48371002	48371023 +	2
chr4	90786113	90786133 -	2
chr10	61791287	61791308 -	2
chr17	48425461	48425482 -	2
chr11	21428379	21428400 -	2
chr8	82623136	82623159 -	2
chr2	95435130	95435149 -	2
chr10	63137828	63137849 +	2

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chr17	50640888	50640913 -	2
chr9	13537242	13537262 -	2
chr2	95641589	95641608 +	2
chr12	70956171	70956192 -	2
chr10	106365013	106365034 -	2
chr10	106539073	106539093 +	2
chr7	114127701	114127726 -	2
chr18	13909579	13909600 +	2
chr4	71503857	71503878 +	2
chr5	17688474	17688495 +	2
chr5	6388551	6388571 -	2
chr7	114694917	114694936 +	2
chr18	1106652	1106673 -	2
chr8	119700703	119700724 +	2
chr4	72202482	72202503 -	2
chr2	56419503	56419524 +	2
chr5	7785776	7785796 -	2
chr4	70065816	70065836 -	2
chr8	118385275	118385296 +	2
chr7	113220459	113220480 +	2
chr8	118636905	118636927 -	2
chr12	24735441	24735462 +	2
chr5	7122902	7122923 -	2
chr17	79891207	79891229 +	2
chr7	97717511	97717533 -	2
chr4	55723433	55723454 +	2
chr4	55316186	55316208 +	2
chr4	55250393	55250414 +	2
chr5	20500939	20500960 +	2
chr17	78058278	78058299 +	2
chr10	100537477	100537498 +	2
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chr10	100423062	100423083 -	2
chr4	72815423	72815444 +	2
chr10	125325714	125325736 -	2
chr2	40015913	40015934 +	2
chr2	58146700	58146724 +	2
chr8	121831630	121831651 +	2
chr5	19144391	19144415 -	2
chr4	56829096	56829121 -	2
chr2	38359528	38359549 -	2
chr10	118835034	118835055 +	2
chr10	113488907	113488927 -	2
chr4	68481072	68481092 -	2
chr12	31128690	31128711 +	2
chr5	12447445	12447466 -	2
chr7	108189516	108189538 +	2
chr5	11321910	11321932 +	2
chr4	66382363	66382385 -	2
chr5	11331975	11331996 +	2

chr18	8174720	8174740 -	2
chr18	9356101	9356122 +	2
chr7	109523116	109523137 +	2
chr8	111710051	111710072 +	2
chr7	104579429	104579449 -	2
chr10	110544952	110544975 +	2
chr10	108498907	108498929 -	2
chr5	8489892	8489914 -	2
chr4	60142163	60142183 -	2
chr12	32838199	32838220 +	2
chr2	50567639	50567661 +	2
chr7	106840301	106840325 +	2
chr18	5301353	5301372 -	2
chr4	186173972	186173994 -	2
chr7	89570307	89570328 +	2
chr12	17123258	17123279 -	2
chr4	79613420	79613440 +	2
chr5	26031460	26031483 +	2
chr2	33055743	33055764 -	2
chr7	120532111	120532132 +	2
chr2	68697994	68698016 -	2
chr12	17224938	17224961 -	2
chr4	188488808	188488829 -	2
chr4	43954828	43954849 +	2
chr18	25623015	25623036 -	2
chr12	16700502	16700525 +	2
chr8	132696763	132696784 +	2
chr7	119615681	119615702 -	2
chr5	25333229	25333250 +	2
chr4	189707502	189707522 +	2
chr8	96670100	96670121 -	2
chr17	69803835	69803856 +	2
chr8	97575402	97575423 +	2
chr8	97453039	97453060 +	2
chr4	42450769	42450791 +	2
chr4	81540407	81540427 +	2
chr4	42742341	42742362 +	2
chr7	87937805	87937828 +	2
chr8	135482069	135482089 +	2
chr8	92210666	92210686 -	2
chr8	133794333	133794354 +	2
chr7	122117130	122117152 -	2
chr7	88342355	88342377 +	2
chr10	87772979	87773000 -	2
chr12	50911606	50911627 +	2
chr8	124102141	124102163 +	2
chr2	36827589	36827610 +	2
chr2	63340484	63340506 +	2
chr2	36553560	36553581 -	2
chr4	48204168	48204191 +	2
chr10	129571258	129571279 -	2

chr12	44261282	44261303 -	2
chr2	61212315	61212337 -	2
chr5	21273009	21273030 +	2
chr4	74534696	74534717 +	2
chr12	21907795	21907816 +	2
chr8	124353696	124353718 +	2
chr4	52203242	52203263 -	2
chr10	97530730	97530751 +	2
chr7	93247576	93247597 -	2
chr12	19654557	19654581 +	2
chr2	35483650	35483671 -	2
chr4	46117095	46117117 +	2
chr10	90847567	90847589 +	2
chr2	34648686	34648707 +	2
chr7	90521943	90521963 +	2
chr7	90815266	90815290 +	2
chr10	129776885	129776906 -	2
chr2	36374900	36374921 +	2
chr8	128605767	128605788 -	2
chr4	47230859	47230880 -	2
chr2	65507584	65507606 -	2
chr4	47458776	47458797 +	2
chr12	44754603	44754624 -	2
chr2	64286967	64286988 -	2
chr4	47035372	47035396 +	2
chr10	15398959	15398984 -	2
chr10	15704707	15704729 +	2
chr4	119038650	119038671 +	2
chr16	87775647	87775672 +	2
chr10	13970035	13970057 -	2
chr8	3842101	3842121 -	2
chr3	180416543	180416564 +	2
chr19	32697852	32697873 -	2
chr4	158125420	158125442 +	2
chr8	2562844	2562865 +	2
chr5	73869551	73869574 +	2
chr11	109854955	109854976 +	2
chr5	73268171	73268192 -	2
chr3	182655926	182655948 +	2
chr2	142370917	142370938 -	2
chr9	77630008	77630029 +	2
chr18	61545801	61545821 -	2
chr10	10148992	10149016 +	2
chr8	47687060	47687083 -	2
chr4	155302965	155302985 +	2
chr10	10105504	10105526 +	2
chr2	143641740	143641762 -	2
chr11	59246849	59246870 +	2
chr2	143808818	143808840 +	2
chr11	56798524	56798545 -	2
chr8	49372207	49372231 -	2

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chr5	75630555	75630579 +	2
chr8	48611850	48611871 +	2
chr2	142181573	142181594 -	2
chr16	85282335	85282359 -	2
chr3	178457270	178457291 +	2
chr11	57602378	57602403 -	2
chr12	97505482	97505503 +	2
chr11	112306629	112306651 +	2
chr12	98786542	98786565 -	2
chr8	423562	423583 -	2
chr10	23823392	23823413 -	2
chr12	98359832	98359852 -	2
chr4	160891608	160891629 +	2
chr10	26073246	26073268 +	2
chr3	190045706	190045726 +	2
chr5	66745928	66745950 +	2
chr10	25300162	25300183 -	2
chr7	158561211	158561233 +	2
chr5	66426441	66426462 -	2
chr11	113220478	113220499 +	2
chr12	96914095	96914116 +	2
chr8	52998283	52998305 -	2
chr9	70151822	70151843 +	2
chr3	184486168	184486188 -	2
chr9	71086071	71086092 +	2
chr9	71661238	71661260 -	2
chr17	5938240	5938263 +	2
chr2	133423302	133423324 +	2
chr11	111861255	111861277 -	2
chr11	50766178	50766199 -	2
chr12	99625121	99625142 +	2
chr17	7529732	7529754 -	2
chr9	69218780	69218805 -	2
chr10	21488162	21488186 +	2
chr5	69423968	69423990 +	2
chr2	152246316	152246339 -	2
chr5	85194875	85194896 -	2
chr3	167699255	167699276 +	2
chr11	68373231	68373252 +	2
chr12	118195394	118195419 +	2
chr8	43068652	43068673 -	2
chr11	103178349	103178374 +	2
chr9	86821884	86821907 +	2
chr3	169040315	169040335 -	2
chr11	67314558	67314580 +	2
chr18	65007998	65008019 -	2
chr9	92826088	92826108 +	2
chr7	46940430	46940452 +	2
chr16	71724480	71724502 +	2

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chr9	93836619	93836640 -	2
chr9	92309691	92309713 -	2
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chr12	121088120	121088142 -	2
chr11	101912308	101912330 -	2
chr8	12285317	12285340 -	2
chr8	39883242	39883263 -	2
chr16	73149377	73149402 -	2
chr11	101693197	101693219 +	2
chr8	12038752	12038775 -	2
chr10	6907883	6907904 -	2
chr5	80665845	80665866 -	2
chr3	174569107	174569126 -	2
chr18	62845485	62845506 -	2
chr16	79938443	79938463 -	2
chr11	105023864	105023885 -	2
chr7	53928564	53928585 +	2
chr10	5799787	5799808 +	2
chr5	80753921	80753943 +	2
chr12	112977364	112977384 -	2
chr11	59519927	59519948 +	2
chr2	145128576	145128597 -	2
chr5	82740301	82740324 +	2
chr9	84844079	84844103 +	2
chr11	65653962	65653983 +	2
chr12	117254027	117254048 +	2
chr18	64715274	64715299 -	2
chr8	9071168	9071189 +	2
chr8	45990727	45990748 +	2
chr16	79086518	79086539 +	2
chr3	172792655	172792676 -	2
chr5	81203835	81203856 -	2
chr4	153963826	153963846 -	2
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chr10	3752386	3752407 +	2
chr19	27488336	27488357 +	2
chr19	27481346	27481367 +	2
chr4	153797504	153797527 -	2
chr8	43845180	43845200 +	2
chr5	82170064	82170085 +	2
chr4	13816586	13816606 -	2
chr7	144775233	144775255 -	2
chr4	13481987	13482008 +	2
chr5	53360317	53360338 -	2
chr11	36570306	36570326 -	2
chr4	12732671	12732692 +	2
chr10	48312819	48312842 +	2
chr2	110200705	110200725 -	2
chr5	53178881	53178906 -	2
chr8	68219825	68219846 +	2

chr4	170778261	170778282 +	2
chr11	127685072	127685094 +	2
chr2	107932231	107932252 +	2
chr10	49556350	49556371 +	2
chr4	102818722	102818744 +	2
chr2	113524987	113525009 +	2
chr11	38113741	38113762 +	2
chr18	47390911	47390934 +	2
chr11	38619129	38619150 -	2
chr4	9938044	9938065 -	2
chr5	53950786	53950808 +	2
chr2	1929992	1930013 -	2
chr4	12398915	12398939 +	2
chr11	37610251	37610270 -	2
chr12	82539184	82539205 +	2
chr5	54435992	54436014 -	2
chr4	173659248	173659269 +	2
chr4	17658995	17659016 -	2
chr9	22431950	22431971 +	2
chr2	102542874	102542895 +	2
chr7	138432390	138432414 -	2
chr11	28869002	28869025 +	2
chr17	42346374	42346394 +	2
chr7	64222286	64222307 -	2
chr2	5470467	5470488 -	2
chr11	128415177	128415198 -	2
chr4	171380802	171380823 -	2
chr2	107624425	107624444 -	2
chr11	30946613	30946634 +	2
chr7	62763575	62763595 +	2
chr11	30819815	30819836 -	2
chr2	6804969	6804990 -	2
chr9	23792198	23792220 +	2
chr11	31339615	31339635 -	2
chr11	31532493	31532514 -	2
chr3	194320620	194320641 +	2
chr17	15145175	15145196 -	2
chr4	163206441	163206462 +	2
chr17	15568142	15568163 -	2
chr4	111365252	111365273 +	2
chr11	43532607	43532627 -	2
chr10	33647082	33647103 +	2
chr5	62345704	62345726 +	2
chr17	16709325	16709346 +	2
chr4	111124797	111124818 -	2
chr4	111290431	111290452 +	2
chr10	33465253	33465273 +	2
chr3	191705435	191705455 -	2
chr4	114445263	114445284 +	2
chr2	128368072	128368093 +	2
chr3	190915698	190915719 -	2

chr4	114739725	114739746 +	2
chr17	14171263	14171284 -	2
chr3	193088365	193088390 +	2
chr18	54523898	54523919 -	2
chr8	64700995	64701017 +	2
chr8	64675286	64675308 +	2
chr19	55426101	55426123 +	2
chr11	121821016	121821036 -	2
chr10	38982930	38982951 +	2
chr4	108150280	108150302 +	2
chr12	85419809	85419831 -	2
chr7	147249898	147249919 -	2
chr11	38891691	38891712 -	2
chr17	28431969	28431990 -	2
chr17	28172449	28172470 +	2
chr17	28163058	28163081 +	2
chr10	41735114	41735134 +	2
chr18	51063792	51063814 +	2
chr18	51137855	51137878 -	2
chr10	36359425	36359446 -	2
chr9	37876407	37876428 +	2
chr17	19577884	19577905 -	2
chr19	52386220	52386241 -	2
chr17	18606068	18606089 -	2
chr3	197315017	197315039 -	2
chr17	18839884	18839905 +	2
chr17	20340009	20340030 +	2
chr10	38300637	38300657 -	2
chr10	38285545	38285566 +	2
chr10	38178575	38178596 +	2
chr8	63690246	63690268 +	2
chr8	63690209	63690231 +	2
chr8	63684622	63684643 -	2
chr7	149095699	149095720 +	2
chr2	118038201	118038222 +	2
chr4	3147691	3147712 +	2
chr5	59708609	59708633 -	2
chr12	88290258	88290279 +	2
chr5	59614481	59614504 -	2
chr14	62665759	62665780 -	2
chrY	8506727	8506750 +	2
chr14	94743641	94743662 -	2
chr21	40771203	40771223 -	2
chr21	40781395	40781414 -	2
chr3	2272176	2272197 +	2
chr14	94227435	94227458 +	2
chr6	64778080	64778104 -	2
chr1	5980491	5980514 +	2
chr1	5957809	5957831 +	2
chr21	33967222	33967243 -	2
chrY	26231699	26231721 -	2

chr6	44242111	44242136 -	2
chr6	44609660	44609681 +	2
chrY	7144299	7144320 +	2
chr21	37476430	37476452 +	2
chr3	5573645	5573666 -	2
chr14	81791522	81791543 +	2
chr14	60591408	60591429 -	2
chr6	43709513	43709534 -	2
chr14	60359181	60359205 +	2
chr21	42973591	42973612 +	2
chr6	47673736	47673757 +	2
chr6	69470389	69470410 +	2
chr1	4048838	4048864 +	2
chr21	41594659	41594680 +	2
chrY	11871961	11871982 -	2
chr6	68234956	68234981 +	2
chrX	145985354	145985375 -	2
chr14	49954672	49954695 +	2
chr21	23804947	23804968 +	2
chr6	33708949	33708974 -	2
chr1	29480215	29480235 +	2
chr14	71341772	71341793 -	2
chr21	26262914	26262935 +	2
chr6	52723021	52723043 +	2
chr1	31166611	31166631 +	2
chr1	31547072	31547093 +	2
chr22	35132104	35132124 +	2
chrY	23438894	23438916 +	2
chrX	142887231	142887252 +	2
chr22	34769512	34769533 +	2
chrX	143364740	143364761 +	2
chr6	85107259	85107279 -	2
chr6	55927040	55927061 +	2
chr6	27468816	27468836 +	2
chr21	20540167	20540188 -	2
chr3	23216863	23216884 +	2
chr6	61503272	61503292 +	2
chr22	22947563	22947584 -	2
chrX	141960154	141960175 -	2
chr14	84119838	84119859 +	2
chr15	20418406	20418427 -	2
chr6	27931808	27931828 +	2
chr3	20109921	20109941 +	2
chr1	34425879	34425901 +	2
chr21	22772585	22772606 -	2
chr21	22786139	22786161 +	2
chr3	20646753	20646774 +	2
chr3	20571950	20571972 -	2
chr14	56608087	56608112 -	2
chr14	56775889	56775910 -	2
chr6	39871379	39871400 -	2

chr1	19006866	19006887 -	2
chr6	76605030	76605051 +	2
chr22	33495177	33495199 -	2
chr21	30056566	30056589 -	2
chr14	58700216	58700236 -	2
chrY	3315200	3315225 -	2
chr22	26422717	26422738 +	2
chr14	99488121	99488142 -	2
chr6	79684348	79684369 -	2
chrX	149816328	149816349 +	2
chr6	80001836	80001858 +	2
chr14	77520335	77520356 -	2
chr6	34877317	34877336 -	2
chr22	25366858	25366879 -	2
chr14	55226679	55226700 +	2
chr14	67068922	67068944 +	2
chr14	67069362	67069384 -	2
chr6	67349054	67349075 -	2
chr22	30169935	30169954 -	2
chr14	81267241	81267262 -	2
chrY	17676894	17676914 +	2
chr14	88624583	88624604 -	2
chr22	47551823	47551844 -	2
chr22	50400007	50400028 -	2
chrY	18229099	18229119 -	2
chr6	98699647	98699668 +	2
chr6	63923845	63923865 -	2
chr20	60958038	60958058 -	2
chr1	45911329	45911350 -	2
chr3	36336306	36336327 +	2
chr3	40005044	40005064 -	2
chr20	58667970	58667991 -	2
chr14	85401509	85401533 -	2
chr20	58345226	58345248 -	2
chr14	85302112	85302132 +	2
chr6	24734382	24734403 +	2
chr20	57734888	57734909 +	2
chr6	12487166	12487188 -	2
chr1	62390893	62390918 -	2
chr1	61861582	61861604 +	2
chr15	23965624	23965645 -	2
chr20	60077999	60078021 -	2
chr14	43140961	43140983 -	2
chr14	32346924	32346947 +	2
chr1	45226250	45226271 +	2
chrX	137532180	137532200 -	2
chr6	89467622	89467644 -	2
chr1	54918564	54918585 +	2
chrX	132989843	132989863 -	2
chr6	95881680	95881701 -	2
chr3	34194280	34194300 +	2

chr14	72013728	72013750 +	2
chr6	95514983	95515004 +	2
chr6	94588284	94588305 +	2
chr3	32252965	32252986 +	2
chr15	31616276	31616297 -	2
chr21	9649026	9649046 -	2
chr6	92268930	92268952 -	2
chr1	49466177	49466197 -	2
chr14	35279716	35279738 -	2
chr6	16469297	16469318 +	2
chr6	91877633	91877654 +	2
chr6	96367170	96367193 +	2
chr3	34710503	34710526 -	2
chr6	96866446	96866467 -	2
chr20	60774105	60774127 +	2
chrX	139390724	139390745 +	2
chr14	46049321	46049340 -	2
chr6	10305924	10305945 +	2
chrX	119684930	119684952 +	2
chr6	10262366	10262387 +	2
chr3	24883658	24883679 -	2
chr14	30218983	30219004 -	2
chr22	40932557	40932578 -	2
chr14	85938009	85938031 +	2
chr14	44390904	44390926 +	2
chr1	66602069	66602091 -	2
chr20	53655479	53655500 -	2
chr14	46010053	46010073 +	2
chr21	18797113	18797134 +	2
chr20	53676804	53676825 +	2
chr21	18762031	18762054 +	2
chr14	87153649	87153669 -	2
chrY	57072472	57072492 +	2
chr12	33450959	33450979 -	2
chr13	83538386	83538406 -	3
chr5	9798503	9798523 +	3
chr4	69205271	69205291 +	3
chr4	68920997	68921017 +	3
chr4	68709820	68709840 +	3
chrX	74370310	74370330 +	3
chr4	69418282	69418302 -	3
chr5	9588089	9588109 -	3
chr5	12254493	12254513 -	3
chr4	63574431	63574451 +	3
chr4	64725770	64725790 +	3
chr5	11969721	11969741 -	3
chr4	62037981	62038001 +	3
chr4	61934564	61934584 +	3
chr4	61864622	61864642 -	3
chr4	61864621	61864641 -	3
chr5	12751206	12751226 +	3

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chr4	63173944	63173964 +	3
chr4	158694222	158694242 -	3
chr4	65864860	65864880 -	3
chr5	4740639	4740659 +	3
chr4	76866030	76866050 +	3
chr4	76844681	76844701 +	3
chr4	76843965	76843985 +	3
chr4	76303474	76303494 -	3
chr4	77056452	77056472 -	3
chr4	77427147	77427167 -	3
chr4	77412335	77412355 -	3
chr4	145971570	145971590 +	3
chrX	70080191	70080211 +	3
chr4	146373659	146373679 -	3
chr4	81032638	81032658 -	3
chr5	7746388	7746408 -	3
chr5	7693887	7693907 -	3
chr5	7693886	7693906 -	3
chr4	73164962	73164982 +	3
chr4	147983791	147983811 -	3
chr4	148064097	148064117 +	3
chr4	71724907	71724927 -	3
chrX	22346178	22346198 -	3
chrX	41883332	41883352 +	3
chrX	71032066	71032086 +	3
chr4	75302397	75302417 -	3
chrX	41927089	41927109 +	3
chrX	36381398	36381418 +	3
chrX	16715435	16715455 -	3
chrX	38177946	38177966 +	3
chrX	77616610	77616630 +	3
chrX	82757476	82757496 +	3
chrX	83600713	83600733 -	3
chr4	42829456	42829476 -	3
chr5	24138417	24138437 +	3
chrX	37999287	37999307 +	3
chr4	45057105	45057125 -	3
chrX	82587528	82587548 +	3
chr4	156216532	156216552 +	3
chr4	156322707	156322727 +	3
chr4	37617262	37617282 +	3
chr5	26500827	26500847 -	3
chr4	151324641	151324661 +	3
chr4	59279346	59279366 -	3
chr4	59364108	59364128 +	3
chrX	40481782	40481802 +	3
chr4	157333833	157333853 -	3
chrX	77926266	77926286 -	3
chr4	61640089	61640109 -	3

chr4	61621303	61621323 +	3
chr5	12789124	12789144 -	3
chr5	13034891	13034911 +	3
chr4	157747330	157747350 -	3
chr5	15288142	15288162 +	3
chr5	14083236	14083256 +	3
chr4	150942589	150942609 -	3
chr4	59634661	59634681 -	3
chr4	53066764	53066784 -	3
chrX	18724628	18724648 -	3
chrX	81741543	81741563 -	3
chr4	52079268	52079288 -	3
chr4	156924262	156924282 -	3
chr4	56506744	56506764 +	3
chrX	80162982	80163002 +	3
chr4	55493028	55493048 -	3
chrX	19378679	19378699 +	3
chr4	114874502	114874522 -	3
chr4	116017229	116017249 -	3
chr4	163547928	163547948 +	3
chr4	83227095	83227115 +	3
chr4	137153759	137153779 +	3
chr4	164172383	164172403 +	3
chr4	119236782	119236802 -	3
chr4	117485524	117485544 +	3
chr4	116682364	116682384 -	3
chr4	117070628	117070648 -	3
chrX	47676453	47676473 -	3
chr4	105873115	105873135 +	3
chr4	106298868	106298888 -	3
chr4	106296172	106296192 +	3
chrX	30397502	30397522 -	3
chr4	110765400	110765420 -	3
chr4	134252475	134252495 +	3
chr4	133127127	133127147 -	3
chr4	133662204	133662224 +	3
chr4	133559433	133559453 +	3
chr4	170891600	170891620 +	3
chr4	122731228	122731248 -	3
chrX	32229010	32229030 +	3
chr4	169791484	169791504 -	3
chr4	169791485	169791505 -	3
chrX	51986892	51986912 +	3
chr4	170198703	170198723 -	3
chr4	126962889	126962909 -	3
chrX	52118500	52118520 -	3
chrX	52118499	52118519 -	3
chr4	170380771	170380791 -	3
chr4	164627569	164627589 +	3
chr4	90995221	90995241 +	3
chr4	187216304	187216324 +	3

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chr4	187798393	187798413 -	3
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chr4	93157634	93157654 +	3
chr4	142821407	142821427 -	3
chr4	189816531	189816551 +	3
chrX	24865866	24865886 +	3
chrX	68190563	68190583 -	3
chr4	84137787	84137807 -	3
chrX	66863379	66863399 +	3
chr4	87631804	87631824 +	3
chr4	86342874	86342894 -	3
chr4	141211375	141211395 +	3
chr4	102137234	102137254 -	3
chr4	179940052	179940072 +	3
chrX	57959266	57959286 +	3
chrX	62836107	62836127 +	3
chr4	101253747	101253767 +	3
chrX	45289608	45289628 +	3
chr4	104651808	104651828 +	3
chr4	96420896	96420916 +	3
chr4	96165864	96165884 +	3
chr4	183261560	183261580 +	3
chr4	183241483	183241503 -	3
chr4	94947878	94947898 -	3
chr4	94022652	94022672 +	3
chr4	94010042	94010062 -	3
chr4	94520494	94520514 -	3
chrX	27058493	27058513 -	3
chr4	181870257	181870277 +	3
chr4	180824021	180824041 -	3
chr4	98819318	98819338 +	3
chrX	63099636	63099656 +	3
chr4	99890962	99890982 -	3
chr4	162041396	162041416 +	3
chr4	98159179	98159199 -	3
chr4	180896992	180897012 -	3
chrX	148981088	148981108 +	3
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chr3	59722487	59722507 -	3
chr3	49577116	49577136 +	3
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chr3	54754636	54754656 +	3
chr3	54754635	54754655 +	3
chr3	67193521	67193541 -	3
chrX	146323625	146323645 +	3
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chr3	63149219	63149239 +	3
chrY	3642589	3642609 +	3
chr3	37305996	37306016 +	3

chrY	2937893	2937913 +	3
chrY	5580734	5580754 -	3
chr3	31923327	31923347 +	3
chr3	31833741	31833761 +	3
chrX	153049037	153049057 -	3
chr3	46594649	46594669 +	3
chr3	46594648	46594668 +	3
chr3	45918461	45918481 +	3
chrX	155617294	155617314 +	3
chrX	153382033	153382053 +	3
chr3	42376466	42376486 -	3
chr3	88327021	88327041 -	3
chrX	140663085	140663105 +	3
chr3	84541962	84541982 -	3
chrX	135485311	135485331 +	3
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chr3	93824331	93824351 -	3
chr3	90164724	90164744 -	3
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chr3	76257233	76257253 -	3
chr3	76209263	76209283 -	3
chr3	76183863	76183883 +	3
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chr3	69553196	69553216 +	3
chr3	71338098	71338118 +	3
chr3	70865073	70865093 +	3
chr3	80303997	80304017 -	3
chr3	77039328	77039348 +	3
chrX	144172227	144172247 -	3
chr3	78708523	78708543 +	3
chrY	22080625	22080645 +	3
chr22	31431692	31431712 +	3
chr22	29379013	29379033 +	3
chrY	23690302	23690322 +	3
chr22	22132784	22132804 +	3
chrY	22505737	22505757 -	3
chrY	22954795	22954815 +	3
chr22	42784763	42784783 +	3
chr22	41791117	41791137 -	3
chr22	35303057	35303077 +	3
chr22	38231385	38231405 +	3
chr22	38231384	38231404 +	3
chr22	35457866	35457886 +	3
chr22	35457864	35457884 +	3
chrY	24588539	24588559 +	3
chr21	37013202	37013222 -	3
chr21	35666613	35666633 +	3
chr1	60066	60086 +	3
chr21	34537104	34537124 +	3
chrY	25979732	25979752 -	3

chrY	25081511	25081531 -	3
chr22	17393234	17393254 -	3
chr22	16945123	16945143 +	3
chr21	42253968	42253988 +	3
chr21	41688937	41688957 -	3
chr21	41384896	41384916 -	3
chr21	40472245	40472265 -	3
chr21	45990116	45990136 +	3
chr3	21246964	21246984 -	3
chr3	16366887	16366907 +	3
chr3	19199511	19199531 -	3
chr3	30232829	30232849 -	3
chrY	6410375	6410395 +	3
chr3	27981362	27981382 -	3
chrY	9754303	9754323 -	3
chr3	27878411	27878431 +	3
chr3	25845080	25845100 -	3
chr3	25496708	25496728 -	3
chr3	2137685	2137705 +	3
chr3	1437308	1437328 -	3
chr3	2219084	2219104 -	3
chr3	4004099	4004119 -	3
chr22	47750653	47750673 +	3
chr22	48917983	48918003 -	3
chr22	48775810	48775830 -	3
chr22	48379318	48379338 +	3
chr3	11740199	11740219 -	3
chr3	4954759	4954779 +	3
chr3	186469057	186469077 +	3
chr3	181916738	181916758 +	3
chr3	181839868	181839888 -	3
chr3	181418196	181418216 -	3
chr3	182841132	182841152 -	3
chr3	189315961	189315981 +	3
chr3	180189489	180189509 -	3
chr3	195283021	195283041 -	3
chrX	97890565	97890585 +	3
chr3	194368511	194368531 +	3
chr3	196781206	196781226 -	3
chr3	193808837	193808857 -	3
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chr3	193808836	193808856 -	3
chrX	98779467	98779487 -	3
chrX	106976739	106976759 +	3
chr3	168103523	168103543 +	3
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chr3	171066081	171066101 +	3
chrX	109028585	109028605 -	3
chrX	108269049	108269069 -	3
chrX	108532739	108532759 +	3

chr3	167001768	167001788 -	3
chrX	104227236	104227256 +	3
chrX	103425634	103425654 +	3
chr3	178966744	178966764 +	3
chr3	178502374	178502394 -	3
chr3	173351569	173351589 +	3
chr3	175725533	175725553 -	3
chr3	175725532	175725552 -	3
chr3	175725531	175725551 -	3
chr3	174996887	174996907 -	3
chrX	89985143	89985163 +	3
chr4	25179489	25179509 -	3
chr4	26261693	26261713 +	3
chr4	19278475	19278495 +	3
chr4	21943668	21943688 +	3
chr4	31516819	31516839 -	3
chr4	33857653	33857673 +	3
chrX	87288608	87288628 +	3
chr4	9208984	9209004 -	3
chr4	10014952	10014972 +	3
chr4	8923049	8923069 -	3
chr4	8767426	8767446 -	3
chr4	1060324	1060344 -	3
chr4	12363414	12363434 -	3
chr4	15861680	15861700 +	3
chrX	92467258	92467278 -	3
chr4	18052472	18052492 +	3
chr4	12417760	12417780 +	3
chr4	13643098	13643118 -	3
chr3	118806037	118806057 +	3
chr3	120360976	120360996 +	3
chr3	118000457	118000477 -	3
chr3	117729768	117729788 -	3
chr3	116448265	116448285 +	3
chr3	115600053	115600073 -	3
chr3	115600052	115600072 -	3
chr3	122291789	122291809 +	3
chr3	114593972	114593992 -	3
chr3	130627710	130627730 +	3
chr3	128003069	128003089 +	3
chr3	132941468	132941488 -	3
chrX	124336819	124336839 +	3
chrX	124336821	124336841 +	3
chr3	123711484	123711504 -	3
chr3	127333908	127333928 +	3
chrX	124825733	124825753 +	3
chrX	125313407	125313427 +	3
chrX	132844492	132844512 -	3
chr3	104950392	104950412 -	3
chr3	107662508	107662528 +	3
chr3	107006647	107006667 -	3

chr3	106578688	106578708 -	3
chr3	103997619	103997639 +	3
chr3	101521686	101521706 -	3
chr3	103823585	103823605 -	3
chrX	133491327	133491347 -	3
chrX	129811981	129812001 +	3
chrX	128817682	128817702 -	3
chrX	113126621	113126641 +	3
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chr3	151331488	151331508 -	3
chr3	153494041	153494061 -	3
chr3	152471180	152471200 +	3
chrX	111692629	111692649 +	3
chr3	160897485	160897505 +	3
chrX	111131336	111131356 -	3
chrX	111131337	111131357 -	3
chr3	159709572	159709592 +	3
chr3	159467899	159467919 -	3
chr3	149027914	149027934 -	3
chr3	138669654	138669674 +	3
chr3	141306591	141306611 -	3
chr3	140023970	140023990 +	3
chr3	140023969	140023989 +	3
chr3	133771417	133771437 +	3
chrX	115548881	115548901 -	3
chr3	146034268	146034288 +	3
chr3	145422833	145422853 +	3
chrX	116060877	116060897 +	3
chr3	148686216	148686236 -	3
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chr3	148452699	148452719 +	3
chrX	115232460	115232480 -	3
chr3	143646667	143646687 -	3
chr3	143646666	143646686 -	3
chr3	143646668	143646688 -	3
chrX	116390865	116390885 -	3
chrX	116464426	116464446 +	3
chr7	35770384	35770404 -	3
chr7	47410783	47410803 +	3
chr7	37546099	37546119 +	3
chr7	30466982	30467002 -	3
chr8	133547243	133547263 -	3
chr8	132786652	132786672 -	3
chr7	43908029	43908049 +	3
chr8	128854387	128854407 -	3
chr8	128854388	128854408 -	3
chr7	38437996	38438016 -	3
chr7	41344223	41344243 +	3
chr7	18660940	18660960 +	3
chr7	17894737	17894757 +	3
chr7	15628309	15628329 +	3

chr7	15628307	15628327 +	3
chr7	15610596	15610616 -	3
chr7	16676208	16676228 +	3
chr7	28002744	28002764 -	3
chr7	28978799	28978819 -	3
chr7	22119353	22119373 +	3
chr7	24840793	24840813 -	3
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chr7	24576632	24576652 -	3
chr8	135188987	135189007 -	3
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chr8	127594277	127594297 +	3
chr7	71874408	71874428 +	3
chr7	78616003	78616023 -	3
chr7	78356318	78356338 +	3
chr7	70345165	70345185 -	3
chr8	114510477	114510497 +	3
chr7	83055746	83055766 +	3
chr8	114338055	114338075 +	3
chr7	86228835	86228855 +	3
chr8	113351427	113351447 +	3
chr7	79825746	79825766 -	3
chr8	114802319	114802339 -	3
chr7	52035762	52035782 -	3
chr8	120907953	120907973 -	3
chr7	53919411	53919431 +	3
chr7	53919410	53919430 +	3
chr7	57220909	57220929 -	3
chr7	56533603	56533623 +	3
chr7	13934973	13934993 +	3
chr9	14615825	14615845 -	3
chr6	137608248	137608268 -	3
chr9	14452142	14452162 +	3
chr9	14452141	14452161 +	3
chr6	147277843	147277863 +	3
chr6	142910641	142910661 -	3
chr6	142840096	142840116 -	3
chr6	142788013	142788033 +	3
chr6	144148586	144148606 +	3
chr6	126826061	126826081 -	3
chr6	120637436	120637456 -	3
chr6	122243155	122243175 -	3
chr6	122492234	122492254 +	3
chr6	132953407	132953427 +	3
chr6	134337888	134337908 +	3
chr9	19629469	19629489 -	3
chr9	19682782	19682802 +	3
chr9	1770111	1770131 -	3
chr7	7276985	7277005 +	3
chr6	166875730	166875750 -	3
chr6	166875729	166875749 -	3

chr6	166114347	166114367 +	3
chr6	170346835	170346855 +	3
chr9	3247325	3247345 -	3
chr9	3338749	3338769 +	3
chr8	141272872	141272892 -	3
chr7	11612181	11612201 +	3
chr7	13926192	13926212 -	3
chr7	7829645	7829665 +	3
chr6	156312239	156312259 -	3
chr9	8891798	8891818 -	3
chr6	152055614	152055634 -	3
chr9	9882232	9882252 +	3
chr6	152687338	152687358 +	3
chr6	161609463	161609483 +	3
chr6	161140182	161140202 +	3
chr9	6548850	6548870 -	3
chr6	159967113	159967133 +	3
chr9	6611856	6611876 +	3
chr7	86558566	86558586 -	3
chr8	15763911	15763931 +	3
chr8	16421480	16421500 +	3
chr8	77971919	77971939 -	3
chr8	78051284	78051304 -	3
chr8	17251458	17251478 -	3
chr8	14685315	14685335 -	3
chr8	11994686	11994706 -	3
chr8	11314272	11314292 -	3
chr8	14364452	14364472 +	3
chr8	25776371	25776391 -	3
chr8	75413114	75413134 +	3
chr8	24378809	24378829 +	3
chr8	26658736	26658756 +	3
chr8	76579988	76580008 +	3
chr8	76579989	76580009 +	3
chr8	76588753	76588773 -	3
chr8	76579987	76580007 +	3
chr8	75669094	75669114 -	3
chr8	75703956	75703976 -	3
chr8	83521755	83521775 +	3
chr8	85836879	85836899 -	3
chr7	152455597	152455617 -	3
chr7	155539831	155539851 +	3
chr7	155539830	155539850 +	3
chr7	155057202	155057222 -	3
chr7	155057201	155057221 -	3
chr8	6220549	6220569 +	3
chr8	81061523	81061543 +	3
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chr8	4896727	4896747 +	3
chr8	3926181	3926201 +	3
chr8	52172078	52172098 -	3

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chr8	55176647	55176667 -	3
chr8	67322895	67322915 -	3
chr8	50010435	50010455 -	3
chr8	49914182	49914202 -	3
chr8	63600270	63600290 -	3
chr8	61179974	61179994 +	3
chr8	64355691	64355711 +	3
chr8	59391495	59391515 -	3
chr8	57748606	57748626 +	3
chr8	71615018	71615038 +	3
chr8	33681784	33681804 -	3
chr8	34803454	34803474 +	3
chr8	34375838	34375858 -	3
chr8	36134638	36134658 -	3
chr8	72584735	72584755 -	3
chr8	42830192	42830212 +	3
chr8	42781580	42781600 +	3
chr8	42270700	42270720 +	3
chr8	40905311	40905331 -	3
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chr8	105376808	105376828 -	3
chr7	106396181	106396201 +	3
chr7	151839187	151839207 -	3
chr8	104187727	104187747 -	3
chr7	109005940	109005960 +	3
chr7	106199776	106199796 +	3
chr8	105505426	105505446 -	3
chr7	104514910	104514930 -	3
chr7	104676871	104676891 +	3
chr7	116003289	116003309 +	3
chr7	115974933	115974953 -	3
chr8	102147655	102147675 +	3
chr7	112311665	112311685 +	3
chr7	92001049	92001069 +	3
chr7	92231227	92231247 +	3
chr8	111023195	111023215 -	3
chr7	88465708	88465728 -	3
chr7	87054403	87054423 +	3
chr7	89603384	89603404 -	3
chr7	89603383	89603403 -	3
chr7	89373230	89373250 -	3
chr8	112055730	112055750 -	3
chr8	108882944	108882964 -	3
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chr7	96861806	96861826 +	3
chr8	110665672	110665692 -	3
chr7	93523147	93523167 -	3
chr7	93523146	93523166 -	3
chr8	109565699	109565719 -	3

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chr8	91323239	91323259 +	3
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chr8	92120384	92120404 -	3
chr7	136009142	136009162 -	3
chr8	87994422	87994442 -	3
chr7	151839185	151839205 -	3
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chr8	87219720	87219740 -	3
chr8	89303310	89303330 -	3
chr7	143811445	143811465 +	3
chr7	143646150	143646170 -	3
chr7	143199599	143199619 +	3
chr7	121853218	121853238 -	3
chr7	121853217	121853237 -	3
chr7	122742651	122742671 -	3
chr8	98203050	98203070 -	3
chr7	118719108	118719128 +	3
chr7	117741452	117741472 -	3
chr7	130097339	130097359 +	3
chr7	132944125	132944145 -	3
chr8	93536508	93536528 +	3
chr8	95734323	95734343 -	3
chr7	127155299	127155319 -	3
chr8	96325514	96325534 -	3
chr9	107867273	107867293 -	3
chr5	119917302	119917322 +	3
chr9	110729634	110729654 -	3
chr5	113701529	113701549 -	3
chr9	110425929	110425949 -	3
chr5	120462007	120462027 +	3
chr5	124710188	124710208 +	3
chr9	103780227	103780247 -	3
chr5	124804369	124804389 -	3
chr5	125438159	125438179 -	3
chr5	125170430	125170450 +	3
chr5	121986902	121986922 +	3
chr9	105402001	105402021 +	3
chr9	116978285	116978305 -	3
chr9	117404606	117404626 +	3
chr9	117404607	117404627 +	3
chr9	117604862	117604882 -	3
chr9	117615414	117615434 +	3
chr9	112562018	112562038 +	3
chr5	109450899	109450919 +	3
chr9	113238045	113238065 -	3
chr5	105936607	105936627 +	3
chr5	105811869	105811889 +	3

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chr5	145481335	145481355 -	3
chr5	147901789	147901809 +	3
chr5	147901788	147901808 +	3
chr5	147767960	147767980 -	3
chr9	89102540	89102560 +	3
chr9	89809312	89809332 -	3
chr9	88799861	88799881 -	3
chr9	88853988	88854008 +	3
chr5	155043438	155043458 +	3
chr5	155951465	155951485 +	3
chr9	90358376	90358396 +	3
chr5	130506541	130506561 +	3
chr5	134770838	134770858 +	3
chr5	133227403	133227423 +	3
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chr9	101165106	101165126 +	3
chr5	129247199	129247219 -	3
chr9	100133552	100133572 -	3
chr5	141609722	141609742 -	3
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chr5	143164433	143164453 -	3
chr5	136425875	136425895 -	3
chr5	136155811	136155831 -	3
chr5	137434905	137434925 +	3
chrX	7616825	7616845 +	3
chrX	7859450	7859470 -	3
chr5	58700463	58700483 -	3
chr5	57815469	57815489 +	3
chrX	7277649	7277669 +	3
chr5	53724738	53724758 +	3
chr5	52577297	52577317 -	3
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chr5	64957151	64957171 -	3
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chr5	37954711	37954731 -	3
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chr5	30147169	30147189 -	3
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chr5	51680656	51680676 +	3
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chr5	40960008	40960028 +	3
chr5	42960677	42960697 +	3
chr5	42470318	42470338 -	3
chr5	42106877	42106897 +	3
chr5	90921652	90921672 -	3
chr5	86682010	86682030 +	3
chr5	91302895	91302915 -	3
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chr5	73281766	73281786 +	3
chr5	73029819	73029839 +	3
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chr5	71813969	71813989 +	3
chr5	68384602	68384622 +	3
chr5	84191626	84191646 -	3
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chr9	133146479	133146499 -	3
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chr5	76214812	76214832 -	3
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chr9	131912935	131912955 +	3
chr5	78992697	78992717 +	3
chr5	78596009	78596029 +	3
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chr6	6129975	6129995 +	3
chr6	5968578	5968598 -	3
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chr6	6606973	6606993 -	3
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chr6	1526794	1526814 -	3
chr6	3898482	3898502 -	3
chr6	3442727	3442747 +	3
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chr6	18088033	18088053 +	3
chr6	17679217	17679237 +	3
chr6	17173366	17173386 -	3
chr6	17045623	17045643 +	3
chr6	12585630	12585650 +	3
chr5	165665642	165665662 +	3
chr5	165608410	165608430 -	3
chr5	167672548	167672568 -	3
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chr5	177212055	177212075 -	3
chr5	175711520	175711540 +	3
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chr6	46682442	46682462 +	3
chr6	46682443	46682463 +	3
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chr6	54051272	54051292 -	3
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chr6	54929492	54929512 +	3
chr6	49722108	49722128 +	3
chr6	51305738	51305758 +	3
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chr6	20641225	20641245 +	3
chr6	18864083	18864103 -	3
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chr6	30319665	30319685 +	3
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chr13	26332865	26332885 -	3
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chr13	31259996	31260016 -	3
chr13	32012895	32012915 +	3
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chr13	33282380	33282400 +	3
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chr12	107371490	107371510 +	3
chr12	106685264	106685284 +	3
chr12	105797329	105797349 -	3
chr12	105132037	105132057 +	3
chr12	107801342	107801362 +	3
chr12	97537087	97537107 +	3
chr12	94021577	94021597 +	3
chr12	94021576	94021596 +	3
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chr12	119595728	119595748 -	3
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chr13	79255626	79255646 -	3

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chr13	69362352	69362372 +	3
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chr13	84716527	84716547 +	3
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chr13	62743046	62743066 +	3
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chr13	55849577	55849597 +	3
chr13	57490410	57490430 +	3
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chr13	60116747	60116767 +	3
chr13	58818786	58818806 -	3
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chr11	129146975	129146995 -	3
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chr11	121564372	121564392 -	3
chr11	117855641	117855661 +	3
chr11	123476976	123476996 +	3
chr11	122246577	122246597 -	3
chr11	130877359	130877379 +	3
chr12	5893039	5893059 +	3
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chr11	133688697	133688717 -	3
chr11	133747988	133748008 +	3
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chr11	134648765	134648785 +	3
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chr12	69568812	69568832 -	3
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chr15	27277459	27277479 -	3
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chr16	13210560	13210580 -	3
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chr15	97352277	97352297 +	3

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chr1	178852637	178852657 +	3
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chr1	68891175	68891195 +	3
chr1	69507297	69507317 -	3
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chr1	34141386	34141406 +	3
chr1	36549134	36549154 -	3
chr1	42451132	42451152 +	3
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chr1	37399987	37400007 -	3
chr1	37399986	37400006 -	3
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chr1	114723529	114723549 +	3
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chr1	107096756	107096776 +	3
chr1	107096757	107096777 +	3
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chr1	117304153	117304173 -	3
chr1	115143972	115143992 +	3
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chr1	82277481	82277501 +	3

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chr1	103892113	103892133 -	3
chr1	96168155	96168175 -	3
chr1	98838839	98838859 -	3
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chr11	37119382	37119402 +	3
chr11	40381875	40381895 +	3
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chr2	101705557	101705577 -	3
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chr18	79016841	79016861 -	3
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chr2	37018665	37018685 +	3
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chr2	16052321	16052341 +	3
chr2	15934597	15934617 +	3
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chr2	14493557	14493577 -	3
chr2	13235875	13235895 -	3
chr2	5217262	5217282 +	3
chr2	4823155	4823175 -	3
chr2	9255258	9255278 +	3
chr2	8654502	8654522 -	3
chr2	7731656	7731676 +	3
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chr2	178299432	178299452 -	3
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chr2	215402885	215402905 -	3
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chr3	51977179	51977199 +	3
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chrX	130871224	130871244 +	3
chr7	34137041	34137061 +	3
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chr14	71303369	71303389 +	4
chr14	74171604	74171624 +	4
chr14	70721536	70721556 +	4
chr6	68797350	68797370 +	4
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chr14	72116046	72116066 +	4
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chr6	26923601	26923621 +	4
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chr6	25852171	25852191 +	4
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chr14	61197384	61197404 +	4
chr15	31455207	31455227 -	4
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chr6	79167945	79167965 -	4
chr6	78893468	78893488 +	4
chr6	78753295	78753315 -	4
chr6	78426648	78426668 +	4
chr6	74847830	74847850 +	4
chr6	74771862	74771882 -	4
chr6	71197320	71197340 +	4
chr14	69256054	69256074 -	4
chr6	62978673	62978693 +	4
chr6	23664905	23664925 +	4
chr6	69332362	69332382 -	4
chr14	67305796	67305816 -	4
chr15	31423282	31423302 -	4
chr14	64478233	64478253 +	4
chr6	72751794	72751814 -	4
chr6	72663464	72663484 -	4
chr6	72663463	72663483 -	4
chr14	65846669	65846689 -	4
chr6	72373647	72373667 -	4
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chr6	46628716	46628736 +	4
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chr14	99460121	99460141 +	4
chr6	34855875	34855895 +	4
chr14	99778809	99778829 -	4
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chr14	95219053	95219073 +	4
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chr6	48247557	48247577 -	4
chr6	47445869	47445889 +	4
chr15	24098559	24098579 +	4
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chr14	104186669	104186689 -	4
chr14	104421889	104421909 +	4
chr14	105294486	105294506 -	4
chr6	42342146	42342166 +	4

chr6	42235475	42235495 -	4
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chr14	106746997	106747017 +	4
chr6	41392463	41392483 +	4
chr6	40940598	40940618 +	4
chr6	40309711	40309731 -	4
chr6	38878456	38878476 +	4
chr6	35769373	35769393 -	4
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chr6	45319162	45319182 -	4
chr14	100946080	100946100 -	4
chr6	44877078	44877098 -	4
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chr6	43966697	43966717 +	4
chr6	37221571	37221591 -	4
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chr6	56412248	56412268 -	4
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chr6	55919302	55919322 -	4
chr6	55912457	55912477 -	4
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chr6	57041930	57041950 +	4
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chr6	38710546	38710566 +	4
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chr6	27995766	27995786 -	4
chr6	61103019	61103039 +	4
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chr6	29905987	29906007 -	4
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chr14	87553738	87553758 -	4
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chr6	54014032	54014052 +	4
chr14	90192350	90192370 -	4

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chr6	120896531	120896551 -	4
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chr13	107518865	107518885 +	4
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chr13	104096503	104096523 -	4
chr6	127186249	127186269 +	4
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chr13	104886768	104886788 -	4
chr6	124872830	124872850 -	4
chr6	124255329	124255349 -	4
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chr14	22332934	22332954 -	4
chr14	22737269	22737289 -	4
chr14	22737270	22737290 -	4
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chr14	21726489	21726509 +	4
chr13	113573337	113573357 -	4
chr13	114184306	114184326 +	4
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chr6	119207116	119207136 -	4
chr6	119080088	119080108 +	4
chr6	118740212	118740232 -	4
chr6	117735193	117735213 +	4
chr14	20053492	20053512 +	4
chr14	20126312	20126332 -	4
chr6	116728141	116728161 +	4
chr6	116212716	116212736 -	4
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chr13	90762422	90762442 +	4
chr6	140537869	140537889 +	4
chr13	90928554	90928574 -	4
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chr13	91330272	91330292 +	4
chr6	140122097	140122117 -	4
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chr13	92322475	92322495 +	4

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chr6	131128383	131128403 -	4
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chr13	98880295	98880315 -	4
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chr13	99673879	99673899 +	4
chr6	132007480	132007500 +	4
chr14	43422576	43422596 +	4
chr6	89562461	89562481 -	4
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chr14	46532392	46532412 -	4
chr14	43146499	43146519 +	4
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chr14	40646785	40646805 -	4
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chr14	51441396	51441416 -	4
chr14	51604099	51604119 -	4
chr14	52172924	52172944 -	4
chr14	53327723	53327743 -	4
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chr6	83554808	83554828 -	4
chr6	87403716	87403736 -	4
chr6	85613509	85613529 -	4
chr6	85437097	85437117 +	4
chr14	49285039	49285059 +	4
chr14	50344411	50344431 +	4
chr14	30450813	30450833 +	4
chr14	30454140	30454160 +	4
chr6	105338337	105338357 -	4
chr6	104715531	104715551 +	4
chr6	104620688	104620708 +	4
chr14	32737741	32737761 +	4

chr6	102471317	102471337 +	4
chr6	102471316	102471336 +	4
chr14	30279637	30279657 +	4
chr6	106381276	106381296 -	4
chr6	101497383	101497403 +	4
chr6	111085613	111085633 +	4
chr6	110894728	110894748 +	4
chr6	109725040	109725060 +	4
chr6	108661652	108661672 +	4
chr14	27776474	27776494 +	4
chr14	27776475	27776495 +	4
chr14	28202691	28202711 +	4
chr14	28453313	28453333 -	4
chr14	29559439	29559459 +	4
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chr6	97727391	97727411 +	4
chr6	97565906	97565926 +	4
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chr6	97436928	97436948 +	4
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chr14	39036638	39036658 -	4
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chr14	36005346	36005366 +	4
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chr6	98902820	98902840 +	4
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chr14	36780316	36780336 -	4
chr15	31819027	31819047 +	4
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chr16	16247954	16247974 +	4
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chr5	123198192	123198212 -	4
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chr5	124806709	124806729 -	4
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chr16	13876614	13876634 +	4
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chr16	14361396	14361416 -	4
chr16	14587868	14587888 -	4
chr16	14587907	14587927 -	4
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chr5	118348403	118348423 -	4
chr16	25861420	25861440 +	4
chr16	26522713	26522733 -	4
chr5	121835070	121835090 -	4
chr16	19821267	19821287 -	4
chr16	19978362	19978382 +	4
chr5	121835069	121835089 -	4
chr5	121796699	121796719 +	4
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chr5	121175324	121175344 +	4
chr16	20916158	20916178 -	4
chr5	125342046	125342066 -	4
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chr5	137101761	137101781 +	4
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chr5	136584918	136584938 +	4
chr5	134324218	134324238 -	4
chr5	134023814	134023834 +	4
chr5	131867964	131867984 +	4
chr5	137044128	137044148 +	4
chr5	130409454	130409474 +	4
chr5	142775199	142775219 +	4
chr5	142273400	142273420 -	4
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chr5	140548709	140548729 +	4
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chr5	138931758	138931778 -	4
chr5	127166515	127166535 -	4
chr5	126987607	126987627 +	4
chr16	10089508	10089528 +	4
chr16	11353296	11353316 +	4
chr5	125680611	125680631 +	4
chr5	127874952	127874972 -	4
chr5	127932505	127932525 +	4
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chr16	6245212	6245232 +	4
chr16	6352627	6352647 -	4
chr16	7470364	7470384 +	4
chr5	128195121	128195141 +	4
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chr16	63578316	63578336 +	4
chr16	63958620	63958640 -	4
chr5	97402407	97402427 +	4
chr16	64360355	64360375 -	4

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chr16	65040942	65040962 -	4
chr16	63007863	63007883 +	4
chr5	102246163	102246183 +	4
chr16	60113847	60113867 -	4
chr5	101192015	101192035 +	4
chr5	101004412	101004432 -	4
chr16	71739786	71739806 +	4
chr5	92412967	92412987 -	4
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chr5	91376600	91376620 +	4
chr5	90482099	90482119 +	4
chr5	92964359	92964379 -	4
chr5	96236551	96236571 +	4
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chr16	67058725	67058745 +	4
chr5	94521821	94521841 +	4
chr16	68917500	68917520 +	4
chr5	93915364	93915384 -	4
chr5	93480513	93480533 +	4
chr16	59691786	59691806 +	4
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chr16	49881445	49881465 +	4
chr16	50003061	50003081 +	4
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chr5	115496334	115496354 -	4
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chr16	56643890	56643910 -	4
chr16	56779065	56779085 -	4
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chr5	102587044	102587064 +	4
chr16	59163718	59163738 +	4
chr16	54353861	54353881 -	4
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chr16	51106686	51106706 +	4

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chr16	51300834	51300854 -	4
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chr15	55780159	55780179 +	4
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chr15	60491334	60491354 -	4
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chr5	170701089	170701109 +	4
chr5	170495025	170495045 -	4
chr5	170380182	170380202 +	4
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chr5	169483232	169483252 -	4
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chr5	175083306	175083326 -	4
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chr15	40747755	40747775 +	4
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chr15	41235564	41235584 +	4
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chr5	151817182	151817202 -	4
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chr15	70600283	70600303 -	4
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chr5	162962496	162962516 +	4
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chr5	164367127	164367147 -	4
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chr5	161793455	161793475 +	4
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chr13	86049361	86049381 +	4

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chr7	85509593	85509613 -	4
chr12	92630939	92630959 +	4
chr12	92764079	92764099 +	4

chr12	92989887	92989907 +	4
chr12	93584667	93584687 +	4
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chr7	39686604	39686624 -	4
chr7	37889488	37889508 -	4
chr7	37590223	37590243 +	4
chr7	37057538	37057558 -	4
chr7	46235350	46235370 -	4
chr7	45903657	45903677 +	4
chr7	45093413	45093433 +	4
chr7	44503458	44503478 +	4
chr13	19268009	19268029 +	4
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chr7	42700779	42700799 -	4
chr7	42395723	42395743 +	4
chr7	41922978	41922998 +	4
chr13	21048226	21048246 +	4
chr7	41845752	41845772 -	4
chr7	36114383	36114403 +	4
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chr7	32527544	32527564 +	4
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chr7	31906978	31906998 +	4
chr7	30919923	30919943 +	4
chr7	30919922	30919942 +	4
chr7	32649618	32649638 +	4
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chr7	33191387	33191407 +	4
chr7	46913090	46913110 +	4
chr7	47220842	47220862 +	4
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chr12	120494751	120494771 +	4
chr7	54584196	54584216 +	4
chr7	53989531	53989551 -	4
chr7	53989530	53989550 -	4
chr12	122788868	122788888 +	4
chr12	122969887	122969907 -	4
chr7	53697524	53697544 -	4
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chr12	125004004	125004024 -	4
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chr12	117241233	117241253 +	4
chr12	117241624	117241644 -	4
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chr12	118307471	118307491 +	4
chr12	118693700	118693720 -	4
chr7	55319964	55319984 +	4
chr7	52969748	52969768 +	4
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chr7	49402628	49402648 -	4
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chr12	131479270	131479290 -	4
chr7	49134687	49134707 +	4
chr12	132471351	132471371 +	4
chr7	48180979	48180999 +	4
chr7	52705751	52705771 +	4
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chr7	50451345	50451365 +	4
chr7	50151860	50151880 -	4
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chr5	89992362	89992382 +	4
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chr3	132220576	132220596 +	4
chr3	127925022	127925042 +	4
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chr2	151157908	151157928 -	4
chr2	148807144	148807164 -	4
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chr3	135353447	135353467 +	4
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chr3	134133414	134133434 -	4
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chr2	134682667	134682687 -	4
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chr3	124235095	124235115 -	4
chr3	127263149	127263169 -	4
chr3	125978147	125978167 -	4
chr3	125552083	125552103 -	4
chr3	125064845	125064865 -	4
chr3	124997139	124997159 -	4
chr3	124997138	124997158 -	4
chr2	156821946	156821966 -	4
chr3	124476164	124476184 +	4
chr3	136037344	136037364 +	4
chr3	136051946	136051966 -	4
chr3	146413511	146413531 -	4
chr2	140673131	140673151 +	4
chr3	145135811	145135831 -	4
chr2	141073519	141073539 -	4
chr3	144656612	144656632 -	4
chr3	146795711	146795731 +	4
chr3	150167220	150167240 -	4
chr3	148748615	148748635 +	4
chr2	137188168	137188188 -	4
chr3	147036717	147036737 +	4
chr3	144382032	144382052 -	4
chr2	142111080	142111100 +	4
chr2	145923675	145923695 +	4
chr3	138899340	138899360 -	4
chr3	138403529	138403549 +	4
chr3	137998039	137998059 -	4
chr2	147048685	147048705 +	4
chr3	137741578	137741598 -	4
chr3	137698802	137698822 +	4
chr2	147459771	147459791 -	4
chr3	137041372	137041392 +	4
chr2	147883047	147883067 -	4
chr2	142427733	142427753 -	4
chr3	143314242	143314262 -	4
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chr3	142539871	142539891 -	4
chr3	141772674	141772694 +	4
chr2	145184749	145184769 +	4
chr2	145573481	145573501 +	4
chr2	145687126	145687146 -	4
chr2	145687127	145687147 -	4
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chr2	179933883	179933903 -	4
chr3	103145266	103145286 -	4
chr2	180042174	180042194 -	4

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chr2	181344991	181345011 -	4
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chr3	106561753	106561773 -	4
chr2	176808402	176808422 -	4
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chr3	105544352	105544372 -	4
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chr2	189175486	189175506 -	4
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chr3	89742020	89742040 +	4
chr2	190060688	190060708 +	4
chr2	185834249	185834269 +	4
chr2	182435844	182435864 -	4
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chr2	183673572	183673592 +	4
chr3	97652606	97652626 -	4
chr2	184472027	184472047 +	4
chr2	184617613	184617633 -	4
chr2	185681262	185681282 +	4
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chr3	113886682	113886702 +	4
chr3	115357611	115357631 -	4
chr3	115206432	115206452 +	4
chr2	165647552	165647572 +	4
chr2	166140294	166140314 -	4
chr3	114205827	114205847 -	4
chr2	166179957	166179977 -	4
chr3	113972058	113972078 -	4
chr2	175643406	175643426 +	4
chr2	167281677	167281697 +	4
chr2	167283785	167283805 +	4
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chr3	115758500	115758520 -	4
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chr2	161259585	161259605 -	4
chr3	118297188	118297208 +	4
chr3	118017509	118017529 +	4
chr2	161776224	161776244 +	4
chr2	162680226	162680246 +	4
chr3	116989424	116989444 -	4
chr3	116863919	116863939 +	4
chr3	116857261	116857281 -	4
chr3	116794536	116794556 +	4

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chr2	163285098	163285118 -	4
chr3	116167655	116167675 +	4
chr3	116167654	116167674 +	4
chr2	171890342	171890362 +	4
chr2	172132408	172132428 +	4
chr2	172477298	172477318 -	4
chr3	109441310	109441330 +	4
chr2	172977219	172977239 -	4
chr2	174630912	174630932 -	4
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chr2	174928449	174928469 +	4
chr3	107404571	107404591 -	4
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chr2	171874743	171874763 +	4
chr3	111459722	111459742 +	4
chr2	169374227	169374247 +	4
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chr2	169958893	169958913 -	4
chr2	169958895	169958915 -	4
chr3	110849452	110849472 +	4
chr2	170039436	170039456 +	4
chr3	110659555	110659575 +	4
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chr3	187122706	187122726 +	4
chr3	188504888	188504908 +	4
chr3	187122707	187122727 +	4
chr3	186655680	186655700 -	4
chr3	188922040	188922060 -	4
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chr3	190091297	190091317 +	4
chr2	85704748	85704768 -	4
chr2	85900107	85900127 +	4
chr3	189282593	189282613 -	4
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chr3	189140782	189140802 -	4
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chr2	92003297	92003317 +	4
chr2	98814239	98814259 -	4
chr3	181276235	181276255 +	4
chr3	180302014	180302034 -	4
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chr3	180119068	180119088 -	4
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chr2	101882222	101882242 -	4

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chr2	97881099	97881119 -	4
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chr3	184430226	184430246 -	4
chr2	95937736	95937756 +	4
chr2	95993152	95993172 +	4
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chr3	182768289	182768309 -	4
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chr2	68910723	68910743 +	4
chr2	68938434	68938454 -	4
chr2	69646399	69646419 +	4
chr4	11330468	11330488 +	4
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chr2	71216112	71216132 -	4
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chr4	10597066	10597086 -	4
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chr2	65524631	65524651 -	4
chr2	65713699	65713719 -	4
chr4	14373919	14373939 -	4
chr2	66961303	66961323 +	4
chr4	13091078	13091098 +	4
chr4	8664472	8664492 -	4
chr4	7200627	7200647 +	4
chr4	2576037	2576057 +	4
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chr3	162745454	162745474 -	4
chr3	162214925	162214945 +	4
chr3	161929442	161929462 +	4
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chr2	121025475	121025495 +	4
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chr2	122476260	122476280 -	4
chr3	157733064	157733084 -	4
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chr3	152965252	152965272 -	4
chr2	132617849	132617869 +	4
chr3	152261346	152261366 -	4
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chr2	127112432	127112452 +	4
chr2	128816575	128816595 -	4
chr2	128816576	128816596 -	4
chr2	128911639	128911659 +	4
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chr3	154390637	154390657 +	4
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chr2	104794669	104794689 -	4
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chr3	168511749	168511769 +	4
chr3	165374927	165374947 -	4
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chr3	165262788	165262808 +	4
chr3	165174095	165174115 -	4
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chr2	114524414	114524434 +	4
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chr2	114921823	114921843 +	4
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chr20	34534154	34534174 +	4
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chr21	44961681	44961701 -	4
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chr21	40892029	40892049 +	4
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chr21	20765659	20765679 +	4
chr21	21249900	21249920 +	4
chr22	12203080	12203100 -	4
chr22	11789136	11789156 +	4
chr21	39362110	39362130 -	4
chr21	39239776	39239796 -	4
chr21	33944556	33944576 -	4
chr21	33810795	33810815 -	4
chr21	30146430	30146450 -	4
chr21	30160909	30160929 -	4
chr21	30651243	30651263 -	4
chr21	30930217	30930237 -	4
chr21	33114422	33114442 +	4
chr21	35679117	35679137 +	4
chr21	26299074	26299094 -	4
chr21	26363614	26363634 -	4
chr21	26906729	26906749 +	4
chr21	37870507	37870527 -	4
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chr21	36962435	36962455 -	4
chr21	19237561	19237581 -	4
chr20	55370598	55370618 -	4
chr22	35886361	35886381 +	4
chr22	35319928	35319948 -	4
chr22	35319927	35319947 -	4
chr20	62173217	62173237 -	4
chr20	62173218	62173238 -	4
chr20	62371137	62371157 +	4
chr22	34781543	34781563 +	4
chr21	18976007	18976027 +	4
chr22	32316410	32316430 +	4
chr21	9299753	9299773 +	4
chr22	30678455	30678475 -	4
chr20	60791075	60791095 +	4
chr20	60473207	60473227 -	4
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chr21	10046951	10046971 -	4
chr22	30626033	30626053 +	4
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chr21	18337765	18337785 -	4
chr21	18456719	18456739 +	4
chr22	21996436	21996456 -	4
chr22	21858549	21858569 -	4

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chr22	29627005	29627025 +	4
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chr22	25584568	25584588 +	4
chr22	25288023	25288043 +	4
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chr20	10353017	10353037 +	4
chr3	30966840	30966860 +	4
chr20	10802944	10802964 +	4
chr3	29626282	29626302 +	4
chr3	29373806	29373826 +	4
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chr3	34576917	34576937 +	4
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chr3	32622392	32622412 +	4
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chr5	18488007	18488027 +	4
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chr4	70116723	70116743 +	4
chr2	8014427	8014447 -	4
chr4	73335851	73335871 +	4
chr2	2481312	2481332 +	4
chr2	2519488	2519508 +	4
chr4	73221079	73221099 -	4
chr2	2802753	2802773 +	4

chr2	2953235	2953255 +	4
chr2	3899903	3899923 -	4
chr2	3899904	3899924 -	4
chr2	4181930	4181950 +	4
chr2	4365622	4365642 -	4
chr2	14237518	14237538 -	4
chr4	63759895	63759915 -	4
chr4	62893295	62893315 -	4
chr4	62893294	62893314 -	4
chr4	62523668	62523688 -	4
chr2	13287439	13287459 -	4
chr4	67016002	67016022 -	4
chr4	66615695	66615715 -	4
chr2	12547777	12547797 -	4
chr2	33645254	33645274 -	4
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chr4	25222125	25222145 -	4
chr2	54414066	54414086 -	4
chr4	24481095	24481115 -	4
chr4	24051760	24051780 +	4
chr2	56300984	56301004 +	4
chr2	56302362	56302382 +	4
chr2	56536797	56536817 +	4
chr4	22969063	22969083 -	4
chr4	25332665	25332685 -	4
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chr2	51117763	51117783 -	4
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chr2	51546406	51546426 +	4
chr2	51988374	51988394 +	4
chr4	27225046	27225066 -	4
chr4	25657748	25657768 +	4
chr4	25657747	25657767 +	4
chr4	25657746	25657766 +	4
chr2	61937538	61937558 -	4
chr4	17129514	17129534 -	4
chr4	16891113	16891133 -	4
chr4	16872688	16872708 -	4
chr2	62960984	62961004 -	4
chr4	16049374	16049394 +	4
chr4	16049373	16049393 +	4
chr4	16049372	16049392 +	4
chr4	15692058	15692078 -	4
chr4	15692057	15692077 -	4
chr2	57974124	57974144 +	4
chr2	58088709	58088729 -	4
chr4	19184228	19184248 +	4
chr4	19076620	19076640 -	4
chr4	18746393	18746413 +	4
chr4	18591219	18591239 -	4
chr4	18455437	18455457 -	4

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chr4	18080028	18080048 +	4
chr2	50480846	50480866 -	4
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chr4	39187028	39187048 +	4
chr4	39173739	39173759 +	4
chr2	39688676	39688696 -	4
chr2	39752733	39752753 +	4
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chr4	38472492	38472512 -	4
chr4	29910257	29910277 -	4
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chr4	37337067	37337087 -	4
chr2	41682375	41682395 +	4
chr2	41718411	41718431 +	4
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chr4	32945185	32945205 +	4
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chr4	32609788	32609808 -	4
chr4	32413647	32413667 +	4
chr4	31544824	31544844 -	4
chr2	48307472	48307492 +	4
chr4	31243694	31243714 +	4
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chr2	48860467	48860487 +	4
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chr2	43672933	43672953 -	4
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chr2	45119094	45119114 +	4
chr2	45518376	45518396 +	4
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chr4	33548019	33548039 +	4
chr4	33478824	33478844 +	4
chr2	1517139	1517159 -	4

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chr4	132032845	132032865 +	4
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chr4	131905423	131905443 -	4
chr18	71192157	71192177 -	4
chr4	130639754	130639774 +	4
chr18	78666232	78666252 -	4
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chr4	133639869	133639889 +	4
chr18	74521911	74521931 +	4
chr18	71909102	71909122 +	4
chr4	136783044	136783064 +	4
chr4	136762415	136762435 +	4
chr4	136246266	136246286 +	4
chr4	136017834	136017854 -	4
chr4	135298992	135299012 -	4
chr18	74354487	74354507 -	4
chr4	129150627	129150647 -	4
chr4	129150626	129150646 -	4
chr4	117100537	117100557 -	4
chr4	115626826	115626846 +	4
chr4	115211410	115211430 +	4
chr4	115211409	115211429 +	4
chr4	114404487	114404507 -	4
chr4	113955649	113955669 -	4
chr4	112653154	112653174 +	4
chr4	111199935	111199955 -	4
chr4	126798504	126798524 -	4
chr4	125241508	125241528 +	4
chr18	80158354	80158374 -	4
chr4	123204326	123204346 +	4
chr4	122767245	122767265 +	4
chr4	122416428	122416448 +	4
chr4	120958790	120958810 +	4
chr4	120501084	120501104 +	4
chr18	71192156	71192176 -	4
chr4	146514934	146514954 -	4
chr4	147539021	147539041 +	4
chr4	147267004	147267024 -	4
chr4	146675571	146675591 +	4
chr18	62043001	62043021 -	4
chr4	145490885	145490905 -	4
chr4	144886888	144886908 +	4
chr18	63884047	63884067 +	4
chr18	64163193	64163213 -	4
chr4	148752665	148752685 -	4
chr4	151736061	151736081 -	4
chr18	55010784	55010804 +	4
chr4	151736060	151736080 -	4
chr18	55235774	55235794 -	4

chr4	151501079	151501099 +	4
chr18	55546496	55546516 +	4
chr18	55937682	55937702 -	4
chr4	149173569	149173589 +	4
chr18	57468939	57468959 +	4
chr18	58366267	58366287 +	4
chr18	64163194	64163214 -	4
chr4	139645633	139645653 +	4
chr18	68989465	68989485 -	4
chr4	139245137	139245157 -	4
chr4	139245113	139245133 +	4
chr18	70555583	70555603 -	4
chr4	137938412	137938432 +	4
chr18	64585854	64585874 +	4
chr18	65130363	65130383 -	4
chr4	143571561	143571581 -	4
chr4	141985153	141985173 +	4
chr18	67076757	67076777 +	4
chr4	140621573	140621593 -	4
chr18	68398567	68398587 +	4
chr4	88964133	88964153 -	4
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chr19	39340806	39340826 +	4
chr4	89048010	89048030 -	4
chr19	40893462	40893482 -	4
chr19	31043644	31043664 -	4
chr19	41111438	41111458 +	4
chr4	87620651	87620671 -	4
chr19	36947951	36947971 -	4
chr19	36236107	36236127 +	4
chr4	93440666	93440686 +	4
chr19	32242613	32242633 +	4
chr4	92946614	92946634 +	4
chr4	92782996	92783016 -	4
chr4	91805502	91805522 +	4
chr19	34587541	34587561 -	4
chr4	91805501	91805521 +	4
chr19	35217265	35217285 +	4
chr4	81002868	81002888 +	4
chr4	81002867	81002887 +	4
chr4	80882172	80882192 +	4
chr4	80882171	80882191 +	4
chr4	79770333	79770353 +	4
chr4	79563494	79563514 +	4
chr4	77902092	77902112 +	4
chr4	77560658	77560678 -	4
chr4	77215379	77215399 -	4
chr4	75161882	75161902 -	4
chr4	74622644	74622664 +	4
chr2	1049738	1049758 +	4
chr4	81093696	81093716 -	4

chr4	81350709	81350729 +	4
chr19	48406722	48406742 +	4
chr19	52349106	52349126 +	4
chr4	84060988	84061008 +	4
chr19	55608033	55608053 +	4
chr19	55909259	55909279 -	4
chr19	56624341	56624361 -	4
chr19	31131277	31131297 -	4
chr4	109956051	109956071 +	4
chr19	5171651	5171671 -	4
chr4	104398011	104398031 +	4
chr4	104258794	104258814 -	4
chr4	103620913	103620933 -	4
chr19	2007955	2007975 +	4
chr4	102159056	102159076 -	4
chr19	6165563	6165583 -	4
chr4	102095113	102095133 +	4
chr4	101757362	101757382 +	4
chr4	104403711	104403731 +	4
chr4	109318172	109318192 -	4
chr4	109090638	109090658 -	4
chr4	109090637	109090657 -	4
chr4	108110803	108110823 -	4
chr4	107982768	107982788 +	4
chr4	105680523	105680543 -	4
chr4	105177653	105177673 -	4
chr4	104983757	104983777 +	4
chr4	100881350	100881370 +	4
chr19	10212889	10212909 +	4
chr19	11006734	11006754 +	4
chr19	22547473	22547493 +	4
chr4	95701384	95701404 -	4
chr4	95609574	95609594 +	4
chr4	95336963	95336983 -	4
chr4	94743815	94743835 +	4
chr19	28559551	28559571 +	4
chr4	94646905	94646925 +	4
chr4	94550498	94550518 -	4
chr19	30178341	30178361 +	4
chr4	96821205	96821225 -	4
chr4	100602515	100602535 -	4
chr19	20879613	20879633 -	4
chr19	15034901	15034921 +	4
chr19	20319265	20319285 +	4
chrX	128689099	128689119 -	4
chrX	128636488	128636508 +	4
chr10	21432936	21432956 +	4
chrX	54007775	54007795 -	4
chr1	81375540	81375560 -	4
chr9	91712436	91712456 -	4
chr1	81584819	81584839 -	4

chr1	179745630	179745650 +	4
chr8	131046180	131046200 +	4
chrX	128689100	128689120 -	4
chrX	128689101	128689121 -	4
chr1	81042191	81042211 -	4
chr1	79915152	79915172 +	4
chr8	129572957	129572977 +	4
chrX	129896804	129896824 +	4
chr10	20638586	20638606 +	4
chr11	4022483	4022503 -	4
chr10	20789214	20789234 -	4
chr10	20855734	20855754 +	4
chr10	20855735	20855755 +	4
chr9	92601137	92601157 -	4
chr9	92498728	92498748 +	4
chr1	193358073	193358093 -	4
chr1	82781855	82781875 +	4
chr1	82895842	82895862 -	4
chr8	133175881	133175901 +	4
chr10	23577040	23577060 +	4
chr10	130498751	130498771 -	4
chr10	129876373	129876393 -	4
chrX	127145216	127145236 +	4
chr1	178958524	178958544 -	4
chr10	130952098	130952118 +	4
chr1	82772233	82772253 +	4
chr10	131279379	131279399 -	4
chr8	131623945	131623965 +	4
chrX	128242809	128242829 -	4
chr8	131930084	131930104 +	4
chr10	132577083	132577103 +	4
chr8	132533417	132533437 +	4
chrX	127438558	127438578 -	4
chrX	127438557	127438577 -	4
chr9	91213715	91213735 +	4
chr10	131439076	131439096 -	4
chrX	127326056	127326076 +	4
chrX	127326054	127326074 +	4
chr9	93992938	93992958 +	4
chr10	17372762	17372782 -	4
chr8	124317406	124317426 -	4
chr9	97468380	97468400 -	4
chr11	8796193	8796213 -	4
chr9	97468378	97468398 -	4
chr11	8669275	8669295 -	4
chr8	129011863	129011883 -	4
chr8	123116011	123116031 +	4
chr11	10827783	10827803 +	4
chr8	123430104	123430124 +	4
chrX	134209553	134209573 -	4
chr10	16716410	16716430 +	4

chr11	9776321	9776341 -	4
chr11	9615632	9615652 +	4
chr1	75014309	75014329 +	4
chr8	125691702	125691722 +	4
chr1	77416509	77416529 -	4
chr10	19187448	19187468 +	4
chr11	5109975	5109995 -	4
chrX	53245636	53245656 -	4
chrX	130987051	130987071 +	4
chrX	130893976	130893996 -	4
chr11	4822594	4822614 +	4
chr11	4804309	4804329 +	4
chr1	180391678	180391698 -	4
chr1	78830219	78830239 +	4
chr1	180354673	180354693 +	4
chr1	78895968	78895988 +	4
chrX	130402435	130402455 -	4
chr9	93992939	93992959 +	4
chr9	95065245	95065265 +	4
chr1	76573804	76573824 +	4
chr9	95132955	95132975 -	4
chr10	18199638	18199658 +	4
chr1	76661818	76661838 -	4
chr1	77112811	77112831 -	4
chr1	77132994	77133014 -	4
chr9	95656637	95656657 +	4
chr10	129261173	129261193 +	4
chr1	178870854	178870874 +	4
chr8	139925371	139925391 -	4
chr9	84347710	84347730 +	4
chr1	88557783	88557803 -	4
chr9	84244360	84244380 -	4
chr10	31121842	31121862 +	4
chr10	120815627	120815647 +	4
chr1	87890081	87890101 -	4
chr8	137468085	137468105 -	4
chr8	137479719	137479739 +	4
chr10	29072562	29072582 +	4
chr10	29537391	29537411 +	4
chr9	85000857	85000877 +	4
chr1	89215856	89215876 +	4
chr8	143895694	143895714 -	4
chr8	144768725	144768745 +	4
chr10	33078312	33078332 +	4
chrX	117739444	117739464 -	4
chr1	174503692	174503712 +	4
chr8	145021429	145021449 +	4
chr1	174459768	174459788 -	4
chr1	90926129	90926149 -	4
chr8	145028009	145028029 +	4
chrX	117541706	117541726 -	4

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chr1	174180336	174180356 -	4
chr10	117706496	117706516 +	4
chr9	81873578	81873598 -	4
chr10	117133298	117133318 -	4
chr10	32885181	32885201 +	4
chrX	118299259	118299279 -	4
chr8	141030325	141030345 +	4
chr10	120308015	120308035 -	4
chr1	174976274	174976294 +	4
chr9	83074255	83074275 +	4
chr10	31875374	31875394 +	4
chr10	32744419	32744439 +	4
chr1	90211225	90211245 +	4
chr10	129172993	129173013 -	4
chr1	84744274	84744294 +	4
chr1	178183900	178183920 +	4
chr10	127192523	127192543 -	4
chr1	177849687	177849707 +	4
chr1	84489206	84489226 -	4
chr1	84536163	84536183 +	4
chr9	88761394	88761414 +	4
chr10	25181466	25181486 +	4
chr8	135469980	135470000 -	4
chrX	124527289	124527309 -	4
chr8	134958920	134958940 +	4
chrX	126175031	126175051 +	4
chr10	24703799	24703819 -	4
chr10	24104038	24104058 -	4
chr1	178812664	178812684 -	4
chr10	24204951	24204971 +	4
chrX	55551017	55551037 +	4
chrX	126742726	126742746 -	4
chr8	134374990	134375010 +	4
chr8	134524671	134524691 +	4
chr10	24349853	24349873 +	4
chr1	83822364	83822384 +	4
chrX	55551018	55551038 +	4
chr9	89503109	89503129 +	4
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chr9	87159044	87159064 +	4
chr1	86135710	86135730 -	4
chr10	26694308	26694328 +	4
chr10	26785946	26785966 +	4
chr10	26918959	26918979 +	4
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chr1	86026131	86026151 +	4
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chr9	87976803	87976823 -	4
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chr10	126121699	126121719 -	4

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chr10	125521056	125521076 -	4
chr8	136327620	136327640 +	4
chr1	85878678	85878698 +	4
chr9	87427600	87427620 -	4
chrX	124295648	124295668 +	4
chr10	26292241	26292261 +	4
chr10	7598567	7598587 -	4
chr1	62182369	62182389 -	4
chrX	145609987	145610007 +	4
chr1	62554028	62554048 -	4
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chr11	28442867	28442887 +	4
chr1	61225963	61225983 +	4
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chr9	111476411	111476431 +	4
chr1	61892304	61892324 -	4
chr1	63049749	63049769 +	4
chr11	24598997	24599017 +	4
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chr11	24265572	24265592 +	4
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chr11	23819004	23819024 +	4
chr10	10247875	10247895 -	4
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chrX	44454719	44454739 +	4
chr8	110563013	110563033 -	4
chr10	8568696	8568716 -	4
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chr9	109133318	109133338 +	4
chr11	25376257	25376277 -	4
chr11	25055578	25055598 +	4
chr9	114496327	114496347 -	4
chr1	192379927	192379947 -	4
chr1	192142127	192142147 -	4
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chr1	192120055	192120075 -	4
chr1	191993345	191993365 +	4
chr9	113908524	113908544 +	4
chr9	114959562	114959582 -	4
chr8	103575423	103575443 +	4
chr8	103195884	103195904 +	4

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chrX	38614785	38614805 +	4
chr1	193108142	193108162 -	4
chr1	191993344	191993364 +	4
chr9	112882409	112882429 +	4
chr11	30001508	30001528 +	4
chrX	146541300	146541320 -	4
chrX	41070436	41070456 -	4
chr1	60304532	60304552 -	4
chr8	106616834	106616854 -	4
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chr11	29196548	29196568 +	4
chr10	5792477	5792497 -	4
chr11	31166843	31166863 -	4
chr9	113879121	113879141 +	4
chr1	58864656	58864676 +	4
chr11	31100315	31100335 -	4
chr10	5036555	5036575 +	4
chr11	30547338	30547358 -	4
chr10	5453731	5453751 -	4
chr11	11301435	11301455 +	4
chr1	72089343	72089363 -	4
chrX	50375028	50375048 -	4
chr1	183741508	183741528 -	4
chr1	183741507	183741527 -	4
chr11	16772730	16772750 +	4
chr8	117292906	117292926 -	4
chr9	102003426	102003446 +	4
chrX	48800871	48800891 -	4
chr8	117784330	117784350 +	4
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chrX	49664789	49664809 +	4
chr8	118018940	118018960 -	4
chr8	118018941	118018961 -	4
chr11	16246336	16246356 -	4
chr11	16246335	16246355 -	4
chr11	12814942	12814962 -	4
chr1	182820261	182820281 +	4
chr10	16260301	16260321 +	4
chr1	73675942	73675962 -	4
chr11	12378225	12378245 -	4
chr11	12378224	12378244 -	4
chr8	122140077	122140097 +	4
chr1	73884080	73884100 -	4
chr10	16483268	16483288 -	4
chr11	11708552	11708572 -	4
chrX	134581370	134581390 -	4
chr9	98969179	98969199 +	4
chr9	98969178	98969198 +	4
chr9	98952137	98952157 +	4
chr1	73214141	73214161 -	4

chr11	13265787	13265807 -	4
chr8	117016331	117016351 -	4
chr1	66455689	66455709 +	4
chrX	45640920	45640940 +	4
chrX	45880607	45880627 +	4
chr9	105997656	105997676 -	4
chr10	13471964	13471984 -	4
chr8	116798255	116798275 -	4
chr1	68409532	68409552 +	4
chr1	185826581	185826601 +	4
chr9	104462623	104462643 -	4
chrX	141702433	141702453 -	4
chr8	113342099	113342119 +	4
chr8	112959303	112959323 +	4
chr9	107046965	107046985 +	4
chr9	106848253	106848273 -	4
chr10	11000295	11000315 -	4
chr8	113026569	113026589 +	4
chrX	44970126	44970146 +	4
chr11	22476271	22476291 -	4
chr9	106796513	106796533 +	4
chr9	106776836	106776856 -	4
chr9	106460008	106460028 +	4
chr11	20894669	20894689 +	4
chrX	139384211	139384231 +	4
chr11	19125583	19125603 +	4
chr8	116054284	116054304 +	4
chr8	116197253	116197273 +	4
chr9	102844832	102844852 -	4
chr1	184691865	184691885 +	4
chr1	184691864	184691884 +	4
chr8	116553664	116553684 -	4
chr8	116750340	116750360 -	4
chrX	138657871	138657891 -	4
chr1	69386780	69386800 -	4
chr1	69456592	69456612 -	4
chr9	103968624	103968644 +	4
chr1	69563074	69563094 +	4
chr9	103735514	103735534 -	4
chr8	115096322	115096342 -	4
chrX	139901041	139901061 +	4
chrX	47759092	47759112 +	4
chr1	69873664	69873684 -	4
chr8	115496468	115496488 +	4
chr9	62514707	62514727 -	4
chr1	158552851	158552871 -	4
chr1	158514548	158514568 -	4
chr9	26360007	26360027 +	4
chrX	79459152	79459172 -	4
chr9	62394446	62394466 +	4
chrX	79479983	79480003 -	4

chrX	79558251	79558271 -	4
chr10	83481491	83481511 +	4
chr1	158118576	158118596 +	4
chrX	79574446	79574466 +	4
chr10	83765960	83765980 +	4
chrX	96766784	96766804 +	4
chr1	158916789	158916809 +	4
chrX	97048355	97048375 -	4
chrX	97042136	97042156 -	4
chr9	26079974	26079994 -	4
chr10	59078347	59078367 -	4
chr10	83851920	83851940 -	4
chrX	96766785	96766805 +	4
chr10	83765961	83765981 +	4
chrX	79574447	79574467 +	4
chrX	95757269	95757289 -	4
chrX	95706483	95706503 -	4
chr1	114908311	114908331 +	4
chr9	27520551	27520571 -	4
chr9	60890706	60890726 -	4
chrX	80830309	80830329 -	4
chr10	61673155	61673175 +	4
chr10	61790918	61790938 -	4
chrX	81072657	81072677 -	4
chr1	115115683	115115703 +	4
chr1	155958871	155958891 -	4
chrX	80734730	80734750 +	4
chr10	61434662	61434682 +	4
chr9	26859946	26859966 +	4
chr10	82771583	82771603 -	4
chr1	114052818	114052838 -	4
chr9	61286991	61287011 +	4
chr9	61166610	61166630 -	4
chr9	27083515	27083535 +	4
chr9	25510197	25510217 +	4
chrX	76970614	76970634 -	4
chr10	88979477	88979497 +	4
chr1	161868693	161868713 +	4
chr9	66364068	66364088 -	4
chr9	66343251	66343271 +	4
chrX	76970613	76970633 -	4
chr9	25326889	25326909 +	4
chr10	56622526	56622546 -	4
chr1	160439049	160439069 -	4
chr9	23354163	23354183 +	4
chrX	98471378	98471398 -	4
chr9	23770944	23770964 +	4
chr9	67015914	67015934 +	4
chrX	101029353	101029373 -	4
chr1	107252629	107252649 -	4
chr10	89640207	89640227 -	4

chrX	99937708	99937728 +	4
chr1	108121089	108121109 +	4
chr10	87733968	87733988 -	4
chr10	57064845	57064865 +	4
chrX	77971435	77971455 +	4
chrX	78214456	78214476 -	4
chrX	97662185	97662205 +	4
chr10	85726342	85726362 +	4
chr9	63630057	63630077 -	4
chrX	97522563	97522583 -	4
chr9	63609105	63609125 +	4
chrX	97467042	97467062 +	4
chr10	58641885	58641905 +	4
chr10	85108898	85108918 -	4
chr1	159129689	159129709 -	4
chrX	78757401	78757421 -	4
chr10	57947286	57947306 -	4
chr10	85995900	85995920 +	4
chrX	98167099	98167119 -	4
chr9	24444451	24444471 +	4
chr10	86485552	86485572 -	4
chr9	24489052	24489072 -	4
chr10	86420244	86420264 +	4
chr1	110005141	110005161 +	4
chrX	93336247	93336267 -	4
chr10	54851530	54851550 -	4
chr9	39332000	39332020 -	4
chr9	33148960	33148980 +	4
chr1	149811545	149811565 -	4
chr10	73018010	73018030 +	4
chr10	72870136	72870156 +	4
chr1	149324057	149324077 -	4
chr10	73750602	73750622 +	4
chr10	74543614	74543634 +	4
chr9	32297436	32297456 -	4
chrX	88842757	88842777 -	4
chr9	39856232	39856252 -	4
chr9	32357345	32357365 +	4
chr1	143668291	143668311 -	4
chrX	88446354	88446374 +	4
chr1	143903825	143903845 -	4
chr10	72591364	72591384 +	4
chr9	33650223	33650243 -	4
chrX	84846429	84846449 -	4
chr10	70244941	70244961 -	4
chr10	70017961	70017981 -	4
chrX	85975622	85975642 +	4
chrX	85975621	85975641 +	4
chr10	69611548	69611568 -	4
chr10	72195973	72195993 -	4
chr1	149028866	149028886 -	4

chr1	148806146	148806166 +	4
chr9	34456803	34456823 +	4
chr10	66865147	66865167 +	4
chr1	148010063	148010083 +	4
chrX	86886628	86886648 +	4
chrX	89000456	89000476 +	4
chr9	42586976	42586996 +	4
chr1	153584928	153584948 +	4
chrX	91589943	91589963 +	4
chr9	29597717	29597737 -	4
chr9	29854742	29854762 -	4
chr10	62584042	62584062 -	4
chr9	30140327	30140347 -	4
chr1	121116464	121116484 -	4
chrX	91088032	91088052 +	4
chrX	90785627	90785647 -	4
chr9	30140328	30140348 -	4
chr1	153143450	153143470 -	4
chr1	153143449	153143469 -	4
chrX	92046788	92046808 -	4
chr1	117306777	117306797 +	4
chrX	81393492	81393512 -	4
chrX	93050733	93050753 +	4
chrX	81393493	81393513 -	4
chr9	28930021	28930041 -	4
chr1	154805845	154805865 +	4
chr10	80684489	80684509 -	4
chr10	80570087	80570107 -	4
chr9	29043722	29043742 -	4
chrX	81467703	81467723 -	4
chr10	80106685	80106705 +	4
chr9	29158919	29158939 +	4
chrX	81467704	81467724 -	4
chr10	80063740	80063760 -	4
chrX	92547169	92547189 +	4
chrX	92417085	92417105 -	4
chr10	78505404	78505424 +	4
chr1	118171069	118171089 +	4
chr1	118171070	118171090 +	4
chr1	119749139	119749159 -	4
chr10	76644244	76644264 +	4
chr10	76472662	76472682 +	4
chr1	120194724	120194744 +	4
chrX	83166765	83166785 +	4
chr1	120703587	120703607 -	4
chr10	64409942	64409962 -	4
chr10	64409943	64409963 -	4
chrX	83324793	83324813 -	4
chr9	32176599	32176619 -	4
chr9	40012031	40012051 +	4
chrX	82077419	82077439 -	4

chr10	78505403	78505423 +	4
chr10	78449374	78449394 +	4
chr10	62858943	62858963 -	4
chr10	62906698	62906718 -	4
chr9	30262569	30262589 -	4
chrX	90582642	90582662 -	4
chrX	90582641	90582661 -	4
chrX	82300834	82300854 +	4
chrX	82373143	82373163 -	4
chr9	30663417	30663437 -	4
chr10	63413752	63413772 +	4
chr9	41452565	41452585 -	4
chr10	77182224	77182244 +	4
chrX	82648610	82648630 +	4
chr9	41431747	41431767 +	4
chr1	119331624	119331644 -	4
chr10	76746605	76746625 +	4
chrX	101324063	101324083 -	4
chr9	8091328	8091348 +	4
chr10	109173756	109173776 -	4
chr9	9145334	9145354 -	4
chr9	9145335	9145355 -	4
chr10	43438617	43438637 +	4
chr1	170253577	170253597 +	4
chr10	107499201	107499221 -	4
chr9	76966714	76966734 +	4
chr1	97914009	97914029 -	4
chr10	109588465	109588485 +	4
chr10	109588466	109588486 +	4
chr1	171435113	171435133 -	4
chrX	113036848	113036868 -	4
chr1	96950526	96950546 +	4
chr1	96950527	96950547 +	4
chr9	7670659	7670679 -	4
chr1	97097562	97097582 -	4
chr10	42540734	42540754 -	4
chr9	7917472	7917492 +	4
chr10	109765746	109765766 -	4
chr10	106940996	106941016 -	4
chr10	106940994	106941014 -	4
chr9	76055719	76055739 +	4
chr10	105969019	105969039 +	4
chr10	105924178	105924198 +	4
chr9	11151017	11151037 +	4
chrX	110866041	110866061 +	4
chrX	110795023	110795043 -	4
chrX	110737571	110737591 -	4
chr9	76055688	76055708 +	4
chr10	45239981	45240001 +	4
chr10	45239982	45240002 +	4
chr10	105639982	105640002 -	4

chrX	111419354	111419374 -	4
chr10	44801789	44801809 -	4
chr1	98041068	98041088 -	4
chr10	106363416	106363436 +	4
chr1	98258025	98258045 -	4
chr9	10265912	10265932 -	4
chr1	169760939	169760959 +	4
chr9	10481615	10481635 +	4
chr10	44688434	44688454 -	4
chr10	44725343	44725363 -	4
chr1	168802721	168802741 -	4
chrX	115656093	115656113 +	4
chr10	35283051	35283071 +	4
chr10	35684667	35684687 +	4
chr10	115383303	115383323 -	4
chr10	115210178	115210198 +	4
chr1	92670633	92670653 +	4
chrX	116622242	116622262 -	4
chr10	34121656	34121676 +	4
chr1	91962726	91962746 +	4
chr9	81133682	81133702 -	4
chr9	81024909	81024929 -	4
chr9	2072335	2072355 -	4
chr9	80861103	80861123 -	4
chr9	80614331	80614351 -	4
chr9	4421628	4421648 -	4
chr10	112759243	112759263 -	4
chr10	37868057	37868077 -	4
chr1	95189954	95189974 +	4
chr10	35965734	35965754 +	4
chrX	114669791	114669811 +	4
chrX	115214658	115214678 +	4
chr10	36174060	36174080 -	4
chr9	3942111	3942131 +	4
chrX	114972807	114972827 -	4
chr10	36372393	36372413 -	4
chr1	93876575	93876595 -	4
chr10	105043134	105043154 -	4
chrX	101878450	101878470 -	4
chr1	104874361	104874381 -	4
chr1	104892119	104892139 +	4
chr9	17866149	17866169 +	4
chr9	17982171	17982191 -	4
chr9	70036536	70036556 +	4
chr1	166138805	166138825 -	4
chr1	105038968	105038988 +	4
chr9	18232659	18232679 -	4
chr1	105038969	105038989 +	4
chrX	103617310	103617330 +	4
chrX	73754278	73754298 -	4
chr9	18299457	18299477 -	4

chr10	93763153	93763173 -	4
chr10	95247347	95247367 +	4
chr10	52107821	52107841 -	4
chr1	103807319	103807339 +	4
chrX	104863662	104863682 +	4
chrX	104863661	104863681 +	4
chrX	104623144	104623164 +	4
chr9	70701785	70701805 +	4
chr1	104463660	104463680 -	4
chrX	74591808	74591828 -	4
chrX	102951167	102951187 +	4
chr10	91354545	91354565 -	4
chr1	106836950	106836970 -	4
chr1	107084902	107084922 -	4
chr9	20813290	20813310 +	4
chrX	103192535	103192555 -	4
chr9	69431788	69431808 +	4
chrX	74325654	74325674 +	4
chr10	93421580	93421600 +	4
chr10	93209379	93209399 -	4
chrX	74225925	74225945 +	4
chrX	103363273	103363293 -	4
chr9	19889473	19889493 -	4
chr9	73560611	73560631 +	4
chrX	109017040	109017060 -	4
chr10	47927882	47927902 -	4
chr10	47927883	47927903 -	4
chr9	13154678	13154698 +	4
chr1	167934165	167934185 +	4
chr1	101401961	101401981 +	4
chrX	108151669	108151689 -	4
chr10	101519636	101519656 -	4
chr9	14020381	14020401 -	4
chrX	70384231	70384251 +	4
chr1	167934166	167934186 +	4
chr1	167950729	167950749 -	4
chr9	75068774	75068794 -	4
chr10	46456697	46456717 +	4
chr10	46456698	46456718 +	4
chr9	74733858	74733878 -	4
chr9	11724496	11724516 -	4
chr10	47012022	47012042 +	4
chr10	103679767	103679787 -	4
chr9	12386625	12386645 +	4
chr1	100480716	100480736 +	4
chr10	103116448	103116468 -	4
chr9	71205866	71205886 +	4
chr10	51690364	51690384 +	4
chr1	103058447	103058467 -	4
chr1	103304239	103304259 +	4
chr10	96466774	96466794 +	4

chrX	72381703	72381723 -	4
chr9	16763755	16763775 -	4
chr1	101995652	101995672 +	4
chr1	101995653	101995673 +	4
chr9	72430222	72430242 +	4
chr10	99778911	99778931 -	4
chrX	70836695	70836715 -	4
chr9	72122392	72122412 +	4
chr9	15502166	15502186 -	4
chr10	50256600	50256620 +	4
chr9	72052873	72052893 +	4
chrX	105864174	105864194 -	4
chrX	134225735	134225755 -	4
chr1	33480137	33480157 +	4
chr1	32883964	32883984 -	4
chr1	33476797	33476817 +	4
chrY	13511998	13512018 +	4
chr1	33622194	33622214 +	4
chrY	13511997	13512017 +	4
chr1	32325705	32325725 -	4
chr8	81282054	81282074 +	4
chrY	15401804	15401824 +	4
chr1	31266943	31266963 +	4
chrY	14837163	14837183 +	4
chr8	82188197	82188217 +	4
chr11	56272496	56272516 +	4
chr8	84907457	84907477 -	4
chr1	206021899	206021919 +	4
chr1	240405768	240405788 +	4
chr11	49751532	49751552 +	4
chr9	131543734	131543754 -	4
chr9	134515493	134515513 -	4
chr8	83484434	83484454 -	4
chr8	83679409	83679429 -	4
chr9	133241083	133241103 -	4
chr1	34711973	34711993 +	4
chrY	12793234	12793254 +	4
chrX	1574769	1574789 +	4
chr1	25474585	25474605 -	4
chr11	61453979	61453999 +	4
chrX	4676538	4676558 +	4
chrY	19212180	19212200 +	4
chr8	81080178	81080198 +	4
chrX	4640691	4640711 -	4
chr8	78796778	78796798 -	4
chr1	235887248	235887268 -	4
chr11	60658591	60658611 -	4
chr8	79135872	79135892 -	4
chr1	234974753	234974773 +	4
chr1	234974754	234974774 +	4
chr11	64949867	64949887 +	4

chrY	19601182	19601202 -	4
chrX	5523836	5523856 -	4
chr1	235735304	235735324 -	4
chr1	26476907	26476927 -	4
chrX	25431686	25431706 +	4
chr8	80756317	80756337 -	4
chr1	237407393	237407413 +	4
chr1	237552872	237552892 -	4
chr11	58539702	58539722 -	4
chrX	2894643	2894663 +	4
chr8	79314302	79314322 -	4
chr1	236320466	236320486 -	4
chr1	26721498	26721518 +	4
chr8	79694601	79694621 +	4
chrX	26028975	26028995 -	4
chrX	3736711	3736731 -	4
chr8	80078159	80078179 -	4
chr1	236984367	236984387 +	4
chr8	85842251	85842271 +	4
chr11	43109446	43109466 +	4
chrX	32345699	32345719 -	4
chr1	200151442	200151462 -	4
chrY	5530241	5530261 -	4
chr8	90366474	90366494 -	4
chr8	90366475	90366495 -	4
chrY	6166958	6166978 +	4
chr11	42448100	42448120 +	4
chr8	91428668	91428688 -	4
chr1	48191202	48191222 +	4
chrY	4367700	4367720 -	4
chr9	122740329	122740349 -	4
chrX	33155033	33155053 -	4
chrY	4160389	4160409 -	4
chrY	4160388	4160408 -	4
chr8	93197066	93197086 -	4
chr1	49222736	49222756 +	4
chr9	122652600	122652620 -	4
chr11	41110853	41110873 +	4
chrX	33380142	33380162 -	4
chr8	92672477	92672497 -	4
chrX	32950568	32950588 -	4
chr1	47606197	47606217 +	4
chrY	5271363	5271383 -	4
chr8	91718524	91718544 +	4
chr1	244484431	244484451 -	4
chrY	4831183	4831203 +	4
chrX	32921032	32921052 -	4
chr1	199564203	199564223 +	4
chr8	92499378	92499398 +	4
chrY	9978523	9978543 +	4
chrY	9211719	9211739 -	4

chr1	203208796	203208816 -	4
chr1	39200027	39200047 -	4
chr8	87977360	87977380 +	4
chr1	39946299	39946319 -	4
chr9	127655016	127655036 +	4
chrX	31252335	31252355 +	4
chr9	130673166	130673186 +	4
chr9	130695025	130695045 -	4
chr8	86243998	86244018 -	4
chr8	86425393	86425413 -	4
chr1	38432938	38432958 -	4
chr8	86716602	86716622 +	4
chrX	30492072	30492092 -	4
chr8	87100074	87100094 +	4
chr1	38686804	38686824 -	4
chr1	241806150	241806170 -	4
chrY	7622775	7622795 -	4
chrX	31562765	31562785 +	4
chrY	7187398	7187418 -	4
chr1	43345597	43345617 +	4
chr1	201278276	201278296 -	4
chr9	127041443	127041463 +	4
chrY	8822745	8822765 -	4
chr1	202881684	202881704 +	4
chr1	242155336	242155356 -	4
chr9	126836163	126836183 -	4
chr8	89001640	89001660 +	4
chr8	89001641	89001661 +	4
chr1	234597365	234597385 -	4
chrY	19601183	19601203 -	4
chr1	234562754	234562774 +	4
chr1	216000121	216000141 +	4
chr8	66973028	66973048 +	4
chrY	26182710	26182730 +	4
chrX	19037391	19037411 -	4
chr1	225089761	225089781 -	4
chrX	11398457	11398477 +	4
chrX	11327246	11327266 -	4
chr1	224417243	224417263 -	4
chrX	12735276	12735296 -	4
chr1	216903516	216903536 +	4
chr1	216415344	216415364 -	4
chr1	216243426	216243446 -	4
chrX	12411812	12411832 +	4
chr1	227123600	227123620 +	4
chrX	10181633	10181653 -	4
chr1	12770971	12770991 -	4
chr1	11847992	11848012 -	4
chr8	67646913	67646933 +	4
chrX	10846473	10846493 -	4
chrX	10712646	10712666 -	4

chr8	68024364	68024384 -	4
chrX	10539386	10539406 -	4
chrX	20051780	20051800 +	4
chr1	215321614	215321634 +	4
chr1	223192963	223192983 +	4
chr1	7827686	7827706 -	4
chrX	15974875	15974895 -	4
chr11	86061625	86061645 -	4
chr1	218801079	218801099 -	4
chrX	14976327	14976347 +	4
chr1	218484599	218484619 +	4
chrX	15974876	15974896 -	4
chr1	218385963	218385983 -	4
chr11	84883768	84883788 -	4
chr1	3489696	3489716 +	4
chr8	62645687	62645707 -	4
chr1	219462085	219462105 +	4
chr1	1276452	1276472 -	4
chr1	219694693	219694713 -	4
chr1	219694694	219694714 -	4
chrX	15832010	15832030 +	4
chrX	14681271	14681291 -	4
chrX	13487882	13487902 -	4
chr1	216967838	216967858 +	4
chr8	65709164	65709184 +	4
chr11	82208142	82208162 -	4
chrX	14015964	14015984 -	4
chr1	220681699	220681719 -	4
chr1	220684914	220684934 +	4
chr8	64113890	64113910 +	4
chr1	217821061	217821081 -	4
chr11	83801497	83801517 -	4
chr1	24280535	24280555 -	4
chr1	212309520	212309540 -	4
chr8	73602826	73602846 -	4
chr11	71828489	71828509 -	4
chr1	19260831	19260851 -	4
chr1	212112995	212113015 +	4
chr1	232678825	232678845 -	4
chr1	211985126	211985146 +	4
chr8	74706846	74706866 +	4
chrX	7879483	7879503 +	4
chr1	19595673	19595693 -	4
chr1	20122128	20122148 -	4
chr11	73757804	73757824 -	4
chr1	230652633	230652653 +	4
chr1	230960309	230960329 -	4
chr1	233914775	233914795 +	4
chr1	24022736	24022756 -	4
chr1	24022737	24022757 -	4
chr1	24022738	24022758 -	4

chr11	66124655	66124675 -	4
chrX	5656645	5656665 +	4
chr1	234346741	234346761 +	4
chr1	210728145	210728165 +	4
chrX	23596889	23596909 -	4
chrX	24203274	24203294 -	4
chr1	211553117	211553137 +	4
chr8	75957874	75957894 +	4
chr1	24001986	24002006 -	4
chrX	5979256	5979276 -	4
chr1	19260832	19260852 -	4
chr1	228207550	228207570 -	4
chr11	77304476	77304496 +	4
chr8	70232511	70232531 -	4
chr8	70547390	70547410 +	4
chrX	7940995	7941015 +	4
chr8	70547391	70547411 +	4
chrX	21369543	21369563 +	4
chr1	228207584	228207604 -	4
chr11	77415252	77415272 -	4
chr1	17226244	17226264 -	4
chr1	14581361	14581381 -	4
chrY	23487856	23487876 -	4
chr11	78195169	78195189 +	4
chr1	227808267	227808287 +	4
chrY	22708292	22708312 +	4
chr11	76453227	76453247 +	4
chrY	21392362	21392382 -	4
chrX	8504178	8504198 +	4
chr1	18756306	18756326 -	4
chr1	229527877	229527897 -	4
chr8	72449720	72449740 -	4
chr1	228785783	228785803 +	4
chrX	9064214	9064234 -	4
chr8	71152072	71152092 +	4
chr1	228207692	228207712 -	4
chrY	21758894	21758914 -	4
chrY	21746704	21746724 +	4
chrY	21654792	21654812 +	4
chr11	40898805	40898825 +	4
chr1	197374786	197374806 -	4
chr8	94437620	94437640 +	4
chrX	35020798	35020818 -	4
chr11	34829878	34829898 +	4
chr11	36690824	36690844 +	4
chrX	152108648	152108668 -	4
chr9	118232709	118232729 -	4
chr11	36857642	36857662 -	4
chr1	51750438	51750458 -	4
chr11	34878362	34878382 -	4
chr9	116378216	116378236 -	4

chr1	51750437	51750457 -	4
chrX	151094537	151094557 +	4
chr10	3445991	3446011 -	4
chr11	38405966	38405986 -	4
chr1	54579589	54579609 -	4
chr11	36805597	36805617 +	4
chr1	55582021	55582041 -	4
chr1	55654752	55654772 +	4
chr1	196953913	196953933 +	4
chr8	95337129	95337149 -	4
chr11	39261935	39261955 +	4
chrX	34466330	34466350 +	4
chr8	94808535	94808555 +	4
chrX	150469941	150469961 -	4
chr1	50789415	50789435 -	4
chr10	3445990	3446010 -	4
chr11	38405965	38405985 -	4
chr9	118232708	118232728 -	4
chr1	51400854	51400874 +	4
chr8	99057869	99057889 -	4
chr8	94310015	94310035 +	4
chr1	194793120	194793140 -	4
chrX	35098737	35098757 -	4
chr1	194939781	194939801 +	4
chrX	152850554	152850574 -	4
chrY	1574769	1574789 +	4
chr9	118788379	118788399 +	4
chr9	118814473	118814493 -	4
chrX	155885952	155885972 +	4
chr1	248735354	248735374 -	4
chr11	36412898	36412918 +	4
chr1	247230714	247230734 -	4
chr11	36412899	36412919 +	4
chr8	94898921	94898941 +	4
chr1	197885694	197885714 -	4
chr9	117452422	117452442 -	4
chr9	120131564	120131584 +	4
chr8	97469265	97469285 +	4
chr8	94898920	94898940 +	4
chr10	3662464	3662484 +	4
chrX	150142613	150142633 -	4
chrX	38346324	38346344 -	4
chr11	37994829	37994849 -	4
chrX	151437091	151437111 +	4
chr8	94106030	94106050 +	4
chr1	52693964	52693984 +	4
chr8	100862273	100862293 -	4
chrX	151750868	151750888 -	4
chr8	99168624	99168644 -	4
chr1	53235474	53235494 -	4
chr4	132710469	132710489 +	5

chr18	7999027	7999047 -	5
chr2	175076566	175076586 +	5

Min_LevDist

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Confidential - Company Proprietary

x000D Confidential - Company Proprietary

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IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC
IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC
IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC
IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC
IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC
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IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC
IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NGC

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IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NC
IGI_Guidescan|CPS1_ONEseq|BWA_V3_WT_NGC|BWA_2p5sens_WT_NGC|BWA_Lev3_WT_NC

Gene	Region
CPS1	Exon
NSDHL	Intron
HS3ST4	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
KLHL3	Intron
none	Intergenic
none	Intergenic
SCAPER	Intron
none	Intergenic
NRG3	Intron
ATP7B	Intron
none	Intergenic
CCDC28A-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
LINC01049	Other
AKT3	Intron
none	Intergenic
GUSBP16	Other
none	Intergenic
GUSBP3	Other
GUSBP17	Other
none	Intergenic
LOC107985511	Other
LOC105371777	Other
LHX1-DT	Other
none	Intergenic
LOC101927815	Other
NRXN3	Intron
none	Intergenic
none	Intergenic
none	Intergenic
PTCHD1-AS	Other
CTPS2	Intron
none	Intergenic
none	Intergenic
GRID2	Intron
ZNF185	Intron
SPRY3	Intron
RIPPLY3	Intron
none	Intergenic
LDB2	Intron
none	Intergenic
FOCAD	Intron

none	Intergenic
none	Intergenic
KCND2	Intron
KCND2	Intron
KCND2	Intron
none	Intergenic
none	Intergenic
MTREX	Intron
MTREX	Intron
ORC3	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
TMEM62	Intron
RASAL2	Intron
LINC00582	Other
none	Intergenic
none	Intergenic
QSER1	Intron
none	Intergenic
none	Intergenic
LINC02621	Other
WDPCP	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LPP	Intron
none	Intergenic
none	Intergenic
none	Intergenic
ARL15	Intron
none	Intergenic
none	Intergenic
SH3GL2	Intron
none	Intergenic
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GPR155	Intron
SPATA17	Intron
CDH8	Intron
FMN2	Intron
CCNH	Intron
none	Intergenic

none	Intergenic
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none	Intergenic
LINC02698	Other
CSMD1	Intron
TNIP3	Intron
NR3C2	Intron
NKX3-1	Intron
STON1	Exon
none	Intergenic
ADK	Intron
CEP112	Intron
none	Intergenic
LOC730100	Other
none	Intergenic
ADGRL4	Intron
none	Intergenic
ARFGEF3	Intron
LOC105374007	Other
none	Intergenic
KLHL32	Intron
PLCL2	Intron
none	Intergenic
ZFYVE1	Intron
LOC105375107	Exon
none	Intergenic
TTLL5	Intron
SYNE2	Intron
RUNX2	Intron
LOC105370689	Exon
RCOR1	Intron
none	Intergenic
TINAG	Intron
CYB5R4	Intron
none	Intergenic
LINC00596	Other
none	Intergenic
LOC101927284	Other
none	Intergenic
MDGA2	Intron
LOC105370438	Other
NOVA1	Intron
none	Intergenic
LINC02201	Other
LINC02201	Other
REXO5	Intron
none	Intergenic
RBFOX1	Intron
LOC105379168	Other

none	Intergenic
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MCTP1	Intron
CDH1	Intron
none	Intergenic
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ZNF423	Intron
KCNN2	Intron
LOC107984867	Other
RPP40	Exon
none	Intergenic
DPH6	Intron
none	Intergenic
PPP2R2B	Intron
LOC105370982	Other
none	Intergenic
PTPN9	Intron
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LINC02227	Other
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EXOC4	Intron
PDZRN4	Intron
ST8SIA1	Exon
FMC1	Intron
none	Intergenic
RAB21	Intron
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ARHGAP42	Intron
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MTMR2	Intron
SLC2A14	Intron
LOC101929432	Other
MSRA	Intron
none	Intergenic
none	Intergenic
LOC101927815	Other
none	Intergenic
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ICA1	Exon
none	Intergenic
none	Intergenic

none	Intergenic
MYCBP2	Exon
UTRN	Intron
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LOC105369995	Other
none	Intergenic
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SEMA3C	Intron
LOC105369146	Other
LOC105375264	Other
ANAPC5	Intron
none	Intergenic
none	Intergenic
LOC105370076	Other
LOC105374124	Other
PARP15	Intron
SPOPL	Intron
LOC105374145	Other
none	Intergenic
none	Intergenic
none	Intergenic
TTC21B	Exon
XIRP2	Intron
SLC4A10	Intron
none	Intergenic
none	Intergenic
none	Intergenic
UBR3	Intron
LOC101928371	Other
LOC101928371	Other
DGKG	Intron
DGKG	Intron
OPA1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
LYPD1	Exon
LYPD1	Exon
none	Intergenic
DPP10	Intron
DPP10	Intron
none	Intergenic
DOK5	Intron
CDH22	Intron
none	Intergenic
none	Intergenic
ZNF385D	Intron

none	Intergenic
LINC01643	Other
PHACTR3	Intron
LOC107985511	Other
none	Intergenic
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none	Intergenic
none	Intergenic
PLCL1	Intron
none	Intergenic
none	Intergenic
LOC105372529	Other
CACNA2D3	Intron
SPHKAP	Intron
LOC105377110	Other
none	Intergenic
none	Intergenic
TRAPPC11	Intron
CDH12	Intron
CDH12	Intron
GRB2	Intron
MAP2K6	Exon
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
DSG2	Intron
LOC105379013	Other
LOC105379013	Other
LOC105378998	Other
CDH13	Intron
LINC01228	Other
none	Intergenic
PDE4D	Intron
LHX1-DT	Other
PDE4D	Intron
ITGA1	Intron
none	Intergenic
LOC105371777	Other
LDAH	Intron
ALK	Intron
BIRC6	Intron
none	Intergenic
CLOCK	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic

BCL11A	Intron
none	Intergenic
none	Intergenic
PABPC4L	Other
UGT8	Intron
ELOVL6	Intron
none	Intergenic
MUC16	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
FAM135B	Intron
none	Intergenic
LOC105378515	Other
none	Intergenic
none	Intergenic
ARHGAP21	Intron
ARHGAP21	Intron
LOC105376131	Other
none	Intergenic
none	Intergenic
THOC2	Intron
LOC105375704	Other
DOCK7	Intron
none	Intergenic
none	Intergenic
COL27A1	Intron
TNFSF15	Intron
AFF2	Intron
none	Intergenic
none	Intergenic
COL14A1	Intron
COL14A1	Intron
none	Intergenic
none	Intergenic
LINGO2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
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DCAF8	Intron
B4GALT1	Intron
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PLS3	Exon
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LOC107984223	Other
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HTR2C	Intron
SLC16A2	Intron
LOC105378429	Other
TJP2	Intron
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TJP2	Intron
IDE	Intron
TJP2	Intron
TMC1	Intron
SORCS3	Intron
TMC1	Intron
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RBM41	Exon
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LOC105373150	Other
IL7	Other
MTR	Intron
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TTC17	Intron
AKT3	Intron
TTC17	Intron
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LRRC4C	Intron
LOC105375630	Other
FRMPD4	Intron
TENM4	Intron
FCHSD2	Exon
KDM1A	Intron
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POLA1	Intron
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KCNT2	Intron
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CFAP47	Intron
LOC105373369	Other
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LOC105377171	Other
GMDS	Intron
LOC107984526	Other
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CFAP97D2	Other
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NDNF	Intron
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LOC105370003	Other
PPFIA1	Intron
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SDK1	Intron
TBCK	Intron
COX10	Intron
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GUSBP16	Other
SHC4	Intron
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GUSBP17	Other
FTO	Intron
GUSBP3	Other
GUSBP15	Other
GUSBP14	Other
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NAALADL2	Intron
DOCK11	Intron
RABGAP1L	Intron
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C1QTNF3	Other
ESF1	Exon
RARS2	Intron
NHSL2	Intron
NHSL2	Intron
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GPR137C	Intron
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PPP2R2B	Intron
TMX2	Intron
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LOC105377700	Other
FHIT	Intron
THSD4	Intron
AFF2	Intron
SLC25A42	Exon
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PPHLN1	Intron
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LOC105377212	Other
FAM135B	Intron
MKLN1	Intron
RANBP17	Intron
ARPP21	Intron
DCC	Intron
LOC730100	Other
CRTAC1	Intron

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[illegible]

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MUC4	Intron
MUC4	Intron
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ARHGEF26	Intron
MUC4	Intron
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LINC02054	Other
MUC4	Intron
MUC4	Intron
LOC105372225	Other
LOC105372225	Other
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MEGF11	Intron
OTUD7A	Intron
CHRNA7	Intron
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FMN1	Exon
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TJP1	Intron
FAM189A1	Intron
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MTMR10	Intron
TRPM1	Intron
KLF13	Intron
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LOC105372225	Other
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PRH1	Intron
PRH1	Intron
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KANSL1	Intron
LRRC37A3	Intron
NSF	Intron
PARN	Intron
PARN	Intron
NOMO1	Intron
BMERB1	Intron
BMERB1	Intron
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KANSL1	Intron
LOC105371760	Other
ABR	Intron
KRT33B	Intron
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TSPB1	Intron
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HCG17	Other
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HCG17	Other
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HCG17	Other
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TSBP1	Intron
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PLPPR1	Intron
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FAM120B	Intron
LOC101929802	Other
APBA1	Intron
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LOC107987370	Other
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LOC105377783	Other
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ANO3	Intron
LOC102724340	Other
CCDC47	Intron
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CATSPERD	Intron
YWHAQ	Intron
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DAB2	Intron
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LOC101929200	Other

LOC105377567	Other
WDR17	Intron
LINC02365	Other
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SGCD	Other
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KDM3B	Intron
ATP10B	Intron
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MCTP1	Intron
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MORC1	Intron
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P2RY12	Intron
CHCHD6	Intron
LOC105374060	Other
LOC105374060	Other
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TBC1D22A	Intron
SYNPR	Other
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PDZRN3	Intron
ARHGAP24	Intron
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LOC105377329	Other
EPHA5	Intron
USO1	Intron
LINC02485	Other
LINC0002	Other
MCF2L2	Intron
NAALADL2	Intron
EXOC1	Intron
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ELAVL2	Intron
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STK3	Intron
CA1	Exon
PTPRD	Intron

RFX3	Intron
TRPS1	Intron
TRPC5	Intron
ZNF449	Exon
TCEAL7	Intron
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RPS6KA3	Intron
SCML2	Intron
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MED27	Intron
RBM18	Intron
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SYNE1	Intron
SERAC1	Intron
EGFR	Intron
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EPB41L2	Intron
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CNTNAP2	Intron
XKR4	Intron
XKR4	Intron
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SEMA3C	Intron
GSAP	Intron
MAGI2	Intron
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STEAP2-AS1	Other
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DRD2	Intron
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ETS1	Intron
LOC107984526	Other
C12orf56	Intron
GRIP1	Intron
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KIF21A	Intron
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DLG2	Intron
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PCDH9	Intron
LOC107984671	Other
ITGBL1	Intron
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GPC6	Intron
ELK3	Intron
LOC107984543	Other
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HMCN1	Intron
ASCL5	Intron
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OR6N2	Exon
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RABGAP1L	Intron
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FOXJ3	Intron
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AK2	Exon
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NEGR1	Intron
LOC105378819	Other
IPP	Intron
UBE2U	Intron
LINC02778	Other
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LOC107984239	Other
LINC02624	Other
TCF7L2	Intron
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LINC02257	Other
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PRKG1	Intron
SLC39A12	Intron
SH3RF3	Intron
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LOC107985905	Other
MBD5	Intron
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KCNH7	Intron
CCDC148	Intron
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LRP1B	Intron
LRP1B	Intron
LOC107985845	Other
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SH3YL1	Intron
NRXN1	Intron
PRKCE	Intron
PLEKHH2	Intron
CAMKMT	Intron
DHX57	Intron
LOC105372548	Exon
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LOC105379418	Other
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MIR99AHG	Other
TIAM1	Intron
MRPL39	Intron
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DIRC1	Other
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SLX4IP	Intron
PLCB4	Intron
DIS3L2	Intron
NYAP2	Intron
SCAPER	Intron
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MFSD13B	Other
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DPH6-DT	Other
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KIAA1328	Intron
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PTPRM	Intron
LINC01915	Exon
LOC105372028	Other
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SETD6	Intron
PHLPP2	Intron
LINC01572	Other
CEP112	Intron
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TNRC6C	Intron
SLC39A11	Intron
RASL10B	Intron
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LINC01938	Other
CLPX	Intron
HTR4	Intron
FBN1	Intron
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CGNL1	Intron
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LOC101927605	Other
MAN2A1	Intron
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FSTL4	Other
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NRXN3	Intron
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DIO2-AS1	Other
FGGY	Intron
DAB1	Intron
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KYAT3	Intron
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SLC44A5	Intron
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CDKAL1	Exon
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UBE3A	Intron
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RIPOR2	Intron
CLIC4	Intron
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ADGRF1	Intron
KHDRBS2	Intron
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RERE	Intron
GCLC	Intron
TCF4	Intron
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DCLK2	Intron
LINC02233	Other
HAUS1	Intron
ANKRD12	Intron
LOC105372152	Other

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NDST4	Intron
MAML3	Intron
LINC00499	Other
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KRBA2	Intron
BCL6B	Intron
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GLG1	Intron
LOC105371314	Other
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KRT33B	Intron
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NELL1	Intron
MIPEP	Intron
ADCY1	Intron
LINC00534	Other
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UBE2W	Intron
FAM168A	Intron
MMP16	Intron
MMP16	Intron
SRRM4	Intron
BTBD18	Intron
PCDH17	Exon
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LOC105370223	Other
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CYP2R1	Intron
ELMO1	Intron
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LINC00548	Other
LINC00548	Other
IGF2BP3	Intron
LOC107986774	Other
PPFIBP2	Intron
GAB2	Intron
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EPHA1-AS1	Other
EPHA1-AS1	Other
TMEM178B	Intron

LINC-PINT	Other
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GNAI1	Intron
MAML2	Intron
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LOC100287944	Other
NKAIN3	Intron
ASPH	Intron
TMTC2	Intron
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MIR100HG	Other
STAG3	Intron
OTOGL	Intron
ZNF804B	Intron
STEAP2-AS1	Other
LINC00333	Other
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GPC5	Intron
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XKRX	Other
LINC01649	Other
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LOC107985704	Other
GPR63	Exon
IL1RAPL2	Intron
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AJUBA	Intron
LINC00333	Other
BICC1	Intron
PCSK5	Intron
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ZNF438	Intron
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CATSPERE	Intron

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LOC105376375	Other
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SLC30A9	Intron
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THRB	Intron
ANTXR2	Intron
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GADL1	Intron
LOC107986285	Exon
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FGF12	Intron
CLRN1	Intron
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LOC107985905	Other
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LOC101927967	Other
LOC105374220	Other
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VWA3B	Intron
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VPS54	Intron
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LRRTM4	Intron
PIK3R4	Intron
M1AP	Exon
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PREX1	Intron
ARHGAP24	Intron
LINC02885	Other
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DSCAM	Intron
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TOP1	Intron
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TBC1D22A	Intron
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SEL1L2	Intron
NDUFAF5	Intron
RORA	Intron
LOC101927605	Other
KIF13B	Intron
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BRDT	Intron
NKAIN2	Intron
FGF14	Intron
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ZNF337-AS1	Other
LINC02787	Other
LOC101928436	Other
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LOC107985670	Other
GPC5	Intron
GABRB2	Intron
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SYNDIG1	Intron
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PALM2AKAP2	Intron
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LOC101929710	Other
COL11A1	Intron
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USP38-DT	Other
MCTP1	Intron
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IQCH	Exon
PTBP2	Intron
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CRNKL1	Intron
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DPYD	Intron
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ZNF609	Intron
ZNF711	Intron
MEGF11	Intron
SNX5	Intron
LINC01169	Other
DPYD	Intron
EEPD1	Intron
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LOC105370108	Other
DCT	Intron
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PRSS23	Exon
RPS27L	Exon
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LOC401324	Other
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ROBO2	Intron
ROBO2	Intron
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CNN3-DT	Other
TLN2	Intron
TLCD4	Intron
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TANGO6	Intron
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NARS2	Intron
LHX8	Intron
COL4A6	Intron
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MEF2C-AS1	Other
ANKRD18CP	Other
CCDC102B	Intron
SQOR	Intron
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ABHD6	Intron
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MYLK4	Intron
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ERC2	Intron
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SLC7A6	Intron
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FH	Exon
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SGCZ	Intron
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CNTN5	Intron
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PLD5	Intron
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LOC105375264	Other
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RAD54L2	Intron
LINC02405	Other
LOC107984449	Other
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LOC101928437	Other
LOC105373294	Other
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SLC4A10	Intron
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CPEB4	Intron
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SLC35F1	Intron
LINC01725	Other
SYNPR	Intron

SYNPR	Intron
LINC01725	Other
TTLL7	Intron
PABPC4L	Other
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NALF1	Intron
RALGAPB	Intron
LOC100128993	Other
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POU6F2	Intron
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TARBP1	Intron
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SLC25A26	Intron
PANX1	Exon
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BAZ2B	Intron
LOC107984618	Other
LOC107986150	Other
NMD3	Intron
LEO1	Intron
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FHIT	Intron
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ZFP62	Exon
UNC13C	Other
C3P1	Other
TNFSF13B	Intron
LUCAT1	Other
ADGRL2	Intron
PPM1L	Intron
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CBFA2T2	Exon
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PARD3B	Intron
LINC01170	Other
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CEP350	Intron
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XPR1	Intron
ACADL	Intron
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LOC105374037	Other
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SUCO	Exon
ASTN1	Intron
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SNX29	Intron
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LOC101927960	Exon
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IQCB1	Intron
DLEU7	Intron
ABLIM3	Intron
DLEU1	Other
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PGAP1	Intron
AIG1	Intron
LINC01720	Other
AKAP13	Intron
AGBL1	Intron
CAB39L	Intron
SEC22A	Exon
BRINP3	Intron
NIBAN1	Intron
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RGL1	Intron
PHKA2	Intron
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EPM2A	Other
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LINC00348	Other
SPOCK1	Intron
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TIAM2	Intron
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DOCK10	Intron
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LOC105370989	Other
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SV2B	Intron
BLZF1	Intron
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RBFOX1	Intron
IFT57	Intron
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ERBB4	Intron
HHLA2	Intron
LOC105379167	Other
SLC27A6	Intron
DPYSL3	Intron
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STK32A	Intron
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PBX1	Intron
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LOC101928627	Other
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PRKN	Intron
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STXBP5	Intron
LUC7L	Intron
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LOC102724087	Other
CHN1	Intron
CHD9	Intron
CASC20	Other
USH2A	Intron
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TAF1	Intron
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CCDC141	Exon

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B3GLCT	Intron
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CADM2	Intron
PDE11A	Intron
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ANKRD20A19P	Exon
SNAP25	Intron
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SHOC1	Intron
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STK39	Intron
CNIH3	Intron
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GPC5	Intron
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CAPN2	Exon
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HDAC8	Intron
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PDE1C	Other
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LOC105376235	Other
FNDC7	Intron
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USP12	Intron
VAV3	Exon
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MED12L	Intron
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AHI1	Intron
LOC105373790	Other
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LINC01881	Other
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NEK7	Intron
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STS	Intron
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HS3ST4	Intron
NR5A2	Intron
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GALNT10	Intron
SP4	Intron
N4BP1	Intron
GAPVD1	Exon
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PHKB	Intron
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PPP1R12B	Intron
RAB6B	Intron
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LOC105370286	Other
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LINC00375	Other
RAPGEF1	Intron
HTR1F	Intron
FBXL17	Intron
CFAP77	Intron
ZNF804A	Intron
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LINC02751	Other
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A2M	Intron
SEMA3C	Intron
SEMA3C	Intron
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TEX14	Intron
AFF1	Intron
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TENM3	Intron
SPON1	Exon
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KLRF1	Other
LOC408186	Other
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SRGN	Intron
PTPRD	Intron
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GRIP1	Intron
PTPRD	Exon
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SLC1A1	Intron
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RASSF3	Intron
ASXL2	Intron
RFC1	Intron
none	Intergenic
LOC105374703	Other
TEX2	Exon
none	Intergenic
NRG3	Intron
TEX2	Intron
ETV6	Intron
none	Intergenic
none	Intergenic
HELZ	Intron
none	Intergenic
none	Intergenic
none	Intergenic
KLHL29	Intron
KLHL29	Intron
MAPK10	Intron
ARNTL	Intron
none	Intergenic
none	Intergenic
LOC107986330	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105374520	Other
LOC105375341	Other
ADGRA3	Intron
BNC2	Intron
CACNA1C	Exon

BNC2	Intron
BNC2	Intron
none	Intergenic
MAPT	Intron
none	Intergenic
STMN2	Intron
EXOC4	Intron
none	Intergenic
none	Intergenic
TRHDE	Other
CACNA1C	Intron
none	Intergenic
CCDC171	Intron
MIR924HG	Other
none	Intergenic
none	Intergenic
GPM6A	Intron
KCNIP4	Intron
ROCK2	Exon
none	Intergenic
CAPS2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105375523	Other
none	Intergenic
none	Intergenic
LOC105374737	Other
LOC105374737	Other
LAPTM4A-DT	Other
CA10	Intron
none	Intergenic
GALNT17	Intron
none	Intergenic
MYRFL	Intron
CTNNA3	Exon
none	Intergenic
CTNNA3	Intron
none	Intergenic
LOC105374553	Other
LOC105369818	Other
none	Intergenic
SKAP1	Intron
CCSER1	Intron
LINC02625	Other
SKAP1	Intron
NELL1	Intron
LOC105375931	Other
none	Intergenic
NRBF2	Intron

LUC7L3	Intron
ABCC3	Intron
none	Intergenic
LOC105373490	Other
none	Intergenic
none	Intergenic
none	Intergenic
FOXP2	Other
MC2R	Intron
SLC4A4	Intron
none	Intergenic
none	Intergenic
none	Intergenic
LOC105371953	Other
none	Intergenic
none	Intergenic
none	Intergenic
ADCY2	Intron
none	Intergenic
SAMD12	Intron
none	Intergenic
SAMD12-AS1	Other
none	Intergenic
LINC02196	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
CDH18	Intron
TNRC6C	Intron
HIF1AN	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
SLC8A1-AS1	Other
VRK2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
ATL2	Intron
none	Intergenic
LOC107984270	Other
TMPRSS11E	Intron
OVOS2	Other
LOC105374655	Other
NRCAM	Intron
CTNND2	Intron
none	Intergenic
CTNND2	Intron

PTPRM	Intron
TWSG1	Intron
none	Intergenic
none	Intergenic
LHFPL3	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
PKP2	Intron
NRXN1	Intron
none	Intergenic
none	Intergenic
FAM149A	Exon
none	Intergenic
none	Intergenic
LOC107986294	Exon
none	Intergenic
LTBP1	Intron
KCND2	Intron
none	Intergenic
none	Intergenic
LINC01060	Other
none	Intergenic
none	Intergenic
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none	Intergenic
LOC105377616	Exon
CPQ	Intron
LINC01483	Other
none	Intergenic
none	Intergenic
ATP8A1	Intron
none	Intergenic
none	Intergenic
ADAM22	Intron
KHDRBS3	Intron
none	Intergenic
none	Intergenic
AASS	Intron
LOC107986815	Other
ATAD1	Intron
none	Intergenic
FER1L6	Intron
none	Intergenic
WDPCP	Intron
FEZ2	Intron
TEC	Intron
MGMT	Intron

TMEM117	Intron
USP34	Intron
none	Intergenic
none	Intergenic
ABCC9	Intron
TMEM65	Intron
none	Intergenic
UBTD1	Intron
VPS50	Intron
LOC101928387	Exon
none	Intergenic
GABRG1	Intron
HTR7	Intron
none	Intergenic
none	Intergenic
CDK14	Intron
none	Intergenic
CRIM1	Exon
none	Intergenic
GABRB1	Intron
LOC105374781	Other
COMMD8	Intron
NELL2	Intron
none	Intergenic
GABRB1	Intron
none	Intergenic
ITGA8	Intron
SYNPO2	Exon
LOC102724467	Other
FRMD4A	Intron
CSMD1	Intron
LINC02053	Other
NUDT19	Intron
GASK1B	Exon
LOC101927815	Other
ARHGEF28	Intron
none	Intergenic
LOC105379031	Other
LINC02031	Other
none	Intergenic
GNA14	Intron
CDH20	Intron
none	Intergenic
SPIDR	Intron
LOC105377502	Other
none	Intergenic
ARHGAP15	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic

KCNMB2	Intron
CCDC3	Intron
ANKDD1B	Intron
LOC101929268	Other
none	Intergenic
GSE1	Other
LINC01014	Exon
SERPING1	Intron
RMST	Other
LINC02762	Other
ANKS1B	Intron
FBXO25	Intron
KIAA1217	Intron
none	Intergenic
none	Intergenic
MYO3A	Intron
P3H2	Intron
MAST4	Intron
GPR158	Intron
PTPRN2	Intron
LOC105379003	Exon
NCAM1	Intron
NEDD1	Intron
none	Intergenic
MAMDC2	Intron
none	Intergenic
TRPM3	Intron
none	Intergenic
none	Intergenic
NCKAP5	Exon
ALG9	Intron
none	Intergenic
ANKS1B	Intron
none	Intergenic
TJP2	Intron
none	Intergenic
MARVELD2	Intron
none	Intergenic
none	Intergenic
PDCD10	Intron
LRP5	Intron
TAOK3	Intron
FNTA	Intron
DYNC2H1	Intron
none	Intergenic
LOC107986051	Other
none	Intergenic
none	Intergenic
ANKRD19P	Other
none	Intergenic
PHLPP2	Exon

none	Intergenic
none	Intergenic
NOL8	Intron
KIF26B	Intron
none	Intergenic
ANGPTL5	Intron
none	Intergenic
none	Intergenic
ZFHX3	Intron
none	Intergenic
none	Intergenic
LOC105376387	Other
MSH3	Intron
NAALADL2	Other
PHLPP1	Intron
none	Intergenic
none	Intergenic
LINC02854	Other
GDI2	Intron
MSH3	Intron
none	Intergenic
OR4D9	Exon
LOC100505498	Other
none	Intergenic
NTRK2	Intron
RELA	Exon
NOS1	Intron
none	Intergenic
ERI1	Intron
none	Intergenic
WWOX	Intron
ECT2	Intron
RASGRF2	Intron
LOC101927947	Other
none	Intergenic
LOC105376361	Other
none	Intergenic
none	Intergenic
LOC101927947	Other
none	Intergenic
ATG10	Intron
LINC01182	Other
TPK1	Intron
RAB28	Intron
none	Intergenic
RAG1	Intron
none	Intergenic
MAPK8	Intron
NPHP1	Intron
none	Intergenic
PREX2	Intron

none	Intergenic
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none	Intergenic
none	Intergenic
UBE2D3	Intron
none	Intergenic
none	Intergenic
MIR4527HG	Other
LINC02759	Other
SLC2A9	Intron
ARL15	Intron
MYT1L	Intron
none	Intergenic
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FAM184B	Intron
none	Intergenic
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STAT3	Intron
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none	Intergenic
DCDC1	Intron
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none	Intergenic
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ELAVL2	Intron
DCDC1	Intron
ELP4	Intron
none	Intergenic
LOC107984976	Other
none	Intergenic
CDRT1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
KIF2A	Intron
CCDC144A	Exon
none	Intergenic
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LOC105377382	Other
COX10	Intron
none	Intergenic
none	Intergenic
CYP7B1	Exon
CYP7B1	Intron
LOC105372462	Other
none	Intergenic
none	Intergenic
LEF1	Intron
LINC02820	Other
CNTNAP2	Intron
none	Intergenic
none	Intergenic
NLK	Intron
NLK	Intron
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SMAD4	Intron
none	Intergenic
none	Intergenic
none	Intergenic
SLC47A1	Exon
ZNF880	Other
CCDC144B	Exon
none	Intergenic
LOC101929141	Exon
CCDC144CP	Exon
none	Intergenic
none	Intergenic
CCNYL4	Other
LOC105375876	Other
LOC105375876	Other
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HTT	Intron
PDE4D	Intron
none	Intergenic
PDE4D	Intron
none	Intergenic
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none	Intergenic
DSCAM	Intron
DSCAM	Intron
CNTN4	Intron
PPP4R4	Intron
EYS	Intron
NPHP4	Intron
NPHP4	Intron
LINC00649	Other
RERP2Y	Other

POLR1C	Intron
none	Intergenic
none	Intergenic
DYRK1A	Intron
none	Intergenic
LOC107984704	Other
none	Intergenic
POLR1C	Intron
none	Intergenic
none	Intergenic
ADGRF2	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
LINC02549	Other
none	Intergenic
LOC100506446	Other
none	Intergenic
UQCC2	Intron
LOC107984933	Other
SIPA1L1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LINC01399	Other
RERP1Y	Other
none	Intergenic
LINC02885	Other
none	Intergenic
none	Intergenic
none	Intergenic
ZNF184	Intron
none	Intergenic
UBE2E2	Intron
none	Intergenic
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none	Intergenic
HERC2P3	Other
none	Intergenic
KAT2B	Intron
none	Intergenic
none	Intergenic
none	Intergenic
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none	Intergenic
TMEM260	Intron
none	Intergenic
DAAM2	Intron

LOC105376815	Other
none	Intergenic
LARGE1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
CCNK	Intron
SH3BGRL2	Intron
none	Intergenic
none	Intergenic
SPTLC2	Intron
UHRF1BP1	Exon
LRP5L	Exon
none	Intergenic
GPHN	Intron
GPHN	Intron
LOC105377842	Other
HORMAD2	Intron
STON2	Exon
none	Intergenic
EML5	Exon
none	Intergenic
PPP6R2	Intron
none	Intergenic
none	Intergenic
EYS	Intron
none	Intergenic
MAST2	Intron
none	Intergenic
MYRIP	Intron
STX16	Exon
LINC00911	Other
RAB22A	Intron
none	Intergenic
none	Intergenic
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PATJ	Exon
LOC107984787	Other
none	Intergenic
none	Intergenic
AKAP6	Intron
none	Intergenic
none	Intergenic
ANKRD6	Intron
none	Intergenic
none	Intergenic
none	Intergenic
LINC01811	Other

RGS6	Intron
none	Intergenic
none	Intergenic
CMTM8	Intron
OTUD7A	Intron
none	Intergenic
none	Intergenic
AGBL4	Intron
PSMA6	Intron
ATXN1	Intron
none	Intergenic
UFL1-AS1	Other
none	Intergenic
none	Intergenic
LOC105372699	Other
none	Intergenic
none	Intergenic
none	Intergenic
SEPTIN6	Intron
none	Intergenic
RARB	Intron
none	Intergenic
XPNPEP3	Exon
LINC02328	Other
LINC02277	Exon
SGIP1	Intron
none	Intergenic
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none	Intergenic
VAMP7	Intron
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none	Intergenic
TAS2R1	Intron
UGT2B11	Intron
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none	Intergenic
ADGRL3	Intron
ADGRL3	Intron
ADGRL3	Intron
ADGRL3	Intron
LINC01194	Other

ADGRL3	Intron
LINC01194	Other
none	Intergenic
ETFDH	Intron
none	Intergenic
LOC107986400	Other
none	Intergenic
none	Intergenic
none	Intergenic
FAM47E-STBD1	Intron
CCNI	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
SLC10A7	Intron
BMP3	Intron
ADCY2	Intron
ADCY2	Intron
ADCY2	Intron
ANKRD17	Intron
ARHGAP10	Intron
ARHGAP10	Intron
none	Intergenic
PTCHD1-AS	Other
CASK	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CFAP47	Intron
none	Intergenic
SRPX	Intron
ATRX	Exon
LOC105373287	Other
none	Intergenic
none	Intergenic
LINC02899	Other
SYTL5	Other
none	Intergenic
none	Intergenic
none	Intergenic
LOC105377508	Other
RELL1	Intron
none	Intergenic
SH3D19	Intron
none	Intergenic
none	Intergenic
none	Intergenic
GRIA2	Intron
ATP7A	Intron
ADGRL3	Intron

ADGRL3	Intron
LINC01194	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LRBA	Intron
none	Intergenic
SCFD2	Intron
PPEF1	Intron
none	Intergenic
SPATA18	Intron
PDGFC	Intron
ARL9	Intron
none	Intergenic
CLOCK	Intron
MAP3K15	Intron
NDST4	Intron
none	Intergenic
MARCHF1	Intron
none	Intergenic
LINC02511	Other
MARCHF1	Intron
USP53	Intron
LINC01378	Other
none	Intergenic
LOC105377387	Other
none	Intergenic
none	Intergenic
TBCK	Intron
TBCK	Intron
none	Intergenic
none	Intergenic
none	Intergenic
PCDH10-DT	Other
none	Intergenic
none	Intergenic
none	Intergenic
CETN4P	Other
DMD	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
none	Intergenic
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none	Intergenic
LINC02512	Other
none	Intergenic
CCSER1	Intron
none	Intergenic

LOC102723906	Other
none	Intergenic
none	Intergenic
none	Intergenic
GRID2	Intron
INPP4B	Intron
FRG1-DT	Other
POLA1	Intron
OPHN1	Intron
LOC101928978	Other
none	Intergenic
none	Intergenic
MAPK10	Intron
RNF150	Other
none	Intergenic
none	Intergenic
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none	Intergenic
PPP3CA	Intron
none	Intergenic
CXXC4-AS1	Other
LINC02267	Other
none	Intergenic
WWC2	Intron
WWC2	Intron
BMPR1B	Intron
none	Intergenic
none	Intergenic
PDLIM5	Intron
none	Intergenic
TENM3	Other
none	Intergenic
LOC105377343	Other
none	Intergenic
LAMTOR3	Intron
FSTL5	Intron
none	Intergenic
none	Intergenic
AFF2	Intron
DNAH12	Intron
LOC105377110	Other
BSN	Intron
CACNA2D3	Intron
CACNA2D3	Intron
CACNA2D3	Intron
none	Intergenic
none	Intergenic
FHIT	Intron
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none	Intergenic
GOLGA4	Intron

ZFY	Intron
PCDH11Y	Intron
OSBPL10	Intron
OSBPL10	Intron
none	Intergenic
none	Intergenic
none	Intergenic
FYCO1	Exon
SPRY3	Intron
none	Intergenic
LYZL4	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
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none	Intergenic
LINC02005	Other
ROBO2	Intron
ROBO2	Intron
ROBO2	Intron
LINC02018	Other
none	Intergenic
FOXP1	Intron
none	Intergenic
none	Intergenic
ROBO2	Intron
none	Intergenic
ROBO1	Intron
PRY2	Intron
DRG1	Intron
AP1B1	Intron
none	Intergenic
none	Intergenic
PRY	Intron
TTY4	Other
none	Intergenic
MEI1	Intron
TOM1	Intron
TMEM184B	Exon
TMEM184B	Exon
none	Intergenic
none	Intergenic
TTY4B	Other
RIPPLY3	Intron
none	Intergenic
none	Intergenic
RCAN1	Intron
none	Intergenic

TTY4C	Other
CECR2	Intron
none	Intergenic
ABCG1	Intron
LINC00111	Other
MX2	Intron
DSCAM	Intron
COL6A1	Intron
none	Intergenic
RFTN1	Intron
KCNH8	Intron
none	Intergenic
TTY2B	Other
none	Intergenic
TTY1	Other
none	Intergenic
LOC105377000	Other
RARB	Intron
CNTN4	Intron
none	Intergenic
CNTN4	Intron
LOC102723512	Other
LOC284930	Other
none	Intergenic
none	Intergenic
none	Intergenic
TAMM41	Other
BHLHE40-AS1	Other
LINC02052	Other
none	Intergenic
none	Intergenic
SOX2-OT	Other
ATP11B	Intron
TPRG1	Intron
none	Intergenic
ACAP2	Intron
none	Intergenic
LRRC15	Intron
PAK2	Intron
none	Intergenic
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none	Intergenic
MORC4	Intron
none	Intergenic
none	Intergenic
LOC105374217	Other
TNIK	Intron
none	Intergenic
COL4A6	Intron
COL4A5	Intron

none	Intergenic
none	Intergenic
LLOXNC01-250H12.3	Other
none	Intergenic
none	Intergenic
none	Intergenic
NAALADL2	Intron
NAALADL2	Intron
NAALADL2	Intron
NAALADL2	Intron
none	Intergenic
SEPSECS-AS1	Other
RBPJ	Intron
LINC02438	Other
KCNIP4	Intron
LINC02501	Other
none	Intergenic
none	Intergenic
none	Intergenic
SLC2A9	Exon
none	Intergenic
none	Intergenic
RNF212	Intron
none	Intergenic
none	Intergenic
PCDH11X	Intron
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LOC105374060	Other
LOC100130701	Other
none	Intergenic
LOC107986022	Other
none	Intergenic
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none	Intergenic
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ZBTB20	Intron
COL6A6	Intron
none	Intergenic
none	Intergenic
TEX13D	Exon
TEX13D	Exon
MYLK	Intron
LINC02016	Other
TENM1	Intron
none	Intergenic
HS6ST2	Intron
none	Intergenic
BBX	Intron
none	Intergenic

LOC101929485	Other
none	Intergenic
FAM172BP	Other
none	Intergenic
none	Intergenic
ZDHC9	Intron
none	Intergenic
LOC101928437	Other
PLCH1	Intron
MED12L	Intron
LINC02006	Other
none	Intergenic
ALG13	Intron
PPM1L	Intron
PAK3	Intron
PAK3	Intron
SCHIP1	Intron
SCHIP1	Intron
GYG1	Exon
PIK3CB	Intron
none	Intergenic
CLSTN2	Intron
CLSTN2	Intron
TF	Intron
PLS3-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105374150	Exon
LRCH2	Intron
SLC9A9	Intron
SLC9A9	Intron
SLC9A9	Intron
none	Intergenic
none	Intergenic
SEPTIN7-DT	Other
TNS3	Intron
none	Intergenic
NOD1	Intron
ST3GAL1	Intron
PHF20L1	Intron
URGCP	Intron
none	Intergenic
none	Intergenic
AMPH	Intron
LOC105375246	Other
HDAC9	Intron
SNX13	Intron
MEOX2	Intron

MEOX2	Intron
none	Intergenic
BZW2	Intron
JAZF1	Intron
none	Intergenic
RAPGEF5	Exon
OSBPL3	Intron
KLHL7-DT	Exon
PALS2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CALN1	Intron
MAGI2	Intron
MAGI2	Intron
AUTS2	Intron
none	Intergenic
PCLO	Intron
none	Intergenic
none	Intergenic
CSMD3	Intron
LOC105375371	Other
none	Intergenic
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none	Intergenic
none	Intergenic
ETV1	Intron
ZDHC21	Exon
none	Intergenic
NFIB	Intron
NFIB	Intron
STXBP5	Intron
HIVEP2	Intron
HIVEP2	Intron
HIVEP2	Intron
STX11	Other
none	Intergenic
none	Intergenic
none	Intergenic
PKIB	Intron
LOC105378008	Other
LOC105378009	Other
SLC24A2	Intron
SLC24A2	Intron
LOC105375951	Other
LOC101927354	Other
none	Intergenic
none	Intergenic

none	Intergenic
FAM120B	Intron
RFX3	Exon
RFX3	Intron
SLC45A4	Intron
THSD7A	Intron
ETV1	Intron
UMAD1	Intron
LOC105378071	Other
PTPRD	Intron
ESR1	Intron
PTPRD	Intron
LOC105378061	Other
PRKN	Intron
AGPAT4	Intron
GLDC	Intron
none	Intergenic
GLDC	Intron
none	Intergenic
TUSC3	Exon
LOC101929028	Other
none	Intergenic
none	Intergenic
VPS37A	Intron
SGCZ	Intron
DEFB134	Intron
MTMR9	Intron
SGCZ	Intron
LOC107986933	Other
HNF4G	Intron
LOC101929294	Other
none	Intergenic
LOC107986952	Other
LOC107986952	Other
LOC107986952	Other
LOC107986952	Other
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CNPY1	Intron
CNPY1	Intron
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PAG1	Intron
CSMD1	Intron
CSMD1	Intron
CSMD1	Intron
ST18	Exon

none	Intergenic
XKR4	Intron
ARFGEF1	Intron
SNTG1	Intron
SNTG1	Intron
none	Intergenic
CLVS1	Other
LINC01414	Other
none	Intergenic
LOC286178	Exon
none	Intergenic
none	Intergenic
LINC01288	Other
none	Intergenic
none	Intergenic
KCNB2	Intron
none	Intergenic
none	Intergenic
IKBKB-DT	Exon
LOC105379389	Other
LOC105379389	Other
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ZFPM2	Intron
none	Intergenic
PRKAG2	Intron
RIMS2	Intron
none	Intergenic
none	Intergenic
ZFPM2	Intron
LHFPL3	Intron
LHFPL3	Intron
TFEC	Intron
TFEC	Intron
none	Intergenic
ZNF277	Intron
AKAP9	Exon
KRIT1	Intron
LINC01608	Other
none	Intergenic
ELAPOR2	Exon
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105375416	Other
none	Intergenic
none	Intergenic
CALCR	Intron
CALCR	Intron
EBAG9	Exon

SYBU	Intron
NECAB1	Intron
LRRC69	Intron
LOC105375631	Other
SLC26A7	Intron
EXOC4	Intron
none	Intergenic
LOC105375523	Other
none	Intergenic
PRKAG2	Intron
CNBD1	Intron
CNBD1	Intron
LOC105375631	Other
TCAF2P1	Other
TCAF2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CADPS2	Intron
NIPAL2	Intron
none	Intergenic
CTTNBP2	Intron
KLHDC10	Intron
CHCHD3	Intron
CIBAR1-DT	Other
CFAP418-AS1	Other
GRM8	Intron
PTDSS1	Intron
none	Intergenic
LOC105379144	Other
MUSK	Intron
LOC107986441	Other
SVEP1	Intron
none	Intergenic
ZNF608	Intron
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none	Intergenic
none	Intergenic
LOC101927421	Other
SRFBP1	Intron
SLC44A1	Intron
ASTN2	Intron
ASTN2	Intron
ASTN2	Intron
none	Intergenic
none	Intergenic
KIAA1958	Intron
none	Intergenic
SLC31A1	Intron
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none	Intergenic

none	Intergenic
FBXL17	Intron
LOC105378211	Other
C5orf46	Intron
C5orf46	Intron
JAKMIP2	Intron
SHC3	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
SGCD	Other
LINC01508	Other
none	Intergenic
DDX46	Intron
FSTL4	Intron
MARCHF3	Intron
MARCHF3	Intron
PLPPR1	Intron
LOC102723654	Other
INVS	Intron
DIAPH1	Intron
GAS2L1P2	Other
ARHGAP26	Intron
none	Intergenic
SMAD5	Intron
SPOCK1	Intron
none	Intergenic
none	Intergenic
RAB3C	Intron
none	Intergenic
STS	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CWC27	Intron
PDE4D	Intron
LOC105378998	Other
NDUFAF2	Intron
PRLR	Intron
none	Intergenic
none	Intergenic
NIPBL	Intron
none	Intergenic
none	Intergenic
none	Intergenic
MID1	Intron
none	Intergenic
none	Intergenic
EMB	Intron
C9	Intron

FYB1	Intron
C7	Intron
LOC105374745	Other
GHR	Intron
none	Intergenic
ADGRV1	Intron
none	Intergenic
none	Intergenic
LOC105379082	Other
C5	Intron
none	Intergenic
none	Intergenic
FCHO2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
EDIL3	Intron
GOLGA2	Intron
RALGDS	Intron
none	Intergenic
SV2C	Intron
OTP	Intron
MED27	Intron
none	Intergenic
LHFPL2	Intron
none	Intergenic
ZCCHC7	Intron
LOC105377865	Other
LOC105377865	Other
none	Intergenic
LOC105376017	Other
LOC100506851	Other
none	Intergenic
none	Intergenic
none	Intergenic
KHDRBS2	Intron
KHDRBS2	Intron
none	Intergenic
CNTNAP3B	Intron
EYS	Intron
LGSN	Exon
none	Intergenic
LOC101927293	Other
ADGRB3	Intron
none	Intergenic
CNTNAP3	Intron
none	Intergenic
ADGRB3	Intron
none	Intergenic
LOC112268034	Exon
AFG1L	Intron

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AFG1L	Intron
LIN28B	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
FAM184A	Intron
none	Intergenic
RWDD1	Intron
none	Intergenic
none	Intergenic
RRAGD	Intron
none	Intergenic
LINGO2	Intron
LINGO2	Intron
FARS2	Intron
LY86	Intron
none	Intergenic
LOC105374898	Other
LOC105374898	Other
LY86	Intron
BMP6	Intron
CAGE1	Intron
none	Intergenic
LOC102723944	Other
none	Intergenic
SLC22A23	Intron
LOC101927329	Other
none	Intergenic
NUP153	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
none	Intergenic
TENM2	Intron
none	Intergenic
NSD1	Exon
none	Intergenic
none	Intergenic
CYP39A1	Intron
SUPT3H	Intron
TDRD6	Other
TDRD6	Other
none	Intergenic
ADGRF5	Exon
CNTNAP3P2	Other

none	Intergenic
LOC102723789	Other
none	Intergenic
POLR1C	Intron
CNTNAP3C	Other
MLIP	Intron
none	Intergenic
FAM83B	Intron
none	Intergenic
none	Intergenic
CDKAL1	Intron
CDKAL1	Intron
none	Intergenic
none	Intergenic
HCG17	Other
none	Intergenic
PLUT	Other
none	Intergenic
CDK8	Intron
none	Intergenic
none	Intergenic
GJA3	Exon
none	Intergenic
B3GLCT	Intron
none	Intergenic
UBL3	Intron
none	Intergenic
MTUS2	Intron
KL	Exon
STARD13	Intron
none	Intergenic
TXNRD1	Intron
BTBD11	Intron
BTBD11	Intron
RFX4	Intron
none	Intergenic
WASHC4	Intron
none	Intergenic
RMST	Other
none	Intergenic
none	Intergenic
none	Intergenic
CLIP1	Intron
CLIP1	Intron
TMEM233	Exon
none	Intergenic
none	Intergenic
MAP1LC3B2	Intron
none	Intergenic
none	Intergenic
none	Intergenic

OBI1-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
PCDH9	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
none	Intergenic
ATP7B	Intron
ATP7B	Intron
DLEU1	Exon
LINC00407	Other
none	Intergenic
ENOX1	Intron
LOC105370198	Other
none	Intergenic
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none	Intergenic
LINC00448	Other
none	Intergenic
none	Intergenic
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LOC105370217	Other
none	Intergenic
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DIAPH3	Intron
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NUDT4	Intron
PIK3C2G	Intron
none	Intergenic
ST8SIA1	Intron
SLC15A5	Intron
none	Intergenic
PRH1	Intron
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CPNE8	Intron
none	Intergenic
none	Intergenic
LOC105369715	Other
none	Intergenic
RASSF8	Intron
SOX5	Intron
SOX5	Intron
none	Intergenic
CDON	Intron
LINC02725	Other
LINC02551	Other

LINC02551	Other
LINC02551	Other
ADAMTS15	Intron
none	Intergenic
BARX2	Intron
ARHGAP32	Intron
GRIK4	Intron
SORL1	Intron
FXYD6	Intron
GRAMD1B	Intron
MIR100HG	Other
SNX19	Exon
ANO2	Intron
DDX12P	Other
none	Intergenic
none	Intergenic
ERC1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
PPP1R12A-AS2	Other
TRHDE	Other
none	Intergenic
none	Intergenic
none	Intergenic
LOC107984543	Other
none	Intergenic
PLEKHG7	Intron
TMTC2	Intron
none	Intergenic
MGAT4C	Intron
VDR	Intron
VDR	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
TMEM117	Intron
SRGAP1	Intron
LOC105369812	Other
FRS2	Intron
none	Intergenic
none	Intergenic
SLC16A7	Intron
none	Intergenic
none	Intergenic
UNC13C	Intron
none	Intergenic
none	Intergenic

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none	Intergenic
ALDH1A2	Intron
none	Intergenic
none	Intergenic
DAPK2	Intron
none	Intergenic
SNHG14	Other
OCA2	Other
GABRG3	Intron
none	Intergenic
none	Intergenic
EIF2AK4	Intron
none	Intergenic
none	Intergenic
none	Intergenic
TRPM1	Intron
none	Intergenic
AQR	Intron
HS3ST2	Intron
REXO5	Intron
PDILT	Intron
LINC02194	Other
GSG1L	Intron
TNRC6A	Intron
HS3ST4	Intron
TXNDC11	Intron
SNN	Exon
none	Intergenic
GRIN2A	Intron
SHISA9	Intron
none	Intergenic
BMERB1	Intron
FTO	Intron
CHD9	Exon
PHKB	Intron
PHKB	Intron
AKAP13	Intron
SLCO3A1	Intron
ANKRD34C-AS1	Other
TMC3-AS1	Other
ZFAND6	Intron
none	Intergenic
none	Intergenic
RBFOX1	Intron
RBFOX1	Intron
RBFOX1	Intron
LOC105369212	Other
IGF1R	Intron
LINC02253	Other

none	Intergenic
none	Intergenic
G2E3-AS1	Other
HEATR5A-DT	Other
none	Intergenic
none	Intergenic
NPAS3	Intron
LOC105370461	Exon
none	Intergenic
LINC02315	Other
LINC02315	Other
NPAS3	Intron
SFTA3	Other
TTC6	Intron
SLC25A21	Intron
PCCA	Intron
GPC5	Intron
GPC6	Intron
GPC6	Intron
HS6ST3	Intron
GPC6	Intron
none	Intergenic
RPGRIP1	Intron
LOC107984626	Other
none	Intergenic
none	Intergenic
NALF1	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
none	Intergenic
NRXN3	Intron
none	Intergenic
none	Intergenic
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LOC105378178	Other
none	Intergenic
MDGA2	Intron
SIPA1L1	Intron
none	Intergenic
none	Intergenic
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PRKCH	Intron
PRKCH	Intron
none	Intergenic
none	Intergenic
LOC105371657	Other

LOC105371657	Other
none	Intergenic
BRINP3	Intron
LOC101928933	Other
TRMT1L	Intron
none	Intergenic
KLHL12	Intron
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none	Intergenic
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PFKFB2	Intron
NFASC	Intron
LOC105371661	Other
none	Intergenic
none	Intergenic
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RGS5	Intron
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KLHL20	Intron
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RALGPS2	Intron
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POU2F1	Exon
NME7	Intron
PRRC2C	Intron
LINC01681	Other
none	Intergenic
KIF26B	Intron
none	Intergenic
RYS2	Intron
RGS7	Intron
none	Intergenic
CHRM3	Intron
CAMK1D	Intron
CELF2	Intron
ADARB2	Intron
none	Intergenic
USH2A	Intron
TRAF3IP3	Intron
none	Intergenic
TRAF3IP3	Intron
LOC105372892	Other
CCSAP	Exon
TP53BP2	Intron

none	Intergenic
DNAH14	Intron
LINC02778	Other
LINC02778	Other
none	Intergenic
DAB1	Intron
SCP2	Intron
ZFYVE9	Intron
LOC105378740	Other
TNNI3K	Intron
LOC105378800	Other
AK5	Intron
none	Intergenic
none	Intergenic
LOC105378789	Other
none	Intergenic
ZBTB40	Other
EIF4G3	Intron
PLA2G5	Other
none	Intergenic
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IPP	Intron
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SDC3	Intron
CSMD2	Intron
none	Intergenic
ZMYND12	Intron
HIVEP3	Intron
HIVEP3	Intron
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SORT1	Exon
CSDE1	Intron
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NTNG1	Intron
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CTXND2	Intron
none	Intergenic
LINC01525	Other
none	Intergenic
EMBP1	Other
WARS2-AS1	Other
WARS2-AS1	Other
none	Intergenic
ADGRL2	Intron
none	Intergenic

SSX2IP	Intron
TTLL7	Intron
none	Intergenic
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LRRC4C	Intron
none	Intergenic
CCDC73	Intron
LOC105376621	Other
none	Intergenic
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LINC02745	Other
none	Intergenic
TSPAN18	Intron
TMEM41B	Intron
LOC105376542	Other
none	Intergenic
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none	Intergenic
PPFIBP2	Intron
none	Intergenic
PDE3B	Intron
none	Intergenic
CCDC179	Intron
none	Intergenic
BDNF-AS	Other
BDNF-AS	Other
SOX6	Intron
none	Intergenic
NELL1	Intron
NELL1	Intron
NAV2	Intron
CNTN5	Intron
none	Intergenic
MMP13	Intron
WTAPP1	Other
none	Intergenic
none	Intergenic
C11orf54	Exon
AMOTL1	Intron
ZBTB16	Intron
ZBTB16	Intron
none	Intergenic
CADM1	Intron
none	Intergenic
none	Intergenic

UVRAG	Intron
GDPD4	Exon
none	Intergenic
none	Intergenic
none	Intergenic
SLC22A20P	Other
LOC107984361	Other
LOC107984361	Other
DISC1FP1	Other
DISC1FP1	Other
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DLG2	Intron
PRKG1	Intron
PRKG1	Intron
PCDH15	Intron
none	Intergenic
PCDH15	Intron
PCDH15	Intron
none	Intergenic
none	Intergenic
TMEM72-AS1	Other
C10orf71	Intron
C10orf71	Intron
none	Intergenic
none	Intergenic
PTPN20	Intron
PTPN20	Intron
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BICC1	Intron
none	Intergenic
RTKN2	Exon
RSU1	Intron
PLXDC2	Intron
HACD1	Intron
ARL5B	Exon
BEND7	Exon
BEND7	Exon
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BEND7	Exon

none	Intergenic
LINC02680	Other
FHIP2A	Intron
none	Intergenic
none	Intergenic
SORCS3	Intron
SORCS1	Intron
none	Intergenic
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TACC2	Exon
none	Intergenic
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LOC105378396	Other
none	Intergenic
KAT6B	Intron
KCNMA1	Intron
LRMDA	Intron
SORBS1	Intron
CC2D2B	Intron
PLCE1	Intron
FRA10AC1	Intron
DNMBP	Intron
PIK3AP1	Intron
RNLS	Intron
TNKS2-AS1	Other
none	Intergenic
N6AMT1	Other
N6AMT1	Intron
LINC01695	Other
none	Intergenic
none	Intergenic
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LRRTM4	Intron
LRRTM4	Intron
LRRTM4	Intron
LOC105374814	Other
ZNF638	Intron
LOC102724355	Other
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LOC105374593	Other

LHCGR	Intron
none	Intergenic
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FSHR	Intron
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NRXN1	Intron
NRXN1	Intron
none	Intergenic
SRBD1	Intron
CAMKMT	Intron
VRK2	Intron
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none	Intergenic
CCDC85A	Intron
none	Intergenic
ACYP2	Intron
INPP4A	Intron
AFF3	Intron
KANSL3	Intron
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MAP4K4	Intron
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LOC101927967	Other
none	Intergenic
CYTOR	Other
RNF103-CHMP3	Intron
RGPD2	Other
none	Intergenic
LOC105372225	Other
LOC105372225	Other
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LOC105372225	Other
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LOC105372225	Other
ATP9B	Intron
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LOC105372225	Other
LOC105372225	Other
LOC105372225	Other
CHST8	Intron
none	Intergenic
ZNF540	Intron
LOC100505851	Exon
ZNF724	Intron
VSTM2B	Intron
LINC00662	Exon
LOC105372225	Other
LOC105372225	Other
LOC105372225	Other
SERPINB13	Intron
none	Intergenic
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LOC105372225	Other
ZNF236-DT	Other
LOC339298	Other
LOC105372225	Other
LOC105372225	Other
LOC105372225	Other
LOC105372225	Other
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LOC105372225	Other
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LOC105372185	Other
DOK6	Intron
none	Intergenic
none	Intergenic
none	Intergenic
TRMT61B	Intron
LOC105373451	Other
HEATR5B	Intron
HEATR5B	Intron
none	Intergenic
YPEL5	Intron
ALK	Intron
GACAT3	Other
MYCNUT	Other
TTYH1	Exon
LOC107985342	Other
LOC107985342	Other
SNTG2	Intron
none	Intergenic
CEACAM7	Intron
LOC105373436	Other
none	Intergenic
LOC105373436	Other
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none	Intergenic
ASAP2	Intron
LOC105373411	Other
none	Intergenic
RNF144A	Intron
SCHLAP1	Other
SCHLAP1	Other
PLCB1	Intron
none	Intergenic
PPP1R1C	Intron
PPP1R1C	Intron
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ZNF343	Intron
ZNF343	Intron
METTL5	Intron
none	Intergenic
LOC101926913	Other
OSBPL6	Intron
SNAP25	Intron
PLCB4	Intron

CCDC141	Intron
none	Intergenic
none	Intergenic
PTH2R	Intron
none	Intergenic
none	Intergenic
DOCK10	Exon
PARD3B	Intron
VWC2L	Intron
SPAG16	Intron
SPAG16	Intron
PLCD4	Intron
DIRC3	Other
FN1	Intron
none	Intergenic
LOC107985988	Other
LOC107985988	Other
ERBB4	Intron
none	Intergenic
DNER	Intron
none	Intergenic
none	Intergenic
NBEAL1	Intron
NYAP2	Intron
none	Intergenic
LINC01807	Other
none	Intergenic
MFF-DT	Intron
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none	Intergenic
LOC105376980	Exon
CNTNAP5	Intron
none	Intergenic
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LOC107987282	Other
none	Intergenic
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THSD7B	Intron
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none	Intergenic
MIR4435-2HG	Other
none	Intergenic
TSHZ2	Intron
CLASP1	Intron
TSHZ2	Intron

PTPN4	Intron
LOC107985955	Other
none	Intergenic
GPD2	Intron
TANC1	Intron
none	Intergenic
CCDC148	Intron
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KCNH7	Intron
none	Intergenic
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BAZ2B	Other
none	Intergenic
none	Intergenic
LOC102724968	Other
none	Intergenic
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LRP1B	Intron
PTPRT	Intron
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RIF1	Intron
BPIFB3	Intron
LOC105373691	Other
RALGAPB	Intron
none	Intergenic
KRBA2	Exon
none	Intergenic
HEATR6	Intron
none	Intergenic
none	Intergenic
ZNF521	Intron
LOC101927571	Other
none	Intergenic
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TRIM25	Intron
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PIEZO2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
KANSL1	Intron
none	Intergenic
none	Intergenic
PIEZO2	Intron
SPIRE2	Intron
none	Intergenic
none	Intergenic
SLFN12L	Exon

SLFN12L	Exon
LOC105371819	Other
ASIC2	Intron
AA06	Intron
AA06	Intron
none	Intergenic
MAPRE2	Exon
SLFN12L	Exon
none	Intergenic
CCDC178	Intron
DSC2	Exon
RARA	Exon
CHST9	Intron
TRIM16L	Exon
ZNF286A-TBC1D26	Other
TRIM16	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
LINC01992	Exon
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ZFH3	Intron
LOC107984878	Other
EMILIN2	Intron
CDH11	Intron
DYNLRB2-AS1	Other
MAFTRR	Other
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COG1	Intron
TCF4	Intron
TCF4	Intron
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AP1G1	Intron
none	Intergenic
LIPH	Intron
LINC02869	Other
FSTL5	Intron
none	Intergenic
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ABHD14A	Intron
none	Intergenic
none	Intergenic
ENOX2	Intron
BMPER	Intron
LOC105377858	Other
none	Intergenic
RREB1	Intron
TMC7	Intron
LOC107984685	Other
BDKRB2	Intron
PTBP2	Intron
LINC01499	Other
none	Intergenic
PAPSS2	Intron
RELCH	Intron
ASXL3	Intron
none	Intergenic
none	Intergenic
PSEN1	Intron
FAM189A1	Intron
ACOT13	Intron
CMAHP	Other
SIPA1L1-AS1	Other
LIN52	Intron
none	Intergenic
ADGRB3	Intron
PCNX1	Intron
none	Intergenic
RGS6	Intron
TJP1	Intron
none	Intergenic
SIPA1L1-AS1	Other
GUSBP2	Other
EYS	Intron
SLC17A3	Intron
NRXN3	Exon
NRXN3	Other
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none	Intergenic
TTLL5	Intron
ESRRB	Intron
ADCK1	Intron
none	Intergenic

MTMR10	Intron
none	Intergenic
IMPG1	Intron
none	Intergenic
PRKCH	Other
none	Intergenic
none	Intergenic
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none	Intergenic
SH3BGRL2	Other
none	Intergenic
IRAK1BP1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
LOC105377858	Other
none	Intergenic
GALNT16-AS1	Other
none	Intergenic
none	Intergenic
ADGRB3	Intron
PALS1	Intron
KLF13	Intron
ZBTB25	Exon
KCNQ5	Intron
KCNQ5	Intron
KCNQ5	Intron
none	Intergenic
RIMS1	Intron
ADGRF5	Intron
TSBP1	Intron
CYP39A1	Intron
none	Intergenic
NUDT3	Intron
SETD3	Intron
UHRF1BP1	Intron
EML1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CLMN	Intron
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LOC107986602	Other
none	Intergenic
none	Intergenic
LOC105370734	Exon
UHRF1BP1	Intron
none	Intergenic
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BRF1	Intron
TRERF1	Intron

TRERF1	Intron
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none	Intergenic
LOC101929555	Other
none	Intergenic
DNAH8	Intron
none	Intergenic
BRPF3	Intron
SUPT3H	Intron
MEG8	Other
SUPT3H	Intron
CPNE5	Intron
MOK	Intron
POLR1C	Intron
TMEM217	Intron
HCRT2	Intron
none	Intergenic
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HMGCLL1	Intron
HMGCLL1	Intron
HMGCLL1	Intron
HMGCLL1	Intron
DST	Intron
none	Intergenic
CEP128	Intron
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LOC105375001	Exon
none	Intergenic
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DGLUCY	Intron
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IL17A	Intron
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MLIP	Intron
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LINC02296	Other
none	Intergenic
none	Intergenic
none	Intergenic

PTPN21	Intron
FBXO9	Other
EFCAB11	Intron
none	Intergenic
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none	Intergenic
RAB20	Intron
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TUBGCP3	Intron
TUBGCP3	Intron
NALF1	Intron
NKAIN2	Intron
none	Intergenic
RSPO3	Intron
none	Intergenic
LOC107984608	Other
none	Intergenic
NKAIN2	Intron
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OXA1L-DT	Other
OXA1L-DT	Other
STXBP6	Intron
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CFAP97D2	Other
MAN1A1	Intron
MAN1A1	Intron
FAM184A	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
KPNA5	Intron
NT5DC1	Intron
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GPC6	Intron
LOC101927284	Other
CLDN10	Intron
GPC5	Intron
ECT2L	Intron
none	Intergenic
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GPC5	Intron
GPC5	Intron

HBS1L	Intron
HS6ST3	Intron
ENPP1	Intron
LOC102723445	Other
none	Intergenic
NALCN-AS1	Other
none	Intergenic
LAMA2	Intron
none	Intergenic
SLC2A12	Intron
none	Intergenic
FARP1	Intron
DOCK9	Intron
none	Intergenic
CLYBL	Intron
none	Intergenic
none	Intergenic
ANKRD6	Exon
none	Intergenic
LOC107984644	Other
LOC105377885	Other
LINC00871	Other
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TRIM9	Intron
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FRMD6	Intron
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LOC112268134	Exon
none	Intergenic
none	Intergenic
SNAP91	Intron
none	Intergenic
SYNCRIP	Exon
none	Intergenic
LOC105378178	Other
CDKL1	Exon
G2E3-AS1	Other
G2E3-AS1	Other
PREP	Intron
none	Intergenic
none	Intergenic
AKAP6	Intron

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CRYBG1	Intron
GRIK2	Intron
none	Intergenic
AMD1	Exon
FIG4	Intron
FOXO3	Intron
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LOC101927314	Other
LOC105370456	Other
LOC101927314	Other
none	Intergenic
SEC23A	Intron
PRORP	Intron
none	Intergenic
none	Intergenic
FBXL4	Intron
SLC25A21	Intron
SLC25A21	Intron
OTUD7A	Intron
OPHN1	Intron
CEP120	Intron
none	Intergenic
NOMO3	Intron
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none	Intergenic
none	Intergenic
PRDM6	Intron
SNX24	Exon
NOMO2	Intron
none	Intergenic
BMERB1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
MRTFB	Exon
MIR193BHG	Other
MIR193BHG	Other
none	Intergenic
PARN	Intron
PARN	Intron
NOMO1	Intron
none	Intergenic

SMG1	Intron
CACNG3	Intron
none	Intergenic
HS3ST4	Intron
none	Intergenic
HS3ST4	Intron
none	Intergenic
LOC105379149	Other
IQCK	Intron
LOC105371117	Exon
LOC105379149	Other
none	Intergenic
none	Intergenic
GP2	Intron
none	Intergenic
LYRM1	Intron
LOC101927421	Other
SNX29	Intron
SPOCK1	Intron
SPOCK1	Exon
none	Intergenic
CDKL3	Intron
VDAC1	Other
MEIKIN	Intron
SPOCK1	Intron
none	Intergenic
ARHGAP26	Intron
none	Intergenic
PCSK6	Intron
EIF4EBP3	Intron
none	Intergenic
CTNNA1	Intron
none	Intergenic
MARCHF3	Intron
GRIN2A	Intron
LOC105371082	Other
none	Intergenic
CCDC192	Intron
CCDC192	Intron
RBFOX1	Intron
RBFOX1	Intron
RBFOX1	Intron
RBFOX1	Intron
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LOC105371308	Other
none	Intergenic
none	Intergenic
LOC105371310	Other

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ERAP1	Intron
CDH11	Intron
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SLCO4C1	Intron
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AP1G1	Intron
LOC105379080	Other
ZFH3	Intron
none	Intergenic
ARRDC3	Exon
ARRDC3	Exon
POLR3G	Intron
none	Intergenic
LOC101929710	Other
none	Intergenic
CBFB	Intron
KIAA0825	Intron
TANGO6	Intron
FAM172A	Intron
NR2F1-AS1	Other
none	Intergenic
none	Intergenic
EPB41L4A	Intron
NREP	Intron
STARD4-AS1	Other
CAMK4	Intron
SIAH1	Other
none	Intergenic
ZNF423	Intron
none	Intergenic
none	Intergenic
ANKRD26P1	Other
AP3S1	Intron
none	Intergenic
LOC101927078	Other
none	Intergenic
none	Intergenic
LPCAT2	Exon
none	Intergenic
MT1DP	Exon
NUP93	Intron
LOC105379105	Other
none	Intergenic
LINC00492	Other
none	Intergenic
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none	Intergenic
none	Intergenic

LOC105379117	Other
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TOX3	Intron
LINC01950	Other
NR3C1	Exon
none	Intergenic
LOC107983981	Other
WDR72	Intron
UNC13C	Intron
ZNF354B	Intron
ZNF354B	Intron
ZNF354B	Intron
PRTG	Intron
none	Intergenic
none	Intergenic
FARS2	Intron
LYRM4-AS1	Exon
none	Intergenic
MIR4713HG	Other
PXDC1	Intron
none	Intergenic
CDHR2	Intron
CPEB4	Intron
MYO1E	Intron
RORA	Exon
RANBP17	Intron
KCNIP1	Intron
KCNIP1	Intron
KCNIP1	Intron
KCNIP1	Intron
DOCK2	Intron
TLN2	Intron
DOCK2	Intron
LOC105377715	Other
TEX9	Intron
none	Intergenic
TCF12	Intron
LINC01951	Other
LINC01951	Other
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LINC01951	Other
ALDH1A2	Intron
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ALDH1A2	Intron
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DPH6-DT	Other
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none	Intergenic

none	Intergenic
FSIP1	Intron
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CHRNA7	Intron
none	Intergenic
FMN1	Exon
LOC105374971	Other
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CDKAL1	Intron
CDKAL1	Intron
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GPR176	Intron
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MYEF2	Intron
CAGE1	Intron
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RMDN3	Exon
RMDN3	Exon
CHP1	Intron
none	Intergenic
STARD9	Exon
none	Intergenic
none	Intergenic
AGBL1	Intron
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LOC105370958	Other
none	Intergenic
LINC01470	Other
AP3S2	Intron
none	Intergenic
CIB1	Exon
none	Intergenic
AKAP13	Intron
AKAP13	Intron
CLINT1	Intron
LOC102723985	Other
LOC102724001	Other
SGCD	Other
SGCD	Other
SGCD	Other
LINC00927	Other
none	Intergenic
PRELID2	Intron
none	Intergenic
none	Intergenic
KCTD16	Intron
none	Intergenic

none	Intergenic
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MCTP2	Intron
SV2B	Exon
none	Intergenic
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none	Intergenic
LINC01581	Other
LINC01581	Other
DPYSL3	Intron
MCTP2	Intron
LOC107984788	Other
none	Intergenic
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LOC105377700	Other
THSD4	Intron
none	Intergenic
MYO9A	Intron
MYO9A	Intron
SPG21	Intron
none	Intergenic
LOC105377706	Other
LOC105377706	Other
MEGF11	Intron
none	Intergenic
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LOC105377703	Other
LOC105377703	Other
LOC105377703	Other
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ATP10B	Intron
PTPN9	Intron
none	Intergenic
SCAPER	Intron
LINC01847	Exon
none	Intergenic
PEAK1	Intron
none	Intergenic
none	Intergenic
CHRNA3	Intron
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GABRG2	Intron
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none	Intergenic
none	Intergenic
none	Intergenic

PLXNA4	Intron
MUC19	Intron
PLXNA4	Intron
MKLN1	Intron
LOC107986849	Other
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PDZRN4	Intron
EXOC4	Intron
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MTPN	Exon
MTPN	Exon
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AGBL3	Intron
LINC-PINT	Other
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ARID2	Intron
SCAF11	Intron
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PPHLN1	Intron
WASL	Intron
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DDX23	Intron
GRM8	Intron
PPHLN1	Intron
LINC02402	Other
METTTL2B	Intron
SND1	Intron
TMEM117	Intron
TMEM117	Intron
SND1	Intron
GRM8	Intron
GRM8	Intron
BICD1	Intron
PDE3A	Intron
SLCO1C1	Intron
SLCO1B3	Intron
CNTNAP2	Intron
CNTNAP2	Intron
C2CD5	Intron
ETNK1-DT	Other
CNTNAP2	Intron

none	Intergenic
CNTNAP2	Intron
PDE3A	Intron
ACTR3C	Intron
none	Intergenic
none	Intergenic
none	Intergenic
ACTR3B	Intron
NUB1	Intron
none	Intergenic
CCDC91	Intron
ERGIC2	Intron
none	Intergenic
IPO8	Intron
DGKI	Intron
LOC349160	Other
PPFIBP1	Intron
PPFIBP1	Intron
SMCO2	Intron
TPK1	Intron
TPK1	Intron
DNAI7	Exon
DNAI7	Exon
none	Intergenic
MGAM	Intron
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SRPK2	Other
none	Intergenic
none	Intergenic
LHFPL3	Intron
LHFPL3	Intron
none	Intergenic
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none	Intergenic
KCNC2	Intron
KCNC2	Intron
CAPS2	Intron
none	Intergenic
none	Intergenic
FBXL13	Intron
LOC107986836	Other
LOC105375448	Exon
none	Intergenic
ZFC3H1	Intron
TRHDE	Other
none	Intergenic
TRHDE	Exon
FBXL13	Intron

PTPRZ1	Intron
OTOGL	Intron
PTPRQ	Intron
PTPRQ	Intron
PTPRQ	Exon
LOC105369867	Other
LIN7A	Intron
PON2	Intron
PON2	Intron
PPP1R9A	Intron
LOC105369873	Other
PPP1R9A	Intron
OTOGL	Intron
none	Intergenic
none	Intergenic
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NAV3	Intron
NAV3	Intron
FAM200A	Other
PTCD1	Intron
none	Intergenic
LRIG3-DT	Other
LOC105375470	Other
LRIG3-DT	Other
CTTNBP2	Intron
SLC16A7	Intron
SLC16A7	Intron
none	Intergenic
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LOC102724495	Other
LINC02388	Other
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CPED1	Intron
CPED1	Intron
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ITGA5	Intron
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GRIP1	Intron
GRIP1	Intron
GRIP1	Intron
GRIP1	Intron
DOCK4	Exon
DOCK4	Intron
LOC105375451	Other

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HMGA2	Intron
TAF2	Intron
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LEMD3	Intron
LEMD3	Intron
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GUCY1A2	Intron
CUL5	Intron
ADAM9	Intron
LOC105375817	Other
none	Intergenic
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HOOK3	Intron
CASP4LP	Other
none	Intergenic
POLB	Intron
GRIA4	Intron
none	Intergenic
NRG1	Intron
ZBTB16	Intron
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none	Intergenic
NRG1	Intron
LINC02698	Other
none	Intergenic
LINC00589	Other
KCNU1	Intron
LOC105379364	Other
LOC105369501	Other
DISC1FP1	Other
DISC1FP1	Other
none	Intergenic
none	Intergenic
TOX	Intron
none	Intergenic
CYP7A1	Exon
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FAT3	Intron
none	Intergenic
none	Intergenic
none	Intergenic
DISC1FP1	Other

none	Intergenic
CLVS1	Other
CLVS1	Other
CLVS1	Other
LOC101929174	Other
LOC101929174	Other
NOX4	Intron
none	Intergenic
none	Intergenic
PRKDC	Intron
CNTN5	Intron
none	Intergenic
SNTG1	Intron
SNTG1	Intron
CNTN5	Intron
LOC105375852	Other
ARHGAP42	Intron
EFCAB1	Intron
none	Intergenic
none	Intergenic
RB1CC1	Intron
none	Intergenic
ANKRD49	Intron
LYN	Intron
none	Intergenic
ATP6V1H	Intron
none	Intergenic
TNKS	Intron
TSPAN9	Intron
ZNF705G	Intron
none	Intergenic
VWF	Intron
LOC105377795	Other
none	Intergenic
DLC1	Intron
DLC1	Intron
MSRA	Intron
none	Intergenic
CSMD1	Intron
KIF13B	Intron
HEBP1	Intron
GSG1	Exon
none	Intergenic
ZNF705A	Intron
none	Intergenic
DPP6	Intron
GPRC5A	Exon
CSMD1	Intron
CSMD1	Intron
CLEC1A	Intron
KLRC3	Intron

LINC02366	Other
LOC105377784	Other
PRH1	Intron
LOC105377783	Other
none	Intergenic
ETV6	Intron
OPCML	Intron
LOC101929294	Other
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SGCZ	Intron
OR8B2	Exon
OR8B3	Exon
HMBOX1	Intron
none	Intergenic
ELP3	Intron
TBCEL	Intron
SORL1	Intron
SORL1	Intron
MIR100HG	Other
KIRREL3	Intron
none	Intergenic
LOC101929028	Other
LOC101929028	Other
NTM	Intron
NTM	Intron
none	Intergenic
OPCML	Intron
OPCML	Intron
SGCZ	Intron
none	Intergenic
MTMR7	Intron
CSGALNACT1	Intron
none	Intergenic
LOC100128993	Other
LOC105379301	Exon
ARHGAP32	Intron
PSD3	Intron
none	Intergenic
PCM1	Intron
TMTC2	Intron
none	Intergenic
THSD7A	Intron
MGC4859	Other
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LOC105375147	Other
LOC105375147	Other
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RCBTB1	Intron
AGMO	Intron
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DLEU7	Intron
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ETV1	Intron
ETV1	Intron
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SDK1	Intron
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RNF216P1	Other
none	Intergenic
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LOC105370219	Other
LOC105370221	Other
LOC105370221	Other
COL28A1	Intron
LOC105375167	Other
SUCLA2	Intron
none	Intergenic
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LOC107986777	Other
FREM2	Intron
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CHN2	Intron
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CPVL	Intron
LINC00457	Other
none	Intergenic
none	Intergenic
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DCLK1	Intron
COG6	Intron
none	Intergenic
GTF2F2	Intron
ZC3H13	Intron
LCP1	Exon
LRRC63	Intron

LOC101927609	Other
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DNAH11	Intron
NAA16	Intron
VWA8	Intron
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DGKH	Intron
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EPSTI1	Intron
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LINC00355	Other
none	Intergenic
SYNE1	Intron
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GINM1	Intron
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LMO7	Intron
IPCEF1	Intron
OBI1-AS1	Other
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ADGRG6	Intron
LINC00375	Other
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SAMD5	Intron
GRM1	Intron
LINC00333	Other
GRM1	Intron
GRM1	Intron
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LOC105378072	Other
none	Intergenic
PCDH9	Intron
PACRG	Intron
PRKN	Intron
LINC00383	Other
AGPAT4	Intron

PCDH9	Intron
CCR6	Intron
CCR6	Intron
CEP43	Intron
RPS6KA2	Intron
none	Intergenic
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ZDHH14	Intron
ZDHH14	Intron
ZDHH14	Intron
LOC105378075	Other
ARID1B	Intron
KLF12	Intron
LOC105370259	Other
none	Intergenic
SNX9	Intron
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SLC22A3	Intron
IGF2R	Intron
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DACH1	Intron
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STARD13	Intron
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LOC105375358	Other
LOC105375358	Other
GTF2IRD1	Intron
NFYB	Intron
CALN1	Intron
WASHC3	Intron
RSBN1L	Intron
MAGI2	Intron
LOC105375371	Other
ANKS1B	Intron
ANKS1B	Intron
MAGI2	Intron
ANKS1B	Intron
MAGI2	Intron
MAGI2	Intron
none	Intergenic
none	Intergenic
UTP20	Intron
LOC105370003	Other
ATXN2	Intron
IFT81	Intron

CUX2	Intron
ATXN2	Intron
TMEM116	Other
none	Intergenic
LOC102723639	Other
LOC102723639	Other
AUTS2	Intron
AUTS2	Intron
TCP11L2	Intron
RFX4	Intron
none	Intergenic
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BTBD11	Intron
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LINC01372	Other
GTF2IP23	Other
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ZNF804B	Intron
ZNF804B	Intron
LOC107986815	Other
none	Intergenic
ABCB1	Intron
STEAP2-AS1	Other
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LINC02820	Other
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none	Intergenic
MGAT4C	Intron
CDK14	Intron
LOC105369880	Other
ELAPOR2	Exon
PCLO	Intron
CACNA2D1	Intron
none	Intergenic
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PLXNC1	Exon
none	Intergenic
GRM3	Intron
none	Intergenic
LOC105369902	Other
none	Intergenic
none	Intergenic
PLEKHG7	Exon

LINC02413	Exon
SOCS2	Other
none	Intergenic
RALA	Intron
NME8	Intron
none	Intergenic
ELMO1	Intron
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none	Intergenic
ANKRD26P3	Other
HECW1	Intron
LINC01448	Other
none	Intergenic
none	Intergenic
LATS2	Intron
LOC107986788	Other
none	Intergenic
HMGB1	Intron
HMGB1	Intron
DPY19L1P1	Other
AVL9	Intron
B3GLCT	Intron
PDE1C	Intron
AQP1	Intron
AQP1	Intron
DPY19L1P1	Other
SEPTIN7	Intron
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FLT1	Intron
NPSR1	Intron
BBS9	Intron
BBS9	Intron
BBS9	Intron
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VPS37B	Intron
NRAV	Intron
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CCDC62	Exon
ABCB9	Other
LINC01446	Other
RFLNA	Intron
BRI3BP	Intron
BRI3BP	Intron
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AACS	Intron

EGFR	Intron
EGFR	Intron
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MED13L	Intron
NOS1	Intron
NOS1	Intron
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TAOK3	Intron
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TMEM132B	Intron
RIMBP2	Intron
RIMBP2	Intron
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LOC101929974	Other
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ABCA13	Intron
none	Intergenic
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LINC00508	Other
none	Intergenic
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SPATA48	Intron
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LOC101929319	Other
none	Intergenic
CPNE4	Other
KBTBD12	Intron
GALNT13	Intron
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LOC105374124	Other
none	Intergenic
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TMEM108	Intron
LOC105373696	Other
KBTBD12	Intron
TMEM163	Intron
CASR	Intron
SLC49A4	Intron
CCDC148	Intron

BAZ2B	Intron
none	Intergenic
PLA2R1	Intron
ROPN1	Intron
KALRN	Intron
none	Intergenic
ALG1L	Intron
OSBPL11	Intron
none	Intergenic
HEG1	Intron
HEG1	Intron
LOC107985955	Other
KALRN	Intron
PPP2R3A	Intron
PPP2R3A	Intron
PLSCR2	Other
LRP1B	Intron
none	Intergenic
LRP1B	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
THSD7B	Intron
none	Intergenic
LOC105374140	Other
LRP1B	Exon
none	Intergenic
none	Intergenic
MRAS	Exon
none	Intergenic
none	Intergenic
none	Intergenic
LOC105374126	Other
none	Intergenic
none	Intergenic
ACVR2A	Intron
none	Intergenic
SLC9A9	Intron
none	Intergenic
ATR	Intron
GRK7	Intron
LOC100505498	Exon
none	Intergenic
none	Intergenic
none	Intergenic
UPK1B	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic

none	Intergenic
SENP7	Intron
LINC01934	Other
none	Intergenic
LOC101929485	Other
none	Intergenic
ALCAM	Intron
ALCAM	Intron
LOC107986108	Other
CCDC141	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CALCRL	Exon
none	Intergenic
COL5A2	Intron
LOC101927252	Other
none	Intergenic
MSTN	Intron
none	Intergenic
PDE1A	Intron
none	Intergenic
none	Intergenic
EPHA6	Intron
none	Intergenic
ZNF804A	Intron
none	Intergenic
none	Intergenic
GRAMD1C	Intron
none	Intergenic
LOC101926886	Other
CSRNP3	Intron
SCN1A	Intron
none	Intergenic
SCN1A-AS1	Other
CCDC191	Intron
LOC107985962	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
TANK-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
SLC4A10	Intron
KCNH7	Intron
none	Intergenic
none	Intergenic
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none	Intergenic

none	Intergenic
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LOC105373727	Other
LSAMP	Intron
LSAMP	Intron
SLC25A12	Intron
none	Intergenic
ITGA6	Intron
LINC01205	Other
RAPGEF4	Intron
WIPF1	Intron
LINC00636	Other
CHN1	Intron
none	Intergenic
ATF2	Intron
SLC25A12	Intron
LOC105374039	Other
none	Intergenic
NECTIN3	Intron
FASTKD1	Intron
UBR3	Intron
UBR3	Intron
none	Intergenic
UBR3	Intron
LOC105374037	Other
CSNKA2IP	Intron
RPL39L	Intron
LPP	Intron
RPL39L	Intron
LOC105374258	Other
none	Intergenic
none	Intergenic
none	Intergenic
FGF12	Intron
LOC107985905	Other
none	Intergenic
P3H2	Intron
none	Intergenic
LOC112268420	Exon
TPRG1	Intron
TPRG1	Other
TPRG1	Other
CHMP3	Intron
none	Intergenic
CRACDL	Exon
SOX2-OT	Other
none	Intergenic
AFF3	Intron
none	Intergenic
none	Intergenic
MAP4K4	Intron

TMEM131	Intron
TMEM131	Intron
none	Intergenic
none	Intergenic
LINC02054	Other
ANKRD36C	Intron
none	Intergenic
EIF2B5-DT	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC107985894	Other
none	Intergenic
ANXA4	Intron
none	Intergenic
PAIP2B	Intron
PAIP2B	Intron
none	Intergenic
none	Intergenic
CLNK	Intron
EXOC6B	Intron
none	Intergenic
C1QTNF7-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
LINC01799	Exon
none	Intergenic
none	Intergenic
SORCS2	Intron
FAM193A	Intron
MUC4	Intron
none	Intergenic
LOC102724542	Other
FAM193A	Intron
ADD1	Intron
HTT	Intron
none	Intergenic
DCTN1-AS1	Other
STK32B	Intron
none	Intergenic
none	Intergenic
TMEM182	Intron
none	Intergenic
SCHIP1	Intron
none	Intergenic
LOC105373578	Other
none	Intergenic
CNTNAP5	Intron
none	Intergenic

IL12A-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
LOC107986049	Other
none	Intergenic
none	Intergenic
none	Intergenic
B3GALNT1	Exon
none	Intergenic
none	Intergenic
ARHGEF26	Intron
LINC02006	Other
none	Intergenic
GPR39	Intron
MBNL1	Intron
MGAT5	Intron
LINC02066	Exon
ARHGEF26	Intron
ARHGEF26	Intron
none	Intergenic
LOC105373605	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
GPR149	Intron
ARHGEF26	Intron
none	Intergenic
none	Intergenic
LOC105373539	Other
NLGN1	Intron
none	Intergenic
ECT2	Intron
LOC100128164	Exon
LINC01885	Other
none	Intergenic
TBL1XR1	Exon
LINC01965	Other
none	Intergenic
none	Intergenic
LOC105373529	Other
UXS1	Intron
NAALADL2	Intron
EGFEM1P	Other
LINC01322	Other
LINC01322	Other
LINC01322	Other
none	Intergenic
none	Intergenic
DPP10	Intron

DPP10	Intron
DPP10	Intron
DPP10	Intron
WDR49	Intron
DPP10	Intron
DPP10	Intron
WDR49	Intron
DPP10	Intron
LOC105374194	Other
MFSD6	Intron
CSNKA2IP	Intron
LOC102724637	Other
GRM7	Intron
SSUH2	Intron
LOC101927394	Other
none	Intergenic
GRM7	Intron
LOC101927182	Other
PTPRT	Intron
PTPRT	Intron
PTPRT	Intron
PTPRT	Intron
none	Intergenic
none	Intergenic
SRGAP3	Intron
CEP250	Intron
EPB41L1	Intron
none	Intergenic
IQSEC1	Intron
none	Intergenic
PPARG	Intron
none	Intergenic
none	Intergenic
LINC01734	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
TSHZ2	Intron
TBC1D22A	Other
none	Intergenic
none	Intergenic
DOK5	Intron
DOK5	Intron
LOC105372631	Other
none	Intergenic
ELMO2	Intron
SLC13A3	Intron
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EYA2	Intron
TRPC4AP	Intron

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MACROD2	Intron
MACROD2	Intron
KIF16B	Intron
PIGU	Intron
RARB	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
MACROD2	Intron
LINC00693	Other
ISM1	Intron
ISM1	Other
none	Intergenic
MACROD2	Intron
none	Intergenic
UBE2E2	Exon
none	Intergenic
LOC105376976	Other
none	Intergenic
LOC339862	Other
NANP	Exon
none	Intergenic
TBC1D5	Intron
DYNLRB1	Intron
none	Intergenic
KIZ	Intron
none	Intergenic
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LOC107985449	Other
none	Intergenic
LOC105376984	Other
none	Intergenic
DOK5	Intron
SHISAL1	Intron
UMODL1	Intron
FAM207A	Intron
LOC105372750	Other
SLC37A1	Intron
UMODL1	Intron
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none	Intergenic
LINC01692	Other
none	Intergenic
none	Intergenic
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none	Intergenic
none	Intergenic
BCL2L13	Intron

none	Intergenic
none	Intergenic
none	Intergenic
LINC00320	Other
NCAM2	Intron
none	Intergenic
none	Intergenic
LOC105372804	Other
BRWD1	Intron
LINC00649	Other
ITSN1	Intron
none	Intergenic
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LOC101928107	Exon
none	Intergenic
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LOC105372760	Other
KCNJ6	Intron
KCNJ6	Intron
HLCS	Intron
none	Intergenic
none	Intergenic
RBFOX2	Intron
TOM1	Intron
TOM1	Intron
SS18L1	Intron
SS18L1	Intron
none	Intergenic
LINC02885	Other
none	Intergenic
SLC5A4	Other
none	Intergenic
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ENTHD1	Intron
none	Intergenic
ZNF831	Intron
PHACTR3	Intron
LOC105372733	Other
TCN2	Intron
none	Intergenic
CHODL	Intron
TMPRSS15	Intron
none	Intergenic
PRAMENP	Other
MAPK1	Intron

MIR548XHG	Other
MAPK1	Intron
none	Intergenic
none	Intergenic
NF2	Intron
ZNRF3	Intron
SEZ6L	Intron
none	Intergenic
GRK3	Intron
none	Intergenic
none	Intergenic
GLS	Exon
none	Intergenic
CPS1	Intron
ERBB4	Intron
ERBB4	Intron
ERBB4	Intron
TAFA4	Intron
TAFA1	Intron
none	Intergenic
ROBO2	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105377164	Other
GXYLT2	Intron
none	Intergenic
LOC101928278	Other
DIRC3	Other
ATXN7	Intron
ATXN7	Intron
SYNPR	Intron
none	Intergenic
SYNPR	Other
none	Intergenic
USP37	Intron
DNPEP	Intron
LOC105373891	Other
ADAMTS9-AS2	Other
SPAG16	Intron
SPAG16	Intron
SPAG16	Intron
SPAG16	Intron
SPAG16	Intron
MAGI1	Intron
MAGI1	Intron
SNHG31	Other
SNHG31	Other
LOC107986094	Other
LOC105377127	Other

DNAH7	Intron
none	Intergenic
SLC39A10	Intron
none	Intergenic
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HECW2	Intron
none	Intergenic
CADM2	Intron
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HTR1F	Intron
HTR1F	Intron
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LOC102723364	Other
none	Intergenic
C2CD6	Intron
ROBO1	Intron
none	Intergenic
none	Intergenic
ANKRD44	Intron
GBE1	Intron
PLCL1	Intron
PLCL1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
ROBO1	Intron
ROBO1	Intron
LOC105373893	Other
LOC105373893	Other
LRRFIP2	Intron
UBOX5	Exon
CAPN10	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
PTPRA	Intron
ZNF343	Intron
ITGA9	Intron
EIF1B-AS1	Other
LOC105377039	Other
none	Intergenic
CSNK2A1	Intron

RSPO4	Intron
SDCBP2-AS1	Other
SIRPD	Intron
ITGA9	Intron
none	Intergenic
none	Intergenic
DYNC1LI1	Intron
PAK5	Intron
none	Intergenic
none	Intergenic
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none	Intergenic
LOC107985398	Other
RBMS3	Intron
RBMS3	Intron
none	Intergenic
LINC01428	Other
none	Intergenic
none	Intergenic
none	Intergenic
LOC105372520	Exon
PDCD6IP	Exon
PDCD6IP	Exon
PDCD6IP	Exon
PLCB1	Intron
PLCB1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
NYAP2	Intron
LOC105373914	Other
none	Intergenic
RHBDD1	Intron
MFF	Intron
SLC19A3	Intron
HYAL2	Exon
none	Intergenic
ARIH2	Intron
ERC2	Intron
LOC105373910	Other
LOC105373897	Other
none	Intergenic
LOC105377110	Other
none	Intergenic
ARHGEF3	Intron
COL7A1	Exon
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105377043	Other

PDE6D	Intron
none	Intergenic
none	Intergenic
C1QTNF7	Intron
AFTPH	Intron
none	Intergenic
DLGAP1	Intron
DLGAP1	Intron
none	Intergenic
none	Intergenic
none	Intergenic
EPB41L3	Intron
none	Intergenic
L3MBTL4	Intron
LOC105374618	Other
LPCAT1	Intron
ADAMTS16	Intron
DLGAP1	Intron
ADAMTS16	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
LOC105371958	Other
LINC02145	Other
ICE1	Intron
none	Intergenic
MYOM1	Intron
PTPRM	Intron
BPTF	Intron
LINC00290	Other
STOX2	Other
TRAPPC11	Intron
GREB1L	Intron
LOC105377613	Other
none	Intergenic
none	Intergenic
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ENPP6	Intron
ENPP6	Intron
none	Intergenic
LOC102723906	Other
none	Intergenic
COLEC12	Intron
none	Intergenic
SSTR2	Intron
CD300H	Intron
KCTD2	Exon
CDH12	Intron
LOC105374689	Other

ARSG	Intron
ARSG	Intron
ABCA5	Intron
MAP2K6	Intron
MAP2K6	Intron
none	Intergenic
LINC02228	Other
none	Intergenic
none	Intergenic
FBXL7	Intron
none	Intergenic
DNAH5	Intron
DNAH5	Intron
CTNND2	Intron
SRP68	Intron
none	Intergenic
none	Intergenic
LOC100507351	Other
RBFOX3	Intron
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
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LINC02233	Other
none	Intergenic
none	Intergenic
none	Intergenic
none	Intergenic
SLC14A2	Intron
SLC14A2	Intron
none	Intergenic
FSTL5	Intron
none	Intergenic
MARCHF1	Intron
MARCHF1	Exon
none	Intergenic
none	Intergenic
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LINC00907	Other
LINC00907	Other
LINC00907	Other
none	Intergenic
LOXHD1	Intron
none	Intergenic
LOC105372121	Other

LOC101927947	Other
DCC	Intron
DCC	Intron
DCC	Intron
ARFIP1	Intron
ARFIP1	Intron
STARD6	Intron
none	Intergenic
KATNAL2	Intron
ME2	Intron
MIR4527HG	Other
none	Intergenic
none	Intergenic
SMAD2	Intron
none	Intergenic
none	Intergenic
MYO5B	Intron
LOC105372115	Other
LOC105372115	Other
none	Intergenic
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LOC105372043	Other
GLRA3	Intron
LINC02268	Other
SCRG1	Intron
LOC101930370	Other
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GPM6A	Intron
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none	Intergenic
GALNTL6	Intron
CBR4	Other
none	Intergenic
FHOD3	Intron
none	Intergenic
KIAA1328	Intron
none	Intergenic
KIAA1328	Intron
CELF4	Intron
CELF4	Intron
LINC01179	Other
none	Intergenic
PALLD	Intron

NEK1	Intron
GALNTL6	Intron
DSG3	Exon
GALNTL6	Intron
B4GALT6	Other
none	Intergenic
CCDC178	Exon
CCDC178	Exon
ARSG	Intron
TMEM220-AS1	Other
none	Intergenic
none	Intergenic
none	Intergenic
HS3ST3A1	Exon
none	Intergenic
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none	Intergenic
LOC339166	Other
LOC339166	Other
LOC339166	Other
LOC339166	Other
LINC01331	Other
LINC01331	Other
ARHGEF28	Intron
PIK3R5	Intron
PIK3R5	Intron
none	Intergenic
none	Intergenic
none	Intergenic
CCDC144NL-AS1	Exon
none	Intergenic
WSB1	Intron
none	Intergenic
none	Intergenic
SEZ6	Intron
NLN	Intron
ZNF286A-TBC1D26	Other
ADAMTS6	Intron
TNFRSF13B	Intron
none	Intergenic
none	Intergenic
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LOC107986418	Other
ATP2A3	Intron
none	Intergenic
CDH13	Intron
CDH13	Intron
CDH13	Intron
none	Intergenic
CDH13	Intron
none	Intergenic

LOC102724637	Other
ADAMTS18	Intron
none	Intergenic
none	Intergenic
MEF2C-AS1	Other
MEF2C	Intron
WWOX	Intron
TMEM161B	Intron
SERINC5	Intron
THBS4	Intron
BHMT2	Exon
LHFPL2	Other
SMG6	Intron
PDE8B	Intron
S100Z	Other
CCDC92B	Intron
none	Intergenic
EMC8	Intron
none	Intergenic
none	Intergenic
XRCC4	Intron
DBNDD1	Intron
none	Intergenic
OSMR	Intron
EGFLAM	Intron
ANKFN1	Intron
none	Intergenic
none	Intergenic
NUP155	Intron
CPLANE1	Intron
CPLANE1	Other
none	Intergenic
none	Intergenic
UGT3A1	Intron
none	Intergenic
CA10	Intron
CCL28	Other
none	Intergenic
SELENOP	Intron
none	Intergenic
OXCT1	Intron
PLCXD3	Intron
DDX42	Intron
none	Intergenic
SMURF2	Intron
SMURF2	Intron
RGS9	Intron
none	Intergenic
none	Intergenic
PRKCA	Intron
LINC02109	Exon

NOL11	Intron
MARCHF10-DT	Other
SMG8	Exon
MARCHF10-DT	Other
PRLR	Intron
none	Intergenic
BRIP1	Intron
none	Intergenic
none	Intergenic
METTL2A	Intron
SLC38A9	Exon
MAP3K1	Intron
CCT6B	Intron
SLFN5	Exon
DDX4	Intron
none	Intergenic
none	Intergenic
MTREX	Intron
CDC20B	Exon
none	Intergenic
LOC105371760	Other
PLXDC1	Intron
MIER3	Exon
PDE4D	Intron
PDE4D	Intron
LOC107984974	Other
RAB11FIP4	Intron
PDE4D	Intron
none	Intergenic
MYO1D	Intron
ASIC2	Intron
none	Intergenic
NSF	Intron
LRRC37A2	Other
none	Intergenic
none	Intergenic
LRRC59	Intron
none	Intergenic
ITGA1	Intron
SMARCE1	Intron
ARL15	Intron
none	Intergenic
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BRCA1	Intron
NBR1	Intron
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LINC01822	Other
none	Intergenic
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LINC01830	Other

none	Intergenic
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LINC02380	Other
SF3B6	Intron
none	Intergenic
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LOC105373456	Other
LOC105373456	Other
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LINC01808	Other
LINC01808	Other
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ALK	Intron
ALK	Intron
ALK	Intron
XDH	Intron
CRACD	Exon
MEMO1	Intron
BIRC6	Intron
BIRC6	Intron
TTC27	Intron
TTC27	Intron
none	Intergenic
ALK	Intron
LINC02358	Other
OTOF	Intron
KIT	Exon
none	Intergenic
PPP1CB	Intron
PPP1CB	Intron
TRMT61B	Intron
SMC6	Intron
SLC4A4	Intron
none	Intergenic
RUFY3	Intron
LOC105373401	Exon
LOC105373401	Exon
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LINC00487	Other
none	Intergenic
LINC00299	Other
ANKRD17-DT	Other
none	Intergenic
none	Intergenic
ANKRD17	Intron
none	Intergenic

LINC01250	Other
none	Intergenic
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LINC00276	Other
none	Intergenic
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LOC105373436	Other
LOC105377262	Other
none	Intergenic
MIR3681HG	Other
LOC105374455	Other
PPP4R3B	Intron
LOC105374535	Other
none	Intergenic
none	Intergenic
PPARGC1A	Intron
CCDC85A	Intron
CCDC85A	Intron
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ZCCHC4	Intron
NRXN1	Intron
LOC730100	Other
LOC730100	Other
LOC730100	Other
LOC730100	Other
LINC02261	Other
SLC34A2	Intron
SLC34A2	Intron
SLC34A2	Intron
COMMD1	Intron
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LDB2	Intron
LDB2	Intron
EHBP1	Intron
PROM1	Intron
PROM1	Intron
PROM1	Intron
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VRK2	Intron
VRK2	Intron
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LOC105374510	Other
LOC105374510	Other
LOC105374510	Other

none	Intergenic
none	Intergenic
NRXN1	Intron
RFC1	Intron
RFC1	Intron
WDR19	Intron
none	Intergenic
TMEM178A	Intron
THUMPD2	Intron
TMEM156	Intron
LINC01258	Other
none	Intergenic
LOC105374506	Other
NWD2	Intron
none	Intergenic
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NSUN7	Intron
APBB2	Intron
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ATP8A1	Intron
ATP8A1	Intron
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LOC107985869	Other
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LINC02501	Other
none	Intergenic
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LOC439933	Other
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PLEKHH2	Intron
LOC105378262	Other
none	Intergenic
none	Intergenic
LOC107985809	Other
SRBD1	Intron
none	Intergenic
none	Intergenic
LOC105374391	Exon
TPO	Intron

none	Intergenic
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LOC105377428	Other
ZNF236	Intron
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CNDP2	Exon
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C18orf63	Exon
none	Intergenic
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LOC105377388	Other
none	Intergenic
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ARSJ	Intron
LARP7	Exon
none	Intergenic
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PARD6G	Exon
SPATA5	Intron
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ADAD1	Intron
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SLC10A7	Exon
EDNRA	Intron
none	Intergenic
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PIGN	Exon
SMAD1	Intron
none	Intergenic
none	Intergenic
LINC01924	Other
LOC107986195	Other
GATB	Intron
none	Intergenic
GATB	Intron
TCF4	Intron

FHIP1A	Intron
TCF4	Intron
none	Intergenic
LINC02355	Other
ONECUT2	Intron
NEDD4L	Intron
LINC01924	Other
LOC101927490	Other
CCDC102B	Intron
LOC105379412	Other
LOC105379412	Other
none	Intergenic
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TBC1D9	Exon
none	Intergenic
FAM13A	Intron
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FAM13A	Intron
CYP2G1P	Other
none	Intergenic
none	Intergenic
none	Intergenic
ZNF568	Intron
ZNF146	Exon
GRID2	Intron
none	Intergenic
GRID2	Intron
GRID2	Intron
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ZNF807P	Exon
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CFAP299	Intron
CFAP299	Intron
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LINC00989	Other
MRPL1	Intron
CXCL13	Intron
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SNTG2	Intron
PRKG2	Intron

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GRIN2D	Intron
ZNF610	Intron
LOC101928978	Other
ZNF865	Intron
NLRP13	Intron
ZNF71	Exon
LOC105372356	Other
EGF	Intron
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TACR3	Intron
BTBD2	Intron
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ACSBG2	Intron
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COL25A1	Intron
COL25A1	Intron
LEF1	Intron
LOC107986298	Other
ARHGEF38	Exon
TET2	Exon
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SMARCA4	Intron
none	Intergenic
none	Intergenic
none	Intergenic
UNC5C	Intron
BMPR1B-DT	Exon
LOC100420587	Other
PDLIM5	Intron
PDLIM5	Intron
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LOC107985698	Other
LOC107985698	Other
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PHF8	Intron
ADGRL2	Intron
LOC105376147	Other
ADGRL2	Intron

FAM163A	Intron
LOC105375760	Other
LOC107985698	Other
LOC107985698	Other
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CCDC26	Other
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STIM1	Intron
NEBL	Intron
NEBL	Intron
NEBL	Intron
CENPP	Intron
ECM2	Intron
LINC01031	Other
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LOC105376454	Other
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EBF3	Intron
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TCERG1L	Intron
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EFR3A	Intron
INPP5A	Intron
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ST8SIA6	Intron
TMEM65	Intron
TDRD7	Intron
DENND2B	Intron
TDRD7	Intron
TRIM66	Intron
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TBC1D31	Intron
LOC112268072	Exon
NTAQ1	Intron
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RSU1	Intron

SBF2-AS1	Other
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AK5	Intron
MALRD1	Intron
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IQSEC2	Intron
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ENOX2	Intron
MMP26	Intron
MMP26	Exon
ACBD6	Intron
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ACBD6	Intron
ADGRL4	Intron
RBMX2	Intron
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AOPEP	Intron
ST6GALNAC3	Intron
FANCC	Intron
CACNB2	Intron
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PIGK	Intron
PIGK	Intron
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RALGPS2	Exon
TRAPPC9	Intron
SLC28A3	Intron
PKN2-AS1	Other
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LOC105376481	Other
WDR11-AS1	Exon
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LOC107984174	Other
SVIL	Intron
NTRK2	Intron
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LOC105375805	Exon
IATPR	Other
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RABGAP1L	Intron
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RABGAP1L	Intron
ZNF644	Intron
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RABGAP1L	Intron
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VAX1	Exon
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LOC105375783	Other
LOC105378515	Other
RABGAP1L	Intron
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ARHGAP12	Intron
CCDC7	Intron
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RASAL2	Intron
DOCK1	Intron
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RPF1	Intron
SPATA1	Intron
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GPR158	Intron
KHDRBS3	Intron
TENM1	Intron
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ARHGAP21	Intron
KIAA1217	Intron
RALGPS2	Intron
KIAA1217	Intron
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ZFAT	Intron
KIAA1217	Intron
LINC01725	Other
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KHDRBS3	Intron
LINC02872	Exon
COL24A1	Intron
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ABI1	Intron
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ASTN1	Intron
COL24A1	Intron
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LOC105376131	Other
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ADAM12	Intron

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GAD2	Intron
ITIH5	Intron
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DOCK7	Intron
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SVEP1	Intron
LOC105376219	Other
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METTL15	Other
NFIA	Intron
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ECPAS	Intron
PATJ	Intron
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LUZP2	Intron
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LOC105376211	Other
LOC105376403	Other
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FRRS1L	Exon
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LUZP2	Intron
WHRN	Intron
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LOC105371661	Other
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ZNF618	Intron
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RIMS2	Intron
BAALC	Intron

DAB1	Intron
TSPAN7	Intron
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SLC46A2	Exon
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OXR1	Intron
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GDI2	Intron
DCDC1	Intron
ZNF618	Intron
LINC01135	Other
DCDC1	Intron
LOC107984198	Other
MPPED2	Intron
NET1	Exon
GALNT18	Intron
NEGR1	Intron
DGKK	Exon
RGL1	Intron
RGL1	Intron
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LOC105375716	Other
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EXT1	Intron
EXT1	Intron
SOX6	Intron
SOX6	Intron
TEAD1	Intron
NPL	Intron
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LINC02238	Other
PARVA	Intron
PARVA	Intron
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PTER	Intron
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PLAC1	Intron
COL15A1	Intron
COL15A1	Intron
COL15A1	Intron
LOC105378800	Other

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SLC30A8	Intron
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BEND7	Exon
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HMCN1	Intron
LOC105376195	Other
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CSMD3	Intron
CSMD3	Intron
LOC340512	Other
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CELF2	Intron
CSMD3	Intron
KDM6A	Intron
LINC01495	Other
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NELL1	Intron
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ZDHHC13	Intron
LINC00536	Other
LINC00536	Other
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EDEM3	Exon
EDEM3	Exon
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EIF3H	Intron
FGF13	Intron
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LOC105378789	Other
LOC105376193	Other
LOC105378790	Other
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ATP11C	Intron
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LRRC7	Exon
TRPS1	Intron
LINC01189	Other
OR6Y1	Intron
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LOC105375999	Other
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FGF7P6	Other
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DIAPH2	Intron
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LOC100506422	Other
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DIAPH2	Intron
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SYCP1	Intron
MOB3B	Intron
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CABCOCO1	Intron
LINC02625	Other
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ARHGEF2	Intron
BRWD3	Intron
TMEM26	Intron
CAAP1	Intron
NRG3	Intron
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LOC107987056	Other
MIR325HG	Other
ACTA2	Intron
ATF6	Intron
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MIR325HG	Other
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ELAVL2	Intron
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TRMT2B	Intron
NTNG1	Intron
PANK1	Intron

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PAPSS2	Intron
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ATP7A	Intron
LOC107985669	Other
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GRID1	Intron
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DIAPH2	Intron
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DIAPH2	Intron
BICC1	Intron
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AIM2	Other
LPAR4	Exon
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GRID1	Intron
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WAPL	Intron
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AHCYL1	Intron
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PCDH15	Intron
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B4GALT1	Intron
H2BC18	Intron
P4HA1	Intron
MCU	Intron
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SEC24C	Intron
ADK	Intron
LOC107987059	Other
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FGF7P3	Other
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H3-2	Exon
MICU1	Intron
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LINC02636	Other
CHM	Intron
CHM	Intron
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ASCC1	Intron
PDE4DIP	Intron

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FAM219A	Intron
CTNNA3	Intron
PDZK1P1	Exon
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H3P4	Other
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PCDH11X	Intron
LINC01525	Other
LOC105373284	Other
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LOC105373284	Other
LINGO2	Intron
KCNN3	Intron
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SH2D4B	Intron
LINGO2	Intron
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LINGO2	Intron
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TMEM254-AS1	Other
PCDH11X	Intron
PCDH11X	Intron
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SPAG17	Intron
SPAG17	Intron
HMGCS2	Intron
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LRMDA	Intron
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LOC107984245	Other
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LOC107984012	Other
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JMJD1C	Intron
LOC107984035	Other
KCNMA1	Intron
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LOC107984035	Other
LINC01780	Other
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PTPRD	Intron
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ZNF487	Intron
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DPYD	Intron
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DPYD	Intron
ZNF37BP	Other
LOC105375971	Other
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SORCS1	Intron
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PCSK5	Intron
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CHRD1	Intron
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PCSK5	Intron
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MIR137HG	Other
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LINC01776	Other
PTPRD	Intron
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CCNY	Intron
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ATRNL1	Intron
ATRNL1	Intron
EVI5	Intron
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PARD3	Intron
BRDT	Exon
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SMARCA2	Intron
LOC107987084	Other
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VTI1A	Intron
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TLCD4	Intron
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HTR2C	Intron
LRCH2	Intron
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GLIS3	Intron
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DNTTIP2	Exon
SORCS3	Intron
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ADAMTSL1	Other
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FAM78B	Intron
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ADAMTSL1	Other
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LOC105373302	Other
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ADAMTSL1	Other

LGI1	Exon
PDLIM1	Exon
PRKG1	Intron
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IL1RAPL2	Intron
IL1RAPL2	Intron
IL1RAPL2	Intron
TRPM3	Intron
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RLIM	Exon
LINC00630	Other
HECTD2-AS1	Other
LINC01661	Other
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FOCAD	Intron
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APBA1	Intron
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MYOF	Intron
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FTX	Other
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SLC24A2	Other
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ANXA8	Other
ANXA8	Other
MPDZ	Intron
MPC2	Intron
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ATG4A	Intron
BTRC	Intron
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KIF4A	Intron
MPC2	Intron
DCAF6	Intron
NMRK1	Exon
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TRPM6	Intron
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SH3PXD2A	Intron
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CDC14A	Intron
NT5C2	Intron
TRPM3	Intron
PRKG1	Intron
COL11A1	Intron
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TLL2	Intron

HDAC8	Intron
BNC2	Intron
OLFM3	Intron
OLFM3	Intron
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TEX11	Intron
GDA	Intron
PSIP1	Intron
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C9orf57	Intron
NRK	Intron
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ZSCAN20	Intron
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ZSCAN20	Intron
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CSMD2	Exon
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HDAC1	Intron
FABP5	Intron
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SNRNP40	Intron
NLGN4Y	Intron
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RALYL	Intron
CTSE	Intron
FMN2	Intron
GRM5P1	Other
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LOC100506532	Other
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LOC105375932	Other
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LOC105378642	Other
USP9Y	Intron
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MACO1	Intron
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PAG1	Intron
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IL7	Intron
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LINC00301	Other
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LOC107985366	Other
LOC107985366	Other
MAJIN	Exon

TXLNGY	Other
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LYST	Intron
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ZNF704	Intron
RYR2	Intron
RYR2	Intron
LPXN	Exon
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ARID1A	Intron
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TPD52	Intron
LOC107985368	Other
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DMD	Intron
NR5A2	Intron
PCDH11Y	Intron
LINC00534	Other
LINC00534	Other
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DMD	Intron
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AGBL4	Intron
OR1B1	Intron
LRRC4C	Intron
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LOC101926956	Other
DMD	Intron
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PCDH11Y	Intron
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CATSPERE	Intron
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DMD	Intron
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LOC105375639	Other
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MACF1	Intron
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STXBP1	Intron
DMD	Intron
PRDM12	Intron
EXOSC2	Intron
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WWP1	Intron
LOC105378657	Other
CNGB3	Intron
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CNBD1	Intron
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DMD	Intron
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MPL	Intron
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RALGPS1	Intron
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RABIF	Intron
PLD5	Intron
ZBTB43	Exon
LOC105375631	Other
LOC105375631	Other
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TXLNGY	Other
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USH2A	Intron
PPP1R42	Intron
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ADGRG2	Intron
DNAH14	Intron
ARHGAP6	Intron
ARHGAP6	Intron
WDR26	Intron
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ESRRG	Intron
USH2A	Intron
USH2A	Intron
FRMPD4	Intron
CDC42BPA	Intron
CLCN4	Intron
none	Intergenic
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CPA6	Intron
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MID1	Intron

PREX2	Intron
MID1	Intron
MAP7D2	Intron
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PER3	Exon
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PICALM	Intron
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TGFB2	Intron
DLG2	Intron
MEGF6	Exon
NKAIN3	Intron
LYPLAL1-AS1	Other
LINC01786	Other
LOC105372926	Other
LOC105372926	Other
AP1S2	Exon
GLRA2	Intron
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ESRRG	Intron
MTFR1	Exon
MIR4300HG	Other
GEMIN8	Intron
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LINC01414	Other
SPATA17	Intron
DLG2	Intron
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PPP2R5A	Intron
STAU2	Intron
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INTS7	Intron
MIR2052HG	Other
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LOC105378614	Other
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RAB6A	Intron
COG2	Intron
TTC13	Intron
SLC35F3	Intron
LOC105376863	Other
LOC105376863	Other
LOC105376863	Other

PACS1	Intron
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KCNH1	Intron
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ZFX	Intron
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NLGN4X	Intron
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OBSCN-AS1	Other
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NCOA2	Intron
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LOC107985675	Other
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LOC105373146	Other
OBSCN-AS1	Other
PAK1	Intron
PADI1	Intron
KAZN	Other
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USP35	Intron
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EMSY	Intron
PRORY	Other
LOC107985715	Other
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ABCB10	Intron
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OBSCN-AS1	Other
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LRR4C	Intron
CRB1	Intron
RAD54B	Intron
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LOC102723568	Other
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LOC105373369	Other
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LOC107984326	Other
OSBPL9	Intron
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PAPPA	Intron

OSBPL9	Intron
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LINC02669	Other
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ACOT11	Intron
LOC107984326	Other
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CFHR2	Intron
CFAP418-AS1	Other
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MAMLD1	Exon
FAF1	Intron
LINC02669	Other
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EPS15	Intron
VPS13B	Intron
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NSDHL	Intron
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VAMP7	Intron
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PRR5L	Intron
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PRR5L	Intron
NDUFAF6	Intron
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LOC105376242	Other
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NDUFAF6	Intron
LOC105376360	Other
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COA7	Intron
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VPS13B	Intron
MAGOH	Intron
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PTPRM
ATF2

Intron
Intron

rs12969929

rs201782266

Location	Name	Origin
chr1:101885582-101885601(+)	GUIDE-seq1	GUIDE-seq only
chr1:117371225-117371245(-)	GUIDE-seq2	GUIDE-seq only
chr1:148055972-148055992(+)	GUIDE-seq3	GUIDE-seq only
chr1:155614892-155614912(-)	GUIDE-seq4	GUIDE-seq only
chr1:187763236-187763256(-)	GUIDE-seq5	GUIDE-seq only
chr1:231540617-231540637(+)	GUIDE-seq6	GUIDE-seq only
chr1:32334556-32334577(-)	GUIDE-seq7	GUIDE-seq only
chr1:45988663-45988682(+)	GUIDE-seq8	GUIDE-seq only
chr1:94757676-94757696(-)	GUIDE-seq9	GUIDE-seq only
chr1_KI270709v1_random:10583-10603(+)	GUIDE-seq10	GUIDE-seq only
chr10:114296211-114296231(-)	GUIDE-seq11	GUIDE-seq only
chr10:24349861-24349881(+)	Shared1	Shared 3
chr10:39392442-39392461(+)	GUIDE-seq13	GUIDE-seq only
chr10:42079675-42079695(-)	GUIDE-seq14	GUIDE-seq only
chr10:45987007-45987026(+)	GUIDE-seq15	GUIDE-seq only
chr10:56324292-56324312(-)	Shared2	Shared 3
chr10:63501384-63501403(-)	GUIDE-seq17	GUIDE-seq only
chr11:104272430-104272450(+)	GUIDE-seq_ONE-seq18	GUIDE-seq+ONE-seq
chr11:106109726-106109744(+)	GUIDE-seq19	GUIDE-seq only
chr11:108029419-108029439(+)	GUIDE-seq20	GUIDE-seq only
chr11:109138384-109138404(-)	GUIDE-seq21	GUIDE-seq only
chr11:122891474-122891494(+)	GUIDE-seq22	GUIDE-seq only
chr11:27616919-27616940(+)	GUIDE-seq23	GUIDE-seq only
chr11:35453141-35453161(+)	GUIDE-seq24	GUIDE-seq only
chr11:37842595-37842615(-)	GUIDE-seq25	GUIDE-seq only
chr11:55052344-55052362(-)	GUIDE-seq26	GUIDE-seq only
chr11:57726496-57726516(+)	GUIDE-seq_ONE-seq27	GUIDE-seq+ONE-seq
chr11:63335538-63335557(-)	GUIDE-seq28	GUIDE-seq only
chr11:74601439-74601458(+)	GUIDE-seq29	GUIDE-seq only
chr11:85448979-85448997(+)	GUIDE-seq30	GUIDE-seq only
chr11:98349120-98349138(-)	GUIDE-seq31	GUIDE-seq only
chr11:99844369-99844389(+)	GUIDE-seq32	GUIDE-seq only
chr12:114850684-114850705(+)	GUIDE-seq33	GUIDE-seq only
chr12:16700502-16700522(+)	GUIDE-seq34	GUIDE-seq only
chr12:3124373-3124392(+)	GUIDE-seq35	GUIDE-seq only
chr12:90832411-90832431(-)	GUIDE-seq36	GUIDE-seq only
chr13:100666619-100666638(+)	GUIDE-seq37	GUIDE-seq only
chr13:102978390-102978410(-)	GUIDE-seq38	GUIDE-seq only
chr13:103687143-103687163(-)	GUIDE-seq39	GUIDE-seq only
chr13:105730448-105730466(+)	GUIDE-seq40	GUIDE-seq only
chr13:105960512-105960532(-)	Shared3	Shared 3
chr13:28478362-28478382(-)	GUIDE-seq42	GUIDE-seq only
chr13:47975530-47975550(-)	GUIDE-seq_ONE-seq43	GUIDE-seq+ONE-seq
chr13:51941587-51941607(-)	Shared4	Shared 3
chr13:69970655-69970676(-)	GUIDE-seq45	GUIDE-seq only
chr13:79419346-79419365(-)	GUIDE-seq46	GUIDE-seq only
chr14:25620214-25620235(-)	GUIDE-seq47	GUIDE-seq only
chr14:36880675-36880695(-)	GUIDE-seq48	GUIDE-seq only
chr14:38007077-38007097(+)	GUIDE-seq_ONE-seq49	GUIDE-seq+ONE-seq
chr14:43408726-43408745(+)	GUIDE-seq50	GUIDE-seq only

chr14:49505304-49505323(-)	GUIDE-seq51	GUIDE-seq only
chr14:99778821-99778841(-)	GUIDE-seq_ONE-seq52	GUIDE-seq+ONE-seq
chr15:25433727-25433746(-)	GUIDE-seq53	GUIDE-seq only
chr15:25963477-25963497(-)	GUIDE-seq54	GUIDE-seq only
chr15:68647164-68647185(+)	GUIDE-seq55	GUIDE-seq only
chr15:71560451-71560470(-)	GUIDE-seq56	GUIDE-seq only
chr15:72575185-72575205(+)	GUIDE-seq57	GUIDE-seq only
chr15:76599706-76599726(+)	GUIDE-seq_ONE-seq58	GUIDE-seq+ONE-seq
chr16:19129826-19129846(-)	GUIDE-seq59	GUIDE-seq only
chr16:34581387-34581407(+)	GUIDE-seq60	GUIDE-seq only
chr16:34586133-34586153(-)	GUIDE-seq61	GUIDE-seq only
chr16:34588127-34588147(+)	GUIDE-seq62	GUIDE-seq only
chr16:34594949-34594969(-)	GUIDE-seq63	GUIDE-seq only
chr16:46386493-46386513(-)	GUIDE-seq64	GUIDE-seq only
chr16:46389076-46389096(+)	GUIDE-seq65	GUIDE-seq only
chr16:46391230-46391250(+)	GUIDE-seq66	GUIDE-seq only
chr16:46398553-46398573(-)	GUIDE-seq67	GUIDE-seq only
chr16:46400236-46400256(-)	GUIDE-seq68	GUIDE-seq only
chr16:46401181-46401201(-)	GUIDE-seq69	GUIDE-seq only
chr16:46401311-46401330(+)	GUIDE-seq70	GUIDE-seq only
chr16:76814991-76815011(+)	GUIDE-seq71	GUIDE-seq only
chr16:82705551-82705571(+)	GUIDE-seq72	GUIDE-seq only
chr17:14085181-14085201(+)	Shared5	Shared 3
chr17:21014472-21014493(-)	GUIDE-seq74	GUIDE-seq only
chr17:26619568-26619587(+)	GUIDE-seq75	GUIDE-seq only
chr17:37868538-37868558(-)	GUIDE-seq76	GUIDE-seq only
chr17:43472085-43472104(-)	GUIDE-seq77	GUIDE-seq only
chr17:7602883-7602903(+)	GUIDE-seq78	GUIDE-seq only
chr17_KI270729v1_random:59740-59759(+)	GUIDE-seq79	GUIDE-seq only
chr18:20922197-20922217(+)	GUIDE-seq80	GUIDE-seq only
chr18:2161219-2161239(+)	Shared6	Shared 3
chr18:28430786-28430806(-)	GUIDE-seq_ONE-seq82	GUIDE-seq+ONE-seq
chr18:50910799-50910819(+)	GUIDE-seq83	GUIDE-seq only
chr18:6641253-6641274(-)	GUIDE-seq84	GUIDE-seq only
chr19:35923620-35923639(-)	GUIDE-seq85	GUIDE-seq only
chr19:37732208-37732227(-)	GUIDE-seq86	GUIDE-seq only
chr19:52675206-52675225(-)	GUIDE-seq87	GUIDE-seq only
chr19:57579217-57579235(+)	GUIDE-seq88	GUIDE-seq only
chr2:107701686-107701706(+)	GUIDE-seq_ONE-seq89	GUIDE-seq+ONE-seq
chr2:131812122-131812141(-)	GUIDE-seq90	GUIDE-seq only
chr2:132665291-132665311(-)	Shared7	Shared 3
chr2:135947775-135947796(+)	GUIDE-seq92	GUIDE-seq only
chr2:161811106-161811126(+)	GUIDE-seq93	GUIDE-seq only
chr2:179715527-179715545(+)	GUIDE-seq94	GUIDE-seq only
chr2:190032040-190032060(+)	GUIDE-seq95	GUIDE-seq only
chr2:191905587-191905607(-)	GUIDE-seq96	GUIDE-seq only
chr2:198087320-198087340(-)	Shared8	Shared 3
chr2:204916812-204916832(+)	GUIDE-seq98	GUIDE-seq only
chr2:210590916-210590936(-)	GUIDE-seq99	GUIDE-seq only
chr2:210591749-210591767(-)	GUIDE-seq100	GUIDE-seq only
chr2:210591873-210591893(-)	OnT	Shared 3

chr2:21395450-21395470(+)	GUIDE-seq102	GUIDE-seq only
chr2:218254089-218254109(-)	GUIDE-seq103	GUIDE-seq only
chr2:51700372-51700394(-)	GUIDE-seq104	GUIDE-seq only
chr2:62015628-62015649(+)	GUIDE-seq105	GUIDE-seq only
chr2:78933334-78933355(-)	GUIDE-seq106	GUIDE-seq only
chr2:79046372-79046392(+)	GUIDE-seq107	GUIDE-seq only
chr2:88552102-88552122(-)	GUIDE-seq_ONE-seq108	GUIDE-seq+ONE-seq
chr2:89826531-89826551(-)	GUIDE-seq109	GUIDE-seq only
chr2:89833404-89833424(-)	GUIDE-seq110	GUIDE-seq only
chr2:91586559-91586578(-)	GUIDE-seq111	GUIDE-seq only
chr2:93754951-93754969(+)	GUIDE-seq112	GUIDE-seq only
chr2:97548295-97548315(-)	GUIDE-seq113	GUIDE-seq only
chr20:18004086-18004106(+)	GUIDE-seq114	GUIDE-seq only
chr20:29885813-29885831(-)	GUIDE-seq115	GUIDE-seq only
chr20:31068519-31068537(+)	GUIDE-seq116	GUIDE-seq only
chr20:31213821-31213839(+)	GUIDE-seq117	GUIDE-seq only
chr20:42667000-42667020(+)	GUIDE-seq118	GUIDE-seq only
chr20:42970387-42970407(+)	GUIDE-seq119	GUIDE-seq only
chr20:46262548-46262568(-)	GUIDE-seq_ONE-seq120	GUIDE-seq+ONE-seq
chr20:47912906-47912926(-)	GUIDE-seq121	GUIDE-seq only
chr21:10691030-10691049(-)	GUIDE-seq122	GUIDE-seq only
chr21:24770731-24770751(+)	GUIDE-seq123	GUIDE-seq only
chr21:40397747-40397766(-)	GUIDE-seq124	GUIDE-seq only
chr21:7255330-7255348(-)	GUIDE-seq125	GUIDE-seq only
chr21:7919637-7919656(-)	GUIDE-seq126	GUIDE-seq only
chr22:16269967-16269987(+)	GUIDE-seq127	GUIDE-seq only
chr22:33548897-33548917(+)	GUIDE-seq_ONE-seq128	GUIDE-seq+ONE-seq
chr3:103265928-103265948(-)	GUIDE-seq129	GUIDE-seq only
chr3:107194685-107194705(+)	GUIDE-seq130	GUIDE-seq only
chr3:108858616-108858636(-)	GUIDE-seq131	GUIDE-seq only
chr3:109441319-109441339(+)	GUIDE-seq132	GUIDE-seq only
chr3:112911040-112911060(-)	GUIDE-seq133	GUIDE-seq only
chr3:122159469-122159488(-)	GUIDE-seq134	GUIDE-seq only
chr3:125726766-125726786(-)	GUIDE-seq135	GUIDE-seq only
chr3:143788738-143788758(+)	GUIDE-seq136	GUIDE-seq only
chr3:145538143-145538162(+)	GUIDE-seq137	GUIDE-seq only
chr3:173691237-173691256(-)	GUIDE-seq138	GUIDE-seq only
chr3:18286238-18286257(+)	GUIDE-seq139	GUIDE-seq only
chr3:184821674-184821695(-)	GUIDE-seq140	GUIDE-seq only
chr3:25248348-25248367(-)	GUIDE-seq141	GUIDE-seq only
chr3:39964863-39964885(-)	GUIDE-seq142	GUIDE-seq only
chr3:40277530-40277550(+)	GUIDE-seq143	GUIDE-seq only
chr3:60384958-60384978(-)	GUIDE-seq144	GUIDE-seq only
chr3:67097709-67097728(+)	GUIDE-seq145	GUIDE-seq only
chr3:96019252-96019272(+)	GUIDE-seq_ONE-seq146	GUIDE-seq+ONE-seq
chr4:129150639-129150659(-)	GUIDE-seq147	GUIDE-seq only
chr4:149238470-149238488(-)	GUIDE-seq148	GUIDE-seq only
chr4:150673751-150673769(-)	GUIDE-seq149	GUIDE-seq only
chr4:159914856-159914876(+)	GUIDE-seq150	GUIDE-seq only
chr4:174877223-174877243(+)	GUIDE-seq151	GUIDE-seq only
chr4:34238119-34238139(-)	GUIDE-seq152	GUIDE-seq only

chr4:42524439-42524458(+)	GUIDE-seq153	GUIDE-seq only
chr4:49103973-49103991(-)	GUIDE-seq154	GUIDE-seq only
chr4:49147625-49147643(+)	GUIDE-seq155	GUIDE-seq only
chr4:52575886-52575906(-)	GUIDE-seq156	GUIDE-seq only
chr4:52735305-52735323(+)	GUIDE-seq157	GUIDE-seq only
chr4:63161261-63161281(+)	GUIDE-seq158	GUIDE-seq only
chr4:64420581-64420601(-)	GUIDE-seq159	GUIDE-seq only
chr4:78956535-78956555(-)	GUIDE-seq160	GUIDE-seq only
chr5:146593816-146593836(+)	GUIDE-seq161	GUIDE-seq only
chr5:19552938-19552958(+)	GUIDE-seq162	GUIDE-seq only
chr5:32045171-32045191(+)	GUIDE-seq163	GUIDE-seq only
chr5:33299687-33299705(+)	GUIDE-seq164	GUIDE-seq only
chr5:39966526-39966546(-)	GUIDE-seq165	GUIDE-seq only
chr5:49601725-49601745(+)	GUIDE-seq166	GUIDE-seq only
chr5:49601750-49601770(+)	GUIDE-seq167	GUIDE-seq only
chr5:49602115-49602135(+)	GUIDE-seq168	GUIDE-seq only
chr5:49657003-49657023(-)	GUIDE-seq169	GUIDE-seq only
chr5:49660745-49660765(-)	GUIDE-seq170	GUIDE-seq only
chr5:50995275-50995295(+)	GUIDE-seq171	GUIDE-seq only
chr5:77742179-77742199(+)	GUIDE-seq172	GUIDE-seq only
chr5:92045471-92045492(-)	GUIDE-seq_ONE-seq173	GUIDE-seq+ONE-seq
chr6:113966592-113966612(-)	GUIDE-seq174	GUIDE-seq only
chr6:137610990-137611008(-)	GUIDE-seq175	GUIDE-seq only
chr6:154331970-154331990(-)	GUIDE-seq176	GUIDE-seq only
chr6:32368599-32368619(-)	GUIDE-seq177	GUIDE-seq only
chr6:41668217-41668235(-)	GUIDE-seq178	GUIDE-seq only
chr6:61383664-61383682(+)	GUIDE-seq179	GUIDE-seq only
chr6:68587058-68587079(+)	GUIDE-seq180	GUIDE-seq only
chr6:71690557-71690577(+)	Shared9	Shared 3
chr6:91554457-91554476(-)	GUIDE-seq182	GUIDE-seq only
chr6:96750602-96750622(-)	GUIDE-seq183	GUIDE-seq only
chr7:121141099-121141119(+)	GUIDE-seq184	GUIDE-seq only
chr7:122094836-122094856(+)	GUIDE-seq185	GUIDE-seq only
chr7:3448464-3448485(-)	GUIDE-seq186	GUIDE-seq only
chr7:37590233-37590253(+)	GUIDE-seq187	GUIDE-seq only
chr7:49502148-49502168(-)	GUIDE-seq_ONE-seq188	GUIDE-seq+ONE-seq
chr7:68154122-68154142(+)	GUIDE-seq189	GUIDE-seq only
chr7:81628563-81628583(+)	GUIDE-seq190	GUIDE-seq only
chr7:86536385-86536405(+)	GUIDE-seq191	GUIDE-seq only
chr8:107998731-107998751(-)	GUIDE-seq192	GUIDE-seq only
chr8:110396641-110396661(+)	GUIDE-seq193	GUIDE-seq only
chr8:123614246-123614266(+)	GUIDE-seq194	GUIDE-seq only
chr8:2040223-2040243(-)	GUIDE-seq195	GUIDE-seq only
chr8:70547400-70547420(+)	GUIDE-seq196	GUIDE-seq only
chr8:99794486-99794506(-)	GUIDE-seq197	GUIDE-seq only
chr9:117808527-117808547(-)	GUIDE-seq198	GUIDE-seq only
chr9:121177557-121177577(-)	GUIDE-seq199	GUIDE-seq only
chr9:5828921-5828941(-)	GUIDE-seq_ONE-seq200	GUIDE-seq+ONE-seq
chr9:73747216-73747236(+)	GUIDE-seq201	GUIDE-seq only
chrUn_KI270438v1:102368-102386(+)	GUIDE-seq205	GUIDE-seq only
chrUn_KI270438v1:104376-104396(+)	GUIDE-seq206	GUIDE-seq only

chrUn_KI270517v1:2631-2649(-)	GUIDE-seq207	GUIDE-seq only
chrX:115223463-115223483(+)	GUIDE-seq208	GUIDE-seq only
chrX:143455204-143455224(+)	GUIDE-seq_ONE-seq209	GUIDE-seq+ONE-seq
chrX:63259190-63259210(-)	GUIDE-seq_ONE-seq210	GUIDE-seq+ONE-seq
chrY:11643825-11643844(-)	GUIDE-seq211	GUIDE-seq only
chr2:98814239-98814259(-)	ONE-seq1	ONE-seq only
chr2:99672541-99672561(-)	ONE-seq2	ONE-seq only
chr19:19076134-19076154(-)	ONE-seq3	ONE-seq only
chr20:13784104-13784124(+)	ONE-seq4	ONE-seq only
chr4:56229938-56229958(-)	ONE-seq5	ONE-seq only
chr4:137601272-137601292(+)	ONE-seq6	ONE-seq only
chr12:122788868-122788888(+)	ONE-seq7	ONE-seq only
chr13:33065684-33065704(+)	ONE-seq8	ONE-seq only
chr12:25111823-25111843(+)	ONE-seq9	ONE-seq only
chr10:120815627-120815647(+)	ONE-seq10	ONE-seq only
chr13:91359585-91359605(-)	ONE-seq11	ONE-seq only
chr15:40747756-40747776(+)	ONE-seq12	ONE-seq only
chr4:140621573-140621593(-)	ONE-seq13	ONE-seq only
chr2:95541686-95541706(+)	CHANGE-seqBE1	CHANGE-seq-BE only
chr5:29153498-29153518(-)	ONE-seq14	ONE-seq only
chr5:55692818-55692838(-)	ONE-seq15	ONE-seq only
chr7:86879335-86879355(-)	ONE-seq16	ONE-seq only
chr8:65709164-65709184(+)	ONE-seq17	ONE-seq only
chr9:125552068-125552088(-)	CHANGE-seqBE2	CHANGE-seq-BE only
chr6:28319161-28319181(+)	ONE-seq_CHANGE-seqBE1	In vitro
chr10:21381234-21381254(-)	ONE-seq_CHANGE-seqBE2	In vitro
chr10:3903005-3903025(+)	ONE-seq_CHANGE-seqBE3	In vitro
chr2:7733220-7733240(-)	ONE-seq_CHANGE-seqBE4	In vitro
chr8:122636872-122636892(+)	ONE-seq_CHANGE-seqBE5	In vitro
chr7:131268494-131268514(+)	ONE-seq_CHANGE-seqBE6	In vitro
chr5:68439824-68439844(+)	ONE-seq_CHANGE-seqBE7	In vitro
chr14:26538238-26538258(+)	ONE-seq_CHANGE-seqBE8	In vitro
chr12:114081726-114081746(+)	ONE-seq_CHANGE-seqBE9	In vitro
chr12:14009521-14009541(+)	ONE-seq_CHANGE-seqBE10	In vitro
chr15:71407301-71407321(-)	ONE-seq_CHANGE-seqBE11	In vitro
chr3:69014309-69014329(-)	ONE-seq_CHANGE-seqBE12	In vitro
chr2:17253817-17253837(+)	ONE-seq_CHANGE-seqBE13	In vitro
chr5:29462611-29462631(+)	ONE-seq_CHANGE-seqBE14	In vitro
chr4:96821205-96821225(-)	ONE-seq_CHANGE-seqBE15	In vitro
chr10:80905054-80905074(+)	ONE-seq_CHANGE-seqBE16	In vitro
chr1:232678825-232678845(-)	ONE-seq_CHANGE-seqBE17	In vitro
chr4:29910257-29910277(-)	ONE-seq_CHANGE-seqBE18	In vitro
chr2:196584615-196584635(-)	ONE-seq_CHANGE-seqBE19	In vitro
chr19:20319265-20319285(+)	ONE-seq_CHANGE-seqBE20	In vitro
chr9:13154678-13154698(+)	ONE-seq_CHANGE-seqBE21	In vitro
chr3:103143974-103143994(-)	ONE-seq_CHANGE-seqBE22	In vitro
chr18:76326696-76326716(-)	ONE-seq_CHANGE-seqBE23	In vitro
chr12:42377204-42377224(+)	ONE-seq18	ONE-seq only
chr10:106940996-106941016(-)	ONE-seq19	ONE-seq only
chrX:94310316-94310336(+)	ONE-seq20	ONE-seq only
chr5:102333534-102333554(-)	ONE-seq21	ONE-seq only

chr5:89092422-89092442(-)	CHANGE-seqBE3	CHANGE-seq-BE only
chr5:153089661-153089681(-)	CHANGE-seqBE4	CHANGE-seq-BE only
chr9:72906365-72906385(-)	CHANGE-seqBE5	CHANGE-seq-BE only
chr14:82199313-82199333(-)	in silico only1	in silico only
chr4:25696309-25696329(+)	in silico only2	in silico only
chr4:25696310-25696330(+)	in silico only3	in silico only
chr13:90518582-90518602(-)	in silico only4	in silico only
chr11:72838746-72838766(+)	in silico only5	in silico only
chr7:8213616-8213636(+)	in silico only6	in silico only
chr14:103879509-103879529(+)	in silico only7	in silico only
chr6:27313497-27313517(-)	in silico only8	in silico only
chr17:69548520-69548540(-)	in silico only9	in silico only
chr13:77205504-77205524(-)	in silico only10	in silico only
chrX:115635016-115635036(+)	in silico only11	in silico only
chrX:107069755-107069775(-)	in silico only12	in silico only
chr6:4998773-4998793(-)	in silico only13	in silico only
chr12:22308939-22308959(+)	in silico only14	in silico only
chr2:48597982-48598003(-)	in silico only15	in silico only
chr2:165919377-165919397(+)	in silico only16	in silico only
chr20:531888-531908(-)	ONE-seq_E1	ONE-seq only
chr2:56536797-56536817(+)	ONE-seq_E2	ONE-seq only
chr18:31525111-31525131(-)	ONE-seq_E3	ONE-seq only
chr18:71192156-71192176(-)	ONE-seq_E4	ONE-seq only
chr19:31131277-31131297(-)	ONE-seq_E5	ONE-seq only
chr2:2481312-2481332(+)	ONE-seq_E6	ONE-seq only
chr2:50480846-50480866(-)	ONE-seq_E7	ONE-seq only
chr20:13784104-13784124(+)	ONE-seq_E8	ONE-seq only
chr20:54569334-54569354(+)	ONE-seq_E9	ONE-seq only
chr4:56229938-56229958(-)	ONE-seq_E10	ONE-seq only
chr4:105489456-105489476(-)	ONE-seq_E11	ONE-seq only
chr3:116794536-116794556(+)	ONE-seq_E12	ONE-seq only
chr21:20131782-20131802(+)	ONE-seq_E13	ONE-seq only
chr21:39362110-39362130(-)	ONE-seq_E14	ONE-seq only
chr3:28647007-28647027(-)	ONE-seq_E15	ONE-seq only
chr3:35964683-35964703(+)	ONE-seq_E16	ONE-seq only
chr3:103377328-103377348(+)	ONE-seq_E17	ONE-seq only
chr12:42377204-42377224(+)	ONE-seq_E18	ONE-seq only
chr12:60336177-60336197(-)	ONE-seq_E19	ONE-seq only
chr13:58498215-58498235(+)	ONE-seq_E20	ONE-seq only
chr13:59089333-59089353(-)	ONE-seq_E21	ONE-seq only
chr10:106940996-106941016(-)	ONE-seq_E22	ONE-seq only
chr10:128590280-128590300(-)	ONE-seq_E23	ONE-seq only
chr11:23310298-23310318(+)	ONE-seq_E24	ONE-seq only
chr11:23819004-23819024(+)	ONE-seq_E25	ONE-seq only
chr11:38405965-38405985(-)	ONE-seq_E26	ONE-seq only
chr13:59092798-59092818(-)	ONE-seq_E27	ONE-seq only
chr16:46526796-46526816(+)	ONE-seq_E28	ONE-seq only
chr16:49741749-49741769(+)	ONE-seq_E29	ONE-seq only
chr16:61032958-61032978(+)	ONE-seq_E30	ONE-seq only
chr16:71935122-71935142(+)	ONE-seq_E31	ONE-seq only
chr17:52735296-52735316(-)	ONE-seq_E32	ONE-seq only

chr13:94810687-94810707(-)	ONE-seq_E33	ONE-seq only
chr14:47343282-47343302(+)	ONE-seq_E34	ONE-seq only
chr14:71303370-71303390(+)	ONE-seq_E35	ONE-seq only
chr14:75771551-75771571(-)	ONE-seq_E36	ONE-seq only
chr14:78582287-78582307(-)	ONE-seq_E37	ONE-seq only
chr14:91205110-91205130(+)	ONE-seq_E38	ONE-seq only
chrX:12101643-12101663(+)	ONE-seq_E39	ONE-seq only
chrX:74492645-74492665(-)	ONE-seq_E40	ONE-seq only
chrX:90582641-90582661(-)	ONE-seq_E41	ONE-seq only
chrX:94310316-94310336(+)	ONE-seq_E42	ONE-seq only
chrX:99977456-99977476(-)	ONE-seq_E43	ONE-seq only
chrX:5844969-5844989(-)	ONE-seq_E44	ONE-seq only
chr8:119822670-119822690(-)	ONE-seq_E45	ONE-seq only
chr9:8207007-8207027(+)	ONE-seq_E46	ONE-seq only
chr9:10481615-10481635(+)	ONE-seq_E47	ONE-seq only
chr9:69177146-69177166(+)	ONE-seq_E48	ONE-seq only
chr9:72624454-72624474(-)	ONE-seq_E49	ONE-seq only
chr9:98969178-98969198(+)	ONE-seq_E50	ONE-seq only
chr9:114797492-114797512(+)	ONE-seq_E51	ONE-seq only
chrY:4160388-4160408(-)	ONE-seq_E52	ONE-seq only
chr8:103195884-103195904(+)	ONE-seq_E53	ONE-seq only
chr5:92964359-92964379(-)	ONE-seq_E54	ONE-seq only
chr5:93612866-93612886(-)	ONE-seq_E55	ONE-seq only
chr5:102333534-102333554(-)	ONE-seq_E56	ONE-seq only
chr5:159669105-159669125(-)	ONE-seq_E57	ONE-seq only
chr5:71257673-71257693(+)	ONE-seq_E58	ONE-seq only
chr5:70553701-70553721(+)	ONE-seq_E59	ONE-seq only
chr5:70257365-70257385(+)	ONE-seq_E60	ONE-seq only
chr4:168790765-168790785(-)	ONE-seq_E61	ONE-seq only
chr4:183698545-183698565(-)	ONE-seq_E62	ONE-seq only
chr5:29153498-29153518(-)	ONE-seq_E63	ONE-seq only
chr5:34216779-34216799(+)	ONE-seq_E64	ONE-seq only
chr5:38430463-38430483(+)	ONE-seq_E65	ONE-seq only
chr5:69677628-69677648(+)	ONE-seq_E66	ONE-seq only
chr7:95118617-95118637(+)	ONE-seq_E67	ONE-seq only
chr7:95815040-95815060(-)	ONE-seq_E68	ONE-seq only
chr7:130096718-130096738(-)	ONE-seq_E69	ONE-seq only
chr8:33172341-33172361(+)	ONE-seq_E70	ONE-seq only
chr8:35134219-35134239(+)	ONE-seq_E71	ONE-seq only
chr8:89001641-89001661(+)	ONE-seq_E72	ONE-seq only
chr8:91428668-91428688(-)	ONE-seq_E73	ONE-seq only
chr6:26923601-26923621(+)	ONE-seq_E74	ONE-seq only
chr6:138770125-138770145(-)	ONE-seq_E75	ONE-seq only
chr6:139651449-139651469(+)	ONE-seq_E76	ONE-seq only
chr6:160766277-160766297(-)	ONE-seq_E77	ONE-seq only
chr10:98353386-98353406(+)	ONE-seq_E78	ONE-seq only
chr10:96683542-96683562(-)	ONE-seq_E79	ONE-seq only
chr1:173744089-173744109(+)	ONE-seq_E80	ONE-seq only
chr1:198803203-198803223(-)	ONE-seq_E81	ONE-seq only
chr10:24703799-24703819(-)	ONE-seq_E82	ONE-seq only
chr10:37410194-37410214(+)	ONE-seq_E83	ONE-seq only

chr10:62298408-62298428(+)
chr10:82028845-82028865(-)

ONE-seq_E84
ONE-seq_E85

ONE-seq only
ONE-seq only

Priority	Gene	Annot.	Lev. Dist.	CHANGE-seq-BE Score	ONE-seq Score
	2 OLFM3	Intron	6	0	0
	2 MAN1A2	Intron	6	0	0
	2 PDE4DIPP1	Other	5	0	0
	1 MSTO1	Exon	6	0	0
	2 none	Intergenic	6	0	0
	1 TSNAX	Intron	6	0	0
	1 MARCKSL1	Exon	6	0	0
	2 MAST2	Intron	6	0	0
	2 SLC44A3-AS1	Other	6	0	0
	2 none	Intergenic	6	0	0
	1 AFAP1L2	Intron	4	0	0
	1 KIAA1217	Intron	3	0.2	0.562660919
	2 none	Intergenic	6	0	0
	2 none	Intergenic	6	0	0
	1 TIMM23	Intron	6	0	0
	1 none	Intergenic	2	0.2	0.104282716
	1 JMJD1C	Intron	6	0	0
	2 none	Intergenic	4	0	0.38084473
	2 none	Intergenic	6	0	0
	2 CUL5	Intron	4	0	0
	2 none	Intergenic	6	0	0
	2 JHY	Intron	6	0	0
	1 BDNF-AS	Other	5	0	0
	2 PAMR1	Intron	6	0	0
	2 none	Intergenic	6	0	0
	2 none	Intergenic	6	0	0
	1 TMX2	Intron	3	0	0.049417474
	2 none	Intergenic	6	0	0
	2 POLD3	Intron	6	0	0
	1 DLG2	Intron	6	0	0
	2 none	Intergenic	6	0	0
	1 CNTN5	Intron	6	0	0
	2 none	Intergenic	6	0	0
	2 none	Intergenic	3	0	0
	1 TSPAN9	Intron	6	0	0
	2 none	Intergenic	6	0	0
	1 TMTC4	Intron	6	0	0
	2 none	Intergenic	6	0	0
	2 none	Intergenic	6	0	0
	1 LINC00343	Exon	6	0	0
	1 none	Intergenic	2	0.1	0.70353089
	1 FLT1	Intron	3	0	0
	1 SUCLA2	Intron	4	0	0.27178127
	1 ATP7B	Intron	2	4.3	5.048108912
	1 KLHL1	Exon	6	0	0
	2 RBM26-AS1	Other	6	0	0
	2 none	Intergenic	6	0	0
	1 SLC25A21	Intron	6	0	0
	2 LOC105370456	Other	4	0	0.061381676
	2 none	Intergenic	6	0	0

2 none	Intergenic	6	0	0
1 EML1	Intron	4	0	0.158263316
1 UBE3A	Intron	4	0	0
1 LINC02346	Other	6	0	0
2 CORO2B	Intron	6	0	0
1 THSD4	Intron	6	0	0
2 ARIH1	Intron	6	0	0
1 SCAPER	Intron	2	0	0.890029975
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	5	0	0
1 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
1 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
1 none	Intergenic	6	0	0
1 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	5	0	0
2 none	Intergenic	5	0	0
1 CDH13	Intron	6	0	0
1 COX10	Intron	3	7.1	5.73915517
2 USP22	Intron	6	0	0
2 none	Intergenic	6	0	0
2 YWHAEP7	Other	6	0	0
2 none	Intergenic	6	0	0
2 FXR2	Intron	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	4	1.5	2.170628891
1 none	Intergenic	3	0	0.156338524
2 ME2	Intron	4	0	0
2 LOC107985176	Other	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
1 ZNF83	Intron	6	0	0
2 none	Intergenic	6	0	0
1 none	Intergenic	4	0	0.035198578
2 none	Intergenic	5	0	0
1 LYPD1	Exon	3	0.1	0.364928286
1 DARS1	Intron	6	0	0
1 SLC4A10	Intron	6	0	0
2 ZNF385B	Intron	6	0	0
1 C2orf88	Other	6	0	0
2 none	Intergenic	4	0	0
1 PLCL1	Intron	3	1.2	1.111771749
1 PARD3B	Intron	6	0	0
1 CPS1	Intron	6	0	0
1 CPS1	Intron	6	0	0
1 CPS1	Exon	1	1	1

2 none	Intergenic	6	0	0
1 ARPC2	Exon	6	0	0
2 LOC730100	Other	6	0	0
2 COMMD1	Intron	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
1 LOC101928371	Other	2	0	1.341129545
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	5	0	0
1 ANKRD36B	Intron	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	4	0	0
2 none	Intergenic	6	0	0
1 PTPRT	Intron	3	0	0
1 PTPRT	Intron	6	0	0
1 CDH22	Intron	3	0	0.287024987
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
1 DSCAM	Intron	6	0	0
2 none	Intergenic	4	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
1 LARGE1	Intron	4	0	1.021746961
2 none	Intergenic	6	0	0
2 LINC00882	Other	6	0	0
2 none	Intergenic	6	0	0
2 LINC01205	Other	4	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	5	0	0
2 none	Intergenic	6	0	0
1 SLC9A9	Intron	6	0	0
2 none	Intergenic	6	0	0
1 NLGN1	Intron	6	0	0
2 none	Intergenic	5	0	0
1 VPS8	Intron	6	0	0
1 RARB	Intron	6	0	0
2 MYRIP	Intron	5	0	0
2 EIF1B-AS1	Other	6	0	0
1 FHIT	Intron	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	3	0	0.689281963
2 none	Intergenic	3	0	0
2 LINC02355	Other	6	0	0
1 LRBA	Intron	6	0	0
2 LOC107986324	Other	6	0	0
2 none	Intergenic	6	0	0
2 LINC02484	Other	6	0	0

2 ATP8A1	Intron	6	0	0
1 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 PPP2R2B	Intron	6	0	0
1 CDH18	Intron	5	0	0
1 PDZD2	Intron	6	0	0
2 none	Intergenic	5	0	0
2 none	Intergenic	5	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	2	0	0
2 TBCA	Intron	6	0	0
2 none	Intergenic	3	0	0.030885509
1 HDAC2	Intron	6	0	0
2 none	Intergenic	6	0	0
1 IPCEF1	Intron	3	0	0
2 TSBP1	Intron	3	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	5	0	0
2 none	Intergenic	6	0	0
1 none	Intergenic	2	2.1	0.612917409
2 none	Intergenic	6	0	0
1 none	Intergenic	4	0	0
1 CPED1	Intron	6	0	0
1 AASS	Intron	6	0	0
1 SDK1	Intron	6	0	0
2 none	Intergenic	2	0	0
2 none	Intergenic	5	0	0.037950979
2 LOC105375341	Other	2	0	0
1 LOC100128317	Other	6	0	0
2 none	Intergenic	6	0	0
1 RSPO2	Intron	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	3	0	0
1 VPS13B	Intron	5	0	0
2 LOC105376244	Other	6	0	0
1 CNTRL	Exon	6	0	0
2 ERMP1	Intron	5	0	0.021233036
2 none	Intergenic	4	0	0
2 none	Intergenic	6	0	0
2 none	Intergenic	6	0	0

2 none	Intergenic	5	0	0
1 LRCH2	Intron	6	0	0
2 none	Intergenic	4	0	0.562756361
2 LOC105377212	Other	3	0	0.069498701
2 none	Intergenic	6	0	0
1 CRACDL	Exon	4	0	0.044623809
1 AFF3	Exon	5	0	0.012231368
1 SLC25A42	Exon	3	0	0.018921308
1 ESF1	Exon	3	0	0.575666784
1 CRACD	Exon	4	0	0.524221234
1 LINC02172	Exon	5	0	0.011292989
1 CCDC62	Exon	4	0	0.011495012
1 KL	Exon	4	0	0.011622892
1 DNAI7	Exon	4	0	0.020016083
1 WDR11-AS1	Exon	4	0	0.016137984
1 LOC107984617	Exon	5	0	0.04061783
1 RMDN3	Exon	4	0	0.072100408
1 TBC1D9	Exon	4	0	0.019032077
1 LOC107985917	Exon	5	0.1	0
1 LINC02109	Exon	4	0	0.930645398
1 SLC38A9	Exon	4	0	0.098453715
1 ELAPOR2	Exon	4	0	0.011640002
1 MTFR1	Exon	4	0	0.028022339
1 MAPKAP1	Exon	5	0.1	0
1 none	Intergenic	2	0.7	1.081259096
1 none	Intergenic	2	0.4	0.108296805
1 none	Intergenic	2	0.1	0.167407567
1 none	Intergenic	2	0.1	2.244927049
1 none	Intergenic	2	0.1	0.707630529
1 MKLN1	Intron	3	0.1	0.292247918
1 LOC105379013	Other	3	0.1	0.63664771
1 NOVA1	Intron	3	0.1	0.119996246
1 LOC105369995	Other	3	0.1	0.012973427
1 none	Intergenic	3	0.1	0.483802131
1 THSD4	Intron	3	0.1	0.604130687
1 none	Intergenic	3	0.2	0.945159977
1 none	Intergenic	3	0.1	0.0473591
1 none	Intergenic	4	0.1	0.048194819
1 none	Intergenic	4	0.4	0.025998184
1 none	Intergenic	4	0.1	0.026009591
1 none	Intergenic	4	0.1	0.11003098
1 none	Intergenic	4	0.2	0.649139917
1 HECW2	Intron	4	0.1	0.353426947
1 none	Intergenic	4	0.1	0.011756475
1 MPDZ	Intron	4	0.1	0.194479229
1 none	Intergenic	5	0.1	0.0371747
1 none	Intergenic	5	0.1	0.97733177
1 PPHLN1	Intron	3	0	1.204710503
1 SORCS1	Intron	4	0	4.042746159
1 FAM133A	Intergenic	3	0	1.423785427
1 SLCO4C1	Intergenic	3	0	1.251672418

1 MEF2C-AS1	Other	3	1	0
1 LINC01470	Intergenic	6	0.3	0
1 ALDH1A1	Intron	6	0.3	0
2 none	Intergenic	2	0	0
2 none	Intergenic	2	0	0
2 none	Intergenic	2	0	0
2 LINC01049	Other	2	0	0
2 FCHSD2	Exon	3	0	0
2 ICA1	Exon	3	0	0
2 LOC105370689	Exon	3	0	0
2 LOC105375107	Exon	3	0	0
2 MAP2K6	Exon	3	0	0
2 MYCBP2	Exon	3	0	0
2 PLS3	Exon	3	0	0
2 RBM41	Exon	3	0	0
2 RPP40	Exon	3	0	0
2 ST8SIA1	Exon	3	0	0
2 STON1	Exon	3	0	0
2 TTC21B	Exon	3	0	0
2 CSNK2A1	Intron	5	0	0.193473301
2 none	Intergenic	4	0	0.162187042
2 DSG2	Intron	3	0	0.239867019
2 none	Intergenic	4	0	0.119843147
2 LOC105372358	Other	4	0	0.123757873
2 none	Intergenic	4	0	0.187107561
2 NRXN1	Intron	4	0	0.159474565
2 ESF1	Exon	3	0	0.575666784
2 DOK5	Intron	3	0	0.123255354
2 CRACD	Exon	4	0	0.524221234
2 none	Intergenic	5	0	0.217769748
2 none	Intergenic	4	0	0.112865634
2 none	Intergenic	4	0	0.104342156
2 LOC105372804	Other	4	0	0.981052582
2 LINC00693	Other	4	0	0.140948303
2 none	Intergenic	4	0	0.168824761
2 none	Intergenic	5	0	0.367282343
2 PPHLN1	Intron	3	0	1.204710503
2 none	Intergenic	3	0	0.403753125
2 none	Intergenic	3	0	0.10644286
2 LOC105370221	Other	4	0	0.101552238
2 SORCS1	Intron	4	0	4.042746159
2 none	Intergenic	3	0	0.306310418
2 none	Intergenic	3	0	0.302051976
2 none	Intergenic	4	0	0.120238193
2 none	Intergenic	4	0	0.174863895
2 LOC105370221	Other	4	0	0.160733846
2 ANKRD26P1	Other	5	0	0.714139744
2 ZNF423	Intron	4	0	0.13280187
2 none	Intergenic	5	0	0.10381023
2 PKD1L3	Intron	5	0	0.250620863
2 none	Intergenic	4	0	0.112672611

2 LOC101927284	Other	3	0	0.240181595
2 MDGA2	Intron	5	0	0.11969486
2 SIPA1L1-AS1	Other	4	0	0.164629056
2 TTLL5	Intron	3	0	0.205395173
2 NRXN3	Intron	5	0	0.118170818
2 DGLUCY	Intron	4	0	0.112794787
2 FRMPD4	Intron	3	0	0.305570764
2 SLC16A2	Intron	3	0	0.140134506
2 none	Intergenic	4	0	0.159138958
2 none	Intergenic	3	0	1.423785427
2 none	Intergenic	5	0	0.113701353
2 none	Intergenic	5	0	0.188406766
2 TAF2	Intron	5	0	0.540894442
2 none	Intergenic	3	0	0.691808636
2 PTPRD	Intron	4	0	0.12001906
2 TJP2	Intron	3	0	0.197490687
2 TMC1	Intron	3	0	0.341119653
2 COL15A1	Intron	4	0	0.487915583
2 TNFSF15	Intron	3	0	0.205267293
2 none	Intergenic	4	0	0.149440858
2 BAALC	Intron	4	0	0.173721086
2 none	Intergenic	4	0	0.448387717
2 none	Intergenic	3	0	0.216065872
2 none	Intergenic	3	0	1.251672418
2 none	Intergenic	3	0	0.275846065
2 GUSBP17	Other	3	0	0.178915501
2 GUSBP15	Other	3	0	0.154128566
2 GUSBP14	Other	3	0	0.134337319
2 PALLD	Intron	4	0	0.490617544
2 TRAPPC11	Intron	4	0	0.23052823
2 LINC02109	Exon	4	0	0.930645398
2 C1QTNF3	Other	3	0	0.112473885
2 EGFLAM	Intron	4	0	0.134653409
2 GUSBP3	Other	3	0	0.114845052
2 PPP1R9A	Intron	4	0	0.184750206
2 DYNC1I1	Intron	3	0	0.198303592
2 KLHDC10	Intron	5	0	0.129416665
2 none	Intergenic	3	0	0.351880715
2 none	Intergenic	3	0	0.117568937
2 LOC105375631	Other	4	0	0.209790495
2 none	Intergenic	4	0	0.161598973
2 GUSBP2	Other	4	0	0.16056934
2 CCDC28A-AS1	Other	2	0	0.319938839
2 none	Intergenic	5	0	0.40093166
2 none	Intergenic	4	0	0.104100209
2 none	Intergenic	3	0	0.184931822
2 PIK3AP1	Intron	4	0	0.102878445
2 KLHL20	Intron	4	0	0.119709564
2 none	Intergenic	5	0	0.195613928
2 ARHGAP21	Intron	4	0	0.42741855
2 LOC107984223	Other	3	0	0.154307776

2 LINC02621	Other	3	0	0.437059617
2 NRG3	Intron	2	0	0.135679745

Max GUIDE-seq+ score	GUIDE-seq+ Cell Line Origin	Site Type
0.01	HUH7	OFF
0.052	U2OS	OFF
0.025	HUH7	OFF
0.013	HUH7	OFF
0.014	HUH7	OFF
0.027	HUH7	OFF
0.012	HUH7	OFF
0.05	HUH7	OFF
0.026	U2OS	OFF
0.01	HUH7	OFF
0.028	HUH7	OFF
0.089	U2OS	OFF
0.013	HUH7	OFF
0.02	HUH7	OFF
0.031	U2OS	OFF
2.901	both	OFF
0.025	U2OS	OFF
0.016	U2OS	OFF
0.021	HUH7	OFF
0.019	U2OS	OFF
0.015	HUH7	OFF
0.033	HUH7	OFF
0.011	HUH7	OFF
0.016	U2OS	OFF
0.018	HUH7	OFF
0.028	U2OS	OFF
0.695	both	OFF
0.014	HUH7	OFF
0.064	HUH7	OFF
0.022	HUH7	OFF
0.012	HUH7	OFF
0.014	HUH7	OFF
0.039	HUH7	OFF
0.048	U2OS	OFF
0.014	HUH7	OFF
0.014	HUH7	OFF
0.024	HUH7	OFF
0.037	U2OS	OFF
0.026	HUH7	OFF
0.01	HUH7	OFF
1.253	both	OFF
3.055	both	OFF
0.011	HUH7	OFF
1.084	both	OFF
0.006	HUH7	OFF
0.056	U2OS	OFF
0.004	U2OS	OFF
0.013	HUH7	OFF
0.026	U2OS	OFF
0.026	HUH7	OFF

0.019 HUH7	OFF
0.014 U2OS	OFF
0.005 HUH7	OFF
0.023 U2OS	OFF
0.015 HUH7	OFF
0.036 HUH7	OFF
0.01 HUH7	OFF
0.004 U2OS	OFF
0.035 U2OS	OFF
0.045 HUH7	OFF
0.025 HUH7	OFF
0.102 HUH7	OFF
0.01 HUH7	OFF
0.016 HUH7	OFF
0.078 HUH7	OFF
0.009 HUH7	OFF
0.026 HUH7	OFF
0.058 HUH7	OFF
0.036 HUH7	OFF
0.038 HUH7	OFF
0.008 HUH7	OFF
0.014 HUH7	OFF
0.126 both	OFF
0.014 HUH7	OFF
0.017 HUH7	OFF
0.009 HUH7	OFF
0.071 U2OS	OFF
0.031 U2OS	OFF
0.021 HUH7	OFF
0.005 HUH7	OFF
0.058 both	OFF
0.21 both	OFF
0.019 U2OS	OFF
0.008 HUH7	OFF
0.048 U2OS	OFF
0.019 HUH7	OFF
0.06 U2OS	OFF
0.01 HUH7	OFF
0.089 both	OFF
0.009 HUH7	OFF
0.015 U2OS	OFF
0.014 HUH7	OFF
0.033 HUH7	OFF
0.009 HUH7	OFF
0.023 HUH7	OFF
0.112 both	OFF
0.01 HUH7	OFF
0.008 U2OS	OFF
0.026 U2OS	OFF
0.13 HUH7	OFF
100 both	ON

0.085 U2OS	OFF
0.003 HUH7	OFF
0.019 HUH7	OFF
0.018 HUH7	OFF
0.013 HUH7	OFF
0.056 HUH7	OFF
1.815 both	OFF
0.006 HUH7	OFF
0.028 HUH7	OFF
0.01 HUH7	OFF
0.046 U2OS	OFF
0.003 HUH7	OFF
0.004 HUH7	OFF
0.006 HUH7	OFF
0.016 HUH7	OFF
0.048 HUH7	OFF
0.248 both	OFF
0.029 HUH7	OFF
0.118 both	OFF
0.013 HUH7	OFF
0.004 U2OS	OFF
0.005 HUH7	OFF
0.011 HUH7	OFF
0.011 HUH7	OFF
0.005 HUH7	OFF
0.017 HUH7	OFF
0.144 both	OFF
0.015 HUH7	OFF
0.018 HUH7	OFF
0.01 HUH7	OFF
0.012 both	OFF
0.032 U2OS	OFF
0.01 HUH7	OFF
0.021 HUH7	OFF
0.014 U2OS	OFF
0.028 HUH7	OFF
0.02 U2OS	OFF
0.013 HUH7	OFF
0.011 HUH7	OFF
0.014 HUH7	OFF
0.008 HUH7	OFF
0.015 HUH7	OFF
0.03 U2OS	OFF
0.013 U2OS	OFF
0.006 U2OS	OFF
0.151 both	OFF
0.021 HUH7	OFF
0.059 U2OS	OFF
0.02 U2OS	OFF
0.007 HUH7	OFF
0.034 HUH7	OFF

0.04 U2OS	OFF
0.055 HUH7	OFF
0.027 HUH7	OFF
0.03 HUH7	OFF
0.022 HUH7	OFF
0.007 HUH7	OFF
0.025 U2OS	OFF
0.007 HUH7	OFF
0.027 U2OS	OFF
0.017 HUH7	OFF
0.064 U2OS	OFF
0.007 U2OS	OFF
0.015 U2OS	OFF
0.032 HUH7	OFF
0.032 HUH7	OFF
0.029 HUH7	OFF
0.005 HUH7	OFF
0.033 HUH7	OFF
0.014 HUH7	OFF
0.026 U2OS	OFF
0.005 HUH7	OFF
0.005 HUH7	OFF
0.021 HUH7	OFF
0.026 HUH7	OFF
0.025 U2OS	OFF
0.023 U2OS	OFF
0.016 HUH7	OFF
0.011 HUH7	OFF
33.009 both	OFF
0.005 HUH7	OFF
0.346 both	OFF
0.031 HUH7	OFF
0.012 HUH7	OFF
0.018 HUH7	OFF
0.036 HUH7	OFF
0.03 U2OS	OFF
0.096 U2OS	OFF
0.011 HUH7	OFF
0.028 HUH7	OFF
0.022 HUH7	OFF
0.007 HUH7	OFF
0.024 HUH7	OFF
0.03 HUH7	OFF
0.011 U2OS	OFF
0.079 U2OS	OFF
0.012 HUH7	OFF
0.025 HUH7	OFF
0.058 U2OS	OFF
0.009 HUH7	OFF
0.13 HUH7	OFF
0.026 U2OS	OFF

[illegible]

[illegible]

[illegible]

0 NA
0 NA

OFF
OFF

GUIDE-seq+ gRNA Origin	Chr	Start	Stop	Strand
CPS1_Mut	chr1	101885582	101885601	+
CPS1_Mut	chr1	117371225	117371245	-
CPS1_Mut	chr1	148055972	148055992	+
CPS1_Mut	chr1	155614892	155614912	-
CPS1_Mut	chr1	187763236	187763256	-
CPS1_Mut	chr1	231540617	231540637	+
CPS1_Mut	chr1	32334556	32334577	-
CPS1_WT	chr1	45988663	45988682	+
CPS1_WT	chr1	94757676	94757696	-
CPS1_Mut	chr1_KI270709v1_random	10583	10603	+
CPS1_Mut	chr10	114296211	114296231	-
CPS1_Mut	chr10	24349861	24349881	+
CPS1_Mut	chr10	39392442	39392461	+
CPS1_Mut	chr10	42079675	42079695	-
CPS1_Mut	chr10	45987007	45987026	+
Both	chr10	56324292	56324312	-
CPS1_Mut	chr10	63501384	63501403	-
CPS1_Mut	chr11	104272430	104272450	+
CPS1_Mut	chr11	106109726	106109744	+
CPS1_WT	chr11	108029419	108029439	+
CPS1_Mut	chr11	109138384	109138404	-
CPS1_Mut	chr11	122891474	122891494	+
CPS1_Mut	chr11	27616919	27616940	+
CPS1_Mut	chr11	35453141	35453161	+
CPS1_WT	chr11	37842595	37842615	-
CPS1_Mut	chr11	55052344	55052362	-
CPS1_Mut	chr11	57726496	57726516	+
CPS1_Mut	chr11	63335538	63335557	-
CPS1_WT	chr11	74601439	74601458	+
CPS1_Mut	chr11	85448979	85448997	+
CPS1_Mut	chr11	98349120	98349138	-
CPS1_Mut	chr11	99844369	99844389	+
CPS1_WT	chr12	114850684	114850705	+
CPS1_Mut	chr12	16700502	16700522	+
CPS1_Mut	chr12	3124373	3124392	+
CPS1_Mut	chr12	90832411	90832431	-
CPS1_Mut	chr13	100666619	100666638	+
CPS1_Mut	chr13	102978390	102978410	-
CPS1_Mut	chr13	103687143	103687163	-
CPS1_WT	chr13	105730448	105730466	+
CPS1_Mut	chr13	105960512	105960532	-
CPS1_WT	chr13	28478362	28478382	-
CPS1_Mut	chr13	47975530	47975550	-
Both	chr13	51941587	51941607	-
CPS1_Mut	chr13	69970655	69970676	-
CPS1_WT	chr13	79419346	79419365	-
CPS1_Mut	chr14	25620214	25620235	-
CPS1_Mut	chr14	36880675	36880695	-
CPS1_Mut	chr14	38007077	38007097	+
CPS1_WT	chr14	43408726	43408745	+

CPS1_Mut	chr14	49505304	49505323 -
CPS1_Mut	chr14	99778821	99778841 -
CPS1_Mut	chr15	25433727	25433746 -
CPS1_Mut	chr15	25963477	25963497 -
CPS1_Mut	chr15	68647164	68647185 +
CPS1_Mut	chr15	71560451	71560470 -
CPS1_Mut	chr15	72575185	72575205 +
CPS1_Mut	chr15	76599706	76599726 +
CPS1_WT	chr16	19129826	19129846 -
CPS1_Mut	chr16	34581387	34581407 +
CPS1_Mut	chr16	34586133	34586153 -
CPS1_Mut	chr16	34588127	34588147 +
CPS1_Mut	chr16	34594949	34594969 -
CPS1_Mut	chr16	46386493	46386513 -
CPS1_Mut	chr16	46389076	46389096 +
CPS1_Mut	chr16	46391230	46391250 +
CPS1_Mut	chr16	46398553	46398573 -
CPS1_Mut	chr16	46400236	46400256 -
CPS1_Mut	chr16	46401181	46401201 -
CPS1_WT	chr16	46401311	46401330 +
CPS1_Mut	chr16	76814991	76815011 +
CPS1_Mut	chr16	82705551	82705571 +
CPS1_Mut	chr17	14085181	14085201 +
CPS1_WT	chr17	21014472	21014493 -
CPS1_WT	chr17	26619568	26619587 +
CPS1_WT	chr17	37868538	37868558 -
CPS1_Mut	chr17	43472085	43472104 -
CPS1_Mut	chr17	7602883	7602903 +
CPS1_Mut	chr17_KI270729v1_random	59740	59759 +
CPS1_Mut	chr18	20922197	20922217 +
CPS1_Mut	chr18	2161219	2161239 +
CPS1_Mut	chr18	28430786	28430806 -
CPS1_Mut	chr18	50910799	50910819 +
CPS1_Mut	chr18	6641253	6641274 -
CPS1_Mut	chr19	35923620	35923639 -
CPS1_WT	chr19	37732208	37732227 -
CPS1_Mut	chr19	52675206	52675225 -
CPS1_Mut	chr19	57579217	57579235 +
CPS1_Mut	chr2	107701686	107701706 +
CPS1_WT	chr2	131812122	131812141 -
CPS1_Mut	chr2	132665291	132665311 -
CPS1_Mut	chr2	135947775	135947796 +
CPS1_WT	chr2	161811106	161811126 +
CPS1_Mut	chr2	179715527	179715545 +
CPS1_Mut	chr2	190032040	190032060 +
CPS1_WT	chr2	191905587	191905607 -
CPS1_Mut	chr2	198087320	198087340 -
CPS1_Mut	chr2	204916812	204916832 +
CPS1_Mut	chr2	210590916	210590936 -
CPS1_Mut	chr2	210591749	210591767 -
Both	chr2	210591873	210591893 -

CPS1_WT	chr2	21395450	21395470 +
CPS1_WT	chr2	218254089	218254109 -
CPS1_Mut	chr2	51700372	51700394 -
CPS1_Mut	chr2	62015628	62015649 +
CPS1_Mut	chr2	78933334	78933355 -
CPS1_WT	chr2	79046372	79046392 +
CPS1_WT	chr2	88552102	88552122 -
CPS1_Mut	chr2	89826531	89826551 -
CPS1_WT	chr2	89833404	89833424 -
CPS1_Mut	chr2	91586559	91586578 -
CPS1_WT	chr2	93754951	93754969 +
CPS1_Mut	chr2	97548295	97548315 -
CPS1_Mut	chr20	18004086	18004106 +
CPS1_WT	chr20	29885813	29885831 -
CPS1_Mut	chr20	31068519	31068537 +
CPS1_Mut	chr20	31213821	31213839 +
CPS1_WT	chr20	42667000	42667020 +
CPS1_WT	chr20	42970387	42970407 +
CPS1_Mut	chr20	46262548	46262568 -
CPS1_WT	chr20	47912906	47912926 -
CPS1_Mut	chr21	10691030	10691049 -
CPS1_Mut	chr21	24770731	24770751 +
CPS1_WT	chr21	40397747	40397766 -
CPS1_Mut	chr21	7255330	7255348 -
CPS1_Mut	chr21	7919637	7919656 -
CPS1_Mut	chr22	16269967	16269987 +
CPS1_Mut	chr22	33548897	33548917 +
CPS1_WT	chr3	103265928	103265948 -
CPS1_Mut	chr3	107194685	107194705 +
CPS1_Mut	chr3	108858616	108858636 -
CPS1_Mut	chr3	109441319	109441339 +
CPS1_Mut	chr3	112911040	112911060 -
CPS1_WT	chr3	122159469	122159488 -
CPS1_Mut	chr3	125726766	125726786 -
CPS1_Mut	chr3	143788738	143788758 +
CPS1_WT	chr3	145538143	145538162 +
CPS1_Mut	chr3	173691237	173691256 -
CPS1_Mut	chr3	18286238	18286257 +
CPS1_Mut	chr3	184821674	184821695 -
CPS1_Mut	chr3	25248348	25248367 -
CPS1_Mut	chr3	39964863	39964885 -
CPS1_Mut	chr3	40277530	40277550 +
CPS1_WT	chr3	60384958	60384978 -
CPS1_Mut	chr3	67097709	67097728 +
CPS1_Mut	chr3	96019252	96019272 +
CPS1_WT	chr4	129150639	129150659 -
CPS1_Mut	chr4	149238470	149238488 -
CPS1_Mut	chr4	150673751	150673769 -
CPS1_WT	chr4	159914856	159914876 +
CPS1_Mut	chr4	174877223	174877243 +
CPS1_WT	chr4	34238119	34238139 -

CPS1_Mut	chr4	42524439	42524458 +
CPS1_Mut	chr4	49103973	49103991 -
CPS1_Mut	chr4	49147625	49147643 +
CPS1_WT	chr4	52575886	52575906 -
CPS1_Mut	chr4	52735305	52735323 +
CPS1_Mut	chr4	63161261	63161281 +
CPS1_Mut	chr4	64420581	64420601 -
CPS1_WT	chr4	78956535	78956555 -
CPS1_WT	chr5	146593816	146593836 +
CPS1_Mut	chr5	19552938	19552958 +
CPS1_WT	chr5	32045171	32045191 +
CPS1_Mut	chr5	33299687	33299705 +
CPS1_Mut	chr5	39966526	39966546 -
CPS1_WT	chr5	49601725	49601745 +
CPS1_WT	chr5	49601750	49601770 +
CPS1_WT	chr5	49602115	49602135 +
CPS1_WT	chr5	49657003	49657023 -
CPS1_WT	chr5	49660745	49660765 -
CPS1_WT	chr5	50995275	50995295 +
CPS1_WT	chr5	77742179	77742199 +
CPS1_Mut	chr5	92045471	92045492 -
CPS1_Mut	chr6	113966592	113966612 -
CPS1_Mut	chr6	137610990	137611008 -
CPS1_WT	chr6	154331970	154331990 -
CPS1_WT	chr6	32368599	32368619 -
CPS1_Mut	chr6	41668217	41668235 -
CPS1_Mut	chr6	61383664	61383682 +
CPS1_Mut	chr6	68587058	68587079 +
Both	chr6	71690557	71690577 +
CPS1_WT	chr6	91554457	91554476 -
CPS1_WT	chr6	96750602	96750622 -
CPS1_Mut	chr7	121141099	121141119 +
CPS1_Mut	chr7	122094836	122094856 +
CPS1_Mut	chr7	3448464	3448485 -
CPS1_WT	chr7	37590233	37590253 +
CPS1_Mut	chr7	49502148	49502168 -
CPS1_WT	chr7	68154122	68154142 +
CPS1_Mut	chr7	81628563	81628583 +
CPS1_Mut	chr7	86536385	86536405 +
CPS1_WT	chr8	107998731	107998751 -
CPS1_Mut	chr8	110396641	110396661 +
CPS1_Mut	chr8	123614246	123614266 +
CPS1_Mut	chr8	2040223	2040243 -
CPS1_WT	chr8	70547400	70547420 +
CPS1_WT	chr8	99794486	99794506 -
CPS1_Mut	chr9	117808527	117808547 -
CPS1_Mut	chr9	121177557	121177577 -
CPS1_Mut	chr9	5828921	5828941 -
CPS1_Mut	chr9	73747216	73747236 +
CPS1_WT	chrUn_KI270438v1	102368	102386 +
CPS1_Mut	chrUn_KI270438v1	104376	104396 +

CPS1_Mut	chrUn_KI270517v1	2631	2649 -
CPS1_Mut	chrX	115223463	115223483 +
CPS1_Mut	chrX	143455204	143455224 +
CPS1_Mut	chrX	63259190	63259210 -
CPS1_Mut	chrY	11643825	11643844 -
NA	chr2	98814239	98814259 -
NA	chr2	99672541	99672561 -
NA	chr19	19076134	19076154 -
NA	chr20	13784104	13784124 +
NA	chr4	56229938	56229958 -
NA	chr4	137601272	137601292 +
NA	chr12	122788868	122788888 +
NA	chr13	33065684	33065704 +
NA	chr12	25111823	25111843 +
NA	chr10	120815627	120815647 +
NA	chr13	91359585	91359605 -
NA	chr15	40747756	40747776 +
NA	chr4	140621573	140621593 -
NA	chr2	95541686	95541706 +
NA	chr5	29153498	29153518 -
NA	chr5	55692818	55692838 -
NA	chr7	86879335	86879355 -
NA	chr8	65709164	65709184 +
NA	chr9	125552068	125552088 -
NA	chr6	28319161	28319181 +
NA	chr10	21381234	21381254 -
NA	chr10	3903005	3903025 +
NA	chr2	7733220	7733240 -
NA	chr8	122636872	122636892 +
NA	chr7	131268494	131268514 +
NA	chr5	68439824	68439844 +
NA	chr14	26538238	26538258 +
NA	chr12	114081726	114081746 +
NA	chr12	14009521	14009541 +
NA	chr15	71407301	71407321 -
NA	chr3	69014309	69014329 -
NA	chr2	17253817	17253837 +
NA	chr5	29462611	29462631 +
NA	chr4	96821205	96821225 -
NA	chr10	80905054	80905074 +
NA	chr1	232678825	232678845 -
NA	chr4	29910257	29910277 -
NA	chr2	196584615	196584635 -
NA	chr19	20319265	20319285 +
NA	chr9	13154678	13154698 +
NA	chr3	103143974	103143994 -
NA	chr18	76326696	76326716 -
NA	chr12	42377204	42377224 +
NA	chr10	106940996	106941016 -
NA	chrX	94310316	94310336 +
NA	chr5	102333534	102333554 -

NA	chr5	89092422	89092442 -
NA	chr5	153089661	153089681 -
NA	chr9	72906365	72906385 -
NA	chr14	82199313	82199333 -
NA	chr4	25696309	25696329 +
NA	chr4	25696310	25696330 +
NA	chr13	90518582	90518602 -
NA	chr11	72838746	72838766 +
NA	chr7	8213616	8213636 +
NA	chr14	103879509	103879529 +
NA	chr6	27313497	27313517 -
NA	chr17	69548520	69548540 -
NA	chr13	77205504	77205524 -
NA	chrX	115635016	115635036 +
NA	chrX	107069755	107069775 -
NA	chr6	4998773	4998793 -
NA	chr12	22308939	22308959 +
NA	chr2	48597982	48598003 -
NA	chr2	165919377	165919397 +
NA	chr20	531888	531908 -
NA	chr2	56536797	56536817 +
NA	chr18	31525111	31525131 -
NA	chr18	71192156	71192176 -
NA	chr19	31131277	31131297 -
NA	chr2	2481312	2481332 +
NA	chr2	50480846	50480866 -
NA	chr20	13784104	13784124 +
NA	chr20	54569334	54569354 +
NA	chr4	56229938	56229958 -
NA	chr4	105489456	105489476 -
NA	chr3	116794536	116794556 +
NA	chr21	20131782	20131802 +
NA	chr21	39362110	39362130 -
NA	chr3	28647007	28647027 -
NA	chr3	35964683	35964703 +
NA	chr3	103377328	103377348 +
NA	chr12	42377204	42377224 +
NA	chr12	60336177	60336197 -
NA	chr13	58498215	58498235 +
NA	chr13	59089333	59089353 -
NA	chr10	106940996	106941016 -
NA	chr10	128590280	128590300 -
NA	chr11	23310298	23310318 +
NA	chr11	23819004	23819024 +
NA	chr11	38405965	38405985 -
NA	chr13	59092798	59092818 -
NA	chr16	46526796	46526816 +
NA	chr16	49741749	49741769 +
NA	chr16	61032958	61032978 +
NA	chr16	71935122	71935142 +
NA	chr17	52735296	52735316 -

NA	chr13	94810687	94810707 -
NA	chr14	47343282	47343302 +
NA	chr14	71303370	71303390 +
NA	chr14	75771551	75771571 -
NA	chr14	78582287	78582307 -
NA	chr14	91205110	91205130 +
NA	chrX	12101643	12101663 +
NA	chrX	74492645	74492665 -
NA	chrX	90582641	90582661 -
NA	chrX	94310316	94310336 +
NA	chrX	99977456	99977476 -
NA	chrX	5844969	5844989 -
NA	chr8	119822670	119822690 -
NA	chr9	8207007	8207027 +
NA	chr9	10481615	10481635 +
NA	chr9	69177146	69177166 +
NA	chr9	72624454	72624474 -
NA	chr9	98969178	98969198 +
NA	chr9	114797492	114797512 +
NA	chrY	4160388	4160408 -
NA	chr8	103195884	103195904 +
NA	chr5	92964359	92964379 -
NA	chr5	93612866	93612886 -
NA	chr5	102333534	102333554 -
NA	chr5	159669105	159669125 -
NA	chr5	71257673	71257693 +
NA	chr5	70553701	70553721 +
NA	chr5	70257365	70257385 +
NA	chr4	168790765	168790785 -
NA	chr4	183698545	183698565 -
NA	chr5	29153498	29153518 -
NA	chr5	34216779	34216799 +
NA	chr5	38430463	38430483 +
NA	chr5	69677628	69677648 +
NA	chr7	95118617	95118637 +
NA	chr7	95815040	95815060 -
NA	chr7	130096718	130096738 -
NA	chr8	33172341	33172361 +
NA	chr8	35134219	35134239 +
NA	chr8	89001641	89001661 +
NA	chr8	91428668	91428688 -
NA	chr6	26923601	26923621 +
NA	chr6	138770125	138770145 -
NA	chr6	139651449	139651469 +
NA	chr6	160766277	160766297 -
NA	chr10	98353386	98353406 +
NA	chr10	96683542	96683562 -
NA	chr1	173744089	173744109 +
NA	chr1	198803203	198803223 -
NA	chr10	24703799	24703819 -
NA	chr10	37410194	37410214 +

NA	chr10	62298408	62298428 +
NA	chr10	82028845	82028865 -

[illegible]

chr18:2161222G>T rs588515

chr2:179715547T>C rs881737

chr2:210591885C>T.

[illegible]

chr2:78933354A>G rs9309541

chr22:33548913C>T rs1547070

[illegible]

chr8:2040236T>C rs13282515

[illegible]

[illegible]

[illegible]

chrX:5844993C>T rs6638568

chr9:10481638C>A rs7870466

chr6:160766302C>T rs1406890

p2
p2

Priority	UNCOVERseq	ONE-seq	Off-target
1	Tier 1, 2, and 3	>=100 score OR >= 10 score AND Annotation = Exon >=10 score OR >=1 score AND Annotation = Exon OR Shared empirical sites >= Priority 3 thresholds	
2	Tier 4, 5, and 6		
3	N/A	>=1 score	

Target Nomination Method

CHANGE-seq-BE

≥ 30 score

OR

Annotation = Exon

Shared empirical sites $\geq$ Priority 3 thresholds

≥ 10 score

Computational

N/A

Lev. distance ≤ 2

OR

Lev. distance ≤ 3 **AND** Annotation = Exon

N/A

SampleName	Cell Line	gRNA	Condition	Replicate	Coverage	%Edited
HUH7_TagOnly_Rep1	HuH-7	None	Negative Contro	1	130925	0.03
HUH7_TagOnly_Rep2	HuH-7	None	Negative Contro	2	147237	0.03
HUH7_TagOnly_Rep3	HuH-7	None	Negative Contro	3	87733	0.03
HUH7_CPS1_Rep1	HuH-7	CPS1*	Treatment	1	127530	87.58
HUH7_CPS1_Rep2	HuH-7	CPS1*	Treatment	2	108221	85.23
HUH7_CPS1_Rep3	HuH-7	CPS1*	Treatment	3	245352	84.59
HUH7_CPS1_WT_Rep1	HuH-7	CPS1_WT	Treatment	1	74963	90.96
HUH7_CPS1_WT_Rep2	HuH-7	CPS1_WT	Treatment	2	116129	91.40
HUH7_CPS1_WT_Rep3	HuH-7	CPS1_WT	Treatment	3	151217	92.57
HUH7_TagOnly_Rep1_LAG3HuH-7	HuH-7	None	Negative Contro	1	201243	0.04
HUH7_TagOnly_Rep2_LAG3HuH-7	HuH-7	None	Negative Contro	2	320083	0.02
HUH7_TagOnly_Rep3_LAG3HuH-7	HuH-7	None	Negative Contro	3	288416	0.02
HUH7_LAG3_Rep1	HuH-7	LAG3	Positive Control	1	154258	83.21
HUH7_LAG3_Rep2	HuH-7	LAG3	Positive Control	2	136733	83.91
HUH7_LAG3_Rep3	HuH-7	LAG3	Positive Control	3	126382	83.22
U2OS_TagOnly_Rep1	U2OS	None	Negative Contro	1	71272	0.03
U2OS_TagOnly_Rep2	U2OS	None	Negative Contro	2	175942	0.03
U2OS_TagOnly_Rep3	U2OS	None	Negative Contro	3	180544	0.02
U2OS_CPS1_Rep1	U2OS	CPS1*	Treatment	1	74400	93.98
U2OS_CPS1_Rep2	U2OS	CPS1*	Treatment	2	84140	95.29
U2OS_CPS1_Rep3	U2OS	CPS1*	Treatment	3	78763	96.26
U2OS_CPS1_WT_Rep1	U2OS	CPS1_WT	Treatment	1	60394	96.64
U2OS_CPS1_WT_Rep2	U2OS	CPS1_WT	Treatment	2	71447	97.00
U2OS_CPS1_WT_Rep3	U2OS	CPS1_WT	Treatment	3	100948	96.26
U2OS_TagOnly_Rep1_LAG3U2OS	U2OS	None	Negative Contro	1	249288	0.02
U2OS_TagOnly_Rep2_LAG3U2OS	U2OS	None	Negative Contro	2	158813	0.02
U2OS_TagOnly_Rep3_LAG3U2OS	U2OS	None	Negative Contro	3	151775	0.02
U2OS_LAG3_Rep1	U2OS	LAG3	Positive Control	1	132285	96.26
U2OS_LAG3_Rep2	U2OS	LAG3	Positive Control	2	76598	96.36
U2OS_LAG3_Rep3	U2OS	LAG3	Positive Control	3	122492	97.07

%Tag Integration

0.00
0.00
0.00
6.90
5.93
6.24
4.61
4.30
4.49
0.00
0.00
0.00
27.66
29.51
25.15
0.00
0.00
0.00
4.95
5.10
5.28
2.94
3.01
3.30
0.00
0.00
0.00
21.16
21.61
28.28

Metric	Cell Line	
	HuH-7	U2OS
# Sites meeting confirmation criteria	46	46
% Confirmed sites nominated	100.00%	97.06%
Max % editing nominated	83.39%	96.54%
Min % editing nominated	0.02%	0.02%
Max % editing not nominated	N/A	0.02%

Average Read Depth Coverage					
Priority	>100,000x	>50,000x	>10,000x	>5,000x	>1,000x
1	1.65%	2.20%	65.01%	81.54%	97.25%
2	2.89%	3.81%	43.99%	68.80%	93.15%

Sensitivity of Confirmation Method at Variable Sequencing Depth on Known Mix

% Indels	<u>Coverage Depth</u>			
	100000x	50000x	10000x	5000x
0.01	60.0	21.1	0.0	0.0
0.05	94.7	69.6	34.8	21.7
0.1	100.0	84.6	36.4	30.4
0.2	100.0	100.0	82.6	56.5
0.5	100.0	95.7	95.7	82.6
1	100.0	100.0	100.0	95.7

xture

1000x
0.0
0.0
17.4
8.7
69.6
82.6

Discloser 1238608
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
AskBio	Data And Safety Monitoring	Self
Category: Data And Safety Monitoring Description: Additional Information:		
LatusBio	Other	Self
Category: Other Description: Advisory Board Member Additional Information:		

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - Compositions and methods for the treatment of car	-	Self
Description: Compositions and methods for the treatment of carbamoyl phosphate synthetase (CPS1) deficiency Patent Status: Filing Jurisdiction: Licensees: Additional Information: Patent Number: Patent Holder:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.



Mohamad-Gabriel Alameh

Discloser 1071364
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239802

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Acuitas Therapeutics	Employment	Self

Title: Vice President Technology Development

Additional Information: Full time salaried employee and shareholder.

Position Description: Responsible for development of underlying core lipid technology related to lipid nanoparticle delivery systems, and translation of this technology to the clinic.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Anne Marie Berry

Discloser Identifier: 1239774

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Sarah Bick

Discloser Identifier: 1239786

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Kevin Briseno

Discloser Identifier: 1238616

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Christian Brommel

Discloser 1239795
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Samantha Burke

Discloser Identifier: 1239784

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser

1239791

Identifier:

Disclosure

25-04747

Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Integrated DNA Technologies	Employment	Self
Title: Senior Staff Scientist Position Description: Enzyme evolution and development. Additional Information:		
Integrated DNA Technologies	Stock	Self
Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser 1239805
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
CSL Behring	Consultant	Self
Category: Consultant Description: Consultant Additional Information:		
Form Bio	Stock Option	Self
Additional Information: Scientific Advisory Board		
Pfizer	Consultant	Self
Category: Consultant Description: consultant Additional Information:		
Regeneron Pharmaceuticals	Consultant	Self
Category: Consultant Description: Consultant on their Hemophilia B gene editing program Additional Information:		
STRM.Bio	Fiduciary Officer	Self
Official Title: Scientific Advisory Board Member Additional Information: I also have stock options Position Description: Scientific Advisory Board		

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - Compositions and Methods for Modulating FVIII Fun	-	Self
Description: Compositions and Methods for Modulating FVIII Function Patent Status: Pending Filing Jurisdiction: USA Licensees: Additional Information: Patent Number: 17/777245 Patent Holder: Current Institution		
Patent - Compositions and Methods for Modulating FVIII fun	-	Self

Type	Is Licensed	Interest Held By
Description: Compositions and Methods for Modulating FVIII function Patent Status: Pending Filing Jurisdiction: USA Licensees: Additional Information:		
Patent Number: 63/334289 Patent Holder: Current Institution		

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser

1239810

Identifier:

Disclosure

25-04747

Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
IMDPath	Consultant	Self
Category: Consultant Description: Additional Information:		
Need Inc	Stock	Self
Additional Information:		
ResearchDx	Consultant	Self
Category: Consultant Description: Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1238613

Disclosure Purpose: 25-04747

Summary of Interests

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - Compositions and methods for treatment of carbamo	-	Self

Description: Compositions and methods for treatment of carbamoyl phosphate synthetase 1 (CPS1) deficiency
Patent Status: Provisional
Filing Jurisdiction: USA
Licensees:
Additional Information:

Patent Number: 63/716,518
Patent Holder:

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Julia Hacker

Discloser Identifier: 1239775

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239778

Disclosure Purpose: 25-04747

Summary of Interests

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - Activity-enhanced engineered SpCas9 PAM Variant e	-	Self

Description: Activity-enhanced engineered SpCas9 PAM Variant enzymes for efficient and specific genome editing.
Patent Status: Provisional
Filing Jurisdiction: USA
Licensees:
Additional Information:

Patent Number: 63/674,450
Patent Holder: Current Institution

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Alvin Hsu

Discloser Identifier: 1239776

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Taylor Hudson

Discloser Identifier: 1238615

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239787

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239793

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Integrated DNA Technologies	Employment	Self
Title: Director, Applications & Market Development Additional Information: Position Description:		
Integrated DNA Technologies	Stock Option	Self
Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser 1239789
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Danaher Corporation	Employment	Self
Title: Principal Scientist R&D Additional Information: Position Description: Analytical method development.		
Danaher Corporation	Stock	Self
Additional Information:		
Danaher Corporation	Stock Option	Self
Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239809

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Danaher Corporation	Employment	Self
Title: CTO/CSO Additional Information: Position Description: Chief Scientific Officer/ Chief Technology Officer		
Danaher Corporation	Stock	Self
Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239792

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239800

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Integrated DNA Technologies	Employment	Self

Title: Staff Scientist
Additional Information:

Position Description: R&D of CRISPR-related technologies

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser 1239806
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Foresite Labs	Consultant	Self
Category: Consultant Description: Consultant Additional Information: Hourly rate		
Jumble Therapeutics	Consultant	Self
Category: Consultant Description: Consulting services Additional Information:		
Life Edit Therapeutics	Stock Option	Self
Additional Information: Scientific advisory board; hourly rate, stock options		
Novartis Venture Fund	Consultant	Self
Category: Consultant Description: Consulting services Additional Information: Hourly rate		
Prime Medicine	Stock	Self
Additional Information: Scientific advisory board, stock options, stocks		

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - IP related to the development of engineered CRISP	-	Self
Description: IP related to the development of engineered CRISPR-Cas9 enzymes Patent Status: Pending Filing Jurisdiction: Licensees: Additional Information: Several patents describing the development of engineered CRISPR-Cas9 enzymes Patent Number: Patent Holder: Current Institution		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.



Gavin Kurgan

Discloser Identifier: 1239797

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Danaher Corporation	Employment	Self
Title: Additional Information:		
Position Description:		
Danaher Corporation	Stock	Self
Additional Information:		

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

Yes.

- a. **Please describe those relationships.**

Integrated DNA Technologies, a Danaher company, sells reagents and services directly related to those used in the manuscript.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser 1239807
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Beam Therapeutics	Consultant	Self
Category: Consultant Description: Additional Information:		
Beam Therapeutics	Stock	Self
Additional Information:		
nChroma Bio	Consultant	Self
Category: Consultant Description: Additional Information:		
nChroma Bio	Stock	Self
Additional Information:		
Pairwise Plants	Consultant	Self
Category: Consultant Description: Additional Information:		
Pairwise Plants	Stock	Self
Additional Information:		
Prime Medicine	Consultant	Self
Category: Consultant Description: Additional Information:		
Prime Medicine	Stock	Self
Additional Information:		

Intellectual Property

Type	Is Licensed	Interest Held By												
Patent - Patents on base editing and prime editing	-	Self												
Description: Patents on base editing and prime editing Patent Status: Filing Jurisdiction: Licensees: Patent Number: Patent Holder: <table border="1"> <thead> <tr> <th>Licensee</th> <th>Title</th> <th>Date</th> </tr> </thead> <tbody> <tr> <td>Pairwise Plants</td> <td></td> <td></td> </tr> <tr> <td>Beam Therapeutics</td> <td></td> <td></td> </tr> <tr> <td>Prime Medicine</td> <td></td> <td></td> </tr> </tbody> </table> Additional Information:			Licensee	Title	Date	Pairwise Plants			Beam Therapeutics			Prime Medicine		
Licensee	Title	Date												
Pairwise Plants														
Beam Therapeutics														
Prime Medicine														

Additional Questions

- Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

- What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

- Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Cathleen Cathleen

Discloser Identifier: 1239804

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Sarah McCague

Discloser Identifier: 1239783

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser 402100
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Beam Therapeutics	Grant / Contract	Self
Recipient Name: University of Pennsylvania Grant / Contract Description: Sponsored Research Agreement for preclinical evaluation of potential gene editing therapies Additional Information: Recipient Type: Institution Grant / Contract Purpose: Research		
Capstan Therapeutics	Consultant	Self
Category: Consultant Description: Scientific advising Additional Information:		
LEXEO Therapeutics	Consultant	Self
Category: Consultant Description: Scientific advising Additional Information:		
National Institutes of Health	Grant / Contract	Self
Recipient Name: University of Pennsylvania Grant / Contract Description: Multiple grants to University of Pennsylvania with me as principal investigator or co-investigator Additional Information: Recipient Type: Institution Grant / Contract Purpose: Research		
Nava Therapeutics	Grant / Contract	Self
Recipient Name: University of Pennsylvania Grant / Contract Description: Sponsored Research Agreement for preclinical evaluation of potential gene editing therapies Additional Information: Recipient Type: Institution Grant / Contract Purpose: Research		
Perelman School of Medicine, University of Pennsylvania	Employment	Self
Title: Professor Additional Information: Position Description: Faculty member		
Variant Bio	Stock Option	Self
Additional Information:		
Verve Therapeutics	Consultant	Self
Category: Consultant Description: Scientific advisor		

Entity	Type	Interest Held By
Additional Information:		
Verve Therapeutics	Stock	Self
Additional Information:		

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - Compositions and methods for treatment of carbamo	-	Self
Description: Compositions and methods for treatment of carbamoyl phosphate synthetase 1 (CPS1) deficiency Patent Status: Provisional Filing Jurisdiction: USA Licensees: Additional Information: Patent Number: 63/716,518 Patent Holder: Current Institution		

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

Yes.

- a. **Please list the other authors' names here.**

Kiran Musunuru, Sarah A. Grandinette, Xiao Wang, Taylor R. Hudson, Kevin Briseno, Anne Marie Berry, Julia L. Hacker, Alvin Hsu, Rachel A. Silverstein, Logan T. Hille, Aysel N. Ogul, Nancy A. Robinson-Garvin, Juliana C. Small, Sarah McCague, Samantha M. Burke, Christina M. Wright, Sarah Bick, Venkata Indurthi, Shweta Sharma, Michael Jepperson, Christopher A. Vakulskas, Michael Collingwood, Katie Keogh, Ashley Jacobi, Morgan Sturgeon, Christian Brommel, Ellen Schmaljohn, Gavin Kurgan, Thomas Osborne, He Zhang, Kyle Kinney, Garrett Rettig, Christopher J. Barbosa, Sean C. Semple, Ying K. Tam, Cathleen Lutz, Lindsey A. George, Benjamin P. Kleinstiver, David R. Liu, Kim Ng, Sadik H. Kassim, Petros Giannikopoulos, Mohamad-Gabriel Alameh, Fyodor D. Urnov, Rebecca C. Ahrens-Nicklas

Certification

I certify that the information provided in this disclosure is complete and accurate.

Kim Choong Wen Ng

Discloser Identifier: 1239808

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239779

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239798

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Integrated DNA Technologies	Employment	Self

Title: Bioinformatics Scientist 2
Additional Information:

Position Description:

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239801

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Integrated DNA Technologies	Employment	Self

Title: Sr. Director Applied Science

Position Description: Directing a team of scientists in the genome writing and editing business unit to execute fee-for service, contract research for pre-clinical/clinical clients

Additional Information:

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Nancy Robinson-Garvin

Discloser Identifier: 1239780

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

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3. Are you the corresponding author?

No.

Certification

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Discloser 1239796
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Danaher Corporation	Employment	Self
Title: Bioinformatics Scientist Additional Information: Position Description:		
Danaher Corporation	Stock	Self
Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Sean Semple

Discloser Identifier: 1239803

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Acuitas Therapeutics, Inc.	Employment	Self
Title: Vice-President, Preclinical Research Additional Information: Position Description: Oversee preclinical research involving lipid nanoparticle delivery systems for nucleic acid therapeutics.		
Acuitas Therapeutics, Inc.	Stock	Self
Additional Information:		

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Shweta Sharma

Discloser Identifier: 1239788

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In-Vivo Gene Editing to Treat Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser

1239777

Identifier:

Disclosure

25-04747

Purpose:

Summary of Interests

Intellectual Property

Type	Is Licensed	Interest Held By
Patent - Generation of Custom CRISPR-Cas9 PAM Variant Enzy	-	Self

Description: Generation of Custom CRISPR-Cas9 PAM Variant Enzymes

Patent Status: Provisional

Filing Jurisdiction: USA

Licensees:

Additional Information:

Patent Number: PCT/IB2025/050835

Patent Holder: Current Institution

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Juliana Small

Discloser 1239781
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

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No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1239794

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Integrated DNA Technologies	Employment	Self

Title: CRISPR Applications Development Manager
Additional Information:

Position Description: Research scientist investigating new applications and techniques related to CRISPR gene editing

Additional Questions

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No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1080128

Disclosure Purpose: 25-04747

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Acuitas	Employment	Self
Title: Chief Scientific Officer Additional Information: Position Description: Oversight of Scientific Research Program		
Acuitas	Stock	Self
Additional Information:		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser 878658
Identifier:

Disclosure 25-04747
Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Cimeio Therapeutics	Consultant	Self
Category: Consultant Description: Paid consultant Additional Information: Flat consulting fee		
Cimeio Therapeutics	Stock Option	Self
Additional Information: Stock options		
Danaher Corporation	Grant / Contract	Self
Recipient Name: Fyodor Urnov Grant / Contract Description: Research support Additional Information: Research reagent support Recipient Type: Institution Grant / Contract Purpose: Research		
Ionis Pharmaceuticals	Consultant	Self
Category: Consultant Description: Consulting fee Additional Information: Flat yearly fee		
Tune Therapeutics	Consultant	Self
Category: Consultant Description: Paid consultant Additional Information: Flat consulting fee		
Tune Therapeutics	Stock	Self
Additional Information: Founder's shares		
Vertex Pharmaceuticals Incorporated	Consultant	Self
Category: Consultant Description: Consultant Additional Information: Flat fee		

Additional Questions

1. **Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?**

No.

2. **What is the manuscript title?**

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. **Are you the corresponding author?**

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

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Global Disclosure System



Discloser

1239790

Identifier:

Disclosure

25-04747

Purpose:

Summary of Interests

Company or Organization

Entity	Type	Interest Held By
Danaher Corporation	Stock	Self
Additional Information:		
Danaher Corporation	Stock Option	Self
Additional Information:		
Integrated DNA Technologies	Employment	Self
Title: Sr. Director of Enzyme Development Additional Information: Position Description: Leader of the Enzyme Development R&D team at IDT developing protein-based product in all business units.		

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Discloser Identifier: 1238614

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

1. Are there other relationships or activities that readers could perceive to have influenced, or that give the appearance of potentially influencing, what you wrote in the submitted work?

No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

Christina Wright

Discloser Identifier: 1239785

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

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No.

2. What is the manuscript title?

Patient-Specific In Vivo Gene Editing to Treat a Rare Genetic Disease

3. Are you the corresponding author?

No.

Certification

I certify that the information provided in this disclosure is complete and accurate.

He Zhang

Discloser Identifier: 1239799

Disclosure Purpose: 25-04747

Summary of Interests

I do not have any interests to disclose at this time.

Additional Questions

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No.

2. What is the manuscript title?

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3. Are you the corresponding author?

No.

Certification

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