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(54) Title: GENEMAP OF THE HUMAN GENES ASSOCIATED WITH CROHN'S DISEASE

(57) Abrégé/Abstract:
The present invention relates to the selection of a set of polymorphism markers for use in genome wide association studies based on linkage disequilibrium mapping. In particular, the invention relates to the fields of pharmacogenomics, diagnostics, patient therapy and the use of genetic haplotype information to predict an individual's susceptibility to Crohn's disease and/or their response to a particular drug or drugs.

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(54) Title: GENEMAP OF THE HUMAN GENES ASSOCIATED WITH CROHN'S DISEASE

(57) Abstract: The present invention relates to the selection of a set of polymorphism markers for use in genome wide association studies based on linkage disequilibrium mapping. In particular, the invention relates to the fields of pharmacogenomics, diagnostics, patient therapy and the use of genetic haplotype information to predict an individual's susceptibility to Crohn's disease and/or their response to a particular drug or drugs.

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JUMBO APPLICATIONS/PATENTS

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GENEMAP OF THE HUMAN GENES ASSOCIATED WITH CROHN'S DISEASE

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CROSS REFERENCE TO RELATED APPLICATIONS

This application is entitled to priority pursuant to 35 U.S.C. §119(e) to U.S. provisional patent application No. 60/710,726, which was filed on August 24, 2005, which is incorporated herein in its entirety.

FIELD OF THE INVENTION

The invention relates to the field of genomics and genetics, including genome analysis and the study of DNA variations. In particular, the invention relates to the fields of pharmacogenomics, diagnostics, patient therapy and the use of genetic haplotype information to predict an individual's susceptibility to Crohn's disease and/or their response to a particular drug or drugs, so that drugs tailored to genetic differences of population groups may be developed and/or administered to the appropriate population.

The invention also relates to a GeneMap for Crohn's disease, which links variations in DNA (including both genic and non-genic regions) to an individual's susceptibility to Crohn's disease and/or response to a particular drug or drugs. The invention further relates to the genes disclosed in the GeneMap (see Tables 8-10), which is related to methods and reagents for detection of an individual's increased or decreased risk for Crohn's disease by identifying at least one polymorphism in one or a combination of the genes from the GeneMap. Also related are the candidate regions identified in Table 1, which are associated with

Crohn's disease. In addition, the invention further relates to nucleotide sequences of those genes including genomic DNA sequences, cDNA sequences, single nucleotide polymorphisms (SNPs), other types of polymorphisms (insertions, deletions, microsatellites), alleles and haplotypes (see Sequence Listing and Tables 2-7).

The invention further relates to isolated nucleic acids comprising these nucleotide sequences and isolated polypeptides or peptides encoded thereby. Also related are expression vectors and host cells comprising the disclosed nucleic acids or fragments thereof, as well as antibodies that bind to the encoded polypeptides or peptides.

The present invention further relates to ligands that modulate the activity of the disclosed genes or gene products. In addition, the invention relates to diagnostics and therapeutics for Crohn's disease, utilizing the disclosed nucleic acids, polymorphisms, chromosomal regions, gene maps, polypeptides or peptides, antibodies and/or ligands and small molecules that activate or repress relevant signaling events.

BACKGROUND OF THE INVENTION

Crohn's disease is an Inflammatory Bowel Disease (IBD) in which inflammation extends beyond the inner gut lining and penetrates deeper layers of the intestinal wall of any part of the digestive system (esophagus, stomach, small intestine, large intestine, and/or anus). Crohn's disease is a chronic, lifelong disease which can cause painful, often life altering symptoms including diarrhea, cramping and rectal bleeding. Crohn's disease occurs most frequently in the industrialized world and the typical age of onset falls into two distinct ranges, 15 to 30 years of age and 60 to 80 years of age. The highest mortality is during the first years of disease, and in cases where the disease symptoms are long lasting, an increased risk of colon cancer is observed. Crohn's disease presently accounts for approximately two thirds of IBD-related physician visits and hospitalizations, and 50 to 80% of Crohn's disease patients eventually require surgical treatment.

Development of Crohn's disease is influenced by environmental and host specific factors, together with "exogenous biological factors" such as constituents of the intestinal flora (the naturally occurring bacteria found in the intestine). It is believed that in genetically predisposed individuals, exogenous factors such as infectious agents, and host-specific characteristics such as intestinal barrier function and/or blood supply, combine with specific environmental factors to cause a chronic state of improperly regulated immune system function. In this hypothetical model, microorganisms trigger an immune response in the intestine, and in susceptible individuals, this immune response is not turned off when the microorganism is cleared from the body. The chronically "turned on" immune response causes damage to the intestine resulting in the symptoms of Crohn's disease.

Current treatments for Crohn's disease are primarily aimed at reducing symptoms by suppressing inflammation and do not address the root cause of the disease. Despite a preponderance of evidence showing inheritance of a risk for Crohn's disease through epidemiological studies and genome wide linkage analyses, the genes affecting Crohn's disease have yet to be discovered (Hugot JP, and Thomas G., 1998). There is a need in the art for identifying specific genes related to Crohn's disease to enable the development of therapeutics that address the causes of the disease rather than relieving its symptoms. The failure in past studies to identify causative genes in complex diseases, such as Crohn's disease, has been due to the lack of appropriate methods to detect a sufficient number of variations in genomic DNA samples (markers), the insufficient quantity of necessary markers available, and the number of needed individuals to enable such a study. The present invention addresses these issues.

The DNA sequences between two human genomes are 99.9% identical. The variations in DNA sequence between individuals can be, as an example, deletions of small or large stretches of DNA, insertions of stretches of DNA, variations in the number of repetitive DNA elements, and changes in single base positions in the genome called "single nucleotide polymorphisms" (SNPs).

Human DNA sequence variation accounts for a large fraction of observed differences between individuals, including susceptibility to disease.

Many common diseases, like Crohn's disease, are complex genetic traits and are believed to involve several disease-genes rather than single genes, as is observed for rare diseases. This makes detection of any particular gene substantially more difficult than in a rare disease, where a single gene mutation that segregates according to a Mendelian inheritance pattern is the causative mutation. Any one of the multiple interacting gene mutations involved in the etiology of a complex disease will impart a lower relative risk for the disease than will the single gene mutation involved in a simple genetic disease. Low relative risk alleles are more difficult to detect and, as a result, the success of positional cloning using linkage mapping that was achieved for simple genetic disease genes has not been repeated for complex diseases.

Several approaches have been proposed to discover and characterize multiple genes in complex genetic traits. These gene discovery methods can be subdivided into hypothesis-free disorder association studies and hypothesis-driven candidate gene or region studies. The candidate gene approach relies on the analysis of a gene in patients who have a disorder in which the gene is thought to play a role. This approach is limited in utility because it only provides for the investigation of genes with known functions. Although variant sequences of candidate genes may be identified using this approach, it is inherently limited by the fact that variant sequences in other genes that contribute to the phenotype will be necessarily missed when the technique is employed. Genome-wide scans (GWS) have been shown to be efficient in identifying Crohn's disease susceptibility genes (NOD2/CARD15 and OCTN). In contrast to the candidate gene approach, a GWS searches throughout the genome without any a priori hypothesis and consequently can identify genes that are not obvious candidates for the disease as well as genes that are relevant candidates for the disease it can also identify chromosomal regions that are structurally important where mutations can influence gene function of specific genes.

Family-based linkage mapping methods were initially used for disorder locus identification. This technique locates genes based on the relatively limited number of genetic recombination events within the families used in the study, and results in large chromosomal regions containing hundreds of genes, any one of which could be the disorder-causing gene. Population-based, or linkage disequilibrium (LD) mapping is based on the premise that regions adjacent to a gene of interest are co-transmitted through the generations along with the gene. As a result, LD extends over shorter genetic regions than does linkage (Hewett *et al.*, 2002), and can facilitate detection of genes with lower relative risk than family linkage mapping approaches. LD-based mapping also defines much smaller candidate regions which may contain only a few genes, making the identification of the actual disorder gene much easier.

It has been estimated that a GWS that uses a general population and case/control association (LD) analysis would require approximately 700,000 SNP markers (Carlson *et al.*, 2003). The cost of a GWS at this marker density for a sufficient sample size for statistical power is economically prohibitive. The use of a special founder population (genetic isolate), such as the French Canadian population of Quebec, is one solution to the problem with LD analysis. The French Canadian population in Quebec (Quebec Founder Population - QFP) provides one of the best resources in the world for gene discovery based on its high levels of genetic sharing and genetic homogeneity. By combining DNA collected from the QFP, high throughput genotyping capabilities and proprietary algorithms for genetic analysis, a comprehensive genome-wide association study was facilitated. The present invention relates specifically to a set of Crohn's disease-causing genes (GeneMap) and targets which present attractive points of therapeutic intervention.

In view of the foregoing, identifying susceptibility genes associated with Crohn's disease and their respective biochemical pathways will facilitate the identification of diagnostic markers as well as novel targets for improved therapeutics. It will also improve the quality of life for those afflicted by this disease and will reduce the economic costs of these afflictions at the individual and societal level. The

identification of those genetic markers would provide the basis for novel genetic tests and eliminate or reduce the therapeutic methods currently used. The identification of those genetic markers will also provide the development of effective therapeutic intervention for the battery of laboratory, radiological, and endoscopic evaluations typically required to diagnose Crohn's disease. The present invention satisfies this need and provides related advantages as well.

DESCRIPTION OF THE FILES CONTAINED ON THE CD-R

The contents of the submission on compact discs submitted herewith are incorporated herein by reference in their entirety: A compact disc copy of the Sequence Listing (COPY 1) (filename: GENI 009 00WO SeqList.ST25.txt, date recorded: August 23, 2006, file size 25,715 kilobytes); a duplicate compact disc copy of the Sequence Listing (COPY 2) (filename: GENI 009 00WO SeqList.ST25.txt, date recorded: August 23, 2006, file size 25,715 kilobytes); a duplicate compact disc copy of the Sequence Listing (COPY 3) (filename: GENI 009 00WO SeqList.ST25.txt, date recorded: August 23, 2006, file size 25,715 kilobytes); a computer readable format copy of the Sequence Listing (CRF COPY) (filename: GENI 009 00WO SeqList.ST25.txt, date recorded: August 23, 2006, file size 25,715 kilobytes).

DEFINITIONS

Throughout the description of the present invention, several terms are used that are specific to the science of this field. For the sake of clarity and to avoid any misunderstanding, these definitions are provided to aid in the understanding of the specification and claims:

Allele: One of a pair, or series, of forms of a gene or non-genic region that occur at a given locus in a chromosome. Alleles are symbolized with the same basic symbol (*e.g.*, B for dominant and b for recessive; B1, B2, Bn for n additive alleles at a locus). In a normal diploid cell there are two alleles of any one gene (one

from each parent), which occupy the same relative position (locus) on homologous chromosomes. Within a population there may be more than two alleles of a gene. See multiple alleles. SNPs also have alleles, *i.e.*, the two (or more) nucleotides that characterize the SNP.

Amplification of nucleic acids: refers to methods such as polymerase chain reaction (PCR), ligation amplification (or ligase chain reaction, LCR) and amplification methods based on the use of Q-beta replicase. These methods are well known in the art and are described, for example, in U.S. Patent Nos. 4,683,195 and 4,683,202. Reagents and hardware for conducting PCR are commercially available. Primers useful for amplifying sequences from the disorder region are preferably complementary to, and preferably hybridize specifically to, sequences in the disorder region or in regions that flank a target region therein. Genes from Tables 8-10 generated by amplification may be sequenced directly. Alternatively, the amplified sequence(s) may be cloned prior to sequence analysis.

Antigenic component: is a moiety that binds to its specific antibody with sufficiently high affinity to form a detectable antigen-antibody complex.

Antibodies: refer to polyclonal and/or monoclonal antibodies and fragments thereof, and immunologic binding equivalents thereof, that can bind to proteins and fragments thereof or to nucleic acid sequences from the disorder region, particularly from the disorder gene products or a portion thereof. The term antibody is used both to refer to a homogeneous molecular entity, or a mixture such as a serum product made up of a plurality of different molecular entities. Proteins may be prepared synthetically in a protein synthesizer and coupled to a carrier molecule and injected over several months into rabbits. Rabbit sera are tested for immunoreactivity to the protein or fragment. Monoclonal antibodies may be made by injecting mice with the proteins, or fragments thereof. Monoclonal antibodies can be screened by ELISA and tested for specific immunoreactivity with protein or fragments thereof (Harlow *et al.* 1988, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring

Harbor, NY). These antibodies will be useful in developing assays as well as therapeutics.

Associated allele: refers to an allele at a polymorphic locus that is associated with a particular phenotype of interest, *e.g.*, a predisposition to a disorder or a particular drug response.

cDNA: refers to complementary or copy DNA produced from an RNA template by the action of RNA-dependent DNA polymerase (reverse transcriptase). Thus, a cDNA clone means a duplex DNA sequence complementary to an RNA molecule of interest, included in a cloning vector or PCR amplified. This term includes genes from which the intervening sequences have been removed.

cDNA library: refers to a collection of recombinant DNA molecules containing cDNA inserts that together comprise essentially all of the expressed genes of an organism or tissue. A cDNA library can be prepared by methods known to one skilled in the art (see, *e.g.*, Cowell and Austin, 1997, "DNA Library Protocols," Methods in Molecular Biology). Generally, RNA is first isolated from the cells of the desired organism, and the RNA is used to prepare cDNA molecules.

Cloning: refers to the use of recombinant DNA techniques to insert a particular gene or other DNA sequence into a vector molecule. In order to successfully clone a desired gene, it is necessary to use methods for generating DNA fragments, for joining the fragments to vector molecules, for introducing the composite DNA molecule into a host cell in which it can replicate, and for selecting the clone having the target gene from amongst the recipient host cells.

Cloning vector: refers to a plasmid or phage DNA or other DNA molecule that is able to replicate in a host cell. The cloning vector is typically characterized by one or more endonuclease recognition sites at which such DNA sequences may be cleaved in a determinable fashion without loss of an essential biological function of the DNA, and which may contain a selectable marker suitable for use in the identification of cells containing the vector.

Coding sequence or a protein-coding sequence: is a polynucleotide sequence capable of being transcribed into mRNA and/or capable of being translated into a polypeptide or peptide. The boundaries of the coding sequence are typically determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus.

Complement of a nucleic acid sequence: refers to the antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

Disorder region: refers to the portions of the human chromosomes displayed in Table 1 bounded by the markers from Tables 2-10.

Disorder-associated nucleic acid or polypeptide sequence: refers to a nucleic acid sequence that maps to region of Table 1 or the polypeptides encoded therein (Tables 8-10, nucleic acids, and polypeptides). For nucleic acids, this encompasses sequences that are identical or complementary to the gene sequences from Tables 8-10, as well as sequence-conservative, function-conservative, and non-conservative variants thereof. For polypeptides, this encompasses sequences that are identical to the polypeptide, as well as function-conservative and non-conservative variants thereof. Included are the alleles of naturally-occurring polymorphisms causative of Crohn's disease such as, but not limited to, alleles that cause altered expression of genes of Tables 8-10 and alleles that cause altered protein levels or stability (*e.g.*, decreased levels, increased levels, expression in an inappropriate tissue type, increased stability, and decreased stability).

Expression vector: refers to a vehicle or plasmid that is capable of expressing a gene that has been cloned into it, after transformation or integration in a host cell. The cloned gene is usually placed under the control of (*i.e.*, operably linked to) a regulatory sequence.

Function-conservative variants: are those in which a change in one or more nucleotides in a given codon position results in a polypeptide sequence in which a given amino acid residue in the polypeptide has been replaced by a conservative amino acid substitution. Function-conservative variants also include

analogs of a given polypeptide and any polypeptides that have the ability to elicit antibodies specific to a designated polypeptide.

Founder population: Also called a population isolate, this is a large number of people who have mostly descended, in genetic isolation from other populations, from a much smaller number of people who lived many generations ago.

Gene: Refers to a DNA sequence that encodes through its template or messenger RNA a sequence of amino acids characteristic of a specific peptide, polypeptide, or protein. The term “gene” also refers to a DNA sequence that encodes an RNA product. The term gene as used herein with reference to genomic DNA includes intervening, non-coding regions, as well as regulatory regions, and can include 5' and 3' ends. A gene sequence is wild-type if such sequence is usually found in individuals unaffected by the disorder or condition of interest. However, environmental factors and other genes can also play an important role in the ultimate determination of the disorder. In the context of complex disorders involving multiple genes (oligogenic disorder), the wild type, or normal sequence can also be associated with a measurable risk or susceptibility, receiving its reference status based on its frequency in the general population.

GeneMaps: are defined as groups of gene(s) that are directly or indirectly involved in at least one phenotype of a disorder (some non-limiting example of GeneMaps comprises varius combinations of genes from tables 8-10). As such, GeneMaps enable the development of synergistic diagnostic products, creating "theranostics".

Genotype: Set of alleles at a specified locus or loci.

Haplotype: The allelic pattern of a group of (usually contiguous) DNA markers or other polymorphic loci along an individual chromosome or double helical DNA segment. Haplotypes identify individual chromosomes or chromosome segments. The presence of shared haplotype patterns among a group of individuals implies that the locus defined by the haplotype has been inherited, identical by descent (IBD), from a common ancestor. Detection of identical by descent haplotypes is the basis of linkage disequilibrium (LD) mapping. Haplotypes are broken down

through the generations by recombination and mutation. In some instances, a specific allele or haplotype may be associated with susceptibility to a disorder or condition of interest, *e.g.*, Crohn's disease. In other instances, an allele or haplotype may be associated with a decrease in susceptibility to a disorder or condition of interest, *i.e.*, a protective sequence.

Host: includes prokaryotes and eukaryotes. The term includes an organism or cell that is the recipient of an expression vector (*e.g.*, autonomously replicating or integrating vector).

Hybridizable: nucleic acids are hybridizable to each other when at least one strand of the nucleic acid can anneal to another nucleic acid strand under defined stringency conditions. In some embodiments, hybridization requires that the two nucleic acids contain at least 10 substantially complementary nucleotides; depending on the stringency of hybridization, however, mismatches may be tolerated. The appropriate stringency for hybridizing nucleic acids depends on the length of the nucleic acids and the degree of complementarity, and can be determined in accordance with the methods described herein.

Identity by descent (IBD): Identity among DNA sequences for different individuals that is due to the fact that they have all been inherited from a common ancestor. LD mapping identifies IBD haplotypes as the likely location of disorder genes shared by a group of patients.

Identity: as known in the art, is a relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity and similarity can be readily calculated by known methods, including but not limited to those described in A.M. Lesk (ed), 1988, Computational Molecular Biology, Oxford University Press, NY; D.W. Smith (ed), 1993, Biocomputing. Informatics and Genome Projects, Academic Press, NY; A.M. Griffin and H.G. Griffin, H. G (eds), 1994, ComputerAnalysis of Sequence Data, Part 1, Humana Press, NJ; G.

von Heinje, 1987, Sequence Analysis in Molecular Biology, Academic Press; and M. Gribskov and J. Devereux (eds), 1991, Sequence Analysis Primer, M Stockton Press, NY; H. Carillo and D. Lipman, 1988, SIAM J. Applied Math., 48:1073.

Immunogenic component: is a moiety that is capable of eliciting a humoral and/or cellular immune response in a host animal.

Isolated nucleic acids: are nucleic acids separated away from other components (*e.g.*, DNA, RNA, and protein) with which they are associated (*e.g.*, as obtained from cells, chemical synthesis systems, or phage or nucleic acid libraries). Isolated nucleic acids are at least 60% free, preferably 75% free, and most preferably 90% free from other associated components. In accordance with the present invention, isolated nucleic acids can be obtained by methods described herein, or other established methods, including isolation from natural sources (*e.g.*, cells, tissues, or organs), chemical synthesis, recombinant methods, combinations of recombinant and chemical methods, and library screening methods.

Isolated polypeptides or peptides: are those that are separated from other components (*e.g.*, DNA, RNA, and other polypeptides or peptides) with which they are associated (*e.g.*, as obtained from cells, translation systems, or chemical synthesis systems). In a preferred embodiment, isolated polypeptides or peptides are at least 10% pure; more preferably, 80% or 90% pure. Isolated polypeptides and peptides include those obtained by methods described herein, or other established methods, including isolation from natural sources (*e.g.*, cells, tissues, or organs), chemical synthesis, recombinant methods, or combinations of recombinant and chemical methods. Proteins or polypeptides referred to herein as recombinant are proteins or polypeptides produced by the expression of recombinant nucleic acids. A portion as used herein with regard to a protein or polypeptide, refers to fragments of that protein or polypeptide. The fragments can range in size from 5 amino acid residues to all but one residue of the entire protein sequence. Thus, a portion or fragment can be at least 5, 5-50, 50-100, l00-200, 200-400, 400-800, or more consecutive amino acid residues of a protein or polypeptide.

Linkage disequilibrium (LD): the situation in which the alleles for two or more loci do not occur together in individuals sampled from a population at frequencies predicted by the product of their individual allele frequencies. In other words, markers that are in LD do not follow Mendel's second law of independent random segregation. LD can be caused by any of several demographic or population artifacts as well as by the presence of genetic linkage between markers. However, when these artifacts are controlled and eliminated as sources of LD, then LD results directly from the fact that the loci involved are located close to each other on the same chromosome so that specific combinations of alleles for different markers (haplotypes) are inherited together. Markers that are in high LD can be assumed to be located near each other and a marker or haplotype that is in high LD with a genetic trait can be assumed to be located near the gene that affects that trait. The physical proximity of markers can be measured in family studies where it is called linkage or in population studies where it is called linkage disequilibrium.

LD mapping: population based gene mapping, which locates disorder genes by identifying regions of the genome where haplotypes or marker variation patterns are shared statistically more frequently among disorder patients compared to healthy controls. This method is based upon the assumption that many of the patients will have inherited an allele associated with the disorder from a common ancestor (IBD), and that this allele will be in LD with the disorder gene.

Locus: a specific position along a chromosome or DNA sequence. Depending upon context, a locus could be a gene, a marker, a chromosomal band or a specific sequence of one or more nucleotides.

Minor allele frequency (MAF): the population frequency of one of the alleles for a given polymorphism, which is equal or less than 50%. The sum of the MAF and the Major allele frequency equals one.

Markers: an identifiable DNA sequence that is variable (polymorphic) for different individuals within a population. These sequences facilitate the study of inheritance of a trait or a gene. Such markers are used in mapping the order of

genes along chromosomes and in following the inheritance of particular genes; genes closely linked to the marker or in LD with the marker will generally be inherited with it. Two types of markers are commonly used in genetic analysis, microsatellites and SNPs.

Microsatellite: DNA of eukaryotic cells comprising a repetitive, short sequence of DNA that is present as tandem repeats and in highly variable copy number, flanked by sequences unique to that locus.

Mutant sequence: if it differs from one or more wild-type sequences. For example, a nucleic acid from a gene listed in Tables 8-10 containing a particular allele of a single nucleotide polymorphism may be a mutant sequence. In some cases, the individual carrying this allele has increased susceptibility toward the disorder or condition of interest. In other cases, the mutant sequence might also refer to an allele that decreases the susceptibility toward a disorder or condition of interest and thus acts in a protective manner. The term mutation may also be used to describe a specific allele of a polymorphic locus.

Non-conservative variants: are those in which a change in one or more nucleotides in a given codon position results in a polypeptide sequence in which a given amino acid residue in a polypeptide has been replaced by a non-conservative amino acid substitution. Non-conservative variants also include polypeptides comprising non-conservative amino acid substitutions.

Nucleic acid or polynucleotide: purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotide or mixed polyribo polydeoxyribonucleotides. This includes single-and double-stranded molecules, *i.e.*, DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as protein nucleic acids (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

Nucleotide: a nucleotide, the unit of a DNA molecule, is composed of a base, a 2'-deoxyribose and phosphate ester(s) attached at the 5' carbon of the deoxyribose. For its incorporation in DNA, the nucleotide needs to possess three phosphate esters but it is converted into a monoester in the process.

Operably linked: means that the promoter controls the initiation of expression of the gene. A promoter is operably linked to a sequence of proximal DNA if upon introduction into a host cell the promoter determines the transcription of the proximal DNA sequence(s) into one or more species of RNA. A promoter is operably linked to a DNA sequence if the promoter is capable of initiating transcription of that DNA sequence.

Ortholog: denotes a gene or polypeptide obtained from one species that has homology to an analogous gene or polypeptide from a different species.

Paralog: denotes a gene or polypeptide obtained from a given species that has homology to a distinct gene or polypeptide from that same species.

Phenotype: any visible, detectable or otherwise measurable property of an organism such as symptoms of, or susceptibility to, a disorder.

Polymorphism: occurrence of two or more alternative genomic sequences or alleles between or among different genomes or individuals at a single locus. A polymorphic site thus refers specifically to the locus at which the variation occurs. In some cases, an individual carrying a particular allele of a polymorphism has an increased or decreased susceptibility toward a disorder or condition of interest.

Portion and fragment: are synonymous. A portion as used with regard to a nucleic acid or polynucleotide refers to fragments of that nucleic acid or polynucleotide. The fragments can range in size from 8 nucleotides to all but one nucleotide of the entire gene sequence. Preferably, the fragments are at least about 8 to about 10 nucleotides in length; at least about 12 nucleotides in length; at least about 15 to about 20 nucleotides in length; at least about 25 nucleotides in length; or at least about 35 to about 55 nucleotides in length.

Probe or primer: refers to a nucleic acid or oligonucleotide that forms a hybrid structure with a sequence in a target region of a nucleic acid due to complementarity of the probe or primer sequence to at least one portion of the target region sequence.

Protein and polypeptide: are synonymous. Peptides are defined as fragments or portions of polypeptides, preferably fragments or portions having at least one functional activity (*e.g.*, proteolysis, adhesion, fusion, antigenic, or intracellular activity) as the complete polypeptide sequence.

Recombinant nucleic acids: nucleic acids which have been produced by recombinant DNA methodology, including those nucleic acids that are generated by procedures which rely upon a method of artificial replication, such as the polymerase chain reaction (PCR) and/or cloning into a vector using restriction enzymes. Portions of recombinant nucleic acids which code for polypeptides can be identified and isolated by, for example, the method of M. Jasin *et al.*, U.S. Patent No. 4,952,501.

Regulatory sequence: refers to a nucleic acid sequence that controls or regulates expression of structural genes when operably linked to those genes. These include, for example, the lac systems, the trp system, major operator and promoter regions of the phage lambda, the control region of fd coat protein and other sequences known to control the expression of genes in prokaryotic or eukaryotic cells. Regulatory sequences will vary depending on whether the vector is designed to express the operably linked gene in a prokaryotic or eukaryotic host, and may contain transcriptional elements such as enhancer elements, termination sequences, tissue-specificity elements and/or translational initiation and termination sites.

Sample: as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual or animal (including, without limitation, plasma, serum, cerebrospinal fluid, lymph, tears, nails, hair, saliva, milk, pus, and tissue exudates and secretions) or from *in vitro* cell culture-constituents, as well as samples obtained from, for example, a laboratory procedure.

Single nucleotide polymorphism (SNP): variation of a single nucleotide. This includes the replacement of one nucleotide by another and deletion or insertion of a single nucleotide. Typically, SNPs are biallelic markers although tri- and tetra-allelic markers also exist. For example, SNP A\C may comprise allele C or allele

A (Tables 2-7). Thus, a nucleic acid molecule comprising SNP A\C may include a C or A at the polymorphic position. For clarity purposes, an ambiguity code is used in Tables 2-7 and the sequence listing, to represent the variations. For a combination of SNPs, the term "haplotype" is used, *e.g.* the genotype of the SNPs in a single DNA strand that are linked to one another. In certain embodiments, the term “haplotype” is used to describe a combination of SNP alleles, *e.g.*, the alleles of the SNPs found together on a single DNA molecule. In specific embodiments, the SNPs in a haplotype are in linkage disequilibrium with one another.

Sequence-conservative: variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position (*i.e.*, silent mutation).

Substantially homologous: a nucleic acid or fragment thereof is substantially homologous to another if, when optimally aligned (with appropriate nucleotide insertions and/or deletions) with the other nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least 60% of the nucleotide bases, usually at least 70%, more usually at least 80%, preferably at least 90%, and more preferably at least 95-98% of the nucleotide bases. Alternatively, substantial homology exists when a nucleic acid or fragment thereof will hybridize, under selective hybridization conditions, to another nucleic acid (or a complementary strand thereof). Selectivity of hybridization exists when hybridization which is substantially more selective than total lack of specificity occurs. Typically, selective hybridization will occur when there is at least about 55% sequence identity over a stretch of at least about nine or more nucleotides, preferably at least about 65%, more preferably at least about 75%, and most preferably at least about 90% (M. Kanehisa, 1984, NucL Acids Res. 11:203-213). The length of homology comparison, as described, may be over longer stretches, and in certain embodiments will often be over a stretch of at least 14 nucleotides, usually at least 20 nucleotides, more usually at least 24 nucleotides, typically at least 28 nucleotides, more typically at least 32 nucleotides, and preferably at least 36 or more nucleotides.

Wild-type gene from Tables 2-7: refers to the reference sequence. The wild-type gene sequences from Tables 8-10 used to identify the variants (polymorphisms, alleles, and haplotypes) described in detail herein.

Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains, unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. Standard reference works setting forth the general principles of recombinant DNA technology include J. Sambrook *et al.*, 1989, Molecular Cloning: A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; P.B. Kaufman *et al.*, (eds), 1995, Handbook of Molecular and Cellular Methods in Biology and Medicine, CRC Press, Boca Raton; M.J. McPherson (ed), 1991, Directed Mutagenesis: A Practical Approach, IRL Press, Oxford; J. Jones, 1992, Amino Acid and Peptide Synthesis, Oxford Science Publications, Oxford; B.M. Austen and O.M.R. Westwood, 1991, Protein Targeting and Secretion, IRL Press, Oxford; D.N Glover (ed), 1985, DNA Cloning, Volumes I and 11; M.J. Gait (ed), 1984, Oligonucleotide Synthesis; B.D. Hames and S.J. Higgins (eds), 1984, Nucleic Acid Hybridization; Quirke and Taylor (eds), 1991, PCR-A Practical Approach; Harries and Higgins (eds), 1984, Transcription and Translation; R.I. Freshney (ed), 1986, Animal Cell Culture; Immobilized Cells and Enzymes, 1986, IRL Press; Perbal, 1984, A Practical Guide to Molecular Cloning, J. H. Miller and M. P. Calos (eds), 1987, Gene Transfer Vectors for Mammalian Cells, Cold Spring Harbor Laboratory Press; M.J. Bishop (ed), 1998, Guide to Human Genome Computing, 2d Ed., Academic Press, San Diego, CA; L.F. Peruski and A.H. Peruski, 1997, The Internet and the New Biology. Tools for Genomic and Molecular Research, American Society for Microbiology, Washington, D.C. Standard reference works setting forth the general principles of immunology include S. Sell, 1996, Immunology, Immunopathology & Immunity, 5th Ed., Appleton & Lange, Publ., Stamford, CT; D. Male *et al.*, 1996, Advanced Immunology, 3d Ed., Times Mirror Int'l Publishers Ltd., Publ., London; D.P. Stites

and A.L Terr, 1991, Basic and Clinical Immunology, 7th Ed., Appleton & Lange, Publ., Norwalk, CT; and A.K. Abbas *et al.*, 1991, Cellular and Molecular Immunology, W. B. Saunders Co., Publ., Philadelphia, PA. Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention; however, preferred materials and/or methods are described. Materials, reagents, and the like to which reference is made in the following description and examples are generally obtainable from commercial sources, and specific vendors are cited herein.

DETAILED DESCRIPTION OF THE INVENTION

General Description of Crohn's Disease

Inflammatory Bowel Disease (IBD) is characterized by excessive and chronic inflammation at various sites in the gastro-intestinal tract. IBD describes two clinical conditions called Crohn's disease (CD) and ulcerative colitis (UC). CD and UC share many clinical and pathological characteristics but they also have some markedly different features. There is strong scientific support suggesting that the main pathological processes in these two diseases are distinct. This patent application will focus primarily on Crohn's disease.

The United Kingdom, northern Europe, and North America have been reported to have the highest incidence rates and prevalence for CD. In North America, prevalence for CD ranges between 0.03% and 0.2%. However, reports of increasing incidence and prevalence from other areas of the world have been published over the past 30 years (reviewed in Loftus 2004). CD may occur in people of all ages, but it is most commonly diagnosed in late adolescence and early adulthood (reviewed in Andres and Friedman 1999). Any part of the gastrointestinal tract can be affected in CD, from the mouth to the anus, and patches of inflammation occur, interspersed with healthy tissue.

Most CD patients experience characteristic periods of remission and flare-ups of the disease, often-requiring long-term medication, and/or hospitalization and

surgery. The symptoms and complications of Crohn's disease differ, depending on what part of the intestinal tract is inflamed. The severity of the disease does not correlate directly with the extent of bowel involvement. It is the disease pattern that is most important in determining the disease course and the nature of the associated complications. Thus, CD can be subdivided into 3 types: predominantly inflammatory CD, non-perforating CD (presence of strictures), or perforating CD (presence of fistulas and/or abscesses) (reviewed in Andres and Friedman 1999).

CD symptoms include chronic diarrhea, abdominal pain, cramping, anorexia, and weight loss. Systemic features include fatigue, tachycardia and pyrexia. Chronic or acute blood loss in the bowel may result in anemia and even shock. The most common complication of CD is the presence of strictures (obstruction) of the intestine due to swelling and the formation of scar tissue. Another complication involves sores or ulcers within the intestinal tract. Sometimes these deep ulcers turn into tracts called fistulas that connect different parts of the intestine. These fistulas often become infected and occasionally form an abscess. Extra-intestinal inflammatory manifestations can occur in joints, eyes, skin, mouth, and liver in patients with either forms of IBD (reviewed in Andres and Friedman 1999). CD patients also carry several risk factors for the development of osteoporosis such as calcium and vitamin D deficiency, and corticosteroid use (Tremaine 2003). Patients with CD are also at increased risk of cancer of both the small and the large intestine (reviewed in Andres and Friedman 1999). CD is associated with an increased mortality rate relative to the general population and independent of whether the small intestine, large intestine, or both are affected. The excess of mortality is most notable in the first few years after diagnosis and is most often attributable to complications of CD, including colorectal cancer as well as other gastrointestinal complications (reviewed in Andres and Friedman 1999). CD is a lifelong disease that causes symptoms that may interfere with social activities, interpersonal relationships, and employment. Impairment relates to disease severity, pattern and side-effects of medication, the possibility of surgery, but also to age, other demographic factors and co-morbid medical conditions, including depression and anxiety (Irvine 2004).

There is no single definitive test for the diagnosis of CD. To determine the diagnosis, physicians evaluate a combination of information from the history and physical examination of a patient and from results of endoscopic, radiologic and histologic (blood and tissue) tests. Endoscopy with biopsy is the cornerstone for diagnosing and evaluating disease activity in CD. Radiology tests are used together with endoscopy to help evaluate the small bowel and look at the entire abdomen for infections, strictures, obstructions, and fistulas. Because CD often mimics other conditions and symptoms may vary widely, it may take some time to confirm the diagnosis.

Because there is no cure for CD, the goal of medical treatment is to suppress the inflammatory response and alleviate the symptoms by decreasing the frequency of disease flare-ups and maintaining remissions. Non-surgical treatment for active disease involves the use of anti-inflammatory (aminosalicylates and corticosteroids), antimicrobial (antibiotics), and immunomodulatory agents to control symptoms and reduce disease activity. The biologic therapies are targeted towards specific disease mechanisms and have the potential to provide more effective and safe treatments for human diseases. Infliximab (Remicade®) is a chimeric monoclonal antibody against TNFalpha, and the first biologic therapy that was approved for CD. Several novel genetically engineered drugs targeting specific sites in the inflammatory cascade are likely to have an impact in the near future. Among them, anti-inflammatory cytokines (recombinant IL-10 and IL-11), antibodies (humanized IgG4, anti-TNFalpha, anti-alpha4-integrin) and antisense therapies (ICAM-1) are currently being evaluated in CD treatment (Sandborn and Faubion 2004).

The frequency of indications for surgery parallels the frequency of local intestinal complications of the disease. Surgery is never curative for CD because the disease frequently recurs at or near the site of surgery; its overall goal is to conserve bowel and return the individual to the best possible quality of life. Up to 74% of all patients eventually require surgical intervention for their disease (Farmer 1985), and nearly 30% of patients require surgery within the first year of diagnosis (Podolsky 1991).

Although the etiology of CD is poorly understood, studies indicate that CD pathogenesis is the result of the complex interaction between environmental factors (i.e. gut micro-flora), genetic susceptibility, and the immune system. It has been proposed that IBD results from a dys-regulated mucosal immune response to the intestinal micro-flora in genetically susceptible individuals. The inappropriate activation of the mucosal immune system observed in CD has been linked to a loss of tolerance to gut commensals. It also appears that the loss of mucosal integrity leading to translocation of bacteria in the bowel wall is a crucial step for the propagation of the inflammatory process. However, it is not known whether barrier function is first compromised by intrinsic defects in epithelial integrity, by infection with enteric pathogens, or by loss of commensal-dependent signals necessary to maintain the physical integrity of the epithelium and hypo-responsiveness of the mucosal immune system (reviewed in Bouma and Strober 2003).

Familial aggregation, twin studies and consistent ethnic differences in disease frequency have strongly supported the important role of genetic factors in the cause of CD (reviewed in Andres and Friedman 1999). However, the incomplete concordance for CD within monozygotic twins, the phenotypic variations and the observed familial pattern of non-Mendelian inheritance suggest that CD has a complex genetic basis with many contributing genes. These facts also underline the presence and importance of environmental factors in the pathogenesis of this disease, such as gut micro-flora as mentioned above, and cigarette smoking which is the best known environmental factor for CD (reviewed in Andres and Friedman 1999). In addition, disease heterogeneity in the phenotype (location, age of onset, number and types of surgery, behavior, extra-intestinal manifestations, response to class of medications) can reflect extensive genetic heterogeneity.

Previously identified genes and loci

Genetic studies have previously indicated the presence of several loci predisposing to Inflammatory Bowel Diseases. Nine IBD loci have been identified:

IBD1 (CARD15/ NOD2, Caspase recruitment domain family, member 15 (NOD2 protein)), IBD2 (Inflammatory bowel disease-2), IBD3 (Inflammatory bowel disease-3), IBD4 (Inflammatory bowel disease-4), IBD5 (Inflammatory bowel disease-5), IBD6 (Inflammatory bowel disease-6), IBD7 (Inflammatory bowel disease-7), IBD8 (Inflammatory bowel disease-8), and IBD9 (Inflammatory bowel disease 9).

Several loci have been identified and replicated to date; they are located on chromosomes 16q12, 12q13.2-q24.1, 6p21, 14q11-q12, 5q31-q33, 19p13, 1p36, 16p, and 3p26 respectively (Wild and Rioux 2004; Duerr *et al.*, 2002). Results from linkage studies have suggested that CD and UC share some loci but do not share others, such as locus 16q12 which is unique to CD (The IBD International Genetics Consortium 2001). Most of the genes determining susceptibility in each of these chromosomal regions remain to be identified. The most widely replicated loci are on chromosomes 16 (caused by mutations in the NOD2/CARD15 gene), 12, 6, 14 and 5 (OCTN2 genes at IBD5 locus), which predispose to early-onset Crohn's disease. Thus, there is a continuing need in the medical arts for genetic markers of Crohn's disease and guidance for the use of such markers.

Several years ago, two different groups reported the association of CARD15 (NOD2) variants with CD (Hugot 2001; Ogura 2001). CARD15 is located at the IBD1 locus. The gene codes for an intracellular receptor involved in the innate immune detection of bacterial products. This detection induces the activation of the NF-kB pathway which is of particular importance in immune and inflammatory responses (Philpott and Viala 2004). Three major mutations represent 82% of the total CARD15 mutations: R702W, G908R, and 1007fsinsC. However they do not explain over 20% of the genetic predisposition to the disease, and altogether, they are carried by 30-50% of CD patients and 15-20% of healthy controls in Caucasian populations. These values are much lower in Japanese or Africans (reviewed in Girardin 2003).

Recently, the OCTN1 and OCTN2 genes at IBD5 locus have been associated with CD (Peltekova 2004). Variants in these genes are in strong linkage disequilibrium and create a two-allele risk haplotype enriched in patients with CD.

Both proteins are trans-membrane sodium-dependent carnitine transporters and sodium-independent organic cation transporters. The variants may cause disease by impairing OCTN activity or expression, reducing carnitine transport in a cell-type and disease-specific manner (Peltekova 2004). The IBD5 locus contains multiple candidate genes including the genes for organic cation transporters (OCTN2/SLC22A4 and SLC22A5), the gene for a LIN4-domain-containing protein (RILIPDLIM3), the gene for the oc2 subunit of proline hydroxylase (P4HA2) and a gene of unknown function (NCBI UniGene identifier Hs.70932). Because of extensive linkage disequilibrium (LD) in this region, it has not been possible to further refine the SNP map and unambiguously identify a single susceptibility gene. With respect to OCTN2, the basal transcription is downregulated by the C allele of G-207C, and this allele disrupts the ability of SLC22A5 to be upregulated in response to heat shock or arachidonic acid as a result of impaired HSF I binding and subsequent transcriptional activation.

The mechanism by which these organic cation transporters contribute to the pathology of Crohn's disease may relate to the in vivo metabolic importance of carnitine. Carnitine facilitates transport of long chain fatty acids across the mitochondrial inner membrane for subsequent P-oxidation, and is also important in the maintenance of cellular CoenzymeA levels. Carnitine uptake into lymphocytes, along with a corresponding decrease in plasma levels, is a physiological response to inflammation. Symptoms of the related condition Ulcerative Colitis may be due to an energy deficiency in colonic epithelium secondary to poor mitochondrial function due to decreased long-chain fatty acid transport to the mitochondria (Roediger WE 1980). The haplotype of mutations in Crohn's disease patients provided previously might affect cellular metabolic energy levels in inflamed tissue by combining impaired OCTN1 transporter function with downregulation and inability to respond to heat or inflammatory stress by the OCTN2 gene. Heat shock proteins and arachidonic acids are involved in response to a variety of cellular stresses, including sepsis, metabolic stress and ischaemia. The heat shock response modulates inflammation through modulation of NF-kB activation. OCTN2 is a heat stress inducible protein. Thus, the OCTN2 gene is normally upregulated in response to inflammation through

binding of HSF I protein to its promoter. This in turn mobilizes carnitine and bolsters metabolism in the inflamed tissue. Impaired OCTN1 carnitine transporter activity and lowered OCTN2 expression level results in reduced metabolism and either triggers or worsens cellular stress in areas of inflammation. The two OCTN transporters may therefore function in the inflammatory pathology of Crohn's disease. Additionally, OCTN1 is a polyspecific cation transporter, and might have a role in the uptake of drugs used to treat CD from the gut. As described above, OCTN2 is a transporter protein with the ability to transport carnitine in a sodium dependent manner. Missense mutations and nonsense mutations in the organic cation transporter OCTN2 had previously been identified in patients with primary Systemic Carnitine Deficiency (SCD), an autosomal recessive disorder characterized by progressive cardiomyopathy, skeletal myopathy, hypoglycemia and hyperammonemia.

Genes encoding proteins involved in the immune system, epithelial functions, and host response to micro-organisms represent good potential candidates for CD and have been examined in numerous case-control studies. However, many of the published associations of genetic variants with CD have not been replicated in follow-up studies.

The genetic variants that have been identified so far in CD explain only a fraction of the genetic predisposition to this disorder. It is clear that multiple components contribute to disease risk, each component having a modest effect on disease susceptibility. Thus the development of GeneMaps for CD may lead to a better understanding of pathogenesis and to the identification of new pathways involved in the disease, ultimately leading to better treatments for the patients. GeneMaps may also lead to molecular diagnostic tools that will identify subjects at risk for CD or for serious complications of the disease.

Genome wide association study to construct a GeneMap for Crohn's disease

The present invention is based on the discovery of genes associated with Crohn's disease. In the preferred embodiment, disease-associated loci

(candidate regions; Table 1) are identified by the statistically significant differences in allele or haplotype frequencies between the cases and the controls. For the purpose of the present invention, 208 candidate regions (Table 1) are identified.

The invention provides a method for the discovery of genes associated with Crohn's disease and the construction of a GeneMap for Crohn's disease in a human population, comprising the following steps (see Example section herein):

Step 1: Recruit patients (cases) and controls

In the preferred embodiment, 500 patients diagnosed for Crohn's disease along with two family members are recruited from the Quebec Founder Population (QFP). The preferred trios recruited are parent-parent-child (PPC) trios. Trios can also be recruited as parent-child-child (PCC) trios. In another preferred embodiment, more or less than 500 trios are recruited. In another embodiment, independent case and control samples are recruited.

In another embodiment, the present invention is performed as a whole or partially with DNA samples from individuals of another founder population than the Quebec population or from the general population.

Step 2: DNA extraction and quantitation

Any sample comprising cells or nucleic acids from patients or controls may be used. Preferred samples are those easily obtained from the patient or control. Such samples include, but are not limited to blood, peripheral lymphocytes, buccal swabs, epithelial cell swabs, nails, hair, bronchoalveolar lavage fluid, sputum, or other body fluid or tissue obtained from an individual.

In one embodiment, DNA is extracted from such samples in the quantity and quality necessary to perform the invention using conventional DNA extraction and quantitation techniques. The present invention is not linked to any DNA extraction or quantitation platform in particular.

Step 3: Genotype the recruited individuals

In one embodiment, assay-specific and/or locus-specific and/or allele-specific oligonucleotides for every SNP marker of the present invention (Tables 2-7) are organized onto one or more arrays. The genotype at each SNP locus is revealed by hybridizing short PCR fragments comprising each SNP locus onto these arrays. The arrays permit a high-throughput genome wide association study using DNA samples from individuals of the Quebec founder population. Such assay-specific and/or locus-specific and/or allele-specific oligonucleotides necessary for scoring each SNP of the present invention are preferably organized onto a solid support. Such supports can be arrayed on wafers, glass slides, beads or any other type of solid support.

In another embodiment, the assay-specific and/or locus-specific and/or allele-specific oligonucleotides are not organized onto a solid support but are still used as a whole, in panels or one by one. The present invention is therefore not linked to any genotyping platform in particular.

In another embodiment, one or more portions of the SNP maps (publicly available maps, proprietary maps from Perlegen Sciences, Inc. (Mountain View, CA, USA), and our own proprietary QLDM map) are used to screen the whole genome, a subset of chromosomes, a chromosome, a subset of genomic regions or a single genomic region.

The 1,500 individuals composing the 500 trios are preferably individually genotyped with at least 80,000 markers, generating at least a few million genotypes; more preferably, at least a hundred million.

Step 4: Exclude the markers that did not pass the quality control of the assay.

Preferably, the quality controls consist of, but are not limited to, the following criteria: eliminate SNPs that had a high rate of Mendelian errors (cut-off at 1% Mendelian error rate), that deviate from the Hardy-Weinberg equilibrium, that are non-polymorphic in the Quebec founder population or have too many missing data (cut-off at 1% missing values or higher), or simply because they are non-

polymorphic in the Quebec founder population (cut-off at 1% ≤ 10% minor allele frequency (MAF)).

Step 5: Perform the genetic analysis on the results obtained using haplotype information as well as single-marker association.

In the preferred embodiment, genetic analysis is performed on all the genotypes from step 3.

In another embodiment, genetic analysis is performed on a total of 248,535 SNPs.

In one embodiment, the genetic analysis consists of, but is not limited to features corresponding to Phase information and haplotype structures. Phase information and haplotype structures are preferably deduced from trio genotypes using Phasefinder. Since chromosomal assignment (phase) cannot be estimated when all trio members are heterozygous, an Expectation-Maximization (EM) algorithm may be used to resolve chromosomal assignment ambiguities after Phasefinder.

In yet another embodiment, the PL-EM algorithm (Partition-Ligation EM; Niu *et al.*., Am. J. Hum. Genet. 70:157 (2002)) can be used to estimate haplotypes from the "genotype" data as a measured estimate of the reference allele frequency of a SNP in 15-marker windows that advance in increments of one marker across the data set. The results from such algorithms are converted into 15-marker haplotype files. Subsequently, the individual 15-marker block files are assembled into one continuous block of haplotypes for the entire chromosome. These extended haplotypes can then be used for further analysis. Such haplotype assembly algorithms take the consensus estimate of the allele call at each marker over all separate estimations (most markers are estimated 15 different times as the 15 marker blocks pass over their position).

In the preferred embodiment, the haplotypes for both the controls and the patients are derived in this manner. The preferred control of a trio structure is the spouse if the patient is one of the parents or the non-transmitted chromosomes (chromosomes found in parents but not in affected child) if the patient is the child.

In another embodiment, the haplotype frequencies among patients are compared to those among the controls using LDSTATS, a program that assesses the association of haplotypes with the disease. Such program defines haplotypes using multi-marker windows that advance across the marker map in one-marker increments. Such windows can be 1, 3, 5, 7 or 9 markers wide, and all these window sizes are tested concurrently. Larger multi-marker haplotype windows can also be used. At each position the frequency of haplotypes in cases is compared to the frequency of haplotypes in controls. Such allele frequency differences for single marker windows can be tested using Pearson's Chi-square with any degree of freedom. Multi-allelic haplotype association can be tested using Smith's normalization of the square root of Pearson's Chi-square. Such significance of association can be reported in two ways:

The significance of association within any one haplotype window is plotted against the marker that is central to that window.

P-values of association for each specific marker are calculated as a pooled P-value across all haplotype windows in which they occur. The pooled P-value is calculated using an expected value and variance calculated using a permutation test that considers covariance between individual windows. Such pooled P-values can yield narrower regions of gene location than the window data (see example 3 for details on analysis methods, such as LDSTATS v2.0 and v4.0).

In another embodiment, conditional haplotype analyses can be performed on subsets of the original set of cases and controls using the program LDSTATS. The selection of a subset of cases and their matched controls can be based on the carrier status of cases at a gene or locus of interest (see conditional analysis section in example 3 herein). Various conditional haplotypes can be derived, such as protective haplotypes and risk haplotypes.

Step 6: Fine Mapping

In this step, the candidate regions that were identified by step 4 are further mapped for the purpose of refinement and validation.

In the preferred embodiment, this fine mapping is performed with a density of genetic markers higher than in the genome wide scan (step 3) using any genotyping platform available in the art. Such fine mapping can be, but is not limited to, typing the allele via an allele-specific elongation assay that is then ligated to a locus-specific oligonucleotide. Such assays can be performed directly on the genomic DNA at a highly multiplex level and the products can be amplified using universal oligonucleotides. For each candidate region, the density of genetic markers can be, but is not limited to, a set of SNP markers with an average inter-marker distance of 1-4 Kb distributed over about 400 Kb to 1 Mb, roughly centered at the highest point of the GWS association. The preferred samples are those obtained from Crohn's disease PPC trios including the ones used for the GWS. Other preferred samples are trios or case control samples from another population, such as a General population.

In the preferred embodiment, the genetic analysis of the results obtained using haplotype information as well as single-marker association (as performed as in step 5, described herein) is performed as described herein (step 5 and Example section). The candidate regions that are validated and confirmed after this analysis proceed to a gene mining step described in Example 5, herein, to characterize their marker and genetic content.

Step 7: SNP and DNA polymorphism discovery

In the preferred embodiment, all the candidate genes and regions identified in step 6 are sequenced for polymorphism identification.

In another embodiment, the entire region, including all introns, is sequenced to identify all polymorphisms.

In yet another embodiment, the candidate genes are prioritized for sequencing, and only functional gene elements (promoters, conserved noncoding sequences, exons and splice sites) are sequenced.

In yet another embodiment, previously identified polymorphisms in the candidate regions can also be used. For example, SNPs from dbSNP, Perlegen Sciences,

Inc., or others can also be used rather than resequencing the candidate regions to identify polymorphisms.

The discovery of SNPs and DNA polymorphisms generally comprises a step consisting of determining the major haplotypes in the region to be sequenced. The preferred samples are selected according to which haplotypes contribute to the association signal observed in the region to be sequenced. The purpose is to select a set of samples that covers all the major haplotypes in the given region. Each major haplotype is preferably analyzed in at least a few individuals.

Any analytical procedure may be used to detect the presence or absence of variant nucleotides at one or more polymorphic positions of the invention. In general, the detection of allelic variation requires a mutation discrimination technique, optionally an amplification reaction and optionally a signal generation system. Any means of mutation detection or discrimination may be used. For instance, DNA sequencing, scanning methods, hybridization, extension based methods, incorporation based methods, restriction enzyme-based methods and ligation-based methods may be used in the methods of the invention.

Sequencing methods include, but are not limited to, direct sequencing, and sequencing by hybridization. Scanning methods include, but are not limited to, protein truncation test (PTT), single-strand conformation polymorphism analysis (SSCP), denaturing gradient gel electrophoresis (DGGE), temperature gradient gel electrophoresis (TGGE), cleavage, heteroduplex analysis, chemical mismatch cleavage (CMC), and enzymatic mismatch cleavage. Hybridization-based methods of detection include, but are not limited to, solid phase hybridization such as dot blots, multiple allele specific diagnostic assay (MASDA), reverse dot blots, and oligonucleotide arrays (DNA Chips). Solution phase hybridization amplification methods may also be used, such as Taqman. Extension based methods include, but are not limited to, amplification refraction mutation systems (ARMS), amplification refractory mutation systems (ALEX), and competitive oligonucleotide priming systems (COPS). Incorporation based methods include, but are not limited to, mini-sequencing and arrayed primer extension (APEX). Restriction enzyme-based detection systems include, but are not limited to,

restriction site generating PCR. Lastly, ligation based detection methods include, but are not limited to, oligonucleotide ligation assays (OLA). Signal generation or detection systems that may be used in the methods of the invention include, but are not limited to, fluorescence methods such as fluorescence resonance energy transfer (FRET), fluorescence quenching, fluorescence polarization as well as other chemiluminescence, electrochemiluminescence, Raman, radioactivity, colometric methods, hybridization protection assays and mass spectrometry methods. Further amplification methods include, but are not limited to self sustained replication (SSR), nucleic acid sequence based amplification (NASBA), ligase chain reaction (LCR), strand displacement amplification (SDA) and branched DNA (B-DNA).

Step 8: Ultrafine Mapping

This step further maps the candidate regions and genes confirmed in the previous step to identify and validate the responsible polymorphisms associated with Crohn's disease in the human population.

In a preferred embodiment, the discovered SNPs and polymorphisms of step 7 are ultrafine mapped at a higher density of markers than the fine mapping described herein using the same technology described in step 6.

Step 9: GeneMap construction

The confirmed variations in DNA (including both genic and non-genic regions) are used to build a GeneMap for Crohn's disease. The gene content of this GeneMap is described in more detail below. Such GeneMap can be used for other methods of the invention comprising the diagnostic methods described herein, the susceptibility to Crohn's disease, the response to a particular drug, the efficacy of a particular drug, the screening methods described herein and the treatment methods described herein.

As is evident to one of ordinary skill in the art, all of the above steps or the steps do not need to be performed, or performed in a given order to practice or use the SNPs, genomic regions, genes, proteins, etc. in the methods of the invention.

Genes from the GeneMap

In one embodiment the GeneMap consists of genes and targets, in a variety of combinations, identified from the candidate regions listed in Table 1. In another embodiment, all genes from Tables 8-10 are present in the GeneMap. In another preferred embodiment, the GeneMap consists of a selection of genes from Tables 8-10. The genes of the invention (Tables 8-10) are arranged by candidate regions and by their chromosomal location. Such order is for the purpose of clarity and does not reflect any other criteria of selection in the association of the genes with Crohn's disease.

In the preferred embodiment, genes identified in the WGAS and subsequent fine mapping studies for Crohn's disease (CD) are evaluated using the Ingenuity Pathway Analysis application (IPA, Ingenuity systems) in order to identify direct biological interactions between these genes, and also to identify molecular regulators acting on those genes (indirect interactions) that could be also involved in CD. The purpose of this effort is to decipher the molecules involved in contributing to CD. These gene interaction networks are very valuable tools in the sense that they facilitate extension of the map of gene products that could represent potential drug targets for CD.

Nucleic acid sequences

The nucleic acid sequences of the present invention may be derived from a variety of sources including DNA, cDNA, synthetic DNA, synthetic RNA, derivatives, mimetics or combinations thereof. Such sequences may comprise genomic DNA, which may or may not include naturally occurring introns, genic regions, nongenic regions, and regulatory regions. Moreover, such genomic DNA may be obtained in association with promoter regions or poly (A) sequences. The sequences, genomic DNA, or cDNA may be obtained in any of several ways. Genomic DNA can be extracted and purified from suitable cells by means well

known in the art. Alternatively, mRNA can be isolated from a cell and used to produce cDNA by reverse transcription or other means. The nucleic acids described herein are used in certain embodiments of the methods of the present invention for production of RNA, proteins or polypeptides, through incorporation into cells, tissues, or organisms. In one embodiment, DNA containing all or part of the coding sequence for the genes described in Tables 8-10, or the SNP markers described in Tables 2-7, is incorporated into a vector for expression of the encoded polypeptide in suitable host cells. The invention also comprises the use of the nucleotide sequence of the nucleic acids of this invention to identify DNA probes for the genes described in Tables 8-10 or the SNP markers described in Tables 2-7, PCR primers to amplify the genes described in Tables 8-10 or the SNP markers described in Tables 2-7, nucleotide polymorphisms in the genes described in Tables 8-10, and regulatory elements of the genes described in Tables 8-10. The nucleic acids of the present invention find use as primers and templates for the recombinant production of Crohn's disease-associated peptides or polypeptides, for chromosome and gene mapping, to provide antisense sequences, for tissue distribution studies, to locate and obtain full length genes, to identify and obtain homologous sequences (wild-type and mutants), and in diagnostic applications.

Antisense oligonucleotides

In a particular embodiment of the invention, an antisense nucleic acid or oligonucleotide is wholly or partially complementary to, and can hybridize with, a target nucleic acid (either DNA or RNA) having the sequence of SEQ ID NO:1, NO:3 or any SEQ ID from any Tables of the invention. For example, an antisense nucleic acid or oligonucleotide comprising 16 nucleotides can be sufficient to inhibit expression of at least one gene from Tables 8-10. Alternatively, an antisense nucleic acid or oligonucleotide can be complementary to 5' or 3' untranslated regions, or can overlap the translation initiation codon (5' untranslated and translated regions) of at least one gene from Tables 8-10, or its functional equivalent. In another embodiment, the antisense nucleic acid is wholly

or partially complementary to, and can hybridize with, a target nucleic acid that encodes a polypeptide from a gene described in Tables 8-10.

In addition, oligonucleotides can be constructed which will bind to duplex nucleic acid (*i.e.*, DNA:DNA or DNA:RNA), to form a stable triple helix containing or triplex nucleic acid. Such triplex oligonucleotides can inhibit transcription and/or expression of a gene from Tables 8-10, or its functional equivalent (M.D. Frank-Kamenetskii *et al.*, 1995). Triplex oligonucleotides are constructed using the basepairing rules of triple helix formation and the nucleotide sequence of the genes described in Tables 8-10.

The present invention encompasses methods of using oligonucleotides in antisense inhibition of the function of the genes from Tables 8-10. In the context of this invention, the term "oligonucleotide" refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits or their close homologs. The term may also refer to moieties that function similarly to oligonucleotides, but have non-naturally-occurring portions. Thus, oligonucleotides may have altered sugar moieties or inter-sugar linkages. Exemplary among these are phosphorothioate and other sulfur containing species which are known in the art. In preferred embodiments, at least one of the phosphodiester bonds of the oligonucleotide has been substituted with a structure that functions to enhance the ability of the compositions to penetrate into the region of cells where the RNA whose activity is to be modulated is located. It is preferred that such substitutions comprise phosphorothioate bonds, methyl phosphonate bonds, or short chain alkyl or cycloalkyl structures. In accordance with other preferred embodiments, the phosphodiester bonds are substituted with structures which are, at once, substantially non-ionic and non-chiral, or with structures which are chiral and enantiomerically specific. Persons of ordinary skill in the art will be able to select other linkages for use in the practice of the invention. Oligonucleotides may also include species that include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the furanosyl portions of the nucleotide subunits may also be effected, as long as

the essential tenets of this invention are adhered to. Examples of such modifications are 2'-O-alkyl- and 2'-halogen-substituted nucleotides. Some non-limiting examples of modifications at the 2' position of sugar moieties which are useful in the present invention include OH, SH, SCH3, F, OCH3, OCN, O(CH2), NH2 and O(CH2)n CH3, where n is from 1 to about 10. Such oligonucleotides are functionally interchangeable with natural oligonucleotides or synthesized oligonucleotides, which have one or more differences from the natural structure. All such analogs are comprehended by this invention so long as they function effectively to hybridize with at least one gene from Tables 8-10 DNA or RNA to inhibit the function thereof.

The oligonucleotides in accordance with this invention preferably comprise from about 3 to about 50 subunits. It is more preferred that such oligonucleotides and analogs comprise from about 8 to about 25 subunits and still more preferred to have from about 12 to about 20 subunits. As defined herein, a "subunit" is a base and sugar combination suitably bound to adjacent subunits through phosphodiester or other bonds. Antisense nucleic acids or oligonulcleotides can be produced by standard techniques (see, *e.g.*, Shewmaker *et al.*, U.S. Patent No. 6,107,065). The oligonucleotides used in accordance with this invention may be conveniently and routinely made through the well-known technique of solid phase synthesis. Any other means for such synthesis may also be employed; however, the actual synthesis of the oligonucleotides is well within the abilities of the practitioner. It is also well known to prepare other oligonucleotides such as phosphorothioates and alkylated derivatives.

The oligonucleotides of this invention are designed to be hybridizable with RNA (*e.g.*, mRNA) or DNA from genes described in Tables 8-10. For example, an oligonucleotide (*e.g.*, DNA oligonucleotide) that hybridizes to mRNA from a gene described in Tables 8-10 can be used to target the mRNA for RnaseH digestion. Alternatively an oligonucleotide that can hybridize to the translation initiation site of the mRNA of a gene described in Tables 8-10 can be used to prevent translation of the mRNA. In another approach, oligonucleotides that bind to the double-stranded DNA of a gene from Tables 8-10 can be administered. Such

oligonucleotides can form a triplex construct and inhibit the transcription of the DNA encoding polypeptides of the genes described in Tables 8-10. Triple helix pairing prevents the double helix from opening sufficiently to allow the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described (see, *e.g.*, J.E. Gee *et al.*, 1994, Molecular and Immunologic Approaches, Futura Publishing Co., Mt. Kisco, NY).

As non-limiting examples, antisense oligonucleotides may be targeted to hybridize to the following regions: mRNA cap region; translation initiation site; translational termination site; transcription initiation site; transcription termination site; polyadenylation signal; 3' untranslated region; 5' untranslated region; 5' coding region; mid coding region; and 3' coding region. Preferably, the complementary oligonucleotide is designed to hybridize to the most unique 5' sequence of a gene described in Tables 8-10, including any of about 15-35 nucleotides spanning the 5' coding sequence. In accordance with the present invention, the antisense oligonucleotide can be synthesized, formulated as a pharmaceutical composition, and administered to a subject. The synthesis and utilization of antisense and triplex oligonucleotides have been previously described (*e.g.*, Simon *et al.*, 1999; Barre *et al.*, 2000; Elez *et al.*, 2000; Sauter *et al.*, 2000).

Alternatively, expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses or from various bacterial plasmids may be used for delivery of nucleotide sequences to the targeted organ, tissue or cell population. Methods which are well known to those skilled in the art can be used to construct recombinant vectors which will express nucleic acid sequence that is complementary to the nucleic acid sequence encoding a polypeptide from the genes described in Tables 8-10. These techniques are described both in Sambrook *et al.*, 1989 and in Ausubel *et al.*, 1992. For example, expression of at least one gene from Tables 8-10 can be inhibited by transforming a cell or tissue with an expression vector that expresses high levels of untranslatable sense or antisense sequences. Even in the absence of integration into the DNA, such

vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a nonreplicating vector, and even longer if appropriate replication elements are included in the vector system. Various assays may be used to test the ability of gene-specific antisense oligonucleotides to inhibit the expression of at least one gene from Tables 8-10. For example, mRNA levels of the genes described in Tables 8-10 can be assessed by Northern blot analysis (Sambrook *et al.*, 1989; Ausubel *et al.*, 1992; J.C. Alwine *et al.* 1977; I.M. Bird, 1998), quantitative or semi-quantitative RT-PCR analysis (see, *e.g.*, W.M. Freeman *et al.*, 1999; Ren *et al.*, 1998; J.M. Cale *et al.*, 1998), or in situ hybridization (reviewed by A.K. Raap, 1998). Alternatively, antisense oligonucleotides may be assessed by measuring levels of the polypeptide from the genes described in Tables 8-10, *e.g.*, by western blot analysis, indirect immunofluorescence and immunoprecipitation techniques (see, *e.g.*, J.M. Walker, 1998, Protein Protocols on CD-ROM, Humana Press, Totowa, NJ). Any other means for such detection may also be employed, and is well within the abilities of the practitioner.

Mapping Technologies

The present invention includes various methods which employ mapping technologies to map SNPs and polymorphisms. For purpose of clarity, this section comprises, but is not limited to, the description of mapping technologies that can be utilized to achieve the embodiments described herein. Mapping technologies may be based on amplification methods, restriction enzyme cleavage methods, hybridization methods, sequencing methods, and cleavage methods using agents.

Amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990), transcriptional amplification system (Kwoh *et al.*, 1989), Q-Beta Replicase (Lizardi *et al.*, 1988), isothermal amplification (*e.g.* Dean *et al.*, 2002; and Hafner *et al.*, 2001), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of

ordinary skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low number.

Restriction enzyme cleavage methods include: isolating sample and control DNA, amplification (optional), digestion with one or more restriction endonucleases, determination of fragment length sizes by gel electrophoresis and comparing samples and controls. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, sequence specific ribozymes (see, *e.g.*, U.S. Pat. No. 5,498,531) or DNAzyme (*e.g.* U.S. Pat. No. 5,807,718) can be used to score for the presence of specific mutations by development or loss of a ribozyme or DNAzyme cleavage site.

Hybridization methods include any measurement of the hybridization or gene expression levels, of sample nucleic acids to probes corresponding to about 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 50, 75, 100, 200, 500, 1000 or more genes, or ranges of these numbers, such as about 2-10, about 10-20, about 20-50, about 50-100, about 100-200, about 200-500 or about 500-1000 genes of Tables 8-10.

SNPs and SNP maps of the invention can be identified or generated by hybridizing sample nucleic acids, *e.g.*, DNA or RNA, to high density arrays or bead arrays containing oligonucleotide probes corresponding to the polymorphisms of Tables 2-7 (see the Affymetrix arrays and Illumina bead sets at www.affymetrix.com and www.illumina.com and see Cronin *et al.*, 1996; or Kozal *et al.*, 1996).

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a single or on multiple solid substrates by a variety of methods, including, but not limited to, light-directed chemical coupling, and mechanically directed coupling (see Pirrung, U.S. Patent No. 5,143,854).

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is

derivatized with a silane reagent containing a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithogaphic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in PCT Publication Nos. WO 93/09668 and WO 01/23614. High density nucleic acid arrays can also be fabricated by depositing pre-made or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing. See WO 99/32660. The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes (*e.g.*, DNA:DNA, RNA:RNA, or RNA:DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency.

Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization tolerates fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency.

In a preferred embodiment, hybridization is performed at low stringency, in this case in 6x SSPET at 37°C (0.005% Triton X-100), to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, 1x SSPET at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25x SSPET at 37°C to 50°C) until a desired level of hybridization specificity is obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, *etc.*).

In general, there is a tradeoff between hybridization specificity (stringency) and signal intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Probes based on the sequences of the genes described above may be prepared by any commonly available method. Oligonucleotide probes for screening or assaying a tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least about 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases, longer probes of at least 30, 40, or 50 nucleotides will be desirable.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes or gene fragments described in Tables 8-10 refer to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequences of said genes. Such hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes (see GeneChip® Expression Analysis Manual, Affymetrix, Rev. 3, which is herein incorporated by reference in its entirety).

The phrase "hybridizing specifically to" or "specifically hybridizes" refers to the binding, duplexing, or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

As used herein a "probe" is defined as a nucleic acid, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

A variety of sequencing reactions known in the art can be used to directly sequence nucleic acids for the presence or the absence of one or more polymorphisms of Tables 2-7. Examples of sequencing reactions include those based on techniques developed by Maxam and Gilbert (1977) or Sanger (1977). It is also contemplated that any of a variety of automated sequencing procedures can be utilized, including sequencing by mass spectrometry (see, *e.g.* PCT International Publication No. WO 94/16101; Cohen *et al.*, 1996; and Griffin *et al.*,1993), real-time pyrophosphate sequencing method (Ronaghi *et al.*,1998; and

Permutt *et al.*, 2001) and sequencing by hybridization (see *e.g.* Drmanac *et al.*, 2002).

Other methods of detecting polymorphisms include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA, DNA/DNA or RNA/DNA heteroduplexes (Myers *et al.*, 1985). In general, the technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labeled) RNA or DNA containing a wild-type sequence with potentially mutant RNA or DNA obtained from a sample. The double-stranded duplexes are treated with an agent who cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of a mutation or SNP (see, for example, Cotton *et al.*, 1988; and Saleeba *et al.*, 1992). In a preferred embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping polymorphisms. For example, the mutY enzyme of E. coli cleaves A at G/A mismatches (Hsu *et al.*, 1994). Other examples include, but are not limited to, the MutHLS enzyme complex of E. coli (Smith and Modrich Proc. 1996) and Cel 1 from the celery (Kulinski *et al.*, 2000) both cleave the DNA at various mismatches. According to an exemplary embodiment, a probe based on a polymorphic site corresponding to a polymorphism of Tables 2-7 is hybridized to a cDNA or other DNA product from a test cell or cells. The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat.

No. 5,459,039. Alternatively, the screen can be performed *in vivo* following the insertion of the heteroduplexes in an appropriate vector. The whole procedure is known to those ordinary skilled in the art and is referred to as mismatch repair detection (see *e.g.* Fakhrai-Rad *et al.*, 2004).

In other embodiments, alterations in electrophoretic mobility can be used to identify polymorphisms in a sample. For example, single strand conformation polymorphism (SSCP) analysis can be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.*, 1989; Cotton *et al.*, 1993; and Hayashi 1992). Single-stranded DNA fragments of case and control nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence. The resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Kee *et al.*, 1991).

In yet another embodiment, the movement of mutant or wild-type fragments in a polyacrylamide gel containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers *et al.*, 1985). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum *et al.*, 1987). In another embodiment, the mutant fragment is detected using denaturing HPLC (see *e.g.* Hoogendoorn *et al.*, 2000).

Examples of other techniques for detecting polymorphisms include, but are not limited to, selective oligonucleotide hybridization, selective amplification, selective primer extension, selective ligation, single-base extension, selective termination

of extension or invasive cleavage assay. For example, oligonucleotide primers may be prepared in which the polymorphism is placed centrally and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki *et al.*, 1986; Saiki *et al.*, 1989). Such oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA. Alternatively, the amplification, the allele-specific hybridization and the detection can be done in a single assay following the principle of the 5' nuclease assay (*e.g.* see Livak *et al.*, 1995). For example, the associated allele, a particular allele of a polymorphic locus, or the like is amplified by PCR in the presence of both allele-specific oligonucleotides, each specific for one or the other allele. Each probe has a different fluorescent dye at the 5' end and a quencher at the 3' end. During PCR, if one or the other or both allele-specific oligonucleotides are hybridized to the template, the Taq polymerase via its 5' exonuclease activity will release the corresponding dyes. The latter will thus reveal the genotype of the amplified product.

Hybridization assays may also be carried out with a temperature gradient following the principle of dynamic allele-specific hybridization or like *e.g.* Jobs *et al.*, (2003); and Bourgeois and Labuda, (2004). For example, the hybridization is done using one of the two allele-specific oligonucleotides labeled with a fluorescent dye, and an intercalating quencher under a gradually increasing temperature. At low temperature, the probe is hybridized to both the mismatched and full-matched template. The probe melts at a lower temperature when hybridized to the template with a mismatch. The release of the probe is captured by an emission of the fluorescent dye, away from the quencher. The probe melts at a higher temperature when hybridized to the template with no mismatch. The temperature-dependent fluorescence signals therefore indicate the absence or presence of an associated allele, a particular allele of a polymorphic locus, or the like (*e.g.* Jobs *et al.*, 2003). Alternatively, the hybridization is done under a gradually decreasing temperature. In this case, both allele-specific oligonucleotides are hybridized to the template competitively. At high temperature

none of the two probes are hybridized. Once the optimal temperature of the full-matched probe is reached, it hybridizes and leaves no target for the mismatched probe (*e.g.* Bourgeois and Labuda, 2004). In the latter case, if the allele-specific probes are differently labeled, then they are hybridized to a single PCR-amplified target. If the probes are labeled with the same dye, then the probe cocktail is hybridized twice to identical templates with only one labeled probe, different in the two cocktails, in the presence of the unlabeled competitive probe.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the present invention. Oligonucleotides used as primers for specific amplification may carry the associated allele, a particular allele of a polymorphic locus, or the like, also referred to as "mutation" of interest in the center of the molecule, so that amplification depends on differential hybridization (Gibbs *et al.*, 1989) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner, 1993). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini *et al.*, 1992). It is anticipated that in certain embodiments, amplification may also be performed using Taq ligase for amplification (Barany, 1991). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known associated allele, a particular allele of a polymorphic locus, or the like at a specific site by looking for the presence or absence of amplification. The products of such an oligonucleotide ligation assay can also be detected by means of gel electrophoresis. Furthermore, the oligonucleotides may contain universal tags used in PCR amplification and zip code tags that are different for each allele. The zip code tags are used to isolate a specific, labeled oligonucleotide that may contain a mobility modifier (*e.g.* Grossman *et al.*, 1994).

In yet another alternative, allele-specific elongation followed by ligation will form a template for PCR amplification. In such cases, elongation will occur only if there is a perfect match at the 3' end of the allele-specific oligonucleotide using a DNA polymerase. This reaction is performed directly on the genomic DNA and the

extension/ligation products are amplified by PCR. To this end, the oligonucleotides contain universal tags allowing amplification at a high multiplex level and a zip code for SNP identification. The PCR tags are designed in such a way that the two alleles of a SNP are amplified by different forward primers, each having a different dye. The zip code tags are the same for both alleles of a given SNPs and they are used for hybridization of the PCR-amplified products to oligonucleotides bound to a solid support, chip, bead array or like. For an example of the procedure, see Fan *et al.* (Cold Spring Harbor Symposia on Quantitative Biology, Vol. LXVIII, pp. 69-78 2003).

Another alternative includes the single-base extension/ligation assay using a molecular inversion probe, consisting of a single, long oligonucleotide (see *e.g.* Hardenbol *et al.*, 2003). In such an embodiment, the oligonucleotide hybridizes on both side of the SNP locus directly on the genomic DNA, leaving a one-base gap at the SNP locus. The gap-filling, one-base extension/ligation is performed in four tubes, each having a different dNTP. Following this reaction, the oligonucleotide is circularized whereas unreactive, linear oligonucleotides are degraded using an exonuclease such as exonuclease I of E. coli. The circular oligonucleotides are then linearized and the products are amplified and labeled using universal tags on the oligonucleotides. The original oligonucleotide also contains a SNP-specific zip code allowing hybridization to oligonucleotides bound to a solid support, chip, and bead array or like. This reaction can be performed at a high multiplexed level.

In another alternative, the associated allele, a particular allele of a polymorphic locus, or the like is scored by single-base extension (see *e.g.* U.S. Pat. No. 5,888,819). The template is first amplified by PCR. The extension oligonucleotide is then hybridized next to the SNP locus and the extension reaction is performed using a thermostable polymerase such as ThermoSequenase (GE Healthcare) in the presence of labeled ddNTPs. This reaction can therefore be cycled several times. The identity of the labeled ddNTP incorporated will reveal the genotype at the SNP locus. The labeled products can be detected by means of gel electrophoresis, fluorescence polarization (*e.g.* Chen *et al.*, 1999) or by

hybridization to oligonucleotides bound to a solid support, chip, and bead array or like. In the latter case, the extension oligonucleotide will contain a SNP-specific zip code tag.

In yet another alternative, a SNP is scored by selective termination of extension. The template is first amplified by PCR and the extension oligonucleotide hybridizes in the vicinity of the SNP locus, close to but not necessarily adjacent to it. The extension reaction is carried out using a thermostable polymerase such as ThermoSequenase (GE Healthcare) in the presence of a mix of dNTPs and at least one ddNTP. The latter has to terminate the extension at one of the allele of the interrogated SNP, but not both such that the two alleles will generate extension products of different sizes. The extension product can then be detected by means of gel electrophoresis, in which case the extension products need to be labeled, or by mass spectrometry (see *e.g.* Storm *et al.*, 2003).

In another alternative, SNPs are detected using an invasive cleavage assay (see U.S. Pat. No. 6,090,543). There are five oligonucleotides per SNP to interrogate but these are used in a two step-reaction. During the primary reaction, three of the designed oligonucleotides are first hybridized directly to the genomic DNA. One of them is locus-specific and hybridizes up to the SNP locus (the pairing of the 3' base at the SNP locus is not necessary). There are two allele-specific oligonucleotides that hybridize in tandem to the locus-specific probe but also contain a 5' flap that is specific for each allele of the SNP. Depending upon hybridization of the allele-specific oligonucleotides at the base of the SNP locus, this creates a structure that is recognized by a cleavase enzyme (U.S. Pat. No. 6,090,606) and the allele-specific flap is released. During the secondary reaction, the flap fragments hybridize to a specific cassette to recreate the same structure as above except that the cleavage will release a small DNA fragment labeled with a fluorescent dye that can be detected using regular fluorescence detector. In the cassette, the emission of the dye is inhibited by a quencher.

Methods to identify agents that modulate the expression of a nucleic acid encoding a gene involved in Crohn's disease.

The present invention provides methods for identifying agents that modulate the expression of a nucleic acid encoding a gene from Tables 8-10. Such methods may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the nucleic acid in a cell. Such cells can be obtained from any parts of the body such as the GI track, colon, esophagus, stomach, rectum, jujenum, ileum, mucosa, submucosa, cecum, rectum, scalp, blood, dermis, epidermis, skin cells, cutaneous surfaces, intertrigious areas, genitalia, vessels and endothelium. Some non-limiting examples of cells that can be used are: muscle cells, nervous cells, blood and vessels cells, dermis, epidermis and other skin cells, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keratinocyte, lamina propria lymphocyte, intraepithelial lymphocyte, epithelial cells and lymphocytes.

In one assay format, the expression of a nucleic acid encoding a gene of the invention (see Tables 8-10) in a cell or tissue sample is monitored directly by hybridization to the nucleic acids of the invention. Cell lines or tissues are exposed to the agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such as those disclosed in Sambrook *et al.*, (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Probes to detect differences in RNA expression levels between cells exposed to the agent and control cells may be prepared as described above. Hybridization conditions are modified using known methods, such as those described by Sambrook *et al.*, and Ausubel *et al.*, as required for each probe. Hybridization of total cellular RNA or RNA enriched for polyA RNA can be accomplished in any available format. For instance, total cellular RNA or RNA enriched for polyA RNA can be affixed to a solid support and the solid support exposed to at least one

probe comprising at least one, or part of one of the sequences of the invention under conditions in which the probe will specifically hybridize. Alternatively, nucleic acid fragments comprising at least one, or part of one of the sequences of the invention can be affixed to a solid support, such as a silicon chip or a porous glass wafer. The chip or wafer can then be exposed to total cellular RNA or polyA RNA from a sample under conditions in which the affixed sequences will specifically hybridize to the RNA. By examining for the ability of a given probe to specifically hybridize to an RNA sample from an untreated cell population and from a cell population exposed to the agent, agents which up or down regulate expression are identified.

Methods to identify agents that modulate the activity of a protein encoded by a gene involved in Crohn's disease.

The present invention provides methods for identifying agents that modulate at least one activity of the proteins described in Tables 8-10. Such methods may utilize any means of monitoring or detecting the desired activity. As used herein, an agent is said to modulate the expression of a protein of the invention if it is capable of up- or down- regulating expression of the protein in a cell. Such cells can be obtained from any parts of the body such as the GI track, colon, esophagus, stomach, rectum, jujenum, ileum, mucosa, submucosa, cecum, rectum, scalp, blood, dermis, epidermis, skin cells, cutaneous surfaces, intertrigious areas, genitalia, vessels and endothelium. Some non-limiting examples of cells that can be used are: muscle cells, nervous cells, blood and vessels cells, dermis, epidermis and other skin cells, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keratinocyte, lamina propria lymphocyte, intraepithelial lymphocyte, epithelial cells and lymphocytes.

In one format, the specific activity of a protein of the invention, normalized to a standard unit, may be assayed in a cell population that has been exposed to the agent to be tested and compared to an unexposed control cell population may be

assayed. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and times. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe.

Antibody probes can be prepared by immunizing suitable mammalian hosts utilizing appropriate immunization protocols using the proteins of the invention or antigen-containing fragments thereof. To enhance immunogenicity, these proteins or fragments can be conjugated to suitable carriers. Methods for preparing immunogenic conjugates with carriers such as BSA, KLH or other carrier proteins are well known in the art. In some circumstances, direct conjugation using, for example, carbodiimide reagents may be effective; in other instances linking reagents such as those supplied by Pierce Chemical Co. (Rockford, IL) may be desirable to provide accessibility to the hapten. The hapten peptides can be extended at either the amino or carboxy terminus with a cysteine residue or interspersed with cysteine residues, for example, to facilitate linking to a carrier. Administration of the immunogens is conducted generally by injection over a suitable time period and with use of suitable adjuvants, as is generally understood in the art. During the immunization schedule, titers of antibodies are taken to determine adequacy of antibody formation. While the polyclonal antisera produced in this way may be satisfactory for some applications, for pharmaceutical compositions, use of monoclonal preparations is preferred. Immortalized cell lines which secrete the desired monoclonal antibodies may be prepared using standard methods, see *e.g.*, Kohler & Milstein (1992) or modifications which affect immortalization of lymphocytes or spleen cells, as is generally known. The immortalized cell lines secreting the desired antibodies can be screened by immunoassay in which the antigen is the peptide hapten, polypeptide or protein. When the appropriate immortalized cell culture secreting the desired antibody is identified, the cells can be cultured either *in vitro* or by production in ascites fluid. The desired monoclonal antibodies may be recovered from the culture supernatant or from the ascites supernatant. Fragments of the monoclonal antibodies or the polyclonal antisera which contain the immunologically significant portion(s) can be used as antagonists, as well as the

intact antibodies. Use of immunologically reactive fragments, such as Fab or Fab' fragments, is often preferable, especially in a therapeutic context, as these fragments are generally less immunogenic than the whole immunoglobulin. The antibodies or fragments may also be produced, using current technology, by recombinant means. Antibody regions that bind specifically to the desired regions of the protein can also be produced in the context of chimeras derived from multiple species. Antibody regions that bind specifically to the desired regions of the protein can also be produced in the context of chimeras from multiple species, for instance, humanized antibodies. The antibody can therefore be a humanized antibody or a human antibody, as described in U.S. Patent 5,585,089 or Riechmann *et al.* (1988).

Agents that are assayed in the above method can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the protein of the invention alone or with its associated substrates, binding partners, etc. An example of randomly selected agents is the use of a chemical library or a peptide combinatorial library, or a growth broth of an organism. As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a non-random basis which takes into account the sequence of the target site or its conformation in connection with the agent's action. Agents can be rationally selected or rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site. The agents of the present invention can be, as examples, oligonucleotides, antisense polynucleotides, interfering RNA, peptides, peptide mimetics, antibodies, antibody fragments, small molecules, vitamin derivatives, as well as carbohydrates. Peptide agents of the invention can be prepared using standard solid phase (or solution phase) peptide synthesis methods, as is known in the art. In addition, the DNA encoding these peptides may be synthesized using commercially available oligonucleotide synthesis instrumentation and produced recombinantly using standard recombinant production systems. The production

using solid phase peptide synthesis is necessitated if non-gene-encoded amino acids are to be included.

Another class of agents of the present invention includes antibodies or fragments thereof that bind to a protein encoded by a gene in Tables 8-10. Antibody agents can be obtained by immunization of suitable mammalian subjects with peptides, containing as antigenic regions, those portions of the protein intended to be targeted by the antibodies (see section above of antibodies as probes for standard antibody preparation methodologies).

In yet another class of agents, the present invention includes peptide mimetics that mimic the three-dimensional structure of the protein encoded by a gene from Tables 8-10. Such peptide mimetics may have significant advantages over naturally occurring peptides, including, for example: more economical production, greater chemical stability, enhanced pharmacological properties (half-life, absorption, potency, efficacy, etc.), altered specificity (*e.g.*, a broad-spectrum of biological activities), reduced antigenicity and others. In one form, mimetics are peptide-containing molecules that mimic elements of protein secondary structure. The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural molecule. In another form, peptide analogs are commonly used in the pharmaceutical industry as non-peptide drugs with properties analogous to those of the template peptide. These types of non-peptide compounds are also referred to as peptide mimetics or peptidomimetics (Fauchere, 1986; Veber & Freidinger, 1985; Evans *et al.*, 1987) which are usually developed with the aid of computerized molecular modeling. Peptide mimetics that are structurally similar to therapeutically useful peptides may be used to produce an equivalent therapeutic or prophylactic effect. Generally, peptide mimetics are structurally similar to a paradigm polypeptide (*i.e.*, a polypeptide that has a biochemical property or pharmacological activity), but have one or more peptide linkages optionally replaced by a linkage using methods known in the art. Labeling of

peptide mimetics usually involves covalent attachment of one or more labels, directly or through a spacer (*e.g.*, an amide group), to non-interfering position(s) on the peptide mimetic that are predicted by quantitative structure-activity data and molecular modeling. Such non-interfering positions generally are positions that do not form direct contacts with the macromolecule(s) to which the peptide mimetic binds to produce the therapeutic effect. Derivitization (*e.g.*, labeling) of peptide mimetics should not substantially interfere with the desired biological or pharmacological activity of the peptide mimetic. The use of peptide mimetics can be enhanced through the use of combinatorial chemistry to create drug libraries. The design of peptide mimetics can be aided by identifying amino acid mutations that increase or decrease binding of the protein to its binding partners. Approaches that can be used include the yeast two hybrid method (see Chien *et al.*, 1991) and the phage display method. The two hybrid method detects protein-protein interactions in yeast (Fields *et al.*, 1989). The phage display method detects the interaction between an immobilized protein and a protein that is expressed on the surface of phages such as lambda and M13 (Amberg *et al.*, 1993; Hogrefe *et al.*, 1993). These methods allow positive and negative selection for protein-protein interactions and the identification of the sequences that determine these interactions.

Method to diagnose Crohn's disease

The present invention also relates to methods for diagnosing inflammatory bowel disease or a related disease, preferably Crohn's disease (CD), a disposition to such disease, predisposition to such a disease and/or disease progression. In some methods, the steps comprise contacting a target sample with (a) nucleic acid molecule(s) or fragments thereof and comparing the concentration of individual mRNA(s) with the concentration of the corresponding mRNA(s) from at least one healthy donor. An aberrant (increased or decreased) mRNA level of at least one gene from Tables 8-10, at least 5 or 10 genes from Tables 8-10, at least 50 genes from Tables 8-10, at least 100 genes from Tables 8-10 or at least 200 genes from Tables 8-10 determined in the sample in comparison to the

control sample is an indication of Crohn's disease or a related disease or a disposition to such kinds of diseases. For diagnosis, samples are, preferably, obtained from inflamed colon tissue. Samples can also be obtained from any parts of the body such as the GI track, colon, esophagus, stomach, rectum, jujenum, ileum, mucosa, submucosa, cecum, rectum, scalp, blood, dermis, epidermis, skin cells, cutaneous surfaces, intertrigious areas, genitalia, vessels and endothelium. Some non-limiting examples of cells that can be used are: muscle cells, nervous cells, blood and vessels cells, dermis, epidermis and other skin cells, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keratinocyte, lamina propria lymphocyte, intraepithelial lymphocyte, epithelial cells and lymphocytes.

For analysis of gene expression, total RNA is obtained from cells according to standard procedures and, preferably, reverse-transcribed. Preferably, a DNAse treatment (in order to get rid of contaminating genomic DNA) is performed. Some non-limiting examples of cells that can be used are: muscle cells, nervous cells, blood and vessels cells, dermis, epidermis and other skin cells, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keratinocyte, lamina propria lymphocyte, intraepithelial lymphocyte, epithelial cells and lymphocytes.

The nucleic acid molecule or fragment is typically a nucleic acid probe for hybridization or a primer for PCR. The person skilled in the art is in a position to design suitable nucleic acids probes based on the information provided in the Tables of the present invention. The target cellular component, *i.e.* mRNA, *e.g.*, in colon tissue, may be detected directly in situ, *e.g.* by in situ hybridization or it may be isolated from other cell components by common methods known to those skilled in the art before contacting with a probe. Detection methods include Northern blot analysis, RNase protection, in situ methods, *e.g.* in situ hybridization, *in vitro* amplification methods (PCR, LCR, QRNA replicase or RNA-transcription/amplification (TAS, 3SR), reverse dot blot disclosed in EP-

B10237362) and other detection assays that are known to those skilled in the art. Products obtained by *in vitro* amplification can be detected according to established methods, *e.g.* by separating the products on agarose or polyacrylamide gels and by subsequent staining with ethidium bromide. Alternatively, the amplified products can be detected by using labeled primers for amplification or labeled dNTPs. Preferably, detection is based on a microarray.

The probes (or primers) (or, alternatively, the reverse-transcribed sample mRNAs) can be detectably labeled, for example, with a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate, or an enzyme.

The present invention also relates to the use of the nucleic acid molecules or fragments described above for the preparation of a diagnostic composition for the diagnosis of Crohn's disease or a disposition to such a disease.

The present invention also relates to the use of the nucleic acid molecules of the present invention for the isolation or development of a compound which is useful for therapy of Crohn's disease. For example, the nucleic acid molecules of the invention and the data obtained using said nucleic acid molecules for diagnosis of Crohn's disease might allow for the identification of further genes which are specifically dysregulated, and thus may be considered as potential targets for therapeutic interventions.

The invention further provides prognostic assays that can be used to identify subjects having or at risk of developing Crohn's disease. In such method, a test sample is obtained from a subject and the amount and/or concentration of the nucleic acid described in Tables 8-10 is determined; wherein the presence of an associated allele, a particular allele of a polymorphic locus, or the likes in the nucleic acids sequences of this invention (see SEQ ID from Tables 2-10) can be diagnostic for a subject having or at risk of developing Crohn's. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest. For example, a test sample can be a biological fluid, a cell sample, or tissue. A biological fluid can be, but is not limited to saliva, serum, mucus, urine, stools,

spermatozoids, vaginal secretions, lymph, amiotic liquid, pleural liquid and tears. Cells can be, but are not limited to: muscle cells, nervous cells, blood and vessels cells, dermis, epidermis and other skin cells, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keranocyte, lamina propria lymphocyte, intraephitelial lymphocyte, epithelial cells and lymphocytes.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, polypeptide, nucleic acid such as antisense DNA or interfering RNA (RNAi), small molecule or other drug candidate) to treat Crohn's disease. Specifically, these assays can be used to predict whether an individual will have an efficacious response or will experience adverse events in response to such an agent. For example, such methods can be used to determine whether a subject can be effectively treated with an agent that modulates the expression and/or activity of a gene from Tables 8-10 or the nucleic acids described herein. In another example, an association study may be performed to identify polymorphisms from Tables 2-7 that are associated with a given response to the agent, *e.g.*, an efficacious response or the likelihood of one or more adverse events. Thus, one embodiment of the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disease associated with aberrant expression or activity of a gene from Tables 8-10 in which a test sample is obtained and nucleic acids or polypeptides from Tables 8-10 are detected (*e.g.*, wherein the presence of a particular level of expression of a gene from Tables 8-10 or a particular allelic variant of such gene, such as polymorphisms from Tables 2-7 is diagnostic for a subject that can be administered an agent to treat a disorder such as Crohn's disease). In one embodiment, the method includes obtaining a sample from a subject suspected of having Crohn's disease or an affected individual and exposing such sample to an agent. The expression and/or activity of the nucleic acids and/or genes of the invention are monitored before and after treatment with such agent to assess the effect of such agent. After analysis of the expression values, one skilled in the art can determine whether such agent can effectively treat such subject. In another

embodiment, the method includes obtaining a sample from a subject having or susceptible to developing Crohn's disease and determining the allelic constitution of polymorphisms from Tables 2-7 that are associated with a particular response to an agent. After analysis of the allelic constitution of the individual at the associated polymorphisms, one skilled in the art can determine whether such agent can effectively treat such subject.

The methods of the invention can also be used to detect genetic alterations in a gene from Tables 8-10, thereby determining if a subject with the lesioned gene is at risk for a disease associated with Crohn's disease. In preferred embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic alteration characterized by at least one alteration linked to or affecting the integrity of a gene from Tables 8-10 encoding a polypeptide or the misexpression of such gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of: (1) a deletion of one or more nucleotides from a gene from Tables 8-10; (2) an addition of one or more nucleotides to a gene from Tables 8-10; (3) a substitution of one or more nucleotides of a gene from Tables 8-10; (4) a chromosomal rearrangement of a gene from Tables 8-10; (5) an alteration in the level of a messenger RNA transcript of a gene from Tables 8-10; (6) aberrant modification of a gene from Tables 8-10, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a gene from Tables 8-10; (8) inappropriate post-translational modification of a polypeptide encoded by a gene from Tables 8-10; and (9) alternative promoter use. As described herein, there are a large number of assay techniques known in the art which can be used for detecting alterations in a gene from Tables 8-10. A preferred biological sample is a peripheral blood sample obtained by conventional means from a subject. Another preferred biological sample is a buccal swab. Other biological samples can be, but are not limited to, urine, stools, spermatozoids, vaginal secretions, lymph, amiotic liquid, pleural liquid and tears.

In certain embodiments, detection of the alteration involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.*,1988; and Nakazawa *et al.*, 1994), the latter of which can be particularly useful for detecting point mutations in a gene from Tables 8-10 (see Abavaya *et al.*, 1995). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic DNA, mRNA, or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a gene from Tables 8-10 under conditions such that hybridization and amplification of the nucleic acid from Tables 8-10 (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with some of the techniques used for detecting a mutation, an associated allele, a particular allele of a polymorphic locus, or the like described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990), transcriptional amplification system (Kwoh *et al.*, 1989), Q-Beta Replicase (Lizardi *et al.*, 1988), isothermal amplification (*e.g.* Dean *et al.*, 2002); and Hafner *et al.*, 2001), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of ordinary skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low number.

In an alternative embodiment, alterations in a gene from Tables 8-10, from a sample cell can be identified by identifying changes in a restriction enzyme cleavage pattern. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicate a mutation(s),

an associated allele, a particular allele of a polymorphic locus, or the like in the sample DNA. Moreover, sequence specific ribozymes (see, *e.g.*, U.S. Pat. No. 5,498,531 or DNAzyme *e.g.* U.S. Pat. No. 5,807,718) can be used to score for the presence of specific associated allele, a particular allele of a polymorphic locus, or the likes by development or loss of a ribozyme or DNAzyme cleavage site.

The present invention also relates to further methods for diagnosing Crohn's disease or a related disorder, preferably IBD, a disposition to such disorder, predisposition to such a disorder and/or disorder progression. In some methods, the steps comprise contacting a target sample with (a) nucleic molecule(s) or fragments thereof and determining the presence or absence of a particular allele of a polymorphism that confers a disorder-related phenotype (*e.g.*, predisposition to such a disorder and/or disorder progression). The presence of at least one allele from Tables 2-7 that is associated with Crohn's disease ("associated allele"), at least 5 or 10 associated alleles from Table Tables 2-7, at least 50 associated alleles from Table Tables 2-7 at least 100 associated alleles from Table Tables 2-7, or at least 200 associated alleles from Table Tables 2-7 determined in the sample is an indication of Crohn's disease or a related disorder, a disposition or predisposition to such kinds of disorders, or a prognosis for such disorder progression. Samples may be obtained from any parts of the body such as the GI track, colon, esophagus, stomach, rectum, jujenum, ileum, mucosa, submucosa, cecum, rectum, scalp, blood, dermis, epidermis, skin cells, cutaneous surfaces, intertrigious areas, genitalia, vessels and endothelium. Some non-limiting examples of cells that can be used are: muscle cells, nervous cells, blood and vessels cells, dermis, epidermis and other skin cells, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keratinocyte, lamina propria lymphocyte, intraepithelial lymphocyte, epithelial cells and lymphocytes.

In other embodiments, alterations in a gene from Tables 8-10 can be identified by hybridizing sample and control nucleic acids, *e.g.*, DNA or RNA, to high density

arrays or bead arrays containing tens to thousands of oligonucleotide probes (Cronin *et al.*, 1996; Kozal *et al.*, 1996). For example, alterations in a gene from Tables 8-10 can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.*, (1996). Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations, associated alleles, particular alleles of a polymorphic locus, or the like. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants, mutations, alleles detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence a gene from Tables 8-10 and detect an associated allele, a particular allele of a polymorphic locus, or the like by comparing the sequence of the sample gene from Tables 8-10 with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxam and Gilbert (1977) or Sanger (1977). It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Bio/Techniques 19:448, 1995) including sequencing by mass spectrometry (see, *e.g.* PCT International Publication No. WO 94/16101; Cohen *et al.*, 1996; and Griffin *et al.* 1993), real-time pyrophosphate sequencing method (Ronaghi *et al.*, 1998; and Permutt *et al.*, 2001) and sequencing by hybridization (see *e.g.* Drmanac *et al.*, 2002).

Other methods of detecting an associated allele, a particular allele of a polymorphic locus, or the likes in a gene from Tables 8-10 include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA, DNA/DNA or RNA/DNA heteroduplexes (Myers *et al.*, 1985). In

general, the technique of "mismatch cleavage" starts by providing heteroduplexes formed by hybridizing (labeled) RNA or DNA containing the wild-type gene sequence from Tables 8-10 with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digest the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of an associated allele, a particular allele of a polymorphic locus, or the like (see, for example, Cotton *et al.*, 1988; Saleeba *et al.*, 1992). In a preferred embodiment, the control DNA or RNA can be labeled for detection, as described herein.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point an associated allele, a particular allele of a polymorphic locus, or the likes in a gene from Tables 8-10 cDNAs obtained from samples of cells. For example, the mutY enzyme of E. coli cleaves A at G/A mismatches (Hsu *et al.*, 1994). Other examples include, but are not limited to, the MutHLS enzyme complex of E. coli (Smith and Modrich., 1996) and Cel 1 from the celery (Kulinski *et al.*, 2000) both cleave the DNA at various mismatches. According to an exemplary embodiment, a probe based on a gene sequence from Tables 8-10 is hybridized to a cDNA or other DNA product from a test cell or cells. The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected using electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039. Alternatively, the screen can be performed *in vivo* following the insertion of the heteroduplexes in an appropriate vector. The whole

procedure is known to those ordinary skilled in the art and is referred to as mismatch repair detection (see *e.g.* Fakhrai-Rad *et al.*, 2004).

In other embodiments, alterations in electrophoretic mobility can be used to identify an associated allele, a particular allele of a polymorphic locus, or the likes in genes from Tables 8-10. For example, single strand conformation polymorphism (SSCP) analysis can be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.*, 1993; see also Cotton, 1993; and Hayashi *et al.*, 1992). Single-stranded DNA fragments of sample and control nucleic acids from Tables 8-10 will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence; the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Kee *et al.*, 1991).

In yet another embodiment, the movement of mutant or wild-type fragments in a polyacrylamide gel containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers *et al.*, 1985). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum *et al.*, 1987). In another embodiment, the mutant fragment is detected using denaturing HPLC (see *e.g.* Hoogendoorn *et al.*, 2000).

Examples of other techniques for detecting point mutations, an associated allele, a particular allele of a polymorphic locus, or the like include, but are not limited to, selective oligonucleotide hybridization, selective amplification, selective primer extension, selective ligation, single-base extension, selective termination of

extension or invasive cleavage assay. For example, oligonucleotide primers may be prepared in which the known associated allele, particular allele of a polymorphic locus, or the like is placed centrally and then hybridized to target DNA under conditions which permit hybridization only if a perfect match is found (Saiki *et al.*, 1986; Saiki *et al.*, 1989). Such allele specific oligonucleotides are hybridized to PCR amplified target DNA of a number of different associated alleles, a particular allele of a polymorphic locus, or the likes where the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA. Alternatively, the amplification, the allele-specific hybridization and the detection can be done in a single assay following the principle of the 5' nuclease assay (*e.g.* see Livak *et al.*, 1995). For example, the associated allele, a particular allele of a polymorphic locus, or the like locus is amplified by PCR in the presence of both allele-specific oligonucleotides, each specific for one or the other allele. Each probe has a different fluorescent dye at the 5' end and a quencher at the 3' end. During PCR, if one or the other or both allele-specific oligonucleotides are hybridized to the template, the Taq polymerase via its 5' exonuclease activity will release the corresponding dyes. The latter will thus reveal the genotype of the amplified product.

The hybridization may also be carried out with a temperature gradient following the principle of dynamic allele-specific hybridization or like (*e.g.* Jobs *et al.*, 2003; and Bourgeois and Labuda, 2004). For example, the hybridization is done using one of the two allele-specific oligonucleotides labeled with a fluorescent dye, an intercalating quencher under a gradually increasing temperature. At low temperature, the probe is hybridized to both the mismatched and full-matched template. The probe melts at a lower temperature when hybridized to the template with a mismatch. The release of the probe is captured by an emission of the fluorescent dye, away from the quencher. The probe melts at a higher temperature when hybridized to the template with no mismatch. The temperature-dependent fluorescence signals therefore indicate the absence or presence of the associated allele, particular allele of a polymorphic locus, or the like (*e.g.* Jobs *et al.* supra). Alternatively, the hybridization is done under a gradually decreasing temperature. In this case, both allele-specific oligonucleotides are

hybridized to the template competitively. At high temperature none of the two probes is hybridized. Once the optimal temperature of the full-matched probe is reached, it hybridizes and leaves no target for the mismatched probe. In the latter case, if the allele-specific probes are differently labeled, then they are hybridized to a single PCR-amplified target. If the probes are labeled with the same dye, then the probe cocktail is hybridized twice to identical templates with only one labeled probe, different in the two cocktails, in the presence of the unlabeled competitive probe.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the present invention. Oligonucleotides used as primers for specific amplification may carry the associated allele, particular allele of a polymorphic locus, or the like of interest in the center of the molecule, so that amplification depends on differential hybridization (Gibbs *et al.*, 1989) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner, 1993). In addition it may be desirable to introduce a novel restriction site in the region of the associated allele, particular allele of a polymorphic locus, or the like to create cleavage-based detection (Gasparini *et al.*, 1992). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany, 1991). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known associated allele, a particular allele of a polymorphic locus, or the like at a specific site by looking for the presence or absence of amplification. The products of such an oligonucleotide ligation assay can also be detected by means of gel electrophoresis. Furthermore, the oligonucleotides may contain universal tags used in PCR amplification and zip code tags that are different for each allele. The zip code tags are used to isolate a specific, labeled oligonucleotide that may contain a mobility modifier (*e.g.* Grossman *et al.*,1994).

In yet another alternative, allele-specific elongation followed by ligation will form a template for PCR amplification. In such cases, elongation will occur only if there

is a perfect match at the 3' end of the allele-specific oligonucleotide using a DNA polymerase. This reaction is performed directly on the genomic DNA and the extension/ligation products are amplified by PCR. To this end, the oligonucleotides contain universal tags allowing amplification at a high multiplex level and a zip code for SNP identification. The PCR tags are designed in such a way that the two alleles of a SNP are amplified by different forward primers, each having a different dye. The zip code tags are the same for both alleles of a given SNP and they are used for hybridization of the PCR-amplified products to oligonucleotides bound to a solid support, chip, bead array or like. For an example of the procedure, see Fan *et al.* (Cold Spring Harbor Symposia on Quantitative Biology, Vol. LXVIII, pp. 69-78, 2003).

Another alternative includes the single-base extension/ligation assay using a molecular inversion probe, consisting of a single, long oligonucleotide (see *e.g.* Hardenbol *et al.*, 2003). In such an embodiment, the oligonucleotide hybridizes on both sides of the SNP locus directly on the genomic DNA, leaving a one-base gap at the SNP locus. The gap-filling, one-base extension/ligation is performed in four tubes, each having a different dNTP. Following this reaction, the oligonucleotide is circularized whereas unreactive, linear oligonucleotides are degraded using an exonulease such as exonuclease I of E. coli. The circular oligonucleotides are then linearized and the products are amplified and labeled using universal tags on the oligonucleotides. The original oligonucleotide also contains a SNP-specific zip code allowing hybridization to oligonucleotides bound to a solid support, chip, bead array or the like. This reaction can be performed at a highly multiplexed level.

In another alternative, the associated allele, particular allele of a polymorphic locus, or the like is scored by single-base extension (see *e.g.* U.S. Pat. No. 5,888,819). The template is first amplified by PCR. The extension oligonucleotide is then hybridized next to the SNP locus and the extension reaction is performed using a thermostable polymerase such as ThermoSequenase (GE Healthcare) in the presence of labeled ddNTPs. This reaction can therefore be cycled several times. The identity of the labeled ddNTP incorporated will reveal the genotype at

the SNP locus. The labeled products can be detected by means of gel electrophoresis, fluorescence polarization (*e.g.* Chen *et al.*, 1999) or by hybridization to oligonucleotides bound to a solid support, chip, bead array or the like. In the latter case, the extension oligonucleotide will contain a SNP-specific zip code tag.

In yet another alternative, the variant is scored by selective termination of extension. The template is first amplified by PCR and the extension oligonucleotide hybridizes in vicinity to the SNP locus, close to but not necessarily adjacent to it. The extension reaction is carried out using a thermostable polymerase such as ThermoSequenase (GE Healthcare) in the presence of a mix of dNTPs and at least one ddNTP. The latter has to terminate the extension at one of the alleles of the interrogated SNP, but not both such that the two alleles will generate extension products of different sizes. The extension product can then be detected by means of gel electrophoresis, in which case the extension products need to be labeled, or by mass spectrometry (see *e.g.* Storm *et al.*, 2003).

In another alternative, the associated allele, particular allele of a polymorphic locus, or the like is detected using an invasive cleavage assay (see U.S. Pat. No. 6,090,543). There are five oligonucleotides per SNP to interrogate but these are used in a two step-reaction. During the primary reaction, three of the designed oligonucleotides are first hybridized directly to the genomic DNA. One of them is locus-specific and hybridizes up to the SNP locus (the pairing of the 3' base at the SNP locus is not necessary). There are two allele-specific oligonucleotides that hybridize in tandem to the locus-specific probe but also contain a 5' flap that is specific for each allele of the SNP. Depending upon hybridization of the allele-specific oligonucleotides at the base of the SNP locus, this creates a structure that is recognized by a cleavase enzyme (U.S. Pat. No. 6,090,606) and the allele-specific flap is released. During the secondary reaction, the flap fragments hybridize to a specific cassette to recreate the same structure as above except that the cleavage will release a small DNA fragment labeled with a fluorescent

dye that can be detected using regular fluorescence detector. In the cassette, the emission of the dye is inhibited by a quencher.

Other types of markers can also be used for diagnostic purposes. For example, microsatellites can also be useful to detect the genetic predisposition of an individual to a given disorder. Microsatellites consist of short sequence motifs of one or a few nucleotides repeated in tandem. The most common motifs are polynucleotide runs, dinucleotide repeats (particularly the CA repeats) and trinucleotide repeats. However, other types of repeats can also be used. The microsatellites are very useful for genetic mapping because they are highly polymorphic in their length. Microsatellite markers can be typed by various means, including but not limited to DNA fragment sizing, oligonucleotide ligation assay and mass spectrometry. For example, the locus of the microsatellite is amplified by PCR and the size of the PCR fragment will be directly correlated to the length of the microsatellite repeat. The size of the PCR fragment can be detected by regular means of gel electrophoresis. The fragment can be labeled internally during PCR or by using end-labeled oligonucleotides in the PCR reaction (*e.g.* Mansfield *et al.*, 1996). Alternatively, the size of the PCR fragment is determined by mass spectrometry. In such a case, however, the flanking sequences need to be eliminated. This can be achieved by ribozyme cleavage of an RNA transcript of the microsatellite repeat (Krebs *et al.*, 2001). For example, the microsatellite locus is amplified using oligonucleotides that include a T7 promoter on one end and a ribozyme motif on the other end. Transcription of the amplified fragments will yield an RNA substrate for the ribozyme, releasing small RNA fragments that contain the repeated region. The size of the latter is determined by mass spectrometry. Alternatively, the flanking sequences are specifically degraded. This is achieved by replacing the dTTP in the PCR reaction by dUTP. The dUTP nucleosides are then removed by uracyl DNA glycosylases and the resulting abasic sites are cleaved by either abasic endonucleases such as human AP endonuclease or chemical agents such as piperidine. Bases can also be modified post-PCR by chemical agents such as dimethyl sulfate and then cleaved by other chemical agents such as piperidine (see *e.g.* Maxam and

Gilbert, 1977; U.S. Pat. No. 5,869,242; and U.S. Patent pending serial No. 60/335,068).

In another alternative, an oligonucleotide ligation assay can be performed. The microsatellite locus is first amplified by PCR. Then, different oligonucleotides can be submitted to ligation at the center of the repeat with a set of oligonucleotides covering all the possible lengths of the marker at a given locus (Zirvi *et al.*, 1999). Another example of design of an oligonucleotide assay comprises the ligation of three oligonucleotides; a 5' oligonucleotide hybridizing to the 5' flanking sequence, a repeat oligonucleotide of the length of the shortest allele of the marker hybridizing to the repeated region and a set of 3' oligonucleotides covering all the existing alleles hybridizing to the 3' flanking sequence and a portion of the repeated region for all the alleles longer than the shortest one. For the shortest allele, the 3' oligonucleotide exclusively hybridizes to the 3' flanking sequence (U.S. Pat. No. 6,479,244).

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid selected from the SEQ ID of Tables 2-7, or antibody reagent described herein, which may be conveniently used, for example, in a clinical setting to diagnose patient exhibiting symptoms or a family history of a disorder or disorder involving abnormal activity of genes from Tables 8-10.

Method to treat an animal suspected of having Crohn's disease

The present invention provides methods of treating a disease associated with Crohn's disease by expressing in vivo the nucleic acids of at least one gene from Tables 8-10. These nucleic acids can be inserted into any of a number of well-known vectors for the transfection of target cells and organisms as described below. The nucleic acids are transfected into cells, *ex vivo* or *in vivo*, through the interaction of the vector and the target cell. The nucleic acids encoding a gene from Tables 8-10, under the control of a promoter, then express the encoded

protein, thereby mitigating the effects of absent, partial inactivation, or abnormal expression of a gene from Tables 8-10.

Such gene therapy procedures have been used to correct acquired and inherited genetic defects, cancer, and viral infection in a number of contexts. The ability to express artificial genes in humans facilitates the prevention and/or cure of many important human disorders, including many disorders which are not amenable to treatment by other therapies (for a review of gene therapy procedures, see Anderson, 1992; Nabel & Felgner, 1993; Mitani & Caskey, 1993; Mulligan, 1993; Dillon, 1993; Miller, 1992; Van Brunt, 1998; Vigne, 1995; Kremer & Perricaudet 1995; Doerfler & Bohm 1995; and Yu *et al.*, 1994).

Delivery of the gene or genetic material into the cell is the first critical step in gene therapy treatment of a disorder. A large number of delivery methods are well known to those of skill in the art. Preferably, the nucleic acids are administered for *in vivo* or *ex vivo* gene therapy uses. Non-viral vector delivery systems include DNA plasmids, naked nucleic acid, and nucleic acid complexed with a delivery vehicle such as a liposome. Viral vector delivery systems include DNA and RNA viruses, which have either episomal or integrated genomes after delivery to the cell. For a review of gene therapy procedures, see the references included in the above section.

The use of RNA or DNA based viral systems for the delivery of nucleic acids take advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (*in vivo*) or they can be used to treat cells *in vitro* and the modified cells are administered to patients (*ex vivo*). Conventional viral based systems for the delivery of nucleic acids could include retroviral, lentivirus, adenoviral, adeno-associated and herpes simplex virus vectors for gene transfer. Viral vectors are currently the most efficient and versatile method of gene transfer in target cells and tissues. Integration in the host genome is possible with the retrovirus, lentivirus, and adeno-associated virus gene transfer methods, often resulting in long term expression of the inserted transgene. Additionally, high

transduction efficiencies have been observed in many different cell types and target tissues.

The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system would therefore depend on the target tissue. Retroviral vectors are comprised of *cis*-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, *e.g.*, Buchscher *et al.*, 1992; Johann *et al.*, 1992; Sommerfelt *et al.*, 1990; Wilson *et al.*, 1989; Miller *et al.*,1999;and PCT/US94/05700).

In applications where transient expression of the nucleic acid is preferred, adenoviral based systems are typically used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and levels of expression have been obtained. This vector can be produced in large quantities in a relatively simple system. Adeno-associated virus ("AAV") vectors are also used to transduce cells with target nucleic acids, *e.g.*, in the *in vitro* production of nucleic acids and peptides, and for *in vivo* and *ex vivo* gene therapy procedures (see, *e.g.*, West *et al.*, 1987; U.S. Pat. No. 4,797,368; WO 93/24641; Kotin, 1994; Muzyczka, 1994). Construction of recombinant AAV vectors is described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin *et al.*, 1985; Tratschin, *et al.*, 1984; Hermonat & Muzyczka, 1984; and Samulski *et al.*, 1989.

In particular, numerous viral vector approaches are currently available for gene transfer in clinical trials, with retroviral vectors by far the most frequently used system. All of these viral vectors utilize approaches that involve complementation

of defective vectors by genes inserted into helper cell lines to generate the transducing agent. pLASN and MFG-S are examples are retroviral vectors that have been used in clinical trials (Dunbar *et al.*, 1995; Kohn *et al.*, 1995; Malech *et al.*, 1997). PA317/pLASN was the first therapeutic vector used in a gene therapy trial (Blaese *et al.*, 1995). Transduction efficiencies of 50% or greater have been observed for MFG-S packaged vectors (Ellem *et al.*, 1997; and Dranoff *et al.*, 1997).

Recombinant adeno-associated virus vectors (rAAV) are a promising alternative gene delivery systems based on the defective and nonpathogenic parvovirus adeno-associated type 2 virus. All vectors are derived from a plasmid that retains only the AAV 145 bp inverted terminal repeats flanking the transgene expression cassette. Efficient gene transfer and stable transgene delivery due to integration into the genomes of the transduced cell are key features for this vector system (Wagner *et al.*, 1998, Kearns *et al.,* 1996).

Replication-deficient recombinant adenoviral vectors (Ad) are predominantly used in transient expression gene therapy; because they can be produced at high titer and they readily infect a number of different cell types. Most adenovirus vectors are engineered such that a transgene replaces the Ad E1a, E1b, and E3 genes; subsequently the replication defector vector is propagated in human 293 cells that supply the deleted gene function in trans. Ad vectors can transduce multiple types of tissues *in vivo*, including nondividing, differentiated cells such as those found in the liver, kidney and muscle tissues. Conventional Ad vectors have a large carrying capacity. An example of the use of an Ad vector in a clinical trial involved polynucleotide therapy for antitumor immunization with intramuscular injection (Sterman *et al.*, 1998). Additional examples of the use of adenovirus vectors for gene transfer in clinical trials include Rosenecker *et al.*, 1996; Sterman *et al.*, 1998; Welsh *et al.*, 1995; Alvarez *et al.*, 1997; Topf *et al.*, 1998.

Packaging cells are used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, and ψ2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are usually generated by a producer cell line that packages a nucleic acid vector into

a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host, other viral sequences being replaced by an expression cassette for the protein to be expressed. The missing viral functions are supplied in trans by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess ITR sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely rep and cap, but lacking ITR sequences. The cell line is also infected with adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, *e.g.*, heat treatment to which adenovirus is more sensitive than AAV.

In many gene therapy applications, it is desirable that the gene therapy vector be delivered with a high degree of specificity to a particular tissue type. A viral vector is typically modified to have specificity for a given cell type by expressing a ligand as a fusion protein with a viral coat protein on the viruses outer surface. The ligand is chosen to have affinity for a receptor known to be present on the cell type of interest. For example, Han *et al.*, 1995, reported that Moloney murine leukemia virus can be modified to express human heregulin fused to gp70, and the recombinant virus infects certain human breast cancer cells expressing human epidermal growth factor receptor. This principle can be extended to other pairs of viruses expressing a ligand fusion protein and target cells expressing a receptor. For example, filamentous phage can be engineered to display antibody fragments (*e.g.*, Fab or Fv) having specific binding affinity for virtually any chosen cellular receptor. Although the above description applies primarily to viral vectors, the same principles can be applied to nonviral vectors. Such vectors can be engineered to contain specific uptake sequences thought to favor uptake by specific target cells.

Gene therapy vectors can be delivered *in vivo* by administration to an individual patient, typically by systemic administration (*e.g.*, intravenous, intraperitoneal,

intramuscular, subdermal, or intracranial infusion) or topical application. Alternatively, vectors can be delivered to cells *ex vivo*, such as cells explanted from an individual patient (*e.g.*, lymphocytes, bone marrow aspirates, and tissue biopsy) or universal donor hematopoietic stem cells, followed by reimplantation of the cells into a patient, usually after selection for cells which have incorporated the vector.

Ex vivo cell transfection for diagnostics, research, or for gene therapy (*e.g.*, via re-infusion of the transfected cells into the host organism) is well known to those of skill in the art. In a preferred embodiment, cells are isolated from the subject organism, transfected with a nucleic acid (gene or cDNA), and re-infused back into the subject organism (*e.g.*, patient). Various cell types suitable for *ex vivo* transfection are well known to those of skill in the art (see, *e.g.*, Freshney *et al.*, 1994; and the references cited therein for a discussion of how to isolate and culture cells from patients).

In one embodiment, stem cells are used in *ex vivo* procedures for cell transfection and gene therapy. The advantage to using stem cells is that they can be differentiated into other cell types *in vitro*, or can be introduced into a mammal (such as the donor of the cells) where they will engraft in the bone marrow. Methods for differentiating CD34+ cells *in vitro* into clinically important immune cell types using cytokines such a GM-CSF, IFN-γ and TNF-α are known (see Inaba *et al.*, 1992).

Stem cells are isolated for transduction and differentiation using known methods. For example, stem cells are isolated from bone marrow cells by panning the bone marrow cells with antibodies which bind unwanted cells, such as CD4+ and CD8+ (T cells), CD45+ (panB cells), GR-1 (granulocytes), and Iad (differentiated antigen presenting cells).

Vectors (*e.g.*, retroviruses, adenoviruses, liposomes, etc.) containing therapeutic nucleic acids can be also administered directly to the organism for transduction of cells *in vivo*. Alternatively, naked DNA can be administered.

Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells, as described above. The nucleic acids from Tables 8-10 are administered in any suitable manner, preferably with the pharmaceutically acceptable carriers described above. Suitable methods of administering such nucleic acids are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route (see Samulski *et al.*, 1989). The present invention is not limited to any method of administering such nucleic acids, but preferentially uses the methods described herein.

The present invention further provides other methods of treating Crohn's disease such as administering to an individual having Crohn's disease an effective amount of an agent that regulates the expression, activity or physical state of at least one gene from Tables 8-10. An "effective amount" of an agent is an amount that modulates a level of expression or activity of a gene from Tables 8-10, in a cell in the individual at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80% or more, compared to a level of the respective gene from Tables 8-10 in a cell in the individual in the absence of the compound. The preventive or therapeutic agents of the present invention may be administered, either orally or parenterally, systemically or locally. For example, intravenous injection such as drip infusion, intramuscular injection, intraperitoneal injection, subcutaneous injection, suppositories, intestinal lavage, oral enteric coated tablets, and the like can be selected, and the method of administration may be chosen, as appropriate, depending on the age and the conditions of the patient. The effective dosage is chosen from the range of 0.01 mg to 100 mg per kg of body weight per administration. Alternatively, the dosage in the range of 1 to 1000 mg, preferably 5 to 50 mg per patient may be chosen. The therapeutic efficacy of the treatment may be monitored by observing various parts of the GI tract, by endoscopy, barium, colonoscopy, or any other monitoring methods known in the art. Other ways of monitoring efficacy can be, but are not limited to monitoring inflammatory conditions involving the upper gastrointestinal tract such

as monitoring the amelioration on the esophageal discomfort, decrease in pain, improved swallowing, reduced chest pain, decreased heartburn, decreased regurgitation of solids or liquids after swallowing or eating, decrease in vomiting, or improvement in weight gain or improvement in vitality.

The present invention further provides a method of treating an individual clinically diagnosed with Crohns' disease. The methods generally comprises analyzing a biological sample that includes a cell, in some cases, a GI track cell, from an individual clinically diagnosed with Crohn's disease for the presence of modified levels of expression of at least 1 gene, at least 10 genes, at least 50 genes, at least 100 genes, or at least 200 genes from Tables 8-10. A treatment plan that is most effective for individuals clinically diagnosed as having a condition associated with Crohn's disease is then selected on the basis of the detected expression of such genes in a cell. Treatment may include administering a composition that includes an agent that modulates the expression or activity of a protein from Tables 8-10 in the cell. Information obtained as described in the methods above can also be used to predict the response of the individual to a particular agent. Thus, the invention further provides a method for predicting a patient's likelihood to respond to a drug treatment for a condition associated with Crohn's disease, comprising determining whether modified levels of a gene from Tables 8-10 is present in a cell, wherein the presence of protein is predictive of the patient's likelihood to respond to a drug treatment for the condition. Examples of the prevention or improvement of symptoms accompanied by Crohn's disease that can monitored for effectiveness include prevention or improvement of diarrhea, prevention or improvement of weight loss, inhibition of bowel tissue edema, inhibition of cell infiltration, inhibition of surviving period shortening, and the like, and as a result, a preventing or improving agent for diarrhea, a preventing or improving agent for weight loss, an inhibitor for bowel tissues edema, an inhibitor for cell infiltration, an inhibitor for surviving period shortening, and the like can be identified.

The invention also provides a method of predicting a response to therapy in a subject having Crohn's disease by determining the presence or absence in the

subject of one or more markers associated with Crohn's disease described in Tables 2-7, diagnosing the subject in which the one or more markers are present as having Crohn's disease, and predicting a response to a therapy based on the diagnosis *e.g.*, response to therapy may include an efficacious response and/or one or more adverse events. The invention also provides a method of optimizing therapy in a subject having Crohn's disease by determining the presence or absence in the subject of one or more markers associated with a clinical subtype of Crohn's disease, diagnosing the subject in which the one or more markers are present as having a particular clinical subtype of Crohn's disease, and treating the subject having a particular clinical subtype of Crohn's disease based on the diagnosis. As an example, treatment for the fibrostenotic subtype of Crohn's disease currently includes surgical removal of the affected, strictured part of the bowel.

Thus, while there are a number of treatments for Crohn's disease currently available, they all are accompanied by various side effects, high costs, and long complicated treatment protocols, which are often not available and effective in a large number of individuals. Accordingly, there remains a need in the art for more effective and otherwise improved methods for treating and preventing Crohn's disease. Thus, there is a continuing need in the medical arts for genetic markers of Crohn's disease and guidance for the use of such markers. The present invention fulfills this need and provides further related advantages.

EXAMPLES

Example 1: Identification of cases and controls

All individuals were sampled from the Quebec founder population (QFP). Membership in the founder population was defined as having four grandparents with French Canadian family names who were born in the Province of Quebec, Canada or in adjacent areas of the Provinces of New Brunswick and Ontario or in New England or New York State. The Quebec founder population has two distinct advantages over general populations for LD mapping. Because it is relatively young (about 12 to 15 generations from the mid 17th century to the present) and because it has a limited but sufficient number of founders (approximately 2600 effective founders, Charbonneau *et al.* 1987), the Quebec population is characterized both by extended LD and by decreased genetic heterogeneity. The increased extent of LD allows the detection of disease associated genes using a reasonable marker density, while still allowing the increased meiotic resolution of population-based mapping. The number of founders is small enough to result in increased LD and reduced allelic heterogeneity, yet large enough to insure that all of the major disease genes involved in general populations are present in Quebec. Reduced allelic heterogeneity will act to increase relative risk imparted by the remaining alleles and so increase the power of case/control studies to detect genes and gene alleles involved in complex disorders within the Quebec population. The specific combination of age in generations, optimal number of founders and large present population size makes the QFP optimal for LD-based gene mapping.

Patient inclusion criteria for the study include diagnosis for Crohn's disease by any one of the following: a colonoscopy, a radiological examination with barium, an abdominal surgical operation or a biopsy or a surgical specimen. The colonoscopy diagnosis consists of observing linear, deep or serpentigenous ulcers, pseudopolyps, or skip areas. The barium radiological examination consists of the detection of strictures, ulcerations and string signs by observing the barium enema and the small bowel followed through an NMRI series.

Patients that were diagnosed with ulcerative colitis, infectious colitis or other intestinal diseases were excluded from the study. All human sampling was subject to ethical review procedures.

All enrolled QFP subjects (patients and controls) provided a 30 ml blood sample (3 barcoded tubes of 10 ml). Samples were processed immediately upon arrival at Genizon's laboratory. All samples were scanned and logged into a LabVantage Laboratory Information Management System (LIMS), which served as a hub between the clinical data management system and the genetic analysis system. Following centrifugation, the buffy coat containing the white blood cells was isolated from each tube. Genomic DNA was extracted from the buffy coat from one of the tubes, and stored at 4°C until required for genotyping. DNA extraction was performed with a commercial kit using a guanidine hydrochloride based method (FlexiGene, Qiagen) according to the manufacturer's instructions. The extraction method yielded high molecular weight DNA, and the quality of every DNA sample was verified by agarose gel electrophoresis. Genomic DNA appeared on the gel as a large band of very high molecular weight. The remaining two buffy coats were stored at –80°C as backups.

The QFP samples were collected as family trios consisting of Crohn's disease subjects and two first degree relatives. Of the 500 trios, 477 were Parent, Parent, Child (PPC) trios; the remainders were Parent, Child, Child (PCC) trios. Only the PPC trios were used for the analysis reported here because they produced equal numbers of more accurately estimated case and control haplotypes than the PCC trios. 382 trios were used in the genome wide scan and 477 trios were used in the fine mapping component of the study. One member of each trio was affected with Crohn's disease. For the 382 trios used in the genome wide scan, these included 189 daughters, 90 sons, 54 mothers and 49 fathers. When a child was the affected member of the trio, the two non-transmitted parental chromosomes (one from each parent) were used as controls, when one of the parents was affected, that person's spouse provided the control chromosomes. The recruitment of trios allowed a more precise determination of long extended haplotypes.

Example 2: Genome Wide Association

Genotyping was performed using Perlegen's ultra-high-throughput platform. Marker loci were amplified by PCR and hybridized to wafers containing arrays of oligonucleotides. Allele discrimination was performed through allele-specific hybridization. In total, 248,535 SNPs, distributed as evenly as possible throughout the genome, were genotyped on the 382 QFP trios for a total of 372,802,500 genotypes. These markers were mostly selected from various databases including the ~1.6 million SNP database of Perlegen Life Sciences (Patil, 2001); several thousand were obtained from the HapMap consortium database and/or dbSNP at NCBI. The SNPs were chosen to maximize uniformity of genetic coverage and to cover a distribution of allele frequencies. All SNPs that did not pass the quality controls for the assay, that is, that had a minor allele frequency of less than 1%, a Mendelian error rate within trios greater than 1%, that deviated significantly from the Hardy-Weinberg equilibrium, or that had excessive missing data (cut-off at 5% missing values or higher) were removed from the analysis. Genetic analysis was performed on a total of 165,785 SNPs (158,775 autosomal, 6869 X chromosome and 141 Y chromosome). The average gap size was approximately 17 kb. Of the 165,785 markers, ~140,000 had a minor allele frequency (MAF) greater than 10% for the QFP.

The genotyping information was entered into a Unified Genotype Database (a proprietary database under development) from which it was accessed using custom-built programs for export to the genetic analysis pipeline. Analyses of these genotypes were performed with the statistical tools described in Example 3. The GWS permitted the identification of 208 candidate chromosomal regions linked to Crohn's disease (Table 1). Some of these regions were further analyzed by the Fine Mapping approach described in Example 4.

Example 3: Genetic Analysis

1. *Dataset quality assessment*

Prior to performing any analysis, the dataset from the GWS was verified for completeness of the trios. The program GGFileMod removed any trios with abnormal family structure or missing individuals (e.g. trios without a proband, duos, singletons, etc.), and calculated the total number of complete trios in the dataset. The trios were also tested to make sure that no subjects within the cohort were related more closely than second cousins (6 meiotic steps).

Subsequently, the program DataCheck2.1 was used to calculate the following statistics per marker and per family:

Minor allele frequency (MAF) for each marker; Missing values for each marker and family; Hardy Weinberg Equilibrium for each marker; and Mendelian segregation error rate.

The following acceptance criteria were applied for internal analysis purposes:

MAF > 1%;
Missing values < 1%;
Observed non-Mendelian segregation < 0.33%;
Non significant deviation in allele frequencies from Hardy Weinberg equilibrium.

Markers or families not meeting these criteria were removed from the dataset in the following step. Analyses of variance were performed using the algorithm GenAnova, to assess whether families or markers have a greater effect on missing values and/or non-Mendelian segregation. This was used to determine the smallest number of data points to remove from the dataset in order to meet the requirements for missing values and non-Mendelian segregation. The families and/or markers were removed from the dataset using the program DataPull, which generates an output file that is used for subsequent analysis of the genotype data.

2. *Phase Determination*

The program PhaseFinderSNP2.0 was used to determine phase from trio data on a marker-by-marker, trio-by-trio basis. The output file contains haplotype data for all trio members, with ambiguities present when all trio members are heterozygous or where data is missing. The program FileWriterTemp was then used to determine case and control haplotypes and to prepare the data in the proper input format for the next stage of analysis, using the expectation maximization algorithm, PL-EM, to call phase on the remaining ambiguities. This stage consists of several modules for resolution of the remaining phase ambiguities. PLEMInOut1 was first used to recode the haplotypes for input into the PL-EM algorithm in 15-marker blocks for the genome wide scan data and for 11 marker blocks for fine and ultra-fine mapping data sets. The haplotype information was encoded as genotypes, allowing for the entry of known phase into the algorithm; this method limits the possible number of estimated haplotypes conditioned on already known phase assignments. The PL-EM algorithm was used to estimate haplotypes from the "pseudo-genotype" data in 11 or 15-marker windows, advancing in increments of one marker across the chromosome. The results were then converted into multiple haplotype files using the program PLEMInOut2. Subsequently PLEMBlockGroup was used to convert the individual 11 or 15-marker block files into one continuous block of haplotypes for the entire chromosome, and to generate files for further analysis by LDSTATS and SINGLETYPE. PLEMBlockGroup takes the consensus estimation of the allele call at each marker over all separate estimations (most markers are estimated 11-15 different times as the 11 or 15 marker blocks pass over their position).

3. *Haplotype association analysis*

Haplotype association analysis was performed using the program LDSTATS. LDSTATS tests for association of haplotypes with the disease phenotype. The algorithms LDSTATS (v2.0) and LDSTATS (v4.0) define haplotypes using multi-marker windows that advance across the marker map in one-marker increments.

Windows can contain any odd number of markers specified as a parameter of the algorithm. Other marker windows can also be used. At each position the frequency of haplotypes in cases and controls was calculated and a chi-square statistic was calculated from case control frequency tables. For LDSTATS v2.0, the significance of the chi-square for single marker and 3-marker windows was calculated as Pearson's chi-square with degrees of freedom. Larger windows of multi-allelic haplotype association were tested using Smith's normalization of the square root of Pearson's Chi-square. In addition, LDSTATS v2.0 calculates Chi-square values for the transmission disequilibrium test (TDT) for single markers in situations where the trios consisted of parents and an affected child.

LDSTATS v4.0 calculates significance of chi-square values using a permutation test in which case-control status is randomly permuted until 350 permuted chi-square values are observed that are greater than or equal to chi-square value of the actual data. The P value is then calculated as 350 / the number of permutations required.

Table 2 lists the results for association analysis using LDSTATs (v2.0 and v4.0) for the 208 regions described above based on the genome wide scan genotype data for 382 QFP trios. For each region that was associated with Crohn disease in the genome wide scan, we report in Table 3 the allele frequencies and the relative risk (RR) for the haplotypes contributing to the best signal at each SNP in the region. The best signal at a given location was determined by comparing the significance (p-value) of the association with Crohn disease for window sizes of 1, 3, 5, 7, and 9 SNPs, and selecting the most significant window. For a given window size at a given location, the association with Crohn disease was evaluated by comparing the overall distribution of haplotypes in the cases with the overall distribution of haplotypes in the controls. Haplotypes with a relative risk greater than one increase the risk of developing Crohn disease while haplotypes with a relative risk less than one are protective and decrease the risk.

4. Conditional Haplotype Analyses

Conditional haplotype analyses were performed on subsets of the original set of 382 cases and 382 controls using the program LDSTATS (v2.0). The selection of a subset of cases and their matched controls was based on the carrier status of cases at a gene or locus of interest. We selected the gene NOD2 (alias CARD15) on chromosome 16 and the gene IL23R on chromosome 1 based on our association findings using LDSTAT (v2.0) in our fine mapping of these two loci with 477 trios (see below). The most significant association signal in NOD2 was obtained with a haplotype window of size 7 containing SNPs corresponding to SEQ IDs 16969, 16970, 16971, 16972, 16973, 16974, 16975 (see Table below for conversion to the specific DNA alleles used). A reduced haplotype diversity was observed and we selected two sets of risk haplotypes for conditional analyses. The first set consisted of haplotypes 2121222 and 1121211 and the second set contained the above two haplotypes and haplotype 2121211. Using the first set, we partitioned the cases into two groups; the first group consisting of those cases that were carrier of a risk haplotype and the second group consisting of the remaining cases, the non carriers. The resulting sample sizes were respectively 125 and 227. LDSTAT (v2.0) was run in each group and regions showing association with Crohn disease are reported in Table 6. Three regions (119, 139 and 163) were associated with Crohn disease in the group of carriers (has_NOD2_caserisk_2hap), indicating the presence of an epistatic interaction between risk factors in those regions and risk factors in NOD2 (Table 6). Seven regions (31, 100, 125, 135, 168, 187 and 196) were associated with Crohn disease in the group of non carriers (not_NOD2_caserisk_2hap), indicating the existence of risk factors acting independently of NOD2. We repeated the process of partitioning the cases into two groups using the second set containing three risk haplotypes. The resulting sample sizes were 200 and 152 for the two groups of cases. Fourteen regions (4, 10, 41, 47, 50, 78, 96, 119, 128, 139, 142, 143, 163 and 171) were associated with Crohn disease in the group of carriers (has_NOD2_caserisk_3hap) indicating the presence of an epistatic interaction between risk factors in those regions and risk factors in NOD2 (Table 6).

A second conditional analysis was performed using the gene IL23R on chromosome 1. The most significant association in IL23R was obtained with a haplotype window of size 9 containing SNPs corresponding to SEQ IDs 16976, 16977, 16978, 16979, 16980, 16981, 16982, 16983, 16984 (see Table below for conversion to the specific DNA alleles used). A reduced haplotype diversity was observed and we selected one set of protective haplotypes and a risk haplotype for conditional analyses. The protective set consisted of haplotypes 212111122 and 212111121 and the risk haplotype was 221211121. However, due to dominance effects involving the risk haplotype, we considered the risk haplotype 221211121 while excluding heterozygotes involving haplotypes 122122212, 222122211 and 212111122 (the "exclusion" set) and the risk haplotype. Using the first set of protective haplotypes, we partitioned the cases into two groups; the first group consisting of those cases that were carrier of a protective haplotype and the second group consisting of the remaining cases, the non carriers. The resulting sample sizes were respectively 204 and 162. LDSTATS (v2.0) was run in each group and regions showing association with Crohn disease are reported in Table 6. Seven regions (31, 38, 52, 73, 143, 161 and 162) were associated with Crohn disease in the group of carriers (has_IL23R_caseprotective_2hap), indicating the existence of risk factors acting independently of IL23R. Eighteen regions (12, 17, 35, 46, 68, 70, 71, 79, 81, 94, 96, 114, 125, 130, 135, 149, 174 and 206) were associated with Crohn disease in the group of non carriers (not_IL23R_caseprotective_2hap), indicating the presence of an epistatic interaction between risk factors in those regions and risk factors in IL23R (Table 6). We repeated the process of partitioning the cases into two groups using the risk haplotype in IL23R and the exclusion set. The carriers were cases with the risk haplotype but without one of the haplotypes in the exclusion set. The non carriers were the remaining set of cases. The sample sizes for the two groups were 184 and 182 respectively. Two regions (5 and 141) were associated with Crohn disease in the group of carriers (has_IL23R_caserisk_not3) indicating the presence of an epistatic interaction between risk factors in those regions and risk factors in IL23R (Table 6). Twenty five regions (18, 19, 29, 32, 35, 44, 51, 69, 81, 86, 88, 96, 102, 112, 113, 121, 122, 129, 130, 146, 167, 175, 184, 186 and 205)

were associated with Crohn disease in the group of non carriers (not_IL23R_caserisk_not3) indicating the presence of risk factors acting independently of IL23R (Table 6).

For each region that was associated with Crohn disease in the conditional analyses, we report in Table 7 the allele frequencies and the relative risk (RR) for the haplotypes contributing to the best signal at each SNP in the region. The best signal at a given location was determined by comparing the significance (p-value) of the association with Crohn disease for window sizes of 1, 3, 5, 7, and 9 SNPs, and selecting the most significant window. For a given window size at a given location, the association with Crohn disease was evaluated by comparing the overall distribution of haplotypes in the cases with the overall distribution of haplotypes in the controls. Haplotypes with a relative risk greater than one increase the risk of developing Crohn disease while haplotypes with a relative risk less than one are protective and decrease the risk.

DNA alleles used in haplotypes (NOD2/CARD15)

SeqID	16969	16970	16971	16972	16973	16974	16975
Position	49303427	49305205	49308676	49308899	49310925	49314041	49314275
Allele	T/C	T/C	T/G	A/G	A/G	G/C	T/C
RISK							
2121222							
	C	T	G	A	G	C	C
1121211	T	T	G	A	G	G	T
2121211	C	T	G	A	G	G	T

DNA alleles used in haplotypes (IL23R)

SeqID	16976	16977	16978	16979	16980	16981	16982	16983	16984
Position	67381537	67382937	67384786	67387749	67388943	67390943	67392949	67395507	67397137
Alleles	T|G	A|G	A|G	T|G	T|C	A|C	T|C	T|C	T|C
RISK									
221211121	G	G	A	G	T	A	T	C	T
Heterozygotes (risk carrier)									
122122212	T	G	G	T	C	C	C	T	C
222122211	G	G	G	T	C	C	C	T	T
212111122	G	A	G	T	T	A	T	C	C
PROTECTIVE									
212111122	G	A	G	T	T	A	T	C	C
212111121	G	A	G	T	T	A	T	C	T

5. Singletype analysis

The SINGLETYPE algorithm assesses the significance of case-control association for single markers using the genotype data from the laboratory as input in contrast to LDSTATS single marker window analyses, in which case-control alleles for single markers from estimated haplotypes in file, hapatctr.txt, as input. SINGLETYPE calculates P values for association for both alleles, 1 and 2, as well as for genotypes, 11, 12, and 22, and plots these as - $\log_{10}$ P values for significance of association against marker position.

Example 4: *Fine Mapping*

Seven of the top regions identified as being associated with Crohn's disease by the GWS were further analyzed by fine mapping using a denser set of markers, in order to validate and/or refine the signal. The fine mapping was carried out using the Illumina BeadStation 500GX SNP genotyping platform. Alleles were genotyped using an allele-specific elongation assay that was ligated to a locus-specific oligonucleotide. The assay was performed directly on genomic DNA at a highly multiplex level and the products were amplified using universal oligonucleotides. For each candidate region, a set of SNP markers was selected with an average inter-marker distance of 1-4 Kb distributed over about 400 Kb to 1 Mb and was roughly centered at the highest point of the GWS curves. The cohort used for the fine mapping consisted of 477 Crohn's disease trios (including the 382 used for the GWS). The algorithms used for genetic analyses were the same as used in the GWS and are described in Example 3. Table 4 lists the fine mapping SNPs for the 7 regions and their respective p values using 477 trios and two analysis methods: LDSTATS(v2.0) and LDSTATS(v4.0). For each region that was associated with Crohn disease in the fine mapping analyses, we report in Table 5a and 5b the allele frequencies and the relative risk (RR) for the haplotypes contributing to the best signal at each SNP in the region. The best signal at a given location was determined by comparing the significance (p-value) of the association with Crohn disease for multiple window sizes, and selecting the most significant window. For a given window size at a given location, the association with Crohn disease was evaluated by comparing the overall distribution of haplotypes in the cases with the overall distribution of haplotypes in the controls. Haplotypes with a relative risk greater than one increase the risk of developing Crohn disease while haplotypes with a relative risk less than one are protective and decrease the risk.

Example 5: *Gene identification and characterization*

A series of gene characterization was performed for each candidate region described in Table 1. Any gene or EST mapping to the interval based on public

map data or proprietary map data was considered as a candidate Crohn's disease gene. The approach used to identify all genes located in the critical regions is described below.

Public gene mining

Once regions were identified using the analyses described above, a series of public data mining efforts were undertaken, with the aim of identifying all genes located within the critical intervals as well as their respective structural elements (*i.e.*, promoters and other regulatory elements, UTRs, exons and splice sites). The initial analysis relied on annotation information stored in public databases (*e.g.* NCBI, UCSC Genome Bioinformatics, Entrez Human Genome Browser, OMIM – see below for database URL information). Table 8 lists the genes that have been mapped to the 208 candidate regions.

Database URLs	
Name	URL
Biocarta	http://www.biocarta.com/
BioCyc	http://www.biocyc.org/
Biomolecular Interaction Network Database (BIND)	http://bind.ca/
Database of Interacting Proteins	http://dip.doe-mbi.ucla.edu/
Gene Expression Omnibus	http://www.ncbi.nlm.nih.gov/geo/
Human Genome Browser	http://www.ensembl.org/Homo_sapiens/
Interdom	http://interdom.lit.org.sg/help/term.php
Kyoto Encyclopedia of Genes and Genomes (KEGG)	http://www.genome.jp/kegg/

Molecular Interactions Database (MINT)	http://mint.bio.uniroma2.it/mint/
National Center for Biotechnology Information (NCBI)	http://www.ncbi.nlm.nih.gov/
Online Mendelian Inheritance in Man (OMIM)	http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=OMIM
OmniViz	http://www.omniviz.com/applications/omni_viz.htm
Pathway Enterprise	http://www.omniviz.com/applications/pathways.htm
Reactome	http://www.reactome.org/
Transpath	http://www.biobase.de/pages/products/transpath.html
UCSC Genome Bioinformatics	http://genome.ucsc.edu/index.html?org=Human
UniGene	http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=unigene

For some genes the available public annotation was extensive, whereas for others very little was known about a gene's function. Customized analysis was therefore performed to characterize genes that corresponded to this latter class. Importantly, the presence of rare splice variants and artifactual ESTs was carefully evaluated. Subsequent cluster analysis of novel ESTs provided an indication of additional gene content in some cases. The resulting clusters were graphically displayed against the genomic sequence, providing indications of separate clusters that may contribute to the same gene, thereby facilitating development of confirmatory experiments in the laboratory. While much of this

information was available in the public domain, the customized analysis performed revealed additional information not immediately apparent from the public genome browsers.

A unique consensus sequence was constructed for each splice variant and a trained reviewer assessed each alignment. This assessment included examination of all putative splice junctions for consensus splice donor/acceptor sequences, putative start codons, consensus Kozak sequences and upstream in-frame stops, and the location of polyadenylation signals. In addition, conserved noncoding sequences (CNSs) that could potentially be involved in regulatory functions were included as important information for each gene. The genomic reference and exon sequences were then archived for future reference. A master assembly that included all splice variants, exons and the genomic structure was used in subsequent analyses (*i.e.*, analysis of polymorphisms). Table 10 lists gene clusters based on the publicly available EST and cDNA clustering algorithm, ECGene.

An important component of these efforts was the ability to visualize and store the results of the data mining efforts. A customized version of the highly versatile genome browser GBrowse (http://www.gmod.org/) was implemented in order to permit the visualization of several types of information against the corresponding genomic sequence. In addition, the results of the statistical analyses were plotted against the genomic interval, thereby greatly facilitating focused analysis of gene content.

Computational Analysis of Genes and GeneMaps

In order to assist in the prioritization of candidate genes for which minimal annotation existed, a series of computational analyses were performed that included basic BLAST searches and alignments to identify related genes. In some cases this provided an indication of potential function. In addition, protein domains and motifs were identified that further assisted in the understanding of potential function, as well as predicted cellular localization.

A comprehensive review of the public literature was also performed in order to facilitate identification of information regarding the potential role of candidate genes in the pathophysiology of Crohn's disease. In addition to the standard review of the literature, public resources (Medline and other online databases) were also mined for information regarding the involvement of candidate genes in specific signaling pathways. A variety of pathway and yeast two hybrid databases were mined for information regarding protein-protein interactions. These included BIND, MINT, DIP, Interdom, and Reactome, among others. By identifying homologues of genes in the Crohn's candidate regions and exploring whether interacting proteins had been identified already, knowledge regarding the GeneMaps for Crohn's disease was advanced. The pathway information gained from the use of these resources was also integrated with the literature review efforts, as described above.

Genes identified in the WGAS and subsequent fine-mapping studies for Crohn's disease (CD) were evaluated using the Ingenuity Pathway Analysis application (IPA, Ingenuity systems) in order to identify direct biological interactions between these genes, and also to identify molecular regulators acting on those genes (indirect interactions) that could be also involved in CD. The purpose of this effort was to decipher the molecules involved in contributing to CD. These gene interaction networks are very valuable tools in the sense that they facilitate extension of the map of gene products that could represent potential drug targets for CD.

Expression Studies

In order to determine the expression patterns for genes, relevant information was first extracted from public databases. The UniGene database, for example, contains information regarding the tissue source for ESTs and cDNAs contributing to individual clusters. This information was extracted and summarized to provide an indication in which tissues the gene was expressed. Particular emphasis was placed on annotating the tissue source for bona fide ESTs, since many ESTs mapped to Unigene clusters are artifactual. In addition, SAGE and microarray data, also curated at NCBI (Gene Expression Omnibus),

provided information on expression profiles for individual genes. Particular emphasis was placed on identifying genes that were expressed in tissues known to be involved in the pathophysiology of Crohn's disease, e.g. intestinal and immune system tissues.

Polymorphism analysis

Polymorphisms identified in candidate genes, including those from the public domain as well as those identified by sequencing candidate genes and regions, are evaluated for potential function. Initially, polymorphisms are examined for potential impact upon encoded proteins. If the protein is a member of a gene family with reported 3-dimensional structural information, this information is used to predict the location of the polymorphism with respect to protein structure. This information provided insight into the potential role of polymorphisms in altering protein or ligand interactions, as well as suitability as a drug target. In a second phase of analysis we evaluate the potential role of polymorphisms in other biological phenomena, including regulation of transcription, splicing and mRNA stability, etc. There are many examples of the functional involvement of naturally occurring polymorphisms in these processes. As part of this analysis, polymorphisms located in promoter or other regulatory elements, canonical splice sites, exonic and intronic splice enhancers and repressors, conserved noncoding sequences and UTRs are localized.

Example 6: *SNP and Polymorphism Discovery (SNPD)*

Candidate regions are selected for sequencing in order to identify all polymorphisms. In cases where the critical interval, identified by fine mapping, is relatively small (~50 kb), the entire region, including all introns, is sequenced to identify polymorphisms. In situations where the region is large (>50 kb), candidate genes are prioritized for sequencing, and/or only functional gene elements (promoters, exons and splice sites) are sequenced.

The samples sequenced are selected according to which haplotypes contribute to the association signal observed in the region. The purpose is to select a set of samples that covered all the major haplotypes in the given region. Each major haplotype must be present in a few copies. The first step therefore consisted of determining the major haplotypes in the region to be sequenced.

Once a region is defined with the two boundary markers, all the markers used in fine mapping that are located within the region are used to determine the major haplotypes. Long haplotypes covering the whole region are thus inferred using the middle marker as an anchor. The results included two series of haplotype themes that define the major haplotypes, comparing the cases and the controls. This exercise is repeated using an anchor in the peripheral regions to ensure that major haplotype subsets that are not anchored at the original middle marker are not missed.

Once the major haplotypes are determined as described above, appropriate genomic DNA samples are selected such that each major haplotype and haplotype subset were represented in at least two to four copies.

The sequencing protocol included the following steps, once a region was delimited:

1. Primer design

The design of the primers is performed using a proprietary primer design tool. A primer quality control step was included in the primer design process. Primers that successfully passed the control quality process are synthesized by Integrated DNA Technologies (IDT). The sense and anti-sense oligos are separated such that the sense oligos were placed on one plate in the same position as their anti-sense counterparts on another plate. Two additional plates are created from each storage plate, one for use in PCR and the other for sequencing. For PCR, the sense and anti-sense oligos of the same pair are combined in the same well to achieve a final concentration of 1.5 μM for each oligonucleotide.

2. PCR optimization

PCR conditions are optimized by testing a variety of conditions that included varying salt concentrations and temperatures, as well as including various additives. PCR products are checked for robust amplification and minimal background by agarose gel electrophoresis.

3. PCR on selected samples

PCR products used for sequencing are amplified using the conditions chosen during optimization. The PCR products are purified free of salts, dNTPs and unincorporated primers by use of a MultiScreen PCR384 filter plate manufactured by Millipore. Following PCR, the amplicons are quantified by use of a lambda/Hind III standard curve. This is done to ensure that the quantity of PCR product required for sequencing had been generated. The raw data is measured against the standard curve data in Excel by use of a macro.

4. Sequencing

Sequencing of PCR products is performed by DNA Landmarks using ABI 3730 capillary sequencing instruments.

5. Sequence analysis

The ABI Prism SeqScape software (Applied Biosystems) is used for SNP identification. The chromatogram trace files are imported into a SeqScape sequencing project and the base calling is automatically performed. Sequences are then aligned and compared to each other using the SeqScape program. The base calling is checked manually, base by base; editing was performed if needed.

Example 7: *Ultra Fine Mapping (UFM)*

Once polymorphisms are identified by sequencing efforts as described in Example 6, additional genotyping of all newly found polymorphisms is performed on the samples used in the fine mapping study. Various types of genotyping

assays may need to be utilized based on the type of polymorphism identified (*i.e.*, SNP, indel, microsatellite). The assay type can be, but is not restricted to, Sentrix Assay Matrix on Illumina BeadStations, microsatellite on MegaBACE, SNP on ABI or Orchid. The frequencies of genotypes and haplotypes in cases and controls are analyzed in a similar manner as the GWS and fine mapping data. By examining all SNPs in a region, polymorphisms are identified that increase an individual's susceptibility to Crohn's disease. The goal of ultra-fine mapping is to identify the polymorphism that is most associated with disease phenotype as part of the search for the actual DNA polymorphism that confers susceptibility to disease. This statistical identification may need to be corroborated by functional studies.

All publications, patents and patent applications mentioned in the specification and reference list are herein incorporated by reference in their entirety for all purposes. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention that are obvious to those skilled in molecular biology, genetics, or related fields are intended to be within the scope of the following claims.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See, for example, Molecular Cloning A Laboratory Manual, 2nd Ed., ed. by Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory Press: 1989); DNA Cloning,

Volumes I and H (D. N. Glover ed., 4); Oligonucleotide Synthesis (M. J. Gait ed., 1984); Mullis *et al.* U.S. Patent No. 4.683,195; Nucleic Acid Hybridization (B.D. Hames & S. J. Higgins eds. 1984); Transcription And Translation (B. D. Haines & S. J. Higgins eds. 1984); Culture Of Animal Cells (R. 1. Freshney, Alan R. Liss, Inc., 1987); Immobilized Cells And Enzymes (IRL Press, 1986); B. Perbal, A Practical Guide To Molecular Cloning (1984); the treatise, Methods In Enzymology (Academic Press, Inc., N.Y.); Gene Transfer Vectors For Mammalian Cells (J.H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); Methods In Enzymology, Vols. 154 and 155 (Wu *et al.* eds.), Immunochemical Methods In Cell And Molecular Biology (Mayer and Walker, eds., Academic Press, London, 1987); Handbook Of Experimental Immunology, Volumes I-IV (D. M. Weir and C. C. Blackwell, eds., 1986); Manipulating the Mouse Embryo, (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986).

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Table 1. List of Crohn's disease candidate regions identified from the genome wide scan and Fine Mapping association analyses. The first column denotes the region identifier. The second and third columns correspond to the chromosome and cytogenetic band, respectively. The fourth and fifth columns correspond to the chromosomal start and end coordinates of the NCBI genome assembly derived from build 35 (B35).

RegionID	Chr	Cytogenetic Band	B35 Start	B35 End
1	1	1p34.2	41335664	41468641
2	1	1p34.2	41725287	42149484
3	1	1p31.3	61493160	61818417
4	1	1p31.3	62624940	62738450
5	1	1p31.1	76261254	76767176
6	1	1p31.1	81954224	82346866
7	1	1p22.3	86515457	86661061
8	1	1p22.2	89156986	89467692
9	1	1q23.3	161010660	161355183
10	1	1q23.3	161892236	162636358
11	1	1q25.3	179252269	179297606
12	1	1q25.3	180891276	181395555
13	1	1q31.3	191642650	191784878
14	1	1q32.1	201183785	201327556
15	1	1q41	217651547	218392303
16	1	1q42.12	221819332	222143412
17	2	2p25.2	4478209	4998554
18	2	2p25.1	10640487	11185834
19	2	2p16.1	60172290	60439045
20	2	2p14	65423719	66015933
21	2	2p14	67379633	67990630
22	2	2p13.3	69497944	70207932
23	2	2q13	113240198	113589249
24	2	2q23.3	152014490	152605675
25	2	2q24.3	167402006	168179485
26	2	2q31.1	175467634	175742264
27	2	2q32.1	186240056	186785784
28	2	2q33.1	198427607	199071714
29	2	2q33.1	203044037	203384037
30	2	2q35	215864845	216015526
31	3	3p26.3	668942	1448261
32	3	3p26.1	6200016	6312319
33	3	3p25.3	10115115	10311291
34	3	3p23	34828660	35249754
35	3	3p22.1	43594314	44252343
36	3	3p21.1	53921874	54060940
37	3	3p14.1	69527828	70257951
38	3	3p12.2	83105104	83497400
39	3	3q13.11	106260663	106845366
40	3	3q13.33	122864870	123261660

41	3	3q21.2	126402467	126511339
42	3	3q24	146954460	147321593
43	3	3q25.2	155804001	156127683
44	3	3q26.32	178142223	178352200
45	3	3q29	195291780	195433210
46	4	4p15.32	15729803	15902068
47	4	4p15.1	33517232	34180581
48	4	4p14	37194643	37294293
49	4	4p13	42090601	42460703
50	4	4p13	43033226	43496420
51	4	4q12	54279961	54623925
52	4	4q12	56117823	56479466
53	4	4q13.2	68502349	68686090
54	4	4q21.3	87970574	88986794
55	4	4q22.3	96334060	96479793
56	4	4q25	114255783	114323984
57	4	4q28.2	129904606	130050868
58	4	4q31.23	150113835	150331683
59	4	4q31.3	155677659	155819753
60	4	4q34.3	181808584	182022355
61	5	5p15.31	8445780	8453859
62	5	5p15.1	17247832	17382406
63	5	5p14.1	24920585	25545459
64	5	5p13.3	33584771	33659517
65	5	5q11.2	55976820	56275126
66	5	5q13.3	76622129	77283634
67	5	5q14.1	80994757	81132011
68	5	5q21.1	102159866	102200395
69	5	5q21.2	103211806	103280273
70	5	5q22.2	112035079	112268058
71	5	5q34	162824472	162944198
72	5	5q34	163672287	164353655
73	5	5q35.2	174814435	175191788
74	6	6p24.2	11280969	11311011
75	6	6p22.3	17419495	17905586
76	6	6p22.3	21140661	21462981
77	6	6p22.2	24477494	24767050
78	6	6p22.1	28228380	28571555
79	6	6p22.1	28735448	29405645
80	6	6p22.1	29761165	30429340
81	6	6p21.31	35927885	36523881
82	6	6p12.2	52558406	52993732
83	6	6p11.2	57753535	62265082
84	6	6q12	64808644	65206215
85	6	6q14.1	78283418	78556850
86	6	6q15	89256799	89648577
87	6	6q16.3	100883255	102084749
88	6	6q16.3	104164733	104648730
89	6	6q22.33	128988117	129448891

90	6	6q23.2	132952928	133286730
91	6	6q24.1	141147720	141312353
92	6	6q25.3	159060617	159192856
93	6	6q26	164223534	164579745
94	6	6q27	167538046	168149491
95	7	7p21.2	13749009	13858986
96	7	7q31.31	119182246	120451698
97	8	8p23.1	11897394	12747610
98	8	8p22	17021982	17086787
99	8	8p22	17804143	17889727
100	8	8q11.21	49970615	50669075
101	8	8q22.1	93426382	93808252
102	8	8q22.3	101940093	102202011
103	8	8q22.3	102502616	102989689
104	8	8q24.12	119397114	119636900
105	8	8q24.13	123884006	123924246
106	9	9q21.13	71307215	72145163
107	9	9q21.31	78411043	78454794
108	9	9q21.33	85928227	86045545
109	9	9q22.2	90800413	90920214
110	9	9q31.1	100188496	100687277
111	9	9q31.3	108740705	109013816
112	9	9q33.2	120936639	121769741
113	9	9q34.13	131664675	132174041
114	10	10p13	13559749	13750842
115	10	10p13	13958759	14485735
116	10	10p12.31	19606357	20176365
117	10	10p12.1	25999792	26446222
118	10	10p12.1	27027421	27250622
119	10	10p11.21	36287333	36680305
120	10	10q11.21	43793799	43947838
121	10	10q21.1	57360183	58912724
122	10	10q21.3	64375192	65234429
123	10	10q22.2	76271373	76969487
124	10	10q22.3	82495793	82613241
125	10	10q23.1	84038722	84460638
126	10	10q24.1	97574013	98176591
127	10	10q24.2	100332431	100541536
128	10	10q25.1	110602526	110890130
129	10	10q25.2	114027468	114179121
130	10	10q25.2	114552665	114937150
131	10	10q26.13	126062195	126247170
132	11	11p15.1	20552900	21088360
133	11	11p14.1	27543012	27659764
134	11	11p13	31269473	31904703
135	11	11q12.3	62431179	62940407
136	11	11q13.3	68497528	69272914
137	11	11q21	92282045	92736858
138	11	11q21	95842433	96271128

139	11	11q22.3	103578975	103844029
140	11	11q24.1	122348745	122476668
141	12	12p12.3	16083756	16626906
142	12	12p12.3	18189189	18379331
143	12	12p12.3	18959566	19668264
144	12	12p12.1	23984329	24127834
145	12	12p11.21	33041207	33694027
146	12	12q12	40879703	40991213
147	12	12q12	41341830	41548186
148	12	12q12	41788288	41898954
149	12	12q14.1	58669336	58784955
150	12	12q21.32	85600523	86709812
151	12	12q24.31	124113077	124615038
152	13	13q12.3	28993758	29452360
153	13	13q13.1	31737224	31804729
154	13	13q14.2	47287583	47644365
155	13	13q14.3	50554432	50785140
156	13	13q21.32	65187336	65831413
157	13	13q21.33	68495875	68573704
158	13	13q22.1	73760424	73911046
159	13	13q31.1	79755980	80261057
160	13	13q33.3	106243933	106377871
161	14	14q11.2	23880999	24361921
162	14	14q13.1	33014942	33351066
163	14	14q21.1	36970890	37145037
164	14	14q21.2	43692035	44097440
165	14	14q22.3	55009781	55308828
166	14	14q31.1	82147133	82226304
167	14	14q31.3	86840424	87482935
168	14	14q32.2	97942526	98137530
169	15	15q13.3	29084144	29317050
170	15	15q15.1	40174495	40252233
171	15	15q15.3	42022068	42602452
172	15	15q21.3	51163737	51284586
173	15	15q22.2	58528133	58636062
174	15	15q22.31	62303537	63028788
175	15	15q22.31	63570070	63746783
176	15	15q26.1	88573386	88993717
177	16	16p12.3	20859599	20985943
178	16	16p12.1	25578533	26460770
179	16	16p12.1	27529217	28027257
180	16	16q12.1	50178482	50340590
181	16	16q21	57771254	57892785
182	16	16q22.1	65329111	65645146
183	17	17p11.2	19381812	19728534
184	17	17q11.2	28595673	28955705
185	17	17q23.3	58581369	58872498
186	18	18q11.2	17660599	17971699
187	18	18q11.2	23189662	23258373

188	18	18q12.3	39397135	39544083
189	18	18q21.1	44810722	45689548
190	18	18q21.1	45866536	46338558
191	18	18q21.31	52559917	52896047
192	18	18q21.32	54839050	55191422
193	19	19p13.11	18310238	18418673
194	20	20p13	947784	1046954
195	20	20p12.2	10313407	10371753
196	20	20p12.1	16842293	17059967
197	21	21q11.2	14572877	14884234
198	21	21q21.1	18675802	19109902
199	21	21q22.12	36165999	36457767
200	22	22q12.2	29573867	29722757
201	X	Xp22.2	13760724	13971625
202	X	Xp22.11	24252580	24289796
203	X	Xp11.4	39060851	39235645
204	X	Xq21.2	84892457	85107122
205	X	Xq21.33	95234712	95478145
206	X	Xq23	110155224	110269647
207	X	Xq27.3	146042507	146210157
208	X	Xq28	147481778	147576685

Table 2. Results from the Crohn's Disease genome wide association study using the Quebec Founder Population (QFP) for 208 associated regions. Individual SNP markers genotyped in the genome wide scan are presented in each row of the table. The corresponding chromosome region ID is presented as identified in Table 1. The chromosome number and coordinate of the SNP according to the NCBI genome assembly build 35 are indicated in columns 2 and 3. The RS# column corresponds to the NCBI dbSNP identifier for the SNP. The Seq ID is the unique numerical identifier for this SNP in the sequence listing for this patent. The column labeled Flanking Sequence corresponds to 21 bp of nucleotide sequence centered at the SNP, which is coded using the standard degenerate naming system. The remainder of the table lists -log10 p values for association of the indicated haplotype centered at the corresponding SNP with the disease as described in the text, using SingleType, LDSTATS V2 and V4. Values for the association of single markers, as well as 3, 5, 7 and 9 marker haplotype windows are shown (see text for explanation of statistical calculations).

						SingleType		LDSTATS v2					LDSTATS v4				
Region ID	Chromosome	B35 Position	RS#	Seq ID	Flanking Sequence	GenotypePValue	AllelePValue	Single Marker	W03	W05	W07	W09	Single Marker	W03	W05	W07	W09
1	1	41335664	6672508	8964	TATGGCTTTGSGGACAGATAA	0.28	0.56	0.56	0.46	0.17	0.10	0.16	0.52	0.44	0.17	0.09	0.16
1	1	41347842	11209701	8965	TCCAAATAATRAATAACTTGG	1.09	1.27	1.27	0.56	0.24	0.12	0.63	1.16	0.57	0.25	0.13	0.64
1	1	41353549	12121121	8966	ATAACTTTCTRTTAAACCACT	0.37	0.68	0.68	0.58	0.52	0.82	1.09	0.65	0.68	0.56	0.84	1.07
1	1	41360416	17358122	8967	GAGAATGCATYGTATCCCAGA	0.01	0.00	0.00	0.62	1.37	1.60	2.12	0.00	0.64	1.33	1.49	1.90
1	1	41372035	10493094	8968	GTGAGATCTTKTATGTTTCTT	1.18	1.36	1.36	1.36	1.65	2.42	2.44	1.27	1.57	1.57	2.15	2.18
1	1	41395566	10524	8969	GGCTTTGGACYATACTTTGGG	1.89	2.19	2.17	1.31	2.16	2.47	1.93	2.07	1.50	1.99	2.27	1.77
1	1	41412997		8970	TTATTGTGTGRACTGAGGAAG	-	-	-	-	-	-	-	-	-	-	-	-
1	1	41413914	1892425	8971	AGGTATTCCCRGGTAAAGAGA	-	-	-	-	-	-	-	-	-	-	-	-
1	1	41452696	16828071	8972	AACCTAGATGRCCAGGAAGAG	0.79	0.23	0.23	1.40	1.94	1.91	1.41	0.20	1.38	1.83	1.80	1.38
1	1	41463496	17362424	8973	TGCTATTTCTKGGTTATCCAT	0.80	0.12	0.12	0.46	1.05	1.09	0.82	0.08	0.48	1.07	1.08	0.86
1	1	41468641	11209895	8974	TGGATAATCAYGTTTTAATAT	0.14	0.35	0.38	0.13	0.07	0.51	1.25	0.34	0.11	0.07	0.52	1.22
2	1	41725287	943374	8975	CACATGGACARGAACATCACC	0.10	0.21	0.22	0.18	0.15	0.43	0.35	0.20	0.18	0.17	0.50	0.35
2	1	41732685	4578215	8976	AGCTAATTCAYCTACTAAGTT	0.41	0.10	0.10	0.26	0.50	0.10	0.16	0.07	0.25	0.51	0.12	0.17
2	1	41740531	6700352	8977	GAAACCCTAAKTGTGTGAGAA	0.22	0.39	0.39	0.30	0.13	0.06	0.13	0.34	0.31	0.14	0.05	0.12
2	1	41749405	6661784	8978	TTACAAAAACWAAATAGGAAC	0.17	0.30	0.30	0.15	0.02	0.12	0.41	0.26	0.13	0.02	0.12	0.43
2	1	41755757	7552928	8979	CTGGTCAGCCYCACACCTGCA	0.54	0.80	0.80	0.07	0.02	0.27	0.25	0.75	0.06	0.02	0.31	0.27
2	1	41763118	6656183	8980	ACCATTATGTRGGAGAAGAGG	0.20	0.17	0.17	0.19	0.24	0.14	0.24	0.16	0.18	0.28	0.16	0.25
2	1	41777183	10890156	8981	TTAACGTGGCYAAATCCAACC	0.11	0.24	0.24	0.35	0.37	0.16	0.76	0.22	0.36	0.39	0.17	0.78
2	1	41790716	10890161	8982	CACCCAAACAYACTGTTGAAT	0.58	1.01	1.01	0.81	0.64	0.42	0.22	0.94	0.80	0.66	0.42	0.21
2	1	41791210	943376	8983	CCCTGGCCCCRATTCCTTTGT	1.31	1.36	1.37	0.25	0.94	0.85	0.41	1.32	0.22	0.95	0.83	0.39
2	1	41808486	17372813	8984	ATGAATAAATYAAGTTTGGTT	0.61	0.60	0.60	0.53	1.04	0.75	0.68	0.56	0.53	1.07	0.73	0.68
2	1	41815828		8985	CCAAAGCTCTYATCATTCCCC	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41826143		8986	AACTACTGACMTGACCATCTG	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41840316		8987	AGACCGAGGCWCAAAACACTG	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41855151	6698845	8988	CGGGAATAGCYTTGGGTCTGT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41861453	12088923	8989	ATACTGAGACWTCTAGAACAA	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41871036	6667709	8990	TTGCATCCCCYGTGGTGTTCA	1.30	1.73	1.67	2.16	1.32	0.33	1.19	1.62	2.32	1.30	0.31	1.19
2	1	41881101	1371805	8991	AAGGGCTTCAMAAGGTGACAT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41886787	11210520	8992	TGCTGGGGAGRTGATGGGTTC	1.36	1.34	1.34	2.24	0.98	0.98	0.83	1.14	2.72	0.99	0.99	0.83
2	1	41899690	2365571	8993	CAACTCAGGGMCATCATCACA	2.08	2.69	2.69	1.74	2.19	1.40	0.58	2.62	1.91	1.93	1.35	0.60
2	1	41906731		8994	ACCCAGTCCCWGGCAGGTTCT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41912668		8995	GAATAGTGGTRTGCATCAGAT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41919549	7517484	8996	TCCGTTTACAYAGAAAAATGC	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41928101	349439	8997	TTCTCTGACTKCTTCAAAGGT	0.47	0.54	0.54	1.52	1.43	1.07	1.02	0.51	1.52	1.39	1.04	1.00
2	1	41936249	732524	8998	CCAGCCTTGGKAATTTTAAGA	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41942746	12563071	8999	ACTTGGACCCYAGAAGTCACT	0.52	0.73	0.73	0.94	0.93	0.83	2.23	0.69	0.93	0.92	0.84	2.05
2	1	41952528	484667	9000	GGCATCAACAYGGCTTCTGAA	1.13	1.61	1.61	1.09	0.58	2.54	1.87	1.53	1.36	0.61	2.35	1.78
2	1	41958831	588203	9001	TTTCAAGCACWTTCATACTAA	0.94	1.39	1.39	0.79	0.92	1.53	2.11	1.30	0.98	0.94	1.46	1.99
2	1	41970688	16828739	9002	TGTTCCTCACRCTTTCACCAA	1.19	1.64	1.73	0.79	1.36	1.50	1.93	1.66	0.85	1.32	1.45	1.80
2	1	41977936	11582555	9003	CACATTTCACRGCATATGCGC	0.12	0.25	0.25	0.91	1.19	1.14	1.84	0.22	0.98	1.21	1.10	1.72
2	1	41983849	17365632	9004	ATCCGAGACAYCAGACTGAGA	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41990428	6662131	9005	TATTCTCACARCACTTTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	41998019		9006	TGGGGGTGATSCCAGTAATGT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	42003886	6670896	9007	CAGTAGAATARAACAGGTGAT	0.80	1.20	1.18	1.33	1.32	1.29	0.49	1.09	1.39	1.30	1.30	0.50
2	1	42009251	945814	9008	AGATTCACAGYGTCTAAGGTT	0.38	0.02	0.02	1.08	1.16	0.55	0.22	0.00	1.14	1.10	0.58	0.21
2	1	42019930	2993120	9009	TGGCATAGGAMAGTCATGAGC	0.70	1.15	1.15	0.35	1.03	0.37	0.20	1.13	0.35	1.01	0.38	0.23
2	1	42029363	1325502	9010	TTCCACTCCCRAAACATGCAG	0.38	0.18	0.18	0.36	0.12	0.36	0.30	0.14	0.34	0.11	0.36	0.28
2	1	42037798		9011	ACATTCCTGASACATGTTTAT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	42043437	1327386	9012	AACTCTACTGRAAACACTAAG	0.19	0.45	0.45	0.48	0.11	0.13	0.66	0.39	0.49	0.10	0.14	0.70
2	1	42049206	16828903	9013	TATGTACATCYAGAAACTGAG	-	-	-	-	-	-	-	-	-	-	-	-
2	1	42070024	1325504	9014	GAAACTCGTCWAATCCACAGA	0.08	0.22	0.22	0.61	0.20	0.36	0.15	0.20	0.66	0.15	0.35	0.12
2	1	42092393	658303	9015	AGATTGGACAYGGAAAGAAAG	0.06	0.02	0.02	0.51	0.36	0.18	0.26	0.00	0.51	0.37	0.18	0.28
2	1	42105774	16828935	9016	TTTGATGTAGRAAAAAAATAT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	42113537	4660592	9017	GAGAAGCATGSGAGCCTTCCT	-	-	-	-	-	-	-	-	-	-	-	-
2	1	42140034	7553696	9018	AAGTGGAAAGYAAGTTGCTGT	0.92	0.91	0.91	0.59	0.22	0.18	0.41	0.78	0.62	0.22	0.22	0.40
2	1	42149484	3909262	9019	TAAATGCTATSATCAATAACA	0.24	0.52	0.47	0.35	0.13	0.16	0.25	0.44	0.34	0.13	0.16	0.26
3	1	61493160	2782541	9020	TCGATTTTCTRATGTTAGAGG	0.34	0.46	0.46	0.39	0.11	0.17	0.78	0.43	0.40	0.11	0.16	0.81
3	1	61504682	6694984	9021	TACTCTGAACRTTCTGTGGGG	0.06	0.01	0.02	0.34	0.10	0.04	0.06	0.00	0.34	0.13	0.04	0.05
3	1	61520071	6704173	9022	TAGGCCATCAMATCCCATCCC	0.11	0.17	0.17	0.15	0.07	0.02	0.04	0.13	0.15	0.07	0.03	0.03
3	1	61532093	17121983	9023	AAATGTTCACSGATCAATATG	0.50	0.04	0.04	0.01	0.06	0.02	0.04	0.00	0.01	0.06	0.03	0.03
3	1	61537819	6587918	9024	TCTTTATTCTRATCTGTACTA	0.04	0.18	0.12	0.07	0.23	0.03	0.02	0.09	0.07	0.24	0.02	0.02
3	1	61543911	1125777	9025	TGGATGACTGYGTTGCACCAC	0.07	0.25	0.25	0.59	0.15	0.11	0.11	0.22	0.59	0.16	0.09	0.10
3	1	61549609	7533561	9026	CCTCACAAGTRCTGGATAAAG	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61554986	12738028	9027	CATAGTGGGCMCTTCATAATT	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61563231	6686758	9028	TTTGTGGAGAKTCCATGAAGA	1.79	0.96	0.94	0.24	0.31	0.17	0.15	0.86	0.23	0.29	0.20	0.17
3	1	61571823	2474388	9029	GTACATTAATKCTAATCCTCA	0.51	0.83	0.74	0.34	0.21	0.37	0.84	0.71	0.32	0.24	0.40	0.85
3	1	61578477	17122148	9030	CCTCAAAATAYAGTTGATGAA	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61584562	10889221	9031	TTGCCAGACCRAGAATCAAAG	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61595452	2474371	9032	CTGATGAAATRATTTTAGTGT	0.36	0.69	0.73	0.27	0.09	1.17	1.43	0.70	0.26	0.08	1.19	1.41
3	1	61603354	7543206	9033	AACAACAAAGSCACTGAATTT	0.30	0.50	0.54	0.10	1.52	1.72	1.63	0.50	0.09	1.46	1.66	1.57
3	1	61609988	2207790	9034	GTTCAGTTCTRTCTTCCCTGG	0.13	0.02	0.04	2.28	0.81	1.25	1.60	0.02	2.46	0.78	1.22	1.54
3	1	61618911	2207789	9035	AAACGCATTGSAATTCCAAGG	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61631191		9036	TGCAGAGGCASTGCAGATTTT	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61637097		9037	ATCATTCGTGYGCAGAGGGCC	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61643372	9436212	9038	CAAAATGTAGRCATAAGGCAT	3.75	4.20	4.11	1.87	1.22	0.91	0.78	3.97	1.87	1.16	0.88	0.79
3	1	61662800	17122262	9039	TACATGGGAAKCTGGCAATAA	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61668419	7555153	9040	AAACAATCAAYCAAAGCATCA	0.06	0.22	0.22	2.72	1.24	0.79	0.80	0.22	2.92	1.20	0.79	0.79
3	1	61673974	3890764	9041	ACAACGGAACRTGCTTACATA	0.04	0.04	0.04	0.05	1.74	0.82	1.31	0.00	0.03	1.65	0.81	1.30
3	1	61676448		9042	TTGGTTCTGAYATCAAGCGGT	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61701847	11207758	9043	GGGGTAACTAYAAAAACATAA	0.10	0.16	0.16	0.50	0.48	0.73	0.79	0.12	0.52	0.51	0.74	0.79
3	1	61706705	7529417	9044	AATAGTAACARCCCTCATTTT	0.75	1.15	1.15	0.63	0.75	0.32	0.39	1.12	0.63	0.76	0.36	0.43

3	1	61726898	1933310	9045	CTGTAGTTTTMTTTCTCTTTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	1	61737059	17122409	9046	ATAACAGAAGRTCCACATAAA	0.97	1.30	1.30	0.34	0.74	0.24	0.12	1.28	0.32	0.74	0.21	0.12		
3	1	61748006	6587933	9047	CTCAAATATCYTTACATTTCA	0.77	0.94	0.94	0.49	0.17	0.69	0.32	0.90	0.52	0.18	0.70	0.32		
3	1	61760033		9048	ATTGGACAGCRGTATACTAGA	-	-	-	-	-	-	-	-	-	-	-	-		
3	1	61765987	2365263	9049	ACTTTCATAARCCTGTATTCC	0.05	0.17	0.17	0.53	0.32	0.27	0.37	0.17	0.55	0.34	0.28	0.35		
3	1	61772234	2365269	9050	ACGTGAAAAGRTCACCCCACA	-	-	-	-	-	-	-	-	-	-	-	-		
3	1	61781761	17122486	9051	GCTTTTGCCGYTTCAACAGCA	0.53	0.63	0.63	0.35	0.23	0.50	0.84	0.59	0.33	0.24	0.49	0.85		
3	1	61792474	17122523	9052	CAATCGCCTAYTGAAAAAAAA	-	-	-	-	-	-	-	-	-	-	-	-		
3	1	61799804	12137416	9053	TTATATGGGAYAGTTTAGGGC	0.47	0.37	0.37	0.37	0.17	0.94	0.66	0.33	0.37	0.16	0.89	0.66		
3	1	61805309	1999881	9054	CCAATAGTGGSTGAGTGTAAG	0.55	0.91	0.86	0.13	2.06	0.68	0.64	0.81	0.11	1.99	0.72	0.67		
3	1	61818417	10889246	9055	CACAATAGAAYGTCTGTCTGT	0.28	0.56	0.59	1.33	0.33	1.23	0.47	0.56	1.34	0.31	1.19	0.48		
4	1	62624940	10158897	9056	AACTGTTATTYATGATATACT	1.45	1.71	1.71	0.87	1.37	0.36	0.22	1.65	0.96	1.29	0.37	0.21		
4	1	62626999	783291	9057	GGGCGGGAAARGCTAAATTCT	-	-	-	-	-	-	-	-	-	-	-	-		
4	1	62652118	1979722	9058	TACTACATCTRCCAATCCGCT	1.38	1.61	1.65	2.29	1.55	0.63	0.31	1.55	2.79	1.45	0.64	0.34		
4	1	62662879	10889332	9059	CCTACTATTTYGAGGGAAAAG	0.92	1.26	1.29	2.04	2.15	0.73	0.42	1.24	2.28	2.03	0.73	0.43		
4	1	62665394	10493326	9060	CTCTAACTAARGTGAGCTGCA	1.64	2.22	2.26	1.60	1.68	1.18	0.53	2.16	1.84	1.66	1.18	0.51		
4	1	62689440	1781212	9061	CATGTCTTTARGAAATTTATG	-	-	-	-	-	-	-	-	-	-	-	-		
4	1	62695714	1168046	9062	ACAACTATACMTATCAACATA	1.27	1.54	1.53	1.18	1.21	0.99	1.00	1.52	1.39	1.21	1.00	1.00		
4	1	62705641	12403207	9063	AATACGGGGCYTTTTCCCATA	1.36	1.65	1.65	0.93	0.90	1.03	0.90	1.60	1.12	0.88	1.02	0.88		
4	1	62714572	1168017	9064	TACTAAAACCRCAAAATCTCT	1.06	1.35	1.35	0.91	0.68	0.82	0.73	1.29	1.02	0.72	0.83	0.73		
4	1	62717020		9065	CAAGGAAATAYTGGCTGTACT	-	-	-	-	-	-	-	-	-	-	-	-		
4	1	62732837	10159255	9066	TCCACTATCAMCAGTGGTACA	1.36	1.65	1.65	1.51	0.66	0.33	0.71	1.57	1.62	0.67	0.37	0.70		
4	1	62738450	10889343	9067	TACTTATAAAKGCAACATCTC	1.33	1.59	1.59	0.88	0.85	0.31	0.27	1.56	0.87	0.86	0.29	0.28		
5	1	76261254	11803060	9068	GTGATTAATAYGAATAAAACA	0.23	0.22	0.22	0.14	0.69	0.40	0.62	0.13	0.12	0.69	0.42	0.60		
5	1	76267681	17660966	9069	AGGTAAGAGTRAGTTAGAGTG	0.07	0.30	0.30	0.60	0.42	0.69	0.30	0.25	0.62	0.43	0.73	0.32		
5	1	76273553	289678	9070	TCTCCCCTCARGGCTGAATGA	0.27	0.05	0.05	0.04	0.42	0.29	0.53	0.02	0.03	0.41	0.31	0.55		
5	1	76284381	491409	9071	TTAAGCACACRGAAAAATCCA	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76300101	17609927	9072	GTCAGCACAGRTCAAACATGC	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76307472	399529	9073	GCATTCACATRCAGCACAGAG	0.17	0.07	0.08	0.52	0.43	0.46	0.38	0.04	0.50	0.44	0.47	0.39		
5	1	76313327	289700	9074	ATGCATTTTAMTGGCTACCAA	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76325165	860154	9075	AGATGCAAGAYCATGTGTGTT	0.04	0.08	0.08	0.45	0.35	0.32	0.45	0.06	0.49	0.37	0.31	0.47		
5	1	76339344	1318243	9076	CTTAAAGTACKTGCTGGGAAG	0.48	0.85	0.89	0.34	0.21	0.38	0.78	0.85	0.32	0.22	0.38	0.74		
5	1	76339765	289696	9077	ACTGTGCTCCMAAATCCTCTA	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76371913	10493585	9078	GTTCATAAAGRTATAAAGATC	0.03	0.17	0.17	0.50	0.33	0.54	1.20	0.13	0.51	0.34	0.57	1.14		
5	1	76377872	481510	9079	ATGGTTGGGCWTCTATTCCAA	0.52	0.63	0.61	0.18	0.17	1.03	0.77	0.51	0.18	0.18	0.98	0.81		
5	1	76386086	3011989	9080	TTTGAAAGCTYGTGTTTATAG	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76404078	531773	9081	TGGCTTCCTTYGGTCTAGTTG	0.67	0.43	0.43	0.33	0.98	1.08	0.78	0.39	0.33	1.00	1.06	0.78		
5	1	76410225	569850	9082	CATCTGGGAGYAAGGGTCCT	0.99	0.55	0.55	1.05	1.18	0.71	0.65	0.51	1.15	1.17	0.73	0.68		
5	1	76416967	17098469	9083	ATATATGGCCMAAGTCAGCAT	1.22	1.71	1.71	0.57	0.90	0.97	1.35	1.63	0.61	0.90	0.99	1.31		
5	1	76417840		9084	TAACATAGGTRTAATACACAG	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76441932	11162104	9085	TTGGGGTTAGMTCTAGGCAGC	0.09	0.00	0.00	0.84	0.46	1.76	1.49	0.00	0.86	0.44	1.65	1.41		
5	1	76446668	6593526	9086	ACTTTATGCCRCCTTGTCTTA	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76458930	17098538	9087	CCTTGAAATCRATATAGATTT	0.48	0.75	0.74	0.45	0.65	0.61	1.47	0.66	0.43	0.69	0.63	1.47		
5	1	76467748	12124554	9088	ATTATCTCACRAGCACTCTTT	0.35	0.63	0.64	0.87	0.14	0.70	1.51	0.59	0.89	0.12	0.71	1.47		
5	1	76475806	3862905	9089	GCTGGAGGAAYAGTCAGAGGT	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76492547	12079106	9090	CATTACTAGGRAGAGTCTTGG	0.08	0.27	0.27	0.35	1.36	0.72	0.91	0.25	0.35	1.36	0.73	0.94		
5	1	76506348	10493590	9091	CTTTTGGACASTATGTATTCA	0.04	0.18	0.19	1.60	1.66	1.48	0.35	0.15	1.76	1.55	1.42	0.35		
5	1	76518295	7539896	9092	AGCAACTAATSTGCCAGATGA	0.27	0.58	0.58	2.03	3.04	0.77	0.70	0.53	2.33	2.67	0.80	0.68		
5	1	76526298	12060625	9093	ACTTTTTTTCYTTCCTGAAAA	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76534397	1325287	9094	AGAATACATCMAAAAGCATTC	0.65	0.78	0.78	1.44	2.47	2.07	0.60	0.76	1.61	2.21	1.93	0.59		
5	1	76546726	12128122	9095	CTATGCTCCARTGCTTAACAA	0.02	0.09	0.12	0.58	0.96	1.60	2.90	0.09	0.58	0.94	1.52	2.70		
5	1	76552749	1540964	9096	AATTCCAAAAMCTTGCAAATT	0.55	0.40	0.40	0.60	0.62	2.04	2.92	0.39	0.65	0.65	1.89	2.70		
5	1	76571522	12029184	9097	ATCCTGGTAAYAAGAGAGTCT	0.65	1.00	1.00	0.83	1.22	3.43	3.16	0.94	0.85	1.18	3.15	2.91		
5	1	76583737	7515898	9098	GTATTTTTCARAACAATTCAT	0.51	0.83	0.86	0.65	3.08	2.45	2.24	0.84	0.64	2.88	2.32	2.13		
5	1	76595098	6691055	9099	GACCAAAATAYCTTTTCCCCT	0.02	0.08	0.07	1.34	0.83	2.54	1.95	0.04	1.36	0.85	2.39	1.94		
5	1	76611485	4949718	9100	TGTTACTAAAYGGAAAAAAAT	0.25	0.56	0.56	0.60	0.86	0.49	0.93	0.54	0.63	0.87	0.51	0.92		
5	1	76622420	7546379	9101	CTGGAGAAGGRAACAGAGGAA	0.69	0.86	0.90	0.32	0.31	0.10	0.22	0.83	0.29	0.30	0.08	0.21		
5	1	76638280		9102	CAGAATCAAGKTACACTGTTG	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76644898	17099040	9103	GGGATTTTTAWTGTTGGCACT	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76650637	11162157	9104	ACAAATGGGGRAAGAAGGATT	0.58	0.93	0.89	0.18	0.02	0.07	0.35	0.83	0.18	0.01	0.08	0.35		
5	1	76676714	4620587	9105	CCCCACTAGAMAACAGGGTTA	0.39	0.65	0.65	0.07	0.03	0.14	0.26	0.57	0.06	0.03	0.15	0.29		
5	1	76689223	315090	9106	AGCACAGCTCRGGTATTTATG	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76702674	7525997	9107	ACATGAAAAGRGAAATTGAAG	-	-	-	-	-	-	-	-	-	-	-	-		
5	1	76713798	315076	9108	AAATAAGGACYGGAGACTCCA	0.25	0.31	0.31	0.33	0.56	0.28	0.09	0.27	0.33	0.59	0.29	0.08		
5	1	76723074	315065	9109	TTGCATAAATWTCGCCTCTTC	0.34	0.40	0.41	0.15	0.46	0.38	0.19	0.36	0.10	0.47	0.38	0.18		
5	1	76732129	984528	9110	AAAAAAACCCYTCAACCTGAA	0.03	0.11	0.11	0.22	0.14	0.19	0.08	0.08	0.21	0.13	0.21	0.08		
5	1	76754426	315029	9111	GAAAAGCTCTRGGGAGCCTGA	0.11	0.02	0.02	0.01	0.06	0.04	0.31	0.00	0.01	0.07	0.03	0.31		
5	1	76760638	12117865	9112	TAAATTTGAAYCCATGTACCA	0.03	0.12	0.12	0.02	0.05	0.03	0.02	0.09	0.02	0.06	0.03	0.02		
5	1	76767176	315040	9113	AGCTTTCCACRATCCCCTTCT	0.13	0.24	0.21	0.01	0.05	0.03	0.03	0.15	0.01	0.05	0.04	0.03		
6	1	81954224	9728563	9114	AAATAGGCATRGTAAAGAGGA	0.24	0.43	0.43	1.00	1.44	1.15	1.21	0.35	1.09	1.38	1.14	1.20		
6	1	81968259	11163377	9115	TTATATAAGAKTTCTAGGTTA	0.81	0.53	0.54	0.14	1.05	1.68	1.03	0.50	0.13	1.06	1.62	1.00		
6	1	81971374	770146	9116	TCTATTTTTGMCCTTACATGA	0.66	0.14	0.18	0.08	0.21	1.05	1.52	0.16	0.06	0.20	1.06	1.44		
6	1	81982293	697984	9117	TAGTTATGTGRGCCAAAAACA	-	-	-	-	-	-	-	-	-	-	-	-		
6	1	81993513	12731297	9118	ACATTTCAGCYTGGAAACCTG	0.17	0.11	0.11	0.16	0.02	0.10	0.46	0.10	0.15	0.02	0.09	0.50		
6	1	82006163	12022861	9119	AGTAGCAATARTAAGTGATAT	0.65	0.50	0.46	0.23	0.03	0.00	0.04	0.40	0.17	0.03	0.00	0.03		
6	1	82016304	1565602	9120	GGGAAGAAAASCTAACTGAAT	-	-	-	-	-	-	-	-	-	-	-	-		
6	1	82024137	3790944	9121	TGTCCCACCAYGAAGATGAAG	0.66	0.43	0.39	0.24	0.04	0.02	0.00	0.34	0.18	0.03	0.01	0.00		
6	1	82031954	6660563	9122	CAGGGATACTKCCGAACCACT	0.07	0.26	0.26	0.06	0.02	0.04	0.18	0.23	0.04	0.03	0.04	0.18		
6	1	82045072	12139921	9123	CTATAAAAACRAACCAAACTT	0.05	0.13	0.13	0.09	0.05	0.30	0.41	0.09	0.06	0.06	0.30	0.39		
6	1	82054388	12143946	9124	TGTGACTCGARGGATCAGATG	0.08	0.08	0.08	0.04	0.29	0.41	0.31	0.05	0.03	0.26	0.41	0.29		
6	1	82068263	284216	9125	CAAACAGCAARAAGGTAATTA	0.30	0.48	0.46	0.78	0.51	0.32	0.58	0.41	0.87	0.51	0.30	0.57		
6	1	82076694	2026596	9126	ACTCTCATAGRGGTCCCTGAT	1.00	0.99	0.99	1.03	0.96	1.36	1.74	0.93	1.07	0.97	1.29	1.70		
6	1	82085294	434619	9127	GTCTTTGGCAWTAGTTGCTAC	0.02	0.11	0.11	0.49	3.54	3.34	1.87	0.11	0.52	2.84	3.04	1.77		
6	1	82091467	284227	9128	CTTTTTACTTYGCAAGCCTTT	0.01	0.07	0.07	1.66	4.22	4.25	1.65	0.03	1.96	3.78	3.67	1.53		
6	1	82097937	10493703	9129	AAACCCATTGWATATCGCTTA	1.80	2.22	2.22	2.95	3.57	2.66	2.57	2.15	3.29	3.01	2.39	2.40		
6	1	82104262	6699460	9130	GTAGGTTAACRTTTTTATAAA	2.30	2.67	2.74	2.51	2.33	1.69	2.04	2.67	2.95	2.22	1.64	1.83		
6	1	82111348	1907675	9131	TATCAACAGCMTATTGTTAAG	0.67	1.10	1.01	1.66	2.28	1.72	1.75	0.96	1.81	2.10	1.60	1.67		
6	1	82118436	17430236	9132	CAGTATTAGCMACCCTGATGC	0.09	0.22	0.22	1.64	1.67	2.35	2.14	0.20	1.75	1.54	2.15	2.00		
6	1	82124231	12044750	9133	TTGCTTTATAKTTACTTAATC	1.31	1.84	1.84	1.40	2.04	2.08	1.87	1.76	1.50	1.76	1.93	1.75		
6	1	82134221	3828121	9134	TCAGGTGAAARTGTGGTCAGT	1.39	1.83	1.77	1.46	1.41	1.66	0.96	1.65	1.55	1.33	1.55	0.95		
6	1	82144639	2296699	9135	TTACTTAGCAKCAGGATAGCT	0.25	0.53	0.53	1.54	1.35	1.18	1.46	0.45	1.62	1.32	1.16	1.39		
6	1	82153537	6598977	9136	CTGCCTCTTGYTCTCATTTCC	0.40	0.17	0.18	1.11	1.06	1.23	1.09	0.16	1.34	1.04	1.19	1.07		
6	1	82162865	1409765	9137	ACCAGATAATSCTACATAGGT	1.49	1.88	1.88	1.02	1.03	0.77	0.52	1.81	1.12	0.98	0.82	0.53		
6	1	82170191	3790868	9138	CCATTCCCACYTTGGTTTAAG	-	-	-	-	-	-	-	-	-	-	-	-		

6	1	82176280	4579802	9139	AATCACATCTRCTTTTATATA	0.34	0.26	0.26	1.43	0.81	0.46	0.50	0.22	1.68	0.84	0.47	0.51
6	1	82184124	7527608	9140	CAGAAACCAGMATAAACTTTG	1.22	1.62	1.62	0.98	0.73	0.50	0.29	1.57	1.13	0.75	0.52	0.32
6	1	82194687	17432411	9141	AACAGAGAAGMCCCAGAGCAT	0.37	0.24	0.18	0.54	0.79	0.41	0.10	0.13	0.63	0.80	0.41	0.12
6	1	82216310	6690297	9142	CATTCCTCCTWTTAATTCTAT	-	-	-	-	-	-	-	-	-	-	-	-
6	1	82238526	4486485	9143	CACTGCGAAASTTTTCCTGAG	0.13	0.22	0.23	0.02	0.28	0.14	0.81	0.18	0.01	0.31	0.14	0.82
6	1	82254302	6598985	9144	GTATGAAAATRGGGAATGAGG	0.19	0.01	0.02	0.05	0.01	1.08	0.78	0.00	0.01	0.01	1.04	0.77
6	1	82266105	4290103	9145	GGTCATTAGTYTATTTCTCTA	0.42	0.18	0.18	0.19	0.35	0.29	1.28	0.10	0.15	0.38	0.27	1.24
6	1	82273580	962249	9146	TGGAAATGCCKCCAAGCCTAA	0.63	0.80	0.80	0.15	0.42	0.56	0.29	0.78	0.13	0.46	0.59	0.29
6	1	82283207	10493708	9147	GTGTTTTGAARATACTAACGC	0.26	0.28	0.28	0.83	0.24	0.36	0.98	0.26	0.84	0.27	0.37	0.97
6	1	82292567	11163432	9148	TTTCTAAGAGSCTTGCAAATG	0.33	0.45	0.45	0.31	0.22	0.26	1.07	0.44	0.29	0.22	0.27	1.03
6	1	82303973		9149	ACCTGCTCTGSATAAATCTTT	0.07	0.00	0.00	0.06	0.19	0.67	0.58	0.00	0.03	0.19	0.68	0.62
6	1	82307339	4970676	9150	GATCATCACARCTTAAAAGGG	-	-	-	-	-	-	-	-	-	-	-	-
6	1	82331135	17473399	9151	CTCTCCAGCTRATCATCCACA	-	-	-	-	-	-	-	-	-	-	-	-
6	1	82341167	4970680	9152	GATCATCATCRCAAAAATATT	0.17	0.04	0.04	0.22	0.32	0.42	0.71	0.02	0.20	0.31	0.41	0.73
6	1	82346866	1414607	9153	TTTTCAATGAYGATTTTTGGT	0.24	0.04	0.04	0.66	0.20	0.34	0.47	0.02	0.71	0.21	0.35	0.50
7	1	86515457	272486	9154	TTTTGATAAAYGGAAGTTCTC	0.03	0.12	0.10	0.65	1.51	1.51	0.78	0.07	0.65	1.37	1.43	0.79
7	1	86527340	272493	9155	GATGAATACARTGAGTTTTAC	0.01	0.10	0.10	1.50	1.64	0.79	1.10	0.08	1.75	1.55	0.85	1.06
7	1	86536227	11161804	9156	TGAGCTATTTRAAGTCTGCTC	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86545674	272504	9157	ACTTTTGTTCRGATGCCATTT	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86557358	272512	9158	AAACAGATTTWTTTACCAAAT	0.22	0.50	0.51	2.40	1.33	1.35	0.75	0.46	2.77	1.27	1.30	0.77
7	1	86564642	2390096	9159	TTTCACTGGTRCACCGTGGTA	1.06	1.40	1.40	0.43	2.67	0.96	0.93	1.38	0.44	2.41	0.92	0.92
7	1	86573108	4288573	9160	GTGATGATTAYTGTTACAGTT	0.36	0.74	0.72	0.81	0.34	2.62	1.05	0.67	0.86	0.37	2.33	1.02
7	1	86581774	17129126	9161	GTTTTTCACARTAGAGCAGGA	0.96	1.40	1.40	0.66	1.11	0.45	2.30	1.37	0.71	1.08	0.48	2.16
7	1	86586103	1999600	9162	TTAAGCAGGAMCTTCATTAGA	0.84	1.29	1.29	1.23	0.73	0.88	0.68	1.21	1.36	0.75	0.85	0.70
7	1	86597625	2151708	9163	AGTCTTTTACRAAAGGCAAGT	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86609283		9164	CTTCTCCTACMATTGCCACTG	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86616346	1889337	9165	TAAATTATGARCATCTTGTTG	2.13	2.62	2.62	0.84	1.31	0.72	1.31	2.52	0.87	1.24	0.70	1.29
7	1	86622308	17129188	9166	AGATAAAAAGWACATGGCTGT	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86628681	17129186	9167	TCATTATGTTRACCTCTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86639021	10493793	9168	TGGCCAATTAYTTTCTATTTC	-	-	-	-	-	-	-	-	-	-	-	-
7	1	86647314	2753345	9169	CCTTCTGATGRGAGAAAACCT	0.35	0.57	0.57	1.94	1.29	1.30	0.36	0.49	1.99	1.25	1.29	0.34
7	1	86652893	2753384	9170	TAAAACCATTYCTTAATAGTG	1.66	0.53	0.68	0.36	1.51	0.34	0.21	0.60	0.36	1.50	0.32	0.26
8	1	89156986	4655890	9172	TCACATCTCCYACCTTCATGG	0.92	0.48	0.48	0.11	0.02	0.42	0.27	0.46	0.10	0.03	0.41	0.29
8	1	89171481	11809016	9173	CAGGTAGGGGYGAGCCTGGAT	0.07	0.17	0.17	0.09	0.13	0.47	0.29	0.12	0.07	0.11	0.50	0.32
8	1	89177535	6682578	9174	CATAGACTTTWAGCTCTTTAA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89184613	10922537	9175	GAAAAGACTARCTTATGCTTT	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89190530		9176	TCAATGCTGAWACTAGGTGGA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89203108	2390678	9177	TAATTTGGCAWAAATTTCAGG	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89217064	2149186	9178	GAAGGCTTGTKGTTCTCCTCC	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89230086	1048848	9179	TAGGACTTTTSACACATAAGA	0.83	0.77	0.77	0.55	0.49	0.29	0.27	0.67	0.58	0.50	0.33	0.25
8	1	89235703		9180	TACGAGGCCCRTTGACCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89242446	17130721	9181	TGAAAAGAACYCGTTTGTAAC	1.06	1.57	1.57	1.28	0.34	0.26	0.14	1.50	1.49	0.35	0.28	0.12
8	1	89243517		9182	ATGGTTTTATRGAAACTGAGC	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89261979	10801713	9183	AAGTCAGGTARAAGTTTCTGT	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89267864	2031834	9184	TCCTCTCAATRTCTCCTCTCA	0.41	0.66	0.66	0.51	0.75	0.14	0.44	0.59	0.55	0.74	0.15	0.43
8	1	89279963	4656092	9185	CAGCAAGTGARGGAAAGGACA	0.48	0.85	0.87	0.18	0.20	1.13	0.18	0.82	0.16	0.22	1.05	0.22
8	1	89287698	2026043	9186	AATTTTGCCTYGGGTAACCAG	0.58	1.00	1.01	0.14	0.88	0.54	0.48	0.97	0.12	0.83	0.55	0.46
8	1	89294711	7537937	9187	CCATTGACTGSAATGCCACCT	0.64	1.06	1.06	1.14	0.41	0.51	0.26	1.01	1.24	0.43	0.52	0.28
8	1	89295594	2209957	9188	TCATTCACAARCATTTATTTA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89308308	1329122	9189	AACAAGAGATKTTCATAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89324951	649641	9190	GTGTAAAATCRTAAGATTCTG	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89331813	4233336	9191	TTCCAAGGCCRACAAGTAATT	0.90	1.34	1.36	1.51	0.56	0.16	0.20	1.24	1.54	0.52	0.16	0.21
8	1	89342747	2893089	9192	GAGGTACTTGKGTCCCTTATT	0.62	0.71	0.71	0.68	0.67	0.20	0.05	0.66	0.70	0.68	0.20	0.05
8	1	89348968	4233337	9193	ATACAAACTAYACTTTAACAT	0.05	0.19	0.19	0.68	0.08	0.15	0.07	0.15	0.68	0.07	0.16	0.08
8	1	89359407	627125	9194	GACACAGTCARTTTCCCTAAC	1.01	1.49	1.49	0.53	0.12	0.02	0.62	1.39	0.54	0.11	0.02	0.65
8	1	89365741	683100	9195	CTTTATTAACYTCTCCATGCA	0.05	0.19	0.19	0.71	0.13	0.27	0.65	0.19	0.71	0.15	0.26	0.69
8	1	89372327	7521137	9196	ATGGACTGATYGCACCTAACA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89385320	12138939	9197	AGAACTTATGRTATATTGGAC	0.58	0.81	0.81	0.71	0.32	0.63	0.42	0.73	0.72	0.34	0.61	0.41
8	1	89393530	551904	9198	GACCATGGAGSTGAGCTTACC	1.10	1.56	1.49	1.03	0.73	0.50	0.65	1.44	1.00	0.72	0.49	0.64
8	1	89437243	17436441	9199	CCATTAGCCTSAGTGATGCCC	1.70	1.29	1.29	1.57	1.23	0.73	0.23	1.23	1.58	1.22	0.76	0.23
8	1	89442744	9628688	9200	TTTCTGAGAAYGTACATTTAA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89448666		9201	AGAGGGAATGMATGTGTCTGA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89461448	17130764	9202	TGGCCATAAAYTCTTCTCTGA	-	-	-	-	-	-	-	-	-	-	-	-
8	1	89467692	623771	9203	ATCCTCACTTWTTTGGGGTTT	0.48	0.64	0.60	1.23	1.32	0.57	0.16	0.54	1.28	1.29	0.55	0.15
9	1	161010660	6704450	9204	TAGCCACAGARGGATAATTCC	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161016188	531802	9205	AGATTCTTCCMGTCTGGGCTG	0.05	0.14	0.14	1.33	1.19	0.91	0.92	0.09	1.52	1.15	0.91	0.85
9	1	161030161	902013	9206	CTCCTGTTATKCTATCCTGCA	1.67	1.79	1.79	1.24	0.93	0.68	0.21	1.71	1.39	0.95	0.68	0.23
9	1	161033601	555908	9207	TAGACACCAGYCTGAAGCTTT	1.70	1.85	1.85	0.76	0.61	0.29	0.53	1.81	0.88	0.67	0.31	0.55
9	1	161046578	10800014	9208	AGGTTGGAATRTCAAATCCTA	1.42	1.54	1.54	0.97	0.23	0.73	0.39	1.50	1.07	0.22	0.73	0.40
9	1	161059491	574944	9209	AGTACAGAAAYCTGTTTCAAT	0.41	0.68	0.65	0.38	0.59	0.26	0.50	0.59	0.36	0.57	0.24	0.50
9	1	161065783	7547121	9210	TTGCAATTTTWAAAAATGTTT	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161071329	2130150	9211	TAAGAAAAATSTTTCAATGCA	0.76	1.21	1.16	0.42	0.43	0.45	0.06	1.09	0.38	0.46	0.47	0.06
9	1	161082177	527203	9212	CAGTAACTGTRGGCCTGAACA	0.16	0.37	0.37	0.39	0.23	0.14	0.18	0.31	0.41	0.24	0.15	0.20
9	1	161092407	1416436	9213	CAAGATAAGAYGCATACTTCT	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161105033	16829814	9214	TATGTGATTARTGTTTCATGT	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161120386	12030152	9215	AGCACTATCCRAACATAATTT	0.78	0.55	0.63	0.22	0.11	0.15	0.56	0.56	0.18	0.08	0.17	0.57
9	1	161126921	2821400	9216	CTGGTAATTAYGGAAGTACAT	0.81	0.56	0.56	0.11	0.43	0.88	1.03	0.47	0.08	0.46	0.92	1.00
9	1	161133228	2634995	9217	AATTTCACAAYGCCCCGAGTC	0.21	0.08	0.08	0.73	1.42	1.10	1.78	0.04	0.81	1.38	1.09	1.68
9	1	161146772	10918005	9218	CTATCAATAARAAGGAGCACT	0.11	0.00	0.00	1.00	1.78	3.23	2.59	0.00	1.17	1.72	2.94	2.37
9	1	161147536	10918008	9219	CCCAGTCAAGWAAAAGGGCAA	1.82	1.93	1.94	1.61	2.51	3.33	2.16	1.80	1.63	2.33	3.07	2.10
9	1	161177015	7416532	9220	GCTATATCTGRCTCACTTAAC	2.62	3.01	3.01	2.69	2.28	1.81	0.89	2.88	3.01	2.14	1.76	0.87
9	1	161186219	2027289	9221	AACCACTGGGYCACACCTGCC	0.28	0.56	0.54	2.08	2.57	1.06	1.06	0.49	2.27	2.38	1.06	1.04
9	1	161188892	7518111	9222	AAATTCACCAYCGCAAACACC	0.18	0.43	0.43	0.40	0.75	1.49	0.88	0.38	0.40	0.76	1.38	0.85
9	1	161198904	16827858	9223	TTAGATCAATRTCATTTCAAA	0.56	0.60	0.60	0.04	0.65	0.90	0.42	0.56	0.03	0.67	0.86	0.42
9	1	161206859	17385225	9224	TCTTCCTGGCRTCAGAGCTCA	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161212898	868376	9225	CGGAAAATCTYTCAGAGAAGA	0.05	0.03	0.02	0.77	0.38	0.21	0.23	0.00	0.76	0.42	0.23	0.22
9	1	161220115	1338626	9226	AATGGCTAATKGAGACCTCCC	0.10	0.31	0.31	0.06	0.22	0.36	0.31	0.28	0.05	0.22	0.38	0.32
9	1	161228480	12091822	9227	ATGAAGAAATRCAACAAAATC	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161237145	1416260	9228	GACCTAGACCKCCAGGTTACA	0.16	0.02	0.02	0.06	0.24	0.48	0.12	0.00	0.04	0.25	0.50	0.15
9	1	161261788	3767374	9229	TGAATTTTATRTATTTCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161286944	1780365	9230	GAACCTGGCARTACAACTTTG	0.48	0.07	0.08	0.07	0.82	0.19	0.32	0.06	0.05	0.85	0.19	0.34
9	1	161295044	10442643	9231	AGATAAGGACRTTGAGCCTCT	0.53	0.71	0.71	0.08	0.07	0.64	0.28	0.66	0.05	0.06	0.67	0.28
9	1	161301512	4607861	9232	CAGAGCTTTTRGCACATTTGA	0.50	0.59	0.59	0.20	0.18	0.16	0.50	0.56	0.18	0.21	0.16	0.50

9	1	161309186	2792260	9233	AAGGAAGGCTYGCAACATCCT	0.01	0.04	0.04	0.59	0.92	0.27	0.10	0.02	0.60	0.92	0.30	0.11
9	1	161315231	2800785	9234	TTGGGAGCCASATTTTAGGAT	0.40	0.77	0.77	1.36	0.67	0.56	0.30	0.71	1.51	0.64	0.59	0.29
9	1	161321166	1780357	9235	ATTTGTATTTRAAGATCCAAA	-	-	-	-	-	-	-	-	-	-	-	-
9	1	161327147	2996669	9236	TTTGGAAATCYTGGGAAAACC	0.06	0.15	0.10	0.84	0.40	0.30	0.32	0.07	0.91	0.45	0.32	0.31
9	1	161332730	17386734	9237	ATATTCGACTRTTTTCATATT	0.08	0.27	0.24	0.19	0.26	0.21	0.14	0.20	0.14	0.26	0.21	0.15
9	1	161341240	16833488	9238	CCTCAGTTTCYCCGGCTAGAA	0.04	0.04	0.04	0.11	0.25	0.26	0.34	0.00	0.08	0.24	0.26	0.36
9	1	161348034	1780358	9239	CCAGTGGTGCRGAGAATAGAC	0.35	0.46	0.46	0.08	0.11	0.43	0.35	0.42	0.06	0.11	0.43	0.36
9	1	161355183	2635022	9240	TAGGATGTGCRTGTGTATTTC	0.09	0.27	0.27	0.08	0.17	0.27	0.57	0.25	0.09	0.18	0.27	0.56
10	1	161892236	1891931	9241	ATGCAACAACKCTTTGCCATG	0.21	0.26	0.26	0.37	0.92	1.47	1.00	0.25	0.37	0.92	1.43	0.97
10	1	161900817	1819768	9242	ATTCAGTTTTMATTCTTGAGG	0.11	0.30	0.33	0.34	1.06	1.49	1.35	0.28	0.35	1.04	1.45	1.30
10	1	161907222	10494435	9243	CTTTCTACGAYAACCCAGTAT	0.16	0.20	0.16	0.92	1.48	1.50	0.74	0.12	0.93	1.40	1.44	0.78
10	1	161914149	12040140	9244	CCCCAAACCAYCACACCAAGT	1.72	2.07	2.07	1.48	0.78	0.75	0.56	1.96	1.59	0.79	0.74	0.56
10	1	161920991	16841238	9245	CTTCTCAAATWTGAATGTTCC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	161926821	16841290	9246	CACATTCTTAYTTTCAGTCAA	0.59	0.72	0.72	1.62	0.97	0.31	0.45	0.68	1.84	1.00	0.34	0.47
10	1	161931540	16841316	9247	AACATGCTGGRAAACAGCACA	0.42	0.49	0.52	0.62	1.44	1.04	0.39	0.48	0.66	1.37	1.01	0.40
10	1	161945820	1394438	9248	GCTGCTTCAARGCCATCAGCA	0.06	0.14	0.15	0.46	0.86	0.83	1.11	0.12	0.47	0.86	0.85	1.10
10	1	161953145	1553608	9249	GTTCACCCTCWTTCTGAAATA	0.01	0.07	0.07	0.24	0.20	0.55	1.12	0.05	0.22	0.22	0.59	1.08
10	1	161956929	4657427	9250	CAGCATGAGCRTGGGCATGAC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	161977542		9251	GATGCAGTGTKTGTAAAGAAA	-	-	-	-	-	-	-	-	-	-	-	-
10	1	161990473	7537922	9252	TCAGGGCTGAYAATGAATTTA	0.20	0.41	0.39	0.14	0.11	1.04	1.10	0.34	0.14	0.12	1.05	1.11
10	1	161997195	10800081	9253	GAGGAAAAGCRAGAAGGGTGT	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162006491	12135437	9254	ACAGCTCCTGRGCAGAGCTTA	0.36	0.31	0.30	0.25	0.44	0.73	0.44	0.26	0.23	0.43	0.73	0.37
10	1	162015128	2174696	9255	ATGTGCAATAKCTGAGCTCTA	0.23	0.42	0.42	0.27	1.30	0.34	0.48	0.39	0.24	1.26	0.36	0.49
10	1	162020279	7549447	9256	CTAAAAACACWTCTATGTTGC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162041544	6666187	9257	AAGCTTTGTGYCCTGGCTAGT	0.03	0.12	0.11	0.36	0.55	1.28	0.29	0.07	0.38	0.56	1.26	0.29
10	1	162051197	17468805	9258	GGAGGATAAAYATCTGGCCAT	0.95	0.90	0.95	0.24	0.29	0.27	1.91	0.90	0.23	0.31	0.27	1.87
10	1	162063514	6675585	9259	GTTACCACGCRGTGAATGTAT	0.89	1.30	1.29	0.34	0.23	1.29	1.24	1.24	0.36	0.24	1.26	1.26
10	1	162095998	12723379	9260	TGGGAATGAARCCAGAGGTGC	0.91	1.35	1.30	0.39	1.74	1.53	0.84	1.28	0.36	1.72	1.55	0.86
10	1	162102415	283690	9261	TGTGATAAAARAGCTGGAAGG	0.59	0.96	0.91	1.18	1.42	1.75	1.01	0.86	1.17	1.37	1.72	0.97
10	1	162109210	2134095	9262	GCTCAGTTAGRACTCTGTTAA	2.14	2.56	2.56	2.78	1.72	0.84	1.21	2.47	2.84	1.62	0.84	1.21
10	1	162115451	10800097	9263	GTGCTTAATGRAAACTGTTAC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162120943	157870	9264	AAGCACAGAGSCAGAGTAAAT	4.01	4.42	4.44	3.67	2.06	0.94	0.69	4.33	3.94	1.93	0.94	0.71
10	1	162131468	10489748	9265	GTCATTCTACRTATGGAGCTT	1.68	1.33	1.33	3.12	3.48	0.83	0.22	1.20	3.43	3.10	0.81	0.22
10	1	162138948	12043501	9266	GAATAATTTCYGCCTTACGGA	0.35	0.73	0.73	0.68	1.96	0.98	0.72	0.66	0.74	1.88	0.99	0.73
10	1	162145304		9267	AGTATCCCAGSAACCCTCAAG	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162152898	285429	9268	AAATCTTGCTSATTAAAGGCC	0.26	0.57	0.62	0.41	0.20	1.24	0.79	0.56	0.42	0.21	1.19	0.78
10	1	162160426	10800100	9269	AATATACACAMCAAAATGCAT	0.23	0.47	0.47	0.39	1.00	0.59	0.61	0.43	0.40	0.97	0.61	0.59
10	1	162168114	182269	9270	GTCAATGCAAYTTTAATGTAA	0.84	1.23	1.23	0.68	1.21	0.49	0.82	1.15	0.71	1.19	0.47	0.82
10	1	162173970	913086	9271	CAAGTGGTTCRCCCTCACAAC	0.05	0.20	0.21	0.60	0.52	1.54	0.85	0.19	0.63	0.54	1.55	0.85
10	1	162186487	17471444	9272	GCATCATCGAKCTTATCATTT	0.30	0.29	0.29	0.66	0.62	0.73	0.40	0.18	0.66	0.61	0.75	0.42
10	1	162192146	10918201	9273	GCCAGCTGTCRCCCACTACAT	0.09	0.30	0.30	0.05	0.31	0.44	0.34	0.27	0.02	0.30	0.43	0.37
10	1	162198198	2433137	9274	TAAAACCCCARTTGATATGGT	0.07	0.06	0.06	0.00	0.06	0.25	0.48	0.04	0.00	0.06	0.24	0.46
10	1	162206941	1025159	9275	GACCAGTGCARCTAATTAAAA	0.04	0.13	0.13	0.18	0.11	0.45	0.46	0.09	0.18	0.10	0.42	0.48
10	1	162213147	285474	9276	CCCCTAACAGYGTCTTAAGCA	0.05	0.18	0.18	0.45	0.64	0.52	0.31	0.16	0.47	0.62	0.55	0.29
10	1	162214829	285476	9277	CGCTGATTTTYTTTTTCTGAA	0.02	0.09	0.16	0.21	1.19	0.27	0.32	0.12	0.18	1.15	0.28	0.33
10	1	162228802	10737514	9278	CTATAAATAGYCTGCTTTTAA	1.26	0.14	0.14	0.33	0.41	0.58	0.31	0.12	0.34	0.44	0.59	0.34
10	1	162237342	2254880	9279	GAATGATCAGMGAGCACCTGA	0.41	0.40	0.40	0.69	0.64	0.45	0.79	0.30	0.66	0.66	0.45	0.74
10	1	162243935	285447	9280	CAATATGTTAYTAATATTCAC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162250534	7535829	9281	CAGTGGAGAAMCTTGAAGGAA	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162257787	6688105	9282	GAATCATCTCYTCTGGGCACC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162264846	367199	9283	AAAATCTCTGMTGGCCATTTC	0.91	0.06	0.06	1.03	0.85	1.02	0.77	0.05	1.08	0.89	1.04	0.79
10	1	162272549	1326377	9284	AGCGCTGAAAYCTCTCAAGTC	0.41	0.76	0.76	1.10	1.69	1.25	0.88	0.70	1.09	1.63	1.19	0.88
10	1	162281387	10918217	9285	CCACTAGTCTRGACACTGCCT	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162290883	952375	9286	GTCATTTGCTRTTCTCATTGC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162296503	7537189	9287	AAAAATGGACSATAACATGCC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162302498	16847544	9288	TCTCGTAACTYTCAGTATTCC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162304956	16847570	9289	CTGGTCACTCYGAATCTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162317364	3930290	9290	CTCATTCACARAGGAGAAGCC	0.06	0.14	0.14	2.31	1.33	1.63	1.86	0.13	2.37	1.29	1.58	1.80
10	1	162323099	4657456	9291	AAAAAATTAGYGTTCACAATT	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162331925	4147593	9292	AGATATATGTWTTTGAGAATG	0.41	0.78	0.83	1.28	1.65	1.39	2.02	0.81	1.31	1.61	1.33	1.93
10	1	162340958	9333413	9293	GTAGCATAATRAGCATTACTT	0.53	0.94	0.94	0.87	1.10	1.87	0.71	0.90	0.94	1.09	1.80	0.73
10	1	162348539	959617	9294	TCTGAAAGCTSACTCTACTGA	0.77	1.12	1.12	1.18	1.04	0.73	0.61	1.08	1.26	1.05	0.70	0.60
10	1	162355939	10800122	9295	TACTATACCTSCTATATCTGA	1.13	1.68	1.84	2.00	1.37	1.06	0.84	1.71	2.10	1.35	0.99	0.86
10	1	162365002	7518869	9296	TGCACTTGTGYCTGTGTGTAC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162373931	17450889	9297	TAAATTTTACRTTAGGCTTTA	1.99	2.58	2.65	2.36	1.88	0.58	0.84	2.57	2.71	1.79	0.61	0.82
10	1	162382274	4578194	9298	GAATGGTTCAYTTGATGAGAG	0.30	0.49	0.47	1.42	1.49	0.82	0.31	0.41	1.39	1.44	0.85	0.30
10	1	162390408	1538115	9299	TGTGCCAGTARTTTCTATTTA	0.93	0.04	0.04	0.11	0.57	0.78	0.58	0.02	0.12	0.57	0.79	0.62
10	1	162401091	3753893	9300	GTGACGAGCARCACTATAGAT	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162408874	12043815	9301	TGGAATGGAGRCTGCCGAGGA	0.09	0.24	0.24	0.50	0.34	0.27	1.08	0.20	0.49	0.36	0.27	1.09
10	1	162416915	10918265	9302	CATCATTAATRCAAGCACTGT	1.38	1.55	1.55	0.54	0.36	0.35	0.45	1.48	0.55	0.38	0.36	0.51
10	1	162426576	6426937	9303	TGGACCTAGASTGTCATCCAA	0.67	0.67	0.67	1.09	0.32	0.34	0.26	0.64	1.28	0.33	0.33	0.26
10	1	162442369		9304	GAAGAAGAGGSAGGCATTCAG	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162450637	7555523	9305	CATTACTTACMTAATGGAAAA	0.49	0.85	0.85	0.27	0.67	0.12	0.32	0.80	0.20	0.72	0.12	0.34
10	1	162458328	10918276	9306	ATCTTTCAAGMAATTCTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162465141	6426940	9307	GATGTTATGCYACACAGATAA	0.69	0.64	0.64	0.40	0.67	0.36	0.28	0.59	0.46	0.67	0.37	0.29
10	1	162471313	2814470	9308	AGCTTCTACTRTATGTCAAGA	0.64	0.67	0.64	0.60	0.83	0.73	0.34	0.61	0.61	0.84	0.74	0.34
10	1	162474074	2790051	9309	ATACCTGAATRAATTCATATC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162496672	6656194	9310	TCTGGCCACAMCAGGTTTTGT	1.56	1.41	1.47	0.74	0.84	0.43	0.25	1.41	0.80	0.87	0.45	0.25
10	1	162512142	12033394	9311	TAGGGTGATAKCCACAGAACA	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162519135	2153264	9312	TGGGCATGCCRAAACTGATAT	0.41	0.39	0.39	0.97	0.35	0.24	0.28	0.36	1.00	0.36	0.24	0.30
10	1	162532572	2348837	9313	ACCTTGGGTARCTCCCCACTG	2.38	1.92	1.98	1.25	0.32	0.21	0.61	1.87	1.22	0.30	0.19	0.61
10	1	162541821	12041574	9314	ATGAATTATCRTATGGTGAAC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162550279	10753694	9315	CGTGGGCTCCRATCTGGGAAA	0.42	0.10	0.10	1.22	0.88	0.78	0.40	0.06	1.27	0.87	0.74	0.40
10	1	162556791	10918295	9316	TACACAATCTRTTCTCTGCTT	0.20	0.08	0.08	0.16	1.18	0.62	0.53	0.05	0.13	1.12	0.64	0.56
10	1	162563307	4657482	9317	GAGGCGAATGRAGATCATGGG	0.00	0.02	0.04	0.86	0.48	0.89	0.52	0.01	0.91	0.46	0.86	0.53
10	1	162567113	16851987	9318	AATGCAAGCTRTTGATTTTTT	0.54	0.95	0.95	0.81	0.59	0.35	0.45	0.91	0.97	0.60	0.38	0.41
10	1	162577302	6687465	9319	GATATTTGATYAGGTAGACAT	0.30	0.61	0.59	1.12	0.77	0.52	0.38	0.59	1.26	0.79	0.55	0.38
10	1	162587778	4657489	9320	TCAACAGTTAYCCGGATTTTT	0.26	0.52	0.56	0.70	1.03	0.82	0.47	0.54	0.75	0.99	0.80	0.47
10	1	162593922	3790654	9321	GAGCTACAGAYGGGTCTATTG	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162599827	3790659	9322	TCCTGATGGAYTCATGGGACT	0.37	0.60	0.60	0.85	1.12	0.63	1.47	0.59	0.87	1.06	0.64	1.42
10	1	162609233	536109	9323	GGGGTTGGAAMACCTTGATTG	0.18	0.40	0.40	0.94	0.46	0.75	1.10	0.36	0.98	0.45	0.80	1.10
10	1	162614961	10494449	9324	GGAATTCTATSCTGAAAAGCC	-	-	-	-	-	-	-	-	-	-	-	-
10	1	162623962	12130978	9325	TTGGAAAATGSCTTTTTTTAC	0.51	0.87	0.87	0.36	0.64	0.59	1.21	0.80	0.35	0.66	0.60	1.19
10	1	162630312	523778	9326	GGAATTCCGTRTGAAGATTTG	-	-	-	-	-	-	-	-	-	-	-	-

10	1	162636358	7525707	9327	TGCGGCCCATRCCATATTGAG	0.08	0.18	0.16	0.09	0.27	1.10	0.59	0.13	0.08	0.27	1.11	0.59
11	1	179252269	266539	9328	CTGAGGGTACRTGGAGAGGAT	1.42	0.24	0.24	0.17	0.10	0.53	1.37	0.22	0.15	0.09	0.56	1.31
11	1	179260273	11581355	9329	TGCTTTTGTCRGGCCCTTGTC	-	-	-	-	-	-	-	-	-	-	-	-
11	1	179269256	17503555	9330	TATCTAAGTAMAAATGCAGCA	0.19	0.08	0.06	0.37	1.10	1.34	1.11	0.03	0.38	1.04	1.31	1.08
11	1	179275323	1048254	9331	GCCCCTTAAGKCAGGTTTTCT	1.22	0.65	0.65	0.30	1.63	1.09	0.65	0.63	0.30	1.57	1.11	0.68
11	1	179281386	12736689	9332	TAGCACATAAYTGGTATTGTA	0.94	0.83	0.94	1.30	0.47	0.47	0.39	0.84	1.38	0.47	0.47	0.41
11	1	179288360	10911100	9333	TTAACAAATTRCTTTCAATGT	-	-	-	-	-	-	-	-	-	-	-	-
11	1	179297606	503280	9334	TCAGGATTAAMGCTGGACTTT	0.78	1.03	1.03	0.58	0.22	0.13	0.89	0.93	0.63	0.24	0.14	0.88
12	1	180891276	12123933	9335	TTAAATTCCCRCAGCCCATAT	0.24	0.30	0.30	0.20	0.22	0.14	0.20	0.27	0.15	0.25	0.13	0.22
12	1	180906456	12128572	9336	GAACTACAACMAGTTCATCCA	0.11	0.22	0.22	0.16	0.16	0.19	0.13	0.18	0.15	0.17	0.22	0.12
12	1	180913351	17574056	9337	TGCCAAGAAAYCCTCACCTAG	0.07	0.17	0.17	0.33	0.13	0.14	0.26	0.15	0.35	0.13	0.13	0.26
12	1	180920194	6424934	9338	CTAAAGAGTARGAAATAGAGA	0.95	0.68	0.61	0.35	0.22	0.26	0.15	0.54	0.33	0.23	0.28	0.17
12	1	180929669	7517993	9339	TCGTTTTCTCYTCCATTAAAC	0.02	0.10	0.10	0.05	0.63	0.14	0.19	0.08	0.06	0.64	0.16	0.20
12	1	180936334	12746749	9340	AAACTGTAAAYCTAAGCAAGA	0.40	0.50	0.50	0.08	0.04	0.30	0.25	0.43	0.07	0.05	0.28	0.26
12	1	180942462	2840274	9341	ACTTCCAGAARATATAGTCAT	0.55	0.37	0.41	0.08	0.09	0.39	1.08	0.39	0.05	0.08	0.43	1.10
12	1	180949636	1930285	9342	TAATTACCATYGTCACCGTAG	0.03	0.10	0.10	0.21	0.28	0.85	0.96	0.08	0.18	0.30	0.83	0.97
12	1	180957392	11806061	9343	TAAAACTTGGYCATGTTACTC	-	-	-	-	-	-	-	-	-	-	-	-
12	1	180962938	6667352	9344	CCCAGATGAGRCACCAAAAAG	0.61	0.84	0.84	0.51	1.01	0.88	0.86	0.77	0.54	1.00	0.92	0.84
12	1	180972165	10797953	9345	TACAATTTTCYGATTTTGTGG	-	-	-	-	-	-	-	-	-	-	-	-
12	1	180982422	17575364	9346	GGTGGTGCTGSTGGTAATGAT	0.88	0.75	0.71	1.59	1.50	0.94	0.57	0.69	1.65	1.47	0.97	0.58
12	1	180992421	10911553	9347	AAAGACCCAGRGTTCTAGCCT	0.44	0.60	0.60	0.79	1.08	0.82	0.69	0.55	0.79	1.07	0.84	0.72
12	1	180997834	6424944	9348	TTATAGATTAKTCTGCTATCT	-	-	-	-	-	-	-	-	-	-	-	-
12	1	180999203	914727	9349	CTTTTATTTCYCACAGCACAC	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181015033	10911556	9350	TTGATGCCATRTAAGACATAT	1.48	1.82	1.82	0.45	0.47	0.75	0.42	1.75	0.48	0.49	0.75	0.43
12	1	181023457		9351	TGGAAGTGTTWGTATTTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181032973	4382670	9352	AAGATTGAGGMAGCATCACTG	0.68	1.01	1.01	1.24	0.19	0.09	0.54	0.95	1.40	0.20	0.09	0.56
12	1	181046877	17838219	9353	AGAATACTGTRCTCAAATAAA	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181052017	12087924	9354	TTTAAAGAACRCAAGGAATCC	1.07	1.52	1.52	0.85	0.76	0.11	0.22	1.45	0.87	0.79	0.11	0.23
12	1	181076235	10911588	9355	GTTTTTCTGAYATATAATTGT	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181084294	10494580	9356	GATAATGAGASTGGTGCCTTT	1.30	1.69	1.69	1.09	0.83	0.79	0.12	1.63	1.19	0.82	0.74	0.13
12	1	181090592	10911593	9357	TAAAGGAGACRCCAAAGGCTG	0.16	0.35	0.35	1.01	0.96	0.88	0.65	0.30	1.30	0.92	0.88	0.66
12	1	181096854	16823101	9358	AATGTAATGAYGTGGAGCCAT	0.30	0.58	0.58	1.43	1.45	0.55	0.50	0.53	1.77	1.34	0.55	0.52
12	1	181105586		9359	GCTTTTCTTTRGTGCCATTAA	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181117728	6666696	9360	ACTTACTTGAYGATTTTGATG	1.16	1.69	1.69	1.21	1.07	0.37	0.56	1.64	1.41	1.03	0.40	0.58
12	1	181126613	12145326	9361	GTTTACAGCAYTGATATAGAC	3.04	2.13	2.02	0.87	0.41	0.58	1.41	1.93	1.03	0.42	0.60	1.38
12	1	181139086	2378885	9362	TTGAGAAAAAKTTTCATTCTC	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181148069	16823155	9363	AAATATATAGYGCTTTGTCTG	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181154210	10489722	9364	GAAGTACTGAYGAATATACAA	0.19	0.45	0.45	1.12	0.56	1.69	1.54	0.40	1.22	0.60	1.58	1.46
12	1	181164537	2207526	9365	GCTAACTTCARAAGGAAGAGG	1.78	1.99	1.99	1.06	3.28	1.55	1.51	1.94	1.21	2.83	1.48	1.42
12	1	181172385	16823238	9366	GACCAGAGCTYGGGCTTCTCA	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181180067	4651210	9367	TGAAACGCTTRACTTTTAAGA	0.05	0.20	0.19	2.84	3.00	2.86	2.56	0.19	3.03	2.69	2.56	2.39
12	1	181189981	1569842	9368	AGAATAATATYTGCAATACAA	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181195821	4651211	9369	GTTCATCTGCWCAGCATGTCA	0.01	0.06	0.08	1.47	2.55	4.26	3.36	0.05	1.49	2.28	3.69	2.93
12	1	181208278	9633308	9370	AGGCCACAGGYGAAAGGGTCT	0.19	0.36	0.36	0.54	3.37	3.21	2.47	0.32	0.59	2.96	2.81	2.23
12	1	181218322	1416752	9371	AGAATAAAGTRAAAGAAACCA	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181230437	1416751	9372	ATAGGAGCAAYGACAGATAAG	0.07	0.19	0.27	0.63	0.68	2.06	1.72	0.25	0.82	0.67	1.86	1.59
12	1	181232819		9373	AACTTTTCAGMCAATTTCATG	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181244519	10911605	9374	CTAAATATACRTTTGTCTTCA	0.85	1.27	1.27	0.84	1.02	0.36	1.45	1.21	0.89	1.05	0.40	1.38
12	1	181254781	1007224	9375	AACCATTCCARCAGTTTCTGC	0.06	0.12	0.12	1.42	0.57	0.41	0.34	0.12	1.56	0.60	0.44	0.35
12	1	181263747	1999996	9376	CTGAGCCTACRTGACCAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181270999	10911612	9377	ATCAGTAAAARACATGGGATC	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181275587	1572767	9378	GAAGAGCCGTRAGAGCAGCAG	0.30	0.56	0.56	0.36	0.49	0.49	0.52	0.52	0.34	0.52	0.50	0.54
12	1	181290313	6424958	9379	GTGTTCATCTRCTGTTCCCTG	0.50	0.63	0.63	0.27	0.38	0.63	0.35	0.59	0.24	0.39	0.65	0.36
12	1	181297229	1339572	9380	AATGCTAAAAMCTCCAACCAG	1.57	0.01	0.00	0.76	0.34	0.29	1.39	0.00	0.81	0.34	0.31	1.37
12	1	181307842	10911620	9381	AATTCTATCAMGTGCAGGCAC	0.81	1.03	1.03	0.65	0.55	0.82	0.84	0.95	0.71	0.54	0.83	0.85
12	1	181320105	4651225	9382	GCTTGGTAAARCTGTCATGCC	0.75	1.05	1.09	0.67	1.26	0.69	0.61	1.01	0.73	1.22	0.71	0.64
12	1	181335237	10911623	9383	GAAGCTTTAARTCAGGTCACC	0.35	0.54	0.56	1.00	0.74	0.89	0.72	0.56	0.99	0.75	0.90	0.74
12	1	181336585	17578245	9384	TAACCATTCCRTCCTCTTGGC	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181374548		9385	ACAATATGTTRACTATAGTCA	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181385290	2024766	9386	TGTGCAATGTYCGTTTTTGAT	0.01	0.10	0.10	0.58	0.69	0.59	0.59	0.09	0.58	0.72	0.63	0.58
12	1	181391862	1046239	9387	ACAATTTTTCWTTTTACTAAT	-	-	-	-	-	-	-	-	-	-	-	-
12	1	181395555	9425635	9388	CCAAGAAGTAYGCTAACCAAT	0.10	0.17	0.15	0.06	0.31	0.25	0.13	0.13	0.03	0.31	0.23	0.12
13	1	191648358	1032828	9389	CTACCTTAATMGAATATTCTG	0.84	1.04	0.98	0.87	0.50	0.63	0.30	0.91	0.88	0.53	0.63	0.28
13	1	191655079	12026667	9390	TCATGTGCTAKATTTCTGTTC	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191660521	182891	9391	ATCCTTAAGAWATTAATCATA	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191667118	184630	9392	GGCTTTAAGGYTAAGCAAATT	1.08	1.61	1.61	1.40	0.61	0.14	0.33	1.58	1.60	0.66	0.12	0.31
13	1	191673295	339573	9393	CATAGTCAAAWTTTGTACAGA	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191677669	866059	9394	CATTTCCTCTYCAAGTTCTAT	0.67	0.81	1.08	1.28	0.87	0.35	0.16	0.95	1.45	0.87	0.38	0.16
13	1	191688565	610038	9395	CACATATTTCRAAATTAATAA	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191699932	12080849	9396	CATTACTTTGYGCATTTATAG	1.19	1.74	1.74	1.61	1.88	0.69	0.13	1.67	1.90	1.67	0.69	0.13
13	1	191721560	4657953	9397	CAGTTTAAAGRTTATCATATT	1.91	2.52	2.52	1.78	2.09	0.99	0.68	2.45	2.24	1.90	1.01	0.64
13	1	191738446	1538551	9398	TCAAGCCTCARGATTAATCTT	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191748701	10801375	9399	AACTCATGTTRGAACTGTTTC	1.76	2.37	2.37	1.75	1.28	1.61	0.66	2.30	2.19	1.23	1.50	0.64
13	1	191763495	10801378	9400	AGGTCTTTGTRAAATATGCAT	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191770294	12141089	9401	CTCTTCTGAGKTTTTTTTGTA	-	-	-	-	-	-	-	-	-	-	-	-
13	1	191777798	11586150	9402	ATTGACAAGAYTCTATGAAGC	0.83	0.15	0.10	1.25	1.38	1.28	1.09	0.08	1.35	1.35	1.25	1.04
13	1	191784226	4657957	9403	CAATCTAGATYCAGTTCTATT	1.48	2.04	2.04	1.12	0.81	0.70	0.93	1.98	1.26	0.82	0.72	0.94
14	1	201183785	7554895	9404	CACGTACAGCRTGGTATGGAC	1.95	0.99	0.99	0.44	0.15	0.10	0.94	0.86	0.46	0.17	0.09	0.91
14	1	201191185	2271417	9405	ATCCCAATGTYCCAGTGTTTT	1.95	0.99	0.99	0.45	0.26	1.80	1.76	0.86	0.54	0.28	1.65	1.64
14	1	201201786	10900594	9406	GATTACTGGTSAGGGAGCAAA	0.21	0.40	0.40	0.34	3.29	3.03	1.26	0.36	0.31	2.65	2.57	1.24
14	1	201219935	1380576	9407	CAAGATAAGASTGAAAATGTG	0.18	0.27	0.27	2.34	3.02	2.19	1.32	0.21	2.68	2.72	2.06	1.31
14	1	201226233	4252675	9408	ATTTTCTGCAYTAGAATAGAT	0.61	0.90	1.22	2.88	2.15	1.34	1.43	1.09	3.04	1.99	1.33	1.37
14	1	201233040	4252697	9409	AGGTATGTCAYATCATATTTC	0.51	0.87	0.87	2.35	1.75	1.77	1.47	0.82	2.52	1.65	1.69	1.43
14	1	201248142	3789050	9410	AAAGAAGACTKGATATTCCAC	-	-	-	-	-	-	-	-	-	-	-	-
14	1	201254146	10900597	9411	GGACCATGTGYTCTGGTTTTC	0.07	0.23	0.23	0.28	2.69	1.67	1.21	0.17	0.30	2.48	1.63	1.18
14	1	201260626	11801289	9412	TTTGTTTTTGSTGGAGTTACA	-	-	-	-	-	-	-	-	-	-	-	-
14	1	201267446	6681905	9413	CTTCAGGGACKCAATGATAAC	-	-	-	-	-	-	-	-	-	-	-	-
14	1	201274237	12039454	9414	TGAAGATGGAYGAGAGTTCCC	0.08	0.16	0.16	0.93	0.50	1.93	0.88	0.11	0.93	0.52	1.83	0.87
14	1	201286100		9415	AGGTCACACGYACACATGGAT	-	-	-	-	-	-	-	-	-	-	-	-
14	1	201292647	4951409	9416	TACAACGTGGWTATTTCTCAG	1.00	1.01	0.96	1.02	0.81	0.29	1.14	0.89	1.04	0.81	0.28	1.13
14	1	201298656	11240762	9417	CAAGTCTTGAYACATTCATGC	1.07	0.08	0.08	0.92	0.58	0.47	0.82	0.07	0.97	0.60	0.48	0.85
14	1	201311517	898385	9418	GCGTTCTCCCRACCTACTAGT	-	-	-	-	-	-	-	-	-	-	-	-
14	1	201324515		9419	AGACTGTCACRTGTATACTTT	-	-	-	-	-	-	-	-	-	-	-	-
14	1	201327556	17335392	9420	TGAATCACAAYCCATTAGTAG	1.17	0.46	0.42	0.38	0.67	0.87	0.54	0.39	0.37	0.68	0.86	0.53

15	1	217651547	7517729	9421	TAAAGTTTCTMCCCATAGGGA	0.75	0.42	0.41	1.12	0.61	0.17	0.63	0.35	1.32	0.62	0.18	0.66
15	1	217662099	6541172	9422	TCAACATTATKCTATCACCTT	0.10	0.14	0.14	0.14	0.53	0.42	0.17	0.09	0.09	0.58	0.45	0.18
15	1	217672697	1372666	9423	TTATTAAGTCYAACATTATAG	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217679983	7511784	9424	AAACCACTTCYAAAGGTATAT	0.49	0.25	0.26	0.12	0.20	0.55	0.28	0.22	0.08	0.20	0.57	0.25
15	1	217680392	989463	9425	ACCTCTCGTTWGTCATTAGTA	0.05	0.18	0.18	0.21	0.13	0.09	0.32	0.13	0.14	0.15	0.09	0.33
15	1	217695066	1981282	9426	ACACAGTACCWTAGTCACATA	0.09	0.24	0.23	0.15	0.04	0.22	0.26	0.18	0.08	0.04	0.23	0.26
15	1	217702615	6656408	9427	TAGTTAGAGCSAGTGGACTGC	0.03	0.15	0.13	0.10	0.33	0.19	0.07	0.10	0.09	0.35	0.18	0.06
15	1	217711827	10779426	9428	TAGTGGGGAGWCAAAGGTAGC	0.72	0.39	0.39	0.49	0.48	0.12	0.22	0.37	0.46	0.47	0.13	0.20
15	1	217718910	12123182	9429	TGAGACCACAYGTTTAGAGTG	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217727869	17009536	9430	AGATCATGGCYAGGACTCGGG	0.48	0.24	0.24	0.60	0.16	0.68	0.48	0.24	0.60	0.17	0.70	0.47
15	1	217735369	17517959	9431	CTTTCACTTTYAAATAAACTT	0.26	0.49	0.51	0.20	0.81	0.61	0.26	0.49	0.15	0.82	0.60	0.28
15	1	217743397	1539140	9432	TGAGTTCCCTSAAGACGGTTT	0.59	0.24	0.24	1.45	0.76	0.30	0.68	0.19	1.54	0.80	0.30	0.69
15	1	217755270		9433	TCTGAGAGAGRCCTTAACAGT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217766389	1442462	9434	ATTTGGGTTTMACAAAGATAA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217779357	17009652	9435	CACAGAGGCARGATGTATTTT	1.80	2.03	2.03	1.18	0.53	0.65	0.44	1.90	1.26	0.48	0.64	0.43
15	1	217789609		9436	TGCAGCCACAYACGCGAAGCC	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217796893		9437	TTTGATAGACMTAAGATGCAA	0.05	0.15	0.15	1.06	0.91	0.63	0.25	0.09	1.15	0.93	0.65	0.24
15	1	217802885		9438	GAGAGTCCTGYGCTGGAAAAG	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217809491	9431455	9439	GGAAAAAGCAYATACTCTAAA	0.13	0.34	0.34	0.41	1.37	0.57	0.45	0.31	0.43	1.31	0.59	0.44
15	1	217813706	6664072	9440	TAAAATTTACRTACATGGCTG	0.44	0.65	0.65	0.50	0.34	0.76	0.62	0.64	0.55	0.35	0.77	0.61
15	1	217828859	3924909	9441	GACTGGAGTCMGGCAATCTTT	0.16	0.40	0.40	0.18	0.32	0.27	0.59	0.35	0.19	0.33	0.26	0.63
15	1	217835004	10489954	9442	TCCTGTGATAYGACCTATGAG	0.14	0.10	0.09	0.46	0.18	0.24	0.44	0.06	0.45	0.20	0.24	0.44
15	1	217845508		9443	AATGGCATCTRACCCAATAAG	1.12	1.33	1.59	0.82	0.44	0.35	0.27	1.54	0.88	0.44	0.35	0.28
15	1	217853557	10746409	9444	GTTTGGAAAAYTTAATCAAAA	1.01	0.95	0.98	0.91	1.05	0.66	0.39	0.95	1.22	1.05	0.69	0.39
15	1	217861304	4415570	9445	ATATCTAAACYTCAAAATTTC	1.03	1.08	1.08	1.11	1.35	0.75	0.97	1.03	1.33	1.24	0.76	0.95
15	1	217873031	11590645	9446	TATTCTATCAKTATCCAGTAT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217884066	4846709	9447	CTGGATGCTCRTGAGACCCCA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217891011	3903829	9448	AAGAGCAACAWATGGACCAAC	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217898589	10863603	9449	TATGTGATTAYGTATCTTCTC	1.08	1.37	1.34	0.64	0.31	0.93	3.20	1.25	0.66	0.33	0.92	2.83
15	1	217906091	11584801	9450	ATAACATCAAYACAGTGGCAA	0.34	0.67	0.65	0.47	0.33	1.89	2.54	0.61	0.48	0.33	1.82	2.31
15	1	217939934	12733856	9451	GATAATAAGAMAATGGAAGAA	0.39	0.74	0.74	0.20	2.20	1.86	1.87	0.68	0.17	2.04	1.76	1.76
15	1	217944661	17436982	9452	ATGACACAGTYTTGCTGACAA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	217955481	10495176	9453	ACATCTATCCSTGGTGCCACT	2.35	0.21	0.31	2.41	3.26	1.62	1.61	0.26	2.56	2.91	1.53	1.55
15	1	217975845	12410403	9454	AGCTTGTAAGRACTGTTTCAG	3.13	3.75	3.75	2.93	2.72	1.93	0.93	3.63	2.95	2.31	1.81	0.97
15	1	217982236	17010009	9455	AAAGCCAACCYGGTAGATATT	1.52	1.49	1.49	2.57	2.51	1.22	1.34	1.34	2.80	2.30	1.19	1.29
15	1	217994227	10495163	9456	ATCAAGAATTWTCGTAACCTA	1.36	1.96	2.03	1.84	1.68	1.61	0.96	1.98	1.86	1.61	1.51	0.96
15	1	218001693	10863613	9457	TGAAAGATAAYATCATGAGCA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218018357	6663387	9458	GACAAGAATARCTAAAGAATG	0.06	0.20	0.20	1.42	1.47	1.32	1.49	0.19	1.39	1.40	1.25	1.44
15	1	218023896	1551670	9459	GGAAATACAAYTAAACACACA	1.07	1.57	1.56	1.47	1.35	1.17	1.47	1.50	1.65	1.31	1.11	1.41
15	1	218033269	11118721	9460	TAAGTTTCCGYCCAAACTAAT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218042923	6694450	9461	TCAAACCTTTKTCACATTCCA	1.17	1.64	1.64	0.77	1.35	1.59	1.23	1.60	0.93	1.32	1.51	1.18
15	1	218052163	1459231	9462	GAGATAAAAAWCTTACCAAAA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218069450	4846718	9463	ACCCAAAAATYCATAGAAAGA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218081418	17010220	9464	AAGTTTCTGTRCTAGGCTCTG	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218087228	17010240	9465	TAGAGAATACYATCTTCCAGG	0.06	0.16	0.22	0.84	2.19	1.20	1.21	0.17	0.99	1.98	1.18	1.19
15	1	218095877	17010245	9466	CAATTTTGACRTTAAAGCCAC	0.68	0.45	0.45	1.08	1.22	1.60	0.42	0.35	1.31	1.17	1.48	0.43
15	1	218106051	12046891	9467	CATGACAAATRATGCCTTAAG	1.67	2.16	2.21	1.45	1.52	0.48	0.37	2.15	1.65	1.36	0.51	0.38
15	1	218113559	4846720	9468	AATTGTTTGTRTACAGAATGT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218121391	12021531	9469	CCTAGCTCTCRAAGCCCCACT	2.34	2.04	2.04	1.41	1.24	0.49	0.20	1.97	1.88	1.19	0.53	0.19
15	1	218127895		9470	ACAACATACGYACATACAAAT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218134630	1933267	9471	CTTTAATTATYGTCTATTTGT	2.18	2.09	1.97	1.04	0.77	0.63	0.57	1.94	1.46	0.78	0.63	0.60
15	1	218147724	7531435	9472	AGAAGGAATGYCTGGATTTAA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218154654	1356701	9473	AGCATGGTAGSATGGGCGTTG	0.92	1.13	1.13	0.77	0.90	0.47	0.49	1.10	0.79	0.91	0.49	0.48
15	1	218162044	12058091	9474	ACACCTTGCAMCTCCTCTCTG	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218178230	17010395	9475	TAATTTGCAGWGTCTCTCCTT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218184376	12568399	9476	GCTTTGAATCYCTATTTTCAA	1.00	1.24	1.27	1.02	0.83	0.62	0.22	1.18	1.03	0.84	0.65	0.25
15	1	218199822	6658755	9477	CATTACTGGCYCTGCTTCCCT	1.10	1.62	1.57	1.15	0.69	0.36	0.47	1.49	1.24	0.68	0.41	0.48
15	1	218206180	12744368	9478	ATTGACTTTTRAGGAGAGGAG	0.22	0.47	0.47	1.10	1.20	0.66	0.23	0.44	1.14	1.18	0.68	0.24
15	1	218212598	11118795	9479	AGGTACAATGSAACCTAACCT	0.21	0.44	0.44	0.99	1.46	0.64	0.85	0.39	0.97	1.40	0.65	0.84
15	1	218217656	10779452	9480	CAGTGCACCASTGAACACAGC	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218226813	12035928	9481	ACTGGCCATARATGAAACAGG	0.72	0.66	0.66	2.11	1.41	0.97	0.70	0.60	2.16	1.35	0.98	0.70
15	1	218245294	10863647	9482	GCAACTCTCARTGTAGACTCC	0.99	1.24	1.24	0.99	1.36	1.28	0.31	1.15	1.00	1.31	1.30	0.33
15	1	218253105	1815577	9483	GACACCCTAGYCCATTTATAA	0.06	0.04	0.06	1.19	0.94	0.78	0.66	0.02	1.21	0.91	0.78	0.69
15	1	218261195	1338076	9484	GTAATATATAYAGAAACCTAA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218269246	12126069	9485	GTCTAGTATARAAAGCTTATA	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218283788	17010629	9486	AATCAGTAATYTGGAGTTCCT	1.98	2.30	2.30	1.45	0.83	0.98	1.39	2.22	1.54	0.86	1.01	1.35
15	1	218290019	6604668	9487	TGTGACGAAAYCTTATAGTTG	1.22	1.59	1.60	1.28	1.50	1.34	1.75	1.52	1.36	1.41	1.30	1.71
15	1	218300756	1141714	9488	CTCGGCTTGGYTCATTGGTAT	0.15	0.38	0.38	0.80	1.11	0.81	1.12	0.36	0.81	1.11	0.82	1.11
15	1	218316700	17491176	9489	GAATCTCACCRAAAGCAGGTT	0.14	0.38	0.38	0.04	0.52	0.71	0.48	0.32	0.05	0.53	0.72	0.49
15	1	218323187	7543041	9490	TTTTATACTCRTAGGTGGTCT	0.01	0.10	0.10	0.01	0.03	0.61	0.61	0.07	0.01	0.03	0.62	0.60
15	1	218328631	4846353	9491	ACTAATCTCAMAGTGATTATC	0.05	0.05	0.11	0.10	0.15	0.08	0.59	0.07	0.09	0.17	0.09	0.61
15	1	218337264	12029988	9492	GACTATGTTTYGAAAATCTTG	0.07	0.22	0.22	0.70	0.22	0.04	0.17	0.20	0.75	0.24	0.03	0.19
15	1	218345594	9441956	9493	GCCATTGATCYCTGGACTGAA	0.15	0.36	0.36	0.35	0.17	0.14	0.29	0.30	0.34	0.18	0.16	0.30
15	1	218354678	4846723	9494	TTCTTGAAGGYGGGGAACTCT	0.27	0.25	0.25	0.03	0.25	0.32	0.07	0.22	0.01	0.27	0.33	0.08
15	1	218360747	10863658	9495	ATAGGATTACRTGCCAAATAT	-	-	-	-	-	-	-	-	-	-	-	-
15	1	218375146	4551601	9496	ATGCATCTTAYGAGGTGGTCC	0.12	0.13	0.13	0.52	0.34	0.16	0.16	0.09	0.51	0.34	0.20	0.17
15	1	218375543	11118869	9497	GTCACCTTTCRAAAACAAGGA	0.91	1.26	1.26	0.60	0.37	0.22	0.18	1.21	0.56	0.38	0.22	0.19
15	1	218392303	4846728	9498	GGTTGTAAACYGAATACCTGC	0.94	1.37	1.37	0.47	0.32	0.50	0.26	1.34	0.53	0.34	0.52	0.27
16	1	221819332	6691715	9499	ATTATCTCAGRAGAGCTTATC	0.43	0.66	0.66	0.20	0.67	0.34	0.10	0.58	0.19	0.67	0.32	0.10
16	1	221826790	4653629	9500	AGTGTATAGAYTGAGAGGCAG	0.17	0.19	0.19	1.90	1.51	0.44	0.25	0.16	2.08	1.42	0.44	0.28
16	1	221832838	12408441	9501	ACTTTTCAAAYTGTGCATGAT	-	-	-	-	-	-	-	-	-	-	-	-
16	1	221838520	6699589	9502	GTAGTAGAGTSTGGGGTATTT	1.86	2.46	2.46	1.90	1.69	1.23	0.69	2.30	2.04	1.57	1.22	0.67
16	1	221846098	12408617	9503	ATTTGAAATARGTGAAAGTCA	0.43	0.66	0.66	1.88	1.97	2.04	0.96	0.59	1.98	1.80	1.88	0.96
16	1	221852907	9659299	9504	TTAATTTTACSTTATCTTCCA	-	-	-	-	-	-	-	-	-	-	-	-
16	1	221859385	12563830	9505	TGTTTGAATGYAAGTCATCTT	-	-	-	-	-	-	-	-	-	-	-	-
16	1	221875976	950210	9506	GAGGAAATATKTAACTCTTTT	0.59	0.89	0.89	0.56	2.07	1.58	1.58	0.81	0.55	1.81	1.48	1.47
16	1	221883798	12028429	9507	GCCAGGCTGCYTCCTATACCA	0.66	0.98	0.98	0.78	0.60	1.63	1.39	0.93	0.92	0.61	1.59	1.34
16	1	221891280	10495240	9508	GACCAAGTTAMACAAGTATAA	0.07	0.22	0.22	0.80	0.61	0.47	1.16	0.18	0.81	0.62	0.50	1.15
16	1	221897485	11551874	9509	TTCAGATTAASGGTTGAAAAT	0.05	0.03	0.03	0.02	0.72	1.00	0.66	0.00	0.03	0.75	1.02	0.64
16	1	221905590	17557867	9510	GTCATAACCTRTAACAGGGCA	0.05	0.03	0.03	0.43	0.71	0.60	1.35	0.00	0.38	0.71	0.64	1.31
16	1	221911606	11799479	9511	TCACAAAAATYCTTGCTAGAG	0.17	0.42	0.42	1.14	0.84	0.96	1.00	0.37	1.14	0.85	0.92	1.00
16	1	221920471	16844878	9512	ATTCTGGGTTRAACAAGTTAA	1.12	1.26	1.30	0.79	1.66	1.12	1.53	1.23	0.77	1.55	1.11	1.49
16	1	221929811	7539651	9513	AAATCTAACCYGCTGGATTAA	1.28	0.81	0.81	0.91	0.75	1.31	1.17	0.75	0.89	0.72	1.26	1.18
16	1	221940732		9514	TCTGAGTAGTRTCTGTCCAGC	-	-	-	-	-	-	-	-	-	-	-	-

16	1	221956274	17500089	9515	GCACAGCTTCRTTTTATAAAA	-	-	-	-	-	-	-	-	-	-	-	-
16	1	221963123	3893032	9516	TGCATTTCATMCCCTGGACTG	-	-	-	-	-	-	-	-	-	-	-	-
16	1	221974766	10799316	9517	CCAGAACTCCRCTTTCCCTAG	0.51	0.23	0.23	0.42	1.35	1.01	1.09	0.20	0.43	1.32	0.97	1.07
16	1	221983065	954534	9518	GCTCATTCAGYTTTGTTAGAA	0.00	0.03	0.03	0.98	1.04	0.91	0.76	0.00	1.08	1.07	0.92	0.78
16	1	221988910	2039620	9519	GTTTTAAGTAYCTGAACGTGT	-	-	-	-	-	-	-	-	-	-	-	-
16	1	221994716	3820226	9520	ATCTTATCACKTACTACTTTT	0.86	0.50	0.54	0.21	0.47	0.75	0.77	0.49	0.17	0.48	0.75	0.77
16	1	222004537	16845004	9521	GGGCTTAGGAMCTGTACCTTT	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222017922	10915846	9522	CAATGCTGGARAATATTTCTA	0.71	0.37	0.48	0.15	0.05	0.39	0.43	0.44	0.11	0.04	0.44	0.46
16	1	222022976	7555139	9523	ACTCTTATTCRGGTTGGTAGA	0.85	0.62	0.62	0.34	0.09	0.01	0.36	0.59	0.35	0.09	0.01	0.41
16	1	222033628		9524	AGTCCTGTTAMTGCAACCTCC	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222044367	554744	9525	AACTTGCATGYTCACCACACT	0.85	0.62	0.62	0.29	0.04	0.15	0.63	0.57	0.26	0.04	0.14	0.67
16	1	222060951		9526	CCGCATGTGTRGCAGGATGAT	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222071826	6671830	9527	GAATACAACARAAACACTGTG	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222085399	16845078	9528	TCAATTAGAAYCTTTTATAAA	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222096699	2657564	9529	ACGAACTCCGYGATGAGACCT	0.88	0.79	0.79	0.18	0.44	0.40	0.65	0.74	0.14	0.49	0.41	0.67
16	1	222111778	2840958	9530	TCCAGGCCCTRTACATTATCC	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222119646	2639703	9531	TAAGCAATCAYTTAAAACAAG	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222134349	2840968	9532	ATGTGTGGAGYCTACCTTACC	-	-	-	-	-	-	-	-	-	-	-	-
16	1	222143412	17503834	9533	TTGACATCCTYGAGCTAAATA	0.24	0.05	0.05	1.16	0.72	0.72	0.23	0.03	1.26	0.70	0.70	0.24
17	2	4478209	2315625	9534	ACTGGTCCTCWTATTAATATC	0.41	0.73	0.71	0.25	0.13	0.05	0.01	0.64	0.23	0.12	0.05	0.00
17	2	4481615	6749621	9535	GCAGATCTAAKGGGACAAAGC	0.31	0.61	0.61	0.74	0.38	0.25	0.01	0.60	0.75	0.40	0.26	0.01
17	2	4490669	6744451	9536	TGAAGGATACYTGTAACCTTG	0.26	0.08	0.07	0.23	0.12	0.13	0.21	0.03	0.23	0.10	0.13	0.22
17	2	4606215	7371570	9537	CGTCAGCCCCRTCGATCAGGA	0.38	0.20	0.20	0.02	0.12	0.20	0.22	0.19	0.01	0.14	0.21	0.21
17	2	4638613	7422175	9538	TTTACATTTTRAAAAATCTTT	0.29	0.16	0.26	0.41	0.19	0.56	0.34	0.21	0.42	0.22	0.57	0.34
17	2	4647542	17040814	9539	AGAAACTAACRAATCAGTGCT	0.14	0.04	0.04	0.12	1.58	0.56	0.70	0.00	0.09	1.49	0.57	0.69
17	2	4660426	6734984	9540	TGAAATATTTYTTTAAGTAAT	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4667206	1078821	9541	AATACGAGGCRCTAAAATTCT	0.05	0.17	0.17	1.71	1.11	2.38	1.36	0.14	1.85	1.06	2.27	1.35
17	2	4673442		9542	TATGGGGGCARTCAGTGGTGC	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4686144	2368693	9543	TCCAACCAAAYTGACTCACCT	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4691321	11677255	9544	ACTGAGATTCMTATCTTGATG	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4704176	17040892	9545	TCTCTCTTGTYATCTCTCAGC	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4711133	10495514	9546	CTATCCACAARCTCAGAATAA	3.50	3.45	3.45	2.73	3.52	2.37	1.36	3.33	2.77	2.92	2.20	1.31
17	2	4715900	2167961	9547	GGGGCCCAAGSCAGCTTGAAA	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4731081	6836	9548	AGAGTTACTAYTGCAGGAACA	0.30	0.62	0.61	4.96	4.57	2.18	0.79	0.54	5.41	4.18	2.07	0.79
17	2	4738674	4854104	9549	TAGTTTTCATMATAAACTCCT	0.05	0.19	0.26	1.99	4.14	1.93	0.94	0.18	2.21	3.63	1.86	0.94
17	2	4744867	4854134	9550	ACACATCCTARCCTTCAGCTT	0.48	0.44	0.44	0.88	1.60	2.70	1.22	0.35	0.93	1.50	2.54	1.20
17	2	4750987	7595702	9551	GTGCACGCTCMTTCAGAATGT	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4754573	7599793	9552	AAAGCCTACCRTGAGCCTGGC	0.04	0.10	0.10	0.46	0.67	0.70	2.32	0.07	0.47	0.71	0.71	2.17
17	2	4766999	4854108	9553	GGCCATGAAGMCACATCAGGG	0.28	0.00	0.00	0.17	0.11	0.82	2.68	0.00	0.11	0.11	0.82	2.49
17	2	4777322	6548135	9554	TGGAGCCACARGAATAGGTCA	0.85	0.83	0.82	0.28	0.19	2.96	2.71	0.72	0.28	0.20	2.69	2.54
17	2	4788216	1869417	9555	CTCTCCTTAAYAGCAGAATCA	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4799024	2694070	9556	GTGTGAATAARTGCATGCTGA	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4816167	4854162	9557	AACCTAGGACRCAGCAGAGAC	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4824833	2694086	9558	TAGTGCTCTCYGTGCTCCAGG	0.50	0.55	0.55	0.21	2.82	2.19	1.69	0.53	0.16	2.59	2.09	1.64
17	2	4851711	6749474	9559	AAAGGAAAAAMAGTGGGCGAG	0.28	0.02	0.00	2.67	2.23	1.53	0.78	0.00	2.83	2.04	1.41	0.80
17	2	4867779	7573861	9560	ATGTTTCACTYGAGAGATTAC	0.79	1.10	1.10	3.14	2.05	0.78	0.99	1.02	3.29	1.97	0.79	0.97
17	2	4885768	7559860	9561	TCCTTTTCTGSAAGAATCGGG	0.63	0.33	0.33	0.65	1.57	1.32	0.86	0.31	0.72	1.50	1.29	0.87
17	2	4905173	4854182	9562	GTCAGCATTCYTGCCAGCCTG	0.12	0.04	0.04	0.33	0.83	1.67	1.11	0.00	0.34	0.81	1.59	1.10
17	2	4920401	6548154	9563	CTGACTCCCTKAGGTTCGGCC	0.79	0.77	0.83	0.35	0.60	0.83	1.09	0.77	0.35	0.63	0.83	1.07
17	2	4941991	7584720	9564	GCGTGCTCCCRGTGGCCCGCC	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4952312	4971502	9565	TCATCTGTGGRAAAATTATAT	0.41	0.04	0.06	0.43	0.57	0.61	0.81	0.04	0.45	0.59	0.60	0.74
17	2	4972615	6548162	9566	TTCTATATAGYAGGTATTTAA	0.44	0.17	0.17	0.69	0.78	0.81	0.71	0.12	0.69	0.80	0.84	0.73
17	2	4978466	6741238	9567	TATACTAAAGWATATATGTAT	-	-	-	-	-	-	-	-	-	-	-	-
17	2	4998554	7572761	9568	TGGTACGTTAMAAAGGCCAGA	1.17	1.16	1.16	0.72	0.78	0.53	0.39	0.91	0.72	0.81	0.55	0.37
18	2	10640487	736725	9569	CCCGGGTTCTSAGACGGCACA	0.12	0.00	0.00	0.19	0.04	0.16	0.22	0.00	0.16	0.04	0.14	0.24
18	2	10651516	7598994	9570	TGCCTGCCCARTGGCTCGTGT	0.31	0.62	0.62	0.38	0.29	0.08	0.18	0.56	0.40	0.30	0.08	0.20
18	2	10666124	6710687	9571	AATAAGTAAARTTTACTGTAA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10673709		9572	TTGGCCACTTSGCAGGACTGA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10679570		9573	TCAATAGCGAYGCTCCCCTCA	0.45	0.62	0.60	0.35	0.33	0.35	0.48	0.58	0.37	0.37	0.36	0.50
18	2	10686889	715247	9574	TGGGTTCCTARCCACAGAATA	0.34	0.22	0.22	0.33	0.43	1.57	0.77	0.20	0.34	0.47	1.50	0.76
18	2	10692647	10454738	9575	GTATACCAACRTTCAGTTATA	0.34	0.27	0.24	0.33	1.98	1.31	0.73	0.22	0.27	1.73	1.27	0.74
18	2	10701844	6721739	9576	CAGGTCAGTAKTAATAAAAGT	0.40	0.10	0.14	0.65	1.37	1.17	0.92	0.14	0.75	1.31	1.15	0.93
18	2	10718689	4669601	9577	GAACTCAATTYAAAGTAAATC	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10730563	7599759	9578	TGAGAGAATTWAAAAAATAAA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10741008	6432129	9579	CTTCAGCCCTYAGAGTATCTG	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10769325	17455388	9580	ATACTTTGCAYATCCCCTGAG	0.51	0.87	0.87	1.39	1.16	1.25	1.05	0.85	1.41	1.13	1.21	1.06
18	2	10780014	4614910	9581	GACTAGGAATSAGGTTAAGTT	0.03	0.14	0.14	1.12	1.24	1.08	0.81	0.12	1.20	1.21	1.07	0.85
18	2	10791525	17364596	9582	CTCCAGAGCTSTAGGGCTGCC	0.26	0.47	0.47	0.23	0.79	0.79	0.98	0.42	0.22	0.80	0.79	0.98
18	2	10808361	6736664	9583	ATTTGGAAAGRGCATCATCTT	0.38	0.30	0.27	0.37	0.06	0.38	0.48	0.23	0.38	0.07	0.39	0.49
18	2	10816924		9584	GGGATTAACAMCATGACTGAC	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10827397	4668694	9585	AACATGCTTARTTACATGCTT	0.36	0.57	0.57	0.15	0.23	0.06	0.63	0.43	0.14	0.21	0.06	0.59
18	2	10842229	16856608	9586	ATCAGTAAGAYGCTATTAACT	0.41	0.49	0.47	0.51	0.40	0.62	0.56	0.43	0.50	0.38	0.63	0.59
18	2	10851593	1198864	9587	ACAAGAGCTTSATCTGAAATG	0.35	0.70	0.70	0.78	1.78	1.39	1.23	0.62	0.83	1.74	1.36	1.20
18	2	10859491	1198849	9588	GGCCGCCTACRACACTCTGAA	0.57	0.28	0.28	2.44	1.73	1.11	1.59	0.24	2.61	1.68	1.09	1.57
18	2	10867291	1734440	9589	GAAACCCTCGYTACCTGGGCA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10874298	1060005	9590	ATTAACAACAYAGAAAGCCTT	3.60	3.52	3.52	2.05	2.15	2.20	1.11	3.37	2.09	1.91	2.10	1.07
18	2	10881033	2969883	9591	TTCTCCAGACKGCACAGATTT	0.21	0.28	0.28	2.34	2.47	2.06	1.30	0.22	2.88	2.31	1.94	1.28
18	2	10887663	1734344	9592	TCGGAGGGTAYAGGAATCACT	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10893588	1734363	9593	CTCCCACTCCYTGGGCTGCAC	0.14	0.22	0.22	0.16	2.42	1.87	0.65	0.21	0.15	2.21	1.81	0.65
18	2	10900117		9594	AAGTAAGACTRAGGCTGGGTG	-	-	-	-	-	-	-	-	-	-	-	-
18	2	10913836	17456225	9595	GTGGCCTGGASAAATCACCTT	0.11	0.32	0.32	0.26	1.00	1.94	0.82	0.31	0.24	0.99	1.89	0.82
18	2	10920162	1686486	9596	GCTATTGCCTRTAATTTGGCC	0.11	0.31	0.31	0.92	0.66	0.44	1.48	0.26	1.03	0.67	0.44	1.44
18	2	10939384	1734396	9597	GAGAACAATTSTGACCCTGCT	0.58	0.95	0.95	0.35	0.56	0.60	0.38	0.92	0.37	0.58	0.61	0.38
18	2	10952457	16856756	9598	TTGTGTGATAYCAACTATTCG	0.44	0.70	0.68	0.51	0.52	0.47	0.40	0.68	0.52	0.57	0.47	0.44
18	2	10952929	11900322	9599	TCCTTAGCTTSGGTTCTTATA	0.14	0.36	0.37	0.58	0.29	0.22	0.57	0.33	0.57	0.28	0.24	0.57
18	2	10978731	7572213	9600	GTGGTCTTAARGGACATAGTT	0.46	0.64	0.64	0.43	0.30	0.34	0.21	0.54	0.43	0.35	0.34	0.21
18	2	10986028	2884316	9601	ACTTTTCTCAWCCTTCCTAGA	0.05	0.12	0.12	0.11	0.06	0.16	0.21	0.10	0.03	0.05	0.18	0.23
18	2	11004338	3732105	9602	GTGGTGTCATYGCCATCGCCC	0.08	0.08	0.11	0.03	0.01	0.03	0.45	0.08	0.04	0.01	0.03	0.42
18	2	11015518	13016124	9603	CCATGGTTCAYGGTTATGCTT	0.60	0.06	0.06	0.02	0.12	0.18	0.02	0.02	0.01	0.12	0.17	0.03
18	2	11026352	10460292	9604	CAGAAACACARGCATCCTTGT	-	-	-	-	-	-	-	-	-	-	-	-
18	2	11032514	4669652	9605	TCCTCTGTGCRTATTTTTTTT	-	-	-	-	-	-	-	-	-	-	-	-
18	2	11038580	13025975	9606	ATCAAACCTCWAATTGGGCAG	0.12	0.29	0.29	0.28	0.41	0.08	0.10	0.23	0.27	0.40	0.08	0.10
18	2	11049691	6432153	9607	CTAATATGCCRTTTTCATTTC	0.49	0.87	0.82	0.81	0.20	0.24	0.12	0.75	0.87	0.20	0.24	0.11
18	2	11062178	16856949	9608	TGATGGAACCYGATTCCTCCA	1.27	1.57	1.57	1.00	0.38	0.25	0.30	1.38	1.01	0.39	0.26	0.28

18	2	11069434	13390165	9609	GAGAAAAACAYGGAAGTTCAA	0.36	0.72	0.72	0.91	0.90	0.57	0.17	0.62	0.99	0.88	0.60	0.16
18	2	11075808	4669661	9610	ATTGGACAAARCCACTGCAGC	0.30	0.66	0.66	0.49	0.99	0.65	0.07	0.60	0.45	0.99	0.64	0.06
18	2	11082210	2357885	9611	TAAAACTAATKTGCTCTACAG	0.73	0.75	0.75	0.62	0.41	0.36	0.17	0.70	0.67	0.43	0.36	0.17
18	2	11095422	16857006	9612	AGTCACATTTWCATTATGCTC	0.72	0.71	0.71	0.49	0.14	0.31	0.56	0.54	0.51	0.15	0.32	0.59
18	2	11101115	4669669	9613	TTCCAGGAAGMGGGTGAAGAA	0.26	0.47	0.47	0.63	0.19	0.64	0.60	0.45	0.59	0.19	0.64	0.57
18	2	11107409	12996749	9614	GGAATTGGAGRGTAGAACTAA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	11116721	16857065	9615	TCTTAGGTCCRCATATTTGAA	0.33	0.64	0.64	0.22	0.19	0.40	0.21	0.62	0.22	0.20	0.43	0.22
18	2	11125776	11694298	9616	CATTAATGGTRCATGAGCACA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	11133435		9617	CAATAAATTTRTATTCTAAGT	-	-	-	-	-	-	-	-	-	-	-	-
18	2	11139730	10208479	9618	TCAAAAGAACWCTCTTCCTTC	0.07	0.25	0.19	0.43	0.36	0.31	0.66	0.15	0.43	0.38	0.32	0.71
18	2	11146393	2100369	9619	AATTGGCTGARGTCAGTTACC	0.53	0.84	0.84	0.73	0.77	0.87	0.64	0.77	0.80	0.78	0.87	0.66
18	2	11150945	7564899	9620	CATCATGCAARGGACTTTAAG	0.16	0.42	0.42	1.19	2.20	0.82	0.52	0.37	1.19	2.06	0.82	0.50
18	2	11158524	10177026	9621	AAGAGGCCCTYGTCTCTCACA	-	-	-	-	-	-	-	-	-	-	-	-
18	2	11166200	6432167	9622	CAGGCCACTGRCTTTGTGTAT	0.01	0.02	0.04	0.95	1.36	1.29	0.55	0.02	0.97	1.31	1.25	0.56
18	2	11185834	4669690	9623	CCTCGTTTTTWAAAAGCTTTA	0.02	0.06	0.06	0.07	0.85	0.91	0.64	0.03	0.07	0.84	0.89	0.63
19	2	60172290	2215897	9624	GAATATCCAGMAGCAATGCCT	0.09	0.29	0.29	0.06	0.05	0.04	0.02	0.25	0.06	0.05	0.04	0.02
19	2	60182556	4672357	9625	TTCCTCGTTTKTAAAGAGTTC	0.52	0.26	0.26	0.20	0.05	0.02	0.06	0.24	0.19	0.06	0.02	0.08
19	2	60191069	994972	9626	AAGGAAACTTYCTGCCTGGCC	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60206928	17030159	9627	CATGATTCACRGATGGAGTGA	1.03	1.22	1.22	0.44	0.09	0.05	0.01	1.11	0.45	0.09	0.05	0.01
19	2	60217515	17011925	9628	GGGGAGATACYCTATAAAATA	0.68	0.45	0.45	0.64	0.28	0.03	0.05	0.33	0.68	0.33	0.03	0.05
19	2	60229084	17027385	9629	TTTTAGGGTASGACCATGAGG	0.37	0.37	0.37	0.49	0.31	0.36	0.29	0.29	0.54	0.31	0.38	0.30
19	2	60235778	13415334	9630	CCTGTAGAGARGTGAGTGTCC	1.18	0.90	0.95	0.36	0.15	1.24	0.76	0.89	0.35	0.17	1.21	0.75
19	2	60242815	17329188	9631	GGACTTCTTARTGATTTTTTT	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60250821	17029624	9632	CTGGAGCAAAMTGGTACCTAG	0.37	0.62	0.48	0.21	0.83	0.67	0.84	0.38	0.19	0.84	0.64	0.85
19	2	60259529	17401147	9633	TGCATGATAAYTGGATGTTTT	0.47	0.60	0.60	1.39	0.46	1.09	0.32	0.56	1.44	0.45	1.10	0.35
19	2	60268436		9634	AGCACTTCCAYAGGGCCAGCG	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60276575	1468757	9635	AGAAGCCTGTSCTAAGGGTCT	2.73	2.93	2.93	1.23	1.59	0.29	0.19	2.86	1.47	1.55	0.28	0.19
19	2	60290466	17036151	9636	GTCACAAAACRTTGTGTCTGA	0.76	1.22	1.22	2.59	1.11	0.33	0.13	1.17	2.99	1.10	0.33	0.14
19	2	60304276	6729620	9637	GACTCTAGATWATTACATAAG	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60309787	6545785	9638	TGCCATGGAGYCCAGACCTCC	0.57	0.07	0.08	1.48	1.07	0.59	0.25	0.05	1.57	1.03	0.61	0.25
19	2	60319988		9639	GGCCACAGATSTGTGGTTCTG	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60347584	17010024	9640	AGAAAGGCCTRGGAGAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60352835	9309322	9641	GCGTAACTCCRAGAGGCAAAC	1.57	2.01	2.01	1.28	1.01	0.66	0.36	1.95	1.25	1.01	0.71	0.38
19	2	60362643	10188396	9642	TCTCACTAGCYGGATTGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60372587	359269	9643	TGAATTCAACKTTTGGACCAT	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60380908	359242	9644	CTGAGTATTTRGAGGGCAGAA	0.45	0.74	0.74	1.35	1.11	0.49	0.50	0.71	1.45	1.14	0.51	0.53
19	2	60399553	17017706	9645	AGCTCAGGAAKGTCATTCAAG	0.59	1.00	1.01	0.65	0.86	1.07	0.95	0.90	0.60	0.86	1.06	0.93
19	2	60405996	4672376	9646	TAAAACCCATKTTCTCCCTAC	0.37	0.67	0.67	0.90	0.86	1.49	0.92	0.64	0.96	0.85	1.42	0.90
19	2	60412135	2110398	9647	GATGCTTCTAYTGGGCCCTGA	0.62	0.92	0.92	0.77	1.39	1.05	0.65	0.86	0.75	1.35	1.04	0.68
19	2	60426015	2419900	9648	CTCCCTTGAGYCTTGGGCAGT	0.73	1.06	1.06	0.72	0.99	0.54	0.30	0.99	0.79	0.97	0.56	0.32
19	2	60432002	9808396	9649	ATAGACCCAGWTAGCTATATT	-	-	-	-	-	-	-	-	-	-	-	-
19	2	60439045	4672384	9650	CTCTCGCTAARGCCCTAGTGC	0.29	0.64	0.64	0.56	0.52	0.69	0.72	0.58	0.57	0.53	0.69	0.75
20	2	65423719	7556894	9651	CCATATTTTCRTCCTTGCAAT	0.38	0.70	0.70	0.38	0.78	0.45	0.74	0.66	0.38	0.77	0.44	0.76
20	2	65435748	906575	9652	CAACACTCCCRCTTCAAGGAA	1.09	0.22	0.22	0.45	0.76	1.06	0.31	0.20	0.47	0.78	1.08	0.34
20	2	65456741	7601027	9653	AGTGCGCACTRTACAAGCAGA	0.47	0.86	0.89	0.47	1.32	0.74	0.56	0.85	0.46	1.30	0.75	0.59
20	2	65468938	871974	9654	CATGGGTCAGYCTCATTTCTG	0.50	0.76	0.76	1.66	1.06	0.81	0.57	0.74	1.86	1.06	0.84	0.59
20	2	65473043	4671658	9655	AGAATCCATTYTCTACTTCTG	0.81	1.15	1.15	1.46	1.17	0.57	0.61	1.09	1.71	1.14	0.54	0.63
20	2	65495925	1396210	9656	CAGGTCCACTRGAAATGGATG	0.98	1.26	1.26	1.55	1.32	0.82	0.36	1.19	1.84	1.32	0.84	0.36
20	2	65508717	11126035	9657	ATTCATTTCCYAGCACTGATC	0.65	0.70	0.70	0.24	0.69	0.42	0.76	0.62	0.21	0.71	0.44	0.77
20	2	65520557		9658	TAGCAAATGGRAACTGTGCAA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65527079	17534670	9659	CCTCAAGGTARAGATCGCGTG	0.74	1.15	1.15	0.36	0.08	0.94	0.92	1.11	0.35	0.08	0.96	0.93
20	2	65533340	10186481	9660	AACATTCATCRGACCACTGGA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65547339	2661798	9661	GTCGCCAGCCWCAGGAATTAG	1.00	1.47	1.47	0.41	1.09	0.94	0.98	1.41	0.44	1.11	0.90	0.98
20	2	65558617	7565437	9662	CACTGGCTAGYAGCATCAGTT	0.35	0.68	0.68	0.69	0.96	1.19	1.00	0.65	0.70	0.94	1.19	1.02
20	2	65591363	1437461	9663	AAAATTTTGTYAAGGGAAATT	1.07	1.33	1.31	1.15	0.95	0.45	0.53	1.25	1.27	0.98	0.45	0.54
20	2	65598112	11675538	9664	CGTGGGTTTGYAGGGAGGATT	0.70	1.06	1.06	0.89	0.59	0.67	0.26	1.01	0.99	0.60	0.70	0.25
20	2	65603411	754110	9665	ATGGGTGTCTYAGAGGTTGGA	0.38	0.42	0.42	0.35	0.65	0.66	0.79	0.41	0.33	0.67	0.65	0.80
20	2	65614900	840970	9666	ACACATCCATWATGTCCGAGG	0.47	0.42	0.42	0.10	0.54	0.52	1.00	0.40	0.06	0.54	0.53	1.00
20	2	65625554	840942	9667	GTGTATTTAGSGCATGCTGAA	0.30	0.13	0.13	0.72	0.17	0.64	1.01	0.10	0.71	0.17	0.66	0.97
20	2	65631592	840952	9668	TGGCAGCAACRCAGAGAAAAC	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65638528	6717262	9669	TAAATCAGTARTTATTGCTAT	0.13	0.34	0.30	0.21	0.81	0.46	1.00	0.28	0.21	0.87	0.48	0.97
20	2	65651816	17030318	9670	CTGGTGTTGCYGGATCTTCCA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65654051	1574	9671	AGGGAATCCCRCTGATCAGGG	0.34	0.59	0.50	0.76	0.63	1.36	0.72	0.48	0.78	0.64	1.32	0.74
20	2	65664691	10496126	9672	AGGCACATATRTTCTTTCGTG	1.60	1.57	1.57	0.88	0.76	0.50	1.52	1.36	0.90	0.71	0.52	1.50
20	2	65675296	11126042	9673	TGCTGTGGTCWTTTGAGAGGA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65683942	702919	9674	TGCTGGTTTGYTGTGGGAATG	0.29	0.40	0.31	0.80	0.91	1.17	0.75	0.27	0.82	0.91	1.13	0.71
20	2	65697020	4671131	9675	GCTTGAAATCRCAAAAGGACA	0.21	0.27	0.30	0.03	0.62	1.22	1.26	0.26	0.03	0.61	1.15	1.23
20	2	65705765	1673441	9676	GGATCAAGACRTGGAAGAGAA	0.01	0.13	0.13	0.30	0.11	0.43	0.91	0.07	0.31	0.11	0.45	0.88
20	2	65718678	1641488	9677	CGCAGAGTATYTCGGTGCATT	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65730097	897875	9678	CCAAGTGGTGKATTTTCATAA	0.59	0.41	0.54	0.26	0.21	0.09	0.42	0.47	0.24	0.24	0.10	0.44
20	2	65736091	12614613	9679	GGGTACTAGASATCTTTTCTG	0.61	0.54	0.54	0.20	0.06	0.06	0.60	0.48	0.19	0.06	0.05	0.61
20	2	65747527	17030462	9680	GGAGGCTGAARTCCAAGTTTG	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65753995	17030504	9681	TCTTATATTTYTATTCAGACA	0.61	0.50	0.62	0.05	0.04	0.61	0.77	0.50	0.03	0.03	0.64	0.77
20	2	65764880	11900826	9682	AATAGACAAAYTAGACAAACA	0.00	0.00	0.00	0.20	0.79	1.05	0.86	0.00	0.18	0.81	0.98	0.85
20	2	65773306	4671675	9683	TTCTGATGGAYTTGAGACGCA	0.18	0.43	0.43	0.63	1.82	1.32	0.80	0.40	0.73	1.65	1.31	0.83
20	2	65780691	4671677	9684	CAAAGATGCTYAGTTATCTGT	1.21	1.19	1.19	0.49	1.94	1.29	1.38	1.04	0.53	1.75	1.23	1.35
20	2	65786536	6745649	9685	TCATGTCTGGRAATGCTTTAA	0.25	0.24	0.24	1.17	0.54	2.01	1.50	0.16	1.23	0.55	1.83	1.50
20	2	65794256	12471196	9686	AGGCTGGAAASTAGAATTCCC	0.77	1.13	1.13	0.45	1.02	0.89	2.13	1.02	0.41	1.03	0.90	1.96
20	2	65801323	840778	9687	GCAGGATCCCRTCACAGCAGG	0.04	0.13	0.13	0.49	0.58	1.32	1.47	0.10	0.54	0.59	1.28	1.43
20	2	65807090	17030616	9688	GTAGGTCGAAYTGCATCTGCT	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65817903	4671679	9689	ACAATGAGGTRCACAGAGCGC	0.01	0.08	0.08	0.24	0.81	1.44	2.33	0.03	0.23	0.80	1.42	2.20
20	2	65825738	10490612	9690	TCTAGTCTTAWGAGAGCACTG	1.81	0.56	0.62	1.36	1.00	1.88	1.87	0.57	1.38	0.99	1.78	1.82
20	2	65833507	1544694	9691	CTTGACATGAYAAAGACAGTC	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65839792	17030656	9692	AGGTCCAGGGYACTTCTAGTG	1.67	2.21	2.21	1.35	1.99	1.89	1.66	2.15	1.36	1.93	1.79	1.56
20	2	65846449	12622132	9693	TACAGGAGAGYAAAATGAAGA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65852315	17628647	9694	TGTGTACAATKGAATAGATAT	1.29	1.19	1.10	1.29	2.13	1.36	1.00	0.98	1.32	2.01	1.33	0.98
20	2	65858219	12990354	9695	GAGAACAGACRATTCTTGGAA	0.02	0.10	0.12	0.67	1.10	1.70	1.39	0.10	0.68	1.07	1.56	1.38
20	2	65869350	3815606	9696	CTTATTGGACSAGCCCCTATG	0.09	0.24	0.24	0.14	0.46	0.91	2.21	0.21	0.13	0.49	0.93	2.04
20	2	65878390	1549022	9697	CACGGAGGCTYCTTTTTAGAT	0.04	0.17	0.17	0.28	0.27	0.23	1.12	0.14	0.28	0.24	0.26	1.10
20	2	65885884	6743531	9698	CCAATAAAAASAAAGTCACTC	0.24	0.51	0.51	0.36	0.20	0.45	0.78	0.47	0.33	0.22	0.47	0.80
20	2	65893738	2193463	9699	AGCGTTCACCRGTTAACCAGG	0.30	0.12	0.12	0.17	0.53	0.72	0.53	0.08	0.16	0.54	0.74	0.54
20	2	65902127	2193466	9700	TTATTCTTGTKTGGAGAACTG	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65911205	875321	9701	TCCTTTATGGWTAATGTGGAT	0.12	0.13	0.13	0.35	0.40	0.56	0.75	0.08	0.32	0.41	0.54	0.79
20	2	65922205	13431395	9702	AGCCTGGGACKGAGGCGTTTC	-	-	-	-	-	-	-	-	-	-	-	-

20	2	65929245	17030814	9703	GGCGCCGAGAYGGATGCTTGA	-	-	-	-	-	-	-	-	-	-	-
20	2	65937885	13424832	9704	TATTTGGTGGRACAATAGGAA	0.18	0.05	0.00	0.50	0.47	0.24	0.81	0.00	0.51	0.46	0.26	0.82
20	2	65945059	6740790	9705	TAAAAACCAASTGAAACAAAA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65950942	961430	9706	CATTAAACTARATACATATGT	-	-	-	-	-	-	-	-	-	-	-	-
20	2	65955364	4141571	9707	CAAATTCAACYCAATGGGATG	2.45	0.99	0.88	0.57	0.33	0.22	0.12	0.86	0.63	0.37	0.19	0.12
20	2	65965124	3845821	9708	AATCTTAGCAYAATTTACTCT	0.91	0.68	0.68	0.60	0.37	0.19	0.05	0.63	0.62	0.38	0.17	0.06
20	2	65974456	13421607	9709	ATAGCTGTTAYGTTGTTGTGT	0.20	0.45	0.42	0.31	0.13	0.11	0.12	0.37	0.30	0.13	0.11	0.11
20	2	65980920	9309380	9710	GGAACATATTSTAAAGGGAGA	0.33	0.42	0.42	0.04	0.11	0.03	0.04	0.38	0.03	0.09	0.01	0.03
20	2	65989798	12713551	9711	GTAACTGGAARTTCAGGGATA	0.20	0.46	0.46	0.16	0.01	0.03	0.15	0.42	0.12	0.00	0.03	0.15
20	2	65990735	7583237	9712	TGGTATATTARTCCGCGGGTA	0.31	0.64	0.64	0.15	0.01	0.43	0.41	0.54	0.14	0.00	0.42	0.36
20	2	66005877	6760229	9713	CCCAGCTATCYGTTGCTTCCA	-	-	-	-	-	-	-	-	-	-	-	-
20	2	66015933	12471713	9714	TTGACACACASAGTGCTTTGT	0.28	0.00	0.03	0.08	0.73	0.61	0.83	0.00	0.09	0.73	0.62	0.83
21	2	67379633	1483342	9715	GGAGCTTTCTYCAAACAAGAT	1.70	1.10	1.02	0.49	0.04	0.04	0.27	0.98	0.53	0.02	0.03	0.27
21	2	67386735	17601323	9716	CTTTACATCCYTAAGACAATT	0.41	0.36	0.36	0.18	0.44	0.16	0.18	0.32	0.15	0.50	0.17	0.19
21	2	67393284	7560230	9717	ATGGGATCTAYTGACACTGCC	0.18	0.20	0.20	0.60	0.39	0.63	0.16	0.15	0.62	0.42	0.66	0.16
21	2	67399278	10198347	9718	AGAATCAAGCYGCTGTCTGCT	1.10	0.85	0.85	0.56	0.85	0.40	0.53	0.78	0.60	0.86	0.43	0.55
21	2	67404868	12999776	9719	CTCAACAACAKTTGGCAAAGT	0.50	0.53	0.53	0.62	0.58	1.04	0.29	0.51	0.65	0.64	1.02	0.31
21	2	67418375	17033369	9720	TACATATATGYACTCTATCAT	0.33	0.30	0.30	0.13	0.57	0.69	0.39	0.26	0.12	0.58	0.68	0.41
21	2	67424769	13385154	9721	CTGTGTTGGTYCCAGAGTCAC	0.60	0.42	0.42	0.72	0.47	0.41	0.50	0.37	0.74	0.48	0.43	0.54
21	2	67433043	11696003	9722	TTAAGAAAAGSTTTACAGACC	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67441931	1483333	9723	TGTTAAGTGAYATTTTAAGTA	1.22	1.52	1.52	0.97	0.36	0.37	0.61	1.45	1.01	0.33	0.40	0.63
21	2	67458005		9724	GTGGTGATTTMTATCATGTTT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67467381	17033455	9725	GGATGTTTAGRATTGGTTAAA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67482099	17603914	9726	ACTCATTCCARTGGCTTCTAC	0.58	0.48	0.59	0.69	0.82	1.13	0.66	0.54	0.68	0.84	1.12	0.66
21	2	67491618	7564335	9727	TTAGGAACACRAAGGGTCTAG	1.39	2.08	2.04	1.50	1.76	1.24	1.15	1.97	1.88	1.62	1.23	1.17
21	2	67510284	6755797	9728	TTTTGTTTTCRTGAGATATCT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67517384	6546302	9729	TTCCATCACTKTCTAGAAACA	1.11	1.69	1.69	1.59	2.29	1.22	1.08	1.63	1.83	2.11	1.20	1.07
21	2	67535953	13016812	9730	GGACCTGACTRCTACCCGAAC	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67542127	13036061	9731	TTTACCCAGAYGATTTCAGAA	0.24	0.10	0.10	0.78	1.08	1.62	0.76	0.07	0.84	1.04	1.52	0.76
21	2	67548488	17545245	9732	TCAAATAGAGRCAGATCCATC	0.11	0.15	0.19	0.21	0.47	0.53	1.20	0.13	0.19	0.49	0.54	1.19
21	2	67551929	13424211	9733	GCTAGACTTAYATAACATTGC	0.93	0.58	0.61	0.47	0.35	0.45	0.30	0.54	0.48	0.36	0.47	0.29
21	2	67574241	17033574	9734	ATAATATGAARAAAAAAACTA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67580498	632647	9735	ATGGAGCCAARCACAAGCTGC	0.40	0.54	0.51	0.25	0.69	0.27	0.53	0.48	0.25	0.67	0.29	0.55
21	2	67586157	12470994	9736	GAGACCCTCTMTGCTTTTGAG	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67601874	581955	9737	TTCTTATCAARAGCTACCCAT	0.23	0.11	0.17	0.17	0.19	0.48	0.32	0.15	0.16	0.20	0.52	0.32
21	2	67607247	17605887	9738	TGCTTACCATYCTCAAAAATT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67614575	17033635	9739	TTAGTTAGCTYTCTGAACTTT	0.64	0.62	0.62	0.46	0.65	0.29	0.45	0.50	0.48	0.64	0.31	0.50
21	2	67620846	7570496	9740	TTAGTGAAAARCAGCAGATTA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67627681	1521043	9741	CATGAGACCTKAAGTTTCCAA	1.50	1.58	1.58	0.39	0.08	0.31	1.81	1.52	0.37	0.08	0.33	1.78
21	2	67634635	6751917	9742	ACCATCATGCRGATAAATGAA	0.20	0.27	0.27	0.36	0.12	1.48	1.26	0.23	0.37	0.12	1.37	1.29
21	2	67640906	10496150	9743	GTGGAATAGAKGCTGAAAGCT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67647621	12713598	9744	GATGAGAAACMGCTGTGAATG	0.51	0.54	0.50	0.13	0.84	0.75	1.05	0.49	0.13	0.85	0.75	1.05
21	2	67653443	1402440	9745	ATGCTGACATYATTTGTTTTA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67664198	2683690	9746	TATCACAGAGRTGGAGCCATG	0.26	0.11	0.11	0.20	0.40	0.82	1.17	0.08	0.20	0.44	0.88	1.13
21	2	67670314	2683687	9747	GACGTAATAARACAGATGTCA	0.51	0.60	0.60	0.29	0.69	0.97	1.04	0.57	0.28	0.74	0.94	1.00
21	2	67691039	4381768	9748	TCACATGGCAYAAAATTTGAA	0.17	0.11	0.13	0.72	0.64	0.78	1.05	0.13	0.70	0.63	0.77	1.01
21	2	67697688	4671186	9749	AATGCTGAGCRATAAGACTTT	0.75	1.25	1.28	0.60	1.25	0.33	0.76	1.24	0.59	1.22	0.36	0.74
21	2	67704977	4671187	9750	TCTCCCCTCCRATCCCAGCAT	0.61	1.08	1.08	1.53	1.68	0.75	0.42	1.04	1.82	1.52	0.75	0.42
21	2	67711916	13005138	9751	GCAGAGGAAASTGTATTTCAT	0.35	0.71	0.71	1.86	1.82	1.07	0.90	0.63	2.11	1.64	1.07	0.91
21	2	67718770	10490722	9752	CACATGAATAKTTGAAGGGCC	1.27	1.82	1.82	0.93	1.69	1.05	0.53	1.72	1.00	1.61	1.02	0.55
21	2	67740265	13398112	9753	GCTTGCCCCGYGTAATATAAT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67748158	2861683	9754	AGAGATGGGGMAAGTTATTAC	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67756672	6746394	9755	ACTTTACTCTMTAAAATGTGC	0.26	0.07	0.07	0.97	0.74	0.85	1.42	0.04	1.05	0.78	0.85	1.33
21	2	67764340	7598674	9756	GTGAAATTCTRTTTTTTCCTT	0.39	0.09	0.06	0.60	1.15	1.59	1.10	0.04	0.68	1.09	1.54	1.07
21	2	67770803	6756226	9757	AGTTCATGGGYCCTTGTAATA	0.36	0.70	0.75	0.70	1.74	1.42	1.42	0.71	0.72	1.65	1.39	1.37
21	2	67777059	11126143	9758	GGTTATATTCYGAGCCCTGCC	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67783039	1897182	9759	AGGCTAGTGTSGCTTAGCATA	0.51	0.93	0.93	0.87	0.79	1.43	1.13	0.89	0.86	0.79	1.40	1.14
21	2	67784222	2902028	9760	ACGAGGAAAAMAGTGCATGCA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67800707	1367463	9761	TGAGATATTAWGCTCAGAATG	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67810040	17040168	9762	TACTCACGTCRTATACATTCC	1.56	1.50	1.50	1.10	1.45	1.19	0.73	1.34	1.31	1.43	1.15	0.70
21	2	67814820	4671822	9763	TTCCGAGGTCKACTATAATTC	0.30	0.48	0.48	2.13	2.14	0.69	1.40	0.42	2.34	1.91	0.68	1.38
21	2	67825191	10174450	9764	TGCATTAAGTWCTGGCTGCTT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67835463	12464252	9765	GGCACCACCCSTTGGATTTTC	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67841853	10496148	9766	CTAGCTCAAAYTACAAAAGCA	0.09	0.08	0.07	1.57	2.20	2.76	1.88	0.05	1.72	1.98	2.60	1.78
21	2	67849063	6724226	9767	AAATGTCTATKTTCAAATCAG	0.65	1.02	1.06	0.46	3.74	4.19	2.33	0.99	0.46	3.33	3.76	2.20
21	2	67858542	10865363	9768	GGAAATATTCYGAATCCCTGA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67866931	2861708	9769	AAATTCAACTYAATCCCAGGC	0.42	0.37	0.41	0.86	2.39	3.09	2.90	0.36	0.93	2.20	2.85	2.65
21	2	67874639	13411734	9770	GGCATCTGAGYCCTAAGGTCC	0.14	0.02	0.02	1.91	1.82	1.96	2.04	0.00	2.15	1.76	1.86	1.96
21	2	67884811	1367474	9771	GGAGATCTCARAAGAAAACAC	0.28	0.33	0.33	1.43	1.74	0.94	1.67	0.27	1.49	1.66	0.96	1.67
21	2	67900726	1346870	9772	AATCTGCCCARGTCTGTTCAA	1.16	1.53	1.53	0.78	1.27	1.61	0.70	1.49	0.73	1.21	1.53	0.70
21	2	67910693	13014491	9773	GGCCCAAAAGYAGGTAAGCTG	0.66	1.09	1.09	0.51	0.43	0.77	0.99	1.03	0.52	0.45	0.78	0.96
21	2	67916224	1036069	9774	CACGATTCTGWACAAGGGCCT	0.27	0.58	0.58	0.95	0.67	0.71	0.47	0.55	1.00	0.64	0.69	0.48
21	2	67925199	4671853	9775	TTTGCCTCACYATATCTCATT	0.94	1.23	1.26	0.71	0.68	0.55	0.39	1.19	0.73	0.67	0.55	0.42
21	2	67932944	765788	9776	ATTCACGTGCRAAGGTTAACT	0.15	0.04	0.04	0.48	0.17	0.28	0.27	0.00	0.48	0.18	0.26	0.25
21	2	67940074	12053579	9777	GAGTCTGCAGSAGCTAATAAT	0.08	0.25	0.25	0.07	0.18	0.14	0.23	0.22	0.06	0.19	0.13	0.24
21	2	67942471	10439491	9778	CTCCTGTGAASTGCTGGTCAG	0.07	0.17	0.17	0.06	0.15	0.17	0.13	0.14	0.06	0.13	0.17	0.13
21	2	67955086	1367464	9779	ACAAGAGAAARGATTACCACA	0.36	0.57	0.57	0.33	0.09	0.05	0.37	0.56	0.31	0.09	0.04	0.38
21	2	67963106	7592215	9780	TTTAGTAACGRAGATCCATTA	0.25	0.50	0.50	0.47	0.13	0.24	0.07	0.47	0.46	0.13	0.27	0.08
21	2	67975534		9781	AAGTGGAGCTRTGCTGTTATA	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67983641	12991815	9782	AGCCCATGAASGGGAAAGGAT	-	-	-	-	-	-	-	-	-	-	-	-
21	2	67990630	966819	9783	GGATAAGCACRGGAATGCCAT	0.24	0.19	0.16	0.26	0.22	0.19	0.17	0.12	0.24	0.24	0.18	0.18
22	2	69497944	6546505	9784	CAAGAAATTAMTTGATGACAC	0.23	0.06	0.06	0.31	0.01	0.00	0.02	0.03	0.27	0.00	0.00	0.01
22	2	69512117	4452195	9785	TTCCAGCCTCWTCTATCTTAA	0.34	0.06	0.06	0.20	0.03	0.01	0.02	0.05	0.17	0.03	0.00	0.01
22	2	69537289	7580642	9786	GTCAAAATAAYCTTGATGTTA	0.31	0.03	0.00	0.09	0.11	0.18	0.35	0.00	0.08	0.10	0.18	0.38
22	2	69598875	4441525	9787	ATGTACCTCTYATCAAAATAA	0.61	0.14	0.14	0.16	0.23	0.90	0.47	0.12	0.16	0.23	0.90	0.51
22	2	69616592	2312205	9788	CAAACCACAGRGGTGATTATT	0.24	0.05	0.05	0.30	0.89	0.74	0.56	0.02	0.26	0.91	0.73	0.54
22	2	69628836	10185225	9789	AGATGATGAAKTGCCATAAAC	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69637691	4852231	9790	CTCAACTAGAYGGGTAACAGG	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69654575	2312210	9791	GAGGATACTGYTTGTCTACTG	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69662006	7566200	9792	TATCATGTTTSAGCCTAGTAC	0.42	0.10	0.10	0.53	0.96	0.58	0.58	0.07	0.55	1.01	0.53	0.58
22	2	69668942	3732271	9793	TAAAGATAGCRGATTGCTACT	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69673480	4852825	9794	CTTCAGGCCAMATCAAACCAT	1.03	1.07	1.07	0.31	0.08	0.76	1.02	1.05	0.32	0.07	0.75	1.00
22	2	69693648	2312213	9795	GCTAATACGCSTCTGGGCCAA	0.47	0.69	0.72	0.25	0.10	0.28	1.57	0.68	0.25	0.11	0.32	1.54
22	2	69703553	6718757	9796	TATCTGACCAYGTGATTGTAT	-	-	-	-	-	-	-	-	-	-	-	-

22	2	69716588		9797	GGGACTCAGAYCAAGAGCCAG	-	-	-	-	-	-	-	-	-	-	-
22	2	69741567	4852866	9798	GTGCCTCACAYAAACTAAGCT	0.33	0.61	0.59	0.30	0.73	0.50	0.56	0.57	0.29	0.75	0.49	0.57
22	2	69759817	17036830	9799	AGGGTGTAAARAACACCAGAG	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69765214	10191956	9800	CTTATCTTGAYGTCTGTAATG	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69770944	17036881	9801	AAACACAGAAMATCTGAATTA	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69784308	1396797	9802	CTTTTTTAAASAAGCTGTGCT	0.28	0.28	0.28	1.06	0.73	0.84	1.29	0.19	1.17	0.72	0.85	1.25
22	2	69795732	12478160	9803	TACACTGTGARCTATTATAGT	1.73	1.86	1.86	0.83	0.86	1.49	1.08	1.80	0.89	0.87	1.44	1.09
22	2	69822665		9804	TCCTAGCTCARGGCCTCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69848286	2048255	9805	AGCACAGACAYGCTCTCTTCT	0.18	0.44	0.42	0.63	1.70	2.59	0.46	0.39	0.62	1.65	2.40	0.43
22	2	69855811	877123	9806	GAAACCAATCRAGAAACAAGG	0.16	0.25	0.22	1.78	3.29	1.40	1.18	0.19	1.95	2.94	1.37	1.16
22	2	69889941	4852988	9807	ACTGACGAGCKTCACAGCCAG	2.19	2.62	2.62	1.66	1.96	1.57	0.73	2.54	1.81	1.82	1.55	0.71
22	2	69901452	13012793	9808	ATCATGCCTCSTTGAATCTAC	2.38	2.62	2.62	1.90	1.25	1.19	0.38	2.56	2.06	1.23	1.16	0.35
22	2	69911087	4852328	9809	CAGCTTATGGRTTGTAGAAAG	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69918766	7586494	9810	AAGAATGAAAYTGGAAGGTAA	0.80	1.16	1.16	1.74	1.65	0.69	0.71	1.07	1.98	1.60	0.71	0.74
22	2	69940961	3771542	9811	AGCAGGGGAGRGACATTGTGA	0.87	1.27	1.27	1.48	1.14	0.93	0.42	1.22	1.71	1.14	0.94	0.39
22	2	69947133	17037082	9812	GAGGGGCCGTSTGGCCCAAAT	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69955038	10173964	9813	ACTATATTGCYCATAAGTAGT	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69966822		9814	CAAGGCAAATSTGTACTCCTT	1.78	1.63	1.63	1.43	0.84	0.69	0.52	1.54	1.60	0.86	0.73	0.54
22	2	69980286	2872075	9815	TTTGTTCATTKAAGAGAAGTG	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69986206		9816	GGCAGAAGGASTGCTGTCATT	-	-	-	-	-	-	-	-	-	-	-	-
22	2	69992048	6711065	9817	TATTTTTAAAMTCAAGAGATA	0.99	1.36	1.31	0.79	0.90	0.23	0.74	1.27	0.97	0.91	0.21	0.71
22	2	69998014		9818	TTTCATTCCARTTTTACAAAT	1.49	1.41	1.41	1.23	0.80	0.30	0.20	1.35	1.40	0.83	0.31	0.20
22	2	70003643		9819	TATTAGTTGCRTATTTTCTAT	-	-	-	-	-	-	-	-	-	-	-	-
22	2	70010459	3214007	9820	ATATGAAAGTRAGGAAGAGCT	-	-	-	-	-	-	-	-	-	-	-	-
22	2	70019722	17037207	9821	GTTTTCTTTCYGTCTCATTAC	-	-	-	-	-	-	-	-	-	-	-	-
22	2	70030078	13028508	9822	ACAGCTCAACWAATTGTGTGT	2.20	2.74	2.74	1.38	0.58	0.67	0.39	2.66	1.54	0.56	0.71	0.35
22	2	70037414	13015457	9823	TAATCTCAGTKGCTGTAAGTT	2.25	2.82	2.82	1.48	0.97	0.72	0.50	2.76	1.87	0.97	0.73	0.49
22	2	70049149	1979214	9824	TTGAATTTGTSAATATAGTTC	2.18	2.74	2.74	1.34	1.65	0.67	0.27	2.69	1.68	1.56	0.68	0.27
22	2	70057484	6546559	9825	TCTCAGATACRCCGTAATTTG	2.33	2.90	2.90	1.41	1.08	0.61	0.39	2.80	2.28	1.08	0.64	0.41
22	2	70068240	6741449	9826	TAGAATCAAGRAAGCATGGTC	2.26	2.82	2.82	1.44	0.98	0.35	0.35	2.77	1.73	0.97	0.35	0.37
22	2	70075685	3771531	9827	TTCAGGGGATYGCTGCAAACA	2.42	2.98	2.98	1.31	0.66	0.42	0.47	2.88	1.38	0.65	0.43	0.50
22	2	70082635	17037263	9828	GCACTTTTTCRGAGTCAAGAG	0.29	0.29	0.29	1.20	0.52	0.62	0.65	0.20	1.25	0.54	0.59	0.66
22	2	70091922	10178406	9829	CCAAAAGCCASTGTTGCGTGT	0.91	0.82	0.82	0.21	1.02	0.75	0.66	0.74	0.23	0.99	0.76	0.67
22	2	70098824	3821276	9830	GTCTTTGATGYTGACTCCCTC	0.38	0.16	0.16	1.06	0.60	1.09	0.88	0.13	1.07	0.60	1.06	0.88
22	2	70107775	12464553	9831	AAATTAGCACWCATGAGACTT	1.12	0.83	0.83	0.44	0.94	0.23	2.01	0.73	0.45	0.96	0.28	1.84
22	2	70128696		9832	GTGATGATGAYGATGGTGACA	-	-	-	-	-	-	-	-	-	-	-	-
22	2	70134214	11682652	9833	CTATGTATCCRTACATTGAGG	0.81	0.75	0.76	0.48	0.17	0.44	0.20	0.63	0.43	0.20	0.44	0.23
22	2	70149011	4853252	9834	CACGGGAGATRCACAAGTGGA	0.82	0.76	0.76	0.34	0.14	0.15	0.41	0.69	0.36	0.16	0.14	0.44
22	2	70163141	4563251	9835	AGTCGTTCATYAGTTGCAGTC	0.83	0.13	0.10	0.25	0.19	0.15	0.17	0.09	0.19	0.19	0.14	0.17
22	2	70174208	10188148	9836	CCAGCAAAACYACAGTGTGAG	0.76	0.71	0.57	0.36	0.19	0.24	0.03	0.47	0.31	0.17	0.24	0.03
22	2	70186569	7369819	9837	AGGCAAAACAYTAAGAAAGGC	-	-	-	-	-	-	-	-	-	-	-	-
22	2	70192488	13421101	9838	ATTCTTCAGGMCCCAATCTGG	0.91	0.85	0.85	0.55	0.28	0.04	0.46	0.75	0.61	0.30	0.03	0.49
22	2	70198785		9839	AGACAGACGCYACCATCTATC	-	-	-	-	-	-	-	-	-	-	-	-
22	2	70207932		9840	AATTAATCTGKATCACAGCCT	0.91	0.84	0.76	0.48	0.14	0.46	0.17	0.67	0.55	0.14	0.47	0.18
23	2	113240198	2048874	9841	ATATCCCACGYAGTGCTGGAG	0.08	0.22	0.22	0.25	0.03	0.65	0.76	0.17	0.26	0.02	0.70	0.74
23	2	113247522	1516790	9842	TATGTGTAATRTGAGCTTTAA	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113253810	3783539	9843	TGTTTTCAAAYGAATGCACTC	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113261909	3783516	9844	TATTGAAGGTYCCAGAATATG	0.65	0.02	0.02	0.25	0.88	0.85	1.74	0.00	0.20	0.89	0.87	1.65
23	2	113269899	10496444	9845	TTTCTCAGACRTTGCTATGTG	0.12	0.19	0.19	1.02	1.89	1.83	1.71	0.16	1.15	1.76	1.71	1.66
23	2	113279593	12613067	9846	CCACCTGACAYGTCTGGACGA	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113287040	11680809	9847	TAAAAGTAACMAAGTGCTGTA	0.45	0.52	0.52	0.94	1.26	1.81	1.16	0.49	1.03	1.27	1.82	1.14
23	2	113303352	2853550	9848	TCCTGTTCCARATGTGCACTG	0.40	0.29	0.29	1.03	1.12	1.07	1.22	0.25	1.06	1.12	1.09	1.23
23	2	113309749	1143629	9849	TGGGCTTGGARTCTTTTCTCC	0.44	0.70	0.71	0.50	1.15	1.19	0.84	0.63	0.49	1.11	1.20	0.84
23	2	113322356	17042486	9850	ATGAATTAAAYATGGGTACTT	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113343582	2723158	9851	ATGAGGCCACSACTGTTCAAA	0.56	0.28	0.23	1.59	1.68	0.92	1.19	0.16	1.69	1.61	0.89	1.15
23	2	113346728		9852	CACTTACACASTGAAAAACTT	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113353093	10496442	9853	CCTGGTTCATYTTAGGCTCTG	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113359859	2723149	9854	ACCATGTTATYATTTGATTGG	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113374306	2723154	9855	GGAAGGAGTTYGGAGTGGTAG	0.15	0.35	0.35	1.33	1.76	1.76	0.98	0.34	1.47	1.66	1.66	1.01
23	2	113383984	2723175	9856	CACAGTCTTCRGTGAAGTTTA	0.76	0.84	0.84	0.50	1.91	1.72	1.58	0.79	0.52	1.73	1.60	1.51
23	2	113389974	2723182	9857	GAATTGCCTAYCACAGATACC	0.41	0.66	0.66	0.45	0.69	1.05	2.19	0.59	0.45	0.70	1.03	2.02
23	2	113396667	13023984	9858	ACTCTAGAACMCATCTTGAAG	0.39	0.62	0.57	0.48	0.97	1.70	2.06	0.52	0.52	0.93	1.60	1.91
23	2	113407730	17659035	9859	GACTCAAAGTRAGATTATTTT	1.27	0.06	0.06	0.81	1.88	2.60	1.67	0.05	0.85	1.72	2.28	1.60
23	2	113420955	4592853	9860	CCAGAGAAAGYTTCCTCCACT	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113429014	12468164	9861	TACCCAACACRTGTCAGCTTT	1.20	0.24	0.24	1.73	2.88	2.30	2.36	0.21	1.97	2.53	2.07	2.22
23	2	113435613	11674086	9862	AAGGTGCCCCRTCTTTGAGTG	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113441630	11902514	9863	AAAAGGTGCCWTTTGGCAATA	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113449040	13418326	9864	GTTGCCCCACSAATTTAAGCG	0.43	0.11	0.11	2.29	1.98	2.56	3.15	0.09	2.47	1.81	2.28	2.70
23	2	113455763	6743744	9865	TCAATTAAGCRCATGTATGGG	1.12	1.38	1.38	0.74	1.36	2.51	4.25	1.27	0.78	1.32	2.16	3.62
23	2	113462043	17042691	9866	CCATAGAAGAYGTAGTATTTT	0.47	0.58	0.57	0.82	0.85	2.33	3.57	0.52	0.89	0.86	2.08	3.13
23	2	113471421	6542108	9867	AAAAAATTCAYTGTTGGACTA	0.23	0.08	0.08	0.20	2.88	2.53	2.52	0.07	0.15	2.56	2.31	2.34
23	2	113476181		9868	CATCTTAGCTKTTGTCACAAA	0.58	0.68	0.68	1.96	2.18	2.33	2.43	0.65	2.08	2.01	2.16	2.28
23	2	113487864	10192773	9869	AGAAATTGTGRTATGTTACAT	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113499462		9870	ATGTTGCCTTYGGTTGGGAAG	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113505547	2305150	9871	GTGAAGAGAAYAAGATAGATC	0.42	0.49	0.49	1.10	1.60	1.95	2.14	0.45	1.10	1.57	1.82	2.02
23	2	113510990	13407508	9872	TCAACGTCCAYGAGGCTGTGT	0.52	0.91	0.91	0.45	1.70	1.72	1.99	0.85	0.42	1.61	1.70	1.88
23	2	113526689	1562302	9873	GTGGGTTTGTRCTAGATGCCA	0.37	0.71	0.71	1.83	1.27	1.83	1.88	0.69	2.00	1.26	1.78	1.77
23	2	113533797	1530551	9874	GCACTTCCCAYGATGTGTTCT	0.19	0.48	0.48	0.25	2.65	1.92	1.73	0.43	0.22	2.35	1.83	1.65
23	2	113539596	17042751	9875	ACAGGCTGGAYATCATGACTC	0.05	0.09	0.09	0.81	1.44	1.79	0.87	0.06	0.85	1.39	1.67	0.86
23	2	113546071	17042795	9876	GGCTCTAGTTRTCTAACCCTT	1.83	1.81	1.81	1.35	0.60	0.50	1.48	1.63	1.48	0.59	0.51	1.47
23	2	113552757		9877	AAAAATTTTCRCATGTAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113558737	13398728	9878	CTTTGGGAGGYAGAGTTAATA	0.69	0.92	0.92	1.05	0.59	0.53	1.29	0.90	1.12	0.59	0.53	1.24
23	2	113566068	1542176	9879	GCCAAGAACGYGCACAAGCAG	0.49	0.66	0.74	0.26	0.28	0.47	1.67	0.70	0.24	0.27	0.50	1.61
23	2	113567390	1446509	9880	GACCCTGGACWGACTCCTGCA	0.76	1.01	1.01	0.22	0.16	0.52	0.71	1.00	0.21	0.17	0.52	0.72
23	2	113578289	1623119	9881	GGGCCTTCTCRTGGTGGGGGC	-	-	-	-	-	-	-	-	-	-	-	-
23	2	113589249	315920	9882	TATCTTGCTCYTCCATTCCTG	0.80	0.03	0.05	0.40	0.22	0.18	0.24	0.02	0.38	0.22	0.19	0.26
24	2	152014490	17805045	9883	ATTTATATTGYTTCAGATAAG	0.91	1.38	1.57	0.85	0.52	0.43	0.52	1.47	0.95	0.51	0.40	0.56
24	2	152020944	6725961	9884	GGGGCAAGTARCCTGAGACGC	0.41	0.12	0.12	0.70	0.34	0.50	0.83	0.09	0.71	0.36	0.52	0.85
24	2	152032487	12466578	9885	GACAATGGACRTAGCATTACA	0.66	0.93	0.93	0.30	0.85	0.68	0.59	0.87	0.32	0.81	0.69	0.60
24	2	152040146	3771889	9886	CAATGCATTTRCAATCAGATT	0.58	0.51	0.51	0.75	0.57	0.67	0.25	0.48	0.80	0.58	0.65	0.26
24	2	152050112	3771897	9887	GGAACAACTCRCTCCTAAAGC	0.44	0.18	0.19	0.91	0.30	0.09	0.14	0.15	1.02	0.31	0.10	0.15
24	2	152056802	3845844	9888	AAAACATCTTRTTGCTGTAGG	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152073833	10490521	9889	CTCTTTCCACRTCACTAATAT	1.10	1.21	1.21	0.24	0.23	0.06	0.10	1.18	0.22	0.24	0.07	0.10
24	2	152077439	17806222	9890	GGATTCAATGRAAACAGAGCT	0.57	0.97	0.97	0.23	0.19	0.19	0.11	0.93	0.19	0.22	0.21	0.10

24	2	152092867	16830019	9891	CCGATGTGTTKGGAAAATGTG	0.49	0.23	0.23	0.30	0.14	0.22	0.19	0.19	0.27	0.14	0.24	0.19
24	2	152113339	2432956	9892	AGAATCTTATRTACACATCCA	0.94	0.80	0.80	0.23	0.22	0.14	0.13	0.75	0.19	0.20	0.15	0.14
24	2	152120649	16830036	9893	AGTGTTAGTCRTAGTACGTAG	0.76	0.14	0.14	0.58	0.16	0.10	0.10	0.13	0.61	0.17	0.11	0.09
24	2	152136436	2444264	9894	TTTGTATCTCKGACTTGTTCA	0.93	0.66	0.71	0.55	0.28	0.05	0.45	0.67	0.64	0.29	0.04	0.48
24	2	152143039	2045025	9895	GGATCATGAGYATCATCAACT	1.02	0.84	0.84	0.43	0.23	0.80	0.46	0.82	0.40	0.26	0.80	0.44
24	2	152151243		9896	AAATGCGTGCRTGTAGATCGT	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152157253	16830067	9897	TAAGTTCAATKTTGTAAGTTC	0.84	0.09	0.09	0.29	1.02	0.79	1.22	0.06	0.24	1.00	0.81	1.20
24	2	152164497	16830086	9898	AGAGAGGTTTYGTCAAATAAG	0.85	0.18	0.12	0.11	1.00	1.56	0.81	0.09	0.02	1.01	1.50	0.84
24	2	152177305	3732308	9899	AGGAAGAATTSTGTTGAAATA	0.65	0.16	0.11	1.50	1.75	0.89	1.79	0.09	1.62	1.65	0.91	1.68
24	2	152187910		9900	CAGATTGACAYACATATATCC	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152193563	7558940	9901	GTTGGACCAGSGAATCTACAT	1.00	1.38	1.38	1.77	1.04	0.45	1.52	1.38	1.89	1.02	0.44	1.46
24	2	152200308	16830136	9902	ATGAATGTGCRCCAGAGGAAA	1.18	1.55	1.65	0.70	0.53	0.53	0.73	1.57	0.69	0.51	0.56	0.77
24	2	152207962	6721666	9903	GCCAAGAGACSGGTGGTTGAT	1.23	1.65	1.65	0.29	0.19	0.67	1.24	1.60	0.24	0.19	0.68	1.24
24	2	152216685	6414089	9904	TTTACCAACTRAGGCTGTGAG	1.07	1.44	1.44	0.52	1.03	1.73	1.26	1.39	0.49	1.04	1.62	1.28
24	2	152223553	16830192	9905	TCTGCTTCTTSCCTGCAGCTC	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152229190	10208825	9906	GAATGATTCCRTGTTGAATGT	1.20	1.48	1.48	1.70	2.32	1.63	1.86	1.43	1.94	2.10	1.54	1.75
24	2	152236240	6731486	9907	CTGAAATAATRTGTAGCTTCT	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152242044	10497084	9908	AAAGGCATAARGAGTTAGAGG	1.53	0.24	0.24	3.18	2.79	2.38	1.67	0.20	3.49	2.56	2.21	1.60
24	2	152247584	2288210	9909	CACCACACTTSTAAAGTTAGG	1.33	1.25	1.25	0.91	4.83	3.28	2.04	1.19	0.95	4.22	2.94	1.90
24	2	152255187	4461258	9910	TGGTGATACAYTTGTAAAGAA	1.79	2.01	1.89	1.05	2.18	3.54	2.24	1.82	1.15	1.98	3.14	2.11
24	2	152257396		9911	TATTTTGAGTYTATCTGAGTC	0.63	0.32	0.32	1.49	1.04	1.46	3.15	0.29	1.53	1.03	1.37	2.82
24	2	152307354	4599105	9912	GTGTCTGTCTRTCTATCTGTC	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152317832	4664493	9913	AGCAAGCACCRCATGTGTTTT	2.22	1.55	1.55	1.16	1.20	1.19	1.65	1.51	1.20	1.18	1.18	1.63
24	2	152327871	4378803	9914	CCTGCAAAGARTGCCTGTCCA	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152346248	7584016	9915	TGGTAAAACAYGTAGATTGCA	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152356585	6711382	9916	ATTAAGTCATRCCAATCCCGT	0.60	0.49	0.45	1.16	1.45	1.40	1.15	0.37	1.16	1.41	1.33	1.12
24	2	152371706	6733909	9917	GTCCATTGCCYACCTAAGCCA	1.11	1.55	1.55	0.92	1.26	1.37	1.24	1.48	1.11	1.20	1.34	1.17
24	2	152377850	4564766	9918	GCATTACTGAWCCTGTGTGCA	1.19	1.61	1.54	0.78	2.02	1.36	1.01	1.51	0.78	1.90	1.37	1.00
24	2	152396978	6433579	9919	TTCTCCCTAAYACAACTATTA	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152411185	4664501	9920	AATGCATCATYAGGGACGAAG	1.39	1.45	1.45	1.14	0.49	1.00	1.44	1.39	1.22	0.49	0.98	1.36
24	2	152423323	4664502	9921	CTCTATGTGCRTCCCTTCTTG	1.03	1.02	1.02	0.67	0.51	0.91	1.06	0.95	0.77	0.53	0.89	1.03
24	2	152437753	4309576	9922	AATGGTATTCRGAAATGGCAG	1.32	1.40	1.40	0.88	1.00	0.84	0.81	1.34	0.94	1.00	0.83	0.82
24	2	152450593	4508594	9923	AAGTGTGGTCRATAGACCTGC	1.49	1.53	1.53	0.56	1.05	0.88	0.60	1.48	0.61	1.02	0.88	0.63
24	2	152469151	2344733	9924	AATTTATGTGRCATATTTTAT	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152481160	2293222	9925	ATAATCTATCRCACATTCTTT	0.18	0.39	0.39	0.80	0.64	0.73	0.88	0.36	0.83	0.68	0.71	0.88
24	2	152487339	9288006	9926	TCAATAATTCRTTATATTTGG	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152494735	2030589	9927	TCTTGAATGCYAATGGACCTA	0.15	0.40	0.36	0.54	0.60	0.69	0.87	0.29	0.58	0.61	0.69	0.89
24	2	152497990	10171724	9928	CAGCATGTGGWAGAAGCTAGT	1.12	0.68	0.68	0.31	0.59	0.73	0.51	0.59	0.32	0.62	0.72	0.53
24	2	152515756	1568673	9929	CAAATTTAACRGTGGATTTTG	0.56	0.55	0.55	0.23	0.57	0.48	0.63	0.45	0.23	0.57	0.50	0.66
24	2	152517337	2344734	9930	GGGTGCCAAASAGCATTTTGG	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152530989		9931	TGTAGTGTATRGATGTATAAT	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152539531	3768655	9932	AGTTTTAAAAKAAATTTTCTT	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152542136	3768653	9933	ACTATGGACTMGCTTCTGTGG	0.20	0.04	0.00	0.19	0.18	0.64	0.61	0.00	0.17	0.18	0.62	0.61
24	2	152555089		9934	GTTATATGGCMCATGACTGTA	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152574226	16830434	9935	GACTGAGAGAYGCTTTCTTCT	-	-	-	-	-	-	-	-	-	-	-	-
24	2	152581106	16830435	9936	AAGAGGACAGKCCTGAGGATG	0.07	0.21	0.21	0.09	0.44	0.45	0.81	0.15	0.09	0.47	0.47	0.83
24	2	152588665	17270290	9937	TCATCTGCTTRTGATTTAAAG	0.39	0.10	0.11	0.25	0.27	0.43	0.52	0.10	0.24	0.30	0.46	0.52
24	2	152605675	6729612	9938	TAATGGGAAAYGTTTTTGCTA	0.20	0.10	0.10	0.19	0.16	0.29	0.30	0.08	0.17	0.16	0.31	0.33
25	2	167402006	1509645	9939	CCAATGTAAAYGACCAAATGA	1.44	1.33	1.33	1.12	0.53	0.43	0.21	1.25	1.13	0.56	0.47	0.23
25	2	167413779	16852587	9940	TTTCGTAGAGWAATTGACCTG	0.46	0.78	0.78	0.73	0.61	0.49	0.74	0.70	0.82	0.66	0.53	0.75
25	2	167415252	1509652	9941	TAGACTTTAAYACAATCTGAA	0.17	0.17	0.17	0.36	0.62	0.87	1.71	0.09	0.37	0.68	0.88	1.55
25	2	167433439	16852625	9942	CAATGCCTTARGTTTGGGACA	0.61	0.97	0.96	0.62	0.51	1.22	1.09	0.90	0.76	0.53	1.14	1.06
25	2	167441518	6736995	9943	TCATTCCCAASATCTGACTGA	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167449883		9944	AATTATCAAGYTCAGCACTTG	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167462718	16852645	9945	TATAGAGAAARTGGCTCTCAA	0.40	0.39	0.39	0.64	1.06	0.66	0.57	0.34	0.68	0.99	0.67	0.55
25	2	167469661	16852657	9946	TGAATTTACCMATCCATCTCA	0.08	0.08	0.11	0.53	0.92	0.30	0.59	0.09	0.57	0.92	0.30	0.61
25	2	167481604	7599628	9947	ATTGCTTTTAYAATTAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167491528	6755015	9948	AGGCTAGCCAYGCTTGGTAAT	0.22	0.10	0.10	0.01	0.17	0.83	0.82	0.03	0.01	0.18	0.79	0.81
25	2	167497156	9287876	9949	ATAGAATGAAKAAAATTGAAG	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167517355		9950	TTCAAAGGCAWAATTCAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167522021	4622745	9951	CATATAAATTRAGAGACTGGT	0.21	0.09	0.10	0.04	0.60	0.95	0.74	0.05	0.03	0.61	0.92	0.69
25	2	167550133	7596044	9952	AGGAATATTTYGCATGAAAGA	0.31	0.07	0.04	1.02	0.77	0.45	0.64	0.02	1.06	0.78	0.45	0.68
25	2	167556651	4316949	9953	CACCTAAAAAKGACACTTTCT	3.15	1.97	1.97	0.92	0.72	0.53	0.27	1.93	1.04	0.73	0.55	0.30
25	2	167569763	13391943	9954	AGAAAGACTTYACTTATTTGA	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167572347	9677390	9955	TCATAGGCTTYGGGCATCAGA	1.35	1.58	1.58	1.25	0.72	0.38	0.25	1.50	1.48	0.74	0.38	0.29
25	2	167579501	6755120	9956	CAGACATCTCRTTATGCAAAA	2.76	1.79	1.79	0.96	1.06	0.38	0.44	1.70	1.12	0.99	0.42	0.44
25	2	167585455	7599152	9957	GAGTGTATCAYTGATAAAAGG	1.41	0.67	0.67	0.88	0.68	1.01	0.60	0.62	0.95	0.67	0.99	0.59
25	2	167604094	1464007	9958	AGACTAGATAMTATTTTGGTA	1.58	0.79	0.79	0.84	1.04	0.75	0.93	0.74	0.87	0.99	0.73	0.90
25	2	167610105	1511210	9959	AAAGAGTTCCSTCATTTTACA	3.02	2.03	2.03	1.18	0.96	0.85	0.29	1.96	1.27	0.98	0.86	0.30
25	2	167615904		9960	GATATTTGCTRTTTCTTGTTG	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167633760	17614686	9961	CAATCTAGCCSCAACCTAGCT	0.18	0.20	0.20	1.61	1.18	0.49	0.29	0.15	1.74	1.15	0.50	0.30
25	2	167644059	1473041	9962	CATAAAAGTTYAAGGGAGGAA	0.79	1.07	1.07	0.41	1.29	0.66	0.19	1.01	0.40	1.29	0.67	0.21
25	2	167653439	16852817	9963	CCTATGTGATRTTAACTTGGG	0.10	0.00	0.00	0.46	0.24	0.76	0.28	0.00	0.46	0.26	0.78	0.27
25	2	167677773	12476945	9964	TAAGCTGTTAYAAAATTTGTA	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167685854	1995948	9965	TACTTAATCAYGTATTTTGGC	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167687361		9966	AATGAAGTCASTGCAGGTGGT	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167694910	10497305	9967	AATTCTCCAGYGTTTTGTTAT	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167701110	10188981	9968	TGAGAAATCTRTACAACACAG	0.95	1.21	1.22	0.52	0.06	0.15	0.43	1.18	0.54	0.05	0.17	0.42
25	2	167721924	1511209	9969	ATATGAATTASAAACTAATGA	0.82	1.23	1.23	0.27	0.33	0.15	0.15	1.17	0.26	0.31	0.15	0.16
25	2	167729549	1511199	9970	AAATAAAATTKTCAGATACAA	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167738111		9971	TAAAAAGTAGRCCAGTTCCTC	0.52	0.93	0.93	0.90	0.48	0.53	0.27	0.90	0.88	0.50	0.53	0.28
25	2	167744054	16852925	9972	CCAGCACCCTSGATCGCTTGG	1.50	1.97	2.03	0.90	0.94	0.65	0.41	1.90	0.99	0.97	0.64	0.44
25	2	167751866	16852935	9973	ACTTCCTTCARACAGATGATT	0.40	0.66	0.66	1.66	1.05	0.41	0.47	0.60	1.80	1.07	0.43	0.49
25	2	167759338	6733384	9974	TTATCTGATAYTACCCTAATT	0.77	1.18	1.16	0.34	1.04	1.25	0.68	1.06	0.35	1.05	1.21	0.67
25	2	167790824	1346722	9975	AGTGTGATTAYGTGTTTCTTG	0.59	0.93	1.02	0.47	0.55	1.30	0.98	0.99	0.45	0.57	1.24	0.97
25	2	167803327	10497316	9976	TTAGTATGATYGTTTGAATAC	1.05	0.68	0.68	1.30	0.89	0.40	1.19	0.62	1.39	0.90	0.40	1.17
25	2	167815198	7569147	9977	GGTATTGTACRCATTTGTTTA	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167821649	11900989	9978	GGGGATCCTTSCAGTCATTAA	0.74	0.55	0.56	1.08	0.74	0.60	0.38	0.50	1.18	0.75	0.62	0.40
25	2	167828849	1155284	9979	GTGAAAGTACRTAATACGACA	0.47	0.79	0.73	1.04	0.74	0.71	1.86	0.67	1.13	0.77	0.70	1.73
25	2	167839233	10497313	9980	AGAGAGCTCARTGTTTTTAGT	0.92	0.85	0.85	0.49	1.15	2.64	2.07	0.78	0.53	1.10	2.38	1.87
25	2	167862089	16853124	9981	AACTTGAAACRCCTTTCACTT	0.84	0.77	0.92	0.57	3.97	3.44	2.24	0.86	0.83	3.03	2.74	2.00
25	2	167868962	16853179	9982	GAAAAGCAATRTCTCCTCTTC	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167874507		9983	CCTGGGAGAGRGTGAACTATG	0.84	0.77	0.77	1.94	2.68	4.22	2.29	0.69	2.15	1.95	3.16	1.99
25	2	167880507	1382891	9984	CAAGAGGCCARTTACCTTTTC	-	-	-	-	-	-	-	-	-	-	-	-

25	2	167888123	6432984	9985	TTACTACAGAYACTCTTCATG	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167894375	6747227	9986	GTAAACAATAYTTGATTTAGG	2.30	2.28	2.28	1.94	1.84	2.81	3.54	2.21	2.14	1.58	2.23	2.76	
25	2	167900895	922536	9987	AAATACTGTCRTGAGATTTAG	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167907629	16853266	9988	ATAGGCCAGCRAATACTCATG	2.02	2.01	2.01	1.69	2.67	3.38	3.27	1.89	1.91	2.38	2.58	2.51	
25	2	167914364	16853286	9989	CCACATGTCARGAGCCAGAAT	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167920417	16853296	9990	AGGCCTCAACWTTTTTTTCTT	1.26	1.78	1.78	2.24	3.41	3.24	2.12	1.69	2.44	2.84	2.68	1.89	
25	2	167933864	1842233	9991	AGACGTGGCARGAGAGTGGAA	0.20	0.29	0.29	2.40	3.43	2.53	2.71	0.24	2.47	2.95	2.19	2.50	
25	2	167945383	1479586	9992	AAATCTTACGKTAAAAAAATC	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	167953373	7604377	9993	GCAAGGACAARCAATATAGGC	2.45	2.42	2.42	2.25	2.28	2.14	0.95	2.31	2.62	1.95	1.97	0.94	
25	2	167984858	10497324	9994	ACATAAATCCRAAAACAAATA	1.67	1.84	1.84	1.70	1.85	0.89	1.02	1.72	1.98	1.69	0.88	0.97	
25	2	167989237	1916743	9995	AAGTGAAATARGAAGAAACAG	0.03	0.04	0.04	0.76	0.99	0.89	0.95	0.02	0.79	1.00	0.93	0.92	
25	2	167996595	10192896	9996	AATATTCAAARCTGTGAATCG	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	168003686	2177440	9997	TTATTTTCTCRGGAATCTTAC	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	168020334	1523879	9998	TTTGTGGTGCRAATGTATTAA	0.06	0.20	0.20	0.10	0.63	1.08	0.90	0.19	0.10	0.70	1.04	0.89	
25	2	168026277	16853464	9999	CAAACTTTTAYCTACTCGCCC	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	168036837	2617365	10000	TGTCTTTTATWGCCTGCACCA	0.71	0.89	0.89	0.55	0.23	0.62	0.92	0.85	0.67	0.27	0.69	0.93	
25	2	168043380	2689825	10001	CAGTCGTATCRTAAGAATCCA	1.38	1.27	1.17	0.73	0.59	0.14	0.38	1.05	0.80	0.67	0.17	0.42	
25	2	168049865	1403899	10002	CTTTACACTASTCTAGTCATT	1.39	1.28	1.28	0.91	0.51	0.32	0.11	1.17	1.21	0.61	0.39	0.12	
25	2	168051988	2689820	10003	TAAGCCAGAARACACTGAATT	1.50	1.38	1.38	0.75	0.58	0.39	0.19	1.26	0.85	0.62	0.43	0.21	
25	2	168066012	1357605	10004	AATGCAAACTRTTTGCACATA	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	168088441	1523888	10005	TGGAGCCACARAAAAGTGGAG	0.78	0.76	0.76	0.58	0.59	0.31	0.16	0.65	0.66	0.63	0.35	0.16	
25	2	168096259	2222504	10006	AGTGTCTTTAMTTCCTAAGAG	1.22	1.16	1.16	0.76	0.34	0.30	0.38	1.07	0.97	0.38	0.32	0.42	
25	2	168105124	940314	10007	AGTCATACCCRTACCAGTCAA	1.45	1.38	1.38	0.56	0.39	0.43	0.25	1.28	0.62	0.42	0.47	0.30	
25	2	168139726	6747599	10008	CTCATCTTGAYTGAATCACTG	1.61	1.44	1.45	0.54	0.57	0.31	0.50	1.31	0.55	0.60	0.32	0.54	
25	2	168154919	4667535	10009	TGTGGGAGAARTCTAAACGTC	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	168167723	16853634	10010	TGAATTAATCWAAACTATGCA	-	-	-	-	-	-	-	-	-	-	-	-	-
25	2	168173371	1112983	10011	GTAACAACTGSGAAACCAGGG	0.34	0.62	0.62	0.96	0.40	0.56	0.68	0.57	1.09	0.45	0.60	0.68	
25	2	168179485	12104575	10012	AAGATGCTCARTTGTACCGAT	0.61	0.60	0.60	0.37	0.83	0.37	0.65	0.44	0.38	0.85	0.40	0.65	
26	2	175467634	2646150	10013	GGACCCTGTCRTTGATTAGAA	0.03	0.04	0.04	0.31	0.44	0.45	0.56	0.01	0.34	0.45	0.43	0.58	
26	2	175492372	12476097	10014	TCAGACGTGTYGACACAGATA	-	-	-	-	-	-	-	-	-	-	-	-	-
26	2	175500663	6711283	10015	ATTTTCTATASAGGAAACTGT	0.62	0.60	0.93	0.72	0.30	0.27	0.88	0.81	0.77	0.30	0.28	0.87	
26	2	175513212	10497430	10016	AACCTTATTAYATTTTAGTGA	0.69	0.93	0.93	0.68	0.36	0.69	0.66	0.90	0.77	0.38	0.71	0.66	
26	2	175519882	12614445	10017	GCCTGCAAAGYTTGCTGCAAA	-	-	-	-	-	-	-	-	-	-	-	-	-
26	2	175533811	1378730	10018	CTCTGCCTGASAACTAGGCAC	0.76	1.01	1.01	0.65	1.02	0.98	0.53	0.95	0.63	1.01	0.97	0.55	
26	2	175550101	10497431	10019	CAACTGAAAAYGACCACTCTT	0.59	0.57	0.57	1.03	1.06	0.78	0.55	0.47	1.07	1.03	0.79	0.56	
26	2	175560002	10930689	10020	AAGGGATGAGRACTACAGCTT	1.25	1.70	1.70	1.41	0.95	0.42	0.62	1.66	1.62	0.93	0.42	0.62	
26	2	175569622		10021	TAGAATCCAAYGTACTATCCA	-	-	-	-	-	-	-	-	-	-	-	-	-
26	2	175592137	4972731	10022	CTTAACCTTAYGAAGAATTAA	-	-	-	-	-	-	-	-	-	-	-	-	-
26	2	175603873	4972732	10023	ATTTCCATGAMCTCCTGTGAC	-	-	-	-	-	-	-	-	-	-	-	-	-
26	2	175606110	4324297	10024	TAAAAAGCCAYCTTACACATT	0.50	0.48	0.48	1.10	0.68	0.58	0.36	0.41	1.10	0.68	0.62	0.36	
26	2	175622691	1193622	10025	CAAGAGGCTGSGAAAATTTAG	1.31	1.61	1.61	0.69	0.79	0.62	0.38	1.56	0.68	0.79	0.62	0.38	
26	2	175629820	2141559	10026	GTCTTACTAAYAAATACTTCA	1.14	1.35	1.36	0.86	0.53	0.71	0.63	1.31	0.94	0.51	0.73	0.62	
26	2	175642569		10027	CACTAAGGGGYATTCAAGGGT	1.32	1.23	1.47	1.04	0.68	0.68	0.41	1.38	1.17	0.67	0.66	0.40	
26	2	175653901	1143989	10028	ACTATGAGTTYTTCTCTGGTT	1.41	1.86	1.86	1.56	1.09	0.40	0.45	1.82	1.76	1.11	0.40	0.42	
26	2	175663703	1143986	10029	GGCCAGGGAARCTAATGACTG	1.04	1.50	1.56	1.40	1.08	0.59	0.44	1.47	1.68	1.08	0.60	0.42	
26	2	175688925		10030	ACTGTGGGTAYTGGCTCTTTC	0.60	0.73	0.73	0.85	0.73	0.72	0.57	0.69	0.89	0.75	0.73	0.58	
26	2	175698177	1320875	10031	TGCTTTCCACRAGCCATTCCT	0.86	1.31	1.39	1.16	0.80	0.82	0.48	1.31	1.22	0.78	0.82	0.52	
26	2	175705852	13421992	10032	AAAAGCTTCTYATGTCTGGTC	-	-	-	-	-	-	-	-	-	-	-	-	-
26	2	175714603	17222732	10033	CTTTACAAACRTAAAAGTTCT	1.55	1.26	1.27	0.21	1.74	0.37	0.41	1.17	0.16	1.70	0.35	0.43	
26	2	175720916	7568572	10034	ACAAGTGTTGSGCAAGAGAGA	0.60	0.74	0.74	0.45	0.14	0.74	0.53	0.69	0.45	0.13	0.78	0.54	
26	2	175724388	11680035	10035	AAGACCAACAKATATTGGGTG	1.62	0.99	0.96	0.18	0.25	0.48	0.86	0.91	0.16	0.24	0.51	0.88	
27	2	186240056	7593254	10036	TAGTTGAATTRTCTTATTTGC	0.08	0.26	0.33	0.09	0.19	0.10	0.12	0.30	0.07	0.19	0.10	0.11	
27	2	186259057	12615448	10037	AAATGTTAGGRGACATAATTA	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186275184	6434136	10038	AAGACCTGTCKTACGAGATAT	0.27	0.52	0.52	0.08	0.05	0.25	0.14	0.48	0.09	0.06	0.24	0.16	
27	2	186301503	17206513	10039	AAGTGATACTYCTCCAAATCA	0.18	0.06	0.07	0.31	0.16	0.21	0.52	0.02	0.28	0.16	0.22	0.57	
27	2	186314691	6749577	10040	TAACATTTCTKAAGTAGTTTT	0.14	0.37	0.43	0.28	0.43	0.40	0.27	0.38	0.28	0.46	0.43	0.26	
27	2	186326863	6755533	10041	AAGACAGAAAYACCATTAGAG	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186340814	17207117	10042	CCAATAAACAYTCAAAGTTTG	0.44	0.18	0.18	0.63	0.80	0.48	0.31	0.16	0.65	0.81	0.50	0.33	
27	2	186346997	2160846	10043	ATGCTATTTCRATTTCTTTCA	0.61	0.58	0.58	0.87	0.65	0.43	0.59	0.52	0.87	0.66	0.44	0.65	
27	2	186359901	11687532	10044	TTTAGAAAGAYGTTCCAGAGT	1.34	1.19	1.19	0.54	0.42	0.46	0.50	1.02	0.52	0.41	0.49	0.52	
27	2	186385745	10208912	10045	GCTCCTTTGCRCTAATGCTTA	0.60	0.56	0.57	0.74	0.32	0.60	0.40	0.55	0.75	0.37	0.61	0.42	
27	2	186402772	6434140	10046	GTGACTCCTTKAAATTGTCCT	0.97	1.27	1.20	0.44	0.82	0.44	1.24	1.16	0.43	0.81	0.42	1.24	
27	2	186414353	17813158	10047	CAGACAAGGGRGAATTCAGAA	0.26	0.54	0.59	0.79	0.53	1.63	1.23	0.56	0.79	0.53	1.53	1.22	
27	2	186424385		10048	TTAGCCTACAMGAATCTTTGA	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186431940	6759616	10049	AGGGAATCTARCTTTCTGATT	1.09	1.41	1.41	0.68	1.81	1.58	1.66	1.33	0.69	1.69	1.47	1.58	
27	2	186437940	7570827	10050	TTTTTAGAACYAGCAGTTCTT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186443759	2887761	10051	GGTAAATTGCWTACATGTTAA	1.07	1.35	1.35	1.98	2.26	1.87	0.78	1.29	2.71	1.93	1.74	0.78	
27	2	186454697	12998112	10052	AAATTTTTTTKTGTGGATCTA	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186469308	11897716	10053	AGTGTTATTTSTTTAGATGCC	1.03	1.35	1.35	1.82	3.23	1.12	0.85	1.30	2.42	2.72	1.08	0.84	
27	2	186477148	10490390	10054	TTTTTTTCAGYTTAATGTTGT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186484865	2161036	10055	CAAAGAGTAAKGGAAGTCACA	1.17	1.46	1.46	1.57	1.95	1.53	0.54	1.41	1.97	1.81	1.53	0.53	
27	2	186491330	11695215	10056	AGCACCATTTRACAAGCATTG	1.10	1.41	1.41	0.61	0.94	1.01	0.94	1.33	0.61	0.93	1.00	0.94	
27	2	186497418	1862066	10057	ATTTTCCAACRTCAGGTTAAC	1.10	1.41	1.41	0.68	0.54	0.67	0.32	1.36	0.71	0.53	0.68	0.30	
27	2	186507479	7608481	10058	TGTTTCACCTRACTAGGAACT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186515065	767042	10059	TTTGAAGGATYATGCCTCTTT	1.44	1.69	1.69	0.96	0.54	0.13	0.48	1.64	1.10	0.52	0.12	0.48	
27	2	186522900	6743211	10060	CAAAAAAAATSCAAATAGGAA	0.80	1.25	1.30	0.86	0.29	0.25	0.18	1.25	0.95	0.29	0.24	0.18	
27	2	186526646	759782	10061	AATTCCATTAYAAAAATTAGT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186550807	4510179	10062	ACCTATCTCAYTGAGTAATCT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186572725	4476313	10063	TTGAAAAAAAWATATTGCCTG	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186583883	6434147	10064	TATGAATTTTWAAAAATCAAT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186599926	6748949	10065	ATTTAATCACKGGACATTTGC	1.00	1.27	1.37	0.65	0.77	0.48	0.26	1.30	0.68	0.77	0.46	0.27	
27	2	186612880	2370506	10066	TATCTTATAARAGTAACAATA	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186640793	16827312	10067	ATTATTTTGAYGTGTGAGTCA	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186642677	1872831	10068	ATAGCTTTATRCATCAAGTTC	0.05	0.17	0.18	0.96	0.59	0.61	0.59	0.15	1.13	0.57	0.63	0.62	
27	2	186667994	17403904	10069	ACATAATATTMGTTATTAAGA	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186676730	7601385	10070	ACCTTAGACTRTGAATAAAGT	1.86	1.94	2.12	1.12	1.09	0.72	0.60	2.04	1.25	1.09	0.73	0.62	
27	2	186682885	16827374	10071	CTATATTCTAYTCATCATATA	0.10	0.14	0.14	1.16	0.96	1.00	0.66	0.12	1.25	0.97	0.97	0.64	
27	2	186688911	4666697	10072	ATAGCAGGACKAAGATAACCA	0.81	1.25	1.25	0.72	0.82	0.71	0.81	1.18	0.75	0.83	0.76	0.80	
27	2	186697461	7587154	10073	TTTTCTTTTGRACAGGAATTT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186705847	12988820	10074	GAAGTCACACRCTTTCAGCCT	0.75	1.19	1.19	0.47	0.36	0.52	0.88	1.15	0.44	0.40	0.54	0.85	
27	2	186709282	1487357	10075	GACATACTACRATTTTTTTTT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186722263	875162	10076	GTTGTCTCCARTGTGCTTGGA	0.05	0.17	0.17	0.30	0.70	0.75	0.72	0.12	0.30	0.70	0.76	0.72	
27	2	186730293	16827445	10077	ATCTTTAAATYTGACTTGTTT	-	-	-	-	-	-	-	-	-	-	-	-	-
27	2	186735722	10931219	10078	AAAATACTCARTGAGACATGG	-	-	-	-	-	-	-	-	-	-	-	-	-

27	2	186745632	725727	10079	TTCCATGTGCYCTTGTTGGTG	0.32	0.08	0.11	0.40	0.89	0.81	0.81	0.08	0.41	0.91	0.82	0.79
27	2	186754123	7566161	10080	TCAATAGAGAYACACATGTGC	0.54	0.65	0.65	0.62	0.64	0.96	0.60	0.62	0.71	0.69	0.96	0.61
27	2	186770169	2046593	10081	CTCTGCACTGMTCCATTAGCA	0.21	0.11	0.11	0.47	0.38	0.25	0.47	0.09	0.48	0.45	0.31	0.46
27	2	186783723	1386517	10082	ACTATGACAGWTATAACAATA	0.73	1.09	1.11	0.61	0.24	0.12	1.16	1.07	0.79	0.25	0.12	1.14
27	2	186785784	13019653	10083	AAGAATGATAMAACGAGCAAG	0.68	0.98	0.98	0.42	0.22	1.06	1.19	0.93	0.41	0.24	1.00	1.20
28	2	198427607	16823385	10084	CATCAAAAAGRAGTCTTGGTA	0.07	0.24	0.21	0.36	0.34	0.51	0.30	0.20	0.33	0.38	0.54	0.30
28	2	198435768	16823457	10085	ATATCAGATAYTAAAAATATG	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198447012	2293255	10086	CTAGAACTTCYTAATGACTGA	0.01	0.10	0.12	0.77	0.70	0.32	0.18	0.09	0.94	0.75	0.36	0.18
28	2	198468927	700654	10087	ATGTACATCTRCTACTTACAT	0.86	1.05	1.00	1.14	0.73	0.18	0.03	0.93	1.29	0.74	0.21	0.03
28	2	198480513	700658	10088	CTTCAGATTGWAGCTCCTAAT	0.95	1.40	1.40	0.73	0.39	0.10	0.04	1.34	0.78	0.41	0.09	0.04
28	2	198488712		10089	ACAAAGAGTGYTAATGAAGTG	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198499690	770657	10090	TTGTGGGGTAMATTATCTTTT	0.90	1.34	1.34	0.42	0.11	0.04	0.06	1.33	0.44	0.11	0.03	0.05
28	2	198509848	16824376	10091	TTTACTAAGCYGGCTGTCTAC	0.02	0.12	0.12	0.44	0.12	0.07	0.04	0.08	0.45	0.13	0.06	0.04
28	2	198516512	771010	10092	TATCATCTACSTACGCTTCAT	0.66	1.00	1.00	0.58	0.23	0.04	0.02	0.94	0.62	0.23	0.03	0.01
28	2	198533144	3851979	10093	TTTGCTAGGCWGTAAGGAATA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198538737	6707521	10094	TGAAGACAAGRACTAGGCCGA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198546560	700686	10095	TAGAAGTCGARATAAGTTAGA	1.14	1.62	1.53	0.81	0.18	0.04	0.01	1.46	0.95	0.17	0.04	0.01
28	2	198554006	700692	10096	CTTGAAGTCAYCCCGTGTATA	1.16	1.51	1.34	0.83	0.36	0.08	0.25	1.28	0.90	0.40	0.08	0.24
28	2	198561218		10097	TTTTCTGGATRTTAAACTACA	0.13	0.18	0.18	1.06	0.65	0.92	0.22	0.17	1.23	0.66	0.93	0.22
28	2	198569830	9288280	10098	AACCCTGAGGRAAATTTAATA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198577143	2060488	10099	CCTTAGGTTTKTATATTCTGT	0.87	1.34	1.34	0.81	1.84	0.70	0.85	1.32	0.89	1.67	0.70	0.87
28	2	198585479	6734781	10100	TCCTCCATTCRTCTCCATTTC	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198593672	6760891	10101	CAAAAATCTAKGTATCTTCCT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198602052	4241195	10102	CTTTTGTCCCRAGTTCCAGTT	0.99	1.46	1.46	1.71	0.98	1.30	0.30	1.45	2.08	0.99	1.28	0.30
28	2	198617826	1401092	10103	ATTACATAAGMCAACTCACAG	0.93	1.41	1.29	1.43	1.93	0.42	0.41	1.23	1.63	1.82	0.43	0.42
28	2	198624136	1464211	10104	CAGTATTTAARTTACTGAGCT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198631344	11887138	10105	AAACTAGACAWCTATACCAAT	1.19	1.70	1.71	1.84	0.83	0.33	0.33	1.61	2.06	0.83	0.34	0.35
28	2	198644132		10106	TCCTGAGTAGWCACCAATGCC	0.90	1.36	1.34	0.51	0.42	0.54	0.31	1.31	0.51	0.45	0.55	0.35
28	2	198651174	10497809	10107	TTGGCAAATARTATTCGATTA	0.51	0.70	0.70	0.30	0.29	0.38	0.36	0.64	0.27	0.29	0.40	0.37
28	2	198671129	16826320	10108	TTTGCAGTTAYAATGGAGCTG	0.06	0.21	0.21	0.61	0.15	0.14	0.40	0.17	0.81	0.14	0.14	0.42
28	2	198678142	2139050	10109	CTTATGTTGGRGAAGTTGATT	0.06	0.21	0.21	0.15	0.45	0.19	0.13	0.19	0.11	0.47	0.21	0.14
28	2	198684689	1518369	10110	AAAGTCATCTRAGTCAGAAAT	0.06	0.21	0.21	0.59	0.37	0.17	0.04	0.19	0.65	0.39	0.16	0.04
28	2	198693707	1976772	10111	CTGGACTCTTKTATTGGTTCG	1.24	1.73	1.73	0.69	0.18	0.23	0.07	1.70	0.72	0.19	0.23	0.06
28	2	198704803	1440090	10112	TTTTGTTGTTKATGTTATCTT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198707174	1016883	10113	CTCAAAGTTARAGACCATGAA	0.16	0.40	0.40	0.52	0.36	0.16	0.30	0.35	0.51	0.37	0.13	0.29
28	2	198719433	16826740	10114	GGCTTTTCTGRTGATTCTTAC	0.25	0.54	0.52	0.86	0.28	0.43	0.49	0.44	0.95	0.29	0.41	0.52
28	2	198730776	892514	10115	TTCTCCTTGGYGGGTGGAATT	0.86	1.30	1.31	1.08	1.41	0.82	1.37	1.23	1.23	1.35	0.86	1.33
28	2	198736751	10497812	10116	CTTTATAATCRAGGGCTAAAT	1.19	1.71	1.71	2.34	1.82	1.03	0.58	1.68	2.59	1.78	1.02	0.58
28	2	198746066	13382697	10117	TAGGGATGAAMTAATCACTGT	0.67	1.01	0.97	2.14	1.55	0.77	0.47	0.92	2.51	1.53	0.74	0.49
28	2	198755222	6434954	10118	GAGGGGCAGCYAAGATTTATG	0.82	1.23	1.19	1.01	0.72	0.66	0.66	1.13	1.04	0.76	0.68	0.66
28	2	198765757	7590828	10119	CTCATAACTGYGTACGAAGCA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198773023	16827521	10120	TAGGAAGGACRATAGGTGAGA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198785109	3755333	10121	TGCCTATCTARTATTTTGTGC	0.05	0.04	0.04	0.22	0.55	0.65	0.15	0.01	0.20	0.57	0.68	0.14
28	2	198791257	7570678	10122	TACATTTATTYGACAGCTACT	0.79	0.86	0.86	1.15	0.57	0.18	0.14	0.77	1.13	0.61	0.18	0.16
28	2	198798289		10123	ATCTTTTTCTRTACGATTCTT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198808027	16827729	10124	AAGCTTCTTARCAATGTATAT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198814784	16827788	10125	TAGTCCTGGGWAATTGGGACC	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198821526	16827819	10126	TTCATGGACASCTCACCTTCT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198834891	16827923	10127	GAAAATGGCCMAGATAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198843361	11896429	10128	ATTGAGGCACWACTGAAAAAG	1.44	1.95	1.87	1.98	0.69	0.10	0.07	1.78	2.19	0.68	0.09	0.05
28	2	198850476	13031577	10129	TAAAAGTTATRTTGACTGGCT	1.17	1.21	1.21	1.80	1.27	0.40	0.03	1.16	2.05	1.22	0.41	0.03
28	2	198863571	1368990	10130	ACACTAACTTYTTTGCTCTCA	0.83	1.10	1.05	1.54	1.14	0.33	0.12	0.98	1.75	1.14	0.34	0.12
28	2	198873644	17793044	10131	GTGGCCATGCMTGAGGTTGAG	1.27	1.78	1.80	0.79	0.61	0.56	0.12	1.69	0.86	0.65	0.58	0.13
28	2	198882620	3937566	10132	GTTTGTATGGYCTATTGCATA	0.20	0.44	0.44	0.79	0.46	0.17	0.40	0.40	0.81	0.48	0.18	0.46
28	2	198899396	4850447	10133	CCATTTATAGYGTTCCATGTG	0.91	1.48	1.34	0.92	0.49	0.32	0.22	1.23	0.92	0.51	0.35	0.25
28	2	198905312	1598660	10134	TTCACTCTGAYTAATGGATGG	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198912596	6746027	10135	CAAGGTTTCAYTTGAGGTGCC	0.43	0.75	0.75	0.67	1.00	0.65	0.28	0.69	0.69	1.00	0.64	0.30
28	2	198918962	13411216	10136	ATGACTGGTAYACTTTACACA	0.46	0.58	0.64	1.34	1.17	0.80	0.94	0.60	1.45	1.18	0.78	0.92
28	2	198924942	12693836	10137	AACAGGAGAAYGGAATCCCTG	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198934154	11674810	10138	CTGCTTTTCTRTGGTCACATC	2.69	2.17	2.01	1.57	1.36	1.27	1.56	1.94	1.74	1.29	1.24	1.55
28	2	198940187	6434961	10139	TAAGCAAATTYGGAGATACAG	2.70	2.83	2.83	1.48	1.33	2.67	1.06	2.72	1.60	1.26	2.49	1.06
28	2	198947953	1456556	10140	AAGCCAAGGAYTGGATCATTT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	198954384	16829186	10141	GATATGGTTCRGCTGTGGCGA	0.47	0.57	0.57	1.72	3.37	2.51	1.44	0.50	1.76	3.13	2.37	1.41
28	2	198964749	4850838	10142	AGGAAATCTCRTAATTGAGAA	0.46	0.26	0.29	2.43	3.16	2.53	1.83	0.25	2.58	2.98	2.42	1.77
28	2	198977567	12471228	10143	TGAACTTAATYCTTTATCCAA	1.16	1.64	1.58	1.27	1.26	1.99	2.28	1.53	1.34	1.25	1.91	2.14
28	2	198987602	1037663	10144	CCTCCAAATCSTTCCTGAGAG	1.02	1.33	1.33	0.35	0.44	1.02	1.98	1.28	0.33	0.45	1.00	1.88
28	2	198995021	13398693	10145	CTTAATGTTAYGGTGATTTTT	0.92	1.27	1.27	0.63	0.62	1.26	0.84	1.18	0.64	0.60	1.19	0.86
28	2	199003237	2529670	10146	TACTACTTTCSCTTAACAAGG	-	-	-	-	-	-	-	-	-	-	-	-
28	2	199009513	13022622	10147	CTGACAAATCRAAGCAGAAAA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	199015891	2727767	10148	TCATATGCTTRTTGTGACTTG	0.18	0.09	0.09	0.99	0.96	0.79	1.05	0.05	1.10	0.92	0.83	1.07
28	2	199018779	16829952	10149	GCTTTTTCCARATAGAGGTGT	-	-	-	-	-	-	-	-	-	-	-	-
28	2	199030492	10490082	10150	TCTGTATTATWCTTAATGGTG	0.04	0.04	0.06	0.76	0.55	0.41	1.16	0.03	0.80	0.55	0.43	1.14
28	2	199042202		10151	CTAGGAATCTKGCAAAGTGGA	-	-	-	-	-	-	-	-	-	-	-	-
28	2	199049683	12468958	10152	TGAAAGAGACRGAGTCTAAGA	0.48	0.46	0.49	0.38	0.21	0.62	0.36	0.43	0.36	0.19	0.63	0.35
28	2	199056937	2467041	10153	ATATGTATTCYGGCTAGACTG	0.23	0.32	0.32	0.24	0.39	0.36	0.24	0.32	0.26	0.38	0.36	0.21
28	2	199063519	6744584	10154	TGTAAGTACAYTGGCTTTTAT	0.48	0.37	0.37	0.34	0.17	0.42	0.18	0.33	0.30	0.16	0.41	0.16
28	2	199071714	2880591	10155	CTTTATAGGTRCATACTTATG	0.64	0.41	0.41	0.28	0.08	0.07	0.26	0.38	0.25	0.07	0.08	0.24
29	2	203044037	1996270	10156	ACTGATTTTCWAAGTATATCC	0.21	0.20	0.20	0.17	0.35	0.16	1.23	0.18	0.13	0.36	0.16	1.18
29	2	203046974	12994463	10157	ACACAACTTARCCATGTATGG	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203071810	6717924	10158	CACTTTGCCTRTGATGAGGCT	0.32	0.64	0.59	0.33	0.13	1.33	1.13	0.55	0.31	0.13	1.30	1.07
29	2	203080991	13426118	10159	CAAGCTTTTCMTGCTTGTCAG	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203088848	17271393	10160	AGTTTTGAATRTTCTTGTGGT	0.27	0.57	0.53	0.45	1.39	0.50	1.97	0.43	0.52	1.32	0.51	1.87
29	2	203096773	6435149	10161	GGAAAGTGAAYGTAGTTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203119293	16839152	10162	CCCATAAATAYCTCTAGAATC	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203149343	12467506	10163	CTAAGGTTTTMGTTTTTTGGA	0.24	0.53	0.53	1.08	1.42	2.50	3.39	0.48	1.29	1.34	2.27	3.01
29	2	203165927	7597257	10164	ACATTACTTAYTTGCCTGATG	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203185798	6751669	10165	GGTCCGGGTGKTCTTGGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203243289	17199228	10166	ACATTTTTGTWTGGTACAAGT	-	-	-	-	-	-	-	-	-	-	-	-
29	2	203250981	6435156	10167	TTCAAGGCATYTTAATAAACT	0.84	0.27	0.26	1.19	2.14	3.10	3.75	0.24	1.30	1.92	2.71	3.33
29	2	203255962	1048829	10168	AGGTATTATCKATGGACATTT	1.01	1.20	1.20	2.24	3.17	3.38	2.23	1.17	2.39	2.90	2.98	2.09
29	2	203284000	17386813	10169	TCTTTTAGCAYGTTAGGACCA	0.41	0.75	0.75	2.65	4.30	2.34	2.39	0.71	2.82	3.68	2.22	2.26
29	2	203295466	13035933	10170	GGCCTTCTCTKCTCTGTTTGC	0.37	0.15	0.10	2.13	2.43	3.14	2.39	0.08	2.29	2.24	2.94	2.26
29	2	203333169		10171	TTGAGAAAGCYGAAAAGAAAG	0.32	0.63	0.59	2.27	2.42	2.52	2.45	0.55	2.44	2.30	2.38	2.30
29	2	203357810	11694172	10172	ATAATTATGTRGAGAGGAATA	0.69	0.95	0.96	0.80	3.08	1.76	1.61	0.87	0.75	2.68	1.66	1.56

29	2	203364809		10173	GTACTACCAAYGTCTTGAGTT	0.89	0.88	0.88	0.70	0.39	1.52	0.64	0.63	0.69	0.42	1.49	0.63
29	2	203384037		10174	GTGTCCAATCRTCTTCTCATT	0.70	0.91	0.91	0.99	0.43	0.23	1.03	0.88	1.01	0.46	0.23	1.03
30	2	215864845	4563222	10175	CATAATTAATYTGTAAAAGTT	0.04	0.07	0.08	0.11	0.36	0.43	0.16	0.05	0.04	0.37	0.43	0.17
30	2	215875822	16853507	10176	CGTTAATTTTRATGTTCAGCC	-	-	-	-	-	-	-	-	-	-	-	-
30	2	215881289	13034856	10177	CAATGAAAGAYAAATGGTGGT	0.04	0.14	0.14	0.43	0.52	0.29	0.78	0.11	0.47	0.53	0.31	0.80
30	2	215905634	12474265	10178	GTTTCTCAATMCTTGAGACAA	-	-	-	-	-	-	-	-	-	-	-	-
30	2	215929412	4673964	10179	GAATACAATAYAAAATGGATA	0.18	0.37	0.40	0.92	0.45	0.43	0.25	0.40	1.05	0.46	0.44	0.23
30	2	215932422	16853623	10180	TGTTTCATTCRCATTTTGGAA	1.63	0.04	0.06	0.14	0.84	0.50	0.42	0.04	0.16	0.85	0.52	0.44
30	2	215966743	10498034	10181	GTGTTATTATYGAAGCTCACA	0.28	0.55	0.55	0.22	0.32	0.63	0.76	0.46	0.22	0.34	0.63	0.74
30	2	215981941	16853697	10182	AACATTATGCYCTATTTTCCT	0.37	0.29	0.29	0.26	0.18	0.61	0.59	0.23	0.24	0.21	0.61	0.60
30	2	215992750	12997662	10183	TGAAGTAGAAYACAAACACTG	0.04	0.04	0.04	0.10	0.17	0.18	0.32	0.02	0.10	0.18	0.18	0.34
30	2	216007374	7585489	10184	TTCGTGGTTAYGACTTTCTAG	0.21	0.00	0.00	0.08	0.04	0.04	0.13	0.00	0.07	0.03	0.04	0.12
30	2	216015526	2372536	10185	CCAGGTGTAASTGTTGAGGAG	0.12	0.13	0.10	0.00	0.00	0.00	0.01	0.07	0.00	0.00	0.00	0.01
31	3	668942	17044991	10186	AATACTAACCRGGTATCTTCA	0.16	0.16	0.16	0.05	0.29	0.41	0.40	0.06	0.06	0.31	0.39	0.40
31	3	675611	2627981	10187	AATGCAAATTWTCAAGGAACC	0.04	0.03	0.03	0.14	0.36	0.88	0.20	0.00	0.12	0.39	0.91	0.20
31	3	684782	9866771	10188	CTCCCTGCAAYGAGTGCAAAT	0.47	0.61	0.53	0.26	0.47	0.27	0.21	0.45	0.24	0.45	0.28	0.20
31	3	693313	716633	10189	ATTATTCAGGRAACATTTTGA	0.72	0.85	0.77	0.51	0.07	0.10	0.12	0.66	0.52	0.08	0.11	0.13
31	3	701617	17472555	10190	TTCTTATATARTTATAGTTGC	-	-	-	-	-	-	-	-	-	-	-	-
31	3	703950	4596136	10191	ACTTGAAATGWTCTTACACAG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	719058	1385194	10192	TAGGATTTCTSTTAGATGCCA	0.65	0.47	0.47	0.14	0.20	0.07	0.33	0.40	0.09	0.25	0.07	0.33
31	3	745685		10193	ATTAGATACAWTCCTTGGTTT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	751632	17047035	10194	CACGTGTTCCYGTCTCAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	766276	7618377	10195	TTATTCATGTKTACTTTATTT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	779791	7640121	10196	GATATTCTTAWCTATTAGATT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	792978	1523896	10197	AATGAGACTCRACTGACATTT	1.12	0.86	0.86	0.38	0.20	0.31	0.16	0.78	0.37	0.20	0.30	0.16
31	3	804036	11131086	10198	AAGGGGCATGYTTTAGCCTTC	1.31	0.48	0.38	0.92	0.53	0.27	0.66	0.33	1.04	0.55	0.28	0.68
31	3	809801	13316610	10199	GCTATTGTGTKTTGCACTTGG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	815276	17486433	10200	TAGAAATTTGYACCTTGAAAT	0.86	1.38	1.38	0.67	0.62	1.10	0.47	1.34	0.63	0.66	1.07	0.42
31	3	844467	2204282	10201	CAGTGTTGCTRTGTTTAAGGT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	855768	12488182	10202	TTAATTTTGGRGTTGGATCAG	0.33	0.62	0.67	0.46	1.90	1.17	0.21	0.61	0.48	1.63	1.15	0.23
31	3	862936	4686228	10203	CATGGCATCASTTGGAACTTT	0.45	0.83	0.83	1.65	0.79	0.48	0.22	0.82	1.87	0.83	0.48	0.24
31	3	873689		10204	AATAGCAAGAYGGCAAATGAA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	882552	13065349	10205	GTGCCACCATYTTTCCTTGCT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	888198	1916758	10206	TTAGTAAAATMCCAAAGGCTG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	895346	10510201	10207	AACATATAATSACAGAAACAA	1.34	1.90	1.90	0.86	0.51	0.39	0.58	1.84	0.93	0.51	0.39	0.59
31	3	916639	9830614	10208	GAAAAAAAGARGCTCAGAAAG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	924345	9812345	10209	ATCTCTCTTCMTGCTAGACTA	0.06	0.06	0.06	0.82	0.38	0.59	1.00	0.00	0.87	0.37	0.64	0.99
31	3	938042	955350	10210	AGCAAAACTTYGTAAAATAAT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	947794	11708965	10211	TCTGCTACCAMTTTGAACCTT	1.10	0.84	0.86	0.32	0.22	0.61	1.35	0.79	0.29	0.21	0.63	1.30
31	3	950836	11920873	10212	TAAAGGAGGGYGGTCAAAAAA	0.82	0.09	0.09	0.16	0.49	1.53	1.60	0.06	0.17	0.50	1.49	1.54
31	3	961917	4686326	10213	TAGGCCTCTTYGGATCAAATG	0.27	0.54	0.54	0.66	1.71	2.34	2.40	0.49	0.68	1.63	2.14	2.27
31	3	970511	12630927	10214	AATTCTTGCTMTGGGAGCTTT	1.71	0.31	0.31	2.21	2.46	1.28	1.44	0.26	2.34	2.33	1.28	1.39
31	3	978642	17488996	10215	CTGCCTGATTYTACGCAGTCC	0.81	1.24	1.18	1.00	1.57	1.57	1.33	1.14	1.03	1.49	1.56	1.27
31	3	987532	17050444	10216	CTAGTTTCCTSTGGGACATTA	0.70	1.12	1.30	1.26	0.59	1.41	1.94	1.21	1.34	0.57	1.38	1.85
31	3	996321	13066780	10217	ACATTCCCATSTAAGGTTACA	0.78	1.08	1.00	1.43	1.05	0.66	1.40	0.94	1.51	1.03	0.65	1.34
31	3	1010817	6792210	10218	TTAGATCACTSCCATTTCACT	0.59	0.78	0.78	0.60	1.61	1.39	1.20	0.71	0.65	1.56	1.33	1.18
31	3	1026760	4234583	10219	GATAAATCCCYAATGTTTATG	0.59	0.40	0.34	1.67	1.09	2.59	1.96	0.28	1.94	1.07	2.36	1.85
31	3	1029048	4476491	10220	TTATGATAGAYATTTTTCAAT	0.62	1.15	1.21	1.09	3.13	3.36	2.16	1.12	1.21	2.71	3.06	2.01
31	3	1037808		10221	GCGTAAGCTTRGGACCACAAC	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1046343	9310358	10222	AAAATGTTACYAATGTTCTAG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1052541	17032572	10223	ACAAAAGCCAYTTGAAGCAAT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1065860	17032728	10224	GAATTAAGAARTTGGGTTAAA	0.29	0.29	0.29	3.12	4.44	3.93	2.69	0.23	3.63	3.84	3.44	2.49
31	3	1072248	2729112	10225	AGCAGCACATKCAAGGACATG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1091152	1504069	10226	ACTGTTTAAGYGAGCCTCAAG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1096947	9869886	10227	TCTCCGCCATSCCTCACGCTT	3.08	3.76	3.76	2.51	3.78	2.76	2.46	3.66	3.03	3.33	2.56	2.30
31	3	1103796	2729140	10228	TTTAAGAGCARTAGTCAATAA	1.03	1.57	1.46	3.09	2.67	1.55	2.15	1.41	3.47	2.40	1.52	2.06
31	3	1113294	9817012	10229	AGTATAGCTTRCAATAAACCT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1118996		10230	GCTTTTAGTGRAAGAACATGA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1124544	6442206	10231	TTACTGAAAGRAGTTAGGTCT	0.57	0.78	0.78	1.40	2.14	1.58	1.67	0.69	1.49	1.99	1.55	1.64
31	3	1142599	1394179	10232	TTTTCGGGCASTGTAGTTTTC	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1149083	2171764	10233	AAAATCAGTTRTCTCATTGAT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1166861	12495445	10234	TTTTGTTAGASGTTTCATGGT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1172989	11925137	10235	ATTTTCTCCTKAAACCTTGAT	0.53	0.69	0.69	0.32	0.99	2.30	2.25	0.65	0.28	0.99	2.16	2.09
31	3	1185218	4684777	10236	AACAAGAGACRAGCTCTGAGA	0.23	0.15	0.15	0.83	2.14	1.64	1.60	0.09	0.93	2.01	1.52	1.54
31	3	1195546	12106966	10237	CCAGAGAGTAKTCTGTTTCAC	1.02	1.46	1.46	1.59	1.47	1.23	0.96	1.37	1.72	1.41	1.18	0.93
31	3	1206334	9840388	10238	GCCTCCTTCAYGTCGACTCCA	0.58	0.88	0.92	0.62	0.76	0.66	0.58	0.85	0.62	0.74	0.68	0.61
31	3	1213954	17440919	10239	TTGGCTGGTCRTTGAGGATAC	0.19	0.39	0.43	0.26	0.43	0.52	0.39	0.38	0.25	0.43	0.55	0.40
31	3	1221312		10240	TTTATTTCAGYTCCCAGTTTA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1226909	3772346	10241	CTTGACCTCTYTAGAATTACT	0.22	0.36	0.50	0.47	0.38	0.24	0.40	0.48	0.43	0.37	0.25	0.42
31	3	1232668	7644569	10242	ATTTCTTTTTYAATGAATTGT	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1240677	9835758	10243	TTCAAGTATAYGCAGCAAAGG	0.28	0.21	0.21	0.33	0.34	0.39	1.29	0.16	0.32	0.32	0.36	1.24
31	3	1247244	6798321	10244	TTGTTCTTTTSTTTTCATGTC	0.20	0.22	0.24	0.19	0.36	1.14	1.87	0.19	0.15	0.40	1.14	1.78
31	3	1249105	6766483	10245	TTCCTGTCTCMACAGAACAGA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1264305	17036319	10246	ATATCTTTCAYTGGATAAAAA	0.00	0.00	0.00	0.13	2.07	1.98	1.21	0.00	0.09	1.99	1.93	1.19
31	3	1273990	17036743	10247	ATTTTAACTTKGCTAGTTGTG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1280712	4088850	10248	ATTATGTTCCRAAAAACAGGA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1286742	7621594	10249	TTTGACAATARCATTGTGCTT	0.66	0.43	0.43	1.88	1.67	2.52	2.74	0.36	2.01	1.62	2.38	2.61
31	3	1292869	3821435	10250	AAGATAACCARTGTGTATTTT	1.74	2.36	2.37	1.76	2.68	2.02	2.92	2.29	1.81	2.46	1.91	2.69
31	3	1299048	6786142	10251	CATCACAGTGMAAAAGAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1305516	3901789	10252	AACATAATCAYACTCTGGGGA	0.40	0.16	0.16	1.89	2.68	2.90	1.75	0.13	1.95	2.52	2.67	1.66
31	3	1312162	2063243	10253	CTATCAACTGRGCAAATAGAG	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1323603	536569	10254	AGTTACTGACRTTTCCTCACT	0.41	0.17	0.17	0.21	2.17	2.72	2.09	0.15	0.22	2.01	2.54	1.95
31	3	1331306	155227	10255	ATGAACTAGGYCAGATGGTTA	0.58	0.98	1.02	1.07	0.34	1.24	2.28	0.98	1.21	0.38	1.20	2.17
31	3	1338767	5012022	10256	AGCAGTGTCAKGTTAAAGCCA	0.66	0.78	0.71	0.88	0.21	0.62	0.61	0.65	0.91	0.22	0.64	0.61
31	3	1344428	265774	10257	TCAAGGTGGTRATTATTATTC	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1351765	2133451	10258	AGTCAAAGATSTGGGTTAAAG	0.33	0.62	0.60	0.23	0.38	0.32	0.45	0.52	0.24	0.35	0.30	0.45
31	3	1362438	6794738	10259	AATTGTGAACRGGAAGAATTT	0.12	0.15	0.17	0.93	0.70	0.28	0.58	0.15	0.96	0.70	0.28	0.60
31	3	1368675	7651808	10260	GGAAAATACASAGTAAATAGT	0.47	0.84	0.84	1.00	0.84	0.34	0.40	0.81	1.09	0.87	0.33	0.41
31	3	1376541	155896	10261	TCAGAGTATTMGCTTTGATTT	0.21	0.45	0.45	0.61	0.72	0.64	0.30	0.41	0.61	0.73	0.60	0.30
31	3	1383344	13063912	10262	GTGGGGTACTYATGTTAGTGC	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1390195	3765098	10263	TATTTTACTTYCTAAGCACAA	0.07	0.22	0.22	0.42	0.57	0.61	0.44	0.17	0.45	0.60	0.64	0.46
31	3	1396900	155391	10264	GTCACAATCTRCCATTACGTT	0.02	0.11	0.11	0.43	0.30	0.37	0.92	0.08	0.45	0.32	0.36	0.93
31	3	1403635	17038510	10265	AGTTAGGAACYATCTCAGAGA	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1412835	17038652	10266	CAAGATCTTTSACAATGTGTC	0.04	0.15	0.15	0.06	0.30	0.52	0.30	0.14	0.05	0.28	0.53	0.32

31	3	1428277	155867	10267	CCCTGCAGCCRAATTAACTAA	-	-	-	-	-	-	-	-	-	-	-	-	-
31	3	1441904	12492544	10268	GGAAGTGCTCRGAGCTCATTG	0.50	0.44	0.44	0.05	0.88	0.82	0.11	0.39	0.05	0.87	0.80	0.12	
31	3	1448261	1124606	10269	ACAGGGAATTKTTTCTGAATC	0.70	0.61	0.61	1.03	1.08	0.13	0.03	0.59	1.18	1.08	0.13	0.02	
32	3	6200016	1394155	10270	TTAAAGGTGGMAATGCAGGCC	0.14	0.17	0.17	0.31	0.29	0.11	0.08	0.14	0.31	0.33	0.11	0.09	
32	3	6213978	17044332	10271	ACAAGACTATYGTAAACACAA	-	-	-	-	-	-	-	-	-	-	-	-	
32	3	6220005	286588	10272	CTCTTCAAAGYGAATTGTGTT	0.81	1.22	1.22	0.90	0.10	0.12	0.11	1.18	0.91	0.10	0.12	0.11	
32	3	6226079	1513436	10273	TGACTGTGCARTAATACTCAC	1.37	1.62	1.62	0.80	0.27	0.11	0.10	1.56	0.85	0.27	0.11	0.11	
32	3	6232785	12497884	10274	GTGATTCACARTGAGAGTGAC	-	-	-	-	-	-	-	-	-	-	-	-	
32	3	6238422	9846434	10275	ATCTGAGGATKATATATTTAT	0.36	0.70	0.74	0.49	0.36	0.29	0.40	0.66	0.49	0.37	0.31	0.41	
32	3	6244892	9855569	10276	GGGTTATGAASCAGAGTGGAA	0.29	0.47	0.41	0.29	0.32	0.13	0.81	0.39	0.30	0.33	0.16	0.84	
32	3	6257028	10490889	10277	GAACCAACTCRATGTATTTGA	0.32	0.45	0.45	0.20	0.18	0.37	0.45	0.42	0.20	0.16	0.37	0.41	
32	3	6265436	12330911	10278	GGTGACCTTCYGTCAGGGTTC	0.37	0.71	0.71	0.24	0.38	0.23	0.26	0.68	0.24	0.38	0.20	0.27	
32	3	6278579	17272131	10279	TATCAGCTTGYGGCTTTCCTT	0.40	0.42	0.42	0.49	0.35	0.30	0.22	0.38	0.47	0.35	0.28	0.22	
32	3	6290882	2164364	10280	AGCAATCATGRAGCAAGCCTG	-	-	-	-	-	-	-	-	-	-	-	-	
32	3	6300946	17599293	10281	TAGTACACCCKTGGGGCTAAG	0.34	0.64	0.64	0.64	0.35	0.23	0.13	0.61	0.65	0.39	0.22	0.12	
32	3	6312319	11707382	10282	CTGTGCACAAYTGAAAGTGAT	0.25	0.37	0.46	0.77	0.29	0.10	0.05	0.39	0.75	0.27	0.11	0.07	
33	3	10115115	2272123	10283	GTTCAGCATCRACTTAGAGTC	0.19	0.28	0.29	0.28	0.20	0.36	0.85	0.25	0.24	0.20	0.37	0.86	
33	3	10126138	7652935	10284	ACACAAATGAYTTTGAATTAC	0.27	0.26	0.25	0.08	0.51	1.05	0.83	0.22	0.03	0.58	1.01	0.81	
33	3	10133302	17032414	10285	AAGTGTTTAASAGAACTTGGC	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10139783	6783705	10286	TGACCATGCTRAGATACCTTT	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10144819	17032440	10287	AAAGACACATKGATTTAATAG	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10158274	779804	10288	CTTAGAGGGGYGAAAAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10164929	1681660	10289	CCTTATAGAAYACCCTCGAGT	0.04	0.15	0.12	0.09	0.60	0.94	0.48	0.09	0.03	0.61	0.96	0.51	
33	3	10170485	1642739	10290	AGTCTCTTCTMTTTCCAACCC	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10177329		10291	TTTCTAACTGMTCCTGGTGGG	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10187494	708030	10292	ACTTCCTACAYTGGATCAGAG	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10195830	17610830	10293	TTCACCTAGCRAAGACCTTGG	0.44	0.58	0.58	0.45	0.47	0.53	0.60	0.53	0.44	0.47	0.54	0.62	
33	3	10204189	17032518	10294	CAGATCATGGYCTAGAGTAGC	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10210666	696040	10295	TGCTTCCTTCRGAGGCCCGAG	0.89	0.64	0.64	0.45	0.20	0.50	1.10	0.58	0.45	0.21	0.51	1.13	
33	3	10217711	263413	10296	ACAATATCGGRAGGTAGAAAA	0.41	0.79	0.79	0.35	0.61	0.88	0.74	0.75	0.38	0.62	0.87	0.72	
33	3	10223082	9842690	10297	GGCTGCTAGAYTCACACAGCA	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10229176	13058968	10298	AGACCAAGAGYGCTGAGCTCG	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10235907	11465906	10299	TGAAAAAACTYACAGTATCAT	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10243017	779905	10300	TGTGCACGAGYGTCTGAACCA	0.06	0.14	0.15	0.75	0.64	0.77	0.76	0.13	0.81	0.61	0.79	0.76	
33	3	10253980	11711184	10301	TTTAGGTGTAMGAAGAGGTAG	1.98	1.87	1.87	0.84	0.31	0.24	0.25	1.78	0.94	0.32	0.26	0.23	
33	3	10264316	11709512	10302	GGGAGAATTGYTACATCGAAT	2.27	1.35	1.35	0.89	0.31	0.07	0.10	1.28	0.90	0.33	0.08	0.12	
33	3	10280551	1630999	10303	GGATGATCGGSAGAATATAAC	-	-	-	-	-	-	-	-	-	-	-	-	
33	3	10286939	2075352	10304	TCAGCCGTTCYGGAGCCTTCT	0.44	0.21	0.20	0.84	0.29	0.12	0.11	0.17	0.86	0.32	0.11	0.10	
33	3	10295968	1063429	10305	CGAGGATGTGWTTAGAGAGCT	1.51	1.89	1.89	0.79	0.33	0.17	0.09	1.84	0.84	0.34	0.18	0.09	
33	3	10301686	35684	10306	GTTGTGGAACRTAAGAGTCAA	0.46	0.79	0.79	0.56	0.20	0.16	0.14	0.75	0.58	0.19	0.16	0.14	
33	3	10311291	1629816	10307	GGGCCATCTCRTCTCAATTTC	0.10	0.06	0.02	0.13	0.44	0.15	0.34	0.00	0.10	0.46	0.15	0.34	
34	3	34828660	6805290	10308	GTTCATCAATRGACAATAATA	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	34843225	7624563	10309	GAGAGCATCARAATTGTGAGA	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	34852224	479207	10310	TTCTTTTCTTSCCAAATGGCA	0.73	0.25	0.38	0.21	0.02	0.02	0.52	0.33	0.18	0.01	0.02	0.53	
34	3	34862685	2358748	10311	CTATATTCTCYGTTTTAGCTT	0.02	0.08	0.08	0.10	0.09	0.04	0.01	0.06	0.08	0.10	0.05	0.01	
34	3	34881768	17032340	10312	ACCAATAAATRCACCTGCTTG	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	34887174	1357430	10313	TAACAGAAAAYGATGATGATG	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	34893508	12163625	10314	AATCTGTTATYTCCTTTCACA	0.30	0.17	0.17	0.37	0.12	0.03	0.15	0.15	0.36	0.12	0.03	0.16	
34	3	34897727	17032385	10315	GTCATTGGCTKGTGGCTCACT	0.22	0.05	0.12	0.28	0.08	0.30	0.34	0.07	0.25	0.06	0.28	0.36	
34	3	34910897	17032404	10316	TTAAAGATAASACAAAGTCAA	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	34919697	17032486	10317	TGGTTAGTGAYGGAGCAATAA	0.38	0.55	0.60	0.05	0.07	0.02	0.96	0.54	0.05	0.05	0.00	0.99	
34	3	34931530	17032494	10318	TCAATTATAARTTTTCTTTCT	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	34938895	17032513	10319	ATTGTGTATGYATGCGTCATG	0.44	0.61	0.66	0.25	0.02	0.74	0.22	0.57	0.18	0.01	0.77	0.21	
34	3	34959718	7618930	10320	TGCTAACTCAYACACCCGTGA	0.61	0.26	0.26	0.20	1.58	0.37	0.27	0.22	0.17	1.51	0.37	0.27	
34	3	34970751	7637034	10321	ACAATAAGCTSTGTATGGGGA	0.28	0.26	0.26	1.47	0.74	0.51	0.46	0.21	1.73	0.74	0.54	0.50	
34	3	34985135	17032548	10322	TAAGAAGATGYTGATTAAATT	2.30	2.27	3.00	1.59	0.59	0.71	1.00	2.90	1.84	0.62	0.69	0.96	
34	3	34989683	17032557	10323	AAGGCAGAACMAGCTAATAGC	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35015028	1382548	10324	GTTTTTATCAYAGCAAAAAAT	0.67	0.41	0.41	1.62	0.90	0.66	1.25	0.37	1.72	0.93	0.69	1.21	
34	3	35024824	1871290	10325	ACCTGGCTCTRTTAGGAGCAT	0.44	0.69	0.69	0.20	0.95	0.60	1.24	0.62	0.18	0.94	0.62	1.19	
34	3	35027805	1993908	10326	TCCTCTTGTCRTACTTCACTT	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35040405	2884663	10327	CAAAGTTAATRTAAGACACAA	0.52	0.43	0.43	0.37	0.22	0.81	0.30	0.37	0.40	0.23	0.82	0.34	
34	3	35052013	17032625	10328	TGTGGTCTTTYGAACTCCAGT	0.37	0.58	0.64	0.67	0.27	0.06	0.19	0.58	0.73	0.28	0.05	0.18	
34	3	35075665	1463551	10329	GTTTTCTGGARTATTCAGCAA	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35089566	7629404	10330	TACTTTATTAWTATTATATTT	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35103050	1478838	10331	AAATTGAGACYGAGAGGAAGT	1.63	1.08	1.14	1.00	0.41	0.04	0.01	1.08	1.21	0.42	0.04	0.00	
34	3	35104903	4678736	10332	CCAGAATGACYGCAGGAATAC	0.96	1.43	1.42	0.56	0.34	0.08	0.01	1.38	0.63	0.43	0.06	0.01	
34	3	35129072	1478836	10333	TTTACACAGAWCCCTTCTACT	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35142169	6771743	10334	CGAGATTAGCWCTCCATACCA	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35153052	4263240	10335	TAATATGTTGMTTCCTTTCCT	1.05	1.55	1.36	0.36	0.24	0.12	0.65	1.30	0.35	0.23	0.12	0.64	
34	3	35167895	7619909	10336	ACTAAAATACRTATTCCCAAA	0.20	0.16	0.16	0.52	0.23	0.51	1.13	0.14	0.52	0.23	0.50	1.08	
34	3	35183715	7626357	10337	GCAGGTTTACYATATGGAAAT	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35204578	7614636	10338	GGTTTTGCTCYTCCTGGGCAG	0.06	0.19	0.19	0.12	0.87	1.79	1.24	0.16	0.11	0.85	1.76	1.20	
34	3	35220131	4346506	10339	TCACGGCACTKAGTTATAGCA	-	-	-	-	-	-	-	-	-	-	-	-	
34	3	35249754	11917407	10340	TTGAAAAGGAYTGAATAAACA	0.03	0.14	0.15	0.30	1.05	1.92	1.83	0.13	0.30	1.03	1.83	1.79	
35	3	43594314	3755602	10341	TTCTACACATRAACTTCCAGA	0.13	0.14	0.11	0.03	0.36	0.45	0.54	0.08	0.03	0.38	0.45	0.60	
35	3	43603851	3772170	10342	CAGTCTAGAAWGGTGCAGGAA	0.32	0.32	0.23	0.10	0.16	0.57	0.21	0.15	0.10	0.17	0.59	0.24	
35	3	43617160	2068969	10343	TATAATGTTTYTAGTCTGGTA	-	-	-	-	-	-	-	-	-	-	-	-	
35	3	43639042	17030517	10344	CAAGTTGTGARAAACGCAGAT	0.25	0.39	0.39	0.63	0.28	0.03	0.22	0.37	0.70	0.33	0.03	0.23	
35	3	43643180	9852783	10345	TATATCTTGAYAGCTACACAT	0.67	1.00	1.00	0.49	0.11	0.07	0.02	0.97	0.50	0.11	0.08	0.01	
35	3	43675296	4432612	10346	TTATGTAAGGYTCAAGACGAG	0.27	0.19	0.19	0.27	0.17	0.07	0.04	0.14	0.24	0.17	0.09	0.03	
35	3	43719412	17075884	10347	CAGCAGGCTTYGTCTAATGTT	0.09	0.09	0.09	0.15	0.16	0.09	0.05	0.04	0.04	0.18	0.10	0.05	
35	3	43728082	17075899	10348	TTTAGCACTARTCTTTAACGT	0.09	0.00	0.04	0.18	0.10	0.13	0.03	0.00	0.12	0.10	0.16	0.04	
35	3	43736445	3733156	10349	TAGGAAATGTRAGGTTGTGTC	0.11	0.29	0.28	0.21	0.09	0.04	0.12	0.27	0.19	0.09	0.03	0.12	
35	3	43744784	17075945	10350	TTGGGAAAATYAGTGTTCTAA	0.28	0.28	0.28	0.12	0.10	0.23	0.08	0.15	0.09	0.07	0.22	0.07	
35	3	43751778	7645010	10351	TGCCAGCATTYTGGTAGGTTT	-	-	-	-	-	-	-	-	-	-	-	-	
35	3	43757672	6441792	10352	ATGGCAGATTRCTGGTGTGAA	0.71	0.24	0.24	0.26	0.25	0.30	0.15	0.22	0.22	0.25	0.31	0.17	
35	3	43771684	2372547	10353	AAGAGTCTACRTTCTTCTCTT	0.85	0.83	0.78	0.41	0.19	0.16	0.58	0.80	0.42	0.19	0.16	0.59	
35	3	43783855	9834526	10354	CTTTAGACAAYGCAAAATCTG	0.32	0.56	0.59	0.55	0.17	0.97	0.66	0.54	0.54	0.15	0.94	0.68	
35	3	43797976	17076032	10355	ATTTAGATAGYTTTCTGGGTA	0.51	0.04	0.04	0.05	1.03	1.02	1.24	0.00	0.05	1.04	0.98	1.24	
35	3	43801826	4682696	10356	AGTCACTAATYTTCAGCAAAT	0.20	0.49	0.53	0.74	1.23	1.30	1.66	0.50	0.74	1.17	1.30	1.63	
35	3	43837255	4392389	10357	GTTCAGCCCTRTGGAAATTTG	1.67	1.21	1.21	0.82	1.03	2.35	1.51	1.15	0.89	1.00	2.13	1.46	
35	3	43849576	4280612	10358	TGGATGGTCTSTAAATACTTC	0.51	0.04	0.04	1.12	1.28	1.22	1.55	0.00	1.20	1.26	1.18	1.48	
35	3	43859425	1826320	10359	GCTTAGTCTARAGAGTGGATT	-	-	-	-	-	-	-	-	-	-	-	-	
35	3	43884703	6790122	10360	TTGCAACTGAWCTTTGTTTAC	1.81	1.89	1.89	1.11	1.65	0.89	0.70	1.86	1.21	1.51	0.89	0.69	

35	3	43892950	17076170	10361	CAAATAGGCAYCTTCTATTAT	0.08	0.14	0.14	1.30	1.14	0.96	0.55	0.12	1.48	1.11	0.93	0.57
35	3	43907049	6789465	10362	TTTTGAGAACRCAGAGCACTA	0.06	0.19	0.19	0.94	1.05	0.51	0.54	0.17	1.07	1.00	0.50	0.57
35	3	43927637	9311345	10363	GTGGCAAACAMAGATGTGGAA	1.31	1.64	1.64	0.68	0.38	0.79	0.62	1.58	0.70	0.41	0.82	0.66
35	3	43937763	3846066	10364	TCCAGCCCAGYGCCAGGATCA	-	-	-	-	-	-	-	-	-	-	-	-
35	3	43949706	6791985	10365	CTTTGCTAAGYACCATTTCTC	0.30	0.25	0.25	0.54	0.42	0.51	0.89	0.22	0.55	0.45	0.53	0.84
35	3	43964599	9861276	10366	ACAGATGAGCYTTCCAAGAGT	1.18	0.46	0.49	0.83	0.68	0.43	0.19	0.45	0.86	0.65	0.46	0.20
35	3	43972670	3843372	10367	CTGCCTATGTYACAGTTAGTG	1.15	0.62	0.62	0.82	0.69	0.21	0.09	0.57	0.93	0.72	0.20	0.10
35	3	43980050	13060222	10368	CCTGCAAAAGWGAATTGTTGC	1.26	0.66	0.66	0.18	0.26	0.11	0.05	0.62	0.10	0.27	0.13	0.05
35	3	43986057	3843373	10369	AGCTACTCCCRTTCTGCTCCC	1.26	0.66	0.66	0.08	0.09	0.18	0.12	0.63	0.04	0.09	0.19	0.13
35	3	43995241	11917515	10370	ATAGCCAAGGRCCTGACATCT	1.49	0.50	0.50	0.26	0.08	0.08	0.47	0.43	0.23	0.07	0.08	0.47
35	3	44019348	1554654	10371	GTCTGAATTCYTGTAGAGTTG	0.19	0.33	0.33	0.50	0.15	0.45	0.87	0.31	0.56	0.17	0.45	0.81
35	3	44031076	17076300	10372	TGGAGAGAGCRCAACCTGCAG	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44043078	7652264	10373	TTGGATTTCTSTTCCTAGTTC	1.05	1.37	1.34	0.54	0.74	1.02	1.01	1.26	0.55	0.77	0.97	1.00
35	3	44051097	10490768	10374	TGTGGGAAATSAGCTCACGTA	0.88	0.83	0.83	1.41	1.13	0.88	0.65	0.82	1.47	1.11	0.88	0.67
35	3	44058056	17076354	10375	TATTGGCCAAWTCTTATCGTT	1.38	0.94	0.81	1.51	1.32	0.57	0.57	0.70	1.60	1.26	0.55	0.55
35	3	44069200	4682934	10376	TGATTTTCTTYCACAGTTGGG	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44080163	1008369	10377	AGAAGGATTCRTAGAAAGATG	0.19	0.36	0.36	0.91	0.59	0.92	0.82	0.32	0.95	0.58	0.95	0.80
35	3	44086949	9844198	10378	GGGGCAAACTRACATAGTCAT	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44100376	9839994	10379	AGAATTCTTCYACCAGTGATT	0.17	0.34	0.34	0.44	0.46	1.22	1.27	0.29	0.46	0.46	1.21	1.23
35	3	44110360	9882688	10380	CATATATGAGRAATCATCTGG	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44116161	6800118	10381	GTTCAACTGGRAAGTTTGCAG	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44126035		10382	CACGGGGACAYGAACTAGAAG	0.81	1.17	1.25	0.67	0.98	0.71	0.90	1.21	0.70	0.96	0.71	0.93
35	3	44136253	6772728	10383	TGAAACAAAGRCAGTGACCCC	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44138138	6767048	10384	AGCCTTCAAAMCTGAGCTAGC	1.08	1.07	1.07	0.63	0.59	0.67	0.19	0.88	0.67	0.60	0.68	0.20
35	3	44161403	4234443	10385	GGTGTGAACGRAAGTGCTGTG	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44174762	7618961	10386	GCATAATTCAYGGATTTACTC	0.76	1.11	1.11	0.75	0.51	0.10	0.16	1.01	0.86	0.52	0.09	0.19
35	3	44186675	17585084	10387	ATTCTAATTARACACCTCCCT	0.70	0.95	0.95	0.42	0.21	0.27	0.07	0.86	0.46	0.22	0.26	0.06
35	3	44208227		10388	AGGTCTTCAAKTAGCCATACA	0.21	0.36	0.36	0.24	0.17	0.15	0.19	0.29	0.20	0.19	0.13	0.18
35	3	44226274	9825080	10389	TTTGGGTCAAYAATCAAACAA	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44239198	10510741	10390	GCAGATGACCRTGGAAAGGAC	0.16	0.10	0.10	0.26	0.12	0.12	0.64	0.07	0.23	0.12	0.10	0.62
35	3	44245841	17076518	10391	TGGAGGAAGAKAATATAATCC	-	-	-	-	-	-	-	-	-	-	-	-
35	3	44252343	9852733	10392	GGCGGCTAGGYAGCAACCAAG	0.24	0.23	0.25	0.18	0.11	0.58	0.59	0.19	0.15	0.11	0.58	0.59
36	3	53921874	2359131	10393	GCCTATTCATRTAACTTCAAA	0.04	0.06	0.08	0.11	0.08	0.21	0.12	0.07	0.07	0.07	0.19	0.13
36	3	53952944	6767076	10394	TGGATTCTACKACTTGTACTA	-	-	-	-	-	-	-	-	-	-	-	-
36	3	53967436	4687597	10395	GTACAGAAACRAGCTGGGAGG	0.01	0.02	0.02	0.13	0.10	0.07	0.21	0.00	0.12	0.10	0.06	0.22
36	3	53980136	6797145	10396	GAGTGCTTTGYCTTTGGGACA	-	-	-	-	-	-	-	-	-	-	-	-
36	3	53992929	4687766	10397	CCTTCAACCARGTAACATAAT	0.06	0.15	0.15	0.19	0.08	0.20	0.37	0.13	0.20	0.07	0.23	0.37
36	3	54004437	6445623	10398	TAGGAGCAGGYGACTCACCAC	-	-	-	-	-	-	-	-	-	-	-	-
36	3	54029518	13324565	10399	TATAAAATAARGGTTTTCAAA	-	-	-	-	-	-	-	-	-	-	-	-
36	3	54044845	17053677	10400	TACATCAGCASCAGGCTTCAC	-	-	-	-	-	-	-	-	-	-	-	-
36	3	54052296	9856661	10401	CTCCATTTTTMAGCCCTCTGC	0.21	0.21	0.21	0.23	0.21	0.22	0.34	0.18	0.23	0.21	0.21	0.33
36	3	54060940	4928043	10402	GAAATCTGTAWGGAACTGACA	0.27	0.28	0.20	0.55	0.17	0.49	0.30	0.17	0.54	0.17	0.52	0.30
37	3	69527828	1967033	10403	CAGTTCCATTWTCTCAGTCTG	0.70	1.11	1.11	0.98	0.68	0.24	0.22	1.05	1.07	0.67	0.22	0.22
37	3	69538104	17005844	10404	TAGAGCACCAYATTTAATGAA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69568443	7645808	10405	CAGATACCCARAAGAATTGAA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69581632	17508572	10406	TTTGGAAAACYCAGAAAAGCA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69585269	962852	10407	GCATAGCGCCRGGCACCTGGA	0.17	0.41	0.41	0.71	0.43	0.62	0.47	0.34	0.75	0.43	0.62	0.46
37	3	69595409		10408	TAGCTATTATSTTTGGCTTAT	0.14	0.18	0.16	0.36	0.35	1.08	0.66	0.15	0.35	0.36	1.10	0.70
37	3	69605808	17633736	10409	CCATCCTGCCRTGTAACTTGT	1.04	0.50	0.50	0.14	0.49	0.37	0.26	0.44	0.15	0.51	0.38	0.27
37	3	69613873	10510979	10410	CTGCAACTAAYTGAATAAACA	0.12	0.15	0.15	0.08	0.06	0.36	0.37	0.11	0.07	0.03	0.32	0.39
37	3	69619641	6783232	10411	GAGGATTCACRGAGAGAGGAA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69625683	17006013	10412	GAGTATGATAYGTTTTGTCAT	0.58	0.26	0.26	0.05	0.23	0.29	0.43	0.20	0.03	0.22	0.29	0.43
37	3	69631985	17006029	10413	GCTGAGCTGGRTCACCACTGT	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69638972	1498852	10414	TAGCCTTTAAYGGAGCTGTTT	0.05	0.19	0.19	0.21	0.13	0.25	0.29	0.18	0.21	0.13	0.25	0.31
37	3	69649252	17006050	10415	ATAGACATCAYAAAGATTAAG	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69659800	11924887	10416	AAAGGAATCAYAAATGCAGAC	0.09	0.28	0.26	0.23	0.09	0.09	0.28	0.23	0.21	0.10	0.09	0.30
37	3	69667090	7643730	10417	TCTTATAAAAYACTAGTCAAC	0.40	0.55	0.55	0.10	0.31	0.32	0.02	0.50	0.08	0.35	0.35	0.02
37	3	69683544	4855413	10418	TTGTATATGCYGCCATGCTAT	0.13	0.32	0.34	0.75	0.80	0.17	0.17	0.28	0.74	0.80	0.19	0.17
37	3	69687225		10419	TATGGCAATCYAGTGCTGGAG	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69702356	2648009	10420	CTCAGGACAASTGTAGATGCT	1.69	1.93	1.93	1.04	0.73	0.76	0.21	1.78	1.10	0.76	0.77	0.23
37	3	69711043	1391777	10421	TAATCTTCAGYGTAAAGGAAG	1.97	0.69	0.69	1.36	1.37	1.08	0.45	0.67	1.54	1.34	1.09	0.46
37	3	69715438	17435790	10422	AAATGTTATTKTCCCTACCTT	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69738540	746948	10423	TGATACTGATRCTTACCTCTT	0.48	0.75	0.75	0.63	0.63	0.82	0.63	0.67	0.65	0.62	0.82	0.60
37	3	69746779	9840980	10424	GATCAGGTTCYGTTTTTTTTC	0.74	0.96	0.96	0.33	0.43	0.48	0.29	0.91	0.34	0.48	0.49	0.27
37	3	69762223	17043824	10425	GTACAATTTTKGTTTTTCAAA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69770992	11707526	10426	TTTAAAATAGMATGAGTTAGA	0.21	0.48	0.46	0.60	0.72	0.35	0.42	0.43	0.59	0.74	0.36	0.44
37	3	69776938	1427416	10427	ACAGTGTGTAWGGCATTAGAA	0.15	0.20	0.24	0.72	1.04	0.55	0.30	0.23	0.77	1.03	0.58	0.29
37	3	69782390	6792167	10428	ACTTTTTACTRAGCCTGAGAA	1.46	1.81	1.81	1.46	1.15	0.59	0.26	1.74	1.64	1.13	0.60	0.25
37	3	69788306	6549245	10429	ATGTTATTTGYTTCTCCTCCA	0.22	0.16	0.15	1.75	1.23	0.62	0.63	0.11	2.07	1.22	0.61	0.66
37	3	69796402	9877101	10430	AGCAATTGTTRTTACTACATT	0.06	0.16	0.19	1.44	1.27	1.04	0.88	0.16	1.72	1.24	1.05	0.83
37	3	69802549	17686914	10431	TATTTTTTTCRTTGATCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69815129	13090155	10432	TGACCCGGTGRCAAGAATGAG	1.60	1.70	1.70	0.71	1.70	1.38	1.73	1.62	0.75	1.60	1.34	1.60
37	3	69821831	17636072	10433	GAAGAAACAGRAAATCAGAGA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69832233	6549248	10434	AGTAGTGAACRCCAGCACATA	1.21	1.31	1.38	1.23	1.06	1.83	1.34	1.33	1.36	1.07	1.76	1.35
37	3	69842594	17006370	10435	CTACCATAAAMCCTTGTACCC	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69852270	1946426	10436	GTCTTTCACTSCCTTTAGTGT	1.48	0.41	0.45	1.52	3.05	1.46	1.31	0.40	1.78	2.79	1.47	1.26
37	3	69859414	7641148	10437	AGAGAATCCTRAGGTTTAAGT	0.17	0.02	0.02	1.99	2.67	1.73	1.36	0.00	2.18	2.39	1.65	1.33
37	3	69893347		10438	TTTTGGTGTTYGGAGGTTTGG	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69903472	12714757	10439	GGAAAGTAAGYGTTACCATTG	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69911493	17006426	10440	AAAAATTCACRGAAACTTAAT	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69919626	7648607	10441	GGATCTCCTAMGTGTCCAACA	0.90	1.25	1.25	0.71	0.96	1.48	1.58	1.23	0.73	0.92	1.40	1.57
37	3	69932756	9832459	10442	TACAAATTAGKATTTATTCTA	-	-	-	-	-	-	-	-	-	-	-	-
37	3	69936491	1430611	10443	TTTTGTGATAYGAGAGCAAGT	1.36	1.49	1.52	0.58	0.27	0.83	1.20	1.45	0.58	0.28	0.87	1.17
37	3	69959120	13093918	10444	GATGTGGATGYGCAGTGAGAC	1.10	1.36	1.36	0.99	0.57	0.42	0.76	1.30	1.10	0.54	0.43	0.77
37	3	69963292	9823839	10445	GCTGTGATGTYGGTTGTCACT	0.74	1.06	1.01	1.27	1.12	0.34	0.30	0.93	1.45	1.10	0.35	0.32
37	3	69999327	2320172	10446	ACAGATACTTKAGATTTTTTT	0.04	0.12	0.08	1.06	1.22	0.77	0.47	0.05	1.12	1.21	0.77	0.46
37	3	70006713		10447	TGGGATTTAGSAAAACGTCAG	-	-	-	-	-	-	-	-	-	-	-	-
37	3	70017219	17006579	10448	CCATACTGCCRGAGGTGAAGG	-	-	-	-	-	-	-	-	-	-	-	-
37	3	70030858	10510992	10449	CCCAAAAAGAYGTATGAACAC	0.19	0.19	0.12	0.49	1.61	0.87	0.80	0.06	0.50	1.56	0.87	0.79
37	3	70049623	11128152	10450	TTGGTTGGTAYATTTTATGTC	0.35	0.53	0.66	1.47	0.94	1.51	1.14	0.57	1.68	0.93	1.43	1.13
37	3	70054974	9820221	10451	AGTTTCAAAASCAGAAATAAT	-	-	-	-	-	-	-	-	-	-	-	-
37	3	70083573		10452	TGTATGTTTGRGAAATGAGAT	-	-	-	-	-	-	-	-	-	-	-	-
37	3	70102313	1491688	10453	TGGCTTTATGWCTGTACCCAT	0.06	0.04	0.09	1.23	2.13	1.55	1.25	0.07	1.28	2.01	1.48	1.25
37	3	70107441	2172211	10454	AATGTGCCTCRTGTAAAGATC	0.09	0.14	0.12	0.37	1.32	1.84	1.69	0.09	0.39	1.28	1.75	1.62

37	3	70118040	9839734	10455	TTTTCATTCAWGTTTCCCCAA	-	-	-	-	-	-	-	-	-	-	-	-	-
37	3	70128128	7611660	10456	TTATGGATGGYGATATAACTG	-	-	-	-	-	-	-	-	-	-	-	-	-
37	3	70138202	9818798	10457	AGGAAGGGAAYGTGTATTAAG	0.44	0.81	0.81	0.57	0.22	1.41	1.80	0.78	0.56	0.24	1.36	1.67	
37	3	70145242	12495615	10458	AGTCAGTCATRTTGCTTTATG	0.26	0.56	0.54	0.51	0.45	0.19	0.62	0.50	0.47	0.50	0.19	0.59	
37	3	70153619	7619924	10459	TAAGGTTTTTRAGTGCATTTG	0.47	0.85	0.85	0.62	0.47	0.18	0.58	0.76	0.63	0.48	0.17	0.61	
37	3	70163580	1491696	10460	GTTAGCTTTTSTAAATGAAAC	0.54	0.92	0.94	0.73	0.19	0.26	1.03	0.88	0.77	0.19	0.28	1.00	
37	3	70174220	4855335	10461	AAGTATTGTTYTTCCATGAAT	0.43	0.69	0.69	0.53	0.36	0.24	0.42	0.64	0.51	0.38	0.22	0.45	
37	3	70185441	6549267	10462	GATACTGTCTRTGAAATATTT	-	-	-	-	-	-	-	-	-	-	-	-	
37	3	70197189	7651972	10463	AGTTTGGCTTYGAAATCCATG	0.21	0.46	0.46	0.14	0.63	0.61	0.18	0.42	0.12	0.63	0.63	0.18	
37	3	70212465	902709	10464	TGTCTATAAAMCTCTTACTGG	0.37	0.21	0.10	0.69	0.77	0.30	0.32	0.05	0.72	0.75	0.33	0.37	
37	3	70218633	765015	10465	CAACAGCAGAKTTAACATGCG	-	-	-	-	-	-	-	-	-	-	-	-	
37	3	70225785	755353	10466	TTTGCAACCCYTAACCTTCTG	-	-	-	-	-	-	-	-	-	-	-	-	
37	3	70234134		10467	CAGATGAAATRTAACAAAGCC	-	-	-	-	-	-	-	-	-	-	-	-	
37	3	70257951	6549270	10468	ACTCTGTTTGYTAGGATTGTG	0.23	0.08	0.08	0.46	0.51	0.42	0.20	0.05	0.44	0.54	0.46	0.21	
38	3	83105104	17043367	10469	CTTTCTCATTMTCAAATATAC	0.80	0.55	0.55	1.07	0.45	0.17	0.60	0.49	1.06	0.45	0.18	0.62	
38	3	83121394		10470	ACTAGGTAGCYGTGAGGTCAC	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83133246	1482637	10471	GGAGCAGACTRTGAAATGTAC	1.36	1.54	1.54	0.72	0.48	1.36	1.04	1.41	0.70	0.53	1.30	1.05	
38	3	83153783	7615127	10472	TTGGTTCTTTRTTAGCGAGTG	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83164216	1482627	10473	TTATTGGCAAWTTGGTCCCTA	1.99	1.83	1.71	0.60	1.25	1.60	2.34	1.53	0.75	1.22	1.52	2.13	
38	3	83178353	1384431	10474	ATATTCAGGCYTGGAGAATTG	2.13	1.71	1.71	1.68	1.37	2.29	2.76	1.58	2.22	1.29	2.10	2.44	
38	3	83189297	9851151	10475	ATAAGCTTCTRAGGAACTTCA	0.80	1.22	1.22	1.62	1.34	0.91	2.80	1.16	1.76	1.30	0.90	2.51	
38	3	83217835	1115816	10476	TAAATTAGTCMTTTTACATAA	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83229441	17020551	10477	TGTACTAAGAYTATTTTTAAA	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83237104	538361	10478	GTTACAAGAARCAGACCAATG	1.27	1.74	1.74	1.17	1.53	1.39	0.79	1.63	1.32	1.45	1.28	0.79	
38	3	83247317	7611473	10479	CTGAAAGGATRATTTGATATT	1.40	1.88	1.94	1.59	1.90	1.34	1.34	1.87	1.81	1.68	1.28	1.23	
38	3	83256237	17020571	10480	GCATCTAAACRCAAGTTCAAA	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83265725	17020584	10481	GTTTATATGGYTCTGTCACTT	2.30	2.02	1.76	1.99	1.89	1.72	1.28	1.59	2.52	1.68	1.59	1.25	
38	3	83273109	1356629	10482	TGCTTTAAATYAGAAGTGTTC	1.29	1.69	1.69	1.66	2.88	1.62	1.07	1.65	2.00	2.33	1.54	1.00	
38	3	83289913		10483	AAAGTCATAAYGGTGTCCTTG	0.49	0.33	0.33	1.95	2.78	1.85	1.11	0.24	2.12	2.33	1.69	1.08	
38	3	83301123	17020612	10484	TTGTTGAGAAYATTTTTCCAA	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83308814	9857892	10485	AACTTACAGCRTATGCCTAAC	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83353484	11714817	10486	GGCACAGACTKGTATTGAAAG	1.07	1.48	1.52	0.55	2.05	1.90	1.48	1.49	0.58	1.83	1.72	1.44	
38	3	83361299	17020636	10487	ACCACATGCCRTGATAAATTG	0.79	1.18	1.14	0.71	0.47	1.63	1.73	1.07	0.80	0.52	1.53	1.62	
38	3	83370236		10488	ATTCAGAGTASCCTTTCAGAG	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83391358	381553	10489	AGTCAACAAGRAATTTCGATG	0.80	1.23	1.22	0.92	0.86	0.65	1.41	1.19	1.10	0.85	0.70	1.36	
38	3	83407928	823624	10490	TTCCTGTGGTRTAAGTATTGT	0.89	1.33	1.33	1.17	1.04	0.69	0.27	1.30	1.35	1.05	0.69	0.31	
38	3	83416563	9821203	10491	ATTATCTTTCRCTTTGGTTTA	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83451611	17491343	10492	GTCATGTTCCRTCCCATTTTG	0.77	0.76	0.76	1.00	0.82	0.48	0.25	0.64	1.11	0.86	0.48	0.25	
38	3	83463849		10493	TGGATAAATCRAACCTTTATT	0.35	0.55	0.55	0.93	0.56	0.35	0.34	0.45	1.02	0.58	0.36	0.35	
38	3	83474702	422541	10494	CTAACGACACRCAATTGCCTA	-	-	-	-	-	-	-	-	-	-	-	-	
38	3	83497400	417281	10495	ATTAATTTGCRTATTCCTACC	0.80	1.22	1.22	0.90	0.52	0.33	0.38	1.14	0.96	0.55	0.33	0.41	
39	3	106260663	10933805	10496	TTGACTACTTSACATACTCAA	0.88	1.00	1.00	1.10	2.15	0.83	0.62	0.96	1.45	1.96	0.85	0.63	
39	3	106266785	11924063	10497	CCTGCTATGAMATGAAAGCCT	0.15	0.39	0.39	0.81	0.36	0.88	0.53	0.34	0.94	0.38	0.90	0.55	
39	3	106272810	17453821	10498	TGGTAGGCTCRTAAGTAGATT	0.81	1.00	1.00	1.01	0.27	0.08	0.51	0.93	1.02	0.27	0.09	0.52	
39	3	106289555	2654238	10499	GCAACTTGAAMCACTGGCTTC	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106298689	6437566	10500	GACAGGAGCARATGAGAAGTT	0.13	0.35	0.35	0.87	0.26	0.27	0.36	0.29	0.92	0.25	0.27	0.39	
39	3	106310856	9848160	10501	GAGTTCTAAGWGGAGAGAAAG	0.29	0.08	0.10	0.35	0.56	0.40	0.45	0.07	0.34	0.58	0.40	0.46	
39	3	106324272	13065509	10502	GCTCTAAAACRTTAGATTTGT	0.15	0.39	0.30	0.69	1.40	0.85	0.55	0.27	0.67	1.34	0.85	0.56	
39	3	106345175	905462	10503	TTTACCTTCCYTCATTCAAAT	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106352213	9861329	10504	CCGGAGTTGAYAAATTGACAT	0.78	1.05	1.16	1.78	0.65	0.86	0.67	1.11	1.92	0.66	0.86	0.67	
39	3	106357874	967557	10505	GGTTTTGTACRTATTAACACA	0.81	1.26	1.37	0.57	0.53	0.29	1.44	1.34	0.59	0.53	0.30	1.41	
39	3	106370032	12695105	10506	AATAGCTTAARGGACTTACCT	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106378366	16850937	10507	TGACACACTTYAAGGTTTTTC	0.15	0.09	0.09	0.62	0.51	0.63	0.70	0.06	0.65	0.52	0.62	0.73	
39	3	106390387	7626224	10508	ATTATTGACCKGATTAAGTGT	1.27	0.52	0.55	0.80	1.22	1.13	1.03	0.54	0.88	1.20	1.10	1.02	
39	3	106396373	16850955	10509	AGCACCCACAYGTGAAAGTGC	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106410709	16850972	10510	ATCCACACTCYTCCCCTAAAC	0.28	0.36	0.36	0.68	0.83	1.26	1.75	0.30	0.74	0.86	1.23	1.68	
39	3	106421339	13087685	10511	CCAGACTCTTRGATGAGATTA	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106435591	1525843	10512	AATCTGTATTWCATGCAGCCC	0.60	0.56	0.56	0.50	0.70	1.50	1.63	0.50	0.51	0.71	1.42	1.56	
39	3	106449405	11708894	10513	GTGGTATCTGKATTCTGGCCA	0.39	0.73	0.76	0.64	1.37	1.41	2.09	0.73	0.57	1.31	1.40	2.01	
39	3	106455621	10511241	10514	GTTAGATTAARTACAGGCCTC	0.24	0.24	0.24	1.26	1.85	2.13	2.31	0.17	1.26	1.80	2.05	2.23	
39	3	106468340	9868520	10515	AAAAATGACTSCATGTAACTA	0.43	0.78	0.78	0.37	1.19	3.32	2.77	0.74	0.34	1.21	3.07	2.61	
39	3	106481164	9834091	10516	TTTAAAAAGGYTTTCAGCATT	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106487779	16851027	10517	CCCAATACTCYCTAGTGCAGC	0.48	0.67	0.67	1.40	1.37	3.06	3.49	0.61	1.44	1.33	2.86	3.24	
39	3	106495495	9816851	10518	CCTAGAATGCRGTTTCTCATT	1.04	1.32	1.32	2.59	1.59	1.33	3.06	1.23	2.64	1.55	1.33	2.87	
39	3	106508811	7618321	10519	GATTTCAATAWCCTATTTTCA	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106527153	7641707	10520	TGGGATGATAYGATGATTGTG	0.30	0.42	0.40	0.90	1.60	1.17	0.81	0.37	0.89	1.55	1.14	0.78	
39	3	106531544	16851056	10521	AATGTGTAGCWCAAATTGTCA	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106541515	9883403	10522	CAAACATTAAYTGCAAGCCTC	0.64	0.97	0.97	0.54	0.70	1.01	2.45	0.90	0.56	0.72	1.00	2.32	
39	3	106552755	9288801	10523	TTCCTGGCTGRTCGTAGACAA	0.48	0.79	0.79	0.34	0.21	0.91	2.73	0.75	0.32	0.22	0.89	2.51	
39	3	106553516	4894921	10524	TGTAGCAAAAYGAAAAGGGCA	1.17	0.06	0.06	0.36	0.57	1.46	1.51	0.04	0.39	0.58	1.37	1.43	
39	3	106558144	16851091	10525	ACACATCCCTRACTGTCTGCC	0.06	0.19	0.19	1.12	1.73	1.11	0.59	0.12	1.14	1.67	1.11	0.63	
39	3	106574919	16851097	10526	ATATCAACCAKCACTCCAACA	1.34	1.92	1.88	2.24	1.91	0.55	1.39	1.83	2.44	1.83	0.55	1.35	
39	3	106582866	16851098	10527	GAATTATAAARTTGCCAGCTG	3.43	3.44	3.56	2.30	1.42	1.96	1.71	3.45	2.74	1.34	1.83	1.59	
39	3	106611723	12491980	10528	ATGCTGTAACRGAACCACCTG	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106617293	1438538	10529	ATACTTTTGCYAGTGGCTTGC	0.74	0.90	0.90	1.69	3.14	2.10	2.16	0.89	1.99	2.62	1.86	1.98	
39	3	106629158	16844719	10530	TAGGACAAGGRCTCTTAACCC	0.06	0.12	0.14	0.92	3.40	3.14	1.62	0.11	0.91	2.95	2.67	1.50	
39	3	106639048	6806304	10531	ATAAGGAAGAMAAGCTGAATG	0.36	0.21	0.20	0.83	2.48	2.12	1.67	0.17	0.86	2.19	1.93	1.54	
39	3	106653509	12494392	10532	GGGTCTGCACYGCAAGTTGTA	0.40	0.65	0.68	2.30	1.55	1.43	1.33	0.64	2.55	1.45	1.32	1.28	
39	3	106660954	16851175	10533	GAAGACAGGGKTATTATCTTG	1.58	2.18	2.21	1.01	1.72	0.89	1.32	2.15	1.07	1.59	0.88	1.26	
39	3	106670239	16851188	10534	CAAGAGTACAYAAAGATAATG	0.04	0.05	0.05	1.00	0.52	1.42	0.89	0.02	1.27	0.55	1.39	0.88	
39	3	106672694	6437592	10535	TAATTTGAATRTCACTTGGAA	0.10	0.06	0.07	0.11	1.13	0.62	1.04	0.06	0.11	1.09	0.60	1.04	
39	3	106691352	6804472	10536	TCTGAACACTRTCCTGACATA	0.18	0.45	0.45	1.77	1.32	1.53	1.87	0.44	1.96	1.26	1.45	1.78	
39	3	106697479	13075944	10537	CTCAAAGCCCRAATAGTTCCA	2.12	2.82	2.95	2.27	2.63	2.36	1.43	2.86	2.45	2.38	2.15	1.36	
39	3	106704122		10538	AGTTTGCTCARTTACCCTTTT	0.21	0.09	0.00	2.08	1.97	1.36	1.28	0.00	2.19	1.88	1.32	1.24	
39	3	106717573	9283550	10539	ACTTCTTTTAMGGATGATGAT	0.62	0.31	0.31	0.17	1.14	1.02	1.39	0.29	0.15	1.12	1.03	1.35	
39	3	106725019	16851258	10540	ATCACATTTAWTTTTCTCAAA	0.68	0.87	0.87	0.63	0.37	0.99	1.53	0.83	0.65	0.36	0.97	1.50	
39	3	106731901	3772556	10541	TTTACTCTTAYGTGAAAGGCT	0.43	0.34	0.34	0.33	0.83	0.71	1.11	0.31	0.32	0.86	0.74	1.08	
39	3	106740175	3772554	10542	ACAGTGACATRCCACAGGCCA	0.14	0.03	0.05	0.04	0.43	0.82	0.91	0.02	0.04	0.46	0.82	0.91	
39	3	106747643	519016	10543	GGAAAAGGTTRTGATTGCGAT	0.06	0.03	0.02	0.21	0.08	0.61	0.23	0.00	0.19	0.06	0.64	0.25	
39	3	106754625	9283551	10544	TCAGAGAAAAWCATGTCATTA	0.60	0.89	0.92	0.32	0.96	0.22	0.50	0.90	0.32	0.95	0.23	0.52	
39	3	106760324	16851303	10545	TTGGTGAGTCYCTGCATGTAA	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106773252	2291374	10546	GCTCACAGATRTGGAAATTTT	0.19	0.09	0.09	1.07	0.19	0.64	0.40	0.06	1.18	0.21	0.64	0.40	
39	3	106783696	6778668	10547	TTACATGCCARTACCTTTCCT	-	-	-	-	-	-	-	-	-	-	-	-	
39	3	106794262	9881500	10548	ATGTAACTCARCAATCTACTT	-	-	-	-	-	-	-	-	-	-	-	-	

39	3	106812734	9812807	10549	ATGAACCTCTSTTTGAAGCTA	-	-	-	-	-	-	-	-	-	-	-
39	3	106818277	7615659	10550	AATCAACATTSAGTCAGTTCC	1.25	1.70	1.70	0.35	0.47	0.44	0.48	1.65	0.33	0.48	0.42	0.48
39	3	106825705	4894936	10551	TACAAAATCTYCAGAGCATCT	0.13	0.00	0.02	1.21	0.32	0.41	0.29	0.00	1.21	0.34	0.42	0.31
39	3	106827576		10552	ACTGCAAATCKGCCACTCTGA	-	-	-	-	-	-	-	-	-	-	-	-
39	3	106845366	16851374	10553	AAACGGTGGAYTGTAAACCTG	0.36	0.06	0.06	0.31	0.75	0.40	0.32	0.04	0.32	0.77	0.41	0.31
40	3	122877397	6791046	10554	CAAATGCCCARTGTGATTCAG	0.57	0.98	1.04	0.46	1.12	1.48	1.32	0.96	0.49	1.09	1.39	1.25
40	3	122883415	1463736	10555	TTAACCAAAGRGAAAGTAAAA	-	-	-	-	-	-	-	-	-	-	-	-
40	3	122932302	7643293	10556	CTTAATCCTCKCTTCACCTAG	0.23	0.31	0.32	1.24	2.01	1.49	1.29	0.27	1.36	1.73	1.40	1.26
40	3	122942279	12498138	10557	TTGAAGATAARTAATGTGAAT	-	-	-	-	-	-	-	-	-	-	-	-
40	3	122947391	9835182	10558	AAGTGGCACTYAGAATTAAGT	-	-	-	-	-	-	-	-	-	-	-	-
40	3	122971685	1135750	10559	TATCCTCATCSTTAGCCACAC	-	-	-	-	-	-	-	-	-	-	-	-
40	3	122984614	6438663	10560	AGCCTAAAATRTTTTATTATA	-	-	-	-	-	-	-	-	-	-	-	-
40	3	122998310	6438666	10561	GTGGCAGTATYTATAAACAGA	2.42	2.72	2.72	1.80	1.69	1.69	1.68	2.65	2.39	1.53	1.53	1.56
40	3	123011301	4676753	10562	TTTAGTGGAAYGTTGGATAAA	2.62	2.95	2.96	1.89	4.01	2.56	2.34	2.86	2.78	2.95	2.21	2.07
40	3	123024031	1881994	10563	CAAACTTCCAYTGAATTCTTG	-	-	-	-	-	-	-	-	-	-	-	-
40	3	123034260	12695416	10564	AACCCAAGAGRTAAAAAACAT	2.70	3.01	3.03	2.55	4.54	3.49	1.31	3.00	3.13	3.24	2.79	1.31
40	3	123045124	7627354	10565	TGTATATATAMCACAGGGAAC	-	-	-	-	-	-	-	-	-	-	-	-
40	3	123051204	16845505	10566	ATATGTATGARGGGTACTCCA	-	-	-	-	-	-	-	-	-	-	-	-
40	3	123056909		10567	ATAGTATAGAYAAAAATTGCT	-	-	-	-	-	-	-	-	-	-	-	-
40	3	123076459	1920299	10568	TATTGGTAAGRATCTTGGTAC	3.30	3.80	3.80	2.26	3.25	2.39	1.07	3.72	2.56	2.66	2.15	1.05
40	3	123089428	7650341	10569	ATGATCCTGAYGTGATTCTAA	0.73	1.14	0.91	2.66	2.08	1.09	1.35	0.80	3.35	1.90	1.07	1.33
40	3	123096865	1881998	10570	ACAGTGTGTCRGCTAAACTCC	0.64	0.75	0.75	0.59	1.67	1.11	0.66	0.69	0.63	1.58	1.12	0.65
40	3	123115197	866929	10571	GCAAGGAAACRTAATGAATGT	0.67	0.71	0.71	0.35	0.15	1.00	0.85	0.67	0.38	0.15	1.01	0.85
40	3	123118913	11914993	10572	ATGGGAATGCRTAGAAGCAAT	0.50	0.64	0.67	0.11	0.33	0.85	0.64	0.64	0.06	0.33	0.87	0.64
40	3	123140772	874741	10573	TTTCCTGAAARTGGCTGAAGA	0.54	0.67	0.67	0.81	0.38	0.57	0.56	0.62	0.86	0.38	0.54	0.58
40	3	123148640	7615571	10574	TCTAGTAACAMGTCTTGAAAC	1.71	2.22	2.22	1.09	0.41	0.47	1.04	2.14	1.21	0.39	0.49	1.04
40	3	123157884	1474327	10575	ATTTAGGGTTRTCTCTCACAT	1.20	1.40	1.37	1.09	0.77	0.99	0.43	1.30	1.22	0.74	0.97	0.47
40	3	123192776	11718322	10576	GGCTTAAAGGRCTTATCCAGT	0.54	0.67	0.67	1.25	0.72	0.75	0.46	0.62	1.34	0.69	0.76	0.47
40	3	123200267	9824120	10577	GTGACAGTGAYTTCTCCATGG	0.90	0.48	0.48	0.15	0.67	0.38	0.29	0.47	0.13	0.65	0.41	0.28
40	3	123212739	11929235	10578	TAGCAGTTTAWTCAACACTCT	-	-	-	-	-	-	-	-	-	-	-	-
40	3	123231202		10579	AAACACACTASACATGCAAAA	-	-	-	-	-	-	-	-	-	-	-	-
40	3	123233014	6797971	10580	GATTACATTTWTCAACTGCTA	-	-	-	-	-	-	-	-	-	-	-	-
41	3	126402467	4679370	10581	ATCAGTAAGCYCCTAAAGCCT	0.76	0.71	0.74	0.94	0.29	0.18	0.47	0.70	0.95	0.31	0.19	0.46
41	3	126408819	9833476	10582	CTACACTTCAWGTCTCTGTGG	-	-	-	-	-	-	-	-	-	-	-	-
41	3	126422361	4679371	10583	GTTTCTCCAAKTAACAACTGG	-	-	-	-	-	-	-	-	-	-	-	-
41	3	126428434	2292803	10584	AATTTCAATGKGATAAGTTTC	0.66	0.82	0.80	0.68	1.00	0.21	0.17	0.76	0.91	1.00	0.25	0.18
41	3	126438708	6807163	10585	TGAATACCGCYGAAATGGTGC	0.53	0.71	0.71	0.50	0.56	1.12	0.50	0.63	0.78	0.67	1.12	0.48
41	3	126445682	9870428	10586	CAAGGGCCCTMAAGTTTCTCT	0.53	0.71	0.71	0.23	1.05	0.50	0.66	0.60	0.08	1.09	0.50	0.68
41	3	126452143	9857356	10587	GTCATTAATTYATTTAGCAAG	0.53	0.71	0.71	0.83	0.77	0.79	0.33	0.67	0.94	0.81	0.78	0.35
41	3	126462475	17264366	10588	TCCTGATTTAYTGATAAGCAG	1.43	1.92	1.92	1.17	0.69	0.74	0.91	1.84	1.18	0.68	0.74	0.90
41	3	126476877	7615139	10589	CTTTTAGATGYTACTATACCT	0.48	0.67	0.71	1.09	1.12	0.93	0.72	0.67	1.11	1.07	0.90	0.76
41	3	126484865	1338543	10590	TTTTAAATGGYAAGCTTTTGA	0.56	0.73	0.75	0.69	2.26	1.02	0.58	0.70	0.77	1.99	1.02	0.60
41	3	126492754	987956	10591	AACCATACCAMCCTCACTGAC	0.73	0.88	0.85	0.66	0.60	1.07	0.49	0.83	0.77	0.59	1.05	0.52
41	3	126502481	2333196	10592	TGTAAAATGGRTAAGCCAAAT	0.59	0.76	0.76	0.58	0.29	0.28	0.51	0.74	0.57	0.32	0.27	0.50
41	3	126511339	4679382	10593	AATAAAAATGYCAGTCTATTG	0.61	0.77	0.75	0.53	0.23	0.10	0.15	0.71	0.52	0.23	0.10	0.14
42	3	146954460	6770324	10594	TGAGGAGTACRTATTTGTTTG	1.84	2.10	2.10	0.85	0.24	0.28	0.31	2.03	0.88	0.26	0.30	0.27
42	3	146962475	16857208	10595	CTCTGTGACCRCCCACCTGAT	0.65	0.46	0.46	1.22	0.19	0.18	0.32	0.40	1.21	0.24	0.17	0.34
42	3	146973070	1523085	10596	GTTGACTAGCRAGATCACTGT	0.98	0.71	0.71	0.34	0.38	0.58	1.02	0.67	0.31	0.39	0.61	1.03
42	3	146982137	9846710	10597	ATCTTTCTATKTCTCAGAACC	0.38	0.60	0.60	0.08	0.17	0.32	1.16	0.56	0.08	0.19	0.35	1.15
42	3	146988820	7636418	10598	TCTCAGACAARCAGTGCAATT	0.64	0.55	0.55	0.06	0.22	0.40	0.71	0.54	0.08	0.22	0.41	0.69
42	3	147009461	6440391	10599	ACTTTTTTATYCTTATAAATT	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147014280	6777069	10600	AACTAAAATAMGTATCAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147033724	1513399	10601	TTTTATTTCTSACTGTCAATT	0.57	0.32	0.34	0.13	0.69	0.58	0.06	0.29	0.13	0.68	0.57	0.06
42	3	147048605	9844982	10602	ATTCTTGGTCRTCTTTTCTTG	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147058658	1398778	10603	TTTGTGATTARATGAAGCAAT	0.34	0.02	0.02	0.33	0.19	0.18	0.10	0.00	0.35	0.20	0.20	0.10
42	3	147064968	16857450	10604	TAGTCACACCRGACCCCCAGT	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147081076	1513412	10605	CATTTTAATCRGTTTCTCAAT	0.08	0.23	0.23	0.33	0.04	0.05	0.12	0.20	0.31	0.04	0.04	0.12
42	3	147087675	1393695	10606	TATTCTTTTAYGACTTTGAAT	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147098550	1849514	10607	CATATAAAACRGGCCACTGAG	0.59	0.54	0.54	0.12	0.10	0.02	0.05	0.51	0.09	0.08	0.03	0.05
42	3	147106499	6440401	10608	TTTTAACAAGRCTTCACATGA	2.74	0.49	0.49	0.21	0.25	0.16	0.45	0.44	0.20	0.27	0.19	0.46
42	3	147113437	16857576	10609	ATTACGTCATRGCCAGCATGG	1.32	0.70	0.70	1.02	0.31	0.25	0.51	0.64	1.14	0.31	0.26	0.50
42	3	147115440	12629663	10610	ATGTACAAACRTTTGCAATTA	0.73	1.17	1.17	0.79	1.02	0.49	0.13	1.10	0.83	1.03	0.49	0.15
42	3	147127121	1553406	10611	CGTACACACASAGCTGAGCCA	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147138486	16857603	10612	TAACATACTTMATTCAAACAG	0.67	1.07	1.07	0.87	0.51	0.51	0.16	1.00	0.98	0.54	0.55	0.14
42	3	147147951	13092361	10613	TAGCCTACCCRAGCAAGTCAG	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147159328	12486130	10614	AATCCTTGCTYTGGAAAACCA	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147168342	12695803	10615	TCTGTGCAAAYAAATGACAAT	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147178052	1039472	10616	CCACTTTCTGKTTCCTGAGAT	0.87	1.37	1.37	0.44	0.24	0.21	0.09	1.32	0.42	0.22	0.24	0.07
42	3	147183771	5029229	10617	CATCCAAGAASAAGAGAGATA	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147192907	16857731	10618	TTTATTACCAYAAGAAAGGCA	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147204185	1449449	10619	TTCAAGCTTTSCATTAATGTA	0.40	0.69	0.69	0.28	0.03	0.01	0.07	0.66	0.24	0.04	0.01	0.05
42	3	147216294	895931	10620	TAGTAGGGAGSCTTATTCATA	0.62	0.93	0.93	0.12	0.01	0.03	0.02	0.89	0.10	0.01	0.02	0.02
42	3	147228259	11720981	10621	AATTTTCAGTKTAGATTTTAG	0.15	0.11	0.11	0.15	0.02	0.05	0.05	0.10	0.13	0.01	0.05	0.04
42	3	147239595	10804708	10622	GGGAGCTGAGRCACGAAAGTG	0.50	0.84	0.81	0.35	0.17	0.08	0.07	0.76	0.32	0.21	0.09	0.06
42	3	147250382	9867807	10623	TCCCAATTGGYAGAAAATGAC	0.06	0.19	0.17	0.54	0.11	0.14	0.18	0.14	0.54	0.11	0.15	0.17
42	3	147266138	3749282	10624	TTTGATAGCAYGATTTTATAA	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147281297	16857897	10625	TAGTCTTTTCWCCTCCACTGT	0.86	1.17	1.17	0.65	0.30	0.43	0.52	1.15	0.73	0.33	0.45	0.50
42	3	147292709	3792340	10626	TTTAAATGGGMTAGTGAGACT	0.79	1.24	1.28	0.75	0.42	0.19	0.61	1.25	0.97	0.44	0.21	0.59
42	3	147309762	7642940	10627	GAGATTTCAARCCAGGCAGTG	-	-	-	-	-	-	-	-	-	-	-	-
42	3	147321593	4681297	10628	GGTGTTTCTCYTACCATTCAG	0.68	1.09	1.04	0.75	0.50	0.31	0.22	0.98	0.84	0.56	0.34	0.23
43	3	155804001	11929204	10629	TTTTGGACTGSCCATCTCAGC	0.50	0.93	0.92	0.80	0.37	0.25	0.29	0.85	0.89	0.37	0.26	0.27
43	3	155829629	6440949	10630	GGAGGTTAAARTGAATCTGTA	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155847887	7634930	10631	ACTTTACACCYCATTTGTTTC	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155873693	7632408	10632	TATTATGTACRTGTCTACTTC	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155885864	7627856	10633	AAGAGAGAAGYACTGATGGCC	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155897007	6764624	10634	GTATCCCTACRTATTTCCTAT	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155913434	6440953	10635	CTGTAAACTGWTACCTGAAAA	0.76	1.01	1.01	0.42	0.29	0.43	0.55	0.93	0.42	0.31	0.44	0.58
43	3	155926000	6809450	10636	GTGTTCCTTGRCTTGTTGCAT	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155938447	7632135	10637	ACAGTAAAATRCTATTAAATG	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155979455	6795316	10638	AAAGCACGATYGCACAGTTCT	-	-	-	-	-	-	-	-	-	-	-	-
43	3	155991817	16824295	10639	AACATGGCTCYCATTCTCCAG	-	-	-	-	-	-	-	-	-	-	-	-
43	3	156003252	6805713	10640	ATTAAACATTYCACCCAGGAA	0.21	0.06	0.13	0.44	0.47	0.74	0.44	0.06	0.44	0.48	0.74	0.45
43	3	156030846	16824326	10641	TGGCTTAAACYCTGCTTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
43	3	156037686	16824336	10642	TATTTTTTCAKTTGAGTACTT	-	-	-	-	-	-	-	-	-	-	-	-

43	3	156043949	6773952	10643	CTGCACGTAGYTGCAAATATA	0.22	0.22	0.24	0.34	0.74	0.39	0.47	0.21	0.35	0.75	0.43	0.48
43	3	156047054	17439905	10644	TTTTCGATCTSTTTGTTTCTA	0.17	0.26	0.28	0.14	0.58	0.62	0.48	0.22	0.13	0.59	0.67	0.48
43	3	156062131	16824360	10645	TTCTTTTTCTKTGGCCTACTG	-	-	-	-	-	-	-	-	-	-	-	-
43	3	156070356	6440961	10646	ACATTCACATYATATACCTAG	-	-	-	-	-	-	-	-	-	-	-	-
43	3	156094601		10647	CTTTTCCGAGRGACATAATAG	-	-	-	-	-	-	-	-	-	-	-	-
43	3	156101221	12633569	10648	AGAACATTAAYTTCCAAAGCA	0.12	0.02	0.02	0.01	0.89	0.59	0.50	0.00	0.00	0.91	0.60	0.51
43	3	156127683	16824404	10649	TCAGTCTTTCRACCCTTAGGG	-	-	-	-	-	-	-	-	-	-	-	-
44	3	178142223	6443419	10650	TTTAAAAAACMTAAATCCTGC	0.15	0.10	0.10	0.57	1.36	0.65	0.26	0.07	0.60	1.28	0.68	0.27
44	3	178154807	936701	10651	AGGCCGTCTTYTTCCCTAAGT	1.33	1.98	1.98	1.01	0.63	0.76	0.55	1.90	1.00	0.63	0.75	0.56
44	3	178178813	13073493	10652	GTATACTGATKCCAGCCAAGT	0.31	0.49	0.49	1.05	1.04	1.10	0.85	0.48	1.15	1.04	1.11	0.82
44	3	178189020		10653	ACAGTATTTAMTGAACATCTA	1.26	1.14	1.11	0.62	0.90	1.24	1.06	1.02	0.64	0.88	1.21	1.09
44	3	178220762	7645116	10654	GTCTCTTTTTYAGCTTCTGTG	-	-	-	-	-	-	-	-	-	-	-	-
44	3	178228051	17560814	10655	AATCAGAAAASTGACCTCTGC	0.23	0.24	0.24	0.65	0.79	0.73	1.21	0.20	0.68	0.81	0.74	1.18
44	3	178235261	10084754	10656	GTAAAAAGTARCATAGGAAAT	0.51	0.59	0.59	0.32	0.46	1.06	0.96	0.57	0.28	0.47	1.07	0.95
44	3	178243367	16827744	10657	TGAACCTATGRGCGAAGAAGG	0.69	0.64	0.64	0.51	0.87	1.37	2.28	0.60	0.51	0.87	1.34	2.04
44	3	178253102	2862644	10658	GAAAAAATTTMGTTTTGCGTT	0.99	0.76	0.76	1.48	2.43	1.44	0.97	0.71	1.59	2.00	1.31	0.97
44	3	178264695	10936927	10659	CATGACATTTRAAATCACCAA	1.32	1.82	1.82	1.64	1.04	1.11	0.80	1.73	1.81	1.03	1.07	0.80
44	3	178274328	7648272	10660	GTGGGATTCASCACGTTTTTG	0.89	0.80	0.78	0.71	1.28	0.44	0.26	0.75	0.76	1.29	0.46	0.27
44	3	178275462	9827927	10661	TGATGTAAGASAACAGCCCCA	0.48	0.37	0.37	0.34	0.49	0.27	0.28	0.34	0.36	0.47	0.29	0.31
44	3	178299336	880210	10662	ATTGCATTACSGTCCAATTAG	1.05	1.37	1.37	0.75	0.36	0.20	0.20	1.30	0.74	0.37	0.21	0.18
44	3	178303912	9290611	10663	TTTCAGAGCAYTTTATCTAAA	-	-	-	-	-	-	-	-	-	-	-	-
44	3	178326057	2141600	10664	CTGACAAGTGYCTTTTTTATT	-	-	-	-	-	-	-	-	-	-	-	-
44	3	178352200	6443429	10665	ACTGTGAAATMTCAGACTAAT	0.65	1.09	1.09	0.84	0.47	0.23	0.13	1.06	0.88	0.48	0.20	0.13
45	3	195291780	7648783	10666	CCAGATGGCTKCAGGGCACAA	0.57	0.99	1.02	0.14	1.16	0.74	0.86	0.94	0.12	1.18	0.76	0.84
45	3	195303920	1986454	10667	ACAGGGTGGCSGAGAGGAAGA	-	-	-	-	-	-	-	-	-	-	-	-
45	3	195317642	6796696	10668	CTTCAAGCAAYAGGAAAAGTA	0.10	0.31	0.31	2.26	2.54	1.96	1.06	0.25	2.29	2.37	1.89	1.04
45	3	195330329	6444772	10669	TCCAGGATGCYCCGCCCCCAC	-	-	-	-	-	-	-	-	-	-	-	-
45	3	195337663	2368048	10670	GGCTCACTCTYGCGTTCCCAC	1.53	2.22	2.22	3.81	3.73	2.75	0.87	2.16	3.91	3.50	2.61	0.87
45	3	195353157	6796328	10671	CCTCCTCTCCSTGAATTTCCT	0.08	0.26	0.26	1.68	2.33	2.69	1.28	0.21	1.70	2.17	2.53	1.30
45	3	195368850	4627708	10672	TATTGAATATYAAACAAAATC	-	-	-	-	-	-	-	-	-	-	-	-
45	3	195382561	2001726	10673	CTCAAAATGCRCTGTAATATT	0.62	0.96	0.96	0.36	1.47	1.21	1.65	0.91	0.36	1.47	1.21	1.64
45	3	195395465	4627709	10674	CAGAGGTGGGRGGAAAGCGAG	-	-	-	-	-	-	-	-	-	-	-	-
45	3	195404262	4687530	10675	CTCCCGGGTAYCCGTCCCCCC	-	-	-	-	-	-	-	-	-	-	-	-
45	3	195420559	7644396	10676	GCCAGTCTGCYGGAGCAAAGC	-	-	-	-	-	-	-	-	-	-	-	-
45	3	195433210	7621717	10677	CCTTGGAGGCYGAGGTGGGAG	0.01	0.10	0.10	0.87	0.26	1.27	1.26	0.05	0.88	0.27	1.21	1.25
46	4	15729803	4698444	10678	CTAGAATCCARTACAAACATG	0.51	0.23	0.23	0.54	0.33	1.15	0.99	0.16	0.58	0.34	1.15	1.00
46	4	15739324	1554243	10679	GAATCTTCATRATTAAATAGA	-	-	-	-	-	-	-	-	-	-	-	-
46	4	15744914	11725717	10680	CAGAAGACTGYCCTATGAAAG	0.81	1.18	1.18	0.42	1.60	2.18	1.32	1.07	0.46	1.56	2.10	1.30
46	4	15748756	1040209	10681	AAGGGAACAGYAGCAAGGACA	0.69	0.65	0.62	1.28	1.31	0.96	2.67	0.58	1.36	1.22	0.92	2.51
46	4	15770263		10682	ATTCTGCAAGWGTAGAAGTTA	-	-	-	-	-	-	-	-	-	-	-	-
46	4	15785365	1443367	10683	ACTCATCATAYTCCATGTACT	1.87	2.42	2.42	1.39	0.96	1.35	1.35	2.33	1.41	0.99	1.31	1.36
46	4	15798374	7666255	10684	CTCCAAGGTTRGCAGCAGCCA	-	-	-	-	-	-	-	-	-	-	-	-
46	4	15808690	16868299	10685	CTGTGAAGTAKTGAGAGAACA	0.92	1.34	1.37	2.14	1.69	0.91	0.72	1.28	2.17	1.62	0.92	0.72
46	4	15819100	4159	10686	AACAGTGTGTRTCTTTGTCCA	1.05	1.13	1.13	2.68	1.85	0.76	0.56	1.10	2.74	1.74	0.76	0.60
46	4	15836861	317858	10687	AAAATAATTGYAGTTTCAAAA	-	-	-	-	-	-	-	-	-	-	-	-
46	4	15842912	16893138	10688	GCTGCTAGTTYTCCAGACGCT	2.09	2.76	2.76	1.83	1.69	1.35	0.79	2.70	1.98	1.56	1.27	0.80
46	4	15852904	317878	10689	ATTTGGGGAARAGTGACTATT	0.71	1.21	1.28	1.65	2.50	0.87	0.72	1.23	1.95	2.25	0.90	0.69
46	4	15861794	16893162	10690	GTCAGGTCCARCATGGCCTCA	0.84	0.95	0.95	0.74	1.78	1.27	0.51	0.83	0.79	1.64	1.23	0.53
46	4	15865548	17479949	10691	CACATGGAACYTAAGAGCAGG	0.04	0.12	0.12	1.44	0.58	0.92	1.14	0.09	1.45	0.58	0.89	1.09
46	4	15902068	961449	10692	CAAATGACTCYAGGTGCTGCC	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33517232		10693	ACCGTACATAYGATTATAGAT	0.84	0.94	0.94	0.32	0.09	0.43	0.26	0.84	0.31	0.10	0.48	0.29
47	4	33523687		10694	CAATACAATGRCAGCAAGGTT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33533150	10033461	10695	TCTAAAAAAAMCAGATTGATT	0.79	0.91	0.98	0.39	0.76	0.45	0.39	0.89	0.39	0.78	0.48	0.40
47	4	33541458	16989190	10696	AAGCTCCAGASAGTGATGGGA	1.29	1.07	1.07	1.17	1.12	0.69	0.71	0.98	1.32	1.10	0.74	0.69
47	4	33548775	9994499	10697	GGAGAAATGARAGACAACAGT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33568143	6858079	10698	CTGAATTTTGSAATATCTATA	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33579774	16989214	10699	AGAGAGACCTYTAAAATGGCT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33588730	1373493	10700	AATCGGTTCAYAAAATCTCTG	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33595184	10014729	10701	TTTTGCAGCAYATCTCCCTCA	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33604859	10024206	10702	AACACTCAGGWCTGATTAAAC	1.81	1.67	1.78	0.96	1.31	1.54	0.72	1.70	1.06	1.25	1.41	0.72
47	4	33608598	16989245	10703	ATTCTTGGCTRTCTTAATATT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33632997	13126161	10704	GGGGCTTGAGRGAGACCAATT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33635299		10705	TAGATGTTGARCTTTGCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33648065	13143780	10706	TGATTAATTTKTTTAAGTGAC	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33658185	16995875	10707	CTTTATTTTCYCTTGTTTACC	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33663401	16995877	10708	GAAGAGTCTCRGTAGAGGAAT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33708142		10709	ACAAAAACTAYTGAATACATC	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33720617	16989258	10710	TTCACATAAGRATTTCGCCTT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33726071	16989259	10711	TTGAATGTTTWATAAATGCTA	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33736984	10517298	10712	AGAATCTGTTKGGTCTATTTC	1.03	1.12	1.12	0.97	1.48	1.28	0.76	1.03	1.07	1.39	1.21	0.76
47	4	33749405		10713	TGAATCAATASTTGTTATGGA	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33755043	13152635	10714	TTCCAGATTCYTGATTTATGC	1.53	1.26	1.26	0.88	1.06	0.79	0.60	1.19	1.14	1.05	0.77	0.61
47	4	33764311	1446287	10715	CAAACAACCAYTAAACTTCAG	1.21	1.29	1.29	0.52	0.44	0.50	0.43	1.18	0.60	0.48	0.55	0.47
47	4	33767314	10009545	10716	TACTAACTCARGAATTAAGCC	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33776530	13142173	10717	TTTCATATGAYCATGTCTTCT	1.20	1.27	1.27	0.49	0.15	0.14	1.71	1.22	0.47	0.14	0.16	1.64
47	4	33788933	9306906	10718	TGTAAAAGCAYGTGTCATTAT	0.87	0.98	0.98	0.39	0.12	0.99	1.12	0.85	0.37	0.12	0.95	1.09
47	4	33797565	6814473	10719	GTCAGCTTTGYTCCTTTGATG	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33815542	16989287	10720	TGTAATAAAAKCATTTTGTTC	0.94	1.04	1.04	0.29	1.26	1.27	1.30	0.97	0.24	1.21	1.26	1.25
47	4	33827951	10517299	10721	TGTATTTGGAYTATTTCTCCC	1.29	1.36	1.26	1.04	2.26	1.97	1.17	1.19	1.30	1.90	1.71	1.15
47	4	33837633	12645236	10722	TCAAAAAGTGYCATAGTCATA	2.09	2.05	2.05	1.59	1.55	1.33	1.19	1.96	1.92	1.42	1.28	1.16
47	4	33851380	7676416	10723	TATTTTTGGCRTGATAAACTT	1.00	1.10	1.10	1.37	1.62	1.25	1.15	1.03	1.70	1.54	1.18	1.12
47	4	33858762	17433735	10724	CACATACGTTRGTTCTGTTTC	1.70	2.02	2.01	0.80	1.65	1.69	1.30	1.83	0.89	1.49	1.59	1.27
47	4	33880816	7435218	10725	TTTTTAAGCTRAGCAATAATC	0.82	0.93	0.93	0.89	0.40	1.66	1.53	0.84	0.93	0.40	1.56	1.47
47	4	33889778	6824096	10726	GCCTTTCTGAYGATTTATTGT	0.96	1.26	1.26	0.55	1.22	0.52	1.38	1.16	0.62	1.17	0.50	1.29
47	4	33905318	7655271	10727	TACTCATTTTWGCAATAACTA	1.10	1.52	1.52	0.67	0.72	1.09	0.57	1.39	0.85	0.77	1.08	0.58
47	4	33913142	6834739	10728	TTGTTTCAGCSTATAATTTGT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33928129	7435619	10729	CATATTGGTAYACTTCAAGTA	0.87	1.14	1.14	0.88	0.56	0.66	1.06	1.06	1.22	0.59	0.66	0.99
47	4	33953423	7687615	10730	AATAAAAGGARCATATCTCAA	-	-	-	-	-	-	-	-	-	-	-	-
47	4	33972065	7434297	10731	GGCTGCTCATWCATTATTCCT	1.06	1.33	1.33	0.70	0.99	0.57	0.37	1.21	0.77	0.97	0.64	0.41
47	4	33981502	6821190	10732	AATCTTTGCAYGTTCAATATC	1.25	1.52	1.61	0.89	0.74	0.54	0.32	1.51	1.06	0.75	0.54	0.31
47	4	33995523	7437087	10733	ACATTGTCACWCATACAAGGA	1.08	1.35	1.33	1.36	0.74	0.29	0.69	1.27	1.62	0.74	0.27	0.70
47	4	34021495	6834907	10734	TAAATGGAATKTATTTTAACT	-	-	-	-	-	-	-	-	-	-	-	-
47	4	34034483	6851568	10735	GCTAGGTTAAYTATTCAATTT	1.01	1.42	1.50	0.79	0.72	0.61	0.65	1.42	0.79	0.66	0.60	0.68
47	4	34037682	7683171	10736	GAACAATCCCRTTAAAAAGTA	1.26	1.79	1.79	0.54	0.62	1.23	1.02	1.72	0.55	0.65	1.19	0.99

47	4	34071851	4266314	10737	GAGTTTATCAYCTTCTAGGAC	-	-	-	-	-	-	-	-	-	-	-	-	-
47	4	34089188	4334773	10738	AGAATATAGCYAGACAATGCA	-	-	-	-	-	-	-	-	-	-	-	-	-
47	4	34094368	7660253	10739	GGAACATTTAKATTTCAGTTT	-	-	-	-	-	-	-	-	-	-	-	-	-
47	4	34126559	16989404	10740	ATGTCATATGYACACAGGAGA	1.33	1.57	1.57	1.17	1.07	1.08	1.45	1.47	1.57	1.06	1.04	1.40	
47	4	34128522	6812923	10741	CACCAAAATTRAATTATGCTA	1.21	1.47	1.57	1.67	2.29	1.29	0.68	1.45	2.17	1.93	1.28	0.70	
47	4	34145743	16989413	10742	CCACCAGTAAYACCGAAGAAT	2.32	2.20	2.20	1.49	2.94	1.20	0.78	2.07	1.80	2.38	1.14	0.77	
47	4	34157622	16989419	10743	ACCTGATAATWCATTTCAGTG	2.15	2.34	2.34	1.95	1.05	1.33	0.94	2.25	2.20	1.06	1.26	0.94	
47	4	34167260	7663859	10744	TAATTGTGGAYATGCAAAGAG	2.15	2.34	2.34	1.38	1.24	0.68	0.49	2.23	1.39	1.15	0.68	0.50	
47	4	34173222	6830027	10745	CAGGCAAAAGRAATTTTTTTA	-	-	-	-	-	-	-	-	-	-	-	-	
47	4	34179185	6849531	10746	GGTTTTTTGASACATATTTAA	-	-	-	-	-	-	-	-	-	-	-	-	
47	4	34180581	6835135	10747	ACATACTGAARTAGAAGTTAA	0.05	0.17	0.17	1.10	0.89	0.55	0.39	0.14	1.23	0.88	0.57	0.41	
48	4	37194643	12646914	10748	AGTAAAATTAYTTTCTTGCCC	0.01	0.06	0.06	0.02	0.35	0.58	0.70	0.03	0.03	0.34	0.57	0.73	
48	4	37202639	10856828	10749	ATTTTGGATGRTGGACCACAA	-	-	-	-	-	-	-	-	-	-	-	-	
48	4	37208360	1351304	10750	GGCTTTTAAASAGTTTATGTC	-	-	-	-	-	-	-	-	-	-	-	-	
48	4	37215170	10517411	10751	TAAGTGTTCAWTTAGAGTTCA	0.10	0.26	0.26	0.30	0.31	0.89	1.09	0.19	0.29	0.33	0.90	1.07	
48	4	37220826	10856830	10752	TCTTCAGCTCRACAGGTCTCA	0.49	0.80	0.80	0.68	0.85	0.47	1.47	0.71	0.66	0.88	0.46	1.39	
48	4	37229283	6531535	10753	ATGATGAATCRATGAACAAAT	1.45	0.57	0.57	1.25	1.00	0.72	0.41	0.51	1.34	0.98	0.72	0.43	
48	4	37239956	4586959	10754	CGAAAGTCCARTTAAGGATTA	0.70	0.56	0.56	1.11	0.50	1.00	1.39	0.53	1.19	0.53	0.98	1.37	
48	4	37246879	2928289	10755	CTCTCACCTGYTTGATTCTCA	0.05	0.13	0.11	0.85	0.83	1.73	2.45	0.07	0.95	0.83	1.68	2.29	
48	4	37254396		10756	GAGGCTTTACRTGTTTGACAT	0.86	1.09	1.07	0.34	1.71	1.54	0.71	1.02	0.31	1.63	1.48	0.72	
48	4	37260934	2973215	10757	TACACAGATGWCTAGAAAAGA	0.62	0.77	0.77	1.12	1.06	1.24	1.00	0.77	1.25	1.05	1.20	0.97	
48	4	37270865	17422084	10758	TGGTTCACGCYTCTGGGATCA	-	-	-	-	-	-	-	-	-	-	-	-	
48	4	37286913	2973231	10759	AATTCAATTTYTAAGCCTATT	-	-	-	-	-	-	-	-	-	-	-	-	
48	4	37293143	11096879	10760	AGGATTTTGAKATACAGTCAT	1.13	1.46	1.46	0.84	0.49	0.60	1.74	1.46	0.91	0.52	0.65	1.67	
49	4	42090601	10029897	10761	GGAAGCATTTSCTAGTGGTTT	0.03	0.11	0.11	0.14	0.22	0.41	0.71	0.07	0.11	0.23	0.41	0.73	
49	4	42096560	10004100	10762	TTCCAGGAGCRCAAAAAATCC	0.10	0.15	0.15	0.18	0.27	0.61	0.56	0.14	0.16	0.27	0.65	0.53	
49	4	42107357	17530914	10763	GCGATTAGAAYGTTAACTCCA	0.50	0.48	0.48	0.32	0.81	0.45	0.59	0.42	0.32	0.83	0.48	0.56	
49	4	42122160		10764	CTTGGGCTACRTCTTGACTTT	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42124804	1032222	10765	ACAGAACTGTSGGTTTGTGAG	0.02	0.04	0.04	0.48	0.42	0.69	0.44	0.02	0.47	0.44	0.69	0.48	
49	4	42148646	16854142	10766	GTGTTCAGAGYACAAGAGGGC	0.06	0.19	0.19	0.23	0.55	0.50	0.70	0.16	0.20	0.56	0.52	0.69	
49	4	42164670	1565114	10767	CAAAATAAAAWCTTCCATCTC	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42177240	1023993	10768	TGGTCTAGGAMTCTATCTACC	0.16	0.01	0.00	0.59	0.38	1.00	0.88	0.00	0.65	0.39	0.99	0.88	
49	4	42187360	1017935	10769	CGGGCAGCAAYGACTGGTTTG	0.30	0.58	0.58	0.65	0.94	0.92	0.87	0.54	0.63	0.92	0.93	0.85	
49	4	42198823	2632698	10770	TGTCTGTAGAWGGTTCACTCT	0.10	0.00	0.00	0.70	0.72	0.84	1.20	0.00	0.71	0.73	0.84	1.19	
49	4	42204324	6855448	10771	AGGCCAAGGTYGAAAGGCAGA	0.21	0.30	0.30	0.43	0.38	0.66	1.68	0.30	0.45	0.40	0.65	1.65	
49	4	42209774	2632702	10772	GCATGGGTGAYGGGTAATCAT	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42217284	923309	10773	CCCAGGGATTKGTCACCAGTC	0.15	0.34	0.31	0.63	0.91	0.65	1.47	0.25	0.63	0.94	0.64	1.40	
49	4	42226227	3103213	10774	AAAATTAGTTKTATCTAACCT	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42236912	3103218	10775	CTTTTGGTTTYCTCAAATCAT	0.05	0.12	0.12	1.18	1.62	1.32	1.00	0.10	1.23	1.54	1.30	1.00	
49	4	42253333		10776	TTGAAGAGTAYGTGCCCTTTA	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42259495	10517024	10777	TCAAGTTAACRTACAGCATTA	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42266042	17630357	10778	ATGATGGTTTWGGTTTACAAT	2.13	2.63	2.72	1.94	2.05	2.07	1.33	2.62	2.09	1.92	1.94	1.29	
49	4	42269138	9994372	10779	TGACCCACAAYGGCATGATCT	0.31	0.50	0.45	1.86	2.76	2.34	1.98	0.39	2.07	2.50	2.20	1.92	
49	4	42290802	7684005	10780	ACCTGAGGGGKTTTTGAAGTG	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42296765	13103298	10781	CAACCAGTAGRCCTGGAACTT	0.16	0.21	0.28	1.67	1.64	2.45	2.98	0.27	1.73	1.54	2.22	2.67	
49	4	42303814		10782	TGATCTGCAGMGCTCCAACAG	1.48	1.93	1.90	1.10	1.43	1.76	3.33	1.79	1.17	1.35	1.63	2.91	
49	4	42309376	17630562	10783	GTAGATACTCKGCACAAATAT	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42316367	11725164	10784	TAGGGAGCCTKGCCAATGGGA	0.04	0.15	0.12	0.65	1.11	1.32	2.33	0.10	0.79	1.08	1.27	2.14	
49	4	42323630	16854406	10785	AAATATTCAGYGTCCCTTTAG	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42331119	10517035	10786	ATACAAAATAYTTAGCACATA	1.43	1.89	1.89	0.70	0.72	1.77	2.64	1.84	0.80	0.76	1.69	2.44	
49	4	42333116	17592940	10787	ATTCTGCTCTSCTCTTCCCAT	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42345633	12510610	10788	TCTGCAGTCAWTTCTTCACCA	0.84	1.14	1.14	1.25	0.87	2.32	1.47	1.05	1.40	0.85	2.10	1.42	
49	4	42352170	10517038	10789	GACAAAAATAYCAACTGTATC	0.91	1.21	1.21	1.13	1.69	0.97	1.15	1.10	1.30	1.63	0.97	1.14	
49	4	42360443	13353762	10790	AGAGGTGTTAMTGTCCACAAT	1.05	1.52	1.52	1.09	0.65	1.00	0.78	1.49	1.17	0.63	0.97	0.79	
49	4	42368261	12649944	10791	TCTCGAAGGGSCTACATGCTA	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42388159	16854487	10792	TTATCCATAAYGCTCCTGGTA	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42396263	12642419	10793	TCTTACTGCAYTGGGGTTATA	0.53	0.79	0.79	1.16	0.63	0.32	0.71	0.76	1.21	0.63	0.36	0.70	
49	4	42404309	10938197	10794	CACTGAGGTGKACATGCCAAT	0.21	0.35	0.29	1.11	0.67	0.31	0.15	0.27	1.22	0.68	0.33	0.15	
49	4	42411539	2345654	10795	TAAAACGCTAWCTTTAATGAT	-	-	-	-	-	-	-	-	-	-	-	-	
49	4	42417400	13148015	10796	TGCTAAACTARAAACGCGAAA	0.71	1.04	1.04	0.41	0.70	0.36	0.15	0.97	0.38	0.70	0.35	0.14	
49	4	42426576	13124088	10797	GGTGTTCCAARGCTTCTGGCA	0.51	0.19	0.19	0.34	0.16	0.43	0.38	0.16	0.31	0.17	0.45	0.39	
49	4	42434168	3749530	10798	TTCTTTCTCAMATTTCTCAAC	0.16	0.39	0.39	0.19	0.14	0.29	0.48	0.34	0.17	0.15	0.30	0.47	
49	4	42440471	17593233	10799	AAACACTTGTSGAATGAATAG	0.24	0.55	0.59	0.27	0.04	0.60	0.58	0.56	0.24	0.03	0.63	0.56	
49	4	42448385	13152628	10800	ATGTAAAAAAYAGCCCTGATC	0.27	0.58	0.55	0.14	0.09	0.06	0.46	0.55	0.10	0.08	0.05	0.46	
49	4	42454478		10801	ACACCTGGGGYTTTAAAAAGC	0.07	0.02	0.02	0.45	0.07	0.30	0.03	0.00	0.47	0.06	0.29	0.03	
49	4	42460703	17532602	10802	AGGCGATCTTMAACATCACTT	0.10	0.09	0.09	0.24	0.18	0.10	0.09	0.07	0.18	0.19	0.11	0.10	
50	4	43033226	4270612	10803	CCATCACTGAMAGCTATAGAG	0.21	0.22	0.21	0.22	0.49	0.72	0.29	0.17	0.22	0.51	0.73	0.27	
50	4	43046027	4290920	10804	TTGCCCACTCYGCTCTTTCTC	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43057749	7666204	10805	GGGAAAAGGTYTGTTTCATTA	0.10	0.09	0.09	0.53	1.37	0.62	0.70	0.06	0.56	1.34	0.66	0.70	
50	4	43069316	4339251	10806	AAGAAAATATRCCATAGAATG	1.84	1.26	1.26	2.16	1.12	1.17	0.57	1.21	2.27	1.09	1.14	0.59	
50	4	43087170	1867168	10807	TGTGTTCTCTRTACTGGGAGG	0.44	0.61	0.60	1.12	2.33	1.19	0.90	0.57	1.23	2.09	1.17	0.89	
50	4	43096551		10808	TCTTTCTTGAKCTGCACAATC	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43109953	6447260	10809	TTTCAAAATCRACATCATGAT	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43117557	7660347	10810	GAAACCTTATWCACATTGGAG	0.19	0.45	0.49	0.53	1.08	1.71	1.05	0.47	0.56	1.04	1.59	1.08	
50	4	43124040	16855706	10811	GTAAGCATGTRAGTTGTGATC	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43134477	17535682	10812	GATCAACTCGYGTGGTGAGTT	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43142933	11735480	10813	AGGTTGATCTRTGAGAAACTT	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43150043	12498572	10814	TCTCTTGTAAWTTTATTCCAT	0.98	1.22	1.22	0.85	2.10	1.49	1.74	1.11	1.01	1.86	1.43	1.61	
50	4	43158245	1036861	10815	GAGGTGGTACYCAATTTTTGA	0.98	1.22	1.22	0.56	2.17	1.91	1.04	1.13	0.77	1.78	1.71	1.04	
50	4	43165491	12510088	10816	ATACTTGATGYCTTTCCATGA	0.49	0.81	0.82	0.75	1.06	1.39	1.06	0.76	0.82	1.00	1.33	1.08	
50	4	43170609	16855843	10817	AATTTTTTCTYGTTCAATACA	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43188399	6842011	10818	CATCACCCTTSTTATCCCATG	0.62	0.61	0.72	1.23	0.93	0.56	1.09	0.59	1.28	0.92	0.59	1.07	
50	4	43197548	932042	10819	CCTACACAAAKTTTTTATTTG	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43205890	974556	10820	GCATCAACTGYGTAAACTAAA	1.63	1.61	1.61	1.48	0.96	0.68	0.41	1.38	1.65	0.96	0.72	0.43	
50	4	43213858	10938272	10821	CAGGGGACAAYAAGAAGACTT	0.97	1.36	1.36	1.16	1.25	0.78	0.33	1.32	1.23	1.24	0.77	0.34	
50	4	43221061	6447264	10822	TTTTGTGAGGKTTAGGGAAGA	0.93	1.25	1.23	0.78	1.13	0.81	0.61	1.17	0.79	1.10	0.84	0.66	
50	4	43234135	1398202	10823	ATTAGAATGAYAGGTTCTGGA	0.84	1.17	1.17	0.45	0.40	0.38	0.58	1.11	0.51	0.42	0.44	0.60	
50	4	43240725		10824	CTCTCTTTCTRGTTAAGCCCT	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43248186	16855985	10825	CTTTCATTCAYTGTTTGCTGA	-	-	-	-	-	-	-	-	-	-	-	-	
50	4	43266538	11721334	10826	AGCAACTCTTKCTCTCAATAA	0.65	1.04	1.04	0.35	0.16	0.36	0.56	0.96	0.34	0.17	0.40	0.57	
50	4	43274803		10827	AATCTCCAAARTAAGTACAGT	0.43	0.42	0.42	0.30	0.27	0.48	1.44	0.39	0.28	0.28	0.50	1.36	
50	4	43298833	4241705	10828	CACAGTTGTCRTAATGCTAAG	0.19	0.41	0.41	0.32	0.54	1.56	2.08	0.34	0.34	0.55	1.46	1.93	
50	4	43304241	4861287	10829	GCATAGGAAASTACTCTGCCT	0.15	0.35	0.35	0.23	1.22	2.34	2.23	0.29	0.16	1.19	2.15	2.11	
50	4	43326593	6858709	10830	CAAGGCCATTRTAGTTAAATC	0.18	0.38	0.38	1.29	2.49	2.35	2.07	0.33	1.43	2.17	2.11	1.94	

50	4	43332753	10938283	10831	ACATTTTCCCRTGGTTTTACC	0.72	1.19	1.24	2.40	2.70	2.03	1.90	1.18	2.64	2.48	1.89	1.79
50	4	43345166	1701014	10832	AACACAGATGMAGTTTTACAG	-	-	-	-	-	-	-	-	-	-	-	-
50	4	43349524	2347049	10833	GACTTGTACTYCATCTCAAAT	0.37	0.68	0.68	0.86	2.55	2.21	1.40	0.63	0.96	2.25	2.02	1.39
50	4	43368927	16856133	10834	TTCAATTCTCMTTCTGAGCAA	-	-	-	-	-	-	-	-	-	-	-	-
50	4	43376384	13133395	10835	GGAGGAGAACRGAATATCAAA	-	-	-	-	-	-	-	-	-	-	-	-
50	4	43388707	4611962	10836	ATCATATAACYGAGATAAGTC	0.48	0.84	0.89	0.43	0.60	1.79	1.61	0.82	0.42	0.63	1.74	1.57
50	4	43399444	6841952	10837	GCAAAGTCTGMCACCAGGTGC	-	-	-	-	-	-	-	-	-	-	-	-
50	4	43422917	4394031	10838	ATTGTCCATCYAAATTGAAGC	0.17	0.41	0.47	0.68	0.87	0.74	1.38	0.39	0.67	0.91	0.76	1.35
50	4	43436374	6447283	10839	AAATATAAGAYGCAAATTGTA	0.41	0.75	0.75	0.90	1.17	0.59	0.38	0.69	0.96	1.13	0.58	0.37
50	4	43448092	11934338	10840	ACCACTGTAAWTCTTTTCTTA	-	-	-	-	-	-	-	-	-	-	-	-
50	4	43454475	10938293	10841	AGTATAATTGKTAAGTGAGGG	1.11	1.58	1.64	1.05	0.62	0.67	0.54	1.53	1.14	0.64	0.71	0.53
50	4	43465723	1434803	10842	CCTAAATGGGMGATATTCTAT	0.79	1.18	1.36	0.94	0.64	0.56	0.75	1.27	0.99	0.61	0.54	0.75
50	4	43475895	2013357	10843	CCTATTTCCCMACTCAGATCA	0.95	1.17	1.17	0.58	0.86	0.87	0.88	1.03	0.57	0.85	0.89	0.89
50	4	43485079	7657755	10844	AAAACCTTCARTAGATTAAAA	-	-	-	-	-	-	-	-	-	-	-	-
50	4	43496420	4450967	10845	CATTACCAAGRTCCACCAAAA	0.20	0.20	0.20	0.76	0.62	0.91	0.77	0.09	0.79	0.65	0.92	0.81
51	4	54279961	4864800	10846	ATTGCTTGGARGACAAAAGTT	0.26	0.29	0.31	0.48	0.06	0.05	0.02	0.27	0.50	0.05	0.04	0.01
51	4	54289761	10021838	10847	AGATTATTTCYGAGGTTACTT	0.10	0.14	0.14	0.03	0.04	0.01	0.01	0.10	0.04	0.03	0.01	0.01
51	4	54296979	9312642	10848	TGTTCCTTTARTACTCAGACA	0.20	0.18	0.17	0.02	0.00	0.02	0.07	0.13	0.01	0.00	0.01	0.07
51	4	54303834	12186283	10849	CATCCTGAAGRCTTCCACATT	0.12	0.15	0.14	0.18	0.02	0.10	0.16	0.09	0.16	0.02	0.10	0.17
51	4	54307398	17083188	10850	AGGACACATGSACACAAAAAA	0.15	0.38	0.36	0.16	0.34	0.11	0.19	0.36	0.15	0.34	0.13	0.19
51	4	54321637	2616416	10851	GCACCCACACYAGAAAAGCCA	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54330287	2572299	10852	AGAGCGTTTGMGTTGAGAGCA	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54343381	1991972	10853	ACTTCATTGTMTTGAAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54352775	17730883	10854	AGATCAGCAGSAACAAGGGGT	0.12	0.33	0.25	0.26	0.18	0.57	0.44	0.20	0.27	0.19	0.56	0.44
51	4	54359950		10855	ACCTTGCCAAMACTTTCAAAG	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54366435	1107027	10856	CAGGTTGGATKTTGTCTTTTT	0.28	0.55	0.55	0.21	0.60	0.64	0.42	0.51	0.22	0.60	0.60	0.39
51	4	54380168	17083261	10857	ACTCAGAAGGSATTTTGGTTC	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54387494	17083276	10858	GTTGAACCTAYGTAAGCAGCT	0.59	0.05	0.08	0.19	1.20	0.68	0.20	0.06	0.20	1.18	0.68	0.20
51	4	54394109	2668534	10859	AAACTCTTAARCCAAACTTGG	1.00	0.03	0.08	0.87	0.84	1.22	0.90	0.05	0.89	0.85	1.20	0.90
51	4	54405439	2668564	10860	CTGTTAAAAAYAAACTTACTT	0.80	0.41	0.41	0.53	1.06	1.16	1.15	0.37	0.50	1.04	1.16	1.11
51	4	54412508	2668538	10861	CCACAGAGACYTCCAGAAGAG	0.36	0.49	0.49	1.16	1.26	1.70	0.69	0.46	1.37	1.20	1.63	0.69
51	4	54419580	7699804	10862	GTGTGCTTTCRTCTGACTCCG	1.39	1.54	1.57	1.23	1.49	2.27	1.06	1.50	1.48	1.46	2.15	1.06
51	4	54431476	17083362	10863	AGGGGATCCCRGGAAGGGTGA	0.86	0.81	0.81	1.82	1.12	1.20	2.39	0.76	2.07	1.11	1.15	2.26
51	4	54441551	17083383	10864	AAAGCACAAARCAATTTCAGC	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54450998	6848989	10865	GTCTCTTCGGYCTTGGCCCTC	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54457577	2616434	10866	AAATCAGATCRTTTCATTTCA	0.23	0.17	0.19	2.07	1.72	2.28	2.38	0.17	2.12	1.63	2.15	2.25
51	4	54464352	2590813	10867	TTGGAGGAAAYCTGCCTGTAA	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54479627	2412493	10868	CCACACAGCCRTGATGCCTCA	0.16	0.09	0.10	0.18	1.99	1.48	2.95	0.07	0.20	1.94	1.46	2.79
51	4	54488689	1498830	10869	TCCATAATATRCTTTTAGAAA	0.08	0.24	0.24	1.00	0.67	1.44	1.21	0.22	1.02	0.69	1.39	1.20
51	4	54497876	17083481	10870	GGTGAGTCAGYGACTGTCTAA	1.05	1.53	1.57	1.18	0.61	0.37	1.25	1.52	1.15	0.62	0.38	1.26
51	4	54504159	7678117	10871	GAAGTAAGGARGCCAGTGATA	2.20	1.76	1.76	1.24	0.89	0.59	0.36	1.72	1.31	0.88	0.60	0.35
51	4	54510068	6554129	10872	GAAGGATCTTMATGAATGGTG	2.19	1.75	1.72	0.87	1.08	0.73	0.72	1.67	0.97	1.07	0.74	0.71
51	4	54521309	17083526	10873	TGCTAGAAACYGAGCCATTTT	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54526791	7662702	10874	TGGCAAGCACMCGGCCTTGTT	0.37	0.00	0.00	1.11	0.82	0.63	0.30	0.00	1.23	0.83	0.66	0.31
51	4	54547451	1498834	10875	CAGACCCAGCMCAGTAAAAAT	0.41	0.17	0.17	0.72	0.47	0.39	1.00	0.13	0.87	0.47	0.41	1.00
51	4	54555681	1014932	10876	TAGTGGATTTYCAAGTGATGG	1.99	1.62	1.62	0.60	0.46	0.45	0.62	1.56	0.63	0.47	0.46	0.64
51	4	54562446	6554137	10877	CCAAACCTCARATTCTCATTT	0.26	0.49	0.49	0.52	0.46	0.19	0.12	0.49	0.51	0.47	0.19	0.12
51	4	54576863	11733664	10878	CTATATTTTARTACAATCATC	2.33	1.76	1.49	0.25	0.24	0.12	0.03	1.41	0.24	0.26	0.10	0.03
51	4	54583483	13139909	10879	CTGCAATTATYTCACCTATCT	-	-	-	-	-	-	-	-	-	-	-	-
51	4	54591635	7658664	10880	CTGAAAGTCTKTGGATAATGG	0.01	0.02	0.02	0.34	0.13	0.04	0.03	0.00	0.36	0.12	0.04	0.04
51	4	54604464	13126724	10881	AAATTGCTGCSTAACATGCCG	1.27	1.57	1.49	0.68	0.05	0.02	0.04	1.41	0.67	0.04	0.02	0.04
51	4	54616153	10866415	10882	GTATGATCGGMTAAACCTCTC	0.20	0.39	0.38	0.43	0.14	0.03	0.30	0.36	0.42	0.14	0.03	0.30
51	4	54623925	7665164	10883	TGGTCAGTGAWCCCATTTCCT	0.11	0.31	0.31	0.06	0.16	0.59	0.57	0.29	0.03	0.15	0.61	0.58
52	4	56117823	17776975	10884	CTTAGCTTCCYGTCGTTCAAA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56126805		10885	TATCAGATTCKCTTTTTATAA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56136184		10886	TTAACTTAACYACTGGCATAA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56142986	3792603	10887	TTTATGTCCTRAAGACCCATA	1.06	1.39	1.35	0.49	0.24	0.31	0.17	1.25	0.48	0.27	0.33	0.19
52	4	56149970	11945370	10888	TGTAATAGAGRTGATATAAAA	0.05	0.17	0.17	0.45	0.58	0.29	0.32	0.16	0.43	0.60	0.28	0.34
52	4	56156106	6811520	10889	CTATGTCTTCYCATCTATATT	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56162745	1554483	10890	ATATAGAGCTSACGTGCTTCA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56169784	4340844	10891	ATACAGCCTAMATCTTTCTAA	0.04	0.17	0.20	0.01	0.93	0.61	0.29	0.18	0.03	0.92	0.65	0.31
52	4	56175895	1533803	10892	TCAGATAAAGYGGTAAGACCT	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56188409	17085816	10893	TTTCCGAGAAYAGAGTTCATA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56196526	2070062	10894	GGTTCAAGGTMCTCTTCTATA	0.06	0.11	0.11	0.06	0.02	0.93	0.36	0.08	0.02	0.02	0.94	0.33
52	4	56205031	3805157	10895	GCAAATGTATRTAGATTTCTG	0.21	0.06	0.06	0.16	0.09	0.08	0.43	0.04	0.06	0.06	0.09	0.46
52	4	56214086		10896	ACAAATAAATWTGGCCAATGA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56228148	6554283	10897	CTATGCTCACKGTTTTTTCAG	0.04	0.09	0.09	0.29	0.21	0.18	0.16	0.07	0.22	0.23	0.19	0.15
52	4	56235747	7673908	10898	AACTAAGCGARGCACAGCCCA	0.34	0.09	0.08	0.24	0.18	0.30	0.63	0.06	0.20	0.19	0.33	0.65
52	4	56241275	11133398	10899	TCAAGTGGAGYATCAGTGCAA	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56242825	17085885	10900	ATTCCAGTGAYGGGAGAATCT	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56262641	726967	10901	ATATTTTCTCWTGATGAATTC	0.40	0.01	0.04	0.28	0.37	0.63	1.40	0.02	0.25	0.40	0.65	1.35
52	4	56299031		10902	CTCCTAGAGGWTTTTTCTCAA	0.25	0.35	0.35	0.63	0.39	1.34	1.70	0.33	0.68	0.39	1.30	1.57
52	4	56307357	17085935	10903	TAAAATGTCAWGGAATTAAAG	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56316375	17725163	10904	AAATGCTAACYACCTGGAAAA	0.91	0.98	0.98	0.71	1.74	1.36	2.29	0.91	0.80	1.67	1.37	2.21
52	4	56324466	3811826	10905	CCTTTTTATCYTCACAGAACT	0.97	1.43	1.43	2.18	1.85	1.94	0.89	1.36	2.57	1.74	1.84	0.91
52	4	56334333	2412667	10906	TGTTCTTGTGMAATTACCATG	2.02	1.96	2.66	2.59	2.64	0.88	1.52	2.49	2.99	2.35	0.88	1.47
52	4	56354726	17085975	10907	AGATAACTTGRCACATAGTGG	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56360650	962354	10908	GTCTACAGAGWTACCATACAC	0.29	0.59	0.59	1.89	1.95	2.38	0.77	0.51	2.24	1.78	2.18	0.80
52	4	56369711		10909	CTCAGCTAAARATTTCTTCTA	0.19	0.47	0.47	0.26	1.91	1.54	0.76	0.42	0.23	1.72	1.53	0.79
52	4	56376466	6823788	10910	TATATCCAAAWGGTTAAATAT	0.16	0.28	0.28	0.05	0.03	0.49	1.49	0.25	0.03	0.04	0.49	1.46
52	4	56393882	12499711	10911	TGAGCTCCTAYGTGCTGAGCA	0.17	0.36	0.36	0.01	0.01	0.09	0.66	0.31	0.01	0.01	0.10	0.64
52	4	56398094	4340845	10912	ATCTCAACTARAAACTAAATG	-	-	-	-	-	-	-	-	-	-	-	-
52	4	56422606	7665149	10913	CCATCTGCTCRGTTATGAGTG	0.00	0.02	0.02	0.04	0.00	0.07	0.11	0.00	0.02	0.00	0.07	0.09
52	4	56425072	12646404	10914	CTAGTCTCTTYTATGCCCCCA	0.23	0.14	0.14	0.06	0.02	0.02	0.03	0.12	0.04	0.01	0.03	0.03
52	4	56438723	9995947	10915	ATTGCCAATGYAGAATCATTT	0.04	0.16	0.16	0.08	0.23	0.01	0.01	0.13	0.06	0.23	0.01	0.01
52	4	56447879	10019472	10916	GAAAAAAATTRATTTCCTTAC	0.17	0.00	0.00	0.51	0.08	0.06	0.03	0.00	0.54	0.08	0.06	0.01
52	4	56449665	9990863	10917	CATTAGCTCCKTGAAGCATTT	0.21	0.06	0.06	0.20	0.15	0.05	0.14	0.04	0.11	0.14	0.04	0.16
52	4	56473216	7691043	10918	ACAAGCTGCTKTCTTAGCCTA	0.66	0.25	0.25	0.08	0.05	0.60	0.18	0.23	0.06	0.04	0.63	0.15
52	4	56479466	4289500	10919	TTATGTTACASAGTTCAAAGA	0.06	0.22	0.22	0.20	0.40	0.25	0.42	0.17	0.17	0.42	0.26	0.40
53	4	68502349	4504308	10920	TCTTATTACARTTTTTATGTC	0.30	0.56	0.56	0.53	0.14	0.21	0.55	0.51	0.54	0.16	0.20	0.57
53	4	68515882	10780055	10921	CTTTCAATTCRTTACTTAGAT	-	-	-	-	-	-	-	-	-	-	-	-
53	4	68526992	6858754	10922	GTGTTGGCAAYAGTTTAGTCA	0.04	0.15	0.15	0.43	0.22	0.30	0.54	0.12	0.41	0.22	0.31	0.55
53	4	68533724	17576689	10923	CTTCAGAAATYAGCTGGGACT	0.70	0.68	0.68	0.13	0.13	0.08	0.59	0.61	0.14	0.13	0.08	0.64
53	4	68542677	6834437	10924	GACATTTGTTKCAATGTCACT	0.02	0.11	0.11	0.09	0.12	0.50	0.63	0.08	0.08	0.14	0.52	0.61

53	4	68556231	7689160	10925	CATGAGACATRTGACTCAACA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
53	4	68567577	6818162	10926	CTAGAGAAAASTTCATGTTTA	0.18	0.12	0.12	0.21	1.21	1.17	0.84	0.10	0.21	1.19	1.13	0.85	0.18	0.12
53	4	68580401	1440743	10927	ACAACAGAACKTGGGGATGAG	0.13	0.28	0.28	0.88	1.83	1.70	1.35	0.27	0.89	1.74	1.69	1.29	0.13	0.28
53	4	68589092	4860863	10928	GTCATAACATYTATACCTATC	0.68	1.01	1.10	1.99	2.01	1.97	1.37	1.07	2.07	1.87	1.89	1.38	0.68	1.01
53	4	68595145	13103008	10929	GCTTTTGATCKGGCTTCTCTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
53	4	68605505		10930	CCCTTGACAAYGACATTCTAA	0.19	0.41	0.41	2.33	1.65	1.86	2.43	0.39	2.55	1.58	1.79	2.28	0.19	0.41
53	4	68612021	353167	10931	TGGTGAGTAAYGAATGGCTGC	0.87	1.35	1.18	2.48	2.43	1.69	1.33	1.11	3.03	2.15	1.63	1.26	0.87	1.35
53	4	68617485	2119382	10932	CTTACTTGCCYGAAGACATTT	0.21	0.40	0.40	2.29	2.76	1.82	1.05	0.37	2.53	2.39	1.73	1.04	0.21	0.40
53	4	68624581	17578509	10933	ATTGTCCTTCRGTCTTACCTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
53	4	68630539	1124642	10934	GACTTGCCCARGTTGACACCA	0.24	0.52	0.52	0.98	2.39	1.78	0.91	0.49	1.06	2.19	1.71	0.90	0.24	0.52
53	4	68637313	10001742	10935	TACACACTATSAATTAGCAGC	0.17	0.25	0.22	0.73	0.84	1.41	1.15	0.20	0.74	0.86	1.36	1.14	0.17	0.25
53	4	68643957	7680472	10936	ACAGAAGCCAYAGGTTAAAGC	0.77	0.75	0.75	0.67	0.35	0.46	1.32	0.71	0.72	0.35	0.47	1.28	0.77	0.75
53	4	68650048	1561385	10937	AACTACTTCTRTGAATTTACC	0.60	0.98	0.98	0.24	0.06	0.10	0.45	0.92	0.23	0.07	0.10	0.46	0.60	0.98
53	4	68657973	6552134	10938	AGAAGTCTACRGCTCAAAGAA	0.37	0.44	0.44	0.25	0.09	0.27	0.36	0.41	0.25	0.10	0.25	0.38	0.37	0.44
53	4	68661201	17088861	10939	ATATAACTTCYCTGATGTGAT	0.47	0.53	0.53	0.26	0.17	0.33	0.31	0.46	0.24	0.15	0.33	0.27	0.47	0.53
53	4	68686090	4860875	10940	GATAATACACRTGGTGGCACA	0.47	0.58	0.60	0.35	0.24	0.35	0.53	0.57	0.31	0.23	0.32	0.54	0.47	0.58
54	4	87970574	17453839	10941	CAAAGATGTGRGATGTTAGTA	0.07	0.09	0.07	0.16	0.16	0.16	0.04	0.05	0.13	0.18	0.20	0.02	0.07	0.09
54	4	87983207	1212166	10942	CTCCATTATTRTATAGTAACT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	87989851	1420621	10943	TCTCCCATTCRCTCTTTTCTT	0.24	0.55	0.53	0.21	0.21	0.12	0.09	0.46	0.17	0.23	0.14	0.07	0.24	0.55
54	4	87998398	4693780	10944	AATTTGGAACYTATGAGTAGT	0.03	0.16	0.13	0.60	0.19	0.11	0.08	0.08	0.72	0.21	0.11	0.09	0.03	0.16
54	4	88001307		10945	TCTGTATCTTSTATCTTGTGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88012932	7698481	10946	CACAGTTTATYTAATCCTTAT	0.15	0.16	0.15	0.07	0.28	0.12	0.05	0.10	0.01	0.31	0.12	0.05	0.15	0.16
54	4	88024385	3775236	10947	GCAGATTTACYACCTATTAGT	0.10	0.01	0.02	0.28	0.02	0.11	0.21	0.00	0.19	0.00	0.11	0.22	0.10	0.01
54	4	88034436	1035191	10948	AACGGTGGGTKATTAAATCTG	0.09	0.05	0.04	0.40	0.02	0.09	0.25	0.01	0.35	0.01	0.10	0.27	0.09	0.05
54	4	88048177	10516782	10949	ATAATCTTATRCCGGAGCAAA	0.03	0.13	0.13	0.05	0.25	0.25	0.37	0.09	0.02	0.27	0.27	0.39	0.03	0.13
54	4	88063685	989902	10950	TGCAGCAGGAKACTCCTGTGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88076875	17012080	10951	GTTCTCCTACMTAGTTTCTCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88089662	2287147	10952	TTTAAAAATGYAATATCTGCA	0.04	0.08	0.08	0.03	0.21	0.58	1.19	0.06	0.02	0.21	0.57	1.17	0.04	0.08
54	4	88099867	4693152	10953	AAAAGATAAAMGAGTAGGTAA	0.06	0.16	0.16	0.19	0.31	0.88	2.27	0.12	0.18	0.34	0.91	2.12	0.06	0.16
54	4	88107040	7670277	10954	CTAATACTCAYGATCACATGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88127641	4693788	10955	TAATTATCACRGGCATGAAAC	0.40	0.69	0.69	0.18	1.07	1.84	2.23	0.64	0.15	1.06	1.80	2.15	0.40	0.69
54	4	88138467	17012132	10956	GCAAGGGCCTKACTTAGCACA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88166566	1550931	10957	TAGGTTTGTGKACCAGGTCTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88184724	2705622	10958	AGGCTCTGACYTCAAATATTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88191786	17751557	10959	TCCATGTTGCRAAAGCATTCA	0.34	0.03	0.00	1.60	1.38	1.83	2.15	0.00	1.90	1.32	1.76	2.00	0.34	0.03
54	4	88218023	17012170	10960	TACTCATACCRTTTCCTTCTT	0.34	0.53	0.53	1.18	2.94	1.64	1.64	0.48	1.38	2.76	1.50	1.54	0.34	0.53
54	4	88230343	1992876	10961	TACAAATGCTRTGTCTAAATT	0.17	0.41	0.47	1.77	2.64	2.62	1.07	0.46	1.92	2.30	2.30	1.04	0.17	0.41
54	4	88241016	4274814	10962	TGTATAATCAYGTGTTCCTGC	1.24	1.67	1.67	2.10	1.80	2.04	1.43	1.60	2.32	1.66	1.89	1.40	1.24	1.67
54	4	88246616	17012216	10963	AGCTGATTATKAGCTAGCAGA	0.27	0.51	0.51	1.21	1.73	0.77	1.38	0.48	1.20	1.64	0.76	1.31	0.27	0.51
54	4	88256464	17752307	10964	TAAAATGATGKCTCATTGATG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88268870	17012234	10965	TACCCCAAGTKTGGTTTCAGA	0.72	0.75	0.75	1.12	0.64	1.08	0.56	0.74	1.14	0.67	1.09	0.57	0.72	0.75
54	4	88277513	10516787	10966	ATTGCTGATCYTCACAGTTAA	0.69	1.09	1.09	0.93	0.57	0.70	1.45	1.02	0.97	0.54	0.68	1.40	0.69	1.09
54	4	88296509		10967	GTATTGAGTAYTTCATTGTTC	0.69	1.13	1.09	0.38	0.50	0.38	0.70	1.06	0.36	0.52	0.39	0.72	0.69	1.13
54	4	88302554		10968	ACATATATCCRTGTGGCCAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88312320	10032200	10969	CACATGCATTMTTCCTTGGGA	0.12	0.12	0.12	0.43	0.72	0.43	0.36	0.06	0.42	0.73	0.42	0.37	0.12	0.12
54	4	88318682	17702203	10970	GGCGGAGATGMTACTAAATTG	0.69	1.10	1.10	1.39	0.85	0.54	0.47	1.04	1.36	0.83	0.57	0.46	0.69	1.10
54	4	88325977	6854749	10971	CGGATTTGAGWTGAAAATGTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88333538	1471251	10972	TGGCAATCTTWTGAAGAAACA	1.72	2.39	2.39	1.60	0.84	0.65	0.75	2.31	1.64	0.87	0.65	0.75	1.72	2.39
54	4	88342294	17604937	10973	TGTGATGAAGKAATGAAACTC	1.67	2.01	2.00	1.29	1.24	1.06	1.59	1.95	1.41	1.21	1.09	1.53	1.67	2.01
54	4	88350096	6827213	10974	ACGGTTGCCTWTTTTCCATAT	0.05	0.02	0.02	1.08	1.49	1.27	1.43	0.00	1.20	1.42	1.24	1.33	0.05	0.02
54	4	88356662	17668731	10975	TAAAGCCATARGAGAAACTTA	1.19	1.71	1.77	1.19	2.52	1.06	0.77	1.68	1.20	2.18	1.03	0.76	1.19	1.71
54	4	88363546	151451	10976	TCCTCATGAAYTGGCATTCTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88372906	236686	10977	GTCACATGGGRCCCAGGGCGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88379398	342455	10978	AAAGTTTCCCRTGAACTTGAA	0.43	0.42	0.42	2.25	1.92	0.93	0.51	0.32	2.66	1.73	0.93	0.52	0.43	0.42
54	4	88386661	3733377	10979	CGTGTTCCCCSTCGAGATGGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88402280	6846074	10980	TTCGTTCTAARTGCACATGAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88409087	342468	10981	GTTTCTCAAGRAAGTTATAGA	3.02	3.09	3.03	1.56	1.17	0.88	1.21	2.97	2.05	1.12	0.90	1.17	3.02	3.09
54	4	88415519	3755979	10982	AATTTGCACASTTACTACAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88421610	10023050	10983	AGTATATTTTRCAGGCTCTTG	3.00	2.93	2.95	1.31	1.34	2.03	1.76	2.86	1.50	1.26	1.83	1.65	3.00	2.93
54	4	88427663	17012517	10984	ATGTGTCCCTRTTAGATAATT	0.40	0.48	0.48	1.49	2.35	1.73	0.88	0.45	1.74	2.13	1.56	0.89	0.40	0.48
54	4	88440286	3193672	10985	ATATACTCAAYAGGCACTGGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88451829	1552144	10986	AAACAAACATYGGTGTCCATT	0.48	0.54	0.56	2.76	1.67	0.63	0.97	0.52	3.46	1.56	0.63	0.94	0.48	0.54
54	4	88460096	17755195	10987	CTAAAACCTAMTACATAAAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88474451	6531956	10988	TGGCCATGAAYTAAAAATCTT	2.47	2.81	2.88	2.82	2.08	0.88	0.75	2.79	3.17	1.93	0.91	0.75	2.47	2.81
54	4	88481941	4693806	10989	GAACTTCAAGMCACTGCACCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88492168	6811473	10990	GTCAGCCATAYGCGACACAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88506074	6531964	10991	CCATTAAACCRTCATTTTAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88526341		10992	ACAACATGGGYGGGGACAAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88557986	4533725	10993	ATAAGATGGARAAGAAAAGGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88566194	6849526	10994	GCCTCATACARCCTGTGGAAC	0.10	0.10	0.10	1.55	2.35	1.54	1.29	0.09	1.59	2.11	1.52	1.27	0.10	0.10
54	4	88583751	6850509	10995	TTGCGTTTAAYTTTCCTCCGT	0.17	0.08	0.08	0.23	1.67	2.29	1.45	0.04	0.19	1.61	2.18	1.42	0.17	0.08
54	4	88595627	6531975	10996	ATATAATCCARAGATGAGAGT	0.27	0.45	0.42	0.76	1.14	1.74	1.35	0.36	0.81	1.12	1.70	1.28	0.27	0.45
54	4	88607382	6840298	10997	AAGAGCATCTRGAGAGAGTGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88616642	7665638	10998	TATTTAGGGASTTGTCACATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88635106	6531978	10999	AGTATGATCTRGTACTCCTTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88643588	7691791	11000	AAGCTCTAATYAATTGACTTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88661697	7682892	11001	GTCAACACTGRAGGAAGAAAA	0.28	0.11	0.11	0.57	0.50	0.28	0.85	0.07	0.58	0.54	0.26	0.85	0.28	0.11
54	4	88665165	6817242	11002	TGAGCATATAYTATATGCTCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88686663	7688038	11003	TGCTTTCACAYACTCTAGTGT	0.84	1.10	1.10	0.26	0.11	0.39	0.29	1.07	0.25	0.13	0.39	0.26	0.84	1.10
54	4	88698148	4314250	11004	TGAACAGAGCYGGTCTAATAC	1.11	0.37	0.40	0.36	0.09	0.23	0.24	0.40	0.40	0.09	0.26	0.26	1.11	0.37
54	4	88726009	4324526	11005	ACCCATAAGCRATTCAATTTA	1.06	0.17	0.17	0.21	0.33	0.19	0.19	0.14	0.17	0.32	0.19	0.19	1.06	0.17
54	4	88768321	6835925	11006	GTGGATAGCAKTATCATAGTG	0.40	0.10	0.10	0.91	0.57	0.58	0.44	0.06	0.90	0.58	0.60	0.45	0.40	0.10
54	4	88775839	6531999	11007	TGTTTTATCAYTATGGGCATA	1.16	1.61	1.65	0.76	0.63	1.10	1.26	1.58	0.75	0.59	1.14	1.28	1.16	1.61
54	4	88791852	10516792	11008	AGTTCCTTCCRATGTCAAAGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88805697	17012816	11009	GTGAGGACTAYGTGCACTTCA	0.96	1.42	1.42	1.18	2.05	1.55	0.48	1.37	1.27	1.95	1.54	0.50	0.96	1.42
54	4	88811363	17012853	11010	ACCATCATAAYTTGACACTGA	0.32	0.24	0.25	1.53	2.45	2.10	0.73	0.23	1.66	2.31	2.04	0.75	0.32	0.24
54	4	88819908	7681694	11011	ATCACTTCACRTCTGACTGTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88828754	16996086	11012	ACTCAAGTAGMTTTTTAGCAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88854025	11724253	11013	TGTTATAAAAYTCTGCTTTTT	0.74	0.04	0.14	1.57	0.80	1.44	1.29	0.10	1.60	0.85	1.43	1.29	0.74	0.04
54	4	88860575	6829013	11014	GTAAACCACTRGGACATTTGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88873296	13143702	11015	GATATTCCAAYACCAGCCATT	3.03	1.57	1.70	0.56	0.85	0.47	1.81	1.64	0.55	0.84	0.49	1.77	3.03	1.57
54	4	88880107	2615486	11016	ATTGGAAAAAMAACTGAATAC	0.30	0.22	0.23	0.54	0.11	0.58	0.28	0.21	0.52	0.11	0.64	0.30	0.30	0.22
54	4	88891244	3750025	11017	GGATAATTCCRATGGGAGTCC	0.06	0.06	0.06	0.06	0.06	0.00	0.49	0.00	0.05	0.04	0.00	0.49	0.06	0.06
54	4	88897127	10028688	11018	CTACACAAGAYACATAAATGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-

54	4	88903496	751810	11019	CGGATGTACAYACTATATACT	1.14	0.60	0.52	0.07	0.07	0.03	0.03	0.46	0.09	0.07	0.03	0.03
54	4	88909987	1381627	11020	GGTTTGCCACYGACAGATGAC	0.32	0.38	0.38	0.20	0.29	0.08	0.01	0.34	0.19	0.32	0.09	0.00
54	4	88947191	13103299	11021	AATAACAGACYAAGGAGAGTA	0.52	0.33	0.30	0.47	0.20	0.06	0.04	0.27	0.51	0.22	0.05	0.03
54	4	88961534	2869683	11022	TCCTCCCACCRAAGGCCACAG	-	-	-	-	-	-	-	-	-	-	-	-
54	4	88972951	17012948	11023	TAACAACAAAYGTCCAGCTAC	0.15	0.36	0.29	0.22	0.06	0.16	0.11	0.26	0.24	0.05	0.14	0.11
54	4	88986794	11933947	11024	GATGAGAAAAYGCAGGATTAG	0.73	0.15	0.19	0.04	0.30	0.35	0.21	0.18	0.03	0.33	0.37	0.21
55	4	96334060	2077385	11025	ACTGAAATTAYTTGGTTTCAC	0.61	0.97	0.97	0.36	0.17	0.07	0.42	0.92	0.33	0.18	0.07	0.47
55	4	96345445	17346363	11026	TGGAATTTTCWAACTGAAGTG	0.59	0.81	0.78	0.46	0.24	0.13	0.36	0.76	0.43	0.26	0.12	0.40
55	4	96358134	17022957	11027	CAACCCAAAAYAAAAGCTATC	-	-	-	-	-	-	-	-	-	-	-	-
55	4	96369089	6822629	11028	GAGGCTTTAASTTGACTCTAA	-	-	-	-	-	-	-	-	-	-	-	-
55	4	96382480	7665167	11029	CCTTGCACTGKATTAAATATA	-	-	-	-	-	-	-	-	-	-	-	-
55	4	96388755	3796434	11030	AATAAAAGGGRCATCTCTCAC	0.08	0.27	0.27	0.74	0.32	0.75	0.49	0.23	0.85	0.31	0.79	0.51
55	4	96397636	7682667	11031	GTTTGGATGCYTCTATCTGTA	0.80	0.79	0.79	0.29	1.97	0.69	0.45	0.67	0.26	1.85	0.70	0.47
55	4	96403665	7662630	11032	TGGTTACAATMCAGACCCTCA	0.92	0.90	0.90	1.13	1.20	1.02	0.52	0.78	1.43	1.18	1.03	0.55
55	4	96409364	17023083	11033	TAGCCTTACTYGTACAATTTT	2.22	2.37	2.37	1.54	1.14	0.66	1.34	2.24	1.95	1.15	0.66	1.27
55	4	96421549	1966548	11034	ACGCCAGGGGYGGTACACCAG	0.13	0.33	0.33	1.43	0.97	1.17	1.15	0.31	1.70	0.99	1.16	1.14
55	4	96427925	1369085	11035	TCTTCGAGTARATTCTGACAC	0.77	1.25	1.25	1.29	0.82	1.67	0.87	1.17	1.61	0.86	1.58	0.86
55	4	96434561	2289044	11036	CTTTATTCATRTACATTTCCT	0.13	0.30	0.30	1.60	1.34	0.75	0.98	0.29	2.02	1.28	0.74	0.98
55	4	96441637	3893828	11037	TACACCAGCTRTAGATTTCTT	-	-	-	-	-	-	-	-	-	-	-	-
55	4	96448702	2241743	11038	TTATTTCTGARGACAAAAGCA	0.25	0.56	0.56	1.91	1.48	0.94	0.59	0.53	2.40	1.38	0.95	0.61
55	4	96456545	11097458	11039	CACTAGTTCTYATGCCATTTC	0.84	1.36	1.36	1.72	1.89	0.91	0.88	1.26	1.89	1.78	0.90	0.89
55	4	96461977	10026552	11040	GCTTTAATTTYCTAAAAGTCT	0.80	0.70	0.74	1.67	1.70	1.36	1.26	0.72	1.73	1.65	1.34	1.20
55	4	96466214	767824	11041	TGGGACATAARCCCTGGGGAA	-	-	-	-	-	-	-	-	-	-	-	-
55	4	96479793	11737434	11042	TTCAATCATGYCTTTTTTCTG	0.46	0.24	0.19	1.07	1.43	2.07	1.32	0.18	1.04	1.41	1.96	1.25
56	4	114255783	17045209	11043	AGCAGGAATTMTTTGTTCCAC	0.55	0.22	0.22	1.99	1.73	1.70	2.19	0.15	2.23	1.63	1.61	2.06
56	4	114268572	2352223	11044	TCTAAACCAASAAATTACAGA	-	-	-	-	-	-	-	-	-	-	-	-
56	4	114279293	7656714	11045	CCAGTGTTTCYCCCATTTTAC	-	-	-	-	-	-	-	-	-	-	-	-
56	4	114286052	1532877	11046	GCTTTTCAGARTGGCGTTTTC	0.05	0.16	0.16	0.93	1.99	1.11	2.11	0.14	1.04	1.87	1.12	2.02
56	4	114292311	17045357	11047	ATAGTTAAAARTCTCCCAGAG	0.07	0.02	0.02	1.03	1.51	1.86	1.43	0.00	1.11	1.45	1.76	1.38
56	4	114303988	1395112	11048	ATGTTGCTGCYCTTTTGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
56	4	114311681	11728485	11049	TAGAGAAATCYGATTTTGGAG	1.58	2.04	2.04	1.35	0.80	2.26	1.66	1.98	1.32	0.79	2.11	1.59
56	4	114318565	10015472	11050	TCTAACATTGRGATTCTTTGT	1.08	0.23	0.23	1.29	1.61	0.82	1.20	0.21	1.28	1.53	0.81	1.17
56	4	114323984	313939	11051	CATATGAAAAYTAGAATAATC	0.27	0.15	0.13	0.73	0.71	0.41	0.47	0.09	0.72	0.70	0.41	0.49
57	4	129904606	1216436	11052	ACAGCAAGAGSGAAAATAATT	0.23	0.04	0.04	0.22	0.14	0.07	0.08	0.01	0.23	0.14	0.08	0.07
57	4	129910110	17013502	11053	TAATTTCCTGYTTTAACTGAG	0.56	0.95	0.95	0.87	0.18	0.07	1.83	0.89	0.87	0.20	0.09	1.77
57	4	129917117	17013510	11054	AAGACAGTACKCATAAGTGCC	-	-	-	-	-	-	-	-	-	-	-	-
57	4	129928052	1216363	11055	TTGTATACTCRCTGAGGTGAC	0.05	0.19	0.22	0.74	0.81	2.35	0.96	0.20	0.72	0.79	2.16	0.97
57	4	129937225	12500045	11056	GGATAGGCCAYTAAATTTCAG	-	-	-	-	-	-	-	-	-	-	-	-
57	4	129944358	17013550	11057	GTGAGAGTCCRGAGAATTTTG	-	-	-	-	-	-	-	-	-	-	-	-
57	4	129950277	17013591	11058	TAGTGACGGGYTAATTAACAT	0.54	0.71	0.71	0.68	2.62	1.25	1.11	0.66	0.73	2.35	1.22	1.13
57	4	129955683	7700079	11059	AATATATAGGRGCTCACATCA	0.54	0.71	0.71	1.05	1.61	1.11	0.48	0.62	1.03	1.54	1.12	0.52
57	4	129989693	17013614	11060	TTAAGTGAAARGGTGATACAC	-	-	-	-	-	-	-	-	-	-	-	-
57	4	129998199	6823074	11061	TTTTTCCCTCRTGGATGCCTT	-	-	-	-	-	-	-	-	-	-	-	-
57	4	130004166		11062	GAGCACCAGAYTCAGGGATAG	-	-	-	-	-	-	-	-	-	-	-	-
57	4	130022217	17013649	11063	AAGCTCTAGGRAAGAATCCTA	-	-	-	-	-	-	-	-	-	-	-	-
57	4	130033668	4975249	11064	CTACAGATTARACATGGCTTC	0.63	1.06	1.06	0.43	1.17	0.90	0.73	1.03	0.44	1.13	0.87	0.75
57	4	130042763	11723731	11065	CACCCACTTARTGTTCTGAAA	0.09	0.05	0.06	0.94	0.63	1.07	1.19	0.04	1.03	0.65	1.06	1.20
57	4	130050868	13123010	11066	ATATACCTCCYGATTCCTCAA	0.06	0.21	0.21	0.64	1.08	1.73	1.26	0.15	0.69	1.03	1.64	1.27
58	4	150113835	17584189	11067	TTGTCTTTCAYACCAAATGCA	0.23	0.50	0.54	0.54	2.67	0.47	0.30	0.53	0.52	2.42	0.45	0.30
58	4	150124097	7673507	11068	ATGCTCTGAAMCCTTTCAAGC	0.43	0.27	0.27	1.88	1.35	1.07	0.36	0.24	1.85	1.28	1.04	0.37
58	4	150130721	1523018	11069	ATAATGATTAYAGTTATGGCC	1.65	2.21	2.35	1.73	1.16	0.61	0.97	2.30	1.75	1.16	0.59	0.96
58	4	150137456	1719688	11070	GAACTGTGCTRTGTTAGGTGA	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150149573	1634083	11071	AAACATGTAASCAAGAAACAG	1.26	1.82	1.82	1.42	0.71	0.66	0.65	1.73	1.54	0.71	0.66	0.68
58	4	150162875	853713	11072	CCAGCTCTAGYTGATGTGAGT	0.37	0.50	0.50	1.18	0.92	0.94	0.71	0.43	1.37	0.91	0.92	0.74
58	4	150168709	853718	11073	GAAATATTGTRGGTGCAAAGG	1.61	2.24	2.24	1.17	0.67	0.48	1.81	2.16	1.28	0.70	0.45	1.71
58	4	150175170	17025399	11074	AGCATAACACRTCTAGTCCTT	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150182120	853697	11075	ATGTGGGAGAYCAGGGAATGC	1.06	0.45	0.49	1.17	0.91	0.40	1.64	0.42	1.20	0.90	0.42	1.58
58	4	150187592	853723	11076	GGAAAAAAAAYATGAGAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150195921	853731	11077	GGCATTTATCRGGTTGTCCTC	1.80	2.44	2.48	1.51	1.10	2.58	0.88	2.40	1.72	1.10	2.38	0.89
58	4	150202500	6535643	11078	TTTCCATAGCRTTAGTATATT	0.50	0.54	0.54	1.98	2.43	1.78	1.31	0.51	2.08	2.29	1.66	1.27
58	4	150213887	.	11079	TGTAGATGTTKAACTAGGGAA	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150221033		11080	CCCATAGTCAWGTCTCTCCCC	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150228550	6846370	11081	TATCTCCCACYTTGACGTCAT	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150237020	17025532	11082	AAGGTAATAAYACATTCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150252322	11939487	11083	GCACCCACTAWCTTTGCTAAG	0.25	0.41	0.41	0.75	1.32	1.17	1.51	0.36	0.80	1.24	1.20	1.42
58	4	150259798	2188536	11084	AGAATTTAGARTGGCCAGGAG	1.81	2.07	2.04	1.15	0.47	1.07	1.54	1.96	1.30	0.48	1.07	1.50
58	4	150267556	2520488	11085	GCACAATCAARACTTATAAAA	0.56	0.89	0.89	1.28	0.83	0.34	0.34	0.84	1.43	0.87	0.33	0.37
58	4	150276232	10489053	11086	CTCAACTCAAYGGCTTTCTTT	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150285573	17025601	11087	CACCAAGGAARTGAAAGATGA	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150293433	10032532	11088	AAAAGAAGAGYTTTACATGCC	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150299866	4072531	11089	CTTGGTTAGAWGAGTGAACTT	-	-	-	-	-	-	-	-	-	-	-	-
58	4	150306193	11724964	11090	CAGAATGCCASGCACATAATA	0.28	0.52	0.52	1.06	0.88	0.72	0.12	0.48	1.10	0.87	0.74	0.13
58	4	150331683	11940147	11091	AGCGGGGGCAKTGGGTTACAT	0.31	0.61	0.61	0.76	0.84	0.34	0.55	0.52	0.82	0.86	0.37	0.52
59	4	155677659	7693455	11092	ATTGGCAGAGRCTTTAAAAGG	0.85	0.43	0.43	0.30	0.53	0.91	1.32	0.41	0.25	0.49	0.89	1.32
59	4	155691319	6851087	11093	GAAATCTTATYCACACTTGAT	0.60	0.03	0.02	0.22	0.50	1.16	2.04	0.00	0.21	0.52	1.13	1.94
59	4	155697744		11094	AAAGAAAAAAYAAGCCTATAT	-	-	-	-	-	-	-	-	-	-	-	-
59	4	155704998	1466662	11095	ATTTTATCGCWTCTAAAAATA	0.16	0.40	0.38	0.66	0.97	1.62	1.90	0.33	0.70	0.94	1.59	1.85
59	4	155710653	17031636	11096	CATTTAAAAAMTTTCTGTCCT	1.10	1.06	1.06	1.59	2.17	1.88	2.11	0.96	1.66	2.08	1.80	2.02
59	4	155720481	1490683	11097	TACGTCACCAYTTATTAGGCT	-	-	-	-	-	-	-	-	-	-	-	-
59	4	155734344	17301637	11098	GGTGGAATTTYAGTGATTTAG	1.01	1.34	1.32	1.98	2.03	2.65	2.10	1.25	2.21	1.89	2.47	1.97
59	4	155742147	3958410	11099	AGCATTTTTCMGGGACATAAA	-	-	-	-	-	-	-	-	-	-	-	-
59	4	155749795	11935196	11100	AGCCCTTCACRGTGGATGAAG	-	-	-	-	-	-	-	-	-	-	-	-
59	4	155755526	6819298	11101	CAGAACATAAKACGCATTACG	2.44	2.97	2.99	1.67	2.04	2.37	2.90	2.92	1.85	1.96	2.24	2.70
59	4	155762305	11099957	11102	AAAACAGGCTKTCATTGTCTT	-	-	-	-	-	-	-	-	-	-	-	-
59	4	155772945	17031740	11103	GTTGGACAGAYGGTTGGTTGA	0.21	0.46	0.44	1.51	1.87	2.22	1.70	0.35	1.58	1.77	2.11	1.60
59	4	155803910	4482740	11104	TTGACAAAAGRGTTTTATTCT	0.31	0.27	0.25	0.44	2.18	1.06	0.86	0.21	0.46	2.03	1.05	0.85
59	4	155818718	7671792	11105	CTGTAATAATYTGTGGTTCTG	0.40	0.75	0.75	0.73	0.24	0.77	0.68	0.73	0.91	0.26	0.78	0.71
59	4	155819753	7700005	11106	AATTTTAGAAWCCTGATTATT	0.30	0.61	0.63	0.39	0.21	0.08	0.72	0.55	0.38	0.21	0.06	0.71
60	4	181808584	2546611	11107	TTCTCCTCTGYTTGCAGTTTT	0.54	0.85	0.90	0.45	0.13	0.37	1.63	0.85	0.47	0.13	0.39	1.57
60	4	181815023	2546597	11108	CAGCGCTAAAWATCTCATATG	0.75	0.45	0.56	0.36	0.31	0.32	1.01	0.52	0.35	0.33	0.32	1.02
60	4	181817053	2059116	11109	ATAGACAATGYGCTCTTAGAG	0.32	0.42	0.44	0.15	0.72	1.01	0.09	0.37	0.13	0.69	1.05	0.10
60	4	181827439	17069621	11110	CTCCAAATGTYTGCAGGATCA	0.03	0.03	0.00	0.97	0.58	0.17	0.50	0.00	1.06	0.60	0.17	0.50
60	4	181834902	17069625	11111	CTGAGCACCCRACCCCTTTCT	0.47	0.45	0.51	0.72	0.51	0.11	0.21	0.44	0.80	0.52	0.13	0.21
60	4	181840436	17069668	11112	TGCAGCTCCTRGGTTATGGTG	0.24	0.23	0.23	0.72	0.27	0.19	0.12	0.16	0.76	0.28	0.19	0.13

60	4	181848191	11732893	11113	CTAGTGTGGTRCTAATCCTAT	0.37	0.49	0.49	0.09	0.09	0.03	0.46	0.46	0.08	0.09	0.03	0.47
60	4	181854368	1030190	11114	CAGTGATCCCWTCAGAATGAT	0.22	0.47	0.47	0.06	0.02	0.31	0.45	0.44	0.05	0.02	0.32	0.44
60	4	181860565	17796970	11115	GGTCGATATARTGATTTCTGA	0.10	0.09	0.09	0.23	0.31	0.37	1.30	0.06	0.25	0.32	0.40	1.26
60	4	181866778	4309876	11116	TTCCTATATGWCCCTGCCAGG	-	-	-	-	-	-	-	-	-	-	-	-
60	4	181873337	7669125	11117	AATCTCATAAYTGTTCAACTG	0.46	0.86	0.86	1.11	0.69	1.08	0.93	0.77	1.18	0.70	1.05	0.96
60	4	181883831		11118	ATATTTTATTSGTAGCAAGGA	-	-	-	-	-	-	-	-	-	-	-	-
60	4	181898855	13109165	11119	TTGCTCTTAAMGAATCTGAAA	-	-	-	-	-	-	-	-	-	-	-	-
60	4	181904923	3113761	11120	GAACTGGCAGRTGATGATTTG	1.12	1.61	1.61	1.52	2.54	1.41	0.70	1.55	1.63	2.33	1.40	0.71
60	4	181912158	17069891	11121	TTGGCAGATGYCAACAATCCC	1.01	1.25	1.29	2.90	2.45	2.42	0.82	1.19	3.06	2.29	2.29	0.79
60	4	181925325	2613089	11122	CAATGGCTTTKAGTTCCAAGT	1.88	2.42	2.41	2.82	3.80	2.67	1.35	2.32	3.05	3.48	2.56	1.30
60	4	181938156	2546278	11123	AAAATTACGCRTAGAATTGTA	1.81	2.43	2.43	2.97	4.65	1.91	1.02	2.34	3.11	4.10	1.81	1.01
60	4	181944800	2613044	11124	AGGGGTAACTSTTCCTCCATT	-	-	-	-	-	-	-	-	-	-	-	-
60	4	181951824	10049675	11125	CTTGGAAATGKTCTGCAATCA	1.98	2.56	2.56	3.51	2.57	1.81	1.15	2.51	3.76	2.33	1.72	1.16
60	4	181963218	17805897	11126	TTGAACATAAKGCCCAAATCA	0.13	0.16	0.16	1.53	2.62	1.56	1.60	0.14	1.54	2.43	1.53	1.62
60	4	181970612	13114138	11127	GTAAAAGATCYTGTCCTCTGA	-	-	-	-	-	-	-	-	-	-	-	-
60	4	181977911	1007747	11128	ATTCATATATYTGAAAATTTT	0.04	0.11	0.12	0.14	1.09	1.51	1.06	0.09	0.11	1.10	1.50	1.06
60	4	181981766	1024986	11129	GCTCTTCTAGYAGCAGTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
60	4	181996764	6828389	11130	AAAACTCTGARTATAACAGGA	0.20	0.46	0.46	0.38	0.88	0.70	1.41	0.41	0.36	0.90	0.72	1.39
60	4	182002951	2251720	11131	CTTCAATGTTYATTTACTTAT	0.00	0.00	0.00	0.71	0.46	0.58	0.61	0.00	0.76	0.47	0.61	0.60
60	4	182016087	1421995	11132	GACTTGGCTGKCTGTCTGGCT	-	-	-	-	-	-	-	-	-	-	-	-
60	4	182022355	1421998	11133	ATTCCTACCARTCTTTACAGT	0.04	0.17	0.17	0.04	0.76	0.44	0.57	0.17	0.03	0.79	0.46	0.57
61	5	8445780	12153019	11134	ATTCCAACTGYTTAATGATTT	0.14	0.37	0.37	0.40	0.54	0.56	0.77	0.33	0.40	0.53	0.56	0.76
61	5	8453859	17278983	11135	CTTGAAAATGYTTCTGTCTGT	0.08	0.23	0.25	0.61	0.63	0.30	0.17	0.24	0.67	0.64	0.30	0.16
62	5	17247832	7729218	11136	GAAAACTTATRGAATTGAAGA	0.23	0.31	0.32	0.05	0.03	0.03	0.21	0.28	0.05	0.03	0.02	0.21
62	5	17255351	6864445	11137	ATGAAAAGCTYGTGGAGTTTG	0.08	0.08	0.08	0.17	0.05	0.20	0.06	0.00	0.17	0.04	0.21	0.07
62	5	17263388	12658039	11138	TTCCTGTAAGYGCTAGTCATT	0.14	0.33	0.33	0.20	0.22	0.14	0.10	0.30	0.18	0.23	0.14	0.10
62	5	17264649	2929726	11139	CAAGAGGGTTRTGGTATCTGT	0.06	0.02	0.02	0.64	0.58	0.13	0.13	0.00	0.65	0.60	0.13	0.13
62	5	17284485	298525	11140	AAGCTTCTATYCTCTCCTGGA	0.01	0.06	0.06	0.97	0.42	0.63	0.25	0.03	0.95	0.43	0.65	0.26
62	5	17292065	298542	11141	ACAGTTGGTTYAGTGCTTGCT	0.34	0.25	0.22	0.24	0.88	0.33	0.40	0.19	0.24	0.87	0.34	0.40
62	5	17310544	298586	11142	TTCAGAGTTAYTCTCTATTCT	0.11	0.06	0.06	1.60	0.56	0.35	0.05	0.03	1.66	0.58	0.37	0.05
62	5	17317914	298592	11143	AACTTTATTCYGCTGGTTCTA	1.33	1.76	1.76	1.56	1.15	0.21	0.05	1.69	1.59	1.14	0.22	0.06
62	5	17329986	298563	11144	TGTTTTACTTYTCTAGTCCCC	-	-	-	-	-	-	-	-	-	-	-	-
62	5	17337132	298580	11145	GTTGCTGTGARGATTTTCAAT	-	-	-	-	-	-	-	-	-	-	-	-
62	5	17346761	298568	11146	TAATTTCTTCMGGCCTGGTAA	0.37	0.71	0.77	1.20	1.09	0.46	0.09	0.77	1.22	1.07	0.48	0.07
62	5	17355143	17543793	11147	CTTTGAGTGGWCGTTGTGGCA	0.31	0.31	0.31	0.26	0.89	0.84	0.47	0.15	0.27	0.92	0.85	0.50
62	5	17359790	298512	11148	CCAGCCCAATYCTATGAGTGT	0.57	0.79	0.79	0.50	0.19	0.69	0.58	0.73	0.49	0.20	0.72	0.57
62	5	17371109	16869693	11149	TTGCCTGGGAMGAGAAGAAGA	0.17	0.00	0.00	0.32	0.33	0.16	0.33	0.00	0.35	0.38	0.16	0.36
62	5	17382406		11150	ACAACCATGAYGAGAACAAAG	0.06	0.05	0.05	0.34	0.47	0.51	0.13	0.00	0.32	0.51	0.55	0.14
63	5	24920585	9293157	11151	AAAGTAGTTTYTACCTCTTAG	0.52	0.20	0.21	0.19	0.44	0.10	0.03	0.17	0.18	0.44	0.09	0.03
63	5	24936517		11152	AAATGTAAAAYGTTGTTGGGG	0.37	0.44	0.44	0.36	0.04	0.08	0.04	0.41	0.34	0.05	0.09	0.05
63	5	24948924	9283778	11153	TATTCTAAAAKGATAATAGTT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	24957374	16894044	11154	ATTTTTAAATYCCTCTCCCGA	0.13	0.28	0.28	0.37	0.26	0.08	0.04	0.21	0.38	0.27	0.09	0.04
63	5	24965881	6452236	11155	TCCAGAAATTRGCAATGCAGT	0.02	0.12	0.12	0.64	0.63	0.12	0.01	0.11	0.62	0.62	0.11	0.00
63	5	24974856	401249	11156	GTCACTGTGCRGAGATTGAAG	0.88	1.35	1.35	1.16	0.58	0.18	0.06	1.29	1.22	0.55	0.21	0.05
63	5	24986761	2454872	11157	GCCATCCCAAYTGCTTGATGC	0.84	1.30	1.24	1.16	0.67	0.37	0.20	1.19	1.24	0.66	0.39	0.21
63	5	25009938	6895998	11158	TACTAGAATTSTTATTTTTGG	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25042107	1493478	11159	GTTTGTCATGRGTAGTTCAGT	0.51	0.58	0.58	0.46	0.62	0.42	0.37	0.54	0.44	0.59	0.44	0.34
63	5	25051322	6869061	11160	ATATACAAACRGTCGATGTCC	1.20	1.71	1.64	0.69	0.36	0.32	0.40	1.55	0.69	0.38	0.31	0.41
63	5	25057669	182842	11161	AAGGGAGATAWGTGTTGTGTC	1.58	2.15	2.15	0.87	0.56	0.42	0.44	2.11	1.02	0.56	0.43	0.49
63	5	25063375	17343615	11162	GATGGCTCCAYTACACATTGG	0.51	0.79	0.79	1.25	1.14	0.75	0.23	0.68	1.28	1.10	0.72	0.25
63	5	25076335		11163	TTTACAAAGCSCTAACACTAT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25089398	11742222	11164	AAACTTTTTCRCCGGCAACTC	1.83	1.07	1.07	0.87	1.51	0.82	0.94	0.96	0.88	1.46	0.81	0.93
63	5	25096228	13186809	11165	TGTATTTCTTMCAAGGCCTTC	0.91	1.03	1.03	1.69	1.20	1.70	0.80	0.98	1.69	1.18	1.62	0.80
63	5	25103129	10520899	11166	AATGTGGAGAYTAAAGCCATA	0.91	1.03	1.03	0.63	3.23	1.57	0.85	0.96	0.64	2.83	1.53	0.84
63	5	25113363	17344507	11167	AAAATTTCTAYAGGTATCTAA	0.25	0.22	0.22	1.38	2.93	2.23	1.38	0.17	1.58	2.65	2.03	1.35
63	5	25120966	1495872	11168	TGTAAACAAAYTGAGCTTATT	0.67	0.54	0.51	1.72	2.60	2.47	2.24	0.48	1.95	2.41	2.36	2.08
63	5	25128996	12657164	11169	CTGTTTTGGARTAAAAACTTC	1.58	1.51	1.51	1.58	1.81	2.46	1.92	1.41	1.69	1.74	2.29	1.88
63	5	25134561	10520898	11170	TAATAACTTARATGCTTATAT	0.94	0.36	0.33	1.99	1.66	1.27	1.07	0.27	2.28	1.63	1.26	1.10
63	5	25156291	13167221	11171	AATTGCTGCCSAAACCTGCTA	1.64	2.20	2.20	1.67	2.44	1.16	0.72	2.18	1.95	2.31	1.12	0.75
63	5	25162586	11959354	11172	ATGACACTCARCTTGTCATCT	1.40	1.94	1.94	1.70	1.96	1.52	1.54	1.91	2.14	1.87	1.47	1.48
63	5	25168511	1390417	11173	AAGGCCCTAAKCCAGAAATAA	0.21	0.48	0.48	1.01	1.66	2.64	1.83	0.43	1.22	1.59	2.44	1.73
63	5	25174754	2132382	11174	TAAAAAAGTTKCATCAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25196335	335591	11175	GTTTTACTACYATAGGTAGTT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25202429	408163	11176	GAACATAAGGYTTCCACTACC	0.72	1.15	1.15	1.50	0.63	1.26	2.37	1.10	1.62	0.65	1.23	2.19
63	5	25232280	6877333	11177	TCCATTTTGAYGAACAGTTGT	1.18	0.57	0.57	1.22	1.00	0.49	1.28	0.50	1.22	1.00	0.50	1.26
63	5	25245913	17412802	11178	TTTTGAAGAARTGCCTCTATT	0.87	1.29	1.29	1.25	0.76	0.88	0.32	1.20	1.26	0.79	0.85	0.32
63	5	25258786	16894257	11179	ATTCACCAATSACCTTTTTCA	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25273003	12653781	11180	CATTATTGAGRATATGTGACT	1.39	1.94	1.94	1.06	1.03	0.67	0.76	1.87	1.30	1.06	0.67	0.79
63	5	25282977	7716159	11181	AACACGTTAAMCGAAGTACTG	1.34	1.88	1.88	0.78	0.78	0.81	0.29	1.80	0.91	0.74	0.84	0.34
63	5	25291423	3846547	11182	TAACACCTTARTATTGACTTT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25298575	17413348	11183	AACTGAGAAARTGAAACTTTT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25312922	3913966	11184	TAAAAAGTACRTACCCTACCT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25318460	3846549	11185	AAACACACTTYTTGATTAATG	0.68	1.10	1.10	0.92	1.01	0.31	0.23	1.02	1.05	1.00	0.32	0.26
63	5	25323946	7737281	11186	CATTGGGTCCRTGAATGCTTG	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25330941	10942102	11187	TTGGCAGACCRTGCAAGCAGC	1.41	1.94	2.00	1.39	0.44	0.32	0.19	1.91	1.42	0.45	0.33	0.17
63	5	25337948	13160123	11188	TGGAAATTAGSCGTCCAAAAG	0.19	0.27	0.27	1.13	0.56	0.16	0.16	0.24	1.20	0.56	0.16	0.18
63	5	25352739	16894299	11189	AAGTACAGACRATTATAACCC	1.18	0.63	0.63	0.62	0.61	0.21	0.16	0.57	0.66	0.64	0.22	0.15
63	5	25354936	11952846	11190	GGCTCTGAGAYCAGGAATCTT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25362514	13157155	11191	AACACAAAGASTCCAGAGCCC	0.64	0.97	0.97	0.41	0.13	0.47	0.23	0.91	0.38	0.15	0.47	0.20
63	5	25368818	17463609	11192	TTGTATTATCRAGGGTTTTGG	0.35	0.56	0.56	0.12	0.58	0.33	0.37	0.46	0.11	0.58	0.30	0.43
63	5	25382764	4701478	11193	CCCATTTTTAYGTGAACACAT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25446205	4701483	11194	TTTGCATGGCRTACCTTTACA	0.02	0.09	0.06	0.61	0.31	0.22	0.86	0.05	0.62	0.32	0.22	0.82
63	5	25455846	1904173	11195	CTAACCCACARTAAGTAGGCA	0.24	0.47	0.47	0.33	0.32	0.92	0.86	0.43	0.36	0.36	0.90	0.86
63	5	25469241	11750642	11196	CTTTACAGTTKCTATGCTCAC	0.47	0.68	0.59	0.52	0.17	0.24	0.47	0.59	0.52	0.18	0.26	0.49
63	5	25477202	13161364	11197	TTAAGAATGARGTGGTGAGTT	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25483206	7713221	11198	ACATTATGAARAATATCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25488871	17525070	11199	ATTACTAAATYATTCTGATAG	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25499370	10520922	11200	CGATGAATTTKAGAATTACCA	0.13	0.32	0.35	0.67	0.37	0.04	0.07	0.29	0.73	0.39	0.04	0.06
63	5	25508139	7718419	11201	ATACAGCTGAWCATGTGTGGC	0.90	1.37	1.45	0.52	0.22	0.13	0.15	1.41	0.53	0.23	0.13	0.16
63	5	25516597	10051336	11202	TATTTTAGAARAGTATCAAAG	-	-	-	-	-	-	-	-	-	-	-	-
63	5	25545459	7715794	11203	TGTGAGGCATYATTACATGTG	1.08	0.83	0.83	0.91	0.18	0.33	0.17	0.73	0.98	0.21	0.35	0.17
64	5	33584771	1501724	11204	ATTGCGTTCAYTTTCCCTGCA	0.24	0.20	0.20	0.41	0.13	0.70	0.51	0.18	0.40	0.14	0.66	0.51
64	5	33592123	256639	11205	AGGTTATCATRCCAGATACAT	0.43	0.08	0.08	0.03	0.52	0.13	0.89	0.03	0.03	0.53	0.14	0.87
64	5	33599501	17567498	11206	CTATTTTACAYGACCACACAG	0.51	0.22	0.22	0.01	0.16	0.36	0.13	0.19	0.02	0.15	0.38	0.13

64	5	33615961	380548	11207	TTACCAATAAYAAGAACTAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
64	5	33623827	436415	11208	ATGAAACCAGRTTCCAAAGTG	0.02	0.02	0.02	0.06	0.04	0.13	0.15	0.00	0.05	0.03	0.14	0.16						
64	5	33631446	16891385	11209	ACCTTTTGTCYGAAGGCTGGT	-	-	-	-	-	-	-	-	-	-	-	-						
64	5	33636898	13156200	11210	TTCAGATCTAMCCTTCATAAT	0.16	0.10	0.10	0.20	0.02	0.01	0.15	0.09	0.16	0.02	0.00	0.15						
64	5	33642508	4560551	11211	CTGACTAGAAYCTGTGGAGAA	0.11	0.15	0.12	0.10	0.17	0.30	0.15	0.12	0.07	0.18	0.30	0.16						
64	5	33659517	7715934	11212	TGTCTGGAAAKTCATAAGGGA	0.08	0.20	0.19	0.04	0.05	0.15	0.17	0.13	0.03	0.04	0.16	0.18						
65	5	55976820	1479612	11213	GCCAATTGTARATATTTGTCA	0.02	0.08	0.08	0.28	1.12	0.73	0.32	0.05	0.26	1.10	0.76	0.34						
65	5	55984755	10072293	11214	GGCATTGGTAYGGCATCCCTC	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	55995250	13181802	11215	TCAGTATTCAMATGTAATTAT	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56001614	10063589	11216	TGCATGGTGCMGAAAAGCTTT	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56007626	1292145	11217	CATCAAATGCRCTGATTCCTT	0.02	0.01	0.02	0.48	0.65	0.55	0.75	0.00	0.48	0.66	0.57	0.76						
65	5	56014886	13362504	11218	TAGTTTAAAAMACAAGGCATC	1.53	1.43	1.43	0.50	0.59	0.20	0.45	1.34	0.48	0.64	0.22	0.48						
65	5	56023055	4700436	11219	TTAGAGTAACRTTTAAAAAGT	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56028475	4699983	11220	AGAGAAGTAGRCTCTTTCCTG	0.77	0.22	0.22	1.17	0.23	0.22	0.11	0.20	1.22	0.25	0.20	0.10						
65	5	56033999	6450398	11221	CAAGATTATCYTAACTCCAGT	0.27	0.52	0.52	0.55	0.30	0.28	0.25	0.48	0.57	0.34	0.31	0.26						
65	5	56048637	10940511	11222	CCTAGGACTTYAGACAACCAC	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56062257	1910020	11223	TATTGTGTCTYTAGATATAAA	0.51	0.51	0.49	0.72	0.35	0.75	0.26	0.46	0.75	0.37	0.76	0.27						
65	5	56067641	889312	11224	TGGAGAAAGGMATGTGCAAAT	0.57	0.57	0.57	0.24	1.31	0.63	0.49	0.54	0.23	1.27	0.64	0.50						
65	5	56073976	16886207	11225	ACTGGATGATRAAGGGCTGAA	0.39	0.38	0.38	0.28	2.23	0.67	0.44	0.28	0.27	2.03	0.68	0.43						
65	5	56080838	11949391	11226	AAGTACCCTTYGTTGCTAAGC	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56089822	10513090	11227	GAAGAAGCCAYGTTGAATGTC	0.04	0.14	0.14	1.90	1.07	0.85	0.41	0.09	2.18	1.03	0.83	0.43						
65	5	56101332	1423623	11228	CTTGAAATCCRCCACACAGCC	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56103191	16886272	11229	CAATACACTCRCCCCAGGCAG	2.57	3.25	3.25	1.96	1.37	0.65	0.77	3.12	2.12	1.34	0.67	0.78						
65	5	56132072	1862618	11230	GTATATCTCTSCATTTCACCA	0.39	0.60	0.60	1.89	1.69	1.27	0.43	0.54	2.24	1.60	1.23	0.46						
65	5	56138569	1559281	11231	GCTGTATTGAMGCAAGAACAC	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56143134	7733041	11232	TGGCTGTAAGKCTTTAGTCTT	0.71	1.01	1.01	0.89	2.00	1.18	0.93	0.92	1.13	1.86	1.15	0.95						
65	5	56157511	252915	11233	CCGTCATTTCRGCATCGTGCT	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56166681	16886389	11234	TGCTAAGGGTKGAGAAGTGAA	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56172927	3099459	11235	TACATAATACSTGCCTCTCTT	0.63	0.87	0.94	1.88	1.26	1.46	1.18	0.93	2.47	1.25	1.39	1.15						
65	5	56178756	16886420	11236	TAGCCCCTTTYGTTTGATGAT	2.18	2.83	2.83	1.58	2.09	1.21	1.17	2.69	1.96	1.81	1.21	1.14						
65	5	56189533	832568	11237	TTATGGGCCCRTGAGTCCTTG	0.80	1.14	1.07	2.35	1.97	1.19	0.72	1.02	2.43	1.80	1.16	0.72						
65	5	56197544	832575	11238	GTACTTCTACRTCTAGTTCAG	0.22	0.19	0.13	2.26	1.78	0.90	0.91	0.07	2.32	1.60	0.90	0.93						
65	5	56206570	16886448	11239	GCTCTGGGTCSATAAGCTTTT	1.95	2.58	2.70	1.33	1.29	1.17	0.84	2.58	1.51	1.24	1.11	0.85						
65	5	56216237	3736430	11240	GAACGTGTTTRTTTGAAACAG	0.08	0.09	0.03	1.31	1.14	1.17	0.78	0.00	1.45	1.14	1.13	0.76						
65	5	56224734	194058	11241	AAATAGCTCTRTATGCTGAAG	-	-	-	-	-	-	-	-	-	-	-	-						
65	5	56232033	12657353	11242	AGAATAAAAARGTAGTGCCTG	2.31	2.66	2.66	1.68	1.50	0.82	0.62	2.55	1.98	1.44	0.83	0.67						
65	5	56249396	1466007	11243	TTCCCGTTTTMTTAGCAATAG	2.11	2.10	2.55	1.94	1.55	0.95	0.44	2.43	2.28	1.46	0.94	0.42						
65	5	56261526	189695	11244	GAAACCAGTAYTTTGAGAGTT	0.47	0.21	0.23	1.63	1.59	0.91	0.65	0.23	1.89	1.57	0.93	0.65						
65	5	56269494	16886518	11245	ATCAGTGCAAMCATATACTAA	0.43	0.29	0.31	0.08	1.06	0.58	0.50	0.28	0.05	1.04	0.61	0.50						
65	5	56275126	2591958	11246	TGTTGAGGGASAAGATGACCA	0.49	0.17	0.17	0.13	0.02	0.26	0.43	0.14	0.08	0.02	0.26	0.46						
66	5	76622129	3797461	11247	GATGCCTTGTRGGAGAAGATC	0.13	0.21	0.26	0.24	0.39	0.26	0.05	0.25	0.20	0.39	0.27	0.05						
66	5	76629985	832787	11248	AGATGGGGAGRATATTGTTAC	1.30	0.12	0.15	0.60	0.43	0.36	0.34	0.11	0.54	0.44	0.40	0.35						
66	5	76650343	10474498	11249	TATGCAGACASAGCTTATGTG	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76659687	7717216	11250	CTTGGAGATCRTGGTTCCCTT	0.68	0.27	0.26	0.70	0.30	0.62	0.22	0.23	0.71	0.33	0.65	0.23						
66	5	76666994	17671296	11251	GCTTCCTCTCYTTCCTTAGCT	0.90	0.02	0.02	0.51	0.67	0.25	0.21	0.00	0.51	0.72	0.27	0.23						
66	5	76673617	4704410	11252	GAATGGCGTCYTGCAGTTGGC	0.85	0.20	0.23	0.59	0.45	0.17	0.07	0.23	0.62	0.46	0.18	0.07						
66	5	76689508	17683162	11253	TCTGCTGCCTRCAACCCTTGG	0.32	0.43	0.43	0.13	0.17	0.14	0.09	0.41	0.10	0.18	0.14	0.09						
66	5	76700977	10061629	11254	GAGCCCTGAGYGAAGGTTTCT	0.64	0.14	0.17	0.14	0.06	0.05	0.11	0.12	0.09	0.06	0.04	0.11						
66	5	76707804	11750661	11255	CAGGTTTCAARGAGCGAGTAG	0.12	0.19	0.17	0.05	0.07	0.16	0.06	0.16	0.01	0.09	0.18	0.05						
66	5	76713522	7713259	11256	CCCAGGCTCAYAGTAGGGTGT	0.05	0.05	0.05	0.05	0.06	0.03	0.49	0.00	0.03	0.04	0.02	0.52						
66	5	76723182	7733908	11257	AGTGGCTGGCRTACATTTCCA	0.68	0.35	0.35	0.31	0.05	0.84	0.69	0.34	0.30	0.04	0.77	0.68						
66	5	76732090	3733952	11258	TCATACTGAAYGCCCTCCCCA	0.79	0.21	0.19	0.30	1.46	1.28	1.64	0.17	0.27	1.37	1.22	1.58						
66	5	76741011	9293713	11259	ATGGACCTCARATTCCTCATG	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76747918	12521494	11260	CATACCACAGYGGCACTAGCT	0.25	0.56	0.63	2.13	1.98	2.62	3.15	0.59	2.15	1.88	2.41	2.91						
66	5	76754382	6860674	11261	TGTGGAGGCARGATAAATAAG	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76767251	335622	11262	CTGTTACCTCMACTGATCTTA	0.06	0.06	0.08	1.55	3.47	3.21	3.60	0.05	1.70	3.07	2.97	3.32						
66	5	76774003	388924	11263	ACAGTAAACCRTATTAATACA	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76780733	17751031	11264	GATCTTGCCAYCTGATGTCAG	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76786142	335604	11265	GAATAAATAAYGCCCAAGTCT	0.28	0.30	0.30	0.66	1.10	3.30	2.72	0.27	0.65	1.08	3.08	2.52						
66	5	76792067	17751165	11266	AGTAACCTGARCTCCTAAGGC	0.47	0.54	0.54	1.13	1.93	1.45	2.51	0.52	1.11	1.74	1.39	2.39						
66	5	76797159	335655	11267	TTATACTAACSCAACAAAGTA	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76819040	10076634	11268	GTTTAACATGSCATGATTTGG	0.34	0.63	0.63	0.78	2.06	1.11	1.07	0.59	0.81	1.89	1.09	1.04						
66	5	76843891	10514104	11269	AAAGCCATGGYCTGTAATTAC	0.93	1.22	1.22	0.74	1.27	0.85	0.75	1.12	0.74	1.26	0.86	0.76						
66	5	76852199	10474516	11270	TGCTTGACATYCTCCCTGCAA	0.18	0.32	0.32	1.04	1.35	0.88	0.80	0.27	1.11	1.29	0.84	0.79						
66	5	76861588	10805911	11271	AAAGGCTTCTMTCAAGATACA	1.23	1.34	1.34	1.45	1.48	1.33	0.97	1.28	1.71	1.42	1.34	0.97						
66	5	76871811	10070168	11272	TGCTTTGATARTTCTGCAAAC	0.32	0.48	0.48	1.63	1.77	1.59	1.55	0.49	1.73	1.67	1.49	1.52						
66	5	76885020	6453320	11273	ATCCCCCTGAYTTAATCACTT	1.22	1.71	1.60	2.57	1.99	2.52	1.97	1.50	2.63	1.84	2.26	1.88						
66	5	76898243	7708594	11274	GTGGTGGGGGRCAGAGGGATT	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	76906379	6453329	11275	CCCATACAACYCAACATTTCC	3.66	3.14	3.05	3.37	3.46	2.72	2.17	2.94	3.50	3.12	2.53	2.05						
66	5	76931821	4473754	11276	AATAATAGCCYTGGTACATTC	0.10	0.30	0.30	2.16	3.40	1.74	1.92	0.27	2.21	3.06	1.69	1.86						
66	5	76949428	4704436	11277	TGTAGGAATASTCTCATAAAA	1.22	1.74	1.74	0.70	1.45	2.11	1.84	1.63	0.76	1.39	2.01	1.78						
66	5	76953175	3901904	11278	CCAATGCTGASCATTCTAGTA	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77000726	4295371	11279	AAATGTTGCTRAGCATGGAGA	0.64	0.26	0.21	1.27	0.41	0.89	1.81	0.17	1.30	0.39	0.93	1.76						
66	5	77015150	13156814	11280	TTTAGTGAGGMGCTGGAGGAC	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77025835	455742	11281	ACTTATCCTCRTGCTTCATTT	0.82	1.32	1.38	1.29	0.52	0.33	0.93	1.32	1.32	0.53	0.34	0.92						
66	5	77037755	17789844	11282	ATTATGCCACRATTTACATGG	1.72	1.04	1.04	0.76	1.04	0.47	0.47	0.95	0.73	1.03	0.49	0.49						
66	5	77053379	2652212	11283	CCTGTAGTTTWAAAAAAGTCT	0.16	0.41	0.41	1.02	0.52	0.63	0.24	0.39	1.04	0.53	0.67	0.24						
66	5	77059328	7724594	11284	CTCAGCCCAAYAGGGAATACC	1.90	1.37	1.37	0.88	0.35	0.17	0.40	1.29	0.93	0.37	0.19	0.42						
66	5	77068624	17787671	11285	TAGGAGAATARCATCCCAAAA	1.74	1.25	1.18	0.59	0.25	0.20	0.64	1.09	0.57	0.25	0.22	0.65						
66	5	77078468	353904	11286	GTTTCTTCGARATAAAATTGT	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77105461	254420	11287	TCTCTTGTAAYACTTCATCAA	0.12	0.32	0.29	0.51	0.27	0.85	1.11	0.28	0.51	0.30	0.80	1.12						
66	5	77113078		11288	ATCTGGCAGARCAAGAGAAAA	1.65	1.25	1.25	0.83	1.22	1.35	1.17	1.19	0.96	1.20	1.27	1.17						
66	5	77119552	17183713	11289	TACAGGTCACRAAGTATGGAT	1.62	1.42	1.42	0.59	1.06	1.25	1.55	1.32	0.64	1.06	1.23	1.52						
66	5	77123252	13160215	11290	GGCACAAAGASAGGAAAGGGT	0.60	0.25	0.25	1.03	0.35	0.44	2.17	0.21	1.04	0.39	0.45	2.08						
66	5	77145469	353940	11291	TGCAACATTCRTTAAGTGAGT	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77156233	6414974	11292	ACGCCTCCCTRTACCTGAGGG	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77163538	4704446	11293	GTGCAAAAGGRTACACAGTAT	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77170345	354598	11294	AACTGTGGAARGGCATTTGGC	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77179822	6881736	11295	AGTGTGAGGCRGCTCCTATTG	0.79	1.10	1.10	0.46	0.19	0.79	0.86	1.06	0.46	0.19	0.79	0.88						
66	5	77191414	13171704	11296	AACTAAAAAAWTTGAAGAAAG	-	-	-	-	-	-	-	-	-	-	-	-						
66	5	77197245	12518218	11297	CTTGCAGTACKCCAGGGCCCG	0.38	0.50	0.50	0.39	0.56	0.76	0.67	0.47	0.40	0.55	0.81	0.66						
66	5	77208631	10042899	11298	AATCTCACAARAAGAGGCTGG	0.68	1.11	1.21	0.69	0.43	0.48	0.24	1.18	0.73	0.41	0.47	0.22						
66	5	77218411	10514128	11299	TCGTAAAAACYATTATCCAGC	0.63	0.59	0.52	0.43	0.22	0.20	0.19	0.47	0.40	0.24	0.22	0.19						
66	5	77224047	10447178	11300	TCTGTCAGCARGAACTTACTT	0.52	0.06	0.04	0.14	0.14	0.10	0.08	0.01	0.15	0.15	0.12	0.07						

66	5	77236317	7717685	11301	AACTGAGACASTCTGTAACAT	0.38	0.17	0.17	0.05	0.01	0.07	0.23	0.14	0.03	0.02	0.07	0.27
66	5	77247426	355425	11302	ACTGTCCTCCRGTCTCACCAG	-	-	-	-	-	-	-	-	-	-	-	-
66	5	77254244	6453360	11303	GTCAAGCTACMTGACTGAATC	0.38	0.12	0.12	0.08	0.05	0.14	0.14	0.10	0.07	0.05	0.15	0.13
66	5	77260963	10062212	11304	GCAGTTTGGGKAGAAGGAGAC	-	-	-	-	-	-	-	-	-	-	-	-
66	5	77269764	837030	11305	ACAGTGCTCCRGGCCACTAGA	-	-	-	-	-	-	-	-	-	-	-	-
66	5	77283634	10044946	11306	TCTCTAAATTKCCTCTTTGGT	0.07	0.21	0.21	0.08	0.32	0.19	0.61	0.17	0.08	0.30	0.18	0.62
67	5	80994757	10942278	11307	ACAGTATTGTKGATTCACAAA	0.08	0.22	0.41	0.43	1.05	1.13	0.26	0.29	0.46	1.06	1.09	0.26
67	5	81004753	10074416	11308	CTAAGAAGCAYTTAGCACCCA	-	-	-	-	-	-	-	-	-	-	-	-
67	5	81008011	13360536	11309	ATGCAAGCACRGTCTTCCTAG	0.15	0.32	0.32	1.62	1.73	0.67	0.52	0.21	2.11	1.58	0.68	0.49
67	5	81044731	406720	11310	GACAAAAGAGMAAATAGGGTT	1.73	2.34	2.34	1.41	1.60	0.49	1.19	2.25	1.80	1.43	0.52	1.17
67	5	81050947	398666	11311	ACTTCATCCARCCAAACCTGT	-	-	-	-	-	-	-	-	-	-	-	-
67	5	81058250	10035917	11312	ACAAATATCCYACTTTTCTCC	0.25	0.51	0.58	1.40	1.26	0.83	2.30	0.54	1.52	1.23	0.86	2.16
67	5	81067342	13178641	11313	TTATAAACTTYCCTATTGACA	-	-	-	-	-	-	-	-	-	-	-	-
67	5	81073847		11314	CATCATAATAYAATCTTCCAT	-	-	-	-	-	-	-	-	-	-	-	-
67	5	81089201	1550802	11315	GAGCTTACCAMAGGGTAATGA	0.68	0.95	0.95	1.46	0.79	1.66	1.75	0.91	1.68	0.79	1.63	1.71
67	5	81093200	10514225	11316	GATTAAGTAAYTTAGGCATGT	1.16	1.65	1.65	1.60	2.53	1.41	1.73	1.57	1.80	2.32	1.38	1.65
67	5	81103321	396900	11317	AATGACTTCCRCTTGAAATAA	-	-	-	-	-	-	-	-	-	-	-	-
67	5	81110411	457008	11318	TGGCCCCTTAYGTGATTCATG	0.30	0.27	0.27	1.87	2.65	2.04	2.16	0.23	1.92	2.41	1.97	2.09
67	5	81116990	457049	11319	GTTCTAGGTCMGGTCCTTAAT	0.07	0.22	0.22	0.62	1.74	1.74	2.27	0.20	0.66	1.69	1.68	2.15
67	5	81123290	410644	11320	AAATTCTTCAKTCCTAGTGGA	0.28	0.27	0.27	0.01	0.40	1.84	1.91	0.26	0.01	0.42	1.73	1.84
67	5	81132011	6895201	11321	GGGTACCTCTKACCGCTGGGT	0.29	0.49	0.56	0.48	0.40	0.71	1.54	0.54	0.48	0.42	0.69	1.51
68	5	102159866	174015	11322	AAAGGTCACCYGCAATCCATG	0.36	0.67	0.67	0.59	0.21	1.20	1.09	0.63	0.64	0.25	1.17	1.08
68	5	102168338	468891	11323	ATCAGGATTARGGGTGTTTTG	0.78	1.21	1.21	0.71	1.33	0.76	1.63	1.14	0.84	1.33	0.71	1.57
68	5	102173779	469192	11324	TCAATAACTARCTCTTTGTAG	0.68	1.00	1.00	1.14	1.37	2.04	1.45	0.94	1.31	1.36	1.94	1.42
68	5	102179573	466199	11325	TCAGTATTTGRGATTTTTTCA	0.78	0.90	0.86	0.44	1.65	1.74	1.77	0.83	0.39	1.64	1.71	1.74
68	5	102187686	32684	11326	CAAAACTAGCRGATGGTTTAG	0.58	0.91	0.91	1.31	0.58	1.16	1.19	0.86	1.44	0.62	1.14	1.16
68	5	102195607	258242	11327	CAAAGTTTTAYCTTCCATTGA	0.99	1.12	1.12	0.87	0.66	0.31	1.07	1.04	0.91	0.65	0.33	1.04
68	5	102200395	6886411	11328	CTATCTTGTARTGAATGTGGA	0.01	0.09	0.09	0.23	0.34	0.85	0.42	0.04	0.19	0.37	0.82	0.44
69	5	103211806	17155913	11329	GGGTGCAATAYGTAGTATGAT	0.23	0.53	0.53	0.08	1.27	1.06	0.36	0.51	0.08	1.23	1.06	0.39
69	5	103227725	1363261	11330	AGAAAACCTTYTGTTTTAAGT	0.15	0.14	0.12	1.87	0.93	0.18	0.71	0.11	1.95	0.94	0.18	0.71
69	5	103234960	17507406	11331	ATATGCATGCRGTTAGAACAT	3.39	3.82	3.94	2.15	0.48	0.34	0.60	3.80	2.22	0.48	0.34	0.60
69	5	103248345	41126	11332	CTAACGATCCYGGCAAAGTAC	-	-	-	-	-	-	-	-	-	-	-	-
69	5	103258543	34245	11333	TATGAGAAAASCCTGGGACTA	0.98	1.11	1.11	2.15	0.93	0.44	0.53	1.05	2.21	0.90	0.48	0.49
69	5	103271534	13186474	11334	GAGGTGTGTGYACCATGACTT	0.20	0.20	0.20	0.29	1.42	0.53	0.56	0.19	0.29	1.33	0.56	0.60
69	5	103280273	808042	11335	GAGTGCCTCAYTCATGGGACA	0.35	0.70	0.70	0.42	0.41	1.00	0.22	0.67	0.45	0.40	0.99	0.23
70	5	112035079	10428561	11336	CATATTCCACYGTATTGCCCA	1.08	1.35	1.37	1.23	0.56	0.70	1.12	1.31	1.49	0.58	0.73	1.12
70	5	112044199	17134858	11337	CAGTGGATGAYGGATATATTT	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112050154	971517	11338	ATCTGCTCTTSAGAAATACTA	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112060943	10051624	11339	AAACAGCTAASATTTTGGTAG	1.37	1.52	1.58	0.64	0.97	0.44	0.78	1.53	0.63	0.97	0.43	0.79
70	5	112069740	6862050	11340	TCATTGGTAARCAAAACGTAT	1.72	2.00	2.00	0.52	0.65	0.31	0.22	1.94	0.49	0.65	0.31	0.20
70	5	112081985	6864688	11341	CTGGGCCACCYAGATGAGTTG	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112088523	4705573	11342	CTTTGAAAGGYAGAAAATACT	1.44	1.69	1.76	0.43	0.36	0.25	0.26	1.69	0.40	0.35	0.26	0.27
70	5	112102255	2020383	11343	TCTGTTAGGCYGAAAAGACAA	1.44	1.95	1.95	0.65	0.14	0.20	0.23	1.86	0.65	0.14	0.21	0.23
70	5	112107781	10071425	11344	CCCATAACACKCCCTTAATAC	1.41	1.81	1.81	0.70	0.27	0.14	0.32	1.75	0.72	0.27	0.14	0.29
70	5	112115226	11954856	11345	CCCCTATAAAKGAATGATTTC	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112127926	6867243	11346	TGAGCCACTTRGGAAATTATT	1.21	1.70	1.70	0.65	0.42	0.39	0.32	1.63	0.71	0.42	0.41	0.30
70	5	112141671	414098	11347	TTCACTACACRTCAGTCTAGT	0.90	1.31	1.46	0.55	0.63	0.68	0.32	1.46	0.59	0.65	0.67	0.34
70	5	112153318	1734242	11348	AAAGCTAGGARGTACTTGCCA	0.26	0.54	0.54	1.10	0.87	0.48	0.79	0.49	1.26	0.88	0.51	0.81
70	5	112167644	2545158	11349	TTCCTTGAGTRTGTCCAGGCC	1.55	1.94	1.94	0.63	0.74	1.36	1.08	1.85	0.65	0.76	1.32	1.06
70	5	112177826	2707761	11350	TAATGAATGGRTTTAGCTGTG	0.39	0.61	0.52	0.95	2.18	1.71	2.25	0.51	0.99	2.01	1.63	2.07
70	5	112186330	2545162	11351	AGAACCATACRCTTAATTCCC	0.55	0.98	0.92	1.89	1.54	3.18	2.94	0.88	2.04	1.52	2.90	2.69
70	5	112192460	351771	11352	AGGTTATTGCRAGTGTTTTGA	1.11	1.65	1.69	1.59	3.22	3.01	2.99	1.64	1.74	3.00	2.83	2.82
70	5	112205070	465899	11353	AAAATACTCCRGTTTGCTTTT	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112213963	481789	11354	GTTTAGTGGTMATGTCAATGT	1.13	1.55	1.55	2.07	2.69	3.00	4.17	1.48	2.19	2.52	2.75	3.79
70	5	112228993	495794	11355	AACGACATCARTATAACAGAA	0.19	0.45	0.45	1.62	2.17	3.07	3.54	0.41	1.76	2.03	2.84	3.26
70	5	112234906	2909904	11356	TTTAAAACAGSCCAAAAAATG	0.39	0.77	0.77	0.74	2.13	2.34	2.73	0.72	0.77	1.91	2.19	2.50
70	5	112243945	10515448	11357	GAACCAGTACRGTGTGTAAGA	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112251249	17135108	11358	TTGTCCATTCYTGAATTCTTC	-	-	-	-	-	-	-	-	-	-	-	-
70	5	112258230	465454	11359	ACAGAGCAATYGTTACTTACT	0.31	0.65	0.64	1.03	0.85	1.74	1.92	0.63	1.23	0.84	1.62	1.77
70	5	112265938	153546	11360	CTATACAGGTMCTGAGATGGA	0.15	0.29	0.29	0.53	0.78	0.38	0.97	0.29	0.55	0.78	0.40	0.98
71	5	162824472	3756648	11361	AATGGGTTAARTGTATGAATC	0.43	0.79	0.79	0.30	0.23	0.14	0.92	0.74	0.25	0.26	0.13	0.89
71	5	162831143	169920	11362	TCAACCTTCTSTTAGTACTTA	0.38	0.59	0.59	0.43	0.30	1.52	0.95	0.54	0.48	0.33	1.41	0.96
71	5	162838621	299292	11363	AACTTTTATGYGCTGAGCCAG	0.39	0.63	0.63	0.41	2.21	1.55	0.78	0.62	0.43	2.00	1.48	0.79
71	5	162850556	299320	11364	TTGGTTGAAAWGATAAATCTA	0.03	0.12	0.12	2.58	2.23	1.11	1.38	0.09	2.69	2.03	1.12	1.38
71	5	162857508	10040698	11365	CAAGAAAAACRGTGAAAGCCA	-	-	-	-	-	-	-	-	-	-	-	-
71	5	162866387		11366	ACTTTCACAAMAAGAAGTTCA	-	-	-	-	-	-	-	-	-	-	-	-
71	5	162876986	4869089	11367	TAAGAGTATTRGTAGGAATTT	2.12	2.43	2.50	2.10	1.77	1.48	2.69	2.40	2.35	1.68	1.44	2.50
71	5	162890205	1496864	11368	TAGCCATTTCRTTTTTGGCTA	-	-	-	-	-	-	-	-	-	-	-	-
71	5	162906243	17061876	11369	GTCCAGAGATRTTTAATTTTC	0.64	0.98	1.12	1.25	2.31	2.66	2.59	1.00	1.38	2.09	2.44	2.39
71	5	162917533	4301242	11370	CAAACACTCARTTTAATGTTT	0.67	1.08	1.08	0.36	1.02	1.93	2.03	0.99	0.39	1.03	1.83	1.95
71	5	162924534	294597	11371	TCCACGCCCAYTAAGTAGGGA	0.03	0.14	0.14	0.25	0.13	0.82	1.17	0.13	0.21	0.12	0.78	1.13
71	5	162932663	17667466	11372	GAAGGGTCATYTCTACCAGTC	0.02	0.10	0.10	0.10	0.14	0.24	1.28	0.09	0.07	0.14	0.24	1.28
71	5	162938246	11749480	11373	TTCCTAGCAAKCACATTCAAA	-	-	-	-	-	-	-	-	-	-	-	-
71	5	162944198	17061994	11374	CGAGGGAGAGRCCTTTTACCT	0.42	0.25	0.24	0.02	0.12	0.65	0.28	0.17	0.01	0.12	0.67	0.30
72	5	163672287	2915850	11375	TTTTTCAGGTRGATGACTTTT	0.03	0.15	0.13	0.36	0.18	0.04	0.01	0.10	0.38	0.20	0.04	0.00
72	5	163677825	11951951	11376	ACAACTGTCAYTGAAAATTAA	1.20	1.17	1.17	0.48	0.06	0.06	0.01	1.04	0.43	0.05	0.05	0.01
72	5	163684666		11377	TGGAATTAAGRGACTTTTTTT	1.30	1.28	1.08	0.43	0.17	0.05	0.00	0.93	0.41	0.19	0.05	0.00
72	5	163695678	17063176	11378	CATGTAAAGTRTCAAAATCCA	0.14	0.17	0.18	0.32	0.29	0.06	0.00	0.18	0.31	0.30	0.06	0.00
72	5	163703402	6874303	11379	TTTTGATCCARTTGTACTATT	0.35	0.02	0.02	0.34	0.10	0.01	0.01	0.00	0.33	0.09	0.00	0.01
72	5	163710999	10515876	11380	GGTCTTAAGTMCAGATTAGGC	0.13	0.28	0.27	0.03	0.03	0.04	0.01	0.24	0.03	0.01	0.04	0.02
72	5	163721769	17360177	11381	GATTACAGCTRAGCAGAGGCC	0.89	0.17	0.17	0.06	0.13	0.03	0.01	0.15	0.05	0.15	0.03	0.01
72	5	163744620	7718895	11382	CTAAGAATACKTTAAAATACA	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163749534	10036340	11383	CTACTGATATYAAAAAGGAGA	2.86	0.33	0.34	0.13	0.05	0.04	0.01	0.31	0.12	0.05	0.04	0.00
72	5	163759627	10073155	11384	ATTGAGGGTAYGAGTTAAGTT	0.52	0.47	0.45	0.24	0.08	0.03	0.05	0.38	0.23	0.07	0.03	0.06
72	5	163769515	13354605	11385	ATTCAACCAAWTCCTTTTTTT	0.20	0.44	0.44	0.47	0.16	0.03	0.16	0.39	0.46	0.16	0.03	0.16
72	5	163782378	10515877	11386	ACCATTTAAARGGTTACAAAG	1.33	1.05	1.05	0.60	0.44	0.91	0.46	0.95	0.63	0.48	0.89	0.48
72	5	163802801		11387	GCCAGTCTACRTCCTGCAGAG	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163809463	10213986	11388	CATTATTCTTYATAACACATG	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163815733	10476473	11389	CAAGAAGAGCKATGAATTCAA	1.20	0.87	0.87	1.00	2.31	1.98	1.13	0.80	1.01	2.11	1.79	1.07
72	5	163821858	6556756	11390	TCTTGGCATTKGTTACAATAA	1.20	0.87	0.87	2.56	3.52	1.90	1.03	0.77	2.77	2.82	1.73	1.03
72	5	163828175	6556762	11391	CATGAAATTCRAAACCTCAGT	1.56	1.85	2.11	2.03	2.98	1.70	0.93	1.99	2.76	2.53	1.56	0.90
72	5	163834951	10072089	11392	TTCTAGTTTCKTGATACATTT	1.37	0.98	0.98	2.08	1.63	1.74	1.63	0.89	2.47	1.50	1.69	1.51
72	5	163841717	13182232	11393	TTATTCAGAARTAGATTTACC	0.81	1.35	1.35	0.40	1.43	1.76	1.55	1.32	0.39	1.40	1.65	1.49
72	5	163848672	17310753	11394	CACGCCCAAAYCCCTGCTCAT	-	-	-	-	-	-	-	-	-	-	-	-

72	5	163854743	10515882	11395	AATCTTCAACRTATTTTGCCC	-	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163862234	10078439	11396	ATCTTTAAGAYCATCACAATT	-	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163880568	17311616	11397	TGCCACTCTCWTTGCTGGAAA	0.15	0.37	0.40	0.49	0.64	1.53	1.97	0.34	0.46	0.65	1.45	1.82
72	5	163890252	6556770	11398	ACAATACATAYGAGAACGGTG	0.32	0.67	0.75	0.57	0.48	0.98	1.73	0.73	0.56	0.49	0.99	1.66
72	5	163900365	1428076	11399	TATTAAATTGYTGGTGGCTGA	0.54	0.87	0.87	0.28	0.60	1.19	1.35	0.82	0.26	0.64	1.17	1.29
72	5	163906466	10061124	11400	TCATGAGGCASCATCTTTCAC	0.49	0.83	0.83	0.78	0.86	1.17	1.22	0.78	0.88	0.86	1.14	1.20
72	5	163912626	6556772	11401	AAACAATCAAYATGCTGAGAA	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163918968	6868405	11402	TATTTGACCTRTTTTCTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163925921	165066	11403	GGTGTTAATAWCATGTTAAGA	1.66	2.14	2.14	1.32	1.09	0.90	1.04	2.08	1.32	1.08	0.90	1.05
72	5	163931994	17074144	11404	ATAGAAAATASCACTTTCTTT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163943844	17313050	11405	TATCGCCACTRACACACTCAT	0.11	0.25	0.25	1.95	1.20	0.82	0.42	0.22	2.18	1.21	0.82	0.44
72	5	163952748	165072	11406	AAAAACTGCCYGTTTATAATA	1.80	2.34	2.34	1.41	1.23	0.53	0.65	2.26	1.61	1.21	0.53	0.65
72	5	163964349	17064551	11407	CAGAGCATCARTATCAGTCAC	-	-	-	-	-	-	-	-	-	-	-	-
72	5	163973215	165076	11408	ATAAGGGATTRGAATTCCTGA	1.33	1.88	1.88	0.84	0.63	1.06	1.46	1.81	0.89	0.66	1.06	1.44
72	5	163980289	250597	11409	TTGGTTACCTYCTTCTTGAAA	1.18	1.63	1.63	1.07	0.79	1.03	0.99	1.58	1.21	0.81	1.02	1.02
72	5	163989172	17065898	11410	ATCACTTCTAYCTGTTTGTCT	1.00	1.21	1.21	1.76	2.31	0.64	0.28	1.15	1.98	2.18	0.69	0.28
72	5	164011560	17314584	11411	TCACCATCCTYGAAAAAATTG	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164023046	17066385	11412	CTCATGCATGWCATTTCCTCT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164033325	17066543	11413	AGTAGTTTGTRCGCTTTTTGT	0.37	0.66	1.16	2.94	2.03	1.15	0.31	0.94	3.19	1.90	1.13	0.33
72	5	164047174	17066799	11414	CAAATGATTCKCTCTGGTCAT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164060882	1293506	11415	AATTCAAATGRTCTTCCCAAG	0.86	0.01	0.06	1.64	2.20	1.27	0.27	0.03	1.77	2.07	1.22	0.28
72	5	164076218	2544848	11416	TTTATTTGGARTACTTCATGA	1.25	1.67	1.67	0.92	0.64	0.56	0.65	1.57	0.96	0.64	0.58	0.66
72	5	164083509	2547009	11417	CAAATATCCTRAAATTCAGAT	1.09	0.10	0.07	0.78	0.22	0.32	0.71	0.05	0.88	0.23	0.34	0.72
72	5	164108869	4868888	11418	AAGCAAAACCMATGAGAAATG	0.52	0.89	0.89	0.37	0.51	0.43	0.43	0.84	0.35	0.51	0.43	0.46
72	5	164136971	6881810	11419	TTTAATCAGTYTTAAGTCAAT	0.02	0.04	0.04	1.02	1.08	0.56	0.28	0.02	1.11	1.09	0.60	0.30
72	5	164154645	2909760	11420	AGTTTTCTAGRTATTGGAAGT	0.42	0.71	0.71	0.24	1.51	0.97	0.67	0.65	0.17	1.38	0.98	0.68
72	5	164166888	7717101	11421	AACCCATTCTRTGATGATCTT	0.56	0.91	0.94	0.29	0.84	1.15	1.51	0.89	0.27	0.86	1.07	1.42
72	5	164179353	17069021	11422	TTACACCTCARTAGCTCCTGT	0.62	1.00	1.00	0.55	1.31	0.76	1.31	0.94	0.52	1.27	0.77	1.29
72	5	164185098	17376891	11423	ATCTTGATGTYGATAGCTAAA	0.01	0.04	0.04	1.00	0.55	2.06	1.39	0.02	1.02	0.58	1.93	1.35
72	5	164191750	7735637	11424	CTTGCACCCARTCCATTCCCA	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164213852	17069715	11425	TTTAGATTACRGATTTTTGGT	0.45	0.44	0.54	0.32	1.96	1.93	1.31	0.46	0.31	1.84	1.87	1.28
72	5	164219602	2963136	11426	TGAATTGAGGWGAGAACATAC	0.02	0.00	0.00	0.19	0.58	1.62	0.92	0.00	0.18	0.60	1.55	0.93
72	5	164226635	17069968	11427	AAAATTTATGRCACATTTTAT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164240803	3923448	11428	TGCCATTTTAYTGCCGATTTA	0.18	0.37	0.40	0.09	0.02	0.20	0.61	0.38	0.06	0.01	0.21	0.63
72	5	164249094	11960382	11429	TTATATCTAAKCATAATTTGT	0.03	0.03	0.04	0.13	0.03	0.00	0.18	0.02	0.11	0.03	0.00	0.19
72	5	164254631	2962867	11430	GTCTCTACCAYGATACCCAAG	0.05	0.14	0.14	0.09	0.03	0.02	0.05	0.11	0.07	0.03	0.02	0.04
72	5	164262139	3923301	11431	ACCTACTACTKTATAAGTCCC	0.38	0.56	0.56	0.03	0.04	0.13	0.31	0.51	0.03	0.03	0.14	0.33
72	5	164270448	2962872	11432	CCAGGGAACTMTAAGAAAATC	0.32	0.33	0.26	0.30	0.28	0.83	0.99	0.23	0.31	0.28	0.84	0.98
72	5	164273895	10038674	11433	CTGAAAATGCRTCTGGTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164305391	4543284	11434	CTATGAATGCRGAAAATTTGG	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164321663	9790906	11435	AGCAAGGATAWTAGCTTAACT	-	-	-	-	-	-	-	-	-	-	-	-
72	5	164339051	4145750	11436	CCAAAAAAATMACATAATTTG	0.15	0.34	0.27	0.25	1.74	1.39	1.37	0.24	0.24	1.66	1.33	1.30
72	5	164349532	4868901	11437	TCTCAGTGTCYCAGCAAATAT	0.06	0.19	0.19	1.54	1.68	1.17	1.23	0.16	1.85	1.58	1.15	1.21
72	5	164353655	10866748	11438	GTTGTCTTGAYTGTAGAACAC	0.13	0.37	0.35	1.49	1.57	0.88	0.64	0.30	1.71	1.43	0.87	0.67
73	5	174814435	267421	11439	TTTATCAAACYTATCATCTTC	0.90	0.86	0.86	0.27	0.21	0.60	0.17	0.82	0.25	0.22	0.58	0.19
73	5	174820027	267409	11440	CTTTCAAGTTWACGTATTCAT	0.26	0.15	0.15	0.15	0.08	0.38	0.45	0.10	0.16	0.09	0.40	0.43
73	5	174827162	931940	11441	GCACCTCAGGRGATTTGCTGT	-	-	-	-	-	-	-	-	-	-	-	-
73	5	174840551	2940478	11442	GCTGTTGTCCRGAAAGTGAAA	0.32	0.59	0.59	0.10	0.03	0.05	0.28	0.56	0.05	0.02	0.04	0.28
73	5	174852056	267384	11443	ATTGCTCGCCMTTAACACAGA	-	-	-	-	-	-	-	-	-	-	-	-
73	5	174854037	7718943	11444	ACAATAGATCRTCTTTATTTG	0.32	0.37	0.38	0.07	0.09	0.05	0.22	0.33	0.05	0.09	0.05	0.20
73	5	174869799	2662170	11445	GAAGTGGAGAYGCACCCCTCA	0.21	0.05	0.05	0.58	0.16	0.45	0.12	0.03	0.63	0.15	0.45	0.12
73	5	174878071	157472	11446	AAAGAGGATAYGACCCCTGAT	0.58	- 0.53	0.49	0.16	1.14	0.43	0.12	0.45	0.14	1.13	0.43	0.13
73	5	174885040	273081	11447	CAGTGTCGTCRTCATCATTTA	0.08	0.08	0.08	0.80	0.24	0.18	0.61	0.05	0.86	0.25	0.18	0.61
73	5	174891865	156378	11448	GAAGTGAAATYGTTTGCCACA	0.25	0.08	0.15	0.10	0.33	0.29	0.80	0.09	0.09	0.33	0.29	0.78
73	5	174902044	267394	11449	GGGTGCCTGCSTCTCCAAGTC	0.10	0.07	0.13	0.69	0.36	0.68	0.74	0.11	0.71	0.40	0.66	0.75
73	5	174907182	10476160	11450	GAGGAGAAACRAGATAAAGCA	-	-	-	-	-	-	-	-	-	-	-	-
73	5	174931599	200461	11451	TGGTCTGCACRGCACACGGGG	0.22	0.49	0.45	0.91	0.88	0.55	0.65	0.41	0.88	0.85	0.58	0.66
73	5	174944615	882978	11452	ATTGTTCATTSATTCACTTAT	-	-	-	-	-	-	-	-	-	-	-	-
73	5	174957332	2115512	11453	CATGATGGGAYTCCACACACT	0.65	1.02	1.19	2.14	1.86	0.87	0.39	1.08	2.27	1.79	0.86	0.41
73	5	174964234	1501745	11454	TTTTCAGCCTYTTGAGGAATT	2.80	2.77	2.77	2.26	2.00	1.02	0.34	2.68	2.65	1.89	1.03	0.37
73	5	174969964	1019808	11455	CGCTAGTTGAYGGCTAGCCCA	0.93	0.99	1.00	1.50	2.07	1.09	0.20	0.91	1.64	1.95	1.08	0.19
73	5	174978794	17572666	11456	AGAACATGAGYTTTTTGTGAA	0.54	0.53	0.53	1.76	1.02	0.89	0.71	0.49	1.87	1.02	0.88	0.72
73	5	174985113	2963838	11457	GAGATGAATCMGATCTGGGTT	1.80	2.29	2.16	1.41	0.79	1.31	1.37	2.09	1.41	0.79	1.25	1.33
73	5	174991457	1650385	11458	GTGGCAAATCWCTTTAATCTA	0.03	0.15	0.10	0.66	2.28	2.14	1.08	0.07	0.72	2.18	2.04	1.06
73	5	175001194	4868527	11459	CCAAGATGCTRACTGCTCAGC	0.05	0.15	0.15	0.80	1.79	1.78	2.28	0.13	0.86	1.70	1.68	2.12
73	5	175007250	2963850	11460	CCATACTCTCRAGGGGCAGCA	1.88	2.45	2.45	1.00	0.37	2.99	1.58	2.37	1.14	0.38	2.63	1.51
73	5	175019973		11461	TGCCTAAATGYCCAACAGTAG	-	-	-	-	-	-	-	-	-	-	-	-
73	5	175025981	6864183	11462	CGAGTTCAGTYAAGTCTGCAA	-	-	-	-	-	-	-	-	-	-	-	-
73	5	175037116	2890892	11463	CTGAAGCCACRTTGGTCCGCA	0.15	0.25	0.25	1.30	1.66	1.44	2.86	0.18	1.55	1.55	1.36	2.61
73	5	175048315	7732442	11464	TTGAACTTGGYCCTGTTTTTG	0.15	0.25	0.25	0.70	2.57	2.02	1.85	0.19	0.78	2.30	1.89	1.79
73	5	175055757	17601481	11465	GTGAGCCACCRTTGGCATGAG	0.21	0.20	0.20	0.58	1.04	2.29	2.43	0.12	0.64	1.06	2.17	2.29
73	5	175063703	10079693	11466	GATCACTGTGYAGTCCTATAT	0.46	0.00	0.00	0.12	1.13	2.10	1.42	0.00	0.09	1.08	1.96	1.33
73	5	175071036	10035429	11467	CAAAGCTTACRGGAACTGCTC	0.29	0.27	0.30	0.87	0.77	1.05	1.25	0.25	0.90	0.78	1.02	1.24
73	5	175076734	6861443	11468	GATACTTTGGSAAGTCACTAA	0.19	0.40	0.40	0.08	0.25	0.44	1.47	0.37	0.06	0.27	0.45	1.43
73	5	175083501	7711026	11469	TGTGGTTTAAYGTTTGATGAA	0.14	0.34	0.34	0.04	0.27	1.29	0.87	0.28	0.02	0.34	1.26	0.82
73	5	175100329	12518169	11470	ACTGATGCAGYCTCTGCTCTT	-	-	-	-	-	-	-	-	-	-	-	-
73	5	175110051	12658312	11471	TAAGCAGGTAYTTTCAAGTCC	0.06	0.07	0.07	0.18	0.42	0.67	0.49	0.03	0.16	0.47	0.66	0.49
73	5	175138227	4435881	11472	TAAATATAAAKCATCCAGCTA	0.62	0.04	0.07	0.42	0.14	0.14	0.99	0.05	0.42	0.15	0.16	1.03
73	5	175145927	10075384	11473	TCTTTGGAGCMCCACATTTTC	-	-	-	-	-	-	-	-	-	-	-	-
73	5	175153034	2443537	11474	TTTCCAGAGTMCATAGTCCAG	0.73	1.04	1.04	0.50	0.26	0.25	0.18	0.93	0.52	0.27	0.25	0.14
73	5	175170884	17065511	11475	GAAAAGTCTTSAGAAGCAAAC	0.62	0.81	0.81	0.55	0.25	0.20	0.31	0.75	0.54	0.28	0.19	0.29
73	5	175178039	17065525	11476	ATGGAAGGGCRAGTTGTTTTT	0.24	0.14	0.14	0.40	0.18	0.17	0.74	0.09	0.39	0.18	0.18	0.76
73	5	175185077	17065534	11477	GCTCTATTCCSTCCTTTTCTA	0.08	0.10	0.10	0.12	0.20	0.28	0.42	0.07	0.10	0.22	0.28	0.41
73	5	175191788	6556225	11478	CATGTCTGACRGCAGGAGATG	0.44	0.77	0.77	0.26	0.39	0.30	0.15	0.71	0.22	0.40	0.31	0.16
74	6	11280969	10946996	11479	AGGGGCTTCARAACATCCTAG	0.06	0.19	0.19	0.02	1.63	0.89	0.53	0.15	0.02	1.58	0.91	0.53
74	6	11296925	6906952	11480	CAAGGCAGTAKTTCCCACTGT	0.06	0.15	0.15	2.85	2.06	0.81	1.29	0.12	2.92	1.97	0.81	1.26
74	6	11306800	11759513	11481	ACACATCTCTRACAGCACTTA	2.31	2.96	2.96	2.24	2.60	2.05	1.15	2.87	2.34	2.38	1.96	1.18
75	6	17419495	1745069	11482	TTATAATAACRCTACAATTTT	0.66	1.10	1.10	0.70	0.69	0.09	0.07	1.04	0.71	0.72	0.11	0.07
75	6	17426095	9477384	11483	AAATTCAAAGRAGCAGTCTGG	0.01	0.00	0.00	1.10	0.22	0.22	0.10	0.00	1.10	0.24	0.21	0.11
75	6	17438834	12526082	11484	TGTATCCAATRTATAAATTCT	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17458478	12181871	11485	CAGATGATGAYGTTTCAAACT	0.34	0.20	0.20	0.04	0.93	0.21	0.16	0.16	0.05	0.93	0.19	0.16
75	6	17463267		11486	AGAGGGAGCTSCTGCAAAGTA	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17494874	7773313	11487	CTTTGTAAAAYGTTTGTATGT	0.22	0.45	0.45	0.17	0.03	0.48	0.05	0.41	0.15	0.03	0.50	0.05
75	6	17506509	7748415	11488	TATCCTGCGGRGTGGTCTAGT	0.13	0.07	0.07	0.16	0.25	0.02	0.16	0.05	0.16	0.26	0.01	0.15

75	6	17523496	7748921	11489	TTTGTGAACTYGTTGTGAGGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17524043	17379883	11490	TTGACATTGCRCCATGGAGTG	0.30	0.59	0.59	0.29	0.16	0.08	0.23	0.56	0.31	0.16	0.06	0.20	0.30	0.59	0.59	0.29	0.16	0.08	0.23	0.56	0.31	0.16	0.06	0.20
75	6	17530515	10485376	11491	AACATAACTAYGTCACGGTGT	0.84	0.65	0.65	0.60	0.15	0.13	0.27	0.56	0.60	0.15	0.13	0.26	0.84	0.65	0.65	0.60	0.15	0.13	0.27	0.56	0.60	0.15	0.13	0.26
75	6	17549398	6918762	11492	TCTTATATTTYAGGAGGCTAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17560679	3777689	11493	TAGGAAAAAGKCCATGGGAAC	0.96	0.30	0.30	0.09	0.37	0.19	0.07	0.25	0.08	0.40	0.20	0.06	0.96	0.30	0.30	0.09	0.37	0.19	0.07	0.25	0.08	0.40	0.20	0.06
75	6	17571645	3777696	11494	AGTCTCACAAYCTTTTTATAA	1.67	0.30	0.30	0.35	0.16	0.23	0.63	0.26	0.34	0.15	0.22	0.64	1.67	0.30	0.30	0.35	0.16	0.23	0.63	0.26	0.34	0.15	0.22	0.64
75	6	17588832		11495	ACTTGCAAGARAAGCAGGATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17591854	3777700	11496	GACGGGAATGYAAACCCTCAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17613923	910039	11497	GTTTCTTTGGRGCACACACAA	1.39	1.84	1.84	0.67	0.19	0.16	1.56	1.76	0.67	0.20	0.16	1.53	1.39	1.84	1.84	0.67	0.19	0.16	1.56	1.76	0.67	0.20	0.16	1.53
75	6	17622616	9367952	11498	GTCATTTGTTKTAGGAGAAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17629962	7769963	11499	GTGGAAGATAYGGCCCATCCT	1.16	1.53	1.52	0.43	0.56	1.04	0.38	1.45	0.40	0.53	1.04	0.42	1.16	1.53	1.52	0.43	0.56	1.04	0.38	1.45	0.40	0.53	1.04	0.42
75	6	17640235	10949429	11500	TTTGTTTAGTRGACTGACAAA	1.17	1.61	1.61	0.80	1.33	1.07	0.58	1.60	0.87	1.30	1.03	0.59	1.17	1.61	1.61	0.80	1.33	1.07	0.58	1.60	0.87	1.30	1.03	0.59
75	6	17651281	10807614	11501	ACAACTGTAARAAACTCGGCC	0.93	1.28	1.28	1.72	2.07	1.01	0.87	1.23	1.84	1.91	0.97	0.93	0.93	1.28	1.28	1.72	2.07	1.01	0.87	1.23	1.84	1.91	0.97	0.93
75	6	17659356	3777709	11502	CATGTTTTGARTCTACTAACA	2.34	2.96	2.96	1.52	1.45	1.57	1.63	2.90	1.72	1.36	1.47	1.53	2.34	2.96	2.96	1.52	1.45	1.57	1.63	2.90	1.72	1.36	1.47	1.53
75	6	17666296	16879836	11503	AAGTGATTTTWTAAATACCAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17677134	2876452	11504	ATGGTTCTCARGCTGTAGACT	1.26	1.36	1.36	1.57	1.44	1.98	2.41	1.28	1.86	1.35	1.84	2.25	1.26	1.36	1.36	1.57	1.44	1.98	2.41	1.28	1.86	1.35	1.84	2.25
75	6	17690486	17389326	11505	AATCGATATGSTCCAACAGCA	2.31	2.85	2.85	2.08	1.20	2.13	1.91	2.78	2.35	1.19	1.94	1.83	2.31	2.85	2.85	2.08	1.20	2.13	1.91	2.78	2.35	1.19	1.94	1.83
75	6	17700711	17389493	11506	AGACCTGATCYGCTTGGAAGA	0.06	0.20	0.15	1.97	1.38	1.04	1.60	0.13	2.12	1.35	1.05	1.54	0.06	0.20	0.15	1.97	1.38	1.04	1.60	0.13	2.12	1.35	1.05	1.54
75	6	17718069	1055111	11507	AGGTTTTTCTKTGACGTTTAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17724535	3777712	11508	TTTTCTGCTAYACCTAACACA	0.13	0.22	0.22	0.36	1.84	1.85	1.31	0.17	0.35	1.77	1.75	1.31	0.13	0.22	0.22	0.36	1.84	1.85	1.31	0.17	0.35	1.77	1.75	1.31
75	6	17730351	6933829	11509	ATGCTGCTACMCAGAGTCAAG	0.19	0.28	0.28	0.29	1.61	1.47	1.33	0.25	0.24	1.53	1.43	1.31	0.19	0.28	0.28	0.29	1.61	1.47	1.33	0.25	0.24	1.53	1.43	1.31
75	6	17736461	10949434	11510	GTTTGATGAGRACTGGTTATC	0.27	0.42	0.42	0.73	1.01	1.25	1.85	0.36	0.76	1.03	1.24	1.79	0.27	0.42	0.42	0.73	1.01	1.25	1.85	0.36	0.76	1.03	1.24	1.79
75	6	17743002	1886328	11511	GTCTTTAATTKTATGTCCTCC	2.94	1.26	1.26	0.30	0.40	1.12	2.47	1.18	0.31	0.43	1.14	2.32	2.94	1.26	1.26	0.30	0.40	1.12	2.47	1.18	0.31	0.43	1.14	2.32
75	6	17752424	6913935	11512	GAGGATCTAGKTTTTAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
75	6	17778418	9350055	11513	AGAATACTGTYCTCCACCAAC	0.57	0.27	0.30	0.65	0.55	0.76	2.21	0.28	0.74	0.59	0.74	2.14	0.57	0.27	0.30	0.65	0.55	0.76	2.21	0.28	0.74	0.59	0.74	2.14
75	6	17796672	16879902	11514	CTCTCCTCATYGGCATATACC	0.53	0.24	0.28	0.38	1.25	1.01	0.86	0.26	0.39	1.24	1.03	0.86	0.53	0.24	0.28	0.38	1.25	1.01	0.86	0.26	0.39	1.24	1.03	0.86
75	6	17803837	9297042	11515	TATGTGTTTAYGATGCACAGC	0.31	0.61	0.61	0.53	1.04	1.27	0.38	0.56	0.54	1.02	1.23	0.39	0.31	0.61	0.61	0.53	1.04	1.27	0.38	0.56	0.54	1.02	1.23	0.39
75	6	17829827	2038742	11516	GTGAAAATTAYTACCGAGCCC	0.44	0.66	0.66	0.91	0.77	0.17	0.46	0.63	1.00	0.75	0.16	0.47	0.44	0.66	0.66	0.91	0.77	0.17	0.46	0.63	1.00	0.75	0.16	0.47
75	6	17847481	10949441	11517	GTGTTTTAAAYGTTTGGTTCT	1.23	1.48	1.48	0.74	0.33	0.17	0.08	1.40	0.78	0.36	0.20	0.08	1.23	1.48	1.48	0.74	0.33	0.17	0.08	1.40	0.78	0.36	0.20	0.08
75	6	17862940	17714754	11518	CACACAAACAYGCATACTTTT	1.23	1.61	1.64	0.56	0.18	0.27	0.12	1.62	0.58	0.19	0.30	0.13	1.23	1.61	1.64	0.56	0.18	0.27	0.12	1.62	0.58	0.19	0.30	0.13
75	6	17872509	9371018	11519	AATCTTTTCCYTCTGACACTC	0.10	0.06	0.06	0.55	0.42	0.34	0.22	0.04	0.57	0.45	0.35	0.24	0.10	0.06	0.06	0.55	0.42	0.34	0.22	0.04	0.57	0.45	0.35	0.24
75	6	17880743	1924466	11520	AGAGTTACTAMAGTGCTAGTC	0.04	0.12	0.12	0.22	0.36	0.34	0.16	0.10	0.21	0.37	0.33	0.15	0.04	0.12	0.12	0.22	0.36	0.34	0.16	0.10	0.21	0.37	0.33	0.15
75	6	17888764	4716184	11521	CTGGATGACAYTGACCTCTGC	0.06	0.22	0.24	0.28	0.10	0.19	0.26	0.21	0.23	0.08	0.18	0.28	0.06	0.22	0.24	0.28	0.10	0.19	0.26	0.21	0.23	0.08	0.18	0.28
75	6	17898749	6939022	11522	AGATTTGAGAYAGGCTTAGGA	0.26	0.03	0.02	0.11	0.07	0.13	0.08	0.00	0.13	0.06	0.13	0.07	0.26	0.03	0.02	0.11	0.07	0.13	0.08	0.00	0.13	0.06	0.13	0.07
75	6	17905586	7341276	11523	AGCAAATTGTYCAAAGTCATA	0.32	0.12	0.12	0.09	0.01	0.01	0.12	0.10	0.07	0.02	0.00	0.12	0.32	0.12	0.12	0.09	0.01	0.01	0.12	0.10	0.07	0.02	0.00	0.12
76	6	21140661	415446	11524	GTTACTTAATYATTCTCCCTT	0.14	0.27	0.24	0.33	0.05	0.05	0.00	0.20	0.32	0.06	0.05	0.01	0.14	0.27	0.24	0.33	0.05	0.05	0.00	0.20	0.32	0.06	0.05	0.01
76	6	21150116	17730046	11525	GATAACACAGRTTTAGCTATT	0.24	0.41	0.42	0.09	0.02	0.02	0.01	0.38	0.08	0.02	0.02	0.01	0.24	0.41	0.42	0.09	0.02	0.02	0.01	0.38	0.08	0.02	0.02	0.01
76	6	21160395	7775602	11526	ATTGTTTCTTMCTAAATTTTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21170545	9465957	11527	AGCTGTAGACSTTTTGATAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21178475	9356760	11528	ATCCTGCCATRAGAATGTTAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21187063	10080639	11529	TTTTGGTGCTYATTTATACCC	0.31	0.14	0.12	0.07	0.01	0.00	0.01	0.10	0.05	0.01	0.00	0.00	0.31	0.14	0.12	0.07	0.01	0.00	0.01	0.10	0.05	0.01	0.00	0.00
76	6	21194764	10946428	11530	GGCGAACACCRAAGTCCTGGC	0.40	0.08	0.08	0.06	0.02	0.01	0.01	0.05	0.01	0.02	0.00	0.01	0.40	0.08	0.08	0.06	0.02	0.01	0.01	0.05	0.01	0.02	0.00	0.01
76	6	21202933	4454125	11531	TCCAGACACTRGGTAAAGAGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21215091		11532	TTTGGACCCAYACACAAATTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21223003	16884514	11533	ATAACTTGAGWGGGATAATTT	0.24	0.13	0.13	0.01	0.05	0.01	0.04	0.08	0.01	0.04	0.01	0.06	0.24	0.13	0.13	0.01	0.05	0.01	0.04	0.08	0.01	0.04	0.01	0.06
76	6	21228748	4076112	11534	TTGTAACCTTRTCCTAGAGAC	0.22	0.02	0.02	0.16	0.02	0.01	0.02	0.00	0.14	0.02	0.01	0.02	0.22	0.02	0.02	0.16	0.02	0.01	0.02	0.00	0.14	0.02	0.01	0.02
76	6	21235291	7751485	11535	GGTCGATTTGSGTTATGTACA	0.32	0.04	0.02	0.02	0.05	0.03	0.01	0.00	0.00	0.05	0.02	0.01	0.32	0.04	0.02	0.02	0.05	0.03	0.01	0.00	0.00	0.05	0.02	0.01
76	6	21241995	9465970	11536	TGTTTTTACTYGTACTAACCT	0.11	0.15	0.17	0.09	0.02	0.04	0.06	0.14	0.10	0.01	0.04	0.06	0.11	0.15	0.17	0.09	0.02	0.04	0.06	0.14	0.10	0.01	0.04	0.06
76	6	21252578	10498701	11537	ATGAACAACTRTTTTTAAAGC	0.31	0.32	0.32	0.18	0.07	0.10	0.82	0.28	0.17	0.07	0.09	0.80	0.31	0.32	0.32	0.18	0.07	0.10	0.82	0.28	0.17	0.07	0.09	0.80
76	6	21260216	10946432	11538	ATTAATAGTARTCTTTGCTGA	0.09	0.00	0.00	0.20	0.59	1.40	0.51	0.00	0.11	0.61	1.36	0.52	0.09	0.00	0.00	0.20	0.59	1.40	0.51	0.00	0.11	0.61	1.36	0.52
76	6	21267832	16884591	11539	TTATGGGACASTTAAATGAAG	0.04	0.04	0.04	1.06	3.25	1.59	0.77	0.00	1.29	2.68	1.59	0.78	0.04	0.04	0.04	1.06	3.25	1.59	0.77	0.00	1.29	2.68	1.59	0.78
76	6	21276570		11540	CATTTTCAGGKTCCTAACATG	0.62	0.44	0.44	2.96	3.40	1.90	1.19	0.37	3.30	2.97	1.78	1.13	0.62	0.44	0.44	2.96	3.40	1.90	1.19	0.37	3.30	2.97	1.78	1.13
76	6	21290957	9295501	11541	ATTGAAAAACRTTAAGAAAGG	3.01	3.33	3.33	1.88	2.07	1.57	1.23	3.17	1.95	1.93	1.53	1.19	3.01	3.33	3.33	1.88	2.07	1.57	1.23	3.17	1.95	1.93	1.53	1.19
76	6	21301492		11542	AGAGGGCTGTRAGCATACATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21319431	9465998	11543	ACCAACGCAAMGTGACAGAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21328510	12203389	11544	AAGTTCTAGARTAATTTCCAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21336582	7754027	11545	CTTCTCAAAGSCATCTATGAC	1.68	1.66	1.66	1.81	1.18	1.05	0.97	1.49	1.98	1.16	1.04	0.97	1.68	1.66	1.66	1.81	1.18	1.05	0.97	1.49	1.98	1.16	1.04	0.97
76	6	21344526	1459042	11546	AGTCCTAATCMCTTCTCAAAA	0.33	0.44	0.44	0.90	1.39	0.71	0.71	0.40	0.98	1.36	0.68	0.69	0.33	0.44	0.44	0.90	1.39	0.71	0.71	0.40	0.98	1.36	0.68	0.69
76	6	21355623	4712593	11547	AAGCTAAGCCYGTGTCCATTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21363822	1459045	11548	ATCATGGAAAYTGGCATTGTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21371234	4712595	11549	ATATCTCATTYGTAACTATTT	0.80	1.12	1.12	0.58	0.66	0.93	0.12	1.09	0.58	0.69	0.94	0.11	0.80	1.12	1.12	0.58	0.66	0.93	0.12	1.09	0.58	0.69	0.94	0.11
76	6	21377104	12664396	11550	GAACTTCAGGRTATGCTAGAG	0.08	0.20	0.22	0.76	0.37	0.19	0.30	0.17	0.82	0.37	0.19	0.32	0.08	0.20	0.22	0.76	0.37	0.19	0.30	0.17	0.82	0.37	0.19	0.32
76	6	21383482	807831	11551	AGCTTATTGCKTGTGTACTTG	1.12	1.43	1.33	0.37	0.29	0.15	1.49	1.15	0.33	0.31	0.17	1.47	1.12	1.43	1.33	0.37	0.29	0.15	1.49	1.15	0.33	0.31	0.17	1.47
76	6	21389013	807838	11552	TAGTGACTCARCATTTGAGGC	0.19	0.17	0.17	0.28	0.04	1.65	2.10	0.14	0.26	0.04	1.57	2.05	0.19	0.17	0.17	0.28	0.04	1.65	2.10	0.14	0.26	0.04	1.57	2.05
76	6	21406274	807848	11553	ATGATCTCTTYGATTGCTCTT	0.11	0.06	0.06	0.00	0.83	2.38	1.86	0.04	0.00	0.84	2.26	1.79	0.11	0.06	0.06	0.00	0.83	2.38	1.86	0.04	0.00	0.84	2.26	1.79
76	6	21416922	807859	11554	CTTTATTAGGRTTTTGCAAGT	0.13	0.12	0.12	0.06	1.31	1.39	0.96	0.10	0.05	1.27	1.35	0.95	0.13	0.12	0.12	0.06	1.31	1.39	0.96	0.10	0.05	1.27	1.35	0.95
76	6	21423154	9358410	11555	TCCACACTACRTTCTTAAATC	0.66	0.08	0.09	0.45	0.61	0.51	0.63	0.05	0.43	0.61	0.54	0.66	0.66	0.08	0.09	0.45	0.61	0.51	0.63	0.05	0.43	0.61	0.54	0.66
76	6	21425850	9358411	11556	CTTTGGAGTAYCCTCCAGCTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21438112	6456414	11557	CACGTAGCACRATGTTAATCT	0.40	0.48	0.48	0.48	0.28	0.42	0.30	0.45	0.46	0.28	0.39	0.28	0.40	0.48	0.48	0.48	0.28	0.42	0.30	0.45	0.46	0.28	0.39	0.28
76	6	21449537	6456416	11558	GAAGAGTCACRTTCTGTAAAA	0.03	0.06	0.06	0.12	0.18	0.29	0.91	0.04	0.11	0.19	0.30	0.92	0.03	0.06	0.06	0.12	0.18	0.29	0.91	0.04	0.11	0.19	0.30	0.92
76	6	21455389	1555083	11559	TGTACAGTTAYAGGCTTATAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
76	6	21462981	1005886	11560	GCTGGCTTTCYTAACTGCAAT	0.29	0.11	0.11	0.26	0.06	0.46	1.04	0.10	0.27	0.06	0.46	1.03	0.29	0.11	0.11	0.26	0.06	0.46	1.04	0.10	0.27	0.06	0.46	1.03
77	6	24477494	793663	11561	CATGTTAAAAYGTATAGGGTA	0.39	0.51	0.51	0.13	0.01	0.22	0.69	0.48	0.12	0.01	0.22	0.69	0.39	0.51	0.51	0.13	0.01	0.22	0.69	0.48	0.12	0.01	0.22	0.69
77	6	24486328	793699	11562	ATATTATGTAWACAGAAATTG	0.51	0.60	0.58	0.18	0.08	0.06	0.58	0.56	0.17	0.08	0.06	0.58	0.51	0.60	0.58	0.18	0.08	0.06	0.58	0.56	0.17	0.08	0.06	0.58
77	6	24517825	7750241	11563	TACAATCTTAYAAAAGTTACC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24530522	7738943	11564	CCTTGTGAGASATTAAATTTA	0.26	0.35	0.35	0.11	0.08	0.40	0.48	0.28	0.11	0.07	0.39	0.50	0.26	0.35	0.35	0.11	0.08	0.40	0.48	0.28	0.11	0.07	0.39	0.50
77	6	24542690	16901722	11565	ATAGTGTAATMCTTAAGGGTA	0.09	0.03	0.03	0.34	0.68	1.10	0.99	0.00	0.33	0.71	1.08	0.97	0.09	0.03	0.03	0.34	0.68	1.10	0.99	0.00	0.33	0.71	1.08	0.97
77	6	24548330	9461011	11566	AGGAAAGAGGRTATCATCTTG	0.66	0.85	0.85	1.63	2.92	1.33	0.93	0.82	1.88	2.59	1.31	0.90	0.66	0.85	0.85	1.63	2.92	1.33	0.93	0.82	1.88	2.59	1.31	0.90
77	6	24556666	13205780	11567	CAAATTATCAYCACCCCCAAT	1.18	1.74	1.60	2.80	3.44	1.97	1.04	1.55	3.14	3.15	1.86	1.02	1.18	1.74	1.60	2.80	3.44	1.97	1.04	1.55	3.14	3.15	1.86	1.02
77	6	24562658	6925475	11568	TACATAACCTRAGAGGATGAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24568686	2744576	11569	AATATAGTCAWGTTAATCACA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24572886	9467176	11570	TCCAACTTATRAACAGCTAAC	0.24	0.22	0.22	2.32	2.50	2.26	1.06	0.17	2.42	2.33	2.10	1.07	0.24	0.22	0.22	2.32	2.50	2.26	1.06	0.17	2.42	2.33	2.10	1.07
77	6	24585113	2817205	11571	GCCTCATGGARTGCCAAATGT	0.92	1.34	1.34	0.70	1.39	1.68	0.81	1.30	0.69	1.34	1.54	0.80	0.92	1.34	1.34	0.70	1.39	1.68	0.81	1.30	0.69	1.34	1.54	0.80
77	6	24595555	16889389	11572	AGTTTTGGTCKTCTTCTATGT	0.77	0.89	0.72	0.87	0.44	0.60	0.73	0.64	0.96	0.45	0.61	0.71	0.77	0.89	0.72	0.87	0.44	0.60	0.73	0.64	0.96	0.45	0.61	0.71
77	6	24597324		11573	TGCTGCCACGYTGCAACCTCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24621268	2817229	11574	TATTCTACTTYTTATTATTTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24625684	17374923	11575	TGCAAACTTAYCCGCAGAAAG	0.91	0.89	0.90	0.19	0.39	0.56	0.63	0.78	0.17	0.42	0.58	0.66	0.91	0.89	0.90	0.19	0.39	0.56	0.63	0.78	0.17	0.42	0.58	0.66
77	6	24641053	2744597	11576	TAGAGTTATCRTAAAGCTGGA	0.81	0.26	0.31	0.75	0.72	0.90	0.50	0.26	0.76	0.75	0.91	0.49	0.81	0.26	0.31	0.75	0.72	0.90	0.50	0.26	0.76	0.75	0.91	0.49
77	6	24649347	2817239	11577	TATTATATACRTGCAAAAAAA	1.09	1.43	1.49	0.65	1.02	0.34	0.34	1.44	0.73	1.02	0.34	0.33	1.09	1.43	1.49	0.65	1.02	0.34	0.34	1.44	0.73	1.02	0.34	0.33
77	6	24659603	2076313	11578	GTTAAATCATRTAAAGGTGCC	0.44	0.40	0.40	1.33	0.56	0.57	0.34	0.38	1.33	0.56	0.59	0.36	0.44	0.40	0.40	1.33	0.56	0.57	0.34	0.38	1.33	0.56	0.59	0.36
77	6	24666654	2744542	11579	ACATTATCATKTCCCTTGTAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24676372	12193738	11580	CTCTTGCCATYCTACAATGCT	0.39	0.42	0.39	0.68	0.92	0.76	0.24	0.34	0.68	0.93	0.78	0.24	0.39	0.42	0.39	0.68	0.92	0.76	0.24	0.34	0.68	0.93	0.78	0.24
77	6	24682880	2744557	11581	AGATTGTCTAWAGATAAATGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24690011	807509	11582	TACTTGCATGSCTGAAACTTT	0.86	1.15	1.22	0.47	0.60	0.52	0.31	1.18	0.48	0.59	0.57	0.34	0.86	1.15	1.22	0.47	0.60	0.52	0.31	1.18	0.48	0.59	0.57	0.34

77	6	24703832	16889506	11583	GGCTGACTCGYGAAGGCAGAA	0.78	0.27	0.27	0.31	0.09	0.10	0.27	0.24	0.30	0.08	0.10	0.27
77	6	24712047	4352670	11584	TAATCGAGAAMCAACTCAAAT	0.76	0.30	0.30	0.15	0.05	0.04	0.13	0.25	0.13	0.06	0.04	0.14
77	6	24724459	16889523	11585	CTCTTGAGGTWTCCTTAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24732836	9467239	11586	CCTTGACACTSAGAATTCATC	0.41	0.61	0.65	0.17	0.10	0.14	0.16	0.59	0.14	0.09	0.18	0.14
77	6	24745978	9393572	11587	GAAGGATCCCRCCTATCAGCT	0.44	0.81	0.81	0.09	0.46	0.19	0.13	0.75	0.09	0.50	0.17	0.13
77	6	24761525	2294688	11588	TATTAAAGCASTAACCCTGTC	-	-	-	-	-	-	-	-	-	-	-	-
77	6	24767050	2143340	11589	AAGAGCCCTARAAGTGACACT	0.19	0.38	0.38	0.80	0.30	0.37	0.30	0.31	0.76	0.29	0.37	0.29
78	6	28228380	2622319	11590	TGACATCTCASAGGTGCTCTC	0.93	0.71	0.61	0.36	0.17	0.03	0.03	0.57	0.34	0.16	0.04	0.03
78	6	28235423	9380058	11591	CTCCATTTGGYCAGCCTTATT	0.79	0.63	0.63	0.34	0.05	0.03	0.40	0.56	0.30	0.04	0.02	0.40
78	6	28241507	9393899	11592	CCTTGTTGCTSAGATACTGTT	0.71	0.80	0.72	0.03	0.06	0.54	0.31	0.67	0.02	0.06	0.58	0.33
78	6	28248272	16893741	11593	TTGATCCTGAYCTTCAGAACC	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28255966	9295761	11594	TGGAATGTTARTTCTAGCCTC	0.79	0.63	0.63	0.18	0.19	0.21	0.32	0.57	0.17	0.19	0.23	0.32
78	6	28262775	1150680	11595	GATATGACAGYTATGTTTGAT	0.09	0.00	0.04	0.57	0.36	0.09	0.26	0.00	0.63	0.41	0.11	0.26
78	6	28286615	16893817	11596	TTTTATGTTTRTATCAATCAG	0.52	0.88	0.87	0.46	0.24	0.41	0.63	0.81	0.48	0.23	0.45	0.66
78	6	28297368	1736890	11597	TTATTTTAATRCCCACCTAAG	0.45	0.81	0.79	0.38	0.30	0.93	0.53	0.72	0.33	0.32	0.91	0.52
78	6	28305162	17719826	11598	CTTTTCCAAGMAGCACATCTA	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28312772	11752073	11599	TGTAGCACATKACTATATGAA	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28320727	1047703	11600	ATAACTCATCRTCTCAGCCAG	0.21	0.03	0.04	0.23	0.50	0.24	0.39	0.03	0.21	0.53	0.27	0.41
78	6	28327249	1736904	11601	AATGCCCCTCRCTCCGATCTG	0.01	0.05	0.05	0.68	0.19	0.15	0.15	0.02	0.71	0.19	0.15	0.13
78	6	28335415	12000	11602	GGATATCGCTRCCATCGTCAC	0.62	0.31	0.33	0.49	0.50	0.13	0.17	0.32	0.50	0.51	0.13	0.15
78	6	28342381	4713155	11603	ATTTATTTTGWTAAAGTGATA	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28351021	1150726	11604	CCTAGCCTTTRAAGAGTTATC	0.39	0.59	0.63	0.32	0.35	0.53	0.15	0.59	0.32	0.39	0.52	0.15
78	6	28363019	1150721	11605	ACTCATCATCSTGAGAGCCAT	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28372660	3800324	11606	AACCTCTGTGRGAACTCAGCT	0.65	0.62	0.62	1.11	0.50	0.35	0.68	0.55	1.30	0.52	0.35	0.69
78	6	28378796	16893929	11607	AGACTAAAAAYCTTAGCATTG	0.53	1.00	1.00	0.55	1.37	0.67	0.38	0.87	0.54	1.30	0.70	0.38
78	6	28391751	4713159	11608	CAGGCAAGCTRTCATGTTAAA	0.44	0.88	0.89	0.80	0.82	1.25	0.64	0.80	0.88	0.79	1.21	0.64
78	6	28402867	4711167	11609	ATTATATTCAYTACAAGGCAG	0.53	1.00	1.00	0.89	0.81	0.82	0.62	0.88	1.30	0.84	0.87	0.65
78	6	28410257	16893975	11610	AAAGAGATCAYGTAAATCACA	0.80	1.33	1.33	0.69	1.09	0.79	0.46	1.23	0.86	1.06	0.83	0.47
78	6	28417732	10484542	11611	GGTAGAAAACRTATTTATAAT	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28422715	17378623	11612	CTATACCAAASGAACAGGAGA	0.65	0.87	0.87	0.93	0.73	0.54	0.44	0.73	1.00	0.75	0.57	0.43
78	6	28435350	733743	11613	AGGATGGCTASAGAATTAAGT	0.93	1.03	1.03	0.62	0.48	0.40	0.27	0.95	0.70	0.50	0.42	0.26
78	6	28445780	9468354	11614	ATCACCATTGWATCCTCAGCA	0.25	0.08	0.11	0.86	0.72	0.23	0.21	0.09	1.03	0.73	0.23	0.20
78	6	28456639	2072319	11615	TAAAACAAAAYGCACAGACAA	0.98	0.75	0.55	0.94	0.73	0.37	0.14	0.48	1.00	0.74	0.42	0.13
78	6	28466872	2232434	11616	AAACTTTTATYACACTGAGTG	0.49	1.05	1.05	0.78	0.49	0.33	0.20	0.95	0.86	0.51	0.32	0.21
78	6	28474241	2232422	11617	TGAAGAATAARCCATCATTAT	0.28	0.15	0.15	0.63	0.57	0.22	0.18	0.08	0.67	0.62	0.23	0.19
78	6	28482881	6905380	11618	GTTGAGTTCCRTCTAGGATTG	0.49	0.82	0.82	0.22	0.22	0.32	0.48	0.80	0.21	0.23	0.33	0.47
78	6	28491568	4412194	11619	TTGCATTTTGYGTAGTATTGT	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28498209	16894095	11620	ATGTACTGTAYAATGACATTT	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28508318	16894106	11621	GGTTGCCCACRCCTTGTTTCC	0.50	0.88	0.88	0.55	0.37	0.40	0.49	0.84	0.56	0.39	0.41	0.49
78	6	28513775	17315739	11622	CTGTAGAATARAATATTTTTG	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28519223	13190937	11623	GACAACCGCARCCCAAAGAAT	-	-	-	-	-	-	-	-	-	-	-	-
78	6	28532702	2531813	11624	CAGGTCTCTTSTAAGTCAGAG	1.30	1.59	1.59	0.82	0.55	0.48	0.36	1.53	0.89	0.56	0.52	0.42
78	6	28544039	2531815	11625	CAGAGCGCTAYGGAAGCAGTC	0.76	1.08	1.17	1.00	0.85	0.45	0.34	1.08	1.08	0.88	0.47	0.35
78	6	28556065	1015811	11626	ACCCAGGTAARCCTGCAGCTA	1.38	1.65	1.65	1.08	0.79	0.49	0.36	1.60	1.20	0.82	0.54	0.40
78	6	28564698	2531820	11627	GACGCAGTTCYTCGTCAAGAA	1.46	1.89	1.89	1.04	0.64	0.64	0.41	1.80	1.15	0.68	0.68	0.43
78	6	28571555	2227228	11628	TGAATTCTGCYTCTGTCTCAC	0.25	0.48	0.48	1.11	0.93	0.51	0.48	0.46	1.19	0.93	0.53	0.47
79	6	28735448	9295775	11629	CACATAATTARTCATGCACTA	0.24	0.00	0.00	0.18	0.27	0.25	0.70	0.00	0.14	0.25	0.27	0.71
79	6	28751875	9380083	11630	GCCTATTGACRTTAGAGGAAA	-	-	-	-	-	-	-	-	-	-	-	-
79	6	28756250	16894197	11631	TATGTCTTAAYTGAAAAGCCA	0.11	0.28	0.30	0.48	0.52	0.47	0.21	0.28	0.49	0.53	0.48	0.22
79	6	28776459	7383248	11632	TGCAACCCAGMAATTTTCTGC	0.30	0.57	0.57	0.75	0.66	0.49	0.36	0.53	0.77	0.64	0.49	0.36
79	6	28784053	6906506	11633	CTATATTGGTSCTGGACTTTC	0.22	0.20	0.20	0.53	0.55	0.51	0.32	0.14	0.49	0.55	0.54	0.33
79	6	28807670	10498733	11634	GAAGAAAACARGTCCCAAATG	-	-	-	-	-	-	-	-	-	-	-	-
79	6	28811223	1233572	11635	CTCATGAATGYTAAGCATACG	0.02	0.10	0.10	0.06	0.28	0.25	0.27	0.08	0.01	0.29	0.28	0.26
79	6	28820226	1233578	11636	GCAATCCAAARTCTCAAAATC	-	-	-	-	-	-	-	-	-	-	-	-
79	6	28832831	17398081	11637	AGACACTTTTSATTCAACGGC	0.19	0.27	0.27	0.10	0.02	0.14	0.26	0.20	0.08	0.01	0.16	0.27
79	6	28892720	377392	11638	TGGGAGTGAAMGCGAGCCGCC	0.12	0.30	0.33	0.05	0.06	0.02	0.17	0.29	0.06	0.06	0.01	0.18
79	6	28901832	209179	11639	ATGAGTAAAASAAAGGATGCA	0.23	0.42	0.42	0.16	0.05	0.15	0.05	0.36	0.12	0.04	0.16	0.05
79	6	28914313	209173	11640	AAGATCAGAAYCTGACCCTTT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	28934241	9257274	11641	ACCCTCATACYGTAGACTTTG	-	-	-	-	-	-	-	-	-	-	-	-
79	6	28954228	209153	11642	TATTATTATCYAGGGACAGTG	0.20	0.42	0.42	0.21	0.28	0.11	0.12	0.36	0.14	0.29	0.09	0.11
79	6	28962248	2032500	11643	GATTTCTAATRGTTGTACCTG	0.13	0.33	0.36	0.41	0.14	0.25	0.09	0.30	0.43	0.15	0.25	0.10
79	6	28975894	1536215	11644	CTGGTATGTCSAGGATTACGT	0.58	0.54	0.45	0.27	0.21	0.19	0.17	0.40	0.25	0.23	0.20	0.17
79	6	28983481	209122	11645	AACAGAATTTYTCACACATTA	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29015034	3130897	11646	CACTTTATTCRTCTGATATTT	0.13	0.27	0.30	0.42	0.16	0.17	0.65	0.26	0.39	0.16	0.17	0.66
79	6	29017444	4713186	11647	TAACAAAAAAYGGATACTCGA	0.13	0.08	0.06	0.18	0.22	0.67	1.36	0.04	0.16	0.23	0.65	1.30
79	6	29053501	16894533	11648	GCAGTTCCGCYCGGGACATCC	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29060014	17839872	11649	AGCTCAGAGARAACGTCGAAA	0.21	0.09	0.08	0.06	0.65	1.31	1.21	0.05	0.04	0.67	1.27	1.13
79	6	29069798	16894540	11650	TCAAGACATAYCTTTTTCACC	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29078348	6456883	11651	TGCTATATACYATCTCCTAGG	0.09	0.06	0.06	1.15	1.72	1.55	0.95	0.04	1.28	1.68	1.47	0.98
79	6	29092734	3129795	11652	GGAGATGGGGKTGCCCAAAGA	1.27	1.47	1.40	1.06	1.58	1.54	1.11	1.35	1.18	1.51	1.53	1.14
79	6	29106631	16894554	11653	GCTCTTTTATYACCATGCTTT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29114229	9468473	11654	AAGTAATGAAYAGTGTCTAAT	0.26	0.12	0.12	1.84	1.13	0.80	1.40	0.10	2.00	1.13	0.83	1.36
79	6	29119939	9391651	11655	AGAAAACATAYTTAATTGCCT	0.25	0.27	0.25	0.86	1.21	0.90	1.09	0.20	0.90	1.16	0.93	1.10
79	6	29122005	2143574	11656	CCTTGGACGCYTTGTCTCTCT	0.01	0.02	0.04	0.90	0.72	1.35	0.78	0.02	1.01	0.74	1.33	0.79
79	6	29140448	12664320	11657	TAAATTATAARTAAGGTCAGA	0.49	0.11	0.11	0.29	0.93	0.40	0.86	0.10	0.29	0.93	0.42	0.82
79	6	29148765	4713200	11658	AAAATCTGTTSGCCCTGGTCA	0.58	0.58	0.61	0.20	0.10	0.48	0.47	0.53	0.20	0.10	0.51	0.49
79	6	29160459	6903904	11659	TCTGTTGCCTRAAATGTTGCC	0.01	0.00	0.00	0.25	0.06	0.20	0.59	0.00	0.22	0.05	0.25	0.60
79	6	29165950	9380109	11660	ATTTTCAATCYTTACGACATT	0.00	0.02	0.02	0.21	0.42	0.22	0.57	0.00	0.14	0.46	0.23	0.59
79	6	29175411		11661	ATTTCTCAAAMGGTAATGATC	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29182795	17342384	11662	ACTAGGCATCRAGGATAATGT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29193207	3129110	11663	TTATATACATRCTCAATTATC	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29210840	3129119	11664	AAATGTGGCTRATACATACCT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29215633	17343049	11665	TTCAGCTAGAMAGTACATTGA	0.71	0.96	0.95	0.51	0.46	0.73	0.44	0.83	0.55	0.46	0.72	0.45
79	6	29248196	3129156	11666	GCAAAACTATKTAGGAATATT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29259650	3116820	11667	AAAATAACTTYTAGTAAACAA	0.02	0.08	0.08	0.31	1.13	0.64	0.51	0.06	0.31	1.11	0.66	0.56
79	6	29263728	3129171	11668	GAATTTATGCRGCAAGCAATT	0.07	0.13	0.13	0.31	0.79	0.47	0.75	0.11	0.30	0.82	0.46	0.80
79	6	29287536	3116834	11669	AGTGGTGGTCSTCTTCTAAGT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29301241	3130811	11670	ATAAGTTATASTGGGAGATTT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29340051	16894681	11671	CCCAGGGCAAKTTGCCTTACA	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29345200	17344153	11672	TAAGGGAAATYCATGTCATCA	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29356440	2394550	11673	CCTTGCTTCGYATTATTTATT	-	-	-	-	-	-	-	-	-	-	-	-
79	6	29365946	1033568	11674	GCAGATGAACRTGCCAAGATG	0.04	0.14	0.15	0.27	0.56	1.21	0.74	0.11	0.26	0.59	1.21	0.76
79	6	29379552	16867630	11675	TGGTTCATTAMGAGTAATCTC	0.45	0.70	0.70	0.66	0.65	0.68	1.07	0.63	0.65	0.66	0.67	1.08
79	6	29390330	9393954	11676	CACTTCATGCWCCTTAAATTG	0.86	0.44	0.40	0.50	0.81	0.62	0.94	0.32	0.52	0.80	0.59	0.94

79	6	29400009	16894722	11677	AAGCAATATARTATTTTACAA	0.47	0.93	1.12	0.85	0.89	0.85	0.74	1.02	0.98	0.91	0.90	0.75
79	6	29405645	9357078	11678	ATATCAATACYTCAAGTAAAC	1.03	0.92	0.92	1.24	1.17	1.56	0.69	0.82	1.34	1.13	1.51	0.74
80	6	29761165	2747442	11679	GCATTATACTRTCTCTGTAAG	1.18	0.74	0.74	2.44	3.37	2.13	2.49	0.69	2.65	2.73	1.98	2.27
80	6	29782267		11680	CATGAGATACYGGTTATAATT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29785814	1610591	11681	GTTGCCCACCRGAAGTTGCAG	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29791923	2517912	11682	TTACTGACATYATGCTAAGCT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29801478	2235383	11683	TCATTTGTAARGCTCCTGTGA	0.31	0.33	0.33	0.17	1.69	1.74	1.19	0.29	0.15	1.55	1.60	1.14
80	6	29815286	9258215	11684	TACCTTAGATRCAGAAAACTA	0.79	0.41	0.45	0.17	0.09	1.21	1.15	0.42	0.18	0.09	1.16	1.13
80	6	29820738	2844845	11685	ATTTCAGATAWCACCATAGCT	1.52	0.50	0.46	0.39	0.09	0.64	1.06	0.40	0.39	0.08	0.66	1.03
80	6	29831140	9258260	11686	TTTCCAATGGYTAAAGGCTTT	0.05	0.18	0.19	0.27	0.91	0.54	0.60	0.15	0.26	0.88	0.57	0.60
80	6	29844026	1737043	11687	GTATCAAGGGYGATCCATGAA	0.14	0.37	0.37	1.18	0.89	0.77	0.67	0.35	1.23	0.88	0.81	0.67
80	6	29871066	1633009	11688	CGGGGAAGTTWAAAAAAGCAG	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29878402	16895826	11689	TGACATTAAGRGCCTCTGGCT	1.10	1.64	1.70	0.91	1.02	1.07	1.19	1.61	0.91	1.02	1.05	1.16
80	6	29890612	1736957	11690	TCTGAGATAGYGATCATCCAG	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29912155	16896052	11691	TGCTCATTGCRTCTTACAAAT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29919729	4084097	11692	CACAACACTTYGAGAACATGG	0.08	0.08	0.08	1.26	0.91	1.04	1.44	0.04	1.24	0.93	1.07	1.39
80	6	29931170	16896139	11693	GGAGACATGAMAATACTGAGC	0.13	0.04	0.08	0.43	0.82	1.11	1.06	0.04	0.41	0.82	1.09	1.04
80	6	29937615	1611719	11694	ATCTACACATKTTGGGGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29979900	2571419	11695	CTCCTAGGCAYTTATTTCAAA	-	-	-	-	-	-	-	-	-	-	-	-
80	6	29985348		11696	TAGGTCTGGGMACTTTGCATC	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30030719	16896742	11697	TCAACAGCTARGCATATGACA	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30044383	6927487	11698	GTGGCAACCAYTCAACTCTCC	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30050836	16896826	11699	TGTCCTTAGAYCATTGGAGTC	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30056791	2844802	11700	TGTCCTTTGCWATGTAGACTC	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30059708	2735066	11701	TGAGAAATCTRTAATTCTACA	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30069984	16897374	11702	TAAGGCCTGGRTGCCCTGCTG	0.77	0.72	0.77	0.59	1.08	0.80	0.77	0.74	0.62	1.04	0.84	0.77
80	6	30084003	16896030	11703	CAGAACCCAGSACCTCGTTAT	1.47	0.57	0.55	1.16	1.08	1.02	1.78	0.50	1.36	1.05	1.01	1.72
80	6	30092231	9357092	11704	AGCTCTCATCRAGTTTTTTTA	1.16	1.61	1.65	0.77	1.02	3.19	3.19	1.60	0.83	1.02	2.71	2.67
80	6	30108666	16896923	11705	AAGGATTTGGYAGAATTGGAG	0.08	0.08	0.08	1.02	2.66	3.19	2.71	0.05	1.05	2.38	2.74	2.37
80	6	30119913	259940	11706	TTCAGATCACRCTTTTAGTAG	0.65	1.13	1.16	2.06	2.95	2.26	2.60	1.09	2.28	2.72	2.04	2.30
80	6	30134269	10484549	11707	TCTGAGACGAYTGTAGGTTCT	0.07	0.09	0.18	2.06	2.22	2.89	1.81	0.10	2.29	2.03	2.59	1.71
80	6	30140896	16896970	11708	GACATTTAACRGAAATTTTAA	0.08	0.08	0.08	1.78	3.09	2.38	1.94	0.03	1.88	2.85	2.19	1.86
80	6	30156284	9261317	11709	AATGTCACTAWTATTTCTATC	0.74	0.29	0.29	1.73	3.56	1.79	1.15	0.22	1.89	3.04	1.65	1.12
80	6	30163622	6909253	11710	TCCAAACAAGKTATTTATTAA	2.98	3.18	3.17	1.75	1.22	2.05	1.44	3.06	1.88	1.19	1.88	1.39
80	6	30173298	1264704	11711	GATGTAAACARTGTGGTGAGT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30185208	2523990	11712	ATCTCAGCTTRTTTTAAGCAC	0.05	0.17	0.17	1.73	1.40	0.90	1.90	0.14	1.75	1.35	0.91	1.79
80	6	30194401	9261431	11713	ACGGTGACTASAAAGAATATT	1.76	2.35	2.27	1.22	1.30	1.20	0.61	2.24	1.33	1.27	1.18	0.61
80	6	30200686	1419675	11714	AACAGCCATTKTATACAGGCT	0.08	0.25	0.25	1.16	0.93	0.93	1.28	0.21	1.23	0.96	0.93	1.25
80	6	30208019	9261456	11715	TTACTGAGCAYCTAATATATT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30217810	9261490	11716	ATGGTGGACCYTATGTGTACT	1.28	1.42	1.52	0.84	1.20	1.18	1.06	1.44	0.93	1.20	1.16	1.04
80	6	30226107	9261525	11717	AAAGCCACGGYACCTTTGTAG	1.28	1.38	1.38	0.82	0.76	0.93	0.79	1.34	0.91	0.71	0.93	0.79
80	6	30230554	2517646	11718	CGCAAGTTGGYTGGTTTCCAA	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30263110	6457165	11719	GAGGGCATTCRGGCATTCGGC	0.07	0.04	0.04	0.99	0.40	0.41	1.30	0.03	1.00	0.43	0.41	1.25
80	6	30276298	2523719	11720	CGTCTAGATGKCAGGAATCCT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30286266	3132671	11721	GCTTTGCATAYACTGTATTTC	0.15	0.08	0.08	0.04	0.58	0.50	0.43	0.06	0.03	0.58	0.50	0.45
80	6	30304657	3130395	11722	CTCTTTTGCCRTATAACATAA	0.18	0.04	0.06	0.00	0.03	0.31	0.27	0.03	0.00	0.02	0.32	0.29
80	6	30310694	885915	11723	CTATTTGGAGYCATAACAGCA	0.07	0.02	0.02	0.11	0.14	0.10	0.24	0.00	0.12	0.15	0.11	0.24
80	6	30317781	1362089	11724	GCATTTACTGKAGACAACATT	0.07	0.02	0.00	0.29	0.13	0.38	0.24	0.00	0.26	0.13	0.43	0.27
80	6	30319882	2523741	11725	TGTCTATCATSTTACTGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30338064	2523746	11726	GCAATTGTGCYCAGTACTCTG	0.66	0.66	0.66	0.32	0.64	0.33	1.03	0.61	0.33	0.66	0.35	1.05
80	6	30367335	1264620	11727	AATGTGAGACRGTTGTATGAT	1.04	1.18	1.18	0.68	0.41	0.86	0.80	1.09	0.80	0.42	0.80	0.82
80	6	30379313	261946	11728	GGTCTGTTTCRGATGGATCTA	0.74	1.08	1.08	1.10	1.28	0.64	0.42	1.05	1.23	1.22	0.67	0.44
80	6	30390311	3094065	11729	CCTTCAATGGYAAGCATAGTA	0.40	0.63	0.65	1.50	1.61	0.51	0.34	0.60	1.66	1.47	0.55	0.34
80	6	30417912		11730	ACCTTCACTGMTACTTTTACT	-	-	-	-	-	-	-	-	-	-	-	-
80	6	30429340	984802	11731	GCAATATTTTKTTTCACTCTC	0.44	0.82	0.82	0.42	0.82	1.13	0.26	0.76	0.41	0.80	1.17	0.28
81	6	35927885	9470138	11732	AACTATAACTYCATCATTCCT	0.73	1.07	1.09	0.62	1.13	0.88	0.76	1.02	0.69	1.10	0.90	0.76
81	6	35936240	17654270	11733	TAAAGGCACCRGAGCCTGAAA	0.61	0.95	0.95	0.61	0.18	0.65	0.62	0.89	0.59	0.16	0.67	0.64
81	6	35948069	3761981	11734	AAATCATCAAMTCATAAGAAA	0.73	1.17	1.23	0.14	0.21	0.08	0.42	1.16	0.08	0.19	0.09	0.45
81	6	35960422	9462143	11735	AGGGAATCAAYGGACAGAAGC	0.61	0.95	0.95	0.51	0.03	0.09	0.11	0.93	0.58	0.03	0.09	0.10
81	6	35966231	2301510	11736	CAGGCAACCTRATGACACCAT	0.61	0.95	0.95	0.33	0.18	0.17	0.15	0.88	0.29	0.18	0.16	0.13
81	6	35969423	7755600	11737	CTACCCCAGASTAAACTTTTC	0.61	0.95	0.95	0.33	0.44	0.36	0.07	0.92	0.27	0.41	0.36	0.08
81	6	35992327	1160828	11738	AATTTTCAATRTATCTCCCAA	0.58	0.90	0.95	0.87	0.36	0.18	0.21	0.94	0.88	0.36	0.19	0.21
81	6	36005903	611735	11739	GGTACTATAAKAAATTCTACA	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36010371	683423	11740	TTTGCTCTTCRGAGAAATCTA	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36018851		11741	AAATTGCCTAYATCTTAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36031224	2295852	11742	ATCAGGTTAAYGGAGGATGCT	0.06	0.06	0.06	0.64	0.35	0.20	0.34	0.04	0.67	0.34	0.23	0.34
81	6	36038104		11743	ATGAGGTCTTYGTGTTTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36049077	10484265	11744	TTCTGAACATRGCCCAAATTT	0.47	0.56	0.56	0.09	0.27	0.42	0.65	0.50	0.06	0.25	0.47	0.69
81	6	36058053	9470186	11745	CCTCTGGCAGSACAGAAAATG	0.20	0.28	0.25	0.34	0.30	0.76	0.76	0.20	0.35	0.30	0.75	0.74
81	6	36070956	969659	11746	CCTTCCATCTYGTAAATGGCA	0.06	0.22	0.22	0.22	0.67	0.69	0.95	0.16	0.20	0.68	0.69	0.94
81	6	36080744	851044	11747	GAAAAGCAGCRTGTAGCATGA	0.16	0.30	0.30	1.16	0.97	0.64	0.64	0.27	1.25	1.00	0.63	0.65
81	6	36090347		11748	TTAAAAAAACWCACTTATGGC	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36099800	9380542	11749	GACACATCAAYGGCATTTGAC	0.85	1.16	1.13	1.49	1.36	0.92	0.70	1.08	1.64	1.29	0.87	0.75
81	6	36113139		11750	GGTTTTGGGCRTGCTTGGCTC	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36122139	851019	11751	GTTGTTCATGRAAACAAGGTT	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36127205	664367	11752	CATTTTTGCTRTAGATGTCCT	0.36	0.68	0.68	1.11	0.95	0.96	2.21	0.65	1.26	0.94	0.96	2.03
81	6	36172014	851007	11753	GCATGCACAARTGTGTTTTAT	0.19	0.46	0.46	0.40	1.39	2.60	2.42	0.45	0.39	1.34	2.37	2.27
81	6	36177950	851004	11754	TCCAAGACTTKCTTTGGGAAT	0.72	1.19	1.19	0.67	4.01	2.40	1.94	1.09	0.72	3.44	2.19	1.87
81	6	36183888	12530381	11755	GAGCACCTCCRTAGAGAGCTT	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36193303	7757672	11756	ATCATTGGTGRCACTGATTAC	2.49	1.12	1.12	3.29	3.28	2.66	3.19	1.04	3.32	2.86	2.47	2.91
81	6	36209540	2007683	11757	GGTAAGATAGYATTGATTCAG	0.88	1.29	1.29	3.10	2.07	3.22	3.03	1.21	3.35	1.95	2.94	2.74
81	6	36215150	2071863	11758	GCATGGCACCRCCGGCCAGAC	0.07	0.02	0.02	0.47	3.60	3.11	2.77	0.00	0.49	3.16	2.78	2.50
81	6	36234628	2213661	11759	CTAGTCTCATRGTTGCGTTCT	1.00	1.50	1.44	0.57	0.30	3.00	1.87	1.40	0.65	0.31	2.60	1.78
81	6	36260489	6457884	11760	ATTCGCAAATRTATAATTCTA	1.72	0.14	0.22	0.73	0.52	0.15	1.54	0.16	0.78	0.56	0.16	1.53
81	6	36286814	17715809	11761	CTGCAGACGTYTCCCAGATTC	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36296558	6457894	11762	ACCTAACTACWGGTTACTGAA	0.21	0.16	0.16	0.64	0.46	0.20	0.58	0.12	0.67	0.49	0.19	0.61
81	6	36304140	7747793	11763	TGTGGAGCTTRTTGCCTCAAG	0.33	0.09	0.09	0.24	0.09	1.09	0.27	0.07	0.19	0.09	1.06	0.26
81	6	36315576	9380559	11764	AACAAAGGATRTGTGAGCAGG	0.02	0.04	0.04	0.09	0.64	0.12	0.62	0.02	0.08	0.61	0.11	0.61
81	6	36325138	4713940	11765	GTTCTAATTTRCCAAACCTTA	0.12	0.00	0.00	0.63	0.15	0.20	1.18	0.00	0.66	0.15	0.20	1.18
81	6	36354548	1547421	11766	ATGAAATAGAWCATTCATTCG	3.35	2.47	2.49	0.67	0.11	0.79	0.76	2.36	0.65	0.10	0.79	0.75
81	6	36366913	9394342	11767	TTCCGTCATGKGCAAGACAGC	1.29	1.16	1.16	0.83	1.65	0.56	0.75	1.09	0.84	1.56	0.56	0.79
81	6	36382131	12197079	11768	CCTTATGTAAYGTAAGTTTCC	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36384727	9470251	11769	GGAACAGACCYGCACTGCTAT	0.14	0.16	0.16	0.56	1.21	0.58	0.87	0.13	0.55	1.15	0.60	0.86
81	6	36398008	12190546	11770	CCTGTGAACTSCATGTGGAAG	0.39	0.56	0.52	0.24	0.37	0.85	1.63	0.48	0.26	0.38	0.85	1.59

81	6	36415022	1034436	11771	ACATCTCCCAYGTACCCAGCA	1.13	0.48	0.48	0.24	0.13	0.36	1.15	0.41	0.25	0.13	0.34	1.13
81	6	36423220	16888069	11772	AAAATGTTCCYTTTGTGGCCC	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36444592	763017	11773	CCCATCAGCTRAGGATTGTCC	-	-	-	-	-	-	-	-	-	-	-	-
81	6	36450159	6457907	11774	CCAGAAATCTYCTTTGACTCA	0.61	1.00	0.89	0.16	0.15	0.13	0.40	0.85	0.16	0.14	0.14	0.41
81	6	36458583	881648	11775	CTCATTTCCTYTGCATCCAAA	0.53	0.03	0.06	0.35	0.04	0.09	0.16	0.03	0.34	0.03	0.10	0.15
81	6	36482075	2894406	11776	AACAGGGTCASTCAGGTTCCT	2.14	0.30	0.30	0.05	0.35	0.11	0.17	0.27	0.03	0.33	0.13	0.20
81	6	36498412	17358499	11777	CGAATTAAAAMAGAAAATGTA	2.04	0.33	0.33	0.24	0.11	0.29	0.10	0.29	0.20	0.11	0.30	0.13
81	6	36503646	566742	11778	GTGACTCATCRTTTTTCAAAT	0.46	0.03	0.02	0.25	0.05	0.08	0.28	0.00	0.24	0.04	0.08	0.31
81	6	36523881	10484615	11779	AATTTTGGAARGCATTGGAAT	0.00	0.02	0.05	0.03	0.13	0.05	0.04	0.02	0.00	0.14	0.04	0.02
82	6	52558406	7746685	11780	CCTTGTCCAAYGGCCGCTAGT	0.13	0.02	0.00	0.08	0.08	0.20	0.54	0.00	0.08	0.08	0.18	0.57
82	6	52566831	17665563	11781	ACCACTAAATYCTCATGACAA	0.10	0.15	0.15	0.20	0.46	0.48	0.07	0.14	0.22	0.48	0.50	0.07
82	6	52573007	10948704	11782	GTCATGCTGAYCGCTTGCTGG	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52586323	2063643	11783	CTCATTCATCRGGCAACTTTC	0.20	0.46	0.53	0.14	1.19	0.20	0.18	0.46	0.13	1.17	0.20	0.16
82	6	52595892		11784	ATGAGGATTTKTACATGCATT	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52617924	13205411	11785	CAGTGACTTCMTAAGTTCTAG	0.27	0.02	0.00	0.12	0.06	0.77	0.77	0.00	0.10	0.06	0.80	0.78
82	6	52620817	7769642	11786	CAGCTGCCACRCTTGCCCACA	0.27	0.57	0.57	0.06	0.28	0.33	1.07	0.54	0.05	0.28	0.37	1.07
82	6	52634448	9296688	11787	AGCCCTAAGCRGCATCATTTG	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52642773	6928478	11788	TCTAGAGCTAYTTCACTATGA	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52649770	13211066	11789	CCATATAAGCRTATCATTTTT	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52656332		11790	GAAACCTTTTYGGCGAGGTAG	0.62	0.13	0.13	0.24	0.49	0.48	1.15	0.08	0.22	0.47	0.47	1.15
82	6	52664730	11969858	11791	TTAAGTTACAYGCTGATTACA	0.10	0.21	0.21	0.36	1.02	1.11	0.54	0.18	0.33	1.04	1.12	0.55
82	6	52672053	7762828	11792	GTATTCTATCYGTTTTACAAT	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52676301	2207953	11793	ATGAGCTTAGYATCAGCAAAC	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52696797	2144690	11794	CAATTATTTCRAAATTCATCT	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52708575	6921519	11795	GCATCCTTGGKTGCTTTCCTA	0.76	1.19	1.19	0.50	0.60	0.71	1.82	1.11	0.48	0.62	0.72	1.75
82	6	52712013	2180312	11796	CCAAATAGTCRTATGAAAATT	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52734228	17606095	11797	TATTTTGTCCRTAGAACTCTA	0.47	0.38	0.37	0.81	0.24	1.02	1.28	0.36	0.82	0.25	1.00	1.24
82	6	52758481	2608668	11798	GACTAAGAAARGAGGAATTTG	1.16	1.11	1.11	0.45	1.92	1.17	0.77	1.07	0.48	1.80	1.16	0.74
82	6	52788741	17816563	11799	TAATCCACTGYCTTCCACCTC	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52825653	17289238	11800	TATCCTGAGGSTGCTGAAGCT	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52852700	13198332	11801	TCTTCAAACCRAAAGCAGAAT	0.70	1.08	1.08	2.07	1.19	1.25	0.93	1.05	2.07	1.12	1.21	0.93
82	6	52859552	641019	11802	GAACCGAAAGWGCTATCATTT	2.54	3.30	3.30	2.13	1.13	0.88	1.10	3.19	2.23	1.13	0.89	1.07
82	6	52866612	4712023	11803	CTGTCATGCTYGTGGTTCAAC	1.43	2.00	1.83	2.56	2.04	1.05	0.34	1.73	2.73	1.89	1.05	0.31
82	6	52875284	16883105	11804	ATGAATCCCASTATTTCAGGA	1.21	1.39	1.39	1.61	3.14	0.82	1.67	1.26	2.01	2.64	0.79	1.65
82	6	52886964	9382157	11805	ACTCTGATCCRTTTTCCCCTG	1.53	2.15	2.15	1.31	1.00	1.44	1.07	2.08	1.53	0.99	1.37	1.07
82	6	52905380	9367508	11806	CCGTGGATAGYTACTGTCTCA	1.45	2.06	2.06	1.07	1.07	0.71	0.87	1.90	1.12	1.07	0.72	0.87
82	6	52911542	9349653	11807	ATGGTTATGCYGTGTAGTGGC	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52918852	4712026	11808	TATAGTATAARCACTTGATGG	0.53	0.04	0.03	1.19	0.90	0.33	0.32	0.00	1.24	0.90	0.34	0.32
82	6	52928947		11809	AAAGTCACCAYCATGACCTAC	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52938820	560788	11810	GGGTCCCTAAYGTAACACTGA	0.36	0.20	0.17	0.09	0.52	0.60	0.13	0.15	0.09	0.53	0.62	0.12
82	6	52945049	400804	11811	AAACTCACAASAGATTGACTT	0.34	0.02	0.02	0.06	0.04	0.32	0.17	0.00	0.03	0.04	0.34	0.16
82	6	52951090	367836	11812	AGATGATCTCKTTGACACAAA	-	-	-	-	-	-	-	-	-	-	-	-
82	6	52957105	316128	11813	TTAGCGCTTAKGTTAGTTCAA	0.27	0.02	0.02	0.04	0.01	0.01	0.15	0.00	0.01	0.00	0.01	0.16
82	6	52969817	182623	11814	TGGTAAAGCAWTTGCTAATCA	0.05	0.04	0.04	0.02	0.02	0.01	0.02	0.01	0.01	0.00	0.01	0.02
82	6	52973861	2397135	11815	TGAACTTTAAMAAAACCTCCA	0.11	0.02	0.02	0.06	0.01	0.13	0.06	0.00	0.02	0.00	0.14	0.06
82	6	52987654	316144	11816	CCATTTCTTAYATGCATCTGT	0.22	0.19	0.19	0.10	0.22	0.15	0.34	0.17	0.06	0.21	0.15	0.33
82	6	52993732	6458895	11817	CTTGCAGTTAYGTTGGATCCA	0.10	0.14	0.14	0.41	0.96	0.80	0.23	0.10	0.40	0.92	0.78	0.24
83	6	57753535	9396406	11818	AGCTCTTCTCYGATTGGCTGG	0.46	0.10	0.10	0.27	0.13	0.39	0.22	0.09	0.23	0.13	0.39	0.24
83	6	57762970	17759019	11819	TGCCTCATTTSACAAATAGTA	0.44	0.40	0.37	0.36	0.67	0.48	0.14	0.32	0.35	0.69	0.50	0.14
83	6	57774347	17759062	11820	TATCTACATTYTTGTCTTGAT	0.31	0.64	0.58	0.43	0.62	0.26	0.12	0.49	0.42	0.65	0.30	0.12
83	6	57781356	7765475	11821	TGCCTTTAAARTTAAGCATCT	0.83	1.16	1.16	0.83	0.35	0.29	0.20	1.09	0.96	0.38	0.29	0.21
83	6	57818197	7758052	11822	TGGATGATGAYGTGTTATTTG	0.06	0.06	0.06	0.99	0.38	0.20	0.23	0.05	1.10	0.43	0.23	0.26
83	6	57828508	6927871	11823	CCCATTACACMTGAAAAATAA	0.17	0.05	0.04	0.05	0.33	0.18	0.08	0.02	0.04	0.35	0.20	0.09
83	6	57936849	6900431	11824	CTTATTGGACSTTCTCTTTTC	0.45	0.15	0.17	0.08	0.20	0.17	0.10	0.14	0.05	0.20	0.16	0.10
83	6	58075927	7760891	11825	GAGTGTACACYCCGTGTGTGG	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58105609	10807572	11826	GGTGTACATCSCCTGCGATAT	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58455280	7770369	11827	ATCTTTAAAASTTTTATGAAG	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58476590	1539604	11828	CAGGTAAAGTRTTTTATATGT	0.06	0.21	0.21	0.65	0.15	0.11	0.17	0.20	0.70	0.13	0.12	0.18
83	6	58508761	1675660	11829	TTGCTAATCCYCAAAAAACGA	1.51	2.01	1.88	0.67	0.18	0.09	0.08	1.84	0.76	0.18	0.09	0.09
83	6	58509641	1777974	11830	TGCTTTCTCCYCAGACAGTCA	1.35	1.88	1.88	0.56	0.25	0.12	0.14	1.83	0.57	0.28	0.13	0.14
83	6	58530793	1381244	11831	GGACAAAAAAWTTGAACAGAT	1.43	1.94	1.94	0.78	0.29	0.32	0.29	1.86	0.76	0.31	0.33	0.32
83	6	58579302	9377807	11832	GGAAGCTCCGYGTAAAACAAA	0.23	0.48	0.40	0.87	0.99	0.99	1.10	0.34	1.02	1.01	0.99	1.13
83	6	58632568	9500123	11833	CATGAAATAGYGTTGCTCAAC	0.99	1.52	1.50	1.43	2.21	2.62	1.28	1.45	1.82	1.97	2.35	1.28
83	6	58654850		11834	ATGTTGTCAGKAATAATGTTT	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58689965	7381940	11835	GCATATTATAWACAATATTAC	0.10	0.23	0.17	2.01	4.05	2.15	1.92	0.12	2.27	3.22	1.93	1.75
83	6	58704047	2063945	11836	ACATTGTTTGYTGTCTTCCAG	1.86	2.49	2.49	3.03	2.43	2.46	1.37	2.43	3.40	2.21	2.09	1.34
83	6	58710081	2693076	11837	AAACTTATACRGTGGCATAGA	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58724802	1517229	11838	CTTGCTATCCMAAGAAAACAA	2.05	2.71	2.71	2.10	2.97	1.56	1.25	2.62	2.72	2.45	1.49	1.21
83	6	58735767	7744380	11839	ATTCCAAGACKAAACTTCTAG	0.08	0.25	0.25	1.75	1.78	1.42	1.04	0.22	2.04	1.64	1.33	1.03
83	6	58777615	2807299	11840	GACAGTGCTARATCCAATTTA	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58784554	17092102	11841	ATCAATTATAYGTGAATATAT	-	-	-	-	-	-	-	-	-	-	-	-
83	6	58819500	4928472	11842	ATTCAGGATARTTTCTCCATC	0.46	0.72	0.74	0.99	1.31	1.24	0.86	0.68	1.19	1.29	1.19	0.91
83	6	58835224	9391305	11843	CACCAGTAATMACCAGTATAC	1.09	1.55	1.48	1.18	0.62	0.79	0.99	1.41	1.27	0.62	0.79	1.00
83	6	58887977		11844	CTGAGTGATGYGTGCGTTCAA	-	-	-	-	-	-	-	-	-	-	-	-
83	6	61940508	11238107	11845	GTTTACAAACYGTTGAAACAA	0.71	1.01	1.01	0.63	0.59	0.45	1.17	0.93	0.60	0.61	0.48	1.10
83	6	62028453	2249973	11846	AAAACACAAAKGTAATTAGCT	0.21	0.30	0.30	0.61	0.35	0.67	0.62	0.25	0.63	0.37	0.70	0.60
83	6	62042047	17151524	11847	CTGTGAATGCYAAAATTATTT	0.05	0.12	0.12	0.10	0.62	0.19	0.68	0.10	0.11	0.63	0.20	0.67
83	6	62051690	2223759	11848	GAGAAACATCRACACTTGGCA	0.25	0.08	0.08	0.04	0.02	0.34	0.32	0.07	0.05	0.00	0.36	0.33
83	6	62069856	1336309	11849	TGTTCAGGGCRTAGATTAAGT	0.22	0.31	0.29	0.10	0.03	0.33	0.33	0.25	0.06	0.01	0.38	0.38
83	6	62078433	17151452	11850	CATTCCATCTSTGTCATAAGT	0.18	0.21	0.23	0.13	0.61	0.33	0.24	0.21	0.05	0.66	0.38	0.25
83	6	62095902	9378066	11851	CCATGTCTTAYATGGCAGCAG	-	-	-	-	-	-	-	-	-	-	-	-
83	6	62105542	7747700	11852	ATTTTCTTTGYTCCTTCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
83	6	62137338	3890682	11853	CATAAGTTGAYTCTGACAAAA	0.05	0.13	0.15	0.32	0.35	0.45	0.24	0.12	0.32	0.40	0.49	0.29
83	6	62156290		11854	AGATAAAACAMATAGACCATC	-	-	-	-	-	-	-	-	-	-	-	-
83	6	62239871	2223798	11855	AAAAGCTTTCKGAGAAGCTGC	-	-	-	-	-	-	-	-	-	-	-	-
83	6	62243303	10806580	11856	AAAGTAGAAASAAGCCCTCTG	0.75	0.94	0.88	0.46	0.33	0.24	0.25	0.82	0.57	0.38	0.26	0.26
83	6	62265082	7763133	11857	TTCTCCCAACMTGTCCCCATT	0.64	0.94	0.94	0.84	0.48	0.16	0.13	0.89	0.99	0.57	0.19	0.14
84	6	64808644	7757884	11858	TAAAATATTCMTTATCTGGCT	0.02	0.04	0.04	1.29	1.14	1.07	1.22	0.02	1.46	1.11	1.08	1.16
84	6	64866190	6906159	11859	AATAACTTCTRCAAATATAAG	-	-	-	-	-	-	-	-	-	-	-	-
84	6	64889079	3003672	11860	ATCTTTTGCCMCATAACTTAA	-	-	-	-	-	-	-	-	-	-	-	-
84	6	64902553	4710465	11861	AAATGGGAACYCAGTGTCTCA	1.06	1.08	1.11	1.47	1.82	1.74	1.50	1.02	1.62	1.66	1.63	1.39
84	6	64928168	3003677	11862	GAACCACTGGWTTGAATTGCA	-	-	-	-	-	-	-	-	-	-	-	-
84	6	64943595	4310034	11863	AAGTTTGTCAYGCAATCTCGG	-	-	-	-	-	-	-	-	-	-	-	-
84	6	64954923	5002649	11864	AATCTGGTCTRTAGATGAACC	0.89	1.29	1.29	1.02	2.23	2.37	1.38	1.24	1.11	1.98	2.06	1.34

84	6	64965624	6907750	11865	TAGGATTGATKTTTTTTTTG	-	-	-	-	-	-	-	-	-	-	-
84	6	64982995	4710263	11866	AGAGTAATAARTATTTATGAA	-	-	-	-	-	-	-	-	-	-	-
84	6	64993841	4710473	11867	GATTTTCAGAYATGGATATTA	0.79	1.13	1.05	2.17	2.01	1.70	1.35	1.06	2.35	1.85	1.61	1.33
84	6	65000140	6916780	11868	TTATTCCTAAYGATGCTTGAT	0.43	0.73	0.73	1.64	1.38	0.95	1.47	0.74	1.99	1.33	0.90	1.42
84	6	65021232	4365910	11869	CAGATTTAAAYGTAAGTGTTT	0.46	0.71	0.71	0.72	0.83	1.19	0.83	0.66	0.81	0.85	1.11	0.84
84	6	65035099		11870	CTGAGAGGCTSGAATGGGACT	-	-	-	-	-	-	-	-	-	-	-	-
84	6	65041175	10806409	11871	TTCTGATCGAMTTCTTTATTT	-	-	-	-	-	-	-	-	-	-	-	-
84	6	65047402	1922954	11872	CAGGGACATGSCTCTCAGCTT	0.84	1.11	1.11	0.43	0.73	0.75	0.61	1.10	0.43	0.73	0.75	0.66
84	6	65054185	1922955	11873	TTCCTCTAACSAATAGGCAGT	0.85	1.16	1.16	0.91	0.65	0.33	0.59	1.08	0.91	0.65	0.35	0.63
84	6	65060287	1884179	11874	AGAAAATAAAYTGAGTTGCTA	0.76	1.08	1.06	0.92	0.40	0.53	0.31	1.03	1.00	0.41	0.58	0.33
84	6	65073171	7768495	11875	AAGTGATATASAGATTTGGTG	-	-	-	-	-	-	-	-	-	-	-	-
84	6	65098673	9451353	11876	AAAACCCCTAYATAACCTTAG	0.79	1.09	1.10	1.16	0.65	0.37	0.56	1.06	1.21	0.66	0.38	0.60
84	6	65116431		11877	AATCCACAACWCTAACTGAGC	-	-	-	-	-	-	-	-	-	-	-	-
84	6	65125419	10806431	11878	CATAAAGGGAYGTGTGTGAAC	0.95	1.25	1.23	0.45	1.09	0.68	0.24	1.18	0.46	1.10	0.71	0.24
84	6	65132087	673676	11879	TTGGCCATGGYTGACTTTGGT	0.85	1.05	1.05	0.57	0.50	0.66	0.40	0.99	0.72	0.54	0.71	0.43
84	6	65141929	9353739	11880	CATTGCCTACSTGGCTACTAG	0.88	1.19	1.16	0.79	0.31	0.24	0.68	1.11	0.92	0.35	0.27	0.69
84	6	65151885	6454819	11881	TTCATTTGTTYTTCAGGAATC	-	-	-	-	-	-	-	-	-	-	-	-
84	6	65155962	617121	11882	CTTAATTAGGRAGATCAGAGT	0.64	0.93	1.01	0.50	0.42	0.31	0.25	0.97	0.53	0.43	0.37	0.26
84	6	65177721	4286758	11883	TGAATCTTCCKTAAAGGGATG	0.70	1.03	1.01	0.37	0.66	0.58	0.23	0.94	0.32	0.66	0.61	0.26
84	6	65183756	1556861	11884	ATACATTACARTGAAAAGCTA	-	-	-	-	-	-	-	-	-	-	-	-
84	6	65190065	1416351	11885	TTCTAATTACKGACAGACATG	0.67	1.01	1.01	0.95	0.50	0.46	0.56	0.94	1.25	0.49	0.49	0.58
84	6	65203365	9351255	11886	TTGTAGAATTRCTGTTAATGG	0.74	1.14	1.06	0.82	0.69	0.48	0.64	1.02	1.00	0.71	0.48	0.68
84	6	65206215	4710478	11887	TTCAACACTGYTTTTACTTAG	0.50	0.86	0.86	0.82	0.57	0.41	0.21	0.80	0.92	0.60	0.46	0.23
85	6	78293015	10943465	11888	CACTTAAATGYCACAATATTC	0.36	0.58	0.69	1.34	0.85	0.89	0.77	0.63	1.52	0.86	0.85	0.75
85	6	78303068	17275722	11889	AAAACTATTGWTTCCTCAAAT	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78313564	1343493	11890	AATGAAGATAYGGCTTTTTGT	0.58	0.86	0.94	0.71	1.56	1.18	0.71	0.90	0.75	1.46	1.16	0.74
85	6	78328677	16889195	11891	GCTTGTAAAAMAGAAGCCTGA	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78359867	1824284	11892	TTCTTCTTCCWTGAGAAGTGC	1.33	1.89	1.89	0.95	1.02	1.18	0.82	1.84	1.01	1.06	1.14	0.80
85	6	78384797	12527916	11893	AGGATCCACCRTGTAAGCTAG	1.14	1.25	1.25	1.20	1.00	0.94	1.43	1.17	1.20	0.95	0.95	1.41
85	6	78391604	2320723	11894	GAAAACTTACKATTGTCATGA	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78397502	13205165	11895	CTTAGACCCARTCAGAATGGC	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78408635	898040	11896	TACGATCTAGRCTAGGCACTT	1.21	1.62	1.62	1.68	1.14	1.21	0.85	1.53	1.73	1.13	1.17	0.88
85	6	78414494	2504280	11897	TAAAGTAACCRTCTTAGAATT	0.83	1.31	1.31	0.95	1.41	0.75	0.70	1.22	0.94	1.38	0.73	0.71
85	6	78423561	2504278	11898	TTCAAAAATAWGGCTACTGCA	0.27	0.52	0.52	2.02	1.63	0.75	1.00	0.48	2.16	1.53	0.69	0.98
85	6	78438052	12525585	11899	TGCATTTTCTRTTTATTAACT	1.37	1.88	1.86	2.14	1.57	1.75	1.82	1.74	2.37	1.48	1.66	1.77
85	6	78440266	9341679	11900	TCAGGTTCTGRTAAGAATTGT	1.21	1.71	1.71	1.16	2.47	3.65	1.75	1.64	1.25	2.20	3.22	1.71
85	6	78460072	3846759	11901	TACCTTAAACYTCAAAAATGA	0.30	0.58	0.58	1.82	2.47	1.87	2.62	0.53	1.87	2.25	1.73	2.39
85	6	78468500	9352515	11902	TATAAGCATGKATTCAGGAAA	0.41	0.73	0.73	1.83	2.43	2.19	1.06	0.68	2.10	2.14	2.01	1.03
85	6	78476645	17840250	11903	CTGGATTCCGRCAGGCCTGTA	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78482591	16889353	11904	TTACAGTCAARGGCAGAAAAC	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78496859	1905263	11905	TGTTAGGAAAYGGAATTAGGA	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78504391	1398579	11906	TAGTAGCAAGSAAGGAAAGCT	0.79	1.23	1.23	1.90	2.15	1.40	1.10	1.19	2.06	1.91	1.33	1.08
85	6	78528910	1483052	11907	ATCCTCTTTAWTTGACTACCA	0.71	1.07	1.14	1.58	1.44	0.94	1.14	1.08	1.82	1.34	0.96	1.09
85	6	78533413	7748475	11908	TTTTATGTTCRTGGCTATTAA	-	-	-	-	-	-	-	-	-	-	-	-
85	6	78542673	1483056	11909	AGTGGTAACARTCACAGATTC	1.77	2.36	2.36	1.41	0.74	0.70	0.52	2.30	1.66	0.75	0.74	0.49
85	6	78551483	17777705	11910	GAAATTTCCCYGTCAGCTAAT	0.15	0.39	0.39	0.86	0.88	0.77	0.50	0.35	1.03	0.94	0.78	0.47
86	6	89256799	6454699	11911	CTGGGAGCCARCAGTTCTCTG	0.02	0.04	0.09	0.67	0.72	1.04	0.63	0.07	0.68	0.73	1.00	0.62
86	6	89266527		11912	ATTCACAGCCSTGGACTCCTC	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89272868	1325010	11913	TGCCCTTGGTRTGAGGAAAGC	0.30	0.06	0.06	0.67	0.63	0.23	0.27	0.02	0.83	0.64	0.25	0.27
86	6	89278512	7769477	11914	CAGTGAGTTTYTATCTTTAAA	0.33	0.00	0.00	0.15	0.24	0.10	0.05	0.00	0.03	0.27	0.11	0.06
86	6	89286040	6918939	11915	TGGTCCTTATYGAGAGAAGGG	0.65	0.14	0.14	0.02	0.00	0.05	0.22	0.11	0.00	0.00	0.05	0.23
86	6	89296136	13208942	11916	AAATGACACTRGGCTTATTCT	0.00	0.00	0.00	0.02	0.02	0.19	0.32	0.00	0.01	0.01	0.21	0.33
86	6	89305047	4555889	11917	GCTCTTCTTTSCTTCAGATCT	0.23	0.31	0.31	0.08	0.21	0.19	0.09	0.29	0.09	0.21	0.20	0.07
86	6	89311046	2610743	11918	GCTAGAACCGYTCATGGATTT	0.56	0.12	0.12	0.23	0.21	0.14	0.15	0.09	0.22	0.25	0.16	0.14
86	6	89317605	4320332	11919	TAGGGCCCTCYGCAGAAATGC	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89323168	2610731	11920	AAAAATGTCTYTTATGGTGAG	0.09	0.25	0.25	0.07	0.14	0.25	0.13	0.22	0.05	0.15	0.27	0.12
86	6	89328725	10498963	11921	GAAATGAGTAYGTTTAGTGAG	0.10	0.02	0.02	0.14	0.69	0.23	0.27	0.00	0.14	0.67	0.22	0.27
86	6	89356479		11922	ATGGGTGCCTKCCTCACCTGC	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89364396	16880938	11923	GTCACTAGACSTAGGTGTTTT	0.10	0.20	0.20	1.04	0.38	0.24	0.21	0.15	1.14	0.40	0.23	0.21
86	6	89373154	17795830	11924	CCTGGAAAATRGCATTCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89380680	2236287	11925	GTTTTAAATAKAATAAGCACT	1.06	1.58	1.58	1.56	0.63	0.30	0.21	1.50	1.54	0.63	0.31	0.23
86	6	89386658	16880966	11926	CATGCCCTTCRGTCAGATACG	0.22	0.31	0.31	1.42	1.48	0.59	0.29	0.24	1.45	1.43	0.63	0.31
86	6	89396253	2756374	11927	AGAAAGTAACYAGCACAATCT	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89407268	911596	11928	TATATATTTAYGTTGTAAGCT	1.57	2.17	2.17	1.67	1.47	1.00	0.65	2.11	1.86	1.38	0.98	0.67
86	6	89414653	2610746	11929	CAGGACCCTTYTGTTATCATC	1.75	2.35	2.27	1.73	1.65	0.83	0.89	2.21	2.05	1.49	0.86	0.83
86	6	89422385	2756385	11930	GAATTAGCATYAAGATTTTTA	1.46	2.05	2.07	1.36	1.03	1.00	0.68	1.97	1.66	0.98	1.00	0.73
86	6	89434716	12173379	11931	ACAGCCACGTKAAACCCACAG	1.58	2.09	2.09	0.89	1.03	0.74	0.58	1.96	1.01	1.01	0.76	0.57
86	6	89440605	2756400	11932	CTTTAGAGAAYGTTTAGATTT	1.45	2.03	2.05	0.88	0.74	0.52	0.29	2.00	1.00	0.76	0.55	0.29
86	6	89448479	3798778	11933	ATTGTTTCCASAAAAGTTTCT	1.58	2.09	2.09	1.04	0.51	0.29	0.26	1.97	1.31	0.51	0.28	0.26
86	6	89458334	2610760	11934	AGATGAATATKTTAAGAGATG	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89466591	9362543	11935	AAAATGGCCARAAAAATCTAT	1.48	1.99	1.99	1.05	0.54	0.25	0.20	1.82	1.29	0.54	0.26	0.20
86	6	89474087	9351170	11936	TGGGTGAATGYCACACACTAT	1.39	1.88	1.88	0.68	0.64	0.36	0.16	1.76	0.75	0.70	0.38	0.20
86	6	89478611	9359807	11937	TAAAACACTTMATTACACACT	1.37	1.87	1.87	0.85	0.41	0.37	0.35	1.76	1.06	0.42	0.37	0.38
86	6	89500929	1406849	11938	TCACTTCAACYGTTAAGGACC	0.73	1.12	1.12	0.89	0.58	0.41	0.26	1.07	1.15	0.61	0.42	0.29
86	6	89517084	17502171	11939	TCACAGTGTGRTCCTGGCCTG	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89526455	6454719	11940	TCACATAAGCRAAAGGTACTA	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89532303	7743595	11941	GTTTAACAGTKATGACAAATT	0.66	1.09	1.09	0.66	1.09	0.44	0.26	1.05	0.69	1.01	0.44	0.27
86	6	89552569	9342160	11942	TCTTACTTCARTTATACAATC	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89561393	3734419	11943	CAGAATGAGAWCAGCTGCTAC	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89569655	9359816	11944	GACACTGAGAYAGAAATTAGA	-	-	-	-	-	-	-	-	-	-	-	-
86	6	89577866	1040676	11945	ATTGGAGGAAYTGACAAAGGT	0.67	0.98	0.98	0.53	0.44	0.64	0.41	0.88	0.65	0.44	0.65	0.41
86	6	89588629	17581788	11946	AGGAAACAAGYAGAGATTTTA	0.78	1.23	1.18	0.53	0.30	0.41	0.41	1.13	0.67	0.31	0.44	0.44
86	6	89592828	13191713	11947	CTTCACTGAASTAATTTCTCA	0.52	0.33	0.30	0.56	0.25	0.10	0.13	0.25	0.64	0.27	0.12	0.13
86	6	89615753	9353625	11948	GAAAAAAATGYCTTTTAATAA	0.61	0.78	0.80	0.16	0.09	0.07	0.04	0.73	0.13	0.11	0.08	0.04
86	6	89623192	1321086	11949	CAAAAAGTAAKGAGCTATTTC	0.75	0.91	0.91	0.18	0.01	0.03	0.02	0.86	0.14	0.01	0.03	0.01
86	6	89643748	4296868	11950	AAATTCTCAGRTATGTTCTTA	0.06	0.06	0.06	0.18	0.06	0.01	0.16	0.04	0.15	0.05	0.01	0.17
86	6	89648577	9359827	11951	TAAACCCAAGRTCCAACTACC	0.69	0.86	0.86	0.41	0.14	0.09	0.44	0.83	0.42	0.14	0.08	0.44
87	6	100883255		11952	TGTGAGGCCTMTGTTCACAGC	0.21	0.16	0.16	0.15	0.01	0.03	0.01	0.14	0.12	0.00	0.02	0.02
87	6	100892159	11753159	11953	CCCATTCTCCRCATGTCTACC	-	-	-	-	-	-	-	-	-	-	-	-
87	6	100900164	2841292	11954	ACCAAGCACAYGACGTCTATG	0.03	0.10	0.10	0.02	0.06	0.02	0.01	0.07	0.03	0.05	0.02	0.01
87	6	100908241	7746743	11955	TAGATGGAGAWTTCTTCATGA	0.49	0.10	0.10	0.40	0.05	0.06	0.01	0.07	0.38	0.06	0.05	0.01
87	6	100917697	9403695	11956	CCTGGAGCCTMCACACACACG	-	-	-	-	-	-	-	-	-	-	-	-
87	6	100927447	9322026	11957	TTTACAGAGARGAGATGGATT	0.02	0.11	0.08	0.12	0.25	0.02	0.05	0.04	0.11	0.26	0.02	0.05
87	6	100934171	9403718	11958	TGACTGAAGAYCAGATGAAAT	0.11	0.00	0.00	0.07	0.04	0.28	0.05	0.00	0.09	0.03	0.28	0.04

87	6	100940996	1395120	11959	AATATCCTACYCTTGAAAGAG	0.26	0.57	0.57	0.07	0.11	0.05	0.32	0.50	0.05	0.11	0.06	0.35
87	6	100950816	3778037	11960	GTACCATCCAYGTGCTTGCCT	0.26	0.41	0.38	0.10	0.06	0.22	0.60	0.34	0.08	0.05	0.22	0.65
87	6	100959474	3798511	11961	ACTATGTGCCYGTGATAACGT	0.44	0.12	0.12	0.19	0.25	0.31	0.32	0.08	0.17	0.26	0.33	0.32
87	6	100966069	4145404	11962	TGTGGCATTTKTCAGACCATC	-	-	-	-	-	-	-	-	-	-	-	-
87	6	100971659	9390366	11963	CACTTCTTCTKTGCTCTCATT	0.13	0.04	0.07	0.06	0.40	0.34	0.35	0.05	0.05	0.43	0.36	0.36
87	6	100979978	9386144	11964	ATGGCCAGAAYACTTTTTAAG	0.06	0.14	0.16	0.41	0.32	0.46	0.33	0.12	0.41	0.36	0.49	0.36
87	6	100990572	3778032	11965	GCCAGTCATGMACTCCCTTAC	0.05	0.17	0.12	0.89	0.47	0.39	0.60	0.08	0.97	0.51	0.41	0.59
87	6	101003010	3830139	11966	TAGACGGAAAKCTCTCAGTCA	0.05	0.14	0.14	0.79	1.13	0.63	0.67	0.14	0.86	1.13	0.69	0.72
87	6	101016119	4839780	11967	GATCAAACAGYGAGCGACATC	0.57	0.93	0.92	1.26	1.47	1.14	1.41	0.89	1.32	1.44	1.15	1.41
87	6	101022997	6942018	11968	TTTTCTAGTTYCAAGTATATT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101028643	9390390	11969	GGTTCCAAAAYCTATTGACCA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101036115	6929748	11970	CCTGTGTTCAYATCGCATGCT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101043486	7766596	11971	GTTAATGAAAYAGAATGCTAA	0.87	1.39	1.28	1.10	1.41	3.26	1.90	1.20	1.11	1.37	2.92	1.80
87	6	101056902	9403816	11972	GATCAGATACRTTGTCCTAAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101064065	240768	11973	AACGTTGAGAYAGATGTCATA	1.14	0.87	0.87	1.01	2.37	2.91	2.35	0.75	1.29	2.16	2.70	2.20
87	6	101070879		11974	ACTCGATGGARGTCCGACCCC	0.74	0.53	0.70	2.58	3.88	1.62	2.04	0.62	2.99	3.15	1.54	1.93
87	6	101081485	7766621	11975	TCTATGAATTYGATAAGGTCA	2.57	2.80	2.80	2.59	2.83	1.96	1.14	2.66	2.87	2.40	1.79	1.14
87	6	101087921	17244650	11976	TGTAGCACTGMAGTTAAGGTT	0.22	0.49	0.49	1.90	1.84	1.65	1.05	0.46	2.17	1.72	1.57	1.01
87	6	101109380	2062635	11977	ACAATCTGGCRTTTACCACAC	0.19	0.45	0.45	0.03	1.41	1.18	1.44	0.44	0.04	1.37	1.14	1.38
87	6	101116922		11978	AATCAAAAGGYATCACTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101130309	1875401	11979	CCGAGTGTACRTTATAAAAAT	0.23	0.52	0.52	0.11	0.03	1.58	1.60	0.46	0.12	0.02	1.53	1.48
87	6	101146000	108422	11980	TCATTGTTTTSCAAGAAATGA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101154918	171257	11981	GAACAAGTGAWTTAAAGCTTC	0.72	0.51	0.50	0.22	0.05	0.02	1.60	0.42	0.20	0.04	0.02	1.51
87	6	101161720	395521	11982	GATGTAGATGYATAACTTTAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101174210	240152	11983	CTCTACCATASATCATCTGTA	0.32	0.59	0.59	0.32	0.07	0.02	0.01	0.57	0.31	0.07	0.02	0.01
87	6	101175215	9322111	11984	TCACTGAACARCAGAATAATT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101194228	4329121	11985	CCTTGAGTTASATGTTCATGG	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101200045	9399638	11986	GGTTAAAACCRTGGTTGGGTA	0.44	0.43	0.43	0.26	0.10	0.04	0.02	0.31	0.18	0.08	0.03	0.01
87	6	101207504	9399641	11987	AAAAAATATAYAAACAGTTGA	0.66	1.11	1.11	0.25	0.09	0.10	0.07	1.07	0.20	0.10	0.11	0.07
87	6	101213810	239227	11988	TGCAACTGTASAGTCTTGCAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101226727	9399652	11989	CCATGGGTCTRGATCAGATTC	0.50	0.84	0.92	0.32	0.21	0.17	0.12	0.91	0.31	0.18	0.18	0.14
87	6	101238680	239194	11990	TAATGATTCARAAAACTGGAA	0.56	0.96	0.96	0.54	0.43	0.22	0.12	0.94	0.57	0.47	0.24	0.14
87	6	101247698	239209	11991	GAATTTAAGAYACATATATAT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101256297	12201852	11992	AAACTATAGCYGGAATTACGA	0.35	0.55	0.55	0.52	0.18	0.11	0.10	0.52	0.49	0.20	0.10	0.09
87	6	101264864	17190683	11993	TGCACACAAAMGATGGAGAGG	0.54	0.93	0.93	0.16	0.13	0.04	0.01	0.90	0.16	0.13	0.03	0.01
87	6	101273530	7748644	11994	CATTCATTTGKTAATTAAAAT	0.43	0.67	0.67	0.12	0.01	0.01	0.05	0.62	0.10	0.01	0.02	0.04
87	6	101281735	13208757	11995	AATTGTTTAAYGACTACTCCA	0.26	0.52	0.52	0.24	0.01	0.01	0.11	0.50	0.23	0.00	0.01	0.12
87	6	101290540	7759463	11996	GTGGCATCTCYATACCCACAT	0.55	0.93	0.93	0.20	0.06	0.10	0.09	0.92	0.16	0.06	0.08	0.09
87	6	101298118	1039033	11997	CTTTTACTCCYTTATCTCCCA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101304674	1336244	11998	TTGACAAAAAYTGCCTGGAAA	0.39	0.59	0.59	0.58	0.46	0.36	0.22	0.55	0.56	0.48	0.37	0.22
87	6	101311694	9390675	11999	GTCCAATTTCRAAATTAAAAT	0.56	0.89	0.88	0.91	0.37	0.69	0.46	0.83	1.02	0.39	0.71	0.44
87	6	101318722	9373590	12000	TTCTTGCATTWGCATCAGTAA	0.30	0.52	0.45	1.01	0.59	0.45	0.61	0.41	1.10	0.57	0.46	0.59
87	6	101331446	9390685	12001	GTTTAAGATAWTCAAACCATA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101343850	9404049	12002	TACATGAGATMTGAAGCTCAG	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101349376	2055162	12003	AAATCAAGTGYTATGTTTGGG	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101356439	9404052	12004	AAAAGTTAACYTGTCTGCAAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101361951	12663536	12005	GTTTAGGACARACAAGGATAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101379522	846803	12006	TTTGCAAGCTYAATGTGAATA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101387229	10485296	12007	AGGTATTCAGYGGTTGGAAGA	0.23	0.45	0.42	0.47	0.67	0.60	0.61	0.40	0.49	0.69	0.59	0.55
87	6	101394881	17672397	12008	GATAGGAGTAYATTCAAAAAG	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101402594	9399696	12009	GAACGTATATRCAGGCCTGCT	0.52	0.50	0.50	0.28	0.20	0.53	0.64	0.40	0.25	0.20	0.56	0.64
87	6	101408981	9404055	12010	GCACCTTTAGYAATACCTTGC	0.43	0.42	0.41	0.32	0.53	0.27	0.32	0.33	0.33	0.50	0.26	0.34
87	6	101415144	9377239	12011	TTGGATTCTCYATACTTCATT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101421667	705603	12012	CTTGCCAAACSTCATGCCCTA	0.15	0.34	0.34	1.03	0.64	0.26	0.36	0.33	0.99	0.71	0.25	0.36
87	6	101433096	4840157	12013	TTAACACCAGRTAAGGACAAG	1.43	1.77	1.77	0.81	0.70	0.34	0.45	1.72	0.97	0.73	0.33	0.48
87	6	101442603	846798	12014	CAGTACATATSCAGGAAAATT	0.13	0.34	0.34	1.01	0.51	0.53	0.51	0.32	1.12	0.52	0.52	0.53
87	6	101460339		12015	TCTTTGTTCARAAGTTTATAA	1.92	2.42	2.42	0.94	1.06	0.73	0.48	2.34	0.99	1.07	0.73	0.47
87	6	101473294	17061235	12016	TGTCTGGGCTRCACAGGTCTA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101480794	17061242	12017	GAGCCATGTARCTGAGACCGG	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101491384	7760062	12018	TGAAGAAACARAAAAGTTAAA	0.25	0.12	0.13	1.65	1.60	0.87	0.48	0.10	1.93	1.53	0.89	0.52
87	6	101510473	7750098	12019	CAGATCTGGARGTTCCACTGA	0.12	0.21	0.21	0.88	1.71	1.08	0.40	0.20	0.95	1.65	1.05	0.38
87	6	101521099	642703	12020	AAATACAGCTRCCATTCACTA	0.07	0.10	0.08	1.21	1.71	0.92	0.70	0.05	1.36	1.64	0.93	0.69
87	6	101548137	17192230	12021	AGGCCCTGAAYGTAGTTTTTG	1.46	1.92	1.84	1.12	0.36	1.09	0.94	1.81	1.20	0.38	1.07	0.94
87	6	101555762	2244658	12022	GAACTGCAGAKAGGAAGTGTG	0.13	0.30	0.30	0.75	0.57	0.46	0.93	0.31	0.72	0.58	0.48	0.94
87	6	101564630	1337385	12023	GAAAAAAACTWCATACAAGAT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101568872		12024	AATATATATCRCCACATTAAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101589764	1626034	12025	CTATATAAACYTGCAGTATCA	0.14	0.18	0.19	0.37	1.36	0.81	0.69	0.17	0.38	1.31	0.85	0.70
87	6	101598146	2749135	12026	TGCTGAAGGCRCTATGCAGAC	0.29	0.31	0.34	2.12	1.80	1.37	0.87	0.31	2.67	1.62	1.34	0.89
87	6	101616270	4557523	12027	AAAATATGACWGAGATTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101628278	9390724	12028	TACTATGCTASTGAGATTTTG	2.22	2.53	2.43	1.88	2.97	1.34	1.09	2.31	2.01	2.52	1.31	1.06
87	6	101637165	9399705	12029	CATGTTTTTAYTCTCTTAATG	0.62	0.77	0.77	1.94	2.32	2.63	1.40	0.70	2.04	2.02	2.24	1.34
87	6	101647596	9390728	12030	TTCTGACTTGMACATTTTATG	3.39	3.16	3.16	1.94	1.81	2.44	2.63	3.06	2.01	1.72	2.06	2.27
87	6	101654668	17193740	12031	AAATCCGATARCATGTCACAT	0.16	0.03	0.03	1.93	1.93	1.87	1.93	0.00	1.90	1.78	1.71	1.80
87	6	101667065	9498518	12032	TCAGATTTTAYGGTTGTTGGA	0.08	0.01	0.00	2.02	1.87	1.67	1.86	0.00	2.04	1.75	1.60	1.77
87	6	101681210	2813642	12033	CCACAATTTTWAAGTGTCAGG	0.93	1.45	1.45	2.18	1.90	1.86	1.92	1.41	2.32	1.79	1.72	1.77
87	6	101694744	2149461	12034	TCACTTGCTASATATAAAGTG	1.28	1.85	1.85	1.34	2.32	2.16	1.63	1.79	1.46	2.13	1.94	1.54
87	6	101704482	4591857	12035	TGTTCTCATTKAACTCTTACA	1.59	2.07	2.07	1.31	2.41	2.07	1.96	2.00	1.47	2.14	1.89	1.75
87	6	101721033	17657328	12036	TTTTCTTTCAYTGTGAGCTTT	1.86	2.32	2.17	1.77	2.39	1.84	1.69	2.06	1.91	2.14	1.69	1.63
87	6	101732895	17061486	12037	ACAAGGTCACSTAAATGCTCA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101734261	3905202	12038	TTTACTATGGSTGCCTCAAAC	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101758813	6900880	12039	GTGCAGCAGTRATTTGTATAA	0.05	0.15	0.15	2.11	2.42	1.45	1.75	0.08	2.21	2.23	1.39	1.70
87	6	101770416	17061541	12040	GGGTAATCATRTACGAAGACA	0.77	0.76	0.76	2.35	2.47	2.16	1.30	0.61	2.48	2.29	2.01	1.26
87	6	101775358	2764274	12041	TTGTGAGTGARTATCTAGACA	1.75	2.18	2.18	1.27	2.29	2.28	2.44	2.07	1.29	2.09	2.08	2.24
87	6	101788746	17061554	12042	GAACACAAGAKACAGGTTTGA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101796899	2518322	12043	AATAACTACARTGATTTCTCT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101811878	2518334	12044	TAAAATCACARTCAAGTGATA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101818315		12045	TTTGTGGACTSATGAGATGAC	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101830413	525685	12046	ATTTTGTTGTRGTAAAGAAAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101835958	283207	12047	GAAGGTATGTRTAAACCAGAA	1.34	1.92	1.92	1.49	2.23	2.62	2.89	1.87	1.49	1.97	2.42	2.55
87	6	101842865	608847	12048	GTCATTCGCAKCAAATTCAGC	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101850928	546327	12049	GAGCTTGTGARAGAAGGAAGA	0.68	1.05	1.05	2.06	2.58	2.64	3.12	1.01	2.21	2.33	2.37	2.68
87	6	101855062	649828	12050	GGCCAACCCAYTCTTCTGGAA	0.18	0.40	0.42	1.57	2.58	3.15	1.85	0.38	1.72	2.15	2.65	1.71
87	6	101869258	501116	12051	TCTGACTCACRTGCTAATATT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101902622	523813	12052	TCCCTGAATGYGGTTTCCACA	1.80	1.42	1.42	1.93	2.62	1.86	1.35	1.28	2.23	2.07	1.66	1.28

87	6	101905980	2518319	12053	AACTCTTCCARATACAAAGAG	0.51	0.86	0.89	1.70	1.69	1.52	1.22	0.83	2.04	1.54	1.40	1.14
87	6	101916721	17061826	12054	AGATGTGAGASAGAATTGCTA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101926551	10485267	12055	AGTGTATCTGYGGTTAGGTTA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101929967	17061871	12056	ATAGTGAATAYCTTATCAGCT	2.04	1.62	1.62	1.36	1.19	0.94	0.89	1.49	1.36	1.14	0.93	0.85
87	6	101935852	2579930	12057	AGATGATTTARTTTAACATGA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	101946584	6930752	12058	TTGCCACTAAMTCATCTCTCC	0.13	0.35	0.35	0.66	0.91	0.85	1.15	0.32	0.67	0.89	0.85	1.13
87	6	101964910	12214708	12059	ACTATCTTTGWTCCATTTGTG	0.00	0.02	0.00	0.10	0.66	1.06	0.44	0.00	0.09	0.68	1.03	0.45
87	6	101980253	1832413	12060	TTTTCTTGCARTCAACTCATG	1.30	0.02	0.02	0.85	0.70	0.37	0.35	0.00	0.87	0.70	0.39	0.35
87	6	101986947	1465168	12061	TTTGCTCTTAYGGAATTCTAG	0.32	0.63	0.63	1.60	0.30	0.08	0.21	0.63	1.59	0.29	0.08	0.22
87	6	101993419	1890278	12062	GATGACAATTRAATTCCTGAG	0.28	0.25	0.25	0.11	0.65	0.07	0.07	0.17	0.11	0.67	0.07	0.08
87	6	102001004	2251408	12063	CTCCTTATTAYGACGATAATA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	102006832	2518160	12064	ATCAGCATAGYATGGTTCCTT	-	-	-	-	-	-	-	-	-	-	-	-
87	6	102014877	10485269	12065	GTCTGTTTACMCAAGGACAAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	102022335	2248237	12066	GCAATACAGTRAAACATCTAC	0.15	0.40	0.40	0.10	0.01	0.33	0.07	0.33	0.06	0.01	0.34	0.06
87	6	102033540	2749066	12067	TCATGCTGATSGTAGCTACAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	102044359	2518236	12068	TGAAATCCCASCATTAGACAA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	102053876	2518242	12069	ATAAAAATGCYTTGGTGAATC	0.26	0.56	0.56	0.11	0.05	0.05	0.44	0.52	0.10	0.05	0.05	0.46
87	6	102062776	9399722	12070	AAAGTTTATARGAGAAAAATA	-	-	-	-	-	-	-	-	-	-	-	-
87	6	102071607	9390754	12071	TATTTTCTGGRTATGTTTTCT	0.31	0.06	0.03	0.32	0.08	0.35	0.15	0.00	0.32	0.07	0.34	0.16
87	6	102077556	2749051	12072	CAATCTTCCAKTTAGAGTGCT	1.13	1.18	1.26	0.82	0.88	0.44	0.14	1.17	0.82	0.89	0.46	0.12
87	6	102084749	2518254	12073	GCTGGTGCATWAAAGAGAGCA	0.98	0.90	0.95	1.34	0.84	0.47	0.11	0.87	1.47	0.86	0.51	0.11
88	6	104164733	4945902	12074	TAACTAAGGAYACTGATGTAA	0.21	0.00	0.00	0.07	0.06	0.02	0.13	0.00	0.05	0.05	0.01	0.13
88	6	104176558	7763417	12075	AAAAGCAAGTYAGTCCACTGA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104182345	4478448	12076	CTTCTTTAGCRCTTATTTCTG	0.23	0.04	0.04	0.10	0.05	0.02	0.02	0.02	0.04	0.06	0.01	0.02
88	6	104203388	6935959	12077	TTTATATATAYCTACACATAA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104227943	7738893	12078	AAAAAAAAAAYGAAAATGCAC	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104242005	6939660	12079	AATAAACAGAYGATTGCTTGG	0.05	0.16	0.16	0.07	0.02	0.01	0.76	0.11	0.03	0.03	0.01	0.76
88	6	104251145	6917911	12080	TGCATCTGAARCAACTAACCC	0.03	0.22	0.16	0.01	0.00	0.42	0.60	0.09	0.03	0.00	0.46	0.61
88	6	104262613	7772782	12081	AGAAACTTTARTTTTCATACT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104278108	7763252	12082	TGGAACAAATYAGCTGTAACA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104288058	6929257	12083	AGGTGTTAAAMATTGCTCATA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104303976	6907113	12084	CGCTATTGCASGTGTTGGTCT	0.08	0.18	0.12	0.02	0.98	0.48	0.20	0.10	0.01	0.98	0.47	0.21
88	6	104332748	4443528	12085	ATATCTTTATKAAGTACTGGG	0.17	0.17	0.17	1.28	0.74	0.35	0.20	0.11	1.31	0.80	0.35	0.20
88	6	104346938	4623274	12086	GTTTTTCTCAYGTATCAATAC	2.19	2.77	2.77	1.57	0.29	0.10	0.53	2.71	1.67	0.30	0.10	0.53
88	6	104352131	4632930	12087	ACCCTTACAAYTGGGCTTAAG	0.03	0.16	0.04	1.03	0.43	0.32	0.22	0.00	1.04	0.42	0.31	0.23
88	6	104372513	7775533	12088	TATTATATAARTGGATCCATC	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104385873	6930883	12089	CTGTGTTTTAYGAGTCAACTT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104396988	4316033	12090	CTTAAATGAGWCTCATGTAAG	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104410507	7752888	12091	GTCCTTAATGMAATTCACCTG	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104424288	7742861	12092	AAATTTCCGTMGTTTTGCTAT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104428882	7775113	12093	ACCTATCCACMAAGACAGAAA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104449492	6930308	12094	TTACTAAGTCRAATTGTAAAC	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104458054	4489183	12095	CATGAATGTGRCTTGAAAGTC	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104474319	4349848	12096	TTTCACATTARGTGTGGACAT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104489676	4946093	12097	TGAACTATTCMATTACAAAAA	0.05	0.04	0.06	0.04	0.85	0.18	0.21	0.04	0.04	0.84	0.19	0.21
88	6	104494630	7741720	12098	TCCAATGACTRAGGCCTTGTA	0.00	0.03	0.02	0.18	0.01	0.45	0.82	0.00	0.13	0.01	0.47	0.84
88	6	104514416	6921682	12099	TACCATGGATYGCTTTTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104542049	10484272	12100	GAATAAATAAYGTCTGAATTT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104547288	2056929	12101	AAGAAAGGAARCACAATTTCA	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104566356	2205749	12102	GGTACTTTCARGGTATTTATG	0.35	0.67	0.71	0.04	0.21	0.39	0.99	0.64	0.04	0.21	0.38	0.93
88	6	104577755	1997650	12103	CTTCTTAGGCWTTTTTTTGAT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104582112	6919215	12104	GTGGAGAATAYTTCTGACCAT	1.51	0.27	0.27	0.51	0.21	0.37	0.31	0.25	0.48	0.25	0.37	0.33
88	6	104606230	859984	12105	TAGCAATACCWTATTCTGGAA	0.85	0.80	0.74	0.53	0.28	0.13	0.22	0.66	0.54	0.29	0.12	0.25
88	6	104613164	1648958	12106	GTATTTATAGRAATGTGAATT	-	-	-	-	-	-	-	-	-	-	-	-
88	6	104619893	11156355	12107	TAACTATAGCYTTTGTTCCAT	1.42	0.19	0.18	0.29	0.12	0.23	0.34	0.14	0.25	0.12	0.26	0.34
88	6	104623766	17310114	12108	CAAAGCATTCRAATTCTAGGG	0.58	0.04	0.06	0.02	0.19	0.05	0.12	0.03	0.03	0.20	0.05	0.12
88	6	104648730	9485933	12109	TCAGTAGACTRTGTCAAACAC	0.11	0.13	0.10	0.17	0.13	0.24	0.21	0.08	0.12	0.12	0.28	0.22
89	6	128988117	1474851	12110	CAGGTAGCCAYCTCTGTATAG	0.14	0.29	0.29	0.05	0.07	0.01	0.03	0.24	0.05	0.09	0.00	0.03
89	6	128994948	17056145	12111	AAGTGCAAGGRTGCCACAGAG	0.26	0.21	0.19	0.08	0.01	0.03	0.02	0.17	0.01	0.00	0.02	0.01
89	6	129000099	9375582	12112	AAGGCAGAGTKTCTTCTTCGG	0.63	0.10	0.10	0.01	0.02	0.03	0.02	0.06	0.01	0.02	0.03	0.02
89	6	129010085	1341591	12113	GAGATATCCAKAATTTCGCCA	0.59	0.21	0.18	0.03	0.01	0.00	0.14	0.15	0.01	0.00	0.00	0.16
89	6	129021415	565685	12114	AACATCCTAARTGGAAAGGCT	0.44	0.02	0.02	0.08	0.00	0.17	0.35	0.00	0.04	0.00	0.21	0.35
89	6	129032517	9388659	12115	AGATAGCCCARGAGCACTGGT	0.32	0.18	0.18	0.00	0.00	0.27	0.56	0.13	0.01	0.01	0.30	0.55
89	6	129039335	1508436	12116	TGGAGGGAAGWTATCAAGAGT	0.44	0.01	0.02	0.05	0.38	0.85	0.28	0.00	0.04	0.40	0.87	0.28
89	6	129045773	544934	12117	AAACAGGATGRTGCAGTCTAA	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129051286	9402063	12118	ACACAGGAGAYGGGCCTGTAC	0.25	0.01	0.06	0.97	1.20	0.54	0.50	0.04	1.06	1.17	0.53	0.53
89	6	129059030	9321128	12119	TGGAAAACACRAGGTTATTCA	0.44	0.23	0.23	0.68	1.14	0.71	0.68	0.20	0.71	1.13	0.66	0.69
89	6	129064484	1396303	12120	CTAGCAAATTKGGGCATTTTC	0.54	0.10	0.10	0.67	0.30	1.07	0.61	0.09	0.70	0.33	1.08	0.58
89	6	129072622	2174934	12121	AGTGAGAATTYAACCTTTTCC	0.80	0.17	0.17	0.04	0.49	0.27	1.43	0.15	0.03	0.49	0.27	1.39
89	6	129079370	7748311	12122	TCTTAAGAGTRAGCTTCATTT	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129086098	774291	12123	CCATTTATTCYGTATAGGCAG	0.64	0.02	0.02	0.32	0.06	0.72	1.98	0.00	0.36	0.07	0.71	1.89
89	6	129087682	7763313	12124	CTACCATATTMAATTGGCAGT	0.59	0.13	0.13	0.39	0.50	2.09	2.80	0.10	0.35	0.57	1.96	2.61
89	6	129103486	774282	12125	CATTTTACTGYGCCATAGTCC	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129118213	17056470	12126	AAAACATTTCYGTGACCCAGG	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129136801	9492080	12127	AAGGAATCCTYTGGACTTTAG	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129147428	4467800	12128	GGATTTTTTTKTGTGTGTTAA	0.25	0.24	0.24	0.88	2.68	2.61	1.97	0.20	0.95	2.39	2.39	1.91
89	6	129179431	6908984	12129	TAACGGGAAGSATCTGCATAA	0.45	0.56	0.56	1.63	1.62	1.42	1.83	0.46	1.81	1.52	1.43	1.75
89	6	129188119	1508442	12130	TACAGTGAGAYATCTAAACAA	2.36	2.39	2.51	1.92	1.97	1.17	1.04	2.43	1.92	1.81	1.16	0.99
89	6	129199413	9375599	12131	TTTATAGTCCYTTTCACTGAG	2.77	3.35	3.25	2.12	1.64	1.48	1.53	3.15	2.16	1.56	1.46	1.49
89	6	129209704	9482942	12132	ACTCCTAATGRCATCTGGGAG	0.76	1.25	1.25	2.40	1.65	2.18	1.88	1.17	2.84	1.59	2.10	1.80
89	6	129215857	7741616	12133	TCAGTACAGARAGGCACAAAG	0.60	1.05	1.10	0.69	3.53	2.02	1.79	1.01	0.69	3.03	1.98	1.68
89	6	129227227	17056587	12134	GGTGCTGAAAKAGTGCAGTTG	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129233502	17056617	12135	CTCCTCATTARTTTATGATGC	0.17	0.05	0.00	1.19	1.06	2.27	2.12	0.00	1.33	1.05	2.07	2.03
89	6	129247983	17779264	12136	CAATCTACTAYAGGCTGCTAT	0.47	0.65	0.46	0.78	0.92	1.06	2.28	0.36	0.88	0.93	1.05	2.05
89	6	129259273		12137	GCCATACACAYTCCAGTAACA	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129280297	9482956	12138	TTTATATATGRCCTATTAACC	0.18	0.41	0.39	0.18	0.80	0.90	0.39	0.35	0.14	0.80	0.90	0.44
89	6	129281463	7776116	12139	TCTTCATTATYTCCACTACAC	0.24	0.43	0.39	0.15	0.13	0.32	0.13	0.35	0.13	0.13	0.37	0.13
89	6	129331822	17779977	12140	TTGGAGGCAARCAATGCTTCT	0.28	0.27	0.27	0.16	0.04	0.02	0.40	0.21	0.19	0.04	0.01	0.40
89	6	129335702	17723635	12141	CAAATCATCTSTCTGTCTCTT	0.28	0.27	0.27	0.18	0.02	0.09	0.36	0.21	0.14	0.02	0.10	0.37
89	6	129358546	9492182	12142	TTTTATGACCWTATATTTTTC	0.27	0.07	0.07	0.05	0.35	0.55	0.34	0.05	0.02	0.38	0.58	0.35
89	6	129372105	6912590	12143	CCATAATCTCYGAAATAATTA	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129378729	9492195	12144	GTGAGGTACARTATATAAACT	0.11	0.05	0.07	0.29	0.25	0.37	0.68	0.05	0.25	0.27	0.41	0.66
89	6	129384699	17056726	12145	AAGACTAATTSGGAATGCTAC	0.74	0.77	0.77	0.82	0.25	0.54	0.37	0.74	0.81	0.28	0.57	0.37
89	6	129388278	17056731	12146	AAATAGTGGCRTGAGAATGGT	-	-	-	-	-	-	-	-	-	-	-	-

89	6	129395364	9402093	12147	GGCAGTATTCKTTGAATGTGA	0.99	0.41	0.41	0.74	0.82	0.27	0.25	0.37	0.78	0.82	0.26	0.26
89	6	129402254	9388679	12148	ATAGCAACAGWTGAGTTCAGA	0.07	0.25	0.25	0.49	0.61	0.42	0.34	0.22	0.47	0.60	0.43	0.38
89	6	129422719	4404787	12149	TGACAATTACMCTGGATTTAC	-	-	-	-	-	-	-	-	-	-	-	-
89	6	129432939	17782500	12150	ATGACTTATGYGTTGGTACAT	0.22	0.46	0.46	0.30	0.16	0.31	0.25	0.42	0.29	0.14	0.33	0.28
89	6	129448891	17056792	12151	CAATTGAGGTMACCACTTTAA	0.15	0.21	0.21	0.09	0.17	0.10	0.14	0.18	0.07	0.20	0.11	0.16
90	6	132952928	17061476	12152	GTATTTTTTGYCAAATGTAAA	0.28	0.28	0.28	0.33	0.86	0.61	0.23	0.18	0.33	0.89	0.64	0.25
90	6	132959516	13204323	12153	CCAATCAAATRTTAAACAATT	-	-	-	-	-	-	-	-	-	-	-	-
90	6	132970969	9399036	12154	ATTACTGAAAYTTAATAGTAT	-	-	-	-	-	-	-	-	-	-	-	-
90	6	132985815	9389016	12155	TAGGCTTAGCRTAATGCCTGA	-	-	-	-	-	-	-	-	-	-	-	-
90	6	132997093	9402435	12156	AGGAGGATACWGGGATTCCAC	0.49	0.61	0.61	0.33	0.28	0.38	0.35	0.57	0.34	0.31	0.40	0.36
90	6	133006529	7764501	12157	CCAAATCCCCRGTGATACTCA	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133022219	9402443	12158	TTCTGAACCARCATCAGGAAG	0.34	0.53	0.53	0.22	0.16	0.38	0.23	0.50	0.18	0.16	0.39	0.23
90	6	133028617	9373029	12159	TTCTTTTTCAYATGGCCTTGT	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133034808	1569654	12160	AAAACTTAAAYGGGCTTGACA	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133048433	2251449	12161	GTAATTGATTYAGCAGACCCA	0.05	0.02	0.02	0.04	0.14	0.39	1.33	0.00	0.03	0.14	0.38	1.29
90	6	133056316	742516	12162	TCTAGCTAAAYTGGGCCTTTA	0.19	0.31	0.28	0.13	0.30	2.01	1.70	0.26	0.10	0.32	1.94	1.68
90	6	133063932	2840827	12163	GAAATGCTAAYGACAAGTCTG	0.19	0.39	0.42	0.71	3.46	1.50	1.15	0.40	0.75	3.21	1.45	1.12
90	6	133077018	4897612	12164	AAAAGACCCTMCCTTATTGCA	0.30	0.58	0.59	3.01	3.02	2.04	1.77	0.54	3.28	2.76	1.91	1.70
90	6	133087595	2294759	12165	AAGCTTGGTGRAGGTAAACTC	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133094309	4895943	12166	TTCTGAATGAYAGTGATAGCA	2.87	3.45	3.45	2.29	1.71	2.83	2.45	3.37	2.37	1.67	2.62	2.33
90	6	133102784	6569843	12167	GCTTGAAGCAYACTTCCATGT	1.22	1.53	1.60	1.88	2.72	1.62	1.91	1.53	2.07	2.56	1.55	1.84
90	6	133114343	1883617	12168	GTGCATAAATRCCACTTCCTG	0.89	1.31	1.31	2.75	3.53	1.75	1.25	1.26	2.87	3.04	1.68	1.26
90	6	133127154	11154696	12169	CTAAAATTATRAACTTAAATT	1.15	0.88	0.88	2.73	1.78	2.62	1.27	0.81	2.91	1.69	2.41	1.26
90	6	133141822		12170	TAAGCAGCACRGATGATGCCC	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133154515	17606700	12171	CACAGCTCCAWGGTAATGGCT	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133159563	10484629	12172	ACATGGTAAGMAAAGTAATTC	0.07	0.20	0.13	0.57	2.52	1.24	1.92	0.10	0.64	2.36	1.24	1.83
90	6	133180442	2236382	12173	ATAAGGTCCCYGTTAGCAAAG	0.81	0.40	0.40	0.75	0.92	1.74	0.87	0.36	0.78	0.90	1.67	0.87
90	6	133193306	6921262	12174	AAAAGAGAAGRCTGGGAGCTG	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133201602	12207260	12175	AAAGAGGAAGWCATCTGTGTA	0.52	0.92	0.92	0.56	0.57	0.43	1.02	0.86	0.58	0.59	0.42	0.97
90	6	133213644	9373031	12176	TGAAATATCARTGAAGACAAG	0.40	0.69	0.69	0.52	0.35	0.22	0.18	0.66	0.52	0.39	0.23	0.17
90	6	133221251	1555621	12177	CTAGTTTACCRCTCAGATCTC	0.33	0.63	0.63	0.15	0.43	0.13	0.25	0.59	0.13	0.48	0.13	0.26
90	6	133229141	9402465	12178	TTAATTGATARATATATACCC	0.31	0.57	0.56	0.20	0.03	0.39	0.17	0.49	0.18	0.02	0.39	0.15
90	6	133246091	718508	12179	TACCTGATACYAAGCTACTCA	0.16	0.41	0.41	0.17	0.15	0.07	0.30	0.36	0.13	0.15	0.07	0.29
90	6	133251924	271179	12180	TGGTTAAATTRTCAACCAGGG	0.14	0.38	0.49	0.36	0.09	0.11	0.04	0.47	0.36	0.08	0.11	0.04
90	6	133257365	6926217	12181	CACAACCTCARTGAAAGGCAG	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133265236	450727	12182	AAATTATGAAWGGATGAATTA	0.43	0.77	0.81	0.38	0.20	0.06	0.02	0.79	0.31	0.21	0.06	0.02
90	6	133273522		12183	TTTAAGTTCAYGATGTCATTT	0.04	0.16	0.09	0.34	0.21	0.05	0.31	0.05	0.32	0.26	0.04	0.33
90	6	133282902	17061987	12184	CTGTGAAACCRAAGGCTTGTT	-	-	-	-	-	-	-	-	-	-	-	-
90	6	133286730	7747305	12185	ATTGTATCTGSTGGGAGGATT	0.77	1.00	1.01	0.46	0.21	0.44	0.17	0.94	0.46	0.23	0.48	0.18
91	6	141147720	7774722	12186	TGTGACAGAARCATGTATATT	0.18	0.04	0.04	0.10	0.13	0.02	0.54	0.01	0.10	0.14	0.02	0.53
91	6	141175866	601084	12187	ACAAACAAAARACAAGTTGTA	-	-	-	-	-	-	-	-	-	-	-	-
91	6	141182308		12188	AAGGAAGTTCMGTGTTGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
91	6	141190449	611438	12189	CTCTTGATACRTTTACAGATT	0.29	0.20	0.18	0.20	0.10	0.04	0.39	0.15	0.17	0.10	0.04	0.39
91	6	141202018	637822	12190	ATATTTCATAYTTACAACAGT	0.15	0.13	0.13	0.19	0.10	0.60	0.42	0.11	0.12	0.10	0.60	0.39
91	6	141210986	655154	12191	AACTTAAAATYTGTCATGATT	0.08	0.08	0.06	0.06	0.65	0.37	1.35	0.04	0.03	0.63	0.38	1.33
91	6	141226736	640539	12192	AGTCTGAAACWTGTCTTACGT	-	-	-	-	-	-	-	-	-	-	-	-
91	6	141239039	6570426	12193	CTTCCAAATAWCCAATCATAC	0.09	0.17	0.17	0.65	0.35	2.17	2.19	0.18	0.71	0.40	1.96	2.00
91	6	141244731	6909528	12194	TGCAAAGAGCYAACAACTAAT	0.22	0.49	0.49	0.52	2.10	2.61	2.10	0.46	0.63	1.90	2.28	1.93
91	6	141254155	6932768	12195	ACTTGTAAAAMTCTAATTTTG	0.21	0.42	0.42	2.74	3.72	1.82	1.14	0.40	3.32	3.16	1.72	1.13
91	6	141267388	2328153	12196	ATATTAATGASCATTTACGGT	2.16	2.50	2.50	3.99	3.08	1.48	1.01	2.44	4.23	2.69	1.46	0.99
91	6	141277271	1856389	12197	AAGTTTTTATRTCCAAAGGCA	-	-	-	-	-	-	-	-	-	-	-	-
91	6	141286061	6924310	12198	ATAGTAATCAYGTCAGAGTTC	2.06	2.40	2.40	2.29	2.03	1.82	1.24	2.32	2.36	1.97	1.76	1.23
91	6	141305365	17816036	12199	TTTGAAAATARTGGGAAATGG	-	-	-	-	-	-	-	-	-	-	-	-
91	6	141312353	9389835	12200	CTGAGACAGAYTAATTTTTCA	0.27	0.57	0.53	1.23	1.49	1.73	1.36	0.52	1.24	1.42	1.65	1.34
92	6	159060617	317801	12201	TTAGCTTCATYAAAAAAATAA	0.55	0.65	0.65	0.56	0.58	0.26	0.20	0.57	0.55	0.60	0.27	0.24
92	6	159066108	2583077	12202	CCGTTTTTATYGCCAAGGCCT	0.26	0.48	0.48	0.73	0.23	0.38	1.50	0.43	0.73	0.23	0.36	1.44
92	6	159115691	7751659	12203	TAGCATAGTGSTGTGAATATA	-	-	-	-	-	-	-	-	-	-	-	-
92	6	159127336	9346766	12204	GCAATTAGCARTAGATGTCAG	0.75	0.93	0.93	0.40	0.49	0.73	1.20	0.90	0.39	0.47	0.70	1.19
92	6	159134353	17513241	12205	TAAGCTTCTCSGCCCCTCAGC	0.64	1.04	1.04	0.39	0.54	0.44	0.61	1.01	0.39	0.57	0.46	0.63
92	6	159145465	901364	12206	TAAAAGTCTCRCTAGAAGCCA	0.19	0.42	0.42	0.86	0.46	0.38	0.32	0.39	0.92	0.47	0.42	0.32
92	6	159153971	2171209	12207	TCATTCAGTAYAGGTGCATTG	1.07	0.85	0.85	1.11	1.30	0.32	0.24	0.83	1.15	1.26	0.36	0.23
92	6	159155972	3123101	12208	GCATGCTCACWATCGAAGCTC	1.52	1.40	1.40	0.51	0.87	0.75	0.39	1.35	0.60	0.84	0.76	0.40
92	6	159169115	3127205	12209	TCAATACTGAYGAGCAATACA	1.08	0.81	0.81	0.42	0.17	0.51	0.96	0.78	0.39	0.18	0.58	0.93
92	6	159179621	901369	12210	GGTATACAGARCATTTGCTTA	1.08	0.81	0.81	0.26	0.14	0.25	0.57	0.77	0.22	0.16	0.25	0.57
92	6	159185817	6455604	12211	TCCCAACTTTYCATTTTATTA	1.61	0.94	0.93	0.50	0.32	0.19	0.17	0.90	0.55	0.34	0.16	0.19
92	6	159192856	3123125	12212	GCTTGTCTATYGGGCTCAGGA	0.24	0.22	0.22	0.87	0.41	0.41	0.50	0.18	0.88	0.41	0.39	0.55
93	6	164223534	876738	12213	ATTTCTATTAYAATTGTCACC	0.10	0.16	0.16	1.15	0.86	0.41	0.31	0.12	1.33	0.84	0.40	0.31
93	6	164229831	9355442	12214	TTTCAGAAAGRCTAATGTAGC	1.07	0.83	0.87	0.67	0.50	0.55	0.96	0.84	0.75	0.49	0.57	0.91
93	6	164236601	7750264	12215	TACAGAAAACRTTTTTTCCAT	0.04	0.07	0.06	0.49	0.57	0.27	0.25	0.04	0.51	0.56	0.27	0.26
93	6	164250017	6902564	12216	TAGTCAGTTTYCTTCTCTGTG	0.46	0.74	0.77	0.52	0.41	0.29	0.07	0.70	0.60	0.40	0.33	0.08
93	6	164256867	16895454	12217	GGATAACTCARTTATTCTGGC	0.46	0.83	0.83	0.67	0.20	0.05	0.03	0.79	0.72	0.21	0.06	0.02
93	6	164263732	4709779	12218	GTATGGGTGCKTACATGAGCG	0.54	0.52	0.52	0.47	0.11	0.01	0.07	0.51	0.46	0.11	0.01	0.08
93	6	164270669	4709021	12219	GATACAAGAARGAGTGAAGGA	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164277550	9295241	12220	GATGAGCCGARGTAAACAGAC	0.06	0.14	0.15	0.04	0.06	0.04	0.02	0.11	0.02	0.05	0.03	0.01
93	6	164284190	4709791	12221	TACAAATATARTCTTCCCAGA	0.23	0.39	0.39	0.05	0.01	0.06	0.24	0.34	0.05	0.01	0.07	0.26
93	6	164293250	12199159	12222	GAGATGCAAARAAAGCATGTT	0.55	0.17	0.18	0.06	0.13	0.47	1.12	0.14	0.05	0.14	0.47	1.11
93	6	164301316	13219578	12223	TTATGCATGAYGGACATTGTC	0.17	0.04	0.00	0.21	0.58	1.06	0.82	0.00	0.19	0.62	1.02	0.84
93	6	164311453	9356170	12224	TTCTATGTGCMTATTTCTCTA	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164324492	10455928	12225	GAGGGGTGCCYCAAGATTAAG	0.10	0.17	0.17	0.31	1.45	1.11	0.34	0.14	0.30	1.41	1.11	0.36
93	6	164334262	16895683	12226	ATGTTTTGCAKGGCAGCTTCT	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164340994	6920924	12227	AAGCACCACTYTGATCATCTA	1.58	1.21	1.21	1.73	1.73	1.28	0.50	1.14	1.78	1.68	1.25	0.55
93	6	164348090	9458957	12228	CCTAATAATARTAATTCCGTG	2.44	2.86	2.94	1.68	1.07	1.12	0.63	2.85	1.68	1.06	1.13	0.65
93	6	164354419	577610	12229	CAAGGATTTGRTGCTGATACT	1.69	1.16	1.16	1.79	1.23	0.74	0.65	1.11	1.85	1.15	0.76	0.63
93	6	164361209	12207355	12230	TCTCCTGTGCYTCGGGACCCC	0.02	0.09	0.09	0.95	1.29	0.87	0.74	0.06	1.01	1.26	0.86	0.75
93	6	164367199	10484514	12231	TAGATTGATAYGCAGAGTAAA	0.01	0.04	0.04	0.35	1.10	1.30	0.29	0.02	0.33	1.05	1.27	0.30
93	6	164380532	473823	12232	TTTTAGTCACYGCAACCTTTT	0.08	0.21	0.21	0.58	0.45	1.00	1.32	0.21	0.60	0.44	1.00	1.25
93	6	164386987		12233	TATTTTCTCGSTGACCTCCAC	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164393437	680946	12234	ATCGGTATCARTTTTTTGAGG	0.25	0.55	0.55	0.17	1.50	1.67	0.70	0.49	0.16	1.43	1.58	0.69
93	6	164403081	189978	12235	GAAATTTCTGYCCTTTGAGTA	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164411046	4709814	12236	AAGTTTATGTRAAGTCATTGA	0.30	0.54	0.54	1.50	1.94	1.18	0.25	0.52	1.57	1.83	1.14	0.26
93	6	164420069	9365639	12237	TACCAAAATGMAACCTTGTAG	1.86	2.38	2.38	1.96	1.56	0.43	0.26	2.30	2.11	1.47	0.42	0.24
93	6	164426388		12238	TGATGGACGTKATGGCCTTGC	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164437009	444865	12239	GAAAGTGTAAYTTAAATTTTT	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164448969	421102	12240	CTGACGGTCTRTTTTCCAGAG	1.51	0.97	0.97	1.36	0.65	0.41	0.21	0.87	1.57	0.70	0.40	0.21

93	6	164458329	206688	12241	CCCAAAACTTKATTAAGTACG	2.51	0.33	0.33	0.51	0.49	0.24	0.14	0.32	0.54	0.49	0.25	0.14
93	6	164471746	12055870	12242	CACGGCTCGTYCCTGGACACG	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164477763	10455932	12243	TCTGTATCCARGTATCAGAGA	0.39	0.72	0.72	0.12	0.51	0.53	0.13	0.67	0.12	0.50	0.52	0.14
93	6	164486176	10484511	12244	GATACTATGARGTTGCAAAAA	0.01	0.06	0.09	0.38	0.30	0.62	0.36	0.06	0.36	0.32	0.62	0.35
93	6	164497757	16896125	12245	CGGCCCAGGTRTGGCAAAATT	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164504318	714981	12246	ATACTGAAGAWTGTTTCCATA	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164510107	206687	12247	CTTCCACAAAKGTAAAGGCCC	0.60	0.79	0.79	0.62	1.08	0.26	0.26	0.75	0.59	1.11	0.27	0.26
93	6	164522383	206715	12248	TCTATGGATTMATGGGTGTCT	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164528636	4382226	12249	CCAGTAAAAGWTCTGTAACAT	0.67	0.45	0.45	0.57	1.13	0.49	0.14	0.38	0.59	1.15	0.49	0.13
93	6	164534982	9459008	12250	ATTCTAAGAAYAATTTTTAAA	-	-	-	-	-	-	-	-	-	-	-	-
93	6	164544569	4501405	12251	ACAACATGTCRCAGTAAATAG	0.13	0.38	0.42	0.39	0.41	1.09	0.80	0.35	0.35	0.44	1.10	0.87
93	6	164558370	9347821	12252	GGAGACTTGGSTTTCAGGCTT	0.13	0.36	0.36	0.07	0.96	1.69	1.71	0.30	0.04	0.94	1.63	1.65
93	6	164571259	1894638	12253	AGCTGCCCTGYGCTACAGTTT	0.84	0.10	0.08	0.56	0.98	1.91	1.42	0.06	0.57	0.98	1.86	1.38
93	6	164579745	811581	12254	ACTTCTGTTTYCTCTGTTACT	0.14	0.38	0.34	1.02	1.74	0.54	0.65	0.29	1.04	1.67	0.55	0.61
94	6	167538046	11759697	12255	TCTGGTTGGGRAAGTAAGCAA	0.86	0.42	0.42	0.02	0.23	0.23	0.21	0.36	0.03	0.20	0.23	0.23
94	6	167550994	16899926	12256	TGGTCACTGAYTATGTGATAT	-	-	-	-	-	-	-	-	-	-	-	-
94	6	167571720	2345969	12257	TCGCACAGCCYAGTCAGCGCA	0.21	0.31	0.34	0.14	0.21	0.44	0.25	0.30	0.13	0.20	0.43	0.27
94	6	167604084	7753816	12258	CAGCGAAGTASGACTGTGACT	0.42	0.67	0.68	0.91	0.31	0.81	0.53	0.65	0.95	0.32	0.83	0.55
94	6	167605543	2346155	12259	GGAAGCCGTTKCCACCGCCCT	0.66	1.03	1.03	0.74	0.48	0.68	0.76	1.00	0.75	0.49	0.71	0.76
94	6	167634047	7773576	12260	GCCCCAGACTYTCATGTGGAT	0.14	0.29	0.29	0.46	0.31	0.23	0.61	0.25	0.48	0.30	0.23	0.61
94	6	167656982	12527165	12261	CAGGCAAGCCRCTAACGTGAA	0.17	0.37	0.37	0.40	0.20	0.16	0.10	0.33	0.42	0.20	0.16	0.10
94	6	167662993	16900164	12262	TTCCTGCAGASTGGTACAAAT	0.75	0.77	0.77	0.17	0.10	0.09	1.03	0.72	0.12	0.08	0.07	1.05
94	6	167669180	206990	12263	CACGTCTTCCYGTGTCTAAAG	0.71	0.76	0.77	0.19	0.04	0.45	0.93	0.68	0.11	0.03	0.48	0.91
94	6	167675355	2076005	12264	CAAATTTACGKGTTCACTGGT	0.30	0.23	0.21	0.16	0.40	0.67	0.83	0.16	0.14	0.40	0.69	0.84
94	6	167682571	17535087	12265	ATTGTCATGAYGAGGCTCATT	0.34	0.22	0.19	0.69	0.64	0.48	0.63	0.18	0.72	0.66	0.46	0.64
94	6	167689847	2072767	12266	CATCCAGTTCRTCGGCTACGT	-	-	-	-	-	-	-	-	-	-	-	-
94	6	167697725	2294236	12267	AACAGTCACCMTCAAAAAACA	0.78	1.13	1.11	1.23	0.85	0.77	0.40	1.08	1.31	0.83	0.78	0.38
94	6	167706365	7749014	12268	ATCCCAGTACRGAACCTGCTA	2.12	2.17	2.28	2.23	1.62	0.37	0.53	2.20	2.31	1.56	0.37	0.53
94	6	167710180	9456267	12269	TTTCTGGTTTRATAATAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
94	6	167722407		12270	GCATGGAACARTTTGAAAGCA	-	-	-	-	-	-	-	-	-	-	-	-
94	6	167732267	17536436	12271	GAGGTTTTTGYCAGCACCGTA	2.81	3.52	3.52	2.63	1.48	1.12	0.46	3.44	2.93	1.41	1.11	0.50
94	6	167741147	2981988	12272	GCTACAATGAYGCATGCACAA	0.41	0.79	0.75	2.41	1.66	1.36	0.60	0.69	2.48	1.58	1.34	0.59
94	6	167785862	4709179	12273	ATCCTGGTGGSGGAGAGAGGG	-	-	-	-	-	-	-	-	-	-	-	-
94	6	167798646	4072270	12274	TTTATTTCCASACATTACAAT	-	-	-	-	-	-	-	-	-	-	-	-
94	6	168043577	9455902	12275	TGGGACCTACMATAAAGTGTA	0.15	0.38	0.36	0.46	1.74	0.86	1.00	0.31	0.46	1.64	0.85	0.95
94	6	168118382	2268947	12276	TCCCATTGTTYTGTTCTACGG	0.32	0.36	0.36	0.39	0.55	1.51	1.18	0.34	0.43	0.56	1.47	1.14
94	6	168127833	9346512	12277	AAATGAATTCRCACGAGGGAG	0.30	0.57	0.57	0.37	0.38	0.26	0.32	0.53	0.38	0.37	0.26	0.30
94	6	168136929	16886299	12278	TTAGCTATTTRTAAAGAGAAA	-	-	-	-	-	-	-	-	-	-	-	-
94	6	168143740	6912127	12279	CCTGGTGCTGYGATTTAAAAT	0.39	0.54	0.57	0.15	0.07	0.12	0.35	0.49	0.12	0.07	0.12	0.37
94	6	168149491	626848	12280	ATAGATTTAGKGAGACTAAGC	0.31	0.61	0.57	0.05	0.20	0.66	0.57	0.54	0.05	0.17	0.63	0.60
95	7	13749009	17167675	12281	TTTTTAATGCRTATACAAACA	0.68	0.26	0.26	0.06	0.35	0.18	0.67	0.24	0.04	0.36	0.19	0.68
95	7	13755660		12282	AAATTGATGAMCTCTATAGCT	0.69	0.15	0.15	0.01	0.01	0.16	0.58	0.16	0.01	0.01	0.16	0.58
95	7	13765700	6946355	12283	GAGACCAAATRCAGAATATGT	0.09	0.14	0.14	0.00	0.06	0.55	0.21	0.13	0.00	0.07	0.56	0.21
95	7	13774056	7794465	12284	TTATTATATARGAATGATTGC	0.04	0.04	0.04	0.43	0.72	0.86	0.65	0.00	0.43	0.75	0.88	0.67
95	7	13782071	917094	12285	TCCAGTATAAMAGAAATCTAC	0.50	0.64	0.64	1.99	1.79	1.13	0.77	0.60	2.04	1.70	1.09	0.75
95	7	13789411		12286	TAATGCAGGTRTCTGTATTAG	-	-	-	-	-	-	-	-	-	-	-	-
95	7	13795762	7790991	12287	TACACATAGTRAGTAACAATA	0.84	1.01	1.01	1.85	3.06	1.14	0.23	0.97	1.92	2.77	1.14	0.24
95	7	13805896	41503	12288	TATGAAGAAAWTGCACGTTGT	-	-	-	-	-	-	-	-	-	-	-	-
95	7	13811866	10270713	12289	GCTTCCCATCYGTGTAGGAGC	0.03	0.14	0.14	1.79	2.15	1.14	0.55	0.09	1.98	1.99	1.08	0.56
95	7	13823289	11973792	12290	GTATTATTAASAAAAATACAG	-	-	-	-	-	-	-	-	-	-	-	-
95	7	13834197	10275495	12291	AAAGGTTACAYCGAAATTCTA	0.61	1.02	1.02	0.66	0.57	1.08	1.08	0.97	0.72	0.59	1.08	1.06
95	7	13841414	6944510	12292	TATTTAAAAAMTTTCAAATGG	-	-	-	-	-	-	-	-	-	-	-	-
95	7	13846907	10440959	12293	TTTAATGGATRGAATAGTGAT	-	-	-	-	-	-	-	-	-	-	-	-
95	7	13853068	10454309	12294	CAAGCTCCACRTTATGTATTT	-	-	-	-	-	-	-	-	-	-	-	-
95	7	13858986	10254238	12295	GCAAATATGAKGTATATCAAT	0.21	0.49	0.45	0.45	0.18	0.62	0.55	0.46	0.46	0.19	0.63	0.55
96	7	119182246	10251196	12296	TTCCTAGTTAYTGCTTTTCAG	0.07	0.06	0.06	0.54	0.12	0.38	0.78	0.04	0.53	0.13	0.41	0.76
96	7	119190120	7808286	12297	GGTAAAATAARCACTAGAATC	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119202282	17142463	12298	TGTTAAACACRTGGATTTCCC	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119210847	6955881	12299	TGAGCTAATGMCATGAGCCCT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119235020	6963628	12300	TTCTCTAATAYAGTCTATCAA	0.31	0.60	0.69	0.24	1.36	0.79	0.65	0.61	0.21	1.32	0.82	0.67
96	7	119252988	3898475	12301	TCAGAAACCTYTGACATCTAG	0.62	0.70	0.71	1.24	1.90	1.86	1.69	0.65	1.50	1.74	1.80	1.59
96	7	119265280	17142487	12302	ATATGTACTCYGATATTCTTT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119283030	17142502	12303	CATTCATTTGWAAAAATTACA	0.18	0.18	0.09	2.03	1.84	3.68	2.44	0.00	2.41	1.64	3.27	2.31
96	7	119310015	7801733	12304	CCAGTTTTTTWAAAATTTGTA	0.27	0.27	0.50	1.11	1.66	1.33	2.06	0.40	1.26	1.59	1.29	1.96
96	7	119315453	2190088	12305	AACTATAATTYTTAAAGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119322098	10248706	12306	TTTAAGTGTAYGATTTAATGT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119329147	10226287	12307	GAAGGATGTARCATAGTTTGA	0.24	0.09	0.09	0.88	1.02	0.78	0.52	0.06	0.96	0.98	0.74	0.54
96	7	119341333		12308	TATTGATAAGYAACCTCCTTT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119362350	10241741	12309	CCAAAAATTTRGAGATTTCTT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119375678		12310	ATTAAATTAAMAAGGAACTAT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119404670	17593328	12311	AATTATGTACMAAATGATGTA	0.44	0.08	0.08	0.35	0.69	0.32	0.44	0.04	0.34	0.72	0.34	0.44
96	7	119415238	17142555	12312	CACCTGGCAAYTTGAGGAAGT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119422282	7792688	12313	TATGATTAATMCTGATTGTTG	1.47	1.23	1.23	0.24	0.04	0.30	0.48	1.18	0.20	0.04	0.32	0.52
96	7	119430456	6956643	12314	AAGTTGCGTCYGGTTTAACTG	1.48	1.23	1.23	0.27	0.10	0.26	0.52	1.15	0.24	0.09	0.25	0.58
96	7	119439481	10247189	12315	AAGCCTTAGARAGAAAATGGT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119450807	10241520	12316	GCCCTAAGTTRGTCAGCTTAA	1.07	0.59	0.59	0.46	0.27	0.16	0.44	0.52	0.50	0.26	0.16	0.47
96	7	119459108	10253133	12317	CCCAAGTCTGWTGGGATTCCA	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119483097	2402522	12318	CAAGATGGTAKATTTATACCT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119493180	2057927	12319	TAAAATAATGYGGATTGCATT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119500141	10276880	12320	TTGGTAGTAARTTAGGTTGAT	0.34	0.34	0.34	0.74	0.60	0.34	0.20	0.25	0.81	0.60	0.36	0.21
96	7	119521944	1860704	12321	CAGAAGTCTTRAATACAGGTA	1.41	1.25	1.21	0.61	1.05	0.54	0.38	1.18	0.67	1.05	0.56	0.41
96	7	119529107	4730956	12322	TTTTCAATATRTAGCAGTAAG	1.11	1.16	1.16	1.05	1.01	1.20	0.50	1.11	1.20	1.04	1.20	0.52
96	7	119544371		12323	CAGAATCTAAYGACAATGAAG	1.42	2.01	2.01	1.08	0.48	0.46	1.02	1.89	1.09	0.50	0.50	1.04
96	7	119555783	17142635	12324	CCATATTTCAYGATTAAGTCT	0.00	0.00	0.07	0.83	0.46	0.38	0.42	0.00	0.84	0.46	0.40	0.42
96	7	119561346	7792980	12325	AGGAGGAAACKTAATTATTAC	1.19	1.22	1.22	0.75	0.62	0.42	0.60	1.12	0.77	0.68	0.43	0.64
96	7	119571922	10953908	12326	AAAAAAGTCTRTTTGAACATA	0.74	0.94	1.00	0.84	0.70	0.85	0.94	0.93	0.91	0.74	0.84	0.90
96	7	119578820	10231689	12327	CATGACTTCARCATCATCCCA	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119587124	6942715	12328	AACAATGTGARATAAATACTT	0.78	0.97	0.94	0.67	0.49	1.43	1.00	0.88	0.93	0.52	1.35	1.01
96	7	119599097	12706280	12329	AAGCCAAGGTRAAGTTCATAG	0.68	0.89	0.94	0.24	1.47	1.34	0.97	0.87	0.21	1.40	1.32	0.97
96	7	119604727	10266602	12330	AGATAACAGCRGAAAAGGGAC	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119610742	7800215	12331	ATGAAAAACTKTAAGCTCAAT	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119618917	1014168	12332	AAGACGAGTTRTATTTTATAG	0.74	1.04	1.04	1.30	1.04	0.83	1.05	0.97	1.37	1.06	0.82	1.01
96	7	119628995	11773299	12333	CACTCTATACMATTCAAATTA	0.15	0.35	0.35	1.64	0.92	0.96	1.36	0.31	1.80	0.95	0.95	1.33
96	7	119635627	10216253	12334	TATTAGAAATRTTACTGTGTT	-	-	-	-	-	-	-	-	-	-	-	-

96	7	119642915	17142709	12335	ATGATATGAGYGCAAAAATAC	-	-	-	-	-	-	-	-	-	-	-	-	-
96	7	119650620	1860705	12336	CAGTGTATTGYTCTCACAACC	0.11	0.18	0.21	0.21	1.70	1.44	1.28	0.19	0.15	1.63	1.39	1.25	
96	7	119657150	11769563	12337	TTGTTTTGATRCCAAAGGGAG	0.12	0.19	0.19	0.29	0.67	2.10	1.36	0.16	0.22	0.70	1.95	1.32	
96	7	119662539	7796685	12338	GTTTGCTTTTYTAATAAAGTT	0.05	0.12	0.12	0.37	0.37	0.66	2.42	0.07	0.30	0.42	0.68	2.15	
96	7	119671086	17142741	12339	GGAAAAACAAMTTCTTTACTA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119677704	11767599	12340	TTTTTTCTGCRTGGCATTTGA	0.00	0.02	0.02	0.32	0.12	0.16	0.46	0.00	0.32	0.11	0.16	0.48	
96	7	119686000	7805718	12341	AACAGAAATCRATAACACATT	0.12	0.22	0.15	0.08	0.11	0.05	0.08	0.11	0.05	0.11	0.05	0.08	
96	7	119693689	10488297	12342	AATAATAAGCRTCTACCAGTT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119703557	10276390	12343	TCTGTTTCAGYAGCAGAGGAT	0.01	0.00	0.00	0.14	0.05	0.05	0.05	0.00	0.10	0.04	0.05	0.03	
96	7	119714273	10953918	12344	TAACGGAGAARTAGAATACTC	0.00	0.03	0.03	0.16	0.05	0.02	1.03	0.00	0.07	0.04	0.01	1.00	
96	7	119721865	17132703	12345	AAGATTCTACRTAACGAGTAA	0.22	0.26	0.27	0.14	0.06	0.97	0.71	0.24	0.09	0.03	1.02	0.74	
96	7	119730142	723908	12346	GAAGCATCCAYTCTGAGTCAG	0.23	0.32	0.32	0.15	2.06	1.38	0.56	0.32	0.05	1.78	1.26	0.58	
96	7	119736059	802354	12347	ATCTTTTAGTYCCTAATGCCT	0.35	0.36	0.32	1.98	2.11	1.33	1.75	0.27	2.25	1.79	1.23	1.61	
96	7	119743100	802359	12348	AGACTATATTWATTTAAAACT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119752747	802335	12349	ACTTTTTGCCWTAGGTTTACC	2.15	2.12	2.12	1.81	2.19	1.74	1.46	1.94	2.18	1.81	1.58	1.33	
96	7	119763267	802372	12350	GCTTAAATGARAAAGATGGTC	0.79	1.26	1.26	1.69	2.20	2.12	1.82	1.15	2.16	1.90	1.86	1.62	
96	7	119772831	802377	12351	GGTGAGAAGGKCCCTGTATTC	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119781736	802340	12352	AGTGCCAGAAMGACTAACAGG	0.11	0.22	0.13	1.77	2.14	2.22	2.22	0.11	2.08	1.90	1.92	1.90	
96	7	119787811	1881024	12353	CAGGAGAAAASGAGATTTCTA	2.68	2.62	2.62	0.98	1.90	2.25	2.33	2.44	1.10	1.71	1.93	2.03	
96	7	119794997	17142829	12354	CATTAGTACTKTCACATTACT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119805000	1358369	12355	ATATGAGGAGWCCCTGCACGC	0.25	0.12	0.23	1.78	2.29	2.33	2.76	0.18	2.27	1.99	2.03	2.48	
96	7	119820844	17142838	12356	TTACTTTTCARGTCCCTTCAA	0.43	0.66	0.66	2.08	1.53	2.28	3.24	0.61	2.45	1.49	2.10	2.87	
96	7	119823474	6466752	12357	CATCCATTTAYTATAAGTGTA	2.48	2.45	2.45	1.58	2.64	3.81	2.24	2.28	1.78	2.35	3.22	2.06	
96	7	119836736	3814461	12358	CCAAACTTCARAAAGACATTG	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119850055	17142860	12359	TTCAGTGTATRACACAGTGCA	0.08	0.07	0.07	1.98	3.01	2.42	3.23	0.03	2.05	2.65	2.20	2.78	
96	7	119860409	12530902	12360	TTTGTATTTTYGAGTATGTAT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119866915	4727911	12361	GAAACATGAGKAATCTCCCAA	1.19	1.49	1.49	1.02	2.28	2.81	2.20	1.42	1.07	2.20	2.49	2.02	
96	7	119878611		12362	AAATATTCCCYCTGGGCAGAA	0.81	1.15	1.13	1.13	0.86	1.94	2.51	1.09	1.33	0.87	1.84	2.28	
96	7	119892157	4727912	12363	ACGTGGGTTCYTGATATTTCA	1.36	1.64	1.64	1.51	1.06	0.69	1.59	1.57	1.58	1.11	0.75	1.57	
96	7	119902220		12364	TTCACACGTCRATGGTAACAT	1.24	0.90	1.06	1.37	1.33	0.66	0.52	1.00	1.57	1.27	0.67	0.53	
96	7	119911893		12365	AAGCTTATTTYTAGGTCAGTA	0.80	1.22	1.15	0.72	0.96	0.80	0.57	1.06	0.94	0.99	0.86	0.59	
96	7	119917678	7795646	12366	CTGAAAATTTRAGGATAGCAG	0.69	1.15	1.15	0.83	1.21	0.80	0.42	1.07	1.01	1.17	0.81	0.44	
96	7	119931148	6466756	12367	GAGTGAGTTTKCATTCTAATT	1.08	1.58	1.58	0.75	0.29	0.46	0.92	1.49	0.78	0.30	0.42	0.93	
96	7	119938239	17142915	12368	ATCAACCATARCGTAGCCAAG	0.94	1.39	1.38	0.61	0.18	0.46	0.54	1.35	0.62	0.17	0.47	0.55	
96	7	119947324	17142923	12369	CATCACGAACYGGGAAGTAGG	0.75	1.18	1.18	0.37	0.90	0.42	0.42	1.12	0.37	0.90	0.44	0.43	
96	7	119959734	16870517	12370	ATGTTGACAAYATTTAACATC	1.01	1.52	1.52	1.13	0.51	0.68	0.57	1.46	1.21	0.50	0.72	0.59	
96	7	119966774	12673992	12371	CTGAAGCCATRTATATTATAG	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	119986284	10245393	12372	AATATCTGAGYAATTGGGACA	0.44	0.43	0.43	1.16	0.69	0.70	0.71	0.29	1.18	0.69	0.72	0.71	
96	7	120004535	2189974	12373	TCCCGTGATCYGCCAGAACTT	0.34	0.66	0.66	0.67	0.81	0.55	0.69	0.64	0.64	0.82	0.53	0.69	
96	7	120020741	41621	12374	AGACATATCAMAAAAAGCAGC	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120041411	4730982	12375	AGCAAAAACTKTCTCTGATCA	0.23	0.49	0.49	0.46	0.43	0.86	0.87	0.41	0.47	0.43	0.89	0.87	
96	7	120053482	12669167	12376	GATGCCAGTTMTCCCATACAA	0.16	0.29	0.29	0.20	0.59	0.44	0.80	0.23	0.20	0.60	0.46	0.80	
96	7	120061998	17142988	12377	TATATTTTTASTATCAAATCT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120068119	6466761	12378	TTTCACACTTRCTAAGAACAA	0.20	0.14	0.14	0.49	0.34	0.29	0.21	0.11	0.48	0.35	0.31	0.21	
96	7	120080748	17142995	12379	TTAATCAACTYATCAGGGATA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120085933	7781985	12380	AAAGACACTCKACAGATGGCA	0.45	0.78	0.79	0.46	0.15	0.22	0.85	0.74	0.43	0.14	0.21	0.85	
96	7	120097678	17143001	12381	CATCCTACCAYGTGTAAAACA	0.46	0.79	0.77	0.13	0.25	0.97	1.04	0.73	0.10	0.23	0.98	1.05	
96	7	120105911	10279837	12382	AACCTGTGGAKATTAGCATGG	0.51	0.81	0.81	0.26	0.87	1.25	0.90	0.78	0.22	0.88	1.24	0.92	
96	7	120114698	2721343	12383	TTTCATCAACYGGGACAGTAA	0.47	0.72	0.72	1.03	1.32	0.81	1.00	0.67	1.14	1.29	0.81	0.99	
96	7	120133814	6979247	12384	GTGTTGATATSATATAGACCT	1.21	1.78	1.78	1.56	1.27	0.98	0.91	1.68	1.74	1.25	0.98	0.91	
96	7	120142047	2721332	12385	ATAAGAGAAAWGGAAAGAGAA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120154665	732568	12386	GAAGGCATAAYTGCATACTTA	1.48	2.10	2.10	1.54	1.29	1.35	1.97	1.97	1.72	1.25	1.29	1.80	
96	7	120162978	2525705	12387	TGATAATTTTKAAGAAAACTT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120171903	10261886	12388	CTGTGAACTGYAGAATTCTTT	0.99	1.66	1.66	1.27	2.07	2.34	1.77	1.48	1.43	1.80	1.96	1.62	
96	7	120178201	17143055	12389	AAGTCTTTCARAATCAAACCT	1.10	1.80	1.80	1.28	1.76	1.50	1.46	1.64	1.60	1.51	1.39	1.39	
96	7	120184033	3757556	12390	AATCAAGGCTSCATCCGTAAT	1.63	2.28	2.28	1.26	1.36	1.23	0.92	2.13	1.61	1.28	1.17	0.92	
96	7	120196963	2721350	12391	CTCTTCCATTYTTCATATATC	0.61	0.37	0.37	1.21	1.35	0.81	1.69	0.34	1.44	1.27	0.82	1.59	
96	7	120206190	2721370	12392	CATGGATTATRTACTTAGAAG	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120216738	2244865	12393	ATATGGCAAARGATTATAAGT	1.15	1.61	1.67	1.57	0.91	1.79	1.03	1.61	1.84	0.93	1.70	0.99	
96	7	120223221	2525739	12394	GACTCCAGATWTACTTTGGTA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120235682	6949989	12395	CAGATCCTGCYGTGACCCATT	1.70	1.64	1.64	0.76	2.33	1.33	1.12	1.62	0.83	2.14	1.27	1.10	
96	7	120242436	1118142	12396	ATGGTACTGGYCTTCAAGGTC	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120248241	10277935	12397	TATATGTTAARTGATCTTGTG	1.70	1.58	1.58	0.47	0.35	1.65	0.87	1.52	0.49	0.38	1.56	0.87	
96	7	120254633	16870531	12398	TGAAGGTTTAYAATAAAATAT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120260073	7808535	12399	GAGATCACTAKGATTTAGGCA	1.11	0.89	0.93	0.69	0.57	0.31	0.86	0.91	0.71	0.59	0.33	0.85	
96	7	120266993	11976117	12400	ACGTTAGGATSCAAGGAGACC	1.84	0.75	0.75	1.24	0.72	0.40	0.34	0.73	1.25	0.72	0.45	0.37	
96	7	120274187	2058501	12401	GGTGAAGAGAYCAGATTTATT	1.66	2.02	2.02	0.95	0.57	0.63	0.16	1.96	0.96	0.58	0.65	0.17	
96	7	120279398		12402	CCAACAACAGSACAATTAAAA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120299241	2721374	12403	AAAATAATCTYAATTCAACTT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120306947	13246689	12404	TCCTCTGTGTYCTTATTATAC	0.18	0.39	0.39	1.06	0.58	0.18	0.16	0.34	1.05	0.59	0.17	0.16	
96	7	120314976	17536644	12405	GATTTGCAACRTATCATCAAT	0.71	0.56	0.56	1.06	0.36	0.13	0.71	0.52	1.16	0.35	0.13	0.73	
96	7	120325528	6466767	12406	TGTAGCTACTSTTTGAAATTT	0.13	0.08	0.08	0.23	0.33	1.47	0.60	0.07	0.24	0.32	1.42	0.62	
96	7	120334054	798937	12407	TTCATTCGACKGGCACAGTTT	0.33	0.65	0.65	0.09	1.65	1.45	1.99	0.63	0.09	1.57	1.41	1.91	
96	7	120341259	13223036	12408	TCCCTAAGACKTTAACAACAA	0.11	0.15	0.15	2.30	1.75	2.31	1.57	0.13	2.47	1.65	2.11	1.50	
96	7	120347265	2037632	12409	GCTGGGCCATRTGAAGAAAGA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120356793	798946	12410	TAAGAAATAAYCATTTTCATT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120367178	10260858	12411	GGCCTGCAGAYGATCCTGCCT	0.02	0.12	0.12	0.13	3.15	2.34	1.45	0.10	0.11	2.77	2.12	1.42	
96	7	120371668	6951990	12412	TAAAGTATTGMTAATAGAGAA	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120405290	4144090	12413	TTTAATACGCYTTTACATATT	-	-	-	-	-	-	-	-	-	-	-	-	
96	7	120416337	7798060	12414	AACAGACTAGYTCTTAGCAAA	0.15	0.37	0.37	0.86	1.01	2.04	2.12	0.34	0.93	1.00	1.95	2.02	
96	7	120419893	17143194	12415	AGGAAGCAACRTGCTGGGAAG	1.32	1.83	1.83	1.19	0.65	0.69	2.07	1.75	1.39	0.70	0.70	2.01	
96	7	120451698	1404268	12416	AGTTAACACARTGATTCATTC	0.34	0.65	0.65	0.93	0.51	0.33	0.56	0.62	0.94	0.52	0.33	0.57	
97	8	11897394	4841664	12417	AACGCTCTCCSAGATACCTCA	0.39	0.38	0.38	0.10	0.39	0.38	0.29	0.32	0.07	0.40	0.41	0.31	
97	8	11933744	17224569	12418	CAGTTCAAAASTCGTCTTCTT	0.10	0.17	0.17	1.32	0.92	0.36	0.34	0.13	1.36	0.92	0.37	0.32	
97	8	12045990		12419	ATGACCTTCCRCAGGACCCAA	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12276641		12420	TCCTGGAGGTRGGCGCCTTCT	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12286039		12421	GTTTCTTAAARGAACGATAAA	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12348902	3989008	12422	TTAGTGAAGCRCTGTGCACAG	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12466783	1060797	12423	GTATATGAGGYGATAAGCCCC	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12498824	2946425	12424	ATCCACTCTGYAGTCTAGGTG	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12537298	17095001	12425	TCCTCTTGTAYGGTGCTCCTA	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12587453	7813131	12426	GCAAGAGCTARGACCCCATTA	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12601449		12427	CGTCATCATCSTCTTTATCCT	-	-	-	-	-	-	-	-	-	-	-	-	
97	8	12605551	17094925	12428	CATCACAGGARCATGTCTTCC	-	-	-	-	-	-	-	-	-	-	-	-	

97	8	12630196	4831770	12429	CCCTGTTAAGWTATCACCAAC	1.73	2.28	2.28	1.46	0.93	0.73	0.21	2.22	1.54	0.92	0.71	0.18
97	8	12637327	13251315	12430	AAACTATCCAMTGAAAAGCTT	0.70	0.36	0.36	1.92	1.57	0.68	0.46	0.32	2.29	1.51	0.67	0.47
97	8	12643838	7014429	12431	AAGCTTTAAAYGTTCCTTGCT	-	-	-	-	-	-	-	-	-	-	-	-
97	8	12651605	6991754	12432	GATCTTTTTARTAACCCTGAG	1.36	1.33	1.33	0.81	2.64	1.50	1.10	1.29	0.86	2.44	1.46	1.07
97	8	12659279	4072535	12433	GAGTTCCTTTYCCTAATAAAT	-	-	-	-	-	-	-	-	-	-	-	-
97	8	12667407	17830061	12434	ACCACAAGCTSCATCTATCAG	1.22	0.32	0.35	0.55	0.71	2.83	2.54	0.31	0.54	0.72	2.71	2.39
97	8	12677215	4316156	12435	AGAGATAGCCYAAGCGTTGTC	-	-	-	-	-	-	-	-	-	-	-	-
97	8	12708688	7828368	12436	TTCTGAGAGGWGTAAAAAAAT	0.12	0.33	0.33	0.05	0.84	2.13	3.29	0.30	0.04	0.83	2.11	3.10
97	8	12719992	17830672	12437	TAAAATCAGAYGAAGCCTCGA	0.28	0.04	0.03	0.52	0.69	1.22	1.27	0.00	0.57	0.71	1.21	1.29
97	8	12730375	7814546	12438	TTCAGAAGGARTGATATATGA	0.41	0.72	0.72	0.64	1.69	0.26	0.92	0.68	0.65	1.60	0.27	0.93
97	8	12740420	4587336	12439	ATGCTTATGTYTATAGGTATC	0.23	0.25	0.25	0.48	0.46	1.76	0.38	0.23	0.47	0.50	1.67	0.39
97	8	12747610	17120712	12440	TTTCCTGGTTKATTCATATAG	0.48	0.87	0.87	0.54	0.79	0.65	0.56	0.81	0.53	0.83	0.70	0.59
98	8	17021982	2705191	12441	CTAAGCCTAARATTGAGGATT	0.52	0.19	0.19	0.22	0.27	0.38	0.42	0.18	0.22	0.27	0.38	0.42
98	8	17030333	1158577	12442	AATACAGGCTRTATGTGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
98	8	17037592	929152	12443	TAATAGGATGWTCTCTGTAAT	0.02	0.04	0.04	0.54	0.44	0.71	1.24	0.02	0.54	0.46	0.70	1.23
98	8	17047096	2959592	12444	CCAAATGTGTYGAATGGATGA	0.21	0.47	0.47	1.14	2.15	1.12	1.06	0.41	1.22	2.01	1.15	1.03
98	8	17062812	2517065	12445	ATGTGGGAAGSTAGACCACTA	-	-	-	-	-	-	-	-	-	-	-	-
98	8	17069804	1034557	12446	GTTTTAGTAGKTTTCAGATAA	0.46	0.71	0.67	1.94	1.11	2.06	1.44	0.64	2.08	1.08	1.99	1.43
98	8	17076986	6993403	12447	TTCTAGCATASTTTAGCTCAG	1.57	1.65	1.55	0.91	1.98	1.55	2.97	1.43	0.98	1.90	1.50	2.83
98	8	17086787	2517086	12448	ATAAATTGTTSTTTGAGAATG	0.97	0.84	0.84	0.71	0.42	0.96	1.32	0.77	0.77	0.43	0.96	1.30
99	8	17804143	537523	12449	AAAGATAATAMATCATTTCAT	0.01	0.00	0.02	0.73	0.71	0.96	0.37	0.00	0.75	0.72	0.98	0.36
99	8	17817119		12450	ATCCTCTCCTSCTTCAACTTC	-	-	-	-	-	-	-	-	-	-	-	-
99	8	17824437	7814692	12451	TAGGCCTAGGRCCCCACGCTC	-	-	-	-	-	-	-	-	-	-	-	-
99	8	17830796	438873	12452	CCTTATGACCRTCTGTGCTTG	-	-	-	-	-	-	-	-	-	-	-	-
99	8	17837133	478420	12453	CATGCAGACTRGTGCTCACAA	0.60	0.65	0.65	0.34	0.73	0.46	0.43	0.60	0.34	0.75	0.49	0.43
99	8	17843521	10108545	12454	GTTTCAGACAYTGACGTTACT	0.83	0.63	0.63	0.87	0.67	0.38	0.29	0.60	0.88	0.71	0.37	0.29
99	8	17849728	208765	12455	GTGAATTAGAYGAAAGTTGTG	1.59	1.82	1.82	0.89	0.73	0.28	0.47	1.78	0.89	0.72	0.27	0.49
99	8	17856857	17514360	12456	CACATGATTCRTAGTGGCCCT	-	-	-	-	-	-	-	-	-	-	-	-
99	8	17862718	208062	12457	AAAGACAGCAYATAGGAATTG	0.73	1.02	1.03	1.39	0.69	0.45	0.20	1.01	1.55	0.71	0.47	0.21
99	8	17869607	208053	12458	TTAGGGGGATRCTAATAGACT	0.08	0.00	0.00	0.98	1.67	0.55	0.24	0.00	1.01	1.59	0.58	0.24
99	8	17872635	6996133	12459	ACTTCAGATTRGACCTCATTT	0.62	0.30	0.33	1.22	0.59	0.83	0.32	0.28	1.36	0.60	0.84	0.33
99	8	17880679	2299598	12460	ATGATGATTTKTTACCAGGAA	-	-	-	-	-	-	-	-	-	-	-	-
99	8	17889727	439511	12461	TCATTCTCTAKATGCTTCTAT	1.51	1.13	1.02	0.84	0.96	0.27	0.40	0.84	0.85	0.95	0.29	0.43
100	8	49970615	6987879	12462	GTGAATTCTGYGAATAAAAAC	0.63	0.87	0.85	0.79	0.37	0.53	0.21	0.78	0.90	0.39	0.54	0.22
100	8	49979886	7011862	12463	ACTTAAATCTSTGCACAAGTA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	49986758	1023768	12464	CCAAGTGCCAMAACGGAAAAG	0.21	0.06	0.08	0.36	0.63	0.27	0.33	0.06	0.33	0.64	0.30	0.31
100	8	50004799	16939083	12465	CTAGCAGAGCRCCATAGCAGG	0.32	0.19	0.19	0.77	0.22	0.48	0.69	0.15	0.78	0.24	0.53	0.74
100	8	50007761	1441005	12466	GAGTAGCACCYGGGAGAGCAG	0.20	0.10	0.10	0.08	0.88	0.74	0.53	0.09	0.10	0.89	0.75	0.55
100	8	50044592	16939200	12467	GATAATGTTAYGGATGTAGAA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50047370	17641971	12468	GGACAGATAGYGTCTTCACTG	0.31	0.15	0.15	1.39	1.67	1.23	0.85	0.13	1.52	1.51	1.18	0.85
100	8	50063318	17642290	12469	ACAGTCATGAYCATACTGTAT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50096190		12470	CCATGTGCCCRAACCTGTTTT	0.64	0.96	0.96	1.55	2.15	1.58	1.21	0.90	1.67	2.00	1.56	1.19
100	8	50105498	17642664	12471	TTCATGTCCARCATTCTCAAT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50114530	12545097	12472	AGAGTCTGAARGAGCCTAGTG	0.57	0.97	0.97	1.47	1.82	1.85	0.89	0.93	1.49	1.75	1.73	0.89
100	8	50123083	1467089	12473	AACCAGGCTGYGCTTCAGGAT	0.47	0.86	0.92	1.23	1.28	1.67	1.00	0.83	1.34	1.25	1.58	1.02
100	8	50129213	7844223	12474	TCTTTCTACTRTCATGCCCCA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50140977	341815	12475	TCCCTATTGAMGTCCGAGTTG	0.56	0.42	0.42	0.48	0.90	0.95	0.84	0.36	0.45	0.90	0.95	0.85
100	8	50147741	3735973	12476	TTTTTATTGCRGTATATTTGG	0.23	0.46	0.46	0.82	0.91	0.74	1.04	0.41	0.84	0.89	0.74	1.03
100	8	50154286	10504071	12477	TGTGTATATCSTCTCTCGTTA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50161898	13439096	12478	TTACAGTCTCYTACAACTAAT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50169001	1511359	12479	GGCTAGAGCTWAAGCCTGTAA	1.15	1.62	1.62	1.51	1.22	0.87	1.14	1.57	1.60	1.20	0.88	1.17
100	8	50181977	17644430	12480	TAAGAATACASCCTGGGTACA	0.09	0.17	0.17	1.19	1.34	0.84	1.10	0.14	1.31	1.26	0.82	1.07
100	8	50187447	12056729	12481	CACTTTTTTGYGTCAGTAAAG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50200379	2667282	12482	CTAATGTTAGYGCACAGGTGC	0.79	1.20	1.20	1.27	0.56	1.68	1.95	1.15	1.39	0.57	1.64	1.86
100	8	50205110	341809	12483	ACATAATTACRTCATTGGGAA	1.32	1.74	1.81	1.16	1.88	1.48	1.55	1.78	1.14	1.81	1.43	1.49
100	8	50226545	2667289	12484	GAAGAAAGCARGACTTGGAGC	1.54	1.87	1.79	1.40	2.44	1.75	1.49	1.75	1.36	2.28	1.64	1.43
100	8	50232651	13264833	12485	CTAGTTCTAAYGTTTTACCTC	2.04	2.53	2.50	1.73	1.64	2.37	1.97	2.44	1.87	1.58	2.18	1.86
100	8	50238674	2726709	12486	GAGCAAAGACRGTGGCTGTAA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50249732	2726713	12487	CAATAGTATAYAGAAAAAAAG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50257441	10093506	12488	CACTTTTGTTWAGGTTTTAAA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50265081	6983404	12489	ATGGCATTCTKCCTTTTGTTT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50271632	4617168	12490	AGCAAGGCTGYCTTCCATATA	2.64	3.02	3.02	2.04	2.35	1.69	2.21	2.89	2.44	2.13	1.63	2.11
100	8	50281080	7012516	12491	CACCTGAATAYGATCCTGTCT	2.07	2.51	2.51	2.75	3.00	2.33	1.40	2.44	3.36	2.69	2.21	1.37
100	8	50291990	11783895	12492	ATACAAAAACKTTCAAATGTT	2.66	2.94	2.94	2.06	2.03	0.93	1.25	2.84	2.17	1.91	0.96	1.23
100	8	50296491	12681413	12493	AAGTACTGAGRTGTATTATGA	0.14	0.13	0.13	1.93	0.90	1.11	1.34	0.06	2.03	0.89	1.08	1.27
100	8	50306408	9792221	12494	TTGCAGTAACWTTTAGGTAAG	1.53	1.56	1.56	1.61	1.32	1.30	1.23	1.51	1.67	1.28	1.22	1.18
100	8	50311915	10095176	12495	GACATATGAGWTCACGTGCTG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50330939	17720676	12496	TTGCCAGTGTRTCAGTGGTTA	2.74	2.94	2.94	1.30	2.12	1.39	1.95	2.85	1.47	1.94	1.31	1.84
100	8	50336884	7001632	12497	AACACGATAGYGTGATTTCCG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50354748	16906401	12498	GTGCTACAGGYACATCATAAA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50362515	17721252	12499	CAAAGCAGGARGACCATAATT	0.16	0.37	0.37	1.70	2.03	2.78	3.13	0.31	1.88	1.84	2.48	2.80
100	8	50370584	16906585	12500	ACTGGAACCCWCCATCTGGTA	2.24	2.25	2.25	1.32	2.34	4.40	3.62	2.18	1.37	2.18	3.72	3.16
100	8	50381333	10808757	12501	ATAACGGTAARTGACCGGAAT	2.66	2.57	2.57	2.39	2.20	2.74	3.08	2.49	2.97	2.00	2.47	2.72
100	8	50395558	9650228	12502	AAATCCAGTCRTCCTTCCTTC	0.49	0.84	0.81	2.85	2.83	2.02	1.13	0.73	3.12	2.48	1.90	1.11
100	8	50401478	12541173	12503	TTTAGCTCCAYTTAAGTTCAT	1.27	0.93	0.93	1.24	2.66	1.18	0.71	0.89	1.41	2.42	1.13	0.71
100	8	50407353	10504078	12504	GATTATATAARCCTAGAGAAT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50416477	7013162	12505	ATTTTTTTTTYACTTGACGTA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50428219	17666866	12506	ACAGGCAGAGMTGCACCATTG	0.89	0.17	0.17	0.28	0.56	0.92	0.84	0.15	0.25	0.60	0.91	0.84
100	8	50443089	6989207	12507	CGCCCAGTGCRTCTGGTCCTG	0.50	0.84	0.84	0.27	0.09	0.42	1.54	0.73	0.31	0.08	0.46	1.48
100	8	50451575	5005696	12508	ATATTTTAAGSAAGGACTGGA	0.57	0.69	0.69	0.21	0.41	0.57	1.19	0.66	0.20	0.42	0.58	1.18
100	8	50459222	13277322	12509	AGGTAGTTCTYCCATGTGTCC	0.48	0.37	0.37	1.33	0.89	1.55	0.99	0.34	1.56	0.89	1.49	0.98
100	8	50465872	13275508	12510	GACAATGAATRTAGTTGTTAA	1.01	0.77	0.69	1.41	2.03	1.63	1.45	0.66	1.63	1.96	1.59	1.40
100	8	50472635	10090221	12511	ATATATGAAAYGAAGCACCTG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50476541	11778771	12512	CAGGAGCAGAMGCCAAGACAG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50492945	1715315	12513	TAATTAGGAGYATTTTATAGA	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50512976	1356753	12514	TCACTTGTAGMATGGGGAAGT	0.87	0.51	0.51	1.52	2.34	1.70	2.04	0.48	1.81	2.27	1.61	1.91
100	8	50521666	769127	12515	ACTTTGAAAARTTACTTTGCC	0.58	0.28	0.26	1.71	1.93	2.73	1.74	0.25	2.08	1.71	2.52	1.65
100	8	50530338	7819847	12516	ACAAAGCCTAYCTTGTTCTTT	0.75	0.42	0.42	1.41	2.15	1.37	1.27	0.39	1.72	1.97	1.30	1.25
100	8	50538708	1674264	12517	ATAGAAATTTRTGAGCTTCTT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50546675	1356751	12518	AGAAAATCAARGTTGGGAGAG	0.81	0.72	0.67	0.54	1.29	1.00	0.79	0.61	0.52	1.28	1.01	0.83
100	8	50564628	1598951	12519	TAAAGACCTAYAATTCAGCCT	0.27	0.38	0.38	0.68	0.17	0.95	0.83	0.33	0.66	0.19	0.95	0.83
100	8	50570760	13279658	12520	CAAAGTTATTKAGAATCTGAC	0.54	0.63	0.62	0.72	0.36	0.15	0.99	0.54	0.74	0.40	0.14	0.97
100	8	50576653	1715329	12521	AAGTTCTCTTRTTTGTTGATT	0.53	0.90	0.90	0.17	0.42	0.35	0.19	0.80	0.12	0.42	0.38	0.19
100	8	50588584	1715338	12522	GGAGTCACCAYAGGGGCAAGA	1.38	1.08	0.88	0.42	0.08	0.31	0.21	0.80	0.40	0.08	0.30	0.25

100	8	50594566	1674241	12523	TTCAACTCTGYGCTTTAGGGA	1.38	1.07	1.07	0.57	0.24	0.08	0.15	1.00	0.57	0.23	0.08	0.15
100	8	50600903	2926111	12524	GCAATTAGCAYATTGTTCAAT	1.44	1.13	1.06	0.42	0.21	0.09	0.14	0.98	0.37	0.19	0.08	0.11
100	8	50622669	2926090	12525	ACATCTCTTCYTGTTTAATGA	1.29	1.00	1.00	0.39	0.10	0.30	0.08	0.91	0.41	0.10	0.35	0.06
100	8	50629668	2926092	12526	TATTTCTGTCWGATGGTGAGT	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50635491	6989187	12527	ACGATTCCTCRTTAACAGGGC	1.24	0.51	0.51	0.33	0.43	0.10	0.10	0.48	0.30	0.43	0.09	0.12
100	8	50641101	2926095	12528	GTTCCTTCTCRTCATCAGCAG	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50654805	1531273	12529	AAATCAGAAARTCCTGTGTTC	-	-	-	-	-	-	-	-	-	-	-	-
100	8	50669075	7838995	12530	TTCCCCACTCRAACTCAGACG	1.19	0.91	0.91	0.47	0.20	0.15	0.04	0.83	0.43	0.20	0.14	0.04
101	8	93426382	1480888	12531	GGACAGGTGCWGTAGTTTTAT	0.06	0.02	0.02	0.30	0.36	0.32	0.32	0.00	0.27	0.39	0.36	0.36
101	8	93438475	16914930	12532	AAATGCCACARTTGGTGGATT	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93456758	4735167	12533	GAGCCCATGARTAGCGAACTC	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93462507	10808648	12534	CAGCTTCCTTRTCTGTCAAAC	0.41	0.76	0.76	0.31	0.42	0.20	0.11	0.70	0.29	0.45	0.20	0.11
101	8	93470854		12535	TACACTAGGGYAGAATATTTG	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93489470	2062009	12536	ATCAATTCGCRTATCTGCAAA	0.52	0.92	0.96	0.36	0.14	0.08	0.07	0.94	0.33	0.15	0.09	0.10
101	8	93493797	9297909	12537	TGGAATTGATKGTGGCCCAAA	0.47	0.88	0.88	0.34	0.08	0.02	0.14	0.82	0.34	0.07	0.02	0.13
101	8	93512633	12156060	12538	TTCTAAGAGCRATCAAAAACC	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93519888	16914981	12539	ACATACTGCTRGCTTATAGTC	0.06	0.22	0.27	0.12	0.06	0.02	0.02	0.22	0.14	0.08	0.01	0.02
101	8	93526313	11776701	12540	TGGAGCTTCCRTCTAACTCCA	0.49	0.06	0.06	0.07	0.04	0.04	0.01	0.04	0.05	0.03	0.03	0.01
101	8	93539837		12541	CATCACTCAASACATCAGCTT	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93551870	13249669	12542	CCTGGGGCTCRCGTTCAGTAC	2.78	0.06	0.06	0.09	0.02	0.02	0.01	0.04	0.06	0.01	0.02	0.01
101	8	93559132	7002123	12543	CCCTAATGCCRAGGATGTCCA	1.60	0.06	0.06	0.06	0.03	0.04	0.02	0.04	0.03	0.03	0.03	0.02
101	8	93571476	549043	12544	TCTTTGTACCRTATTGCCCTT	0.11	0.32	0.32	0.09	0.06	0.09	0.58	0.27	0.06	0.05	0.09	0.57
101	8	93582042	532481	12545	GTATCAAATAYCTTTCCAGCA	0.35	0.00	0.00	0.56	0.16	0.77	0.69	0.00	0.57	0.16	0.78	0.70
101	8	93590941	543027	12546	TCTTCTAGATRAGGCATTAAG	1.10	1.65	1.65	0.96	2.23	1.15	0.46	1.53	1.05	1.97	1.17	0.46
101	8	93617489	16915030	12547	AATATGAACAYGTTAAGATGT	0.37	0.72	0.72	3.05	2.86	1.08	0.58	0.65	3.48	2.61	1.07	0.60
101	8	93626803	2069134	12548	GAGCACATTGYTTTTGTATTA	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93633773	935712	12549	AAGCAAAATAYACAGAAACAT	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93660187	1900897	12550	CTATATTTTGRTTTAAGTTGA	1.97	2.68	2.68	3.51	3.57	1.40	0.73	2.58	3.68	3.15	1.32	0.74
101	8	93673501	2339654	12551	TTTTTGGCCCRTGTGGGAAGG	1.76	2.35	2.35	2.96	2.42	1.94	1.48	2.33	3.17	2.22	1.88	1.47
101	8	93684765	10156291	12552	TGAGTTTTCCRTTCCACTACA	1.10	1.62	1.62	1.20	2.83	2.10	2.95	1.55	1.27	2.58	2.03	2.74
101	8	93688001	2167029	12553	CAGTAATGGTRTTTTGGATGA	0.00	0.00	0.00	0.65	1.07	3.09	2.33	0.00	0.64	1.05	2.80	2.24
101	8	93712381	10088474	12554	CATGCTAGCCRCTGGATATAC	0.84	0.83	0.83	0.69	0.48	1.11	1.33	0.78	0.66	0.49	1.10	1.30
101	8	93722238	2053851	12555	CTGGGGGCATRTTCTATAAAG	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93729883	7819644	12556	TCTCAAAGACRGACGTAATGC	1.09	1.32	1.36	0.54	0.38	0.38	0.82	1.30	0.56	0.42	0.40	0.83
101	8	93738014	7820708	12557	TGAGGGCTCARACATGTGGAG	1.48	1.10	1.10	0.47	0.34	0.14	0.19	1.02	0.47	0.35	0.14	0.20
101	8	93750484	873545	12558	ATGTTTCCACRTGTATCCTAC	1.09	0.94	0.93	0.71	0.29	0.21	0.17	0.87	0.74	0.29	0.22	0.19
101	8	93752448	2461430	12559	ATCCTCTCACRGTGGACAGAA	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93765637	7817246	12560	AATTTTGTATRAGAAAATGAC	0.10	0.08	0.08	0.43	0.38	0.26	0.19	0.03	0.45	0.37	0.27	0.21
101	8	93775732	16915212	12561	TCGCAAGAGASAGTTTTTGCA	0.09	0.04	0.05	0.23	0.19	0.25	0.10	0.03	0.19	0.18	0.26	0.11
101	8	93784931	16915215	12562	AAATTTTTCAYGTGACAAATT	-	-	-	-	-	-	-	-	-	-	-	-
101	8	93794699	17686978	12563	GAATCAGATGYTTGCCAGACA	0.01	0.04	0.04	0.14	0.08	0.04	0.21	0.02	0.11	0.09	0.04	0.24
101	8	93800460	16915218	12564	GGAGATTGCCYGCCTACTGGC	0.60	0.07	0.08	0.15	0.00	0.02	0.09	0.05	0.13	0.00	0.02	0.11
101	8	93808252	16915219	12565	GTCCACAAAAYTGGGAGAGGC	0.51	0.03	0.03	0.03	0.10	0.03	0.03	0.00	0.02	0.10	0.03	0.02
102	8	101940093	1995564	12566	CGAGAAGTCGYCACTGGAAAT	0.04	0.13	0.07	0.17	0.27	0.07	0.47	0.04	0.14	0.29	0.06	0.48
102	8	101947090	4734491	12567	CCCCTTCCTAYTCTGATCCTG	0.06	0.10	0.10	0.40	0.31	0.29	0.24	0.08	0.41	0.31	0.28	0.22
102	8	101956206	2135121	12568	ATGGCTCCTTRTTTCCTGCTG	0.52	0.78	0.78	0.77	0.41	0.41	0.06	0.76	0.76	0.47	0.41	0.07
102	8	101967883	6993937	12569	GATATCAAGGYGCCTTAAGAC	0.87	1.13	1.13	1.45	0.73	0.15	0.17	1.09	1.58	0.74	0.17	0.17
102	8	101980812	1354588	12570	AGTTATGGAGSCCAGGGTCAC	0.61	0.97	0.98	1.45	1.37	0.76	0.34	0.96	1.52	1.34	0.74	0.39
102	8	101986993	4734495	12571	AAACATGGGTMAAAAATGCAC	-	-	-	-	-	-	-	-	-	-	-	-
102	8	102000610	11551356	12572	CAGAAGGCTARAACAGGAAGG	0.82	1.31	1.22	1.91	3.56	2.22	0.74	1.11	1.99	3.16	2.09	0.74
102	8	102006550	3105460	12573	AAACTTAAACRCCCAGTCACT	-	-	-	-	-	-	-	-	-	-	-	-
102	8	102012580	17365661	12574	CAGTTTCCAAMAGATGCCTTA	-	-	-	-	-	-	-	-	-	-	-	-
102	8	102019214	1470764	12575	GTGATTCTCARTAAGTACAGC	2.52	3.33	3.33	4.20	3.47	3.30	2.61	3.29	4.59	3.16	2.91	2.39
102	8	102028785	1901362	12576	GATACAAATARTAGCTATCAT	1.85	2.42	2.56	2.54	4.26	4.13	1.49	2.47	2.63	3.67	3.49	1.45
102	8	102044655	2386922	12577	TAAATTTTCTKTATGTTCATT	1.54	2.19	2.19	3.01	5.45	3.01	1.95	2.12	3.38	4.52	2.78	1.80
102	8	102058355	16898877	12578	TGTGACACTTRAATGTAGCTT	0.25	0.65	0.60	1.48	3.31	2.76	2.76	0.51	1.55	2.98	2.56	2.53
102	8	102070403	16898881	12579	GAGTAGAACARTCTGTGTTTT	0.07	0.07	0.04	0.07	1.02	2.98	2.70	0.00	0.06	1.00	2.72	2.52
102	8	102081250	17366941	12580	CCTGCAGTATSAGAACAGTAC	0.06	0.21	0.21	0.17	0.24	1.29	2.28	0.18	0.14	0.24	1.25	2.16
102	8	102085828	17367026	12581	GAATACTTTTYGTGAGAGAAT	0.02	0.09	0.09	0.64	0.59	0.17	1.11	0.07	0.72	0.63	0.18	1.11
102	8	102097272	16898901	12582	AAATTGAACAYTAAAATGTAT	1.01	1.58	1.20	1.02	0.66	0.46	0.19	1.06	1.18	0.63	0.46	0.19
102	8	102110383		12583	AACTTAATACRTGCCCAACTT	-	-	-	-	-	-	-	-	-	-	-	-
102	8	102123518		12584	GAGACAGGAGMAGGGGGCCTG	0.71	0.71	0.55	0.82	0.78	0.67	0.13	0.39	0.87	0.77	0.68	0.13
102	8	102129591	4734512	12585	TGATTCGCTARGCAGCTGTTG	-	-	-	-	-	-	-	-	-	-	-	-
102	8	102143162	13277673	12586	CTTTTCCAGAYGCTGTACTTG	0.24	0.46	0.53	0.74	0.89	0.32	0.25	0.51	0.77	0.86	0.35	0.26
102	8	102160689	809605	12587	TCCTGGCTGGSTTTATCAGAT	0.40	0.62	0.56	0.21	0.22	0.19	0.14	0.52	0.20	0.24	0.17	0.13
102	8	102172569	776259	12588	TCCTGGGAGGYGAGAGAGGAG	0.28	0.59	0.59	0.17	0.03	0.15	0.88	0.54	0.14	0.02	0.16	0.87
102	8	102177767	287207	12589	GCAGAGGCCTSGTCCCACAGT	-	-	-	-	-	-	-	-	-	-	-	-
102	8	102189451	7823735	12590	TTTACAGTTAYATTTGACTAC	0.18	0.34	0.41	0.26	0.04	0.34	0.35	0.35	0.25	0.04	0.37	0.33
102	8	102200330	3886153	12591	TGACTAGATTYTTCTCCCCTG	0.26	0.54	0.54	0.59	0.45	0.13	0.23	0.51	0.61	0.48	0.12	0.23
102	8	102202011	895602	12592	CTGCTTTACARATGAAGTGAC	1.57	1.59	1.59	1.21	1.12	0.11	0.01	1.51	1.17	1.08	0.13	0.01
103	8	102502616	1264475	12593	GAGAAAGGAGKATTTTATTTC	0.58	0.64	0.64	0.19	0.62	0.24	0.24	0.57	0.18	0.65	0.23	0.25
103	8	102513596	17473848	12594	AGAGGGAAGTYAGTTCCAATG	0.12	0.12	0.12	0.58	0.13	0.15	0.01	0.06	0.57	0.12	0.16	0.01
103	8	102538911	10108791	12595	TAAGATTGGARACCAAATGTC	0.18	0.04	0.04	0.02	0.21	0.01	0.03	0.03	0.01	0.21	0.01	0.04
103	8	102544654	519526	12596	ATGTGACTAASAACGGGCGGT	0.40	0.14	0.14	0.24	0.01	0.01	0.02	0.09	0.24	0.00	0.01	0.02
103	8	102551719	7813465	12597	GCAGTTTAGGRATGAGAGAAA	0.48	0.41	0.41	0.01	0.03	0.02	0.00	0.38	0.01	0.03	0.03	0.00
103	8	102559664	7006940	12598	ATTCTTCTTAYGTGGAAGACC	0.03	0.03	0.03	0.05	0.01	0.02	0.03	0.00	0.05	0.01	0.01	0.03
103	8	102569031	665572	12599	GCTAAGGGTGKGCAACTTTAT	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102578495	502216	12600	GTATCACCAGYTTAATGTTGA	0.71	0.37	0.23	0.07	0.16	0.06	0.15	0.17	0.03	0.16	0.06	0.17
103	8	102585680	475304	12601	TATCTGTGTCKCCACAACCTT	0.45	0.23	0.14	0.06	0.07	0.38	0.77	0.07	0.03	0.07	0.38	0.79
103	8	102591229	485194	12602	TCTTCTCCTAYTTTTTTTTAC	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102597016	471757	12603	CCTTTCTCCCRTGAGGCATGC	0.12	0.17	0.17	0.36	0.07	0.53	0.68	0.15	0.36	0.06	0.54	0.67
103	8	102603243	1871236	12604	TGGTAATAAGYTGACTTGAAC	0.86	1.09	1.09	0.36	0.97	0.35	0.76	0.94	0.38	0.95	0.36	0.78
103	8	102613751	922466	12605	GGTCATTTTTYTGCTAGGGAG	0.54	0.22	0.22	1.52	0.74	0.80	0.46	0.19	1.65	0.72	0.78	0.47
103	8	102624477	6984360	12606	ATAGACAGTARAAAAATAAAT	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102641028	2509767	12607	ATCAAGTGTGYGTATGTGTGC	0.65	0.18	0.18	0.25	1.78	0.37	0.43	0.15	0.24	1.70	0.39	0.43
103	8	102655564	11787301	12608	GTAAGTCAGARCCCCTCTGTG	0.06	0.17	0.17	0.34	0.30	1.05	0.61	0.14	0.32	0.29	1.01	0.63
103	8	102662638	11996871	12609	TGGAAGCCAGWTTGATATGCG	0.07	0.01	0.04	0.42	0.06	0.39	1.55	0.00	0.43	0.06	0.38	1.50
103	8	102668373	17477457	12610	TAAATACCTCYGAGACTTAAT	0.22	0.33	0.33	0.13	0.16	0.26	1.37	0.30	0.10	0.19	0.26	1.35
103	8	102681248	6999402	12611	TCTTTGATTTYATGAAAACCC	0.30	0.28	0.28	0.20	0.10	0.20	0.49	0.22	0.15	0.10	0.21	0.48
103	8	102688350	7829364	12612	AGGAGTAAATYGGAGAAAACA	0.34	0.32	0.32	0.15	0.20	0.37	1.00	0.28	0.09	0.21	0.36	0.94
103	8	102695424	2032120	12613	TCAAAGGTAGRCCCATTTATT	0.08	0.27	0.31	0.15	0.27	1.85	0.83	0.28	0.14	0.28	1.82	0.82
103	8	102702489	1357984	12614	TCTGTGAACAMACCAGATGGG	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102718857	13275653	12615	CCTTTTCAATYGTAGGTAAGA	0.34	0.27	0.27	0.53	1.82	0.99	1.22	0.25	0.56	1.73	0.97	1.17
103	8	102727585	2387623	12616	CTTTAAAAAAWTTTCTGATTT	0.44	0.78	0.78	2.39	1.33	1.36	0.95	0.73	2.71	1.32	1.29	0.98

103	8	102733591	16868138	12617	ACTAGTGCACRACACTTTACC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102740226	4734570	12618	AAAGTTCAAAWAAAACCAACT	2.40	2.97	2.99	2.29	2.81	1.26	0.90	2.87	2.47	2.62	1.22	0.93	2.40	2.97	2.99	2.29	2.81	1.26	0.90	2.87	2.47	2.62	1.22	0.93
103	8	102746981	4734573	12619	AGTGAGATTTSAGTCGTGTCT	1.54	1.93	1.93	1.93	2.01	2.01	0.45	1.86	2.26	1.95	1.96	0.43	1.54	1.93	1.93	1.93	2.01	2.01	0.45	1.86	2.26	1.95	1.96	0.43
103	8	102752027	16868197	12620	TCTCCCCAGCKGTCCAAGTAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102771226	6990400	12621	GGCAGCACCCRGTTGGTTCCC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102781933	6468785	12622	GGGTCCCCTGSTGGCAAGTAA	2.78	3.36	3.31	1.66	0.98	0.94	0.83	3.22	1.73	0.95	0.91	0.81	2.78	3.36	3.31	1.66	0.98	0.94	0.83	3.22	1.73	0.95	0.91	0.81
103	8	102788809	7844804	12623	AGGAGGATAARCTGTTTTTGC	1.30	1.77	1.77	1.74	0.93	0.62	0.66	1.71	1.94	0.95	0.66	0.67	1.30	1.77	1.77	1.74	0.93	0.62	0.66	1.71	1.94	0.95	0.66	0.67
103	8	102801328	12681368	12624	TCAGAGAGAGYGTGAGGTAGA	0.74	0.98	0.98	1.37	1.16	0.71	0.54	0.96	1.43	1.15	0.70	0.54	0.74	0.98	0.98	1.37	1.16	0.71	0.54	0.96	1.43	1.15	0.70	0.54
103	8	102812245	16868264	12625	ACTTATTCTTRTACATCTATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102818744	7844292	12626	TTTCTTAATCMAAGCCTTCAC	2.19	1.75	1.75	1.31	0.76	0.96	0.79	1.66	1.41	0.77	0.96	0.79	2.19	1.75	1.75	1.31	0.76	0.96	0.79	1.66	1.41	0.77	0.96	0.79
103	8	102825162	13252722	12627	TATCAGAATCRAATTATAAAA	2.05	1.06	1.06	1.09	0.81	0.68	1.02	1.05	1.20	0.82	0.66	1.03	2.05	1.06	1.06	1.09	0.81	0.68	1.02	1.05	1.20	0.82	0.66	1.03
103	8	102831972	1111886	12628	TAAAATGGCARCAGGCACGCC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102838560	10955275	12629	GTTTACCCACSATGGCCTTCA	2.25	1.00	1.00	0.56	0.84	1.11	0.69	0.90	0.60	0.82	1.08	0.69	2.25	1.00	1.00	0.56	0.84	1.11	0.69	0.90	0.60	0.82	1.08	0.69
103	8	102851284	10108160	12630	ACTTACATTCKCAGGACTCTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102857476	16868417	12631	GGGAACAGCAYGAACCCCAGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102863297	16868426	12632	GAACATTCTGRTAGTTGCCAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102868670	7830291	12633	TATCAAGTTGYTAGAGACTCA	1.72	0.88	0.88	0.63	0.58	0.71	1.11	0.82	0.65	0.61	0.70	1.09	1.72	0.88	0.88	0.63	0.58	0.71	1.11	0.82	0.65	0.61	0.70	1.09
103	8	102875570	7009385	12634	CAGGGTAGATKGCTCAAGTGT	2.11	0.83	0.83	0.45	0.27	0.42	0.64	0.78	0.49	0.28	0.39	0.64	2.11	0.83	0.83	0.45	0.27	0.42	0.64	0.78	0.49	0.28	0.39	0.64
103	8	102889113	11783384	12635	ACTTGCAGTCRTAAAGGGTTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102901192	16868487	12636	AGCAGCAGCGSCGGTGGTACA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102910537	7828175	12637	TCTCACCTTCMTTCTTCATGA	0.58	0.36	0.36	0.15	0.30	0.24	0.31	0.31	0.12	0.34	0.26	0.31	0.58	0.36	0.36	0.15	0.30	0.24	0.31	0.31	0.12	0.34	0.26	0.31
103	8	102916438	2155938	12638	AGATTAACTGSGTCAAAAGTT	0.32	0.30	0.30	0.09	0.16	0.19	0.19	0.24	0.08	0.13	0.19	0.20	0.32	0.30	0.30	0.09	0.16	0.19	0.19	0.24	0.08	0.13	0.19	0.20
103	8	102922577	16868516	12639	ATCTTTCTAAYTCACTGGGTC	0.37	0.37	0.37	0.27	0.20	0.15	0.11	0.26	0.25	0.19	0.15	0.10	0.37	0.37	0.37	0.27	0.20	0.15	0.11	0.26	0.25	0.19	0.15	0.10
103	8	102927953	1148499	12640	CATTCTAGCTSTATTTGGGTG	0.23	0.07	0.07	0.54	0.13	0.23	0.09	0.05	0.58	0.13	0.26	0.08	0.23	0.07	0.07	0.54	0.13	0.23	0.09	0.05	0.58	0.13	0.26	0.08
103	8	102935663	478092	12641	TGCTGCCCTGRACATGACTGT	0.41	0.12	0.12	0.04	0.15	0.18	0.20	0.08	0.02	0.17	0.21	0.21	0.41	0.12	0.12	0.04	0.15	0.18	0.20	0.08	0.02	0.17	0.21	0.21
103	8	102946349	489973	12642	AATCTTTATCYGTCTTAAGGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
103	8	102954321	544928	12643	TCACATCATAYGAGAGAGAGA	0.68	0.27	0.27	0.17	0.36	0.14	0.11	0.25	0.17	0.34	0.16	0.11	0.68	0.27	0.27	0.17	0.36	0.14	0.11	0.25	0.17	0.34	0.16	0.11
103	8	102965317	490032	12644	CTATCAGCAGWGTCATTATAC	0.58	0.31	0.33	0.04	0.24	0.26	0.07	0.31	0.03	0.24	0.26	0.08	0.58	0.31	0.33	0.04	0.24	0.26	0.07	0.31	0.03	0.24	0.26	0.08
103	8	102970569	11996557	12645	GGAGGAAGATYTATCTCTTGC	0.35	0.51	0.51	0.10	0.25	0.17	0.13	0.42	0.07	0.26	0.17	0.11	0.35	0.51	0.51	0.10	0.25	0.17	0.13	0.42	0.07	0.26	0.17	0.11
103	8	102989689	16868698	12646	TGGCATCCGGYTTGATTTTAC	0.58	0.43	0.46	0.80	0.28	0.10	0.31	0.43	0.84	0.29	0.09	0.33	0.58	0.43	0.46	0.80	0.28	0.10	0.31	0.43	0.84	0.29	0.09	0.33
104	8	119397114	1385807	12647	AGAAAAAAAAMCTTCCAGAAG	0.25	0.49	0.47	0.65	0.10	0.04	0.56	0.44	0.66	0.10	0.04	0.57	0.25	0.49	0.47	0.65	0.10	0.04	0.56	0.44	0.66	0.10	0.04	0.57
104	8	119405814		12648	CTTTCTATTTMACAGCTATCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119412850	2450222	12649	ACTCTAAGAARAAGACACTTC	0.09	0.02	0.02	0.38	0.18	0.44	0.48	0.00	0.36	0.18	0.45	0.50	0.09	0.02	0.02	0.38	0.18	0.44	0.48	0.00	0.36	0.18	0.45	0.50
104	8	119423413	16890873	12650	AAATTCCTATRAAAAAGTTTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119437899	17828843	12651	ATATATAAACRCCCACCTGCA	0.29	0.61	0.61	0.08	0.45	0.49	1.21	0.58	0.07	0.46	0.48	1.18	0.29	0.61	0.61	0.08	0.45	0.49	1.21	0.58	0.07	0.46	0.48	1.18
104	8	119443303	7839234	12652	GAGCCCAAGTSCCTACTAGAA	0.73	0.02	0.02	0.09	0.06	1.23	1.23	0.00	0.07	0.05	1.19	1.23	0.73	0.02	0.02	0.09	0.06	1.23	1.23	0.00	0.07	0.05	1.19	1.23
104	8	119454759	11786582	12653	AACAAGTCTAYTGCTCCATTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119465188	7006721	12654	GTTTTTCACAYTGCTCTTACT	0.01	0.06	0.06	0.00	3.71	0.90	0.53	0.05	0.00	2.89	0.92	0.51	0.01	0.06	0.06	0.00	3.71	0.90	0.53	0.05	0.00	2.89	0.92	0.51
104	8	119476263	2291371	12655	AGAAGGAAGTYGAGCTCATAC	0.01	0.06	0.06	1.32	1.84	1.85	0.32	0.04	1.35	1.69	1.76	0.34	0.01	0.06	0.06	1.32	1.84	1.85	0.32	0.04	1.35	1.69	1.76	0.34
104	8	119484583	4876821	12656	TGACAGCCTTSCAGTTCAGTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119490813	11985716	12657	TGGTTTTTAARGATTTATTAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119496775	4876414	12658	AACCACACCASCATGCGAACC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119503774	13250709	12659	CTAACAATAAKAGCTGTCATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119516196	13255144	12660	CCTAATGCCTYTCCAGTGTTC	1.91	2.13	2.13	0.98	0.78	1.07	0.61	2.05	1.06	0.78	1.03	0.60	1.91	2.13	2.13	0.98	0.78	1.07	0.61	2.05	1.06	0.78	1.03	0.60
104	8	119522430	17682712	12661	TTCTCCATACRCATAATTTCC	0.33	0.17	0.17	1.15	0.38	0.09	0.56	0.12	1.22	0.39	0.08	0.52	0.33	0.17	0.17	1.15	0.38	0.09	0.56	0.12	1.22	0.39	0.08	0.52
104	8	119530170	9656928	12662	GTGATGTGATRAAACAAACTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119537790	7835295	12663	AACACATCCCRTCTTCACTAT	1.69	2.25	2.28	1.44	0.55	0.12	0.07	2.20	1.63	0.57	0.13	0.07	1.69	2.25	2.28	1.44	0.55	0.12	0.07	2.20	1.63	0.57	0.13	0.07
104	8	119561458	2515010	12664	CATATAAAACRAAGAAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119567293	2515037	12665	ATATCACAGARTCACTATGGG	0.84	0.68	0.68	1.13	0.85	0.42	0.11	0.62	1.14	0.87	0.42	0.11	0.84	0.68	0.68	1.13	0.85	0.42	0.11	0.62	1.14	0.87	0.42	0.11
104	8	119572825	2515020	12666	CATTCAACTAMAGAATTCATG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119581045	2515027	12667	AGTTTCATATKTCTATGTGTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119595498	4242583	12668	GGTCAGGCAARÇACACCTATT	0.25	0.52	0.52	0.33	0.84	0.69	0.54	0.51	0.33	0.86	0.70	0.57	0.25	0.52	0.52	0.33	0.84	0.69	0.54	0.51	0.33	0.86	0.70	0.57
104	8	119608104	4563917	12669	GGCACAGTTAWCAGAAAGTGC	0.27	0.34	0.34	0.44	0.28	0.73	0.43	0.29	0.39	0.32	0.74	0.49	0.27	0.34	0.34	0.44	0.28	0.73	0.43	0.29	0.39	0.32	0.74	0.49
104	8	119620626	7006970	12670	TCTGCTTTGCRTTTGCTCAGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119628765		12671	GAGGCTTTTTWTTTGGTGTCC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
104	8	119636900	4641102	12672	CTAGTGCATCMCTTTGTGTTA	1.11	1.11	1.11	0.69	0.92	0.27	0.32	1.04	0.70	0.93	0.26	0.35	1.11	1.11	1.11	0.69	0.92	0.27	0.32	1.04	0.70	0.93	0.26	0.35
105	8	123884006	748856	12673	GTGGAAAGCCYGCATGGTGTT	0.01	0.02	0.00	0.38	1.37	0.79	0.70	0.00	0.34	1.31	0.78	0.71	0.01	0.02	0.00	0.38	1.37	0.79	0.70	0.00	0.34	1.31	0.78	0.71
105	8	123894786	4870816	12674	GCATCAGAGCYGCCTTTCAGT	0.53	0.05	0.00	0.09	0.17	1.92	0.87	0.00	0.09	0.20	1.84	0.85	0.53	0.05	0.00	0.09	0.17	1.92	0.87	0.00	0.09	0.20	1.84	0.85
105	8	123903070	13270236	12675	GAGCGGGTAGRCATTAGAACT	0.57	0.68	0.62	0.15	0.11	0.65	1.73	0.59	0.10	0.11	0.65	1.69	0.57	0.68	0.62	0.15	0.11	0.65	1.73	0.59	0.10	0.11	0.65	1.69
105	8	123924246	17288269	12676	GATGATCAGCYAGATTTGGCA	0.01	0.10	0.10	0.19	0.08	0.53	0.48	0.04	0.17	0.07	0.53	0.48	0.01	0.10	0.10	0.19	0.08	0.53	0.48	0.04	0.17	0.07	0.53	0.48
106	9	71307215	11142837	12677	GGCCCAGGAAYGCCAGATTAT	0.25	0.55	0.57	0.35	0.05	0.25	0.23	0.53	0.36	0.05	0.24	0.22	0.25	0.55	0.57	0.35	0.05	0.25	0.23	0.53	0.36	0.05	0.24	0.22
106	9	71321779	10512004	12678	ATGCATATACSTAATAGTAAG	0.30	0.27	0.27	0.08	0.92	0.33	0.54	0.24	0.09	0.93	0.36	0.51	0.30	0.27	0.27	0.08	0.92	0.33	0.54	0.24	0.09	0.93	0.36	0.51
106	9	71327934	11142847	12679	GAGGAAGCCCKGGAATTATAC	0.42	0.69	0.69	0.83	0.51	0.54	0.43	0.63	0.82	0.55	0.55	0.45	0.42	0.69	0.69	0.83	0.51	0.54	0.43	0.63	0.82	0.55	0.55	0.45
106	9	71334362	4549848	12680	CAGTGAGCAGRGAAACTAAGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71353952	2309970	12681	TATAAAGCATYGTATGAATTC	0.87	1.30	1.30	0.90	0.47	0.30	0.18	1.24	0.89	0.51	0.30	0.20	0.87	1.30	1.30	0.90	0.47	0.30	0.18	1.24	0.89	0.51	0.30	0.20
106	9	71359840	10869031	12682	AGTGGGCTGGKCTAATGACTG	0.55	0.78	0.78	0.46	0.55	0.34	0.25	0.72	0.44	0.56	0.32	0.26	0.55	0.78	0.78	0.46	0.55	0.34	0.25	0.72	0.44	0.56	0.32	0.26
106	9	71365648	11791628	12683	AGAAAATTGCRTTGTTTCATA	0.80	1.00	1.06	0.67	0.76	0.70	0.51	1.01	0.69	0.80	0.68	0.54	0.80	1.00	1.06	0.67	0.76	0.70	0.51	1.01	0.69	0.80	0.68	0.54
106	9	71385727	10512000	12684	AGGAATTCTCRTAATGTGGCG	0.17	0.35	0.35	0.63	0.87	0.99	0.99	0.27	0.62	0.85	0.96	1.00	0.17	0.35	0.35	0.63	0.87	0.99	0.99	0.27	0.62	0.85	0.96	1.00
106	9	71396956	2309979	12685	TTTGATCTCCYACACAACTTA	0.96	1.00	1.00	0.50	0.82	0.83	1.11	0.89	0.48	0.82	0.85	1.08	0.96	1.00	1.00	0.50	0.82	0.83	1.11	0.89	0.48	0.82	0.85	1.08
106	9	71411288	11142892	12686	GGCAAATCCAYAGTTCTGCTA	0.21	0.23	0.24	0.64	0.60	1.13	1.05	0.21	0.61	0.65	1.12	1.04	0.21	0.23	0.24	0.64	0.60	1.13	1.05	0.21	0.61	0.65	1.12	1.04
106	9	71414327	4744634	12687	CTGAGGGAAARTCTATAAGAA	0.88	1.04	1.04	0.43	1.02	1.48	0.53	1.00	0.42	1.02	1.40	0.54	0.88	1.04	1.04	0.43	1.02	1.48	0.53	1.00	0.42	1.02	1.40	0.54
106	9	71422728	1360142	12688	CCATACTTCAWTTCTTACCTG	0.14	0.36	0.37	1.12	2.24	0.64	1.15	0.34	1.28	2.02	0.67	1.13	0.14	0.36	0.37	1.12	2.24	0.64	1.15	0.34	1.28	2.02	0.67	1.13
106	9	71429639	11142902	12689	CAGAGGTGCTSACTTAACTCC	1.84	2.34	2.34	1.22	0.92	1.32	0.88	2.24	1.33	0.94	1.25	0.84	1.84	2.34	2.34	1.22	0.92	1.32	0.88	2.24	1.33	0.94	1.25	0.84
106	9	71459413	1329411	12690	TAGAAGGATARTACTTTTTTG	0.94	0.95	0.94	1.11	0.71	0.91	0.72	0.89	1.12	0.71	0.90	0.72	0.94	0.95	0.94	1.11	0.71	0.91	0.72	0.89	1.12	0.71	0.90	0.72
106	9	71474980	6560218	12691	TCCCTGGAAGYAAACTGCCCA	0.29	0.55	0.55	1.42	1.43	0.56	0.70	0.53	1.46	1.40	0.58	0.63	0.29	0.55	0.55	1.42	1.43	0.56	0.70	0.53	1.46	1.40	0.58	0.63
106	9	71491126	10746883	12692	AATGACAGGTYAGACACACTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71503980	10781034	12693	CCTACTGAACWGCATTAGTCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71508034	11142952	12694	AAATCCCTACYACCCTCCACT	0.52	0.91	0.87	1.66	0.54	0.88	0.53	0.79	1.69	0.53	0.81	0.53	0.52	0.91	0.87	1.66	0.54	0.88	0.53	0.79	1.69	0.53	0.81	0.53
106	9	71520952	10869050	12695	CATAATCCTTRGCTTTGGTAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71530194	2310021	12696	GAACTTCATGRAATAATACAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71535996	13296053	12697	AAAGACTAGAYATGATTTCCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71542301	1293	12698	TGCTTCTTACRCGCTTCACAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71547691	11142963	12699	TAGATGACTTYAGGAGCTGGA	0.37	0.71	0.76	0.54	0.86	0.47	0.99	0.74	0.55	0.84	0.50	0.99	0.37	0.71	0.76	0.54	0.86	0.47	0.99	0.74	0.55	0.84	0.50	0.99
106	9	71562852	4745120	12700	ATCAGGAAGTMTGTCATGTGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71578163	1027237	12701	TGAGTTCAAARGAAAAGCAAT	0.42	0.10	0.12	0.34	0.44	0.97	0.71	0.11	0.34	0.43	0.96	0.70	0.42	0.10	0.12	0.34	0.44	0.97	0.71	0.11	0.34	0.43	0.96	0.70
106	9	71589650	25689	12702	GCTCTCATTGYGGTATTCATG	0.42	0.23	0.25	0.17	0.85	0.69	0.91	0.22	0.13	0.86	0.69	0.89	0.42	0.23	0.25	0.17	0.85	0.69	0.91	0.22	0.13	0.86	0.69	0.89
106	9	71601895		12703	TTTTGCTTTCRGAGAGTTTCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71620932	6560232	12704	ATAATACCAAYATCCTGAAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71640001	1404192	12705	CACCTATGATYGCTTTTTCCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71646224	7871483	12706	TTTAATTGTCRTCTTCGTGGA	0.44	0.34	0.26	1.07	0.80	1.06	0.43	0.23	1.21	0.82	1.06	0.42	0.44	0.34	0.26	1.07	0.80	1.06	0.43	0.23	1.21	0.82	1.06	0.42
106	9	71657788	12002194	12707	ATGAACAATGYGTGTGCTGTA	0.80	0.70	0.70	1.62	2.15	0.64	0.81	0.65	1.90	1.94	0.65	0.85	0.80	0.70	0.70	1.62	2.15	0.64	0.81	0.65	1.90	1.94	0.65	0.85
106	9	71663791	10869066	12708	GCATCTTCTGRGCGCCCCCTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71674094	13291120	12709	CACTTGGTTTMTACTAAGAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71708533	12004767	12710	CAGCAAGCGARAATCTCCAGA	0.57	0.70	0.70	1.49	1.02	1.18	1.47	0.61	1.73	1.04	1.12	1.42	0.57	0.70	0.70	1.49	1.02	1.18	1.47	0.61	1.73	1.04	1.12	1.42

106	9	71716356	1880327	12711	TGCCAGGCCCYGAGTTTCTTT	0.66	0.91	0.91	0.43	1.49	1.41	1.61	0.87	0.43	1.45	1.40	1.57
106	9	71734808	10746893	12712	CCTAATTCCCRCCTTCTATGC	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71747069	10123159	12713	TTAAAAAGCTSGGAAGAAAAT	1.02	1.10	1.00	0.97	1.38	1.88	1.77	0.88	1.13	1.36	1.83	1.70
106	9	71760607		12714	TATGAAAGAAYGGTCTAGGGA	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71772974	10746896	12715	TGTAGACAATRAAGAGATGGT	0.07	0.07	0.08	1.29	1.98	1.65	1.77	0.00	1.39	1.87	1.56	1.68
106	9	71783495	10781053	12716	GCTGCAAAGTRTAGAATCTCT	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71788926	13288268	12717	CTTGTTGAACRAACTAAATGA	0.40	0.65	0.71	2.53	2.17	1.59	1.37	0.62	3.02	2.06	1.51	1.31
106	9	71795441	4745138	12718	CCATTTGTTCRTGCGATCCAA	0.97	0.97	0.79	0.47	2.32	0.91	1.14	0.58	0.47	2.23	0.94	1.12
106	9	71804086	2310093	12719	TCTATTTCTGSCTTTTATTTT	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71816674	11795366	12720	TTAATTTATTYGAGCCTACTT	0.64	0.92	0.85	0.80	0.67	1.24	0.82	0.76	0.80	0.69	1.18	0.81
106	9	71829269	7045421	12721	TGGGAAAATAYACCAACACAG	0.45	0.50	0.50	0.40	0.76	0.54	1.15	0.48	0.44	0.82	0.52	1.10
106	9	71857083	12378487	12722	TAGGAAAGTGKGAATAGAAGA	0.20	0.18	0.22	0.30	0.31	0.95	0.70	0.21	0.30	0.34	0.92	0.73
106	9	71866683	2147244	12723	CTAGATGCCCRTGAAAGCTTC	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71872203	4745150	12724	AGAAACCATCRAGTGGAATTG	1.03	1.29	1.29	0.75	0.62	0.55	0.29	1.23	0.80	0.60	0.54	0.29
106	9	71878185	12380601	12725	GAGGCATTTTRTACACTTTTC	0.85	1.27	1.27	1.00	0.99	0.28	0.44	1.21	1.03	1.00	0.30	0.45
106	9	71890264	10869087	12726	CAATAGCACCYATATGCAAGC	0.25	0.33	0.33	1.57	0.61	1.47	0.35	0.31	1.59	0.63	1.46	0.35
106	9	71902546	10869089	12727	TTGTATTTTASATCTGCAGAA	2.33	2.50	2.50	1.21	2.71	1.62	0.87	2.46	1.34	2.45	1.54	0.87
106	9	71908680	10869092	12728	TGAATTTTAGKTTGGCAAAGA	0.15	0.38	0.40	1.36	2.69	1.99	1.32	0.35	1.68	2.38	1.89	1.25
106	9	71933526	12344267	12729	AGAGTGACAGSCTGAAGAATC	-	-	-	-	-	-	-	-	-	-	-	-
106	9	71945991	17057428	12730	TTGTCAGTGARGAAGGAAAGG	0.45	0.15	0.12	0.78	2.46	2.73	1.97	0.09	0.78	2.19	2.34	1.85
106	9	71954680	10735612	12731	GGACATGCTCRTCTCTTCTCT	1.34	1.31	1.27	0.67	0.48	2.72	2.69	1.17	0.74	0.55	2.40	2.41
106	9	71968301	4745159	12732	GTGAAATAGAMCTTGTGCAGT	1.17	0.83	0.88	0.73	1.42	1.45	2.27	0.80	0.84	1.37	1.41	2.11
106	9	71972554	7044784	12733	TTGTTAGTTAYCCACGTCCTC	0.85	0.81	0.84	0.90	1.39	1.62	1.47	0.82	1.02	1.36	1.56	1.42
106	9	71983656	4745170	12734	TGTTCGAACCMAGCATTTTGG	1.34	1.34	1.14	1.02	1.19	2.38	1.67	1.08	1.17	1.16	2.17	1.56
106	9	71994939	7857832	12735	CAAATGACACRGGTAACTTGA	0.53	0.80	0.85	1.20	1.52	1.96	2.28	0.77	1.45	1.49	1.81	2.09
106	9	72011320	12347198	12736	CACCAATTTCSTTTTTCTCAG	0.83	1.11	1.11	0.71	1.56	2.07	1.99	1.04	0.84	1.50	1.89	1.84
106	9	72019151	11143145	12737	AGGAGGTACAYAGCTTGATGG	-	-	-	-	-	-	-	-	-	-	-	-
106	9	72030079	4484759	12738	CTGGTTTTATYTCCCCTCACA	0.29	0.25	0.25	0.65	0.51	1.40	1.04	0.21	0.72	0.51	1.37	1.06
106	9	72048638	17494172	12739	ATTCAGTGCARTTGTGGATCT	0.22	0.25	0.17	0.20	0.50	0.41	1.13	0.12	0.15	0.53	0.40	1.10
106	9	72058527	17494333	12740	ATGGAGTTAGRGATGGAAAAA	0.28	0.59	0.54	0.27	0.41	0.36	0.17	0.53	0.25	0.40	0.38	0.19
106	9	72065909	17579286	12741	GAAACCCCGTRCTTCCACCGA	0.20	0.08	0.08	0.65	0.84	0.35	0.23	0.04	0.65	0.85	0.35	0.25
106	9	72075658	17057536	12742	ACAGGTTAGTRGTTCACCATT	0.06	0.19	0.19	0.76	0.85	0.38	0.20	0.17	0.87	0.85	0.40	0.20
106	9	72083489	11143193	12743	GTGATTTCTCYTTCTATCCTA	0.01	0.08	0.08	0.35	0.07	0.28	0.18	0.08	0.32	0.08	0.28	0.16
106	9	72094631	2208744	12744	CAGCTTTATCMCTCAACCCCT	0.05	0.08	0.08	0.01	0.16	0.20	0.18	0.04	0.01	0.16	0.20	0.19
106	9	72113006	11143218	12745	TAAAATGATAWTCTCATAATT	0.04	0.08	0.08	0.25	0.22	0.16	0.18	0.09	0.23	0.25	0.16	0.15
106	9	72120355	17628566	12746	GGCACTACATWTTTCCAAGGT	-	-	-	-	-	-	-	-	-	-	-	-
106	9	72127506	2310126	12747	GCCTTGCTCAYAGCCAACTCT	0.08	0.19	0.21	0.36	0.15	0.19	0.48	0.17	0.36	0.16	0.20	0.50
106	9	72138081	12380305	12748	CATCCATTACMGAGGGTCTAA	0.55	0.52	0.52	0.35	0.27	0.44	0.39	0.44	0.33	0.30	0.46	0.41
106	9	72145163	11143245	12749	CTTAATGCCAYAAGATGATCT	0.70	0.65	0.65	0.46	0.06	0.35	0.31	0.57	0.43	0.04	0.37	0.33
107	9	78411043	12685972	12750	GATTAGCAGCRTTCCTTCATT	0.14	0.10	0.10	0.49	0.13	0.06	0.19	0.08	0.48	0.12	0.08	0.18
107	9	78423768	1505644	12751	TTTAGGTCCCYGAGAGCAATG	0.87	1.12	1.12	0.71	0.22	0.21	0.34	1.05	0.76	0.23	0.23	0.31
107	9	78431152	6559398	12752	ATCAAAAGGCRAGACAATATC	0.87	0.94	0.88	0.42	0.71	1.76	0.76	0.85	0.41	0.70	1.72	0.78
107	9	78436348	1505635	12753	TGACAAGGTCMGTAGCTTCAA	0.65	0.61	0.66	0.52	0.30	1.61	1.82	0.57	0.52	0.29	1.59	1.73
107	9	78447050	769290	12754	CTTTCTATTTYTCAGGCAGCA	0.13	0.00	0.00	0.67	0.36	0.40	1.57	0.00	0.72	0.36	0.42	1.56
107	9	78454794	7027554	12755	CGTTTACTAGYCTCAGTCACT	0.47	0.20	0.20	0.25	0.76	0.73	0.48	0.15	0.20	0.76	0.70	0.46
108	9	85928227	957617	12756	TCTGTGTTTAYGAACTCTTAC	0.70	0.57	0.57	0.79	0.15	0.65	0.10	0.54	0.80	0.16	0.66	0.10
108	9	85939004	7862366	12757	AGTGGTAGGTRGTAGAAACAC	0.67	0.89	0.89	0.60	1.93	0.31	0.18	0.85	0.59	1.82	0.29	0.18
108	9	85963487	7870214	12758	CGTCTCTTCCRTCCCTCTCTA	0.17	0.41	0.41	2.15	1.37	0.85	0.16	0.37	2.42	1.33	0.86	0.18
108	9	85980982	4567122	12759	AAAAGCAGTTYGATCGACTGG	-	-	-	-	-	-	-	-	-	-	-	-
108	9	86012111	7023926	12760	TGGGACAGGAYAGTGAGGCAG	4.07	4.35	4.20	2.40	1.31	1.15	0.59	4.11	2.73	1.31	1.10	0.62
108	9	86019273	6559907	12761	GTTAGAATTCKTCTCAAGGCT	0.37	0.71	0.71	2.35	2.50	0.72	0.40	0.69	2.62	2.26	0.71	0.42
108	9	86031138	7033215	12762	AGGAACTGATSACTGCTGCAG	0.18	0.20	0.19	0.21	1.26	1.34	0.49	0.15	0.19	1.23	1.31	0.49
108	9	86045545	13293650	12763	TCATTGGCTAKGTACTTTTCT	0.16	0.43	0.43	0.65	0.20	0.70	0.67	0.41	0.68	0.21	0.71	0.69
109	9	90800413	10991725	12764	AGTTCTTATCRTCCACATGGA	0.11	0.32	0.32	0.93	1.03	0.79	0.32	0.30	0.97	1.00	0.78	0.33
109	9	90813390	296696	12765	TGGTGCCCATRGCCAATCTAA	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90821873	296717	12766	CTGAAGACCARATGATTGCAT	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90839092	296701	12767	TGTTTGTCAARGTAAATGGTG	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90847321	296642	12768	CTCATCTGTTKTCCTGGGATG	1.47	1.41	1.42	0.45	0.69	0.47	0.65	1.37	0.43	0.70	0.47	0.66
109	9	90854518	167200	12769	AAATATAAATKGTCCTTGCTC	1.32	1.21	1.19	1.54	0.55	0.91	0.73	1.12	1.64	0.54	0.92	0.71
109	9	90868417	296626	12770	GAGGGGAAAAYGCTGCATTAG	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90878254	753791	12771	AGGAGCAAATRAACCCTGGAC	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90884232	10991750	12772	GCTTCAGCCARTTTCCTTTTC	0.70	1.08	1.05	0.47	1.62	0.56	0.41	1.00	0.46	1.57	0.55	0.44
109	9	90903017	10512204	12773	CCAGAGGCGAYCACGTGAAAG	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90907876	7025659	12774	GAACCACGGCMCAAGTCATTG	-	-	-	-	-	-	-	-	-	-	-	-
109	9	90920214	296639	12775	TTCTTGTTGGYTTTAAGGAAA	1.13	1.10	1.11	0.43	0.24	0.63	0.45	1.03	0.43	0.24	0.66	0.47
110	9	100188496	2151131	12776	TTCAATACAGSAAAACTGTGT	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100231157	953382	12777	ACCTCCAGTARGAAACAACCT	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100252377	1930242	12778	TAATGAGTTARAGACCATATG	0.80	0.91	0.91	0.36	0.28	0.17	0.21	0.86	0.34	0.28	0.16	0.23
110	9	100256889	17740576	12779	CAACTGCCCTKTAAAAAGCTC	0.28	0.55	0.55	0.53	0.48	0.33	0.25	0.50	0.51	0.50	0.34	0.28
110	9	100277132	10512270	12780	TAAGATCAGCRGTCTATTAAT	0.01	0.01	0.24	0.77	0.16	0.28	0.30	0.15	0.76	0.16	0.32	0.29
110	9	100290373	12056981	12781	TCCATGGTTGRGCGTGTTGGG	0.29	0.29	0.18	0.66	0.54	0.15	0.12	0.07	0.64	0.53	0.16	0.13
110	9	100297568	17813801	12782	ATGATTATATKTGGCAAAGCC	0.42	0.75	0.73	0.39	0.97	0.26	0.09	0.69	0.43	1.00	0.26	0.09
110	9	100312024	7046408	12783	TACATCCTGTWAAAATTCACT	0.50	0.59	0.59	0.39	0.16	0.37	0.34	0.54	0.41	0.16	0.41	0.35
110	9	100329704	16919142	12784	ATTGGAACCCSAAGTCTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100331950	10512271	12785	TAGTATGCAAMATGGAATGAA	0.18	0.18	0.18	0.42	0.37	0.37	0.37	0.08	0.40	0.40	0.39	0.38
110	9	100351187	17814243	12786	TACTACATTGYTAAGGCTTAA	0.40	0.73	0.82	0.43	0.44	0.37	0.55	0.74	0.43	0.48	0.37	0.55
110	9	100360016	10989127	12787	TGACATCTGCRTAATAGGCTG	0.27	0.45	0.45	0.43	0.41	0.49	2.68	0.41	0.40	0.41	0.48	2.39
110	9	100366020	12683122	12788	CACACTATACYCGTAGTTCTG	0.18	0.18	0.18	0.29	0.36	2.69	1.84	0.09	0.29	0.34	2.58	1.76
110	9	100377154	10989145	12789	GCTTAGTGAAYGCTTTGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100385290	10465149	12790	TCTATTACTTWGTTGTGGGTA	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100393972	16919174	12791	GGGCCAGATTKTGTAGAGTGT	0.18	0.18	0.18	0.24	2.63	1.95	1.26	0.09	0.25	2.45	1.83	1.27
110	9	100403949	10989154	12792	TGCCTGTCTGYGGATACACCT	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100414164	2800281	12793	AGGTGAAAGAMGCACCATGTA	0.73	0.50	0.50	2.79	2.86	1.15	1.17	0.44	2.99	2.53	1.12	1.14
110	9	100421158	10989161	12794	TATGGTATATYTTCAAAACTC	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100432572	1226593	12795	AGACTGTGCTKCTTAAGGTCA	1.32	0.88	0.87	2.53	1.83	1.28	0.57	0.84	2.90	1.74	1.28	0.57
110	9	100440669	10989168	12796	CCGGCTCCGCRGGCAGGAGGA	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100447170	4474081	12797	GAGTCGGAATMAGGTTAATTC	0.29	0.58	0.57	1.07	1.46	1.10	0.82	0.52	1.09	1.41	1.09	0.87
110	9	100457069	7869768	12798	CAGGTGTTGCRTTATATAATA	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100463754	10760734	12799	CATGGCCTGGSATTGGAATTG	0.66	0.21	0.21	0.28	0.60	0.88	0.48	0.17	0.26	0.62	0.90	0.50
110	9	100485445	10122565	12800	ACTGAGATCARTTTGGTCGTC	1.18	0.01	0.00	0.56	0.59	0.32	0.84	0.00	0.59	0.65	0.32	0.85
110	9	100494212	12349919	12801	AAAAAAACTTYCAATAATGCA	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100506710	12238759	12802	TGTCTGCCACYGTTAGTCCAT	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100517539	10819806	12803	ATAGGTTCATRTGTGGTGTAG	1.02	1.53	1.53	0.98	0.83	0.42	0.48	1.52	1.05	0.83	0.45	0.46
110	9	100531623	10123021	12804	TCAGAGGCAGKTTGAGGTACT	0.41	0.74	0.74	0.85	0.70	0.31	0.33	0.67	0.85	0.71	0.32	0.36

110	9	100541387	10989219	12805	CCTAAGGAGAYGGATATAACC	-	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100564688	6479028	12806	CTGGGTCCCAKAGATGATTCC	1.26	1.37	1.37	0.56	0.39	0.31	0.29	1.30	0.57	0.39	0.32	0.31
110	9	100568349	7022939	12807	CTTCTTAAAASAGGTGTTTCA	0.51	0.27	0.31	1.43	0.47	0.60	0.32	0.27	1.53	0.50	0.63	0.34
110	9	100597451	10739802	12808	CCAATGTAACRAATATGTATG	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100602968	7026119	12809	CCATAAATCTRGGTAACATTC	0.39	0.38	0.38	0.73	0.72	0.35	0.31	0.31	0.74	0.75	0.39	0.30
110	9	100616355		12810	AATTAAGGCASCAGGGAAGGC	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100627097	10512275	12811	TCCAAATTCCKTTTCCCTAGT	0.07	0.06	0.04	0.50	0.81	0.67	0.88	0.03	0.52	0.80	0.67	0.91
110	9	100637370	1338747	12812	GCTTCCCTTARCACACAATTG	0.30	0.31	0.32	1.01	0.34	0.32	0.44	0.28	1.05	0.35	0.32	0.48
110	9	100650943	1338729	12813	CCTGAGAAATRCGTGTCAGTG	0.26	0.33	0.36	0.89	0.75	0.38	0.40	0.32	0.92	0.74	0.41	0.41
110	9	100657350	1538409	12814	AATCATCCTTKTCATCTCTTT	0.45	0.52	0.52	0.53	1.09	0.79	0.20	0.51	0.50	1.09	0.78	0.25
110	9	100663829	10760767	12815	CCTCTCTCCTMCCATTCACAG	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100681464	10819852	12816	GATGGCATACYACGAATTTTA	-	-	-	-	-	-	-	-	-	-	-	-
110	9	100687277	16919543	12817	GCTATTGTGARCTTCAAGTGA	0.30	0.30	0.29	1.14	0.61	0.59	0.29	0.17	1.28	0.62	0.60	0.29
111	9	108740705	4978760	12818	ATGCCAAGCTRCTATCACTGG	0.90	0.56	0.52	0.93	0.75	1.05	0.32	0.49	1.04	0.79	1.03	0.34
111	9	108751255	838822	12819	CATCAAACACMATCTTTGAAA	0.13	0.30	0.30	0.80	0.92	0.36	0.75	0.23	0.85	0.93	0.37	0.74
111	9	108759914	16913693	12820	TTTTTAAGACKTCACCAAATG	0.73	0.72	0.72	0.56	0.49	0.42	0.32	0.56	0.54	0.51	0.45	0.36
111	9	108766934	10979612	12821	TTATCTTTCAYCTGGATTCCT	0.75	0.87	0.74	0.40	0.17	0.43	0.17	0.69	0.38	0.17	0.43	0.18
111	9	108776982	1616727	12822	CCTTTCATTCRGTGATAATGG	0.17	0.33	0.33	0.45	0.34	0.08	0.11	0.31	0.41	0.42	0.08	0.10
111	9	108780720	838819	12823	GATTTTCCCAYACTTTTGAAA	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108796693	7044275	12824	ATTTCTAAAAYTCCAGACTTA	0.09	0.00	0.00	0.50	0.19	0.08	0.79	0.00	0.49	0.19	0.07	0.79
111	9	108805625	16913731	12825	AGTGCAGGGTRTATTCATGCC	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108812143	7043345	12826	TTGGACTCTARTTATGAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108821935	4978378	12827	CCTCTAATAGYTCCTCGCCAT	0.52	0.66	0.66	0.12	0.10	1.06	0.72	0.60	0.14	0.12	1.06	0.70
111	9	108834563	2297581	12828	CAGCCTTTATYACTCCTGTTT	0.90	0.37	0.35	0.13	0.89	0.72	1.30	0.31	0.12	0.85	0.74	1.29
111	9	108845292	12555920	12829	GAGAAATCTAYGCAGCTGCAA	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108853948	10816766	12830	ATCACTGCTCYGTTAGCCATG	0.19	0.07	0.07	1.28	1.29	0.96	0.85	0.03	1.27	1.22	0.97	0.86
111	9	108866680	17802292	12831	GGGCAAATTARTGTGTTAGCT	1.09	1.65	1.65	1.81	1.80	1.28	1.22	1.56	2.00	1.71	1.18	1.21
111	9	108880908	3750452	12832	CGTGACCTTGYACATGCAAAA	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108889085	10512391	12833	ATACTATGGARCCAAGACATA	1.02	0.49	0.49	2.50	2.26	2.11	1.56	0.43	2.82	2.05	1.93	1.51
111	9	108895472	13296451	12834	TGACCAACAASGCCTCACCAT	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108902719	7850283	12835	CTATAAACACRAATCCTTCCT	0.98	1.46	1.46	1.37	2.55	2.43	1.51	1.44	1.61	2.35	2.16	1.44
111	9	108911436	16913786	12836	TCTGACCTGCYTTCCCCAGCT	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108925058	7049112	12837	CCAACTCCCASAAAGACTGAA	1.01	1.52	1.52	1.70	2.23	1.65	1.24	1.49	1.84	2.08	1.59	1.20
111	9	108936287	11789183	12838	CTGTAATTTGRAAGCCAGAGC	1.57	2.21	2.21	1.18	1.65	1.09	0.89	2.15	1.31	1.56	1.10	0.85
111	9	108936995	10816769	12839	AGAGGAAAGCSTAAGTTAGAT	1.12	1.63	1.63	1.48	0.68	0.65	0.73	1.54	1.75	0.69	0.68	0.76
111	9	108949640	10979690	12840	GTACCACGCTRAAAAATCAAC	0.08	0.47	0.47	1.45	1.47	0.62	0.19	0.39	1.56	1.36	0.66	0.17
111	9	108960248	6477689	12841	TATGAATCAAYTGGCATTCTT	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108967191		12842	CTTTTTTGCAYTTGCTCCAGT	-	-	-	-	-	-	-	-	-	-	-	-
111	9	108973624	17552439	12843	AACCAATTCCRTTTAGAGAAC	0.62	0.94	1.00	0.71	1.46	0.64	0.12	0.99	0.77	1.35	0.67	0.11
111	9	108980232	17552584	12844	AATAATCCATYTGAAACTTGG	1.03	0.46	0.38	0.51	0.16	0.54	0.37	0.36	0.53	0.14	0.57	0.33
111	9	108991022	16913851	12845	ATGCCTGAGAKAACAAGCTAG	0.79	1.08	1.08	0.48	0.17	0.20	0.54	1.02	0.50	0.16	0.22	0.54
111	9	108997920	6477693	12846	TCAGGATTCCMGGTAATAATC	0.40	0.70	0.73	0.28	0.36	0.41	0.15	0.71	0.28	0.34	0.39	0.17
111	9	109004841	12380418	12847	AAGGGTCAGGYGGTTAACATC	0.26	0.56	0.56	0.33	0.51	0.35	0.20	0.50	0.34	0.54	0.38	0.21
111	9	109013816	10759332	12848	TGCTGAAACCRTGGAATCCTC	0.06	0.02	0.03	0.53	0.27	0.24	0.15	0.00	0.61	0.27	0.25	0.16
112	9	120936639	10760146	12849	ATCAAACAGAYCCTGATGCAC	-	-	-	-	-	-	-	-	-	-	-	-
112	9	120950235	10156476	12850	ACTCAGCCCAYTGAAAACCTT	0.23	0.50	0.50	0.49	0.42	2.33	1.75	0.45	0.54	0.46	2.18	1.63
112	9	120955859	2146838	12851	GTCACAATTARTAATAACTGA	0.29	0.08	0.08	0.32	1.64	1.16	1.09	0.05	0.33	1.51	1.16	1.09
112	9	120960248		12852	AATAAATTACRCCAGGAAGCT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	120966287	10818509	12853	TTAGGATCTASTTTTGCAATG	0.18	0.09	0.09	0.71	0.88	0.43	0.51	0.07	0.72	0.86	0.45	0.55
112	9	120984916	10760151	12854	ATAGTTACCARTCTCAAATAG	0.52	0.80	0.80	0.22	0.07	0.35	0.18	0.73	0.22	0.06	0.33	0.17
112	9	120996574	3736855	12855	ATGGAAATGTWGAGAGTCTTA	0.53	0.84	0.84	0.14	0.05	0.02	0.26	0.78	0.12	0.06	0.01	0.25
112	9	121008123	1535655	12856	AGCAGATACCRTAGGGCCATT	0.09	0.04	0.04	0.38	0.05	0.04	0.26	0.02	0.40	0.04	0.04	0.27
112	9	121013927	16910381	12857	AGTCTTTTGGRTGACCCCACG	1.16	1.48	1.48	0.74	0.20	0.42	0.42	1.40	0.79	0.20	0.43	0.46
112	9	121020638		12858	TACTAATCTGMAGGCCTCCTC	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121032208	10760157	12859	TAAAAACTTTYGGAAAATATC	0.08	0.06	0.06	0.92	0.94	0.91	0.62	0.04	0.96	0.90	0.90	0.62
112	9	121041311	12335895	12860	CATCTCTCAAYAGCCCAAGTT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121068215	16910434	12861	GGAAAAGCAAYCCAGATTGTA	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121081070	16910445	12862	ATGAACTCATWTCTGTTAGGA	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121094287	10985191	12863	CTACATATGAYGGAGACATTT	0.82	0.81	0.81	0.75	1.79	1.47	0.94	0.64	0.83	1.69	1.37	0.96
112	9	121100579	10739593	12864	TCCCAGCAGCRTAAGTGAGCA	0.18	0.22	0.19	0.51	0.91	1.84	1.44	0.17	0.54	0.88	1.66	1.36
112	9	121119425	4837827	12865	TTGTCTTTGAYATCTGACTTA	0.25	0.42	0.42	0.39	0.38	1.40	2.94	0.41	0.37	0.37	1.32	2.67
112	9	121131831	10818525	12866	TGGGGACACCRAACCAGGACA	0.24	0.22	0.22	0.68	0.24	1.01	2.23	0.18	0.82	0.26	1.00	2.03
112	9	121138731	4837834	12867	CAGAGCTATAYGGCAGGCAAA	0.25	0.49	0.49	0.49	1.07	0.48	1.28	0.45	0.53	1.07	0.47	1.24
112	9	121152151	306783	12868	TGGGAAACGCYGGTTTTGAGG	0.24	0.46	0.46	0.97	0.65	1.41	2.57	0.40	0.97	0.66	1.37	2.36
112	9	121159355	2900193	12869	AACATCTAACYGTATGGTCAG	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121171909	306772	12870	ATGATTGCAGYTTGAGCCATT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121177890	767769	12871	GATCAGAAAGRATGTTTTTGG	0.29	0.58	0.57	0.31	1.54	2.29	2.29	0.53	0.29	1.51	2.10	2.14
112	9	121186088	3789313	12872	CTGTATTCCARGGTAGGCACT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121191182	3747847	12873	GCAATTTTACMTCTGTCAACG	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121204068	394572	12874	AATTAGAAATKATAGCTCAAC	0.64	0.62	0.68	0.29	1.10	2.64	2.04	0.62	0.26	1.08	2.38	1.94
112	9	121212434	1771889	12875	GTGCAAGTGARGAAAAGTCGC	0.67	1.11	1.11	0.53	0.33	0.88	2.22	1.05	0.55	0.37	0.87	2.07
112	9	121219264		12876	AAAGATAACTRTGAAGCTGCT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121227635	2793267	12877	GAGAAAAGAAMTTAACAGCTA	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121264498	7048044	12878	GAAGGCCCACRGATGCTATCT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121272036	306777	12879	ATAAATAAACYAACAGCCAAC	1.15	1.02	1.02	0.37	0.21	0.26	0.87	0.93	0.36	0.24	0.27	0.86
112	9	121277446	1369443	12880	GAGAGACACTRTGTCAGATGG	0.84	1.25	1.25	0.75	0.29	0.19	0.22	1.22	0.85	0.29	0.19	0.22
112	9	121289735	1539005	12881	TAGAACTAGAYATGCACTACC	0.76	1.20	1.20	0.49	0.24	0.14	0.18	1.19	0.45	0.26	0.15	0.21
112	9	121295611	10739597	12882	TTTCACAGAAYCGCCCTACCC	0.18	0.18	0.18	0.37	0.14	0.26	0.13	0.09	0.38	0.12	0.28	0.13
112	9	121301587	3816094	12883	CACATCCTTCYAGTTGATCCT	0.79	1.15	1.15	0.57	0.25	0.23	0.10	1.11	0.61	0.25	0.26	0.11
112	9	121307156	9299275	12884	CAGGCAGGAAMCCCAAAGGGT	0.47	0.41	0.51	0.67	0.66	0.09	0.04	0.47	0.72	0.62	0.09	0.05
112	9	121314669	4837862	12885	TGGAAACATTRGCGCTTACAT	0.83	1.25	1.25	1.01	0.36	0.11	0.02	1.25	1.05	0.37	0.11	0.03
112	9	121320923	871670	12886	CCGGCATCCTKCTTCCAGGTC	0.71	0.83	0.83	0.37	0.19	0.05	0.01	0.78	0.38	0.21	0.05	0.01
112	9	121336240	12341605	12887	GTGGTCTCCTYGCCACATTTG	0.48	0.70	0.70	0.34	0.07	0.03	0.09	0.66	0.31	0.05	0.02	0.10
112	9	121349036	4837867	12888	CTTAAGGAGTRAGCATGTTGC	0.86	1.30	1.30	0.28	0.05	0.08	0.23	1.24	0.28	0.05	0.09	0.27
112	9	121386129	1964930	12889	TGGTTTGGTTYAGCTCATTTT	0.45	0.83	0.83	0.35	0.17	0.25	0.56	0.82	0.35	0.18	0.29	0.57
112	9	121406087	6478519	12890	CACAATAACTRTCTGAAGTAA	0.24	0.07	0.07	0.29	0.18	0.90	0.42	0.00	0.28	0.18	0.86	0.42
112	9	121417259	476807	12891	GTGCAGAGTCRAAGATCTTTA	0.12	0.18	0.23	0.44	0.92	0.64	0.35	0.19	0.45	0.90	0.66	0.36
112	9	121428876	634328	12892	TCAAGGGTGTKTCTGATGCTT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121434380	10513376	12893	GAAAATCTCAYTGGAACCCTT	1.02	1.24	1.24	1.67	1.20	0.66	0.54	1.18	1.67	1.17	0.63	0.56
112	9	121451790	10985333	12894	TCCTGGCGTCSGTGTGGCTTA	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121459342	1984035	12895	CCCAATACAGYGGTTTCCGTG	2.21	2.95	2.95	1.87	1.52	1.63	0.57	2.86	1.90	1.49	1.58	0.57
112	9	121466691	537143	12896	AGGAACGTACRTGAAGCATTT	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121480399	12352132	12897	GGAAGAGTGARTGCGAGTCAG	1.62	2.15	2.16	2.46	2.53	1.25	1.73	2.09	2.48	2.35	1.20	1.67
112	9	121501957	7025486	12898	GCAGACCACTRGGAATCAAAG	1.35	1.62	1.62	2.47	2.21	3.56	2.03	1.55	2.92	2.08	3.25	1.92

112	9	121515732	7029004	12899	TCCATGGGTGRCTCCCAGGCA	0.96	0.88	0.88	0.92	3.83	3.45	3.50	0.79	1.00	3.35	3.11	3.25
112	9	121521402	12005159	12900	CCTTTCTCCASGGAGCTCAGG	0.18	0.22	0.18	0.39	1.09	2.87	2.79	0.13	0.38	1.08	2.60	2.60
112	9	121531259	10985354	12901	AATCCTCTCCYAAAATGGTGC	0.32	0.63	0.63	0.17	0.23	0.65	2.47	0.55	0.16	0.24	0.68	2.31
112	9	121562249		12902	AATAATTAACWTCGGCATGGC	0.15	0.15	0.15	0.35	0.12	1.12	1.22	0.08	0.35	0.12	1.10	1.19
112	9	121567049	13290547	12903	GTTGTCGTCAYGTCTTCTTAA	0.82	0.74	0.81	0.27	0.62	0.62	0.46	0.70	0.31	0.64	0.61	0.48
112	9	121600814	3747851	12904	TCCGGCGAGCRGTGCATCCCA	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121607743	12000210	12905	GAGCTGTGTTSTCCCACCGTG	0.07	0.07	0.07	0.80	0.32	0.27	0.14	0.00	0.80	0.34	0.26	0.15
112	9	121661850	4348572	12906	AGGGAGGCTCYGTGCCCTGCG	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121675827	6478531	12907	GTTTCTGTCTYATCGTACAAT	1.04	1.22	1.27	0.51	0.31	0.19	0.12	1.23	0.51	0.31	0.21	0.13
112	9	121697454	12375949	12908	GTATGGGTGAYGATCCAGTCC	0.73	1.11	1.11	0.23	0.12	0.19	0.50	1.07	0.22	0.12	0.20	0.52
112	9	121703427	10739600	12909	ACCACCAGCARCGTGTCCTCA	0.29	0.59	0.59	0.22	0.06	0.42	0.48	0.57	0.22	0.06	0.44	0.50
112	9	121709887	7047365	12910	CTTCATGTTCYCTGATCTTGA	0.23	0.52	0.55	0.15	0.23	0.28	0.09	0.54	0.13	0.22	0.28	0.10
112	9	121719341	10121618	12911	CCTAGACCCAYGTTGAGCCTA	0.45	0.80	0.80	0.27	0.02	0.02	0.15	0.71	0.25	0.01	0.02	0.17
112	9	121726532		12912	GCCTATTCAAMAGGCCAGTTC	0.21	0.40	0.40	0.24	0.01	0.02	0.13	0.36	0.23	0.01	0.02	0.12
112	9	121733267	13285113	12913	ATGCAACAGCRGGATCACAAC	-	-	-	-	-	-	-	-	-	-	-	-
112	9	121758165	2900196	12914	ACAGGTTTCARTATCACTAAG	0.05	0.18	0.18	0.04	0.04	0.19	0.05	0.14	0.03	0.03	0.21	0.05
112	9	121769741	7025547	12915	ACATGTTATTYGGTTTGGATC	0.05	0.18	0.18	0.08	0.41	0.22	0.21	0.12	0.06	0.43	0.22	0.20
113	9	131664675	13294330	12916	TCAGTGAGACSCTACAGCAAT	0.18	0.41	0.41	0.08	0.30	0.11	0.21	0.39	0.05	0.33	0.11	0.21
113	9	131675321	3012724	12917	TTGACCAAAAYAGTCAGGGAG	0.09	0.29	0.32	0.14	0.04	0.25	0.07	0.28	0.11	0.03	0.27	0.07
113	9	131682303	3012738	12918	TGATAACTGARAACATAAGCG	0.40	0.27	0.25	0.03	0.19	0.28	0.22	0.23	0.04	0.20	0.30	0.21
113	9	131689827	3012748	12919	CAGCTACCGAMAATGACAGGG	0.13	0.17	0.17	0.55	0.16	0.18	0.19	0.15	0.56	0.17	0.17	0.20
113	9	131703841	10125655	12920	CCGTGGCTGCYGCAACATCCC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131710086	3012755	12921	TGAGGGAAGTYGCCCCATGGA	1.18	1.82	1.82	0.64	0.38	0.24	0.17	1.75	0.64	0.37	0.24	0.17
113	9	131715550	7850199	12922	CGGGCTTTCARTCCCTCGCTC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131722862	7018957	12923	CACAATGTCAWCTGAGTGGCG	0.70	0.65	0.65	0.79	0.76	0.33	0.14	0.61	0.81	0.79	0.34	0.14
113	9	131733511	2987383	12924	TGCCAATAAGYGTACTTACAT	0.19	0.17	0.17	0.64	0.26	0.37	0.34	0.13	0.65	0.27	0.36	0.35
113	9	131750624	10122844	12925	TCCAACACTGRCCAAGAGATT	0.30	0.36	0.36	0.44	0.27	0.34	0.40	0.34	0.43	0.29	0.33	0.39
113	9	131762107	4740321	12926	GATCTCAAATRTACTCCCGTT	0.40	0.59	0.59	0.26	0.60	0.50	0.40	0.48	0.25	0.58	0.50	0.41
113	9	131767656	2987405	12927	ACTGCACGATYTGTTAATTCA	0.30	0.47	0.47	0.52	0.66	0.77	0.77	0.38	0.55	0.71	0.80	0.76
113	9	131792348	4380988	12928	ATTTACCTGGYGCGCATGGGT	0.44	0.79	0.75	0.61	2.06	0.78	1.54	0.67	0.73	1.84	0.81	1.44
113	9	131807548	4615623	12929	TTCTTCCATASTGAAGGTCAC	0.32	0.63	0.63	2.08	2.13	1.43	0.39	0.59	2.49	1.90	1.37	0.39
113	9	131831021	7025118	12930	CCCTCACTCCKGTGCTCTGGC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131833409	4740334	12931	CATTGAAAAGRGGAGGAAAGA	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131857081	4740192	12932	AAGCCTTTTTSCTCTCTGGCT	3.21	3.38	3.38	2.29	2.08	1.02	0.56	3.26	2.37	1.90	0.96	0.55
113	9	131868699	7045484	12933	TATAGTTCTGYCCATCTCCTC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131877138	7038876	12934	AGTACTAAAAYGATCTATTCC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131895445	7039772	12935	AGTGCCTGGARGAGTACTCAG	1.00	1.13	1.14	1.92	1.29	0.74	0.87	1.11	2.09	1.28	0.73	0.85
113	9	131904197	10512418	12936	GAGAAGTTTCRGCTCAACCAT	0.85	1.35	1.38	0.60	0.94	1.06	0.67	1.31	0.67	0.96	1.03	0.66
113	9	131912973	9411331	12937	AATAAGATCTMGGTTTGCTGG	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131921679	4266768	12938	TCCATGCAAGYTCAGCCATTC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131942932	10512416	12939	GCATTGACGCRACCAATATGC	0.23	0.51	0.51	0.74	0.42	1.03	0.70	0.40	0.78	0.40	1.04	0.70
113	9	131951039	9411433	12940	ATGACCACGTRTAAATATGAA	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131960571	4246176	12941	TCATAGCACTSATAAGCCACC	0.86	1.08	1.08	0.61	0.74	0.37	1.12	1.05	0.59	0.76	0.38	1.09
113	9	131973982	7851262	12942	AAGGACAAATKACAGAGACAA	0.32	0.53	0.45	0.85	0.48	0.95	0.96	0.44	0.92	0.50	0.96	0.94
113	9	131978237	11243614	12943	GTACTTCATCRAAAATACAAG	-	-	-	-	-	-	-	-	-	-	-	-
113	9	131991388	4962112	12944	ATTTCCTTCCYATGATGATTT	0.06	0.02	0.02	0.42	1.39	0.83	1.97	0.00	0.41	1.37	0.83	1.85
113	9	132011357	11243627	12945	CTTGTTCCAARAGCTGTTTGT	0.35	0.68	0.68	0.95	1.00	1.04	0.96	0.57	0.95	0.99	1.03	0.97
113	9	132017199	9411345	12946	ACACATGATCMCAATGGTAAT	2.03	2.02	1.89	0.78	0.36	0.45	0.23	1.83	0.79	0.40	0.48	0.25
113	9	132024822	7865653	12947	CAAGAATTTCYAAGAAGGCCA	0.22	0.48	0.60	0.94	0.90	0.24	0.99	0.56	1.01	0.91	0.26	0.97
113	9	132031257	11243634	12948	TTTACGACTAYGATTTCCAGC	0.88	0.48	0.48	0.16	0.63	0.35	0.29	0.47	0.14	0.67	0.39	0.27
113	9	132038875	7872552	12949	TTGGTAGTTTYGGGTGGAAAT	0.20	0.47	0.52	0.35	0.15	0.39	0.34	0.48	0.34	0.15	0.39	0.33
113	9	132054624	7046350	12950	ATTGCTTGTCKGGTCATTCAG	-	-	-	-	-	-	-	-	-	-	-	-
113	9	132078443	6597547	12951	CCTTTCCGGTYTGCGCATCCC	-	-	-	-	-	-	-	-	-	-	-	-
113	9	132090054	7851764	12952	GGAGGCCCCARCCAAGGCGGG	-	-	-	-	-	-	-	-	-	-	-	-
113	9	132103617	3739929	12953	TGGGACGTTAYTGGATACCTG	0.72	1.13	1.19	0.49	0.14	0.17	0.58	1.10	0.51	0.15	0.18	0.54
113	9	132111064	6597555	12954	ACTGTCAGGGWTACAGAGAAA	0.42	0.02	0.02	0.44	0.55	0.81	0.30	0.00	0.44	0.57	0.75	0.30
113	9	132117446	7025107	12955	GCCTGATTGCRTTCCAGGAGG	0.14	0.06	0.06	0.11	0.23	0.52	0.33	0.04	0.11	0.26	0.51	0.33
113	9	132118808	11243672	12956	AATGTGGGGAYGGGTGGTAAC	0.30	0.06	0.08	0.26	0.11	0.15	0.17	0.06	0.25	0.11	0.17	0.17
113	9	132141124	933174	12957	TGGACTGTGGYGGGTGAAGGG	-	-	-	-	-	-	-	-	-	-	-	-
113	9	132155343	4962059	12958	GTGGAGAAGAYGGGCCTATAA	0.84	0.32	0.27	0.16	0.17	0.38	0.32	0.25	0.16	0.19	0.41	0.36
113	9	132166918	997784	12959	ACGGTGAACAYAGGAAATGGC	0.23	0.03	0.04	0.38	0.58	0.58	0.57	0.00	0.37	0.61	0.58	0.57
113	9	132174041	11243703	12960	TGTACCATTTRTCTACTGAAG	0.02	0.08	0.11	0.37	0.26	0.25	0.73	0.06	0.39	0.26	0.27	0.72
114	10	13560730	11258408	12961	TATATGTCTAYGAATAAACAC	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13568350	7098325	12962	TTTATTAAATSCTATGCTGAG	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13575323	12572570	12963	AATAATCTACWGGTGCCAAAA	1.05	0.40	0.40	0.06	0.12	1.47	0.77	0.36	0.02	0.12	1.39	0.74
114	10	13581280	4750370	12964	TTACAAAATAYGGATCACTGG	1.05	0.40	0.40	0.17	0.31	0.26	1.06	0.35	0.14	0.29	0.26	1.03
114	10	13587970	7906371	12965	ACAGGGAAGAMTGAAAACGTA	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13594437	2226030	12966	AGGAAAAATASAACAAGACTG	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13602477		12967	CATACTAGACMCTCAGTGAAG	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13609273	12249508	12968	GCCAAGTATTYTGAATGCGTG	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13646505	7088854	12969	GACAAGGGAAWGAAGCCAAGA	0.47	0.55	0.55	0.48	0.28	0.14	0.57	0.49	0.46	0.29	0.12	0.60
114	10	13657560	2502225	12970	TTTCCCCATGKAATCTGGACT	-	-	-	-	-	-	-	-	-	-	-	-
114	10	13668534	2478106	12971	TCCAAACTGCYTTAAATGGTT	1.35	0.82	0.85	0.79	0.30	0.74	0.63	0.77	0.76	0.32	0.77	0.67
114	10	13675877	2478112	12972	AGGATGGGAARTTCGTGAGAA	1.16	1.26	1.40	0.40	1.77	1.12	1.23	1.36	0.40	1.67	1.13	1.23
114	10	13685216	2399985	12973	GCTCAGCGAGYGTCTATTGAA	1.81	0.73	0.77	0.66	1.29	2.77	1.51	0.70	0.65	1.24	2.57	1.45
114	10	13691543	2502205	12974	ATGAACCATAYGTGCATAAAA	0.82	1.29	1.38	0.94	1.60	1.31	2.85	1.28	1.16	1.47	1.26	2.65
114	10	13700863	2502230	12975	TTGCTCTTTTYCTAGTCCTCG	0.69	1.13	1.17	1.56	1.95	1.55	1.10	1.12	1.98	1.84	1.52	1.11
114	10	13711577	1983888	12976	TTTGAAAAACMGTTCCACCAT	1.05	1.38	1.42	1.43	3.18	1.55	0.97	1.36	1.60	2.87	1.46	0.96
114	10	13718003	7079169	12977	GAACCGAGAAMAGAAACTTGT	1.17	1.56	1.56	2.02	2.29	1.77	0.78	1.45	2.37	2.12	1.63	0.77
114	10	13724911	11258494	12978	AGCATCAACTRGCTCTAGTGG	0.23	0.36	0.36	1.39	1.45	1.36	0.95	0.33	1.53	1.40	1.33	0.96
114	10	13732687	12264819	12979	TGTCCTAATTSCCCATCTGTC	0.28	0.57	0.56	0.18	0.93	0.98	0.29	0.53	0.16	0.93	1.03	0.30
114	10	13750842	7093256	12980	TGGAAATACCYGACCTCAATC	0.33	0.37	0.37	0.48	0.39	0.18	0.19	0.35	0.46	0.41	0.16	0.20
115	10	13958759	10508468	12981	ATACGTGTGAYTAAAATAGAA	0.86	0.51	0.51	0.30	0.33	0.08	0.14	0.49	0.28	0.35	0.10	0.13
115	10	13969136	751498	12982	AGAGCCTACAMGGAACTTCTC	1.03	0.59	0.66	0.07	0.05	0.26	0.24	0.60	0.09	0.04	0.24	0.25
115	10	13976560	1547834	12983	TCACTGCTCTRCTTAAAGACT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	13982176	10906535	12984	GGGATAATTCYGTCTCCTGTC	0.05	0.15	0.15	0.14	0.07	0.41	0.42	0.15	0.14	0.06	0.42	0.46
115	10	13987657	12776420	12985	ATAATTTCTGYGGCAACACAA	0.26	0.15	0.15	0.01	1.00	0.32	0.28	0.12	0.01	1.00	0.32	0.26
115	10	14000356	2797868	12986	AGCTCTGATAKTATGAACAAG	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14009613	17154219	12987	ATGAGGAAACRATCAGAACGA	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14016797	7082056	12988	TATCAGGTTAYGAAGAGAACC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14023576	7067738	12989	GTCTCAGATCRTAGACACCAG	0.25	0.08	0.08	0.39	0.05	0.29	0.15	0.03	0.40	0.05	0.29	0.15
115	10	14030453	11258743	12990	ATCAAGAGCCRCTAAAGGTAC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14036592	2446575	12991	TGGCTCCAGGKGCTCAAGTCA	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14039003	2446574	12992	TGAGAACTGGKTGTCTGCTTG	0.13	0.23	0.23	0.03	0.11	0.03	0.14	0.20	0.04	0.11	0.03	0.13

115	10	14050128	2447014	12993	CAGTGGCTCCRGGTGGACTGC	0.03	0.06	0.06	0.33	0.18	0.06	0.02	0.03	0.34	0.18	0.06	0.02
115	10	14062431		12994	TCCATAAATGRTCGGTTAAAA	0.05	0.16	0.13	0.08	0.04	0.19	0.46	0.10	0.06	0.05	0.18	0.46
115	10	14069319	4748066	12995	GAAAATCGACWCTTAAGAAAC	0.01	0.07	0.06	0.00	0.31	0.51	0.50	0.04	0.00	0.33	0.53	0.48
115	10	14075639	11258786	12996	AAACAAAAAAMTGTTGCTGAT	1.38	0.04	0.04	0.56	0.53	0.77	0.16	0.02	0.58	0.54	0.77	0.18
115	10	14087929	1841557	12997	TAAGGTCTTCYGCGTCATTAG	0.50	0.90	0.82	1.53	1.08	0.76	0.79	0.75	1.67	1.09	0.76	0.76
115	10	14094112	10508471	12998	TGGATGACACRGTACCCTCAG	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14100811	11258801	12999	ATGCACAGGARGAGGGGAAGA	0.16	0.12	0.12	1.85	1.59	1.41	0.62	0.09	2.05	1.50	1.34	0.62
115	10	14111789	2457855	13000	TGATCACCCARTTAGTCCCAC	1.46	2.05	2.05	1.58	2.33	1.42	0.91	1.92	1.77	2.05	1.34	0.92
115	10	14119126	10906576	13001	GGCATAAAATRTTACCATTGG	0.37	0.23	0.22	1.77	1.33	0.83	0.84	0.18	2.09	1.27	0.84	0.86
115	10	14126889	11258819	13002	TTGAATTCAGYGATACCTTTG	0.35	0.32	0.34	0.77	0.85	0.39	0.30	0.25	0.81	0.83	0.41	0.30
115	10	14133186	11258834	13003	CCTTTCGATGYTCTCTTTCTC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14139124	12265397	13004	GGCCTCAAAGKGTTTTGCAAT	0.21	0.00	0.00	0.25	0.16	0.17	0.08	0.00	0.26	0.17	0.16	0.07
115	10	14145065	11258846	13005	TTACACAACTYAGCTATGACT	0.27	0.10	0.10	0.03	0.02	0.02	0.12	0.08	0.02	0.02	0.02	0.14
115	10	14151001	12770674	13006	TGCATCATTTYTGTTTTCTGT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14165641	922239	13007	TTGACAGAGGWCTTGGACAGT	0.21	0.06	0.06	0.04	0.01	0.05	0.07	0.04	0.04	0.00	0.05	0.08
115	10	14178618	1026581	13008	CTTTAGGTGAWTTATGTTTTG	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14191283	17154656	13009	TTGTACCCTGMAAAACCTGAG	0.00	0.00	0.00	0.07	0.60	0.04	0.04	0.00	0.05	0.63	0.05	0.03
115	10	14202583	2104551	13010	GTGAGCTAAAYGTTTCCAGAG	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14209168	7914952	13011	GAAGTGTTACYTGAACTGAAA	0.29	0.61	0.61	1.27	0.27	0.22	0.21	0.56	1.44	0.27	0.22	0.24
115	10	14221414	17154726	13012	ACATAGAAGTYAATAAATCCT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14230820	10796161	13013	ACCCTGTTTCYAGGAGGACTT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14239551		13014	TCACGGTGACWGGAACTCGGC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14248658	10796166	13015	GCAGCTATTCRAACAGTCAGT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14258297	11258918	13016	CCAACCTCTCYCCATGTTTTT	2.30	3.06	2.98	1.03	0.77	0.67	0.25	2.90	1.10	0.79	0.66	0.23
115	10	14267784	6602711	13017	GCAACAGATAMGTACAATCCA	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14274358	7068441	13018	AGAGATTGATYAACTTGTTTA	1.40	1.89	1.89	1.27	0.42	0.15	0.42	1.79	1.40	0.45	0.15	0.44
115	10	14283559	10906626	13019	CTCCCATTCGSTTTTCTGCCT	1.39	1.95	1.95	1.09	0.31	0.08	0.11	1.89	1.16	0.30	0.07	0.11
115	10	14293817	12570552	13020	AAAACTGTCAYGCATTATAGC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14300506	11258947	13021	TGTATTTACARTCTCATGTCA	1.71	2.21	2.21	0.78	0.36	0.21	0.04	2.14	0.77	0.35	0.19	0.04
115	10	14312086		13022	AATAGTTACTRCCCATCTTTC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14322529	1218403	13023	TTCAATTCAGKGGCTACGGGC	0.22	0.12	0.12	1.13	0.42	0.19	0.41	0.10	1.17	0.42	0.20	0.45
115	10	14331548	11258977	13024	TTCTGCAGCCRCTTCCCTTTC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14338989	1547220	13025	GGGAAAAAAAAKTTATAGTGTA	0.02	0.11	0.07	0.08	0.89	0.99	0.24	0.04	0.05	0.90	1.00	0.24
115	10	14348848	1218341	13026	TTTAGGGTGAMTAGATGTATA	0.01	0.04	0.06	0.14	0.40	0.86	0.30	0.04	0.12	0.44	0.87	0.35
115	10	14354836	1218347	13027	TTTCTCAGATRTGTTTGAGGT	0.03	0.12	0.12	0.60	0.10	0.23	0.32	0.10	0.64	0.08	0.23	0.33
115	10	14360697	17155012	13028	AGAATTTGAAYGGGGATCATG	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14373243	11598717	13029	TACCATCTAAWATTTGTAATG	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14382622	1755153	13030	TGTATAATCTRAATGAGGAAG	0.15	0.06	0.06	0.10	0.17	0.34	0.03	0.04	0.08	0.18	0.35	0.02
115	10	14390736	1041337	13031	AAAACAATGTMCTGATACCCT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14400409	17155043	13032	AGCATGTAAASGAAAAAAACA	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14406320	1018665	13033	TTTACCTTGGKTGCAATAATT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14413136	17155060	13034	GCATTTTCCCYGGAAGATGTC	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14417420	1755115	13035	AATGCATACTSTATTACTCTT	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14426738	612589	13036	TTGATTGTTTWACTAACATTT	0.33	0.66	0.66	0.05	0.32	0.06	0.08	0.63	0.05	0.33	0.06	0.07
115	10	14437734	11595334	13037	TTTCCCAAGAKTAAATATGAT	0.16	0.12	0.14	1.08	0.33	0.23	0.05	0.12	1.08	0.35	0.24	0.04
115	10	14445908	17155131	13038	CCTGGCAATGYTGAGCCTGCA	-	-	-	-	-	-	-	-	-	-	-	-
115	10	14452774	582671	13039	CAGAAGTCAAKCTGTGATCAC	0.76	1.22	1.26	0.22	0.44	0.23	0.20	1.24	0.20	0.45	0.21	0.22
115	10	14459288	589345	13040	CCTGTCTTCARAAAAAGCAGC	0.03	0.15	0.15	0.35	0.14	0.55	0.42	0.11	0.35	0.15	0.55	0.43
115	10	14465626	657771	13041	CGGGACCCAGKAGCTGGTATT	0.46	0.11	0.09	0.37	0.48	0.43	0.59	0.07	0.37	0.50	0.43	0.59
115	10	14475686	17338398	13042	TAAAACCTCAMCTTCAATGGT	0.72	0.13	0.13	1.01	0.94	0.20	0.42	0.10	0.99	0.90	0.20	0.41
115	10	14485735	10906666	13043	AAACCAGGTTWTTCCTATTAA	1.21	1.84	1.61	0.70	0.75	0.53	0.08	1.54	0.82	0.74	0.55	0.07
116	10	19606357	16918455	13044	TTCCTGGTCTSTCTTCATCCT	0.18	0.44	0.56	0.69	0.39	0.23	0.45	0.53	0.69	0.41	0.24	0.46
116	10	19612142	2484099	13045	TTTTGAATATSTCTCTTGGGA	0.12	0.35	0.35	0.35	0.42	0.98	0.33	0.28	0.33	0.43	0.98	0.37
116	10	19619134	11009331	13046	TATCCTTGGTMCATCAGAAGT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19625777	2484098	13047	AAATTAGTTTSCAGTCTTTTA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19637710	1889516	13048	CTCAGGCCCTYCGAGCTTTAG	1.01	0.86	0.86	0.60	0.70	0.50	0.44	0.81	0.63	0.71	0.49	0.43
116	10	19651227	1984114	13049	ATATAAGAGARCTGGAAATGC	0.89	0.45	0.45	0.75	0.29	0.33	0.29	0.37	0.86	0.30	0.30	0.30
116	10	19658017	7071861	13050	TGAATTTCTARTTTTTCACAT	0.90	0.26	0.28	0.81	0.33	0.06	0.14	0.25	1.01	0.35	0.07	0.15
116	10	19664637	7101338	13051	CTCTGAGAAGSCTTTGAAAAT	0.95	0.81	0.85	0.18	0.38	0.07	0.03	0.78	0.14	0.43	0.05	0.03
116	10	19671862	1609748	13052	AAAATTATATRTGAAGGACCT	0.77	0.66	0.70	0.32	0.32	0.21	0.44	0.65	0.30	0.33	0.24	0.45
116	10	19678742	4265504	13053	GTTGACCTCTMAGCTTTTCTA	0.44	0.02	0.05	0.75	0.63	0.60	0.80	0.02	0.84	0.64	0.62	0.82
116	10	19684664	7077218	13054	GTAAAAGTGAWATGCTAAACT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19690726	1577302	13055	ATAAAATTACRTTCTGCTTAA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19703857	1889521	13056	CATCTAAGAAYTGTAAATCAG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19717815	4748576	13057	ATAGGTCTACWGAAAAAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19729041	4433483	13058	AGCTTTTCCTWAATACACTGT	0.49	0.61	0.51	0.70	1.15	1.16	1.24	0.47	0.74	1.11	1.14	1.19
116	10	19735266	11009788	13059	AAAACTGTGCRATCTATTACT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19743142	7908470	13060	TTTTCCAGAAYGTTGTCGTAG	1.54	0.24	0.24	0.20	1.08	1.18	0.97	0.20	0.17	1.04	1.15	0.97
116	10	19756832	11009849	13061	GGAATTTGCCWTGAATGCAAT	1.30	0.02	0.02	0.02	0.13	1.41	1.68	0.00	0.01	0.15	1.36	1.67
116	10	19763168	16918789	13062	CTGTTTAAAAYGATTTTATAA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19769181	16918798	13063	TTCAATTTGTRTTATGGTAAA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19781375	10458692	13064	TATAGTTCTTYCTTTTTCATT	0.10	0.12	0.12	0.27	0.20	0.83	1.73	0.10	0.27	0.23	0.85	1.66
116	10	19788566	7069355	13065	AAGCCATGGAKGAATCTAATT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19794809	10827483	13066	TAATTCAAAAMCCTAAACCTT	0.41	0.11	0.14	0.81	0.65	1.01	0.96	0.11	0.83	0.63	1.04	0.95
116	10	19801974	11010096	13067	CCACACTCAAYGGAAACTGAA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19808296	16918829	13068	CTTCGTGGAARGAACAGCACC	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19814743	1544113	13069	ACATAACTACKTCCAATTATG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19820325	16918861	13070	GGGAAGTCCAYCTTAGGCAAC	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19825907	10740910	13071	TGAGATTGAGWGAATGAAATG	0.85	0.80	0.75	1.17	0.69	0.53	0.81	0.71	1.36	0.71	0.50	0.82
116	10	19831763	7897363	13072	TGAGAACAAGWTTAAAGTATA	0.27	0.56	0.56	0.44	0.44	0.46	0.61	0.49	0.45	0.47	0.48	0.62
116	10	19847826	7905333	13073	CAGTGCAACAYTAGTCATAAA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19855274	7901638	13074	TAAGCAACTTKCATCTTTATG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19863644	10764053	13075	TAAAGAAACAKATATTCATTG	1.55	0.96	0.96	0.45	0.39	0.72	0.24	0.92	0.45	0.41	0.76	0.26
116	10	19871964	10764059	13076	TTCATTTTTTKTTGGATTCAT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19875650	3852473	13077	ATGTATTTTCWTCAAAAAGTT	0.94	1.47	1.49	1.03	1.07	0.25	0.25	1.39	1.10	1.05	0.23	0.25
116	10	19892650	3852477	13078	CCTAATCATTKTCTTTCAAGG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19899999	3852478	13079	TTTGAGTCTTRTGTTTTTCCA	1.63	1.41	1.41	2.08	0.87	0.37	0.18	1.36	2.26	0.87	0.39	0.20
116	10	19905763	11010520	13080	ATCCTCCCCAYAGGAAACCAC	1.01	0.71	0.71	1.08	0.95	0.44	0.20	0.60	1.12	0.94	0.47	0.18
116	10	19916301	12249318	13081	ATATCACTGCRTATGACAATG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19924660	11010622	13082	GGGAGATGCCRTTATGTGTTC	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19935038	3844359	13083	CATTTTCAGARTTAATTGTGT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19942794	3904905	13084	GATCTTTATGYTCACCTTTAC	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19951897	12261476	13085	ATTTGGAAAARGGTAAAATTA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	19958526	12219684	13086	CCAAGCTTCAYGGGGTAGCCG	0.23	0.51	0.50	0.24	0.75	0.59	0.35	0.44	0.24	0.75	0.63	0.34

116	10	19964003	10827695	13087	TTGGATCAAAYCTTTTATAGG	0.18	0.44	0.44	0.11	0.42	0.57	0.79	0.37	0.10	0.44	0.55	0.76
116	10	19976791	7474617	13088	ACATGACACARCTTTTTTCCA	0.35	0.09	0.09	0.85	0.87	1.69	1.22	0.05	0.85	0.93	1.60	1.20
116	10	19986172		13089	TTTTGCTTTGYGGACTAATCT	1.26	1.24	1.55	1.43	2.83	1.78	1.83	1.34	1.44	2.44	1.67	1.75
116	10	19994710		13090	TTGCTCATCTRAATTAATCCT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20004919	7916152	13091	TATCCTTAAARGTAAAGATGA	1.38	1.37	1.37	2.23	1.47	2.13	2.07	1.33	2.54	1.37	2.00	1.93
116	10	20014936	4748608	13092	TATCTGAGTCRTGCAGCACCT	0.39	0.39	0.39	1.95	1.74	1.59	1.54	0.37	2.13	1.62	1.50	1.46
116	10	20019440	16919291	13093	CTCTAAATGGRTGACGAGGTT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20031847	12256382	13094	TTGAAGTAAAMTTTTGTATTG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20042742	2025789	13095	AGTCTGGTTCYGGAGTTAGCA	0.69	0.96	0.87	0.28	2.57	1.59	0.68	0.84	0.27	2.38	1.51	0.73
116	10	20043985	2478746	13096	AAATATGTACRTGCACTCTTT	0.34	0.67	0.67	1.38	0.44	1.26	0.86	0.61	1.56	0.45	1.24	0.89
116	10	20050326	16919309	13097	CAACTCAGATYCACCATTAAT	0.89	0.88	0.88	0.74	0.63	0.16	0.92	0.66	0.81	0.65	0.15	0.91
116	10	20057858	7100283	13098	ACACAACTTAMTCAAATTAAT	0.30	0.57	0.56	0.32	0.45	0.34	0.18	0.54	0.32	0.50	0.36	0.19
116	10	20069776	7073601	13099	TGGTCTGGCTYTTTTAGAGGT	0.26	0.50	0.46	0.17	0.14	0.20	0.35	0.42	0.16	0.17	0.19	0.38
116	10	20106875	4748610	13100	CTCAGTGCTTYGATATAGGAG	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20119156	12763948	13101	GGTCTTTCAAYTGAAACTAGA	1.23	0.71	0.79	0.38	0.12	0.13	0.19	0.69	0.35	0.11	0.14	0.21
116	10	20125405	12263244	13102	CCTATCCCCARTTTGATACTA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20131169	16919362	13103	CAGCAGTCAGYATTGAATGGT	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20140825	11011581	13104	CACTCTGCATYGTACAGCATA	0.72	0.83	0.84	0.53	0.21	0.14	0.23	0.75	0.60	0.22	0.15	0.28
116	10	20150341	11011636	13105	GACGTGTTGTYTTAGAATTCT	0.65	0.78	0.70	0.37	0.18	0.31	0.17	0.59	0.44	0.20	0.31	0.18
116	10	20159308	12263862	13106	TTCAGGTCAGYATCTACCATG	0.56	0.69	0.62	0.14	0.55	0.51	0.19	0.52	0.09	0.57	0.56	0.21
116	10	20170064	333693	13107	TCCTTCTCTTYAAATCTTACA	-	-	-	-	-	-	-	-	-	-	-	-
116	10	20176365	7900249	13108	GTCATTATCTSTGGTGGAAAA	0.14	0.22	0.22	0.51	0.35	0.44	0.51	0.20	0.50	0.38	0.48	0.54
117	10	25999792	2367977	13109	ACCCAAGCGARTATGTTCTGT	0.30	0.50	0.50	0.05	0.31	0.12	0.07	0.47	0.05	0.32	0.12	0.08
117	10	26009152	10828845	13110	GGTGTTTGGTRTCTATCCCAT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26022011	12762156	13111	TGTCCCTGAAMAAGGCAAAGC	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26028092	2505500	13112	CACTCTCAAARCCAAAGGGGA	0.18	0.28	0.35	0.25	0.29	0.27	0.27	0.30	0.25	0.31	0.30	0.31
117	10	26034751	2442904	13113	TGCAAGCCCGYACTCCACTAG	0.60	1.00	1.00	0.56	0.75	0.38	0.99	0.92	0.56	0.74	0.41	0.99
117	10	26038070	11014699	13114	GCTGTTAAAAKCTGACTGGGT	0.03	0.12	0.12	1.14	0.18	0.53	0.68	0.09	1.10	0.18	0.54	0.69
117	10	26060909	2504206	13115	TTATCAACAAYAAATTTTCAT	0.60	0.87	0.82	0.16	0.25	0.51	0.47	0.75	0.18	0.27	0.54	0.51
117	10	26087707	2505471	13116	TCTAGGTACTKCAAGATTCTT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26096689	2442843	13117	ATTATCAAACRTAGCACTCCT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26106666	16926346	13118	ACAGCTTTATMGTTAAAATGG	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26112115	16926350	13119	ATTCATTCACRAAGTTATCCT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26118661	2442833	13120	CTACACACTTKAAGAAAAAAG	0.09	0.27	0.31	0.37	0.13	0.15	0.48	0.31	0.39	0.11	0.17	0.48
117	10	26125305	2505494	13121	GAGAGGTGGARTGTGCTATGG	0.16	0.33	0.33	0.15	0.31	0.16	0.14	0.28	0.13	0.28	0.15	0.14
117	10	26133887	17812509	13122	GCATATTCTCRTAAGTGATAA	0.10	0.27	0.27	0.32	0.19	0.28	0.16	0.23	0.31	0.18	0.28	0.15
117	10	26148416	17665193	13123	CAATACTCAAKTCCTGCTGGA	0.31	0.19	0.19	0.63	0.42	0.10	1.36	0.14	0.61	0.46	0.11	1.32
117	10	26161432	2505438	13124	TCAGACCCCARTTATGCTATT	0.44	0.71	0.71	0.34	0.30	0.97	1.16	0.65	0.34	0.34	0.95	1.11
117	10	26179323	11014778	13125	CTGTCAAGCARGAAGGAGCTG	0.36	0.36	0.48	0.24	0.88	0.75	0.55	0.35	0.19	0.86	0.74	0.56
117	10	26191367	12251932	13126	GTAAGCAGCCRTTAGAAATGA	0.47	0.80	0.80	1.65	1.35	0.78	0.42	0.78	1.84	1.30	0.78	0.44
117	10	26198596	3006263	13127	TGTTCTGAGASACACTAATGA	0.20	0.16	0.19	2.10	1.35	0.76	0.46	0.15	2.11	1.30	0.76	0.46
117	10	26216749	10764588	13128	TTATCTTAAGSGCTTTCTGTT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26223055	17745539	13129	ACACAGAACASATCAATAGTC	0.53	0.54	0.54	1.02	1.32	0.92	0.54	0.52	0.97	1.29	0.92	0.51
117	10	26229615	7896398	13130	TAGCAATTAAYATAAAGTGAT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26236550	4749083	13131	CCAATATGCCYGGGAGAGCTG	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26243725	1538645	13132	ACTGTATGTCWGGGATGTGCA	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26252100	10828912	13133	ATGCTGAAAGRTGTAAATTCC	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26261873	7071526	13134	TTTGATGAGAYAACTTCTTGA	0.87	1.30	1.40	0.68	0.65	1.01	0.67	1.35	0.70	0.66	0.99	0.68
117	10	26269148	10764595	13135	CTTGTTATTTYATGCTGTCTA	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26281462	7923691	13136	CTCAACCGACRATATTATTAA	0.47	0.29	0.29	0.70	0.19	0.40	0.67	0.28	0.77	0.20	0.44	0.64
117	10	26283716	12247318	13137	ACCTTGACATMATGAAATTCT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26332020	10828928	13138	ACACAGAATCKGCAAGGGCAT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26347297	11014914	13139	TTTTAAATAAKCAGCTTTCTA	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26353986	1339813	13140	AAAGTTTTGCRTGAATAAAAT	0.28	0.60	0.60	0.14	0.12	0.01	0.24	0.57	0.09	0.13	0.01	0.26
117	10	26359891	1361376	13141	GTTATAATACRCTCCTCAAAA	0.31	0.64	0.64	0.18	0.02	0.02	0.01	0.61	0.12	0.02	0.01	0.00
117	10	26373946	1402436	13142	CAGCAGAGGARCAAAATCCCT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26380371	17666263	13143	AATACTAATCKTTGCTACTGG	0.50	0.67	0.67	0.16	0.02	0.01	0.02	0.61	0.15	0.02	0.00	0.02
117	10	26386604	11014937	13144	AATCTTTCAGKCGTGAGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26392018	4998839	13145	ATGAGTAACTYCAGGGTCCAG	0.34	0.06	0.06	0.38	0.07	0.07	0.02	0.03	0.36	0.06	0.08	0.01
117	10	26397404	12773390	13146	ACATCACTTASTGCTATTACT	-	-	-	-	-	-	-	-	-	-	-	-
117	10	26415664	1546701	13147	ATTCTAAAAGRTTTTAACAAC	0.28	0.60	0.60	0.49	0.20	0.10	0.06	0.55	0.50	0.22	0.11	0.06
117	10	26423940	7910068	13148	CTAAGTTTGCWGATAAAGGCT	0.88	0.20	0.21	0.51	0.47	0.18	0.03	0.17	0.50	0.47	0.17	0.03
117	10	26438392	1402437	13149	ATGCCAGACAWAGAGAAGATT	0.24	0.49	0.48	0.14	0.36	0.22	0.04	0.44	0.10	0.40	0.20	0.03
117	10	26446222	7921390	13150	CTCATTATATYGGTAACATCC	0.44	0.00	0.00	0.14	0.08	0.10	0.01	0.00	0.09	0.07	0.09	0.01
118	10	27027421	2489584	13151	AGAATCTCAGYGATAGCCCAT	0.47	0.78	0.73	0.84	0.18	0.18	1.65	0.66	0.92	0.21	0.21	1.60
118	10	27034987	2489581	13152	CATTGCCAGTSTGCCCCAAAT	1.23	1.14	1.14	0.40	0.55	0.84	0.91	1.07	0.42	0.55	0.83	0.90
118	10	27040897		13153	GTACTATCACYCACTGTCCCC	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27049340	1780196	13154	TGAATCACACRCTTTTCGGAC	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27055197	2927922	13155	TGGACCCTTAWTAAAAATGAA	0.21	0.12	0.17	0.80	1.28	0.98	0.35	0.15	0.80	1.22	0.96	0.38
118	10	27061012	2448111	13156	ACAAAACAGTYAGCCGAGCTC	0.64	0.37	0.33	1.53	0.98	0.55	0.54	0.30	1.63	0.99	0.56	0.56
118	10	27068155	3802610	13157	GACTCATACTSATCACCTTAG	0.27	0.49	0.49	0.65	1.28	0.71	0.52	0.46	0.61	1.22	0.72	0.49
118	10	27074368	11015262	13158	GCTACCTAACMGAAGTAATCA	1.25	1.49	1.49	0.45	0.28	0.94	0.52	1.41	0.44	0.29	0.89	0.53
118	10	27082923	11015265	13159	ACTGATGTTCWTTATGGCTAT	0.07	0.07	0.07	1.07	0.38	0.42	1.00	0.04	1.06	0.39	0.42	1.00
118	10	27088476	16927324	13160	TTTTTTGTGCRTTTTCAAATA	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27100816	3802616	13161	AGCCTACACARCATGAAACAA	0.74	1.04	1.04	0.72	0.57	0.46	0.18	0.97	0.79	0.61	0.48	0.19
118	10	27106385	10829062	13162	TTTGATTCTAWAACAATTCTC	0.66	1.00	1.00	0.91	0.58	0.36	0.15	0.92	0.99	0.60	0.39	0.17
118	10	27113541	17816509	13163	ACATTCTTTAKAGGCACACAC	0.03	0.15	0.17	0.58	0.95	0.14	0.26	0.13	0.68	0.98	0.14	0.27
118	10	27121908	2018904	13164	AGGAAAGAAGYATGACATAGC	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27132514	10829068	13165	GACTTTTTCASGAAACAGGCA	0.72	1.08	1.08	0.55	0.49	0.55	0.33	1.03	0.57	0.52	0.59	0.32
118	10	27140563	17747961	13166	GAAATTTTTCRTGTTTTCCTT	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27142528	4747575	13167	CTCCTGAAGTYCCCAAGATCC	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27157707	10829077	13168	GCTGGTGTTARTACTGAAATT	0.85	1.24	1.24	0.56	0.89	0.68	0.57	1.19	0.57	0.92	0.71	0.56
118	10	27165547	2505971	13169	CACAATAGCCRCGTAACATTT	0.62	0.74	0.74	1.12	0.85	0.97	0.62	0.70	1.19	0.85	0.96	0.62
118	10	27173687	11015333	13170	TAGGGGAAAAYAGATACCGGT	0.60	0.93	0.93	0.96	1.22	0.73	0.70	0.88	1.03	1.22	0.75	0.72
118	10	27179841	17748178	13171	GTGAGATGTGKAGAAAAGAGC	0.49	0.18	0.20	1.17	0.92	0.67	0.56	0.16	1.31	0.91	0.69	0.58
118	10	27191311	4749194	13172	ACCTCTGAAARGAAAAACTCA	1.00	1.53	1.63	1.19	0.92	0.82	0.21	1.55	1.38	0.90	0.84	0.21
118	10	27200938	2505963	13173	AAGATTTTTCYTGCACTTTCA	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27210249	1853873	13174	TTGTAATAATRACAAAAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27228106	16927375	13175	AGAAGAGCAAMAAAATTAAAG	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27233922	7918574	13176	TACATCACACRATTTTCTCTT	-	-	-	-	-	-	-	-	-	-	-	-
118	10	27241392	12251191	13177	GGGGATATAAYTGTTTTTGTA	0.98	0.97	0.97	1.57	0.62	0.18	0.41	0.78	1.68	0.65	0.18	0.41
118	10	27250622	11015383	13178	GCCATAATTCKTTTCCCAGTA	0.22	0.17	0.18	0.35	0.42	0.26	0.38	0.12	0.34	0.41	0.25	0.37
119	10	36287333	1406029	13179	CCAGTAAACAMTGTTGCATGA	0.39	0.14	0.14	0.00	0.02	0.11	0.41	0.09	0.00	0.02	0.09	0.42
119	10	36292960	708415	13180	GGACAGGTACYGAAAAGAAAA	-	-	-	-	-	-	-	-	-	-	-	-

119	10	36322755	7067945	13181	TGTAGATTACRTTTTGAAGCT	0.40	0.09	0.05	0.10	0.27	1.20	1.53	0.03	0.06	0.28	1.19	1.51
119	10	36329182	11818053	13182	CAAAGGCATGSACAGTGTGTA	0.11	0.16	0.15	0.34	2.33	2.68	1.86	0.12	0.33	2.11	2.53	1.77
119	10	36336848	16936535	13183	CTGAAAAGGTYGGTGGAGAAT	0.86	0.49	0.49	2.07	2.93	3.07	2.19	0.41	2.09	2.65	2.77	2.08
119	10	36346748	12218305	13184	GTATTGATTTYTTATTAACCA	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36357558	4934562	13185	TCAGATTCCTSATGCATAGAT	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36368005	3851073	13186	CGTGAGAAATKGTTAGTCCAT	2.35	2.68	2.79	2.17	3.29	2.10	2.20	2.70	2.25	2.94	1.94	2.07
119	10	36382902	12258844	13187	AGCTGTCACAYTACCATAACC	1.73	1.81	1.81	2.84	2.08	2.29	1.47	1.68	3.11	1.88	2.14	1.40
119	10	36392682	16936624	13188	TCGCATGCCCRGGAGGAAAGC	2.07	2.13	2.11	2.26	1.43	1.23	1.59	1.98	2.74	1.39	1.18	1.49
119	10	36403233	10827592	13189	TTTCCAACCCMTGGCACCAGT	2.18	2.64	2.64	1.72	1.42	0.99	0.57	2.54	1.87	1.33	0.97	0.56
119	10	36419509	7906685	13190	ATAATATGCAMATACAACATG	1.51	1.95	1.95	1.46	1.22	0.65	0.22	1.87	1.61	1.16	0.65	0.21
119	10	36435072	16936674	13191	CACATATTTGKATGCACTGAG	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36441291	12261634	13192	CTAGGTAACTRAGGTCATGTC	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36448564	11010464	13193	TCATGTCTGARGCCACGGCAA	1.70	2.21	2.21	1.38	0.82	0.37	0.69	2.08	1.56	0.82	0.37	0.71
119	10	36455232		13194	AAAATGGGACYAGTTAAACAA	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36461835	11010489	13195	TAGGAGCAAASCAATCTGCTT	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36474682	315567	13196	CCCAAGCATGRCACCTATAGA	1.43	1.94	2.08	1.40	1.05	0.80	0.92	1.97	1.80	1.02	0.78	0.91
119	10	36475107	1413610	13197	AGAGAAATGAYCTAATTGTAG	1.56	1.90	1.86	1.48	1.49	1.20	1.06	1.80	1.68	1.44	1.18	1.08
119	10	36501573	1451193	13198	TGTGTTGTATRGTTCTTGTCT	1.01	1.25	1.25	1.82	1.95	1.65	1.16	1.17	1.86	1.82	1.60	1.13
119	10	36513050	899865	13199	AAATGTGGCAYTGGCTTCCTA	0.60	0.97	0.97	0.66	1.39	1.76	1.39	0.92	0.65	1.34	1.66	1.35
119	10	36524725	315584	13200	AATTGTAGAGRGCTGGGTGTG	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36535755	315604	13201	CTTCAGCAGCYAGAGTTGGCC	0.30	0.40	0.40	0.31	0.24	1.41	2.04	0.38	0.29	0.24	1.39	1.97
119	10	36540188	315615	13202	AGCTCACATGYATTTGCATTT	0.31	0.41	0.41	0.12	0.12	0.43	1.75	0.36	0.08	0.13	0.44	1.70
119	10	36578529	2122724	13203	GGTCTGAGATRCCAATTATTA	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36582264	17614505	13204	ATTTCACATCRTTGCATAAAA	0.30	0.18	0.18	0.38	0.54	0.43	0.74	0.14	0.38	0.52	0.44	0.72
119	10	36592101	1219583	13205	GTTGGGAAAGMAGGATCAGTA	0.12	0.34	0.37	0.31	0.91	0.96	0.38	0.32	0.29	0.94	0.98	0.37
119	10	36602520	17542837	13206	TCCAGCAGAARTTAGAAAATG	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36610727	16936889	13207	TACAAGTCTTMCATATTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36630600	4537709	13208	ATATATGCCTRAGGTAATTTT	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36638433	10508840	13209	TGGCATTGTAMTAAAAATTAT	0.55	0.25	0.25	0.39	0.55	1.03	0.55	0.21	0.34	0.56	0.99	0.58
119	10	36643830	16936914	13210	ACTGATTGCTSCCTGTGTCCA	0.66	0.77	0.77	0.58	0.53	0.28	1.06	0.73	0.63	0.59	0.28	1.07
119	10	36655388	10508843	13211	TACGGGATCGYGGTAATCACA	0.86	0.96	0.96	1.08	0.49	0.39	0.68	0.91	1.44	0.48	0.39	0.70
119	10	36664054	16936949	13212	CATCGCAAGCYGTTTTAAATC	-	-	-	-	-	-	-	-	-	-	-	-
119	10	36674073	11010629	13213	AATCTGCTTGYATGTGTCCTT	0.53	0.65	0.65	0.74	0.79	1.00	1.00	0.62	0.78	0.80	0.99	0.97
119	10	36680305	17627066	13214	GATTTTCATCRTGTTACTGGA	0.23	0.39	0.37	0.63	0.83	0.43	0.77	0.32	0.61	0.86	0.44	0.75
120	10	43793799	1254673	13215	TTAACAAGTTWGGGTTGACTC	0.79	1.20	0.93	0.92	1.21	0.89	0.55	0.90	0.94	1.17	0.87	0.58
120	10	43803527	4145117	13216	CTTCCCTTATRGATTATGGAA	1.80	2.13	2.13	1.39	1.19	1.25	1.12	2.03	1.56	1.17	1.19	1.08
120	10	43812051	17154842	13217	CCAGTTCACCRTGTCTCATCC	0.82	0.81	0.97	2.19	1.95	1.21	1.66	0.75	2.46	1.77	1.15	1.60
120	10	43824365	4948595	13218	ATTCTCACCCYGGTGGGTTGT	0.74	0.46	0.50	0.86	1.75	1.93	1.90	0.45	1.03	1.56	1.84	1.78
120	10	43832576	1472168	13219	GTGCAGTGGARAAGCTTACCC	0.88	1.25	1.25	0.59	1.19	2.79	2.94	1.17	0.63	1.13	2.42	2.64
120	10	43838498	1492705	13220	TGAATTCTAASAACAAATCCT	0.15	0.07	0.10	1.52	1.56	2.01	3.97	0.08	1.76	1.47	1.84	3.29
120	10	43844681	17154929	13221	TGCTGTGTTAYAGTGTAATTT	1.03	1.33	1.32	1.21	2.06	2.18	1.48	1.09	1.26	1.88	1.97	1.41
120	10	43857712	4615977	13222	AATAAGAGCCRAAGTGGATGT	0.44	0.05	0.05	1.24	1.89	1.57	1.38	0.03	1.31	1.73	1.45	1.32
120	10	43869773	2624695	13223	CTGCATATGGYGGAAGGGCAG	-	-	-	-	-	-	-	-	-	-	-	-
120	10	43877508	187901	13224	GTTCCTGTATYAGTGAGGAGG	0.17	0.28	0.28	0.30	2.87	2.24	1.15	0.22	0.30	2.42	2.02	1.14
120	10	43884370	182075	13225	CATCTTCCAARCCAAGGATGT	0.00	0.03	0.03	1.12	1.66	2.53	1.35	0.00	1.22	1.52	2.22	1.28
120	10	43901431	268301	13226	TTTACAATCARCAAAATGGAG	-	-	-	-	-	-	-	-	-	-	-	-
120	10	43919019	2802490	13227	GTTGCTCTCTRCAGCCCACCT	1.85	2.07	2.07	1.24	1.01	0.83	0.47	2.04	1.27	1.01	0.81	0.45
120	10	43933893	2804021	13228	TTGTTTATGAKAGTTTAAATA	-	-	-	-	-	-	-	-	-	-	-	-
120	10	43947838	169162	13229	AAAGAATTCAYATCGAGGAAA	0.73	0.72	0.60	1.66	0.56	0.19	0.14	0.49	1.66	0.55	0.19	0.17
121	10	57360183	1572689	13230	AATGGTTCCAYGAGATGTCCA	1.68	0.54	0.54	0.17	0.09	0.05	0.01	0.48	0.16	0.08	0.06	0.00
121	10	57368160	12770116	13231	ATGCACAAAAMCATATATGAT	0.41	0.49	0.46	0.07	0.01	0.03	0.04	0.42	0.08	0.00	0.02	0.03
121	10	57381466		13232	TTAGGAAACAYAGATGTGCAA	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57390396	10763276	13233	AAGGGATAAARTCAATGATCA	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57414685	10825703	13234	CTATCTAGCTRCCTAGTTGCT	1.01	0.63	0.63	0.02	0.02	0.08	0.01	0.57	0.03	0.01	0.09	0.01
121	10	57424570	10763287	13235	TCTGATTTCAYTGACTAGATC	2.19	0.53	0.54	0.11	0.30	0.03	0.02	0.51	0.09	0.31	0.03	0.01
121	10	57438214	1500765	13236	TTATTTCATGKTATACTGGAA	1.85	0.47	0.47	0.52	0.23	0.12	0.02	0.44	0.55	0.27	0.10	0.02
121	10	57453603		13237	TTATAGGTGTRCGTATTGATA	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57463252	9416416	13238	CATTTTATTGYTCCATCAGAG	1.77	0.96	0.91	0.22	0.27	0.21	0.11	0.86	0.18	0.29	0.22	0.11
121	10	57473247	7085164	13239	TTGTAGTGAARGAGGTATCTT	1.85	1.10	1.10	0.44	0.06	0.15	0.21	1.05	0.42	0.04	0.14	0.23
121	10	57478092	1604204	13240	TAGTTCCTTTWTTTTTCCTGC	2.61	0.46	0.47	0.38	0.10	0.08	0.37	0.43	0.39	0.12	0.08	0.35
121	10	57489081	17561205	13241	TATTTACTAAYTTATGACTTT	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57500433	1392729	13242	TGATTACAACWCATTCTTCAA	1.73	0.87	0.87	0.22	0.42	0.31	0.22	0.79	0.19	0.44	0.32	0.22
121	10	57512355	9416462	13243	AAGATCAATASGGAGATTAAG	2.40	0.39	0.45	0.61	0.58	0.78	0.62	0.41	0.62	0.59	0.77	0.64
121	10	57516173	7089102	13244	GCCCAGAGTGMCTTAATAAAA	2.77	0.66	0.66	1.20	1.11	0.99	1.14	0.61	1.48	1.10	0.99	1.13
121	10	57531487	9416489	13245	TGTAAATCATRGCTGACATAT	2.56	0.91	0.91	1.16	2.35	1.04	0.77	0.84	1.53	2.12	1.00	0.81
121	10	57551326	1500747	13246	CCTGTCGCTGMATAGTTCCTG	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57554214	3104863	13247	ACTTGCACAAYTTTATTTTTA	2.78	0.91	0.91	1.53	1.67	1.27	1.00	0.81	1.77	1.60	1.24	1.01
121	10	57566079	11005230	13248	AGAAAATGTAYATTCATCCAG	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57582773	7086809	13249	ATAACATGCARAAGTATAAGT	1.78	0.72	0.73	1.26	0.97	1.16	1.35	0.65	1.39	0.93	1.15	1.31
121	10	57591336	11005235	13250	GACAGGGTTAYTAAGCAAATT	0.24	0.47	0.47	1.14	1.12	1.39	1.38	0.43	1.15	1.10	1.38	1.33
121	10	57601497	7916378	13251	TGAATAGACTRCTTTTGCATA	1.41	0.63	0.63	0.77	2.02	1.52	1.24	0.59	0.80	1.95	1.43	1.24
121	10	57615599	2893677	13252	TTGTCAAGATRTGGAGCAAAT	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57625632	2392993	13253	CCACTCTCTTWCTTGTTTCCT	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57647623	16908398	13254	AATAACTACTRTCTAGAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57665487	11005271	13255	TGATAGTAGTWTTTTTAGTGG	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57671146		13256	TACCTATTTTMGTTTATGCCA	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57693590	2245618	13257	CTTGCTTCTGMTATCCAAGCT	1.84	1.05	1.05	0.36	1.12	2.08	1.04	0.98	0.35	1.11	1.97	1.04
121	10	57699215	2435872	13258	AGGGTTGAGTYAGGCTTACTT	0.55	0.94	0.96	0.53	0.51	0.83	1.42	0.87	0.53	0.54	0.84	1.38
121	10	57705383	10825777	13259	AACTGGCATGYGTTCACAAAT	1.38	0.15	0.13	0.27	0.27	0.39	0.21	0.11	0.26	0.31	0.43	0.23
121	10	57717939	10465986	13260	ACTTCCAGGGYGTGATGAATC	0.50	0.87	0.87	0.35	0.13	0.13	0.53	0.82	0.35	0.13	0.14	0.54
121	10	57724242	10450291	13261	CTGTGTAACTYTGGGACACTC	2.65	1.26	1.31	0.52	0.06	0.20	0.32	1.28	0.56	0.05	0.19	0.33
121	10	57733352	10825782	13262	CTCCTAAACTRGAATGGAATA	1.07	0.22	0.18	0.50	0.91	0.20	0.11	0.16	0.49	0.90	0.21	0.11
121	10	57744944	16908708	13263	AAGCAGCAAARGCTTCCTCAG	0.90	0.08	0.08	0.96	1.10	0.41	0.17	0.06	1.13	1.06	0.41	0.19
121	10	57751812	7907075	13264	ATGTACCTGCWCCTATACAGC	0.77	1.20	1.20	1.11	0.81	1.08	0.57	1.17	1.20	0.82	1.06	0.57
121	10	57759297	2393065	13265	AATGGCTCTTYCAGCCCAAGG	0.01	0.06	0.07	1.16	1.13	0.93	1.16	0.06	1.25	1.13	0.91	1.14
121	10	57770911	9629903	13266	ACTGAAATAGRGAAGACACTC	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57779853	7909011	13267	TCTCTGAAACSTTGATAAGGA	1.72	1.68	1.68	1.09	1.06	1.12	1.34	1.65	1.13	1.03	1.10	1.32
121	10	57788636	2241666	13268	TGAAACACCCYGTCAAGCTCC	2.88	1.66	1.66	1.22	1.33	1.55	2.08	1.60	1.29	1.28	1.58	2.03
121	10	57797797	10740667	13269	AGTTGCATTARCACTTAAATA	3.06	1.82	1.79	1.27	1.58	2.26	1.92	1.76	1.28	1.52	2.14	1.88
121	10	57808127	3849972	13270	TCCAGAATGCRGATTGAATAA	1.40	0.15	0.15	1.86	2.98	2.07	1.62	0.14	2.07	2.69	2.03	1.56
121	10	57818074	16908858	13271	GCAAATTAGCMATTGGAAAGT	1.38	1.35	1.57	1.81	2.71	2.17	1.81	1.39	2.19	2.56	2.09	1.70
121	10	57829962	10825791	13272	GCCATCCAGTKGTTTTCTTTA	1.07	0.15	0.15	1.97	2.76	2.47	2.05	0.15	2.31	2.40	2.26	1.93
121	10	57850134	16908862	13273	TTTCACCTCAYTGCTGGCACT	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57860764	7918710	13274	TTATACAGCTRCCTTTGTCAG	2.93	1.50	1.48	1.40	2.47	2.35	1.64	1.45	1.79	2.26	2.10	1.52

121	10	57868644	16908876	13275	TCAGGCTGTTKATTCACAGTA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57882588	16908140	13276	CAGGCCTTTTYTGCATACCAC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57890177	11005359	13277	AAAACATGCASACAAACAACA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57900628	2172407	13278	CCAGTGATCAYACTATTTCAC	1.34	0.03	0.02	1.47	1.86	1.50	1.85	0.00	1.77	1.70	1.47	1.74
121	10	57914102	17575600	13279	GGACTTGGAAYGAGTGGGGAG	1.48	1.97	1.97	1.49	1.11	0.87	1.73	1.88	1.88	1.08	0.92	1.68
121	10	57920685	10825805	13280	GGATTATATTKATGGTCAAAG	3.30	1.71	1.71	0.88	1.04	0.97	0.69	1.63	0.94	1.04	0.96	0.72
121	10	57927025	2393082	13281	AAGCCAGAGASAAACGAGGTA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57934990	10763372	13282	AAGAGGAAGAYCAAATTTACG	2.56	1.49	1.51	0.59	0.84	0.76	0.73	1.44	0.65	0.82	0.79	0.73
121	10	57946551	11005382	13283	TGCTATATGGRAATTGTAGAG	0.15	0.22	0.17	0.87	0.21	0.70	1.23	0.11	0.93	0.20	0.72	1.17
121	10	57953140	10825817	13284	TTGAAGAGGGSAGATTTCAAA	1.23	0.98	0.98	0.22	0.72	0.78	0.63	0.94	0.21	0.74	0.77	0.66
121	10	57960756	10763374	13285	AAAACAGCCTKGTGTAGACAG	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57966260	10825819	13286	ACTACTCCCARGCAAAGAAGG	0.03	0.02	0.02	0.82	0.68	0.91	0.47	0.00	0.83	0.67	0.93	0.49
121	10	57973438		13287	TACTTGGAAAMCATTGAGAAG	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	57993008	16908981	13288	CTGGATGTGAWCAAAATGAGG	0.09	0.09	0.05	1.58	0.98	0.55	0.83	0.00	1.75	0.96	0.57	0.81
121	10	58000526	6481214	13289	TCTCTGCATGYGTACTAGATT	0.37	0.70	0.71	1.62	1.73	1.08	0.82	0.68	1.79	1.64	1.07	0.84
121	10	58009247	1907926	13290	GCTATAGGAAYAAACAGCTAT	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58019892	17577793	13291	GTTTCAGAGGKGATACCAGAA	1.13	1.67	1.67	0.89	1.33	1.34	1.42	1.59	0.98	1.26	1.28	1.35
121	10	58030946	16909040	13292	AGCTCTTTGAYCTATTTACAT	1.92	1.92	1.97	0.81	0.45	1.64	1.69	1.87	0.97	0.51	1.52	1.63
121	10	58037173	12412000	13293	TCACAGTCTCWTTCCCTGAAT	0.56	0.77	0.77	1.02	0.73	1.31	2.52	0.73	1.19	0.74	1.27	2.33
121	10	58042845	16909108	13294	CTGTTGCTTCRACAAATCTTT	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58062030	17662259	13295	TGATCAAAAGSACCTGACAAC	0.72	1.18	1.32	0.76	0.68	0.39	2.15	1.23	0.79	0.67	0.39	1.98
121	10	58092947	1914577	13296	AGGATCAGAAYAGTTTCAGTC	0.05	0.12	0.10	0.62	0.42	0.67	0.37	0.07	0.63	0.44	0.71	0.38
121	10	58101479	10763384	13297	TCTTCTTAAARTCAGTGCCTC	0.17	0.34	0.34	0.37	0.52	0.36	0.82	0.28	0.39	0.53	0.36	0.82
121	10	58108952	17585827	13298	CTCTGCTCTGRGAATCTGCTC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58122801	16909194	13299	AACCAGGCTGYGGAGTTTGGA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58128261	16913916	13300	GGGTTTACTGSAAGCAAATGA	0.02	0.12	0.12	0.17	0.26	0.56	0.72	0.07	0.16	0.28	0.55	0.73
121	10	58138020	16909221	13301	GAGCCTCTCASAGTCCATCAG	0.02	0.12	0.12	0.37	0.48	0.53	0.69	0.09	0.33	0.47	0.53	0.71
121	10	58147012	6481230	13302	GGTTTGCAAAWGATCCAGGCT	0.26	0.39	0.42	0.19	0.26	0.85	0.74	0.36	0.17	0.24	0.85	0.79
121	10	58155891	1996435	13303	CCAAACAAGTMTTAACTATTG	0.37	0.49	0.49	0.14	0.17	0.24	0.85	0.46	0.12	0.18	0.25	0.84
121	10	58162260	1914570	13304	GACATCTGACRCTGTTATCGA	0.38	0.42	0.42	0.14	0.25	0.22	0.27	0.39	0.10	0.27	0.22	0.27
121	10	58172964	10825866	13305	TCACCCAGTCRGTTCACAGAG	0.22	0.42	0.42	0.11	0.12	0.20	0.44	0.41	0.05	0.11	0.19	0.48
121	10	58180556	10825878	13306	TCATTTTCTGYTCACCCTTTA	0.07	0.24	0.28	0.25	0.07	0.35	0.82	0.22	0.22	0.08	0.36	0.78
121	10	58187844	1547153	13307	AATTCTATGGWAAAAAAAGTT	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58188418	723125	13308	CGGTATAAACRTAAGACAGAA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58211893	10509061	13309	GTCATTGAAGRTATTGAGATT	0.09	0.22	0.22	0.22	0.33	0.78	0.93	0.21	0.18	0.35	0.81	0.91
121	10	58221470	7073569	13310	CAAAGGCTGGYTTCTGGCACA	0.04	0.10	0.10	0.25	0.83	1.14	1.66	0.08	0.21	0.86	1.10	1.55
121	10	58229823	7922739	13311	AAAAAGCTAASTTTGTATTTT	0.05	0.17	0.19	1.31	1.29	2.00	2.49	0.17	1.50	1.30	1.81	2.24
121	10	58238641	1475301	13312	ATCTGGAGACYTACAGTAAAA	0.04	0.12	0.12	1.23	2.59	2.22	1.64	0.12	1.43	2.25	2.00	1.56
121	10	58249266	10825906	13313	TGAGACTATAYGCAAGATTAA	0.07	0.06	0.06	1.17	1.94	1.90	2.64	0.04	1.29	1.72	1.77	2.48
121	10	58265671	16909569	13314	GAATTGGCACWCCCAAGAATA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58272012	12769674	13315	CAGTATCACCYGGTTAGATGT	0.97	1.49	1.49	1.55	1.06	2.06	1.89	1.39	1.70	1.05	1.96	1.80
121	10	58278439	12781661	13316	AGTAAATATGMATCACTGACT	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58289293	11005560	13317	ATGAGCTGGGRAAATAAAGGT	0.27	0.43	0.43	1.00	1.67	1.52	1.90	0.44	1.09	1.61	1.49	1.84
121	10	58305213	4935153	13318	TATGGCAATAYAATGTTGTTC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58316702	10825922	13319	TTGTTACTTASAGCACAACTT	0.30	0.14	0.14	0.93	1.30	2.20	2.19	0.12	0.94	1.34	2.13	2.09
121	10	58322949	4360622	13320	GTATGTTTTTKGCTCATAGGA	0.01	0.10	0.00	0.66	0.88	1.28	2.36	0.00	0.66	0.87	1.25	2.22
121	10	58328975	10825929	13321	TTCATGTGTGKTTAAGATTGT	0.06	0.22	0.22	1.04	0.88	1.06	2.80	0.18	1.04	0.89	1.09	2.54
121	10	58338741	12359616	13322	CAGCATAGGARACTAAATTGG	0.25	0.30	0.30	0.06	1.14	1.89	3.16	0.26	0.04	1.12	1.79	2.89
121	10	58357206	2251096	13323	TAATATTTAGMTGTTTTTAGA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58366815	16909827	13324	AGTTAAAAGCWGAGTGACAAT	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58385634	17605552	13325	TTCTTGTAAAYATCAAGTTTT	0.32	0.37	0.38	0.76	2.94	1.69	1.26	0.32	0.77	2.63	1.59	1.24
121	10	58391713	12772977	13326	TCTCCATTGCRGCATTAATAT	1.12	1.70	1.71	1.43	1.99	2.03	2.35	1.66	1.63	1.85	1.86	2.12
121	10	58400341	7902645	13327	ACTTTGTACAYTTCTTAGCAG	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58406127	7068823	13328	ATCTACTTAARGCACCTTCAA	0.60	0.41	0.41	1.02	0.88	1.41	1.95	0.37	1.11	0.87	1.38	1.86
121	10	58421576	11005601	13329	GTAACTGAGGWCAGTGATTCC	0.46	0.74	0.74	0.20	0.43	0.87	1.83	0.70	0.19	0.49	0.87	1.75
121	10	58425723	10825954	13330	CATCCTGCTTMACTCCTCTGA	0.34	0.65	0.65	0.22	0.55	1.45	1.22	0.62	0.13	0.52	1.41	1.19
121	10	58434478	10740696	13331	TGCCGTGTGGYTACATTCTGG	0.01	0.04	0.04	1.08	2.24	0.86	1.17	0.02	1.16	2.00	0.88	1.15
121	10	58441435	10732423	13332	ATTTAGCATCRTGGTTGGGCC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58448567	16909960	13333	AATTTTTGCAWTTTTCCTGCC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58474305	16910063	13334	TTCCTTGGAARAACCACTTTT	0.55	0.91	1.12	2.48	1.34	1.79	2.05	1.07	2.73	1.30	1.73	1.95
121	10	58476641	16910083	13335	TTGACTCAAGWGACTTATTTT	2.30	2.58	2.58	2.10	2.42	2.74	4.32	2.42	2.15	2.27	2.52	3.84
121	10	58499801		13336	TTAACCTCCCRTCATCACTTA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58506956	3104656	13337	CACTTAAATTKCGGGAAATGA	0.34	0.02	0.04	2.67	3.89	5.23	3.69	0.02	2.80	3.38	4.64	3.42
121	10	58515323		13338	TAACAAGGATYACCCAAATAC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58551838	1503904	13339	GACATTATTTKTATAGCCTGA	0.43	0.32	0.32	1.38	4.70	4.14	3.76	0.27	1.60	4.07	3.66	3.48
121	10	58559774	1875773	13340	TGAGTTAGTTSCTACAGCCCA	0.13	0.20	0.18	0.43	2.26	3.64	3.33	0.15	0.42	2.16	3.26	3.07
121	10	58589097	1503913	13341	GAAAAAAAAGRTTAATCCCTG	0.33	0.45	0.45	0.26	0.58	1.53	3.70	0.40	0.26	0.59	1.47	3.20
121	10	58603797	2036510	13342	AGAATATTTTRTAACAGAGTT	0.20	0.38	0.38	0.19	0.21	0.54	1.72	0.34	0.18	0.22	0.53	1.63
121	10	58615343	12240853	13343	TCTATAAAAAWGAATTATCTC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58623771	17609262	13344	AAGATATCAARCATACCAGTA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58630081	7084661	13345	ACCATTGCTCYCTGCTAGACT	0.25	0.36	0.33	0.01	0.19	2.10	2.50	0.30	0.02	0.22	1.90	2.29
121	10	58639864	7085848	13346	TTTGTAGACAYTAACTCAGAG	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58656142	11005707	13347	AGTCTGATATRAAGTTGTCAT	0.19	0.33	0.33	0.25	0.38	1.74	3.09	0.29	0.21	0.42	1.62	2.76
121	10	58666619	11005714	13348	TGGGGTACCTWATGCAAATAT	0.20	0.39	0.39	0.81	1.62	1.97	2.92	0.36	0.92	1.48	1.81	2.58
121	10	58682026	16910385	13349	CATGGGAACTSCCTTCATGTG	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58690705	1679496	13350	CCTCAGAAACYGTGTGCCATC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58698423	2393230	13351	AGATCATTCCRCAAGTTGGAA	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58719701		13352	CAGCTGAGTTMTAAATGCAAC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58728366	16910451	13353	TAAATGTTTTSTGCAAACTGT	1.10	1.40	1.39	1.77	2.63	2.55	1.67	1.28	1.82	2.19	2.22	1.56
121	10	58737513	1275279	13354	TTCGTTTTTTWTACTTTGTGT	0.85	0.61	0.53	1.55	2.37	2.92	2.80	0.42	1.85	2.09	2.43	2.35
121	10	58744627	10826015	13355	CGTGTGATGAYAGAAGTTAGA	0.28	0.27	0.22	1.20	1.63	2.59	2.95	0.15	1.38	1.54	2.22	2.42
121	10	58753290	17679397	13356	AAGCGGCCTCYATTATAGAAA	0.41	0.76	0.76	1.32	1.32	1.28	2.21	0.70	1.55	1.28	1.24	1.92
121	10	58759936	10826017	13357	GGAACTTGTTYGTTCTTTCCC	-	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58762357	1904761	13358	TATGGAATTAYGGGCAGGGAT	1.25	1.42	1.47	0.80	1.54	1.33	1.98	1.39	0.94	1.46	1.26	1.77
121	10	58767800	2928472	13359	ATGGAATTGASTAAGGTGACA	0.66	0.45	0.45	1.04	1.05	2.01	1.96	0.41	1.39	1.10	1.81	1.74
121	10	58783714	1011077	13360	CAAAACAGCAMGAACGGTATT	0.55	0.36	0.30	0.25	2.62	1.60	1.79	0.23	0.21	2.20	1.51	1.64
121	10	58793223	3008770	13361	TGGACTAAAARGAGCTTATAA	0.44	0.28	0.22	0.99	1.06	2.13	1.34	0.16	1.33	1.13	1.86	1.26
121	10	58801359	2928426	13362	GGTATGAATCMTTAAATACTA	0.66	0.45	0.45	1.29	1.01	0.38	1.75	0.36	1.63	1.03	0.42	1.61
121	10	58824063	2127615	13363	GTCCTATGTTYAAATACTGCA	1.01	0.74	0.74	0.55	0.67	1.21	0.93	0.66	0.60	0.65	1.16	0.93
121	10	58831419	7922619	13364	TGTTATGTAGYGAGAACTCTC	0.24	0.26	0.29	0.27	0.69	1.15	0.75	0.26	0.23	0.74	1.11	0.75
121	10	58838026	11005792	13365	TGCCTTATATRTTGTAATTCA	0.04	0.05	0.08	0.62	0.81	0.58	0.70	0.05	0.83	0.86	0.57	0.71
121	10	58848752	4297386	13366	ATATCTATCARTTCATTGCTA	0.23	0.06	0.05	0.08	0.23	0.54	0.63	0.03	0.05	0.24	0.56	0.64
121	10	58855375	4298830	13367	TGATAGGGAGRTGAAAGACAG	0.06	0.22	0.22	0.24	0.11	0.39	1.00	0.20	0.25	0.10	0.40	1.00
121	10	58862284		13368	TAATTGTACCRTATAAGTGGA	-	-	-	-	-	-	-	-	-	-	-	-	-

121	10	58880087	4342947	13369	CATATTATTTYTAGAACAGTG	-	-	-	-	-	-	-	-	-	-	-
121	10	58889042		13370	TCGATGCCAGWATATGTAAAA	-	-	-	-	-	-	-	-	-	-	-
121	10	58894849	10458674	13371	GCATCAAAAGYTCTGTTTTCC	0.18	0.31	0.31	0.31	0.41	0.43	0.33	0.27	0.30	0.45	0.45	0.34
121	10	58903069		13372	GGAAACATGASATAGCTCAGG	-	-	-	-	-	-	-	-	-	-	-	-
121	10	58912724	7081956	13373	GATCATTTCTYGCTACCTGAC	0.73	0.03	0.05	0.25	1.44	0.48	0.19	0.02	0.22	1.38	0.53	0.18
122	10	64375192	1115705	13374	GCTATATGTCYGATCATCTAC	0.29	0.30	0.30	0.46	0.63	1.05	0.51	0.24	0.52	0.63	1.04	0.49
122	10	64389346	12776743	13375	GGTTCTTGAAYGAAATCCAGC	0.03	0.02	0.03	0.14	0.48	0.33	0.78	0.00	0.12	0.51	0.33	0.77
122	10	64395746	10509179	13376	CTAAAACTACRTATTGACTAC	0.31	0.19	0.19	0.17	0.14	0.50	0.13	0.13	0.06	0.15	0.51	0.13
122	10	64402320	16917985	13377	ACTCCTACTCYTAATGCCTGC	0.47	0.35	0.28	0.17	0.16	0.16	0.06	0.23	0.07	0.19	0.15	0.07
122	10	64410154	16917994	13378	GAATACTGCAYCAAGTTAAAT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64418672	10822102	13379	AGATCCCTTGRAACTGCCTTC	0.67	0.01	0.02	0.09	0.08	0.04	0.07	0.00	0.02	0.11	0.04	0.06
122	10	64425615	12784493	13380	ATGTCTACTCYGGCATTCAGT	0.02	0.02	0.06	0.18	0.03	0.03	0.03	0.03	0.15	0.02	0.03	0.04
122	10	64432375	2664317	13381	GTCAGACCTTRGGAATCCTTT	0.66	1.07	1.07	0.24	0.09	0.01	0.18	1.02	0.21	0.10	0.02	0.17
122	10	64439634	2842284	13382	GGCAGAATGTRTGAAATGCAA	0.33	0.64	0.64	0.43	0.12	0.45	0.59	0.60	0.41	0.11	0.45	0.60
122	10	64449789	2842288	13383	TCTTTTAGAGRTAATAGGTCT	0.38	0.25	0.25	0.41	0.55	0.79	0.68	0.21	0.42	0.60	0.77	0.69
122	10	64467160	7085374	13384	TACTAGAGACYTTCCTTCTCT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64479908	7078424	13385	CTCTGATGATWGTTTGTTTGT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64486450	2495012	13386	ACAATAGTCARTTTCAGATGC	0.34	0.65	0.65	0.49	0.85	0.55	0.47	0.61	0.52	0.81	0.54	0.49
122	10	64492834	4746855	13387	GGAAGTAATCRGGGCAGTGCA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64504358	2036791	13388	TATCTTTAAAWTACAGCGCAA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64518165	16918175	13389	AATACTATCAYTGTTTTTTTT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64529990	10509185	13390	CTGTTGACTAYACAAAATTTG	0.48	0.86	0.84	0.77	0.62	0.56	0.49	0.80	0.76	0.60	0.55	0.52
122	10	64544760	10995445	13391	CTTATGATTTWGATCATTTCT	1.25	1.48	1.41	0.43	0.78	0.41	0.51	1.38	0.43	0.77	0.43	0.50
122	10	64549235	1553789	13392	ACTGGATTATYATGATGGTAA	0.01	0.02	0.02	0.99	0.53	0.83	0.46	0.00	1.06	0.51	0.84	0.51
122	10	64566483	12416113	13393	ACTCATCATGWTCATTTCAGT	0.02	0.12	0.14	0.06	1.44	0.62	0.58	0.11	0.03	1.39	0.63	0.58
122	10	64584199	16918239	13394	TGATTCCGACYTGGCAGACGC	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64594223	11817689	13395	AGCATATCTAYCTAGGTTTAC	0.06	0.12	0.17	0.39	0.28	0.72	0.36	0.13	0.35	0.27	0.75	0.38
122	10	64623317	4747098	13396	ACAATATTTTRTATTATAATT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64642182	7920159	13397	GTTGTCTCCTSGGAGTTTAAA	0.10	0.30	0.28	0.51	0.14	0.08	0.41	0.23	0.54	0.13	0.07	0.44
122	10	64658937	7916868	13398	ATACTTTTTTWAAAAAAAGGA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64670499	6479890	13399	AAAATAGGCTYAAGATTTGGT	1.35	1.53	1.54	0.52	0.11	0.08	0.31	1.43	0.55	0.10	0.07	0.32
122	10	64699007	7081938	13400	CTTAGGGCACRCTGAGAGAAG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64725539	7907462	13401	TGAGCTACTGYTCTTAAGGAA	0.20	0.43	0.43	0.60	0.26	0.43	0.34	0.40	0.63	0.27	0.44	0.38
122	10	64740169	7085869	13402	ATATTTAAGAYATTGTTCTAT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64751978	6479893	13403	ATCAATTTACRTAAAAGAGAA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64785433	7098614	13404	GTGAGAGTTGYTCTTGGTTGG	0.06	0.15	0.15	0.36	1.00	0.85	0.34	0.11	0.34	1.02	0.85	0.33
122	10	64791571	12355784	13405	AAAGCAAAGTMCAAAATTATA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64798283	7909692	13406	CTATCCATGAWAATATCCAGC	0.14	0.36	0.36	0.95	1.24	0.79	0.34	0.35	1.19	1.17	0.84	0.36
122	10	64803828	7923609	13407	ACAATATCCCRTTGCATAGAC	0.70	1.15	1.15	1.72	1.47	0.58	0.49	1.05	2.08	1.38	0.61	0.49
122	10	64809053	6479899	13408	CAGCTTTTAAWATATTTCTTT	0.02	0.10	0.14	0.56	1.02	0.89	0.55	0.13	0.57	1.00	0.88	0.56
122	10	64836676	17813747	13409	TGCTGGATGAYGAGGATTGTA	1.12	0.81	0.81	0.89	0.60	0.87	0.83	0.74	0.98	0.63	0.89	0.82
122	10	64843379	2393971	13410	CTTTTCTTCCRTTTAGCTGAG	1.29	1.78	1.78	0.50	0.24	0.44	0.87	1.75	0.47	0.27	0.44	0.87
122	10	64862294	3740331	13411	GACAACAACARTATCAGCTAT	0.63	1.05	1.10	0.39	0.28	0.50	0.83	1.05	0.37	0.29	0.53	0.86
122	10	64871932	17741131	13412	TAATCAAGAGYTGAGTTTTGC	1.22	1.73	1.73	0.92	0.69	0.46	0.50	1.66	1.02	0.70	0.44	0.51
122	10	64878327	2466128	13413	CTCAACCCTAYCAATGTTTAA	0.04	0.14	0.14	1.49	1.28	0.69	1.00	0.11	1.64	1.24	0.70	1.01
122	10	64890934	10159609	13414	CAAGTCTTTAYCAGCAATAGC	0.11	0.31	0.29	0.86	1.86	1.99	0.95	0.28	0.95	1.65	1.87	0.95
122	10	64903341	10995541	13415	GGAATTACAGKTCACTTATTG	0.14	0.36	0.32	0.86	2.00	1.72	1.73	0.29	0.97	1.80	1.60	1.67
122	10	64908783	12414159	13416	GTCTTAATATWAGCAAGAATT	0.03	0.12	0.14	1.63	2.36	2.60	1.48	0.11	1.78	2.20	2.41	1.43
122	10	64916453	7085862	13417	ACAGTACATTKCTTGAAAAGT	0.05	0.20	0.18	1.09	2.54	1.83	1.50	0.14	1.15	2.43	1.74	1.41
122	10	64923706	7910662	13418	GAGAGAGAAAYCATGGAGTCT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64934132	10509189	13419	AGTGATTAGGYGGTTAGGTGA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64947032	7082470	13420	CTGTTGCTCTRCTAATAAATG	0.67	1.10	1.15	1.72	0.90	1.48	2.77	1.09	1.83	0.86	1.42	2.59
122	10	64958700	7076568	13421	ACTTCTTTAAYCTATCATCTG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64964676	16918567	13422	TGAGAAAGGAMAGCAGTCAGT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64977659	4746195	13423	AACACTAACARCTCATATTTT	0.25	0.45	0.45	0.59	0.81	2.02	2.58	0.40	0.62	0.79	1.92	2.43
122	10	64985769	12412012	13424	GCATTTATCTYTTTATTTATG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64992995		13425	ATGCATGCATYTCTGTAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	64998746	7907451	13426	TTTTTATTGCWATATTCAGTA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65013137	16918638	13427	GTTCTTGACAYTTAAATACTT	0.45	0.32	0.32	0.43	1.63	2.40	2.42	0.31	0.46	1.56	2.26	2.23
122	10	65020389	10822186	13428	CTCCTATAATRCAAGCCCCCT	0.69	1.15	1.15	1.79	2.75	2.68	2.01	1.08	1.86	2.49	2.45	1.94
122	10	65026315	11817169	13429	AAGAACTCAARTTTGCTCAGC	0.04	0.08	0.08	1.41	2.88	2.33	2.23	0.04	1.38	2.65	2.24	2.09
122	10	65033172	10995566	13430	AAAAATGCCAYGAAAACAAAA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65052334	3847327	13431	ATTTATATGAYCTGGTACTAG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65063743	16918693	13432	CTTCAGATGCYTCCTATGCAA	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65069857	3858120	13433	AATGGCGTCAYACAAAAAAGA	0.14	0.23	0.23	0.32	1.39	2.45	1.58	0.19	0.30	1.35	2.30	1.49
122	10	65079188	2619602	13434	CTCTCAGCACRCACTCAGATC	0.17	0.25	0.25	0.57	0.76	0.92	0.97	0.20	0.56	0.78	0.91	0.96
122	10	65089899	16918757	13435	TAGTCTTGGCSTTGTGAACTC	0.05	0.05	0.05	0.16	0.48	0.47	0.28	0.00	0.08	0.56	0.51	0.27
122	10	65100822	16918762	13436	ATATATTCAGYGGAATCTCTT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65108003	1255484	13437	TCTTGATGCTYATCTTAGTAT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65115156	7093440	13438	CAAATGTCCCRGTTGTGGTGA	0.00	0.00	0.00	0.26	0.26	0.12	0.39	0.00	0.20	0.28	0.14	0.38
122	10	65122552	1255476	13439	ATCTGATGATRTGAACAAAAT	0.64	0.45	0.46	0.10	0.01	0.06	0.08	0.44	0.06	0.00	0.06	0.09
122	10	65128334	1255466	13440	AGCAGGGACTRTGATTTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65136629	12571482	13441	AATCCCTTGTRTATTCCCAGG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65142903	10509194	13442	AGTAGCTTTAYTGATTGGAAC	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65154489	7910647	13443	GGTGCGCCACMAGCATTGAGG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65166113	11599596	13444	TGTCCCAGTGRCCTCATGGCT	0.21	0.31	0.31	0.01	0.05	0.03	0.04	0.29	0.01	0.04	0.03	0.03
122	10	65180980	3864802	13445	CAATAAGCCTYACCCAGGAGT	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65187210	7100414	13446	TCAGGAATAAMTGAAAATAAG	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65194129	4746396	13447	TTCAACTTGGSAAATGTTTGA	0.77	0.43	0.43	0.32	0.06	0.03	0.10	0.38	0.32	0.06	0.02	0.08
122	10	65203592	16918850	13448	CATGCCTCCTSTGGATTTACC	-	-	-	-	-	-	-	-	-	-	-	-
122	10	65214873	12765658	13449	ATTGCAGATARTAGACAGCTC	0.82	0.64	0.64	0.17	0.11	0.21	0.10	0.60	0.11	0.09	0.20	0.10
122	10	65233212	17825120	13450	GGGGCAGCCARTGGGACTTCT	0.43	0.68	0.72	0.16	0.08	0.15	0.12	0.67	0.14	0.08	0.17	0.13
122	10	65234429	7091964	13451	TTCACTCATAYACCTCACATT	0.54	0.72	0.72	0.37	0.03	0.11	0.06	0.69	0.34	0.03	0.11	0.06
123	10	76271373	7906881	13452	TTCGACCCTTWAATCTGTTAT	1.07	0.69	0.69	0.35	0.08	0.08	0.20	0.61	0.34	0.07	0.08	0.18
123	10	76280515	958320	13453	AGAGACTTCCRTTATCACTGC	0.92	0.56	0.56	0.23	0.08	0.09	0.11	0.49	0.23	0.09	0.09	0.12
123	10	76303670	16931793	13454	ATCAGGTGCARACAGAAATTT	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76313833	11001192	13455	AGCCTACTTARACAGTTCCTT	0.75	0.43	0.43	0.13	0.13	0.06	0.13	0.38	0.09	0.11	0.06	0.12
123	10	76323726	7095910	13456	TGAAATTTTAYTAGCTTGAAC	1.12	0.72	0.72	0.25	0.08	0.05	0.03	0.66	0.22	0.08	0.04	0.03
123	10	76334688	1880690	13457	AGTTTAGATTRTTAGAGAACT	0.78	0.68	0.74	0.31	0.09	0.05	0.04	0.71	0.30	0.08	0.03	0.04
123	10	76340855	2395121	13458	GTAGTCCAGCRGAGAGTGATA	0.94	0.83	0.83	0.39	0.17	0.07	0.07	0.76	0.37	0.19	0.06	0.08
123	10	76348654	7097121	13459	TTGTCAATCTMAGGTAATTGT	0.97	0.85	0.85	0.54	0.18	0.16	0.04	0.77	0.64	0.19	0.18	0.04
123	10	76358088	7909358	13460	CCTGAAGAGARTATAAAGGTG	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76364882	10762648	13461	CAAGACTCGARCGTAACACTG	0.86	0.77	0.77	0.30	0.37	0.11	0.02	0.70	0.30	0.41	0.10	0.01
123	10	76380082	11001217	13462	GTTCTACCCCRAAGGATGTGA	-	-	-	-	-	-	-	-	-	-	-	-

123	10	76389685	4746249	13463	AATGTTTTTAMTTTTGAAATG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76399638	3213967	13464	CTTTCTAAAGYTTTAAATACA	0.47	0.70	0.74	0.40	0.15	0.05	0.13	0.68	0.37	0.15	0.05	0.13	0.47	0.70	0.74	0.40	0.15	0.05	0.13	0.68
123	10	76410747	10824255	13465	CCTCATATGTRTGCAGATTGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76420762	16931904	13466	ATGATCACCTYGTCCTTTCCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76430599	1868628	13467	TTCGGGGAATYCCCTTTGCTG	0.54	0.47	0.47	0.27	0.04	0.17	0.40	0.40	0.23	0.03	0.17	0.40	0.54	0.47	0.47	0.27	0.04	0.17	0.40	0.40
123	10	76438438	4746250	13468	TTAAAAACTTRTAGAACATAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76453026		13469	CTAAGGCTCCRCCCCAAGGCC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76465217	16931936	13470	CGAATGCTCCKGCACATTTGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76478827	7904278	13471	GAAAGATTTAYGTCAGAATGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76482866	2395130	13472	ATGGACTGCAKTGTGAGTGAG	0.79	0.69	0.69	0.19	0.35	0.41	0.38	0.61	0.16	0.32	0.40	0.39	0.79	0.69	0.69	0.19	0.35	0.41	0.38	0.61
123	10	76517394	17688487	13473	GGATCAAGAAKCACGGATGAG	0.30	0.48	0.48	1.14	1.24	0.72	0.98	0.44	1.13	1.21	0.75	1.01	0.30	0.48	0.48	1.14	1.24	0.72	0.98	0.44
123	10	76528722	17688962	13474	TCACTAACCCWTCTGCTTCCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76543433	11001296	13475	AGTGGAATAGYAATTGTTTCT	1.09	1.57	1.57	1.43	1.91	2.05	1.14	1.49	1.45	1.79	1.92	1.12	1.09	1.57	1.57	1.43	1.91	2.05	1.14	1.49
123	10	76548031	9299525	13476	GATGGTAGGARTTAGTGCAAG	1.75	2.19	2.19	1.40	2.87	2.20	1.59	2.09	1.41	2.53	2.01	1.54	1.75	2.19	2.19	1.40	2.87	2.20	1.59	2.09
123	10	76567763	10509354	13477	TGACTGAAACMTGGAGAATTA	0.32	0.54	0.54	1.88	2.15	2.16	2.63	0.47	2.01	1.99	2.04	2.46	0.32	0.54	0.54	1.88	2.15	2.16	2.63	0.47
123	10	76581937	16913572	13478	TGATAGCATGMTGTTTTATTA	0.70	1.19	1.23	0.87	2.16	2.51	3.11	1.18	0.93	2.07	2.36	2.81	0.70	1.19	1.23	0.87	2.16	2.51	3.11	1.18
123	10	76586022		13479	CCATTCCTCAMGAAAATGAAC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76594126	11001311	13480	TGTGCTATAGSATGGGAGAAA	0.61	0.56	0.62	2.37	3.30	3.11	3.13	0.61	2.63	2.97	2.79	2.88	0.61	0.56	0.62	2.37	3.30	3.11	3.13	0.61
123	10	76604587		13481	TTTTAGGCGTRTGTGTGGGAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76631338	879154	13482	CAGGCACTGGMTTGACTTTTG	1.43	1.88	1.88	1.67	4.14	4.20	3.02	1.86	1.69	3.63	3.60	2.79	1.43	1.88	1.88	1.67	4.14	4.20	3.02	1.86
123	10	76647123	12269517	13483	TCTAGTGTTTYCTAACATGAT	0.10	0.33	0.33	2.22	3.30	4.67	4.22	0.26	2.30	2.89	3.99	3.54	0.10	0.33	0.33	2.22	3.30	4.67	4.22	0.26
123	10	76653264	12249405	13484	AGTTTGGAAAYGTACCTAGCC	2.03	2.16	2.16	1.76	2.63	3.14	4.89	2.08	1.77	2.40	2.67	4.21	2.03	2.16	2.16	1.76	2.63	3.14	4.89	2.08
123	10	76687012	1700982	13485	ATTCACATCASGCCCAGCCTT	0.01	0.03	0.04	1.00	2.00	2.79	1.70	0.02	1.10	1.89	2.54	1.64	0.01	0.03	0.04	1.00	2.00	2.79	1.70	0.02
123	10	76695947	1149705	13486	GGCCTGCCGCRGTGAAAACAT	0.27	0.56	0.55	0.84	2.64	1.69	1.35	0.47	0.92	2.44	1.61	1.32	0.27	0.56	0.55	0.84	2.64	1.69	1.35	0.47
123	10	76711175	1149711	13487	TGATGAGCACRTTACTGTCGA	0.09	0.25	0.25	1.54	0.54	1.38	1.02	0.22	1.65	0.59	1.36	1.02	0.09	0.25	0.25	1.54	0.54	1.38	1.02	0.22
123	10	76717387	16932187	13488	GCTTCCTGAGRGTAGGTTGAA	0.25	0.47	0.47	1.11	1.41	0.49	1.25	0.38	1.13	1.37	0.53	1.22	0.25	0.47	0.47	1.11	1.41	0.49	1.25	0.38
123	10	76775745	2435882	13489	AACTGTGCGGRATCAGTGTTC	0.08	0.15	0.15	0.19	0.62	1.06	1.05	0.12	0.18	0.66	1.03	1.07	0.08	0.15	0.15	0.19	0.62	1.06	1.05	0.12
123	10	76782306	1652713	13490	TTCCACTTGAYGTGAGCCTCT	0.11	0.23	0.23	0.04	0.19	0.60	0.44	0.21	0.01	0.19	0.62	0.44	0.11	0.23	0.23	0.04	0.19	0.60	0.44	0.21
123	10	76791088	1262398	13491	GTCAATATTGYTCTGGAAAAC	0.17	0.26	0.26	0.26	0.25	0.10	0.25	0.22	0.25	0.24	0.10	0.26	0.17	0.26	0.26	0.26	0.25	0.10	0.25	0.22
123	10	76797239	1259589	13492	TCTGCCGGACRGGGCCATACA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76808701	2488703	13493	AACCACAAGARGGTCCCTGTT	0.37	0.63	0.63	0.87	0.28	0.39	0.68	0.62	0.87	0.27	0.39	0.66	0.37	0.63	0.63	0.87	0.28	0.39	0.68	0.62
123	10	76848073	16932252	13494	ACATTTCAGAYCCTGGAGCAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76867176	17769639	13495	AGGTTATAGCYGTGTCTTGGG	0.06	0.10	0.10	0.17	0.58	0.86	0.66	0.09	0.17	0.59	0.86	0.68	0.06	0.10	0.10	0.17	0.58	0.86	0.66	0.09
123	10	76882173	4746298	13496	ACTTGGGGTCRCATCATAGCC	0.45	0.03	0.03	0.17	0.34	0.61	0.58	0.00	0.17	0.36	0.59	0.61	0.45	0.03	0.03	0.17	0.34	0.61	0.58	0.00
123	10	76906484	4745774	13497	TTTCCCAGCTYTTGGTGTTTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76919635	2915032	13498	TGTCATGGGTRATAAGAATAA	0.43	0.38	0.38	0.33	0.12	0.21	0.52	0.34	0.31	0.14	0.21	0.54	0.43	0.38	0.38	0.33	0.12	0.21	0.52	0.34
123	10	76926587	3012041	13499	AAAAATGCACRTATGTTTATA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76936473	3012044	13500	TCCCTTGGCCRGTGCCCAGTG	0.05	0.00	0.00	0.05	0.09	0.08	0.36	0.00	0.04	0.10	0.09	0.37	0.05	0.00	0.00	0.05	0.09	0.08	0.36	0.00
123	10	76943082	2915028	13501	TCTTGCGTGCRTGTTGGCTTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
123	10	76954380	2395289	13502	CCCTAATGGARTTCTCTGTGT	0.07	0.17	0.15	0.13	0.28	0.13	0.08	0.13	0.10	0.30	0.14	0.07	0.07	0.17	0.15	0.13	0.28	0.13	0.08	0.13
123	10	76969487	2915021	13503	CTCAGAGATTYGGCTTAGTAT	0.45	0.41	0.41	0.49	0.14	0.12	0.06	0.35	0.53	0.13	0.14	0.06	0.45	0.41	0.41	0.49	0.14	0.12	0.06	0.35
124	10	82501022	11186821	13504	TCAGAAATGAYGGGTCCTTTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
124	10	82511054	4934479	13505	ACTCAACAGAYATTCATCACT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
124	10	82521896	11186902	13506	GAGGGCTAGCRTGCCAGATGC	0.30	0.62	0.74	1.47	0.86	1.10	0.78	0.70	1.49	0.86	1.10	0.81	0.30	0.62	0.74	1.47	0.86	1.10	0.78	0.70
124	10	82533692	11186988	13507	GGCAGACATCRTTGTTTTATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
124	10	82538595		13508	GACTGTTTGAKCAGGAATGGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
124	10	82550935		13509	TAAGGCAGGTRGCTCGCTAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
124	10	82561669	1989530	13510	ATAAAACTAGMATTCTTGTTA	0.67	0.28	0.28	0.40	1.60	1.23	1.18	0.21	0.37	1.53	1.20	1.15	0.67	0.28	0.28	0.40	1.60	1.23	1.18	0.21
124	10	82565186	1702223	13511	ATGTATTTAGYGGCTTTTTTT	0.00	0.00	0.00	1.06	0.83	0.99	0.33	0.00	1.13	0.83	0.95	0.35	0.00	0.00	0.00	1.06	0.83	0.99	0.33	0.00
124	10	82603841	10509418	13512	TCTGTTTAAARATATGTCAAA	1.39	1.88	1.88	1.17	0.92	0.30	0.15	1.78	1.32	0.95	0.31	0.17	1.39	1.88	1.88	1.17	0.92	0.30	0.15	1.78
124	10	82613241	7074252	13513	GGTTGGCTTTYTATGATGTTT	0.10	0.06	0.06	1.13	0.78	0.19	0.20	0.05	1.21	0.82	0.18	0.18	0.10	0.06	0.06	1.13	0.78	0.19	0.20	0.05
125	10	84038722	951203	13514	ACAATGATTTSTAAGCACCTG	0.38	0.31	0.31	0.03	0.00	0.08	0.11	0.26	0.02	0.00	0.06	0.11	0.38	0.31	0.31	0.03	0.00	0.08	0.11	0.26
125	10	84045291	10787027	13515	CTTCCATACCKCTGGAGCTGG	0.26	0.19	0.18	0.06	0.17	0.04	0.05	0.18	0.05	0.16	0.04	0.04	0.26	0.19	0.18	0.06	0.17	0.04	0.05	0.18
125	10	84052323	1414763	13516	ATACAAACATRAAAGGGCAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84061945	10884515	13517	ACACAGGAAAYGATCAAAAGA	0.25	0.46	0.44	0.12	0.10	0.10	0.10	0.41	0.09	0.11	0.11	0.08	0.25	0.46	0.44	0.12	0.10	0.10	0.10	0.41
125	10	84069164	11193683	13518	AATTCCGCCGMAAGGCAAATT	0.06	0.18	0.18	0.04	0.04	0.07	0.15	0.17	0.02	0.04	0.08	0.17	0.06	0.18	0.18	0.04	0.04	0.07	0.15	0.17
125	10	84078553	17099789	13519	GGGAAGATGTRGGAGCATACT	0.29	0.41	0.34	0.08	0.04	0.05	0.36	0.30	0.03	0.04	0.05	0.35	0.29	0.41	0.34	0.08	0.04	0.05	0.36	0.30
125	10	84084032	7900818	13520	TACGTTTTCCYCGAAGCATGG	0.10	0.25	0.25	0.06	0.14	0.35	0.12	0.22	0.03	0.16	0.37	0.13	0.10	0.25	0.25	0.06	0.14	0.35	0.12	0.22
125	10	84091786	3904729	13521	ATGGTATTTAYGGTATATGGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84100544	7917348	13522	GAAAGGGTTTRTCAATCTCGT	0.10	0.24	0.22	0.15	0.67	0.38	0.35	0.17	0.11	0.70	0.43	0.33	0.10	0.24	0.22	0.15	0.67	0.38	0.35	0.17
125	10	84109812	1317093	13523	CTCACCCCTGRCATGTGGTGT	0.25	0.53	0.53	0.63	0.36	0.57	0.34	0.42	0.71	0.38	0.57	0.34	0.25	0.53	0.53	0.63	0.36	0.57	0.34	0.42
125	10	84121889	11194002	13524	CTCATTTGGARGCCTACTCTT	0.02	0.06	0.06	0.32	0.55	0.38	0.28	0.02	0.28	0.55	0.42	0.28	0.02	0.06	0.06	0.32	0.55	0.38	0.28	0.02
125	10	84128941	10884635	13525	CACCTGTGACWCTCACTTCAA	0.03	0.13	0.14	0.48	0.30	0.34	0.56	0.10	0.46	0.30	0.33	0.54	0.03	0.13	0.14	0.48	0.30	0.34	0.56	0.10
125	10	84133874	7083166	13526	AATATTGACARACTTATTTAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84141992	7078757	13527	TGTGATAAAGYGAGAAATAAT	0.27	0.58	0.48	0.07	0.15	0.73	1.75	0.44	0.07	0.16	0.76	1.64	0.27	0.58	0.48	0.07	0.15	0.73	1.75	0.44
125	10	84148952	12245090	13528	CCAAAATGACYACTGCTATGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84159896	1954640	13529	TTGGTAAAGAYGATGACTGCT	0.04	0.17	0.17	0.20	0.10	1.46	1.70	0.16	0.17	0.09	1.40	1.64	0.04	0.17	0.17	0.20	0.10	1.46	1.70	0.16
125	10	84166922	7089201	13530	CAAAATTAAARTAACAACTTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84172473	12266855	13531	GTTTTGTTTTKGGAAGAACTA	0.52	0.47	0.56	0.64	2.25	1.59	1.42	0.49	0.66	2.11	1.53	1.35	0.52	0.47	0.56	0.64	2.25	1.59	1.42	0.49
125	10	84188927	7094481	13532	GTTCTACCATRTCACACCAAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84200736	7074029	13533	TATCATCTACRTTAACTGCTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84208644	17100097	13534	ATTCATGCTCRGAATTTTCAG	1.05	1.51	1.51	3.23	2.43	1.97	1.29	1.40	3.46	2.27	1.86	1.24	1.05	1.51	1.51	3.23	2.43	1.97	1.29	1.40
125	10	84227329	7073972	13535	TCACATTTTARAGGGCTGACC	3.07	3.58	3.58	3.55	3.68	2.09	1.31	3.47	4.06	3.23	1.94	1.24	3.07	3.58	3.58	3.55	3.68	2.09	1.31	3.47
125	10	84227698	10884753	13536	TAAGGAAAACRGGACTACTCT	1.53	1.97	1.97	2.70	3.85	2.29	1.32	1.94	2.99	3.30	2.10	1.30	1.53	1.97	1.97	2.70	3.85	2.29	1.32	1.94
125	10	84244151	17100118	13537	AATAATAGGAYGTGTGATGAT	1.01	0.63	0.63	1.69	2.09	2.24	1.38	0.49	1.94	2.02	2.04	1.37	1.01	0.63	0.63	1.69	2.09	2.24	1.38	0.49
125	10	84250674	608159	13538	ATGGAGTATGMTTTAGATTTA	2.29	2.73	2.64	1.69	1.31	1.21	1.93	2.53	1.83	1.25	1.17	1.82	2.29	2.73	2.64	1.69	1.31	1.21	1.93	2.53
125	10	84256231	612113	13539	ACTGCTTGGGKCTTTCCTCTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84261869	12263568	13540	CTGAAGTTTAYTGTTCTTACT	1.70	1.88	1.88	1.33	1.23	0.78	1.25	1.82	1.36	1.26	0.77	1.23	1.70	1.88	1.88	1.33	1.23	0.78	1.25	1.82
125	10	84269929	999889	13541	TATGAGCCCTRTAAATGTTAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84277602	656298	13542	GCAGTTTTATRCAGTCTTATA	2.09	1.63	1.63	0.65	1.01	1.11	1.23	1.53	0.70	0.99	1.11	1.24	2.09	1.63	1.63	0.65	1.01	1.11	1.23	1.53
125	10	84286508	683668	13543	TGGCTGATTARTCAGAGGATG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84293692	659561	13544	AATTGTCAAGKGAGTCCATAA	0.29	0.60	0.55	0.85	0.37	1.04	1.11	0.48	0.95	0.38	1.05	1.08	0.29	0.60	0.55	0.85	0.37	1.04	1.11	0.48
125	10	84307871	616012	13545	AAATTGCAGARACAAGGAAGG	2.03	1.60	1.60	0.98	0.59	0.25	0.64	1.55	1.01	0.59	0.25	0.67	2.03	1.60	1.60	0.98	0.59	0.25	0.64	1.55
125	10	84316220	2348331	13546	AAAGAAGAAGSCATGGCCAAA	0.15	0.16	0.16	0.76	0.70	0.45	0.51	0.14	0.79	0.68	0.47	0.55	0.15	0.16	0.16	0.76	0.70	0.45	0.51	0.14
125	10	84325671	1416851	13547	TCTGGGTCTCYGTATTCTTCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84341183	4454667	13548	TAACAATCAAYGAGTTAGTAA	0.80	1.21	1.11	0.31	0.50	1.13	0.46	1.03	0.27	0.53	1.13	0.48	0.80	1.21	1.11	0.31	0.50	1.13	0.46	1.03
125	10	84347728	10884989	13549	AATGCATGTAYCTTGATGATA	0.20	0.47	0.55	0.30	0.70	0.32	1.08	0.49	0.30	0.73	0.33	1.07	0.20	0.47	0.55	0.30	0.70	0.32	1.08	0.49
125	10	84353307	639839	13550	TTTCCTTTTAMTTATGACCAC	0.72	0.03	0.03	1.31	0.43	0.59	0.75	0.00	1.63	0.46	0.60	0.71	0.72	0.03	0.03	1.31	0.43	0.59	0.75	0.00
125	10	84367195	608009	13551	TGACACCAGCRAGTTTGTGAG	0.88	0.08	0.14	1.21	1.20	0.74	0.53	0.10	1.32	1.20	0.73	0.51	0.88	0.08	0.14	1.21	1.20	0.74	0.53	0.10
125	10	84376073	661469	13552	ATAACCTACCRGCTGTATGGA	0.41	0.52	0.52	0.77	1.27	1.19	0.58	0.47	0.71	1.25	1.11	0.57	0.41	0.52	0.52	0.77	1.27	1.19	0.58	0.47
125	10	84383006	12415032	13553	CCTGGCATAGRAAAATAGAAT	0.43	0.79	0.79	0.13	1.20	1.36	0.63	0.70	0.12	1.21	1.30	0.66	0.43	0.79	0.79	0.13	1.20	1.36	0.63	0.70
125	10	84394962	1339797	13554	ACATTTACACMAGACTTGAAA	0.35	0.55	0.55	0.33	0.18	0.60	0.79	0.48	0.30	0.21	0.60	0.78	0.35	0.55	0.55	0.33	0.18	0.60	0.79	0.48
125	10	84405285	2820111	13555	AGATACCCTCMTCTACTCTGG	0.27	0.26	0.26	0.42	0.07	0.15	0.68	0.23	0.39	0.06	0.17	0.72	0.27	0.26	0.26	0.42	0.07	0.15	0.68	0.23
125	10	84413711	17100442	13556	CTTGGATCAAYGAACTGGGCA	0.43	0.77	0.77	0.22	0.18	0.45	0.38	0.70	0.19	0.19	0.43	0.40	0.43	0.77	0.77	0.22	0.18	0.45	0.38	0.70

125	10	84421766	7080154	13557	TCTAGGTTTTWTCCTTACTGA	0.26	0.31	0.32	0.10	0.32	0.50	0.50	0.28	0.08	0.35	0.54	0.51
125	10	84435120	7922963	13558	TGAGATCAAAYTCAGTCCTGC	0.15	0.12	0.12	1.05	0.33	0.31	0.52	0.10	1.07	0.31	0.33	0.54
125	10	84442056	2249964	13559	AATGTATGCARTTTGTTGACT	-	-	-	-	-	-	-	-	-	-	-	-
125	10	84448055	7068082	13560	TGTAAAACTGRTTAGTGTGTG	0.04	0.09	0.09	1.23	0.53	0.36	0.17	0.07	1.25	0.54	0.36	0.17
125	10	84454665	2484452	13561	CAAGAAGGCARGTTGGACACA	0.24	0.53	0.53	1.02	0.70	0.12	0.17	0.50	1.17	0.70	0.14	0.16
125	10	84460638	10885239	13562	TTTTGAACTTYGGTGACTTTT	0.02	0.06	0.06	0.54	0.37	0.26	0.16	0.03	0.56	0.41	0.29	0.16
126	10	97574013	10882671	13563	TATATCTAGAMGTTAACTTGA	0.07	0.08	0.11	0.14	0.05	0.19	0.06	0.08	0.14	0.05	0.22	0.05
126	10	97586266	4614366	13564	ATATTGAAATRATCCCGAGGG	0.07	0.20	0.23	0.04	0.06	0.02	0.04	0.21	0.01	0.08	0.03	0.05
126	10	97594931	3176883	13565	GCTATGTCTTYGAAGCCCCTC	0.02	0.10	0.10	0.23	0.07	0.02	0.00	0.08	0.21	0.06	0.02	0.00
126	10	97615089	4512761	13566	CCGTTGTTTARAAGCCAGGCT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97622072	2051052	13567	GATCCATGGCYGCCAGCTCTC	0.97	0.33	0.33	0.13	0.06	0.01	0.01	0.29	0.09	0.05	0.01	0.01
126	10	97628214	7897988	13568	CATAATGACTYTCTCTATACA	0.03	0.14	0.14	0.08	0.13	0.07	0.00	0.12	0.06	0.13	0.07	0.00
126	10	97640499	7074866	13569	GGGAAGAACAKTTCTTTAGGT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97651672	7895056	13570	GTACTACCAASAATATACAGT	0.24	0.43	0.43	0.49	0.25	0.03	0.01	0.37	0.49	0.26	0.04	0.00
126	10	97656528	10786240	13571	TGGGTTGTTAYCAAGTATGAC	0.06	0.07	0.10	0.79	0.32	0.02	0.10	0.07	0.87	0.33	0.02	0.10
126	10	97687136	10736095	13572	GAGTATGATAYATTCATTTTA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97694299	10882696	13573	GGTGTAATTAYCTGGGATCAT	1.06	1.03	1.03	0.56	0.30	0.37	0.05	0.90	0.57	0.32	0.35	0.05
126	10	97702109	2027200	13574	ATACGTTCTCMCTGGAAAAGA	0.70	0.04	0.04	0.31	0.40	0.23	0.66	0.02	0.29	0.42	0.26	0.67
126	10	97714237	7904410	13575	TACTGATGTCRTATTGATTGC	0.59	0.04	0.04	0.47	0.45	0.87	0.24	0.01	0.46	0.46	0.92	0.25
126	10	97721189	10509695	13576	TAAACTTATAYGGAATTGTAG	0.26	0.55	0.56	0.22	1.87	0.69	1.00	0.52	0.21	1.69	0.68	0.97
126	10	97727238	4344425	13577	GTTTTTCTTAYACACACTAGT	0.14	0.39	0.39	2.21	0.78	1.86	1.48	0.35	2.69	0.81	1.72	1.41
126	10	97740935	10882703	13578	TGACAGTGTCRAAGTTGGAAA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97749573	2015026	13579	CTCCTTCCCAYTGGGTCTCAC	2.21	2.09	2.09	1.22	2.90	1.60	1.04	2.00	1.28	2.54	1.51	1.04
126	10	97755982	11188552	13580	CTTCTCATGARTAATAGAAAC	0.81	1.10	1.22	1.97	1.79	1.95	1.00	1.16	2.21	1.69	1.83	0.97
126	10	97765629	12770030	13581	ATATGTCCCTKCTTGCCCAGG	2.43	2.56	2.56	1.62	1.55	0.99	2.22	2.47	1.86	1.50	0.97	2.10
126	10	97782913	10509699	13582	CTGAGGTTTCYTGGTTCACTC	0.43	0.22	0.42	1.63	1.05	2.64	0.79	0.29	1.66	1.05	2.31	0.80
126	10	97804806	4145226	13583	AGGCAATAAGMTGGATAACTA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97824720	11188583	13584	TCCTCTTTCTSCCTACGGACT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97832105	7079761	13585	GATGCATGACRGTACTTAGAG	0.21	0.20	0.20	0.20	2.70	1.36	1.96	0.11	0.20	2.47	1.32	1.88
126	10	97843002	11188596	13586	CAACGAACCTRAAAATCACCC	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97869221		13587	CTGAGGATCTRTCTGTCTCAA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97876681	11188622	13588	TCAGGATGCARACAGTCTTAG	0.26	0.27	0.27	1.28	1.43	1.96	0.42	0.24	1.39	1.36	1.84	0.42
126	10	97886002	17111359	13589	TGTAAAATTAYTCATTTTGGC	1.17	1.14	1.28	0.89	1.50	0.68	0.69	1.09	0.97	1.43	0.70	0.70
126	10	97895295	11188627	13590	AACATAATTCWTCATTCTCTT	0.60	0.99	1.19	1.10	0.68	0.70	0.66	1.11	1.14	0.67	0.71	0.68
126	10	97914430	10509703	13591	TGTTACAAGAKTGGAAACTTT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97942032	11188657	13592	GTATTAAGTAYGAAGAAAAAC	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97951468	11188662	13593	ATGTGAAATAYGAAAAAGACT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97958817	736070	13594	CATTACAATCSTCACCTGACT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97966024		13595	ATTTTTTCACKCCTCTGCAGA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97974301	1007764	13596	GTCCTTCTCAKCAGGTATCAG	0.11	0.22	0.22	0.37	0.89	0.77	0.90	0.20	0.36	0.86	0.76	0.91
126	10	97983455	17111485	13597	TTTTTCTGGGMCCTCTTGGAA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	97992875	3789928	13598	GGTAAGTGTTSATAAGAAGGT	0.77	0.15	0.09	0.65	0.77	0.79	0.88	0.07	0.64	0.76	0.78	0.85
126	10	98001354	3789930	13599	TAACAAAATARAATGAAGAAC	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98008856	12411820	13600	ACTTGTTTCARCTTGGCCCCT	0.82	0.77	0.76	0.55	0.66	1.24	0.71	0.67	0.57	0.65	1.23	0.70
126	10	98016172	6584061	13601	GACATGTGGAYTCTGGTTTAG	0.41	0.09	0.03	0.83	0.97	0.86	0.90	0.00	0.99	0.99	0.83	0.91
126	10	98026333	10882767	13602	GCTTTCCCACRCATGCGGGCC	0.96	0.89	1.18	0.71	0.41	0.61	0.50	1.06	0.74	0.45	0.62	0.52
126	10	98040506	2146390	13603	CTGGCAATGCYGTACCACCTT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98059154	10509708	13604	TACCTTTGTCRTCACCTGGAA	0.13	0.26	0.30	0.45	0.54	0.21	0.12	0.23	0.42	0.55	0.21	0.12
126	10	98066200	11188709	13605	GCTATCAATGYTCTGCTCACA	0.04	0.22	0.22	0.22	0.15	0.11	0.03	0.20	0.18	0.16	0.11	0.03
126	10	98075328	3789940	13606	GTAAACTGGAYTTTTGTTCTT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98081924	3818313	13607	GGGAAGATAAKGCAACCACTT	0.04	0.19	0.22	0.29	0.06	0.03	0.03	0.19	0.26	0.04	0.03	0.03
126	10	98088606	7096643	13608	TCCCTGCCATYGTGCTGAAGG	0.60	0.69	0.69	0.14	0.01	0.01	0.06	0.65	0.11	0.01	0.00	0.05
126	10	98095612	3814224	13609	CTTGGCATCTYTCCTCTCCAA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98105674	1923702	13610	AATTTAAAGAKCGTGGGCTCA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98114705	7077344	13611	AGTTAGCAGGMTTTTACAAAT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98122006	17479671	13612	GGATGCTGGTYGCCATTTTGT	0.11	0.14	0.12	0.05	0.00	0.09	0.09	0.08	0.05	0.00	0.09	0.08
126	10	98128558	3827865	13613	AGATGCCCTGRGGAAAACTCT	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98141172	1885682	13614	TCTGTGGTATYGGGAAGGTAG	0.64	0.22	0.22	0.02	0.13	0.09	0.15	0.19	0.02	0.13	0.08	0.16
126	10	98150243	7893983	13615	TTTGGAAACASACAAGTAGGA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98155787	11599403	13616	ATGAGGAGCAYCTTGGCAGCC	0.19	0.31	0.28	0.32	0.09	0.22	0.05	0.26	0.32	0.09	0.21	0.05
126	10	98174962	2146388	13617	AATATTCTGCRTGTTTGGTTA	-	-	-	-	-	-	-	-	-	-	-	-
126	10	98176591	17111856	13618	ATTTGTTAGCYCTGTAATGTT	0.44	0.59	0.59	0.39	0.38	0.07	0.12	0.58	0.38	0.36	0.06	0.12
127	10	100332431	11189687	13619	CTTTTATGGCRTAACTGTCTC	0.08	0.26	0.26	0.32	0.49	0.97	0.58	0.14	0.29	0.49	0.99	0.63
127	10	100340328	10883146	13620	AGCCATGATGYGCTTATCTGT	0.53	0.71	0.75	0.89	0.72	0.45	1.23	0.67	0.98	0.70	0.46	1.23
127	10	100351260	560749	13621	ACTACCAACCSTGATTATCTC	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100359992	526465	13622	TCCACACCATRGCTTGGCAGT	1.03	1.52	1.57	0.56	0.29	1.11	1.31	1.52	0.54	0.29	1.11	1.25
127	10	100370950	10883151	13623	ACTAGTCCAGKTATATTGTAA	0.09	0.11	0.15	0.65	1.11	1.61	1.35	0.13	0.67	1.11	1.55	1.34
127	10	100379797	11189719	13624	GCTAACTGCTWTATTTAACTT	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100389254	17110455	13625	CATCTCTCAGKGGCTCTACTG	0.69	0.47	0.47	2.11	3.52	1.64	0.77	0.42	2.27	3.19	1.62	0.79
127	10	100396734	563060	13626	TAAACCTGTAYTCCAGATCCT	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100402147	528556	13627	TTCAACAACCRGTCCCACATA	1.76	2.16	2.00	1.95	2.66	2.09	0.73	1.89	1.93	2.37	1.97	0.72
127	10	100409703	475945	13628	ACTTCACTGARTACTTGTGAG	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100424345	3021452	13629	TCTCAAGATTRTGTATAAAAG	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100425944	965934	13630	ATGAGTGGCCRGTGTTATTAA	0.19	0.41	0.37	1.95	1.86	1.57	1.09	0.36	1.99	1.77	1.54	1.07
127	10	100445675	10748750	13631	ACCAGCTCTTRAATGAATAGA	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100455887	17110699	13632	CTCAAATTCAYGTAGTTAGTG	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100463182	17110721	13633	ATCCTCCAAAYTGTAATTCTT	0.81	0.57	0.48	0.72	1.89	1.01	0.52	0.40	0.72	1.84	0.98	0.50
127	10	100471417	17110744	13634	TCTAGGAGGGYGATGACATTC	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100483316	17110762	13635	TGGTACTTACKGCTGCCTTTA	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100491881	11189793	13636	GGAATACGAARAACTTCAGGC	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100500931	10786467	13637	TTGACAGAGASGATTAACATT	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100524479	17110835	13638	TAAGTAACCGRTACTGGCAGC	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100530404	17110853	13639	AGGCTTTTGAYTGCTTGGCTA	-	-	-	-	-	-	-	-	-	-	-	-
127	10	100541536	1414971	13640	TGCCTGACATWCCACAGCTAG	0.18	0.27	0.27	0.34	0.58	0.68	0.41	0.25	0.31	0.58	0.68	0.43
128	10	110602526	2685476	13641	TGTCACTCCTSAGTACGAATT	0.13	0.22	0.22	1.08	1.15	0.53	0.35	0.21	1.24	1.15	0.55	0.35
128	10	110615884	2786583	13642	AACCCCTAGTYGTAAAAGGAT	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110618069	2685483	13643	TGAGGAAAAGMAATTGCCCCA	0.52	0.47	0.42	1.04	1.16	0.60	0.29	0.40	1.14	1.10	0.65	0.29
128	10	110638719	11194292	13644	CTGGGGGACASAGTTTTAGTT	1.15	1.65	1.56	1.29	0.97	0.50	0.44	1.47	1.48	0.98	0.52	0.46
128	10	110650450	7920080	13645	TGCATACCATRTAATTCAGTG	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110680293	17700389	13646	CCATACACACKTTGCAATAGA	1.17	1.66	1.66	1.09	0.91	0.91	0.34	1.57	1.17	0.89	0.92	0.33
128	10	110693774	17125438	13647	CAAACAACAAYCATTTTTTGT	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110708276	7917300	13648	CACAAATTGTYCATCATAACA	0.04	0.08	0.08	1.49	0.89	0.35	0.73	0.06	1.82	0.89	0.37	0.74
128	10	110713892	7905093	13649	TACATCTTCAYCTGTGCTCTA	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110720530	10509882	13650	TCAAGGCCACRTATTTGTCAC	0.19	0.14	0.16	1.07	0.82	0.18	0.28	0.14	1.23	0.86	0.20	0.29

128	10	110725913	10082437	13651	CTGCACCTCTRCTCTTACTGA	0.92	1.35	1.35	0.67	0.25	0.53	0.23	1.30	0.73	0.24	0.54	0.24
128	10	110739774	11194325	13652	CAGAGAGAGGYAAGCCATGTC	0.12	0.18	0.18	0.73	0.56	0.35	0.26	0.16	0.74	0.55	0.37	0.26
128	10	110754522	12253338	13653	TCTCATAACCRGGAAAATAAT	0.60	1.00	1.00	1.12	0.66	0.26	0.23	0.91	1.19	0.70	0.29	0.27
128	10	110761451	17779947	13654	TCAAACCAGASTCTGCTAATG	1.63	2.01	2.01	1.19	0.46	0.48	0.27	1.93	1.25	0.45	0.50	0.27
128	10	110769683	17125571	13655	GGACATGAATYACTGGGACTC	0.91	1.19	1.19	1.52	0.74	0.31	0.45	1.15	1.60	0.75	0.29	0.47
128	10	110783195	12264337	13656	TTAAAATATASCACCAAAATA	0.70	1.07	1.07	0.55	1.29	0.59	0.68	0.99	0.68	1.26	0.60	0.65
128	10	110788984	7085262	13657	TCAGGTAACAMATTGTTGTTC	0.92	1.35	1.35	0.86	0.32	1.83	0.87	1.29	0.97	0.32	1.76	0.85
128	10	110798961	10509887	13658	CAAAAATGACSTGTATCCTTA	0.70	1.08	1.08	0.60	1.40	0.50	1.48	1.00	0.63	1.38	0.51	1.46
128	10	110807480	11593905	13659	CGCATGGGGTRAGAAGCAGGG	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110817885	17125661	13660	GGTAAACTACRAGGCCTCAAA	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110823513	17125668	13661	TCCTCTTGGAYGCCCTTGGGT	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110831230	7084033	13662	TACAATCCACSTGCTCAGTAT	0.12	0.35	0.35	1.59	0.94	1.25	0.78	0.26	1.89	0.94	1.24	0.75
128	10	110837416	7071522	13663	ACATGGGCCAYCTGGGTGCCT	1.22	1.70	1.82	1.32	1.54	1.03	0.47	1.74	1.43	1.47	1.00	0.47
128	10	110840345	17125686	13664	CTTCACCAGGRGAATGGGTTA	0.88	1.32	1.30	1.91	1.22	0.56	0.46	1.24	1.99	1.19	0.56	0.47
128	10	110856427	10884698	13665	ATATAATATAKAGTACCAGGC	0.50	0.56	0.53	0.81	0.88	0.54	0.49	0.47	0.87	0.90	0.57	0.50
128	10	110865888		13666	TCTCCTGGTAYTTTTTTCTTT	-	-	-	-	-	-	-	-	-	-	-	-
128	10	110890130	1324277	13667	GTAGGGAGAASGGTCTGTATG	1.18	1.40	1.31	0.82	0.25	0.71	0.27	1.24	0.89	0.26	0.71	0.26
129	10	114027468	10885323	13668	TAACATAGGCRTTGCAATTCT	0.78	0.34	0.32	0.08	0.33	0.54	1.17	0.28	0.04	0.35	0.59	1.12
129	10	114033776	10885325	13669	TAGAGAATGCYTGCTCTATTT	-	-	-	-	-	-	-	-	-	-	-	-
129	10	114044591	10509958	13670	GGAACTAATCRGATAGGAGGT	1.14	0.08	0.08	0.36	0.62	1.42	1.61	0.05	0.34	0.64	1.38	1.53
129	10	114051969	10749114	13671	CTTTGGCCCCRGCAAAACTTT	0.10	0.27	0.31	1.06	1.47	2.12	2.17	0.26	1.15	1.45	1.94	2.07
129	10	114060787	12247848	13672	AACCTCCAGAWGGAAAACAGT	1.01	1.39	1.39	1.40	1.97	2.90	2.80	1.32	1.62	1.73	2.65	2.64
129	10	114074379	2076869	13673	GAAAGGAAGGYATCCAGCCCT	0.78	1.18	1.14	2.45	3.14	2.45	3.25	1.10	2.81	2.71	2.26	3.05
129	10	114084921	7898941	13674	GAGCTTTAACRATTGAACAGA	0.12	0.31	0.31	1.74	3.59	3.26	2.30	0.31	1.93	3.14	2.90	2.15
129	10	114092662	7087000	13675	AATCTGAAACRGTCAAGCCAT	1.20	0.84	0.84	2.43	3.43	3.04	2.86	0.81	2.61	3.15	2.72	2.60
129	10	114101227	10885337	13676	CTGTTGTTGTSTGATACGGAA	1.60	2.08	2.08	2.83	2.13	2.53	2.68	2.00	2.91	1.98	2.36	2.50
129	10	114101533	2148493	13677	TTCTCCAGTGYTGAGTCCCAG	2.46	2.51	2.48	1.46	1.88	2.29	2.26	2.40	1.66	1.73	2.15	2.14
129	10	114114699	10509961	13678	GTTACTTGGCSTCTCTTAGAT	-	-	-	-	-	-	-	-	-	-	-	-
129	10	114124265	3808920	13679	ATTGGAAGGGWACACTGATTT	1.69	2.15	2.15	1.28	1.95	1.63	1.78	2.12	1.42	1.83	1.55	1.67
129	10	114129886	1926564	13680	GATTTGGACTRTGACTCACTT	0.64	0.58	0.51	1.94	1.79	1.37	2.01	0.44	1.95	1.74	1.32	1.88
129	10	114138679	12255316	13681	GAACAGACTTYGAATAGGGTT	0.33	0.32	0.39	0.06	1.12	2.42	1.53	0.37	0.06	1.12	2.13	1.51
129	10	114146731	17129754	13682	CTCTCACTTTKGATACTAATT	-	-	-	-	-	-	-	-	-	-	-	-
129	10	114154136	11195949	13683	GGACATATAAKAGAAGCTCAA	0.18	0.39	0.39	0.69	0.92	0.84	2.45	0.35	0.70	0.87	0.83	2.25
129	10	114164803	17129773	13684	CAGTTTCTTASCATGCTACGC	1.36	1.33	1.69	1.21	0.84	1.05	0.96	1.57	1.44	0.87	1.01	0.98
129	10	114179121	723373	13685	AATGCAAATAYCCCAAAGCAC	0.60	0.14	0.14	0.62	1.18	0.58	0.82	0.10	0.65	1.15	0.59	0.83
130	10	114552665	4633389	13686	GAAAGGGCATRTTCTCAGAGA	0.51	0.85	0.85	0.27	0.50	0.98	1.42	0.82	0.26	0.50	0.95	1.39
130	10	114561821	1213134	13687	TTGATGTTTCRGGCCCACATT	0.64	0.92	0.98	0.28	0.39	0.43	0.44	0.94	0.30	0.41	0.48	0.43
130	10	114568865	12766378	13688	AATTTGCAACYTGTTCAGCAG	0.01	0.09	0.09	0.95	0.25	0.15	0.22	0.06	0.94	0.23	0.13	0.24
130	10	114571183	12358731	13689	CAACTTTGCTRTTTTTCACTT	0.01	0.05	0.06	0.38	0.25	0.14	0.28	0.04	0.34	0.26	0.13	0.27
130	10	114592734	10885388	13690	GGTGATTTACRGGAGCTCACC	0.44	0.43	0.47	0.23	0.12	0.28	0.36	0.42	0.19	0.13	0.27	0.39
130	10	114602962	1547191	13691	CTCACTATTTYGCCTGCAATC	0.25	0.47	0.47	0.09	0.08	0.51	0.53	0.40	0.06	0.07	0.53	0.57
130	10	114608919	2475177	13692	AGTTCTAATGMGAATCCAACC	0.40	0.50	0.50	0.16	0.15	0.41	0.66	0.46	0.13	0.17	0.41	0.67
130	10	114630787	10885390	13693	GAGCTATCGCWCAACAGATTC	0.23	0.53	0.50	0.57	0.23	0.26	0.26	0.46	0.57	0.23	0.28	0.26
130	10	114639457	17746501	13694	GAAAGTGACARCCTACTCAAA	0.30	0.58	0.58	0.63	0.54	0.40	0.09	0.55	0.63	0.56	0.41	0.09
130	10	114645907	11196145	13695	CTTGATATCCWTAACAATCCC	0.43	0.82	0.82	0.87	0.85	0.13	0.41	0.79	0.99	0.85	0.14	0.42
130	10	114653987	11196146	13696	ACATAGGAGGYGAGATGATAA	1.00	1.42	1.42	0.55	0.22	0.52	0.41	1.34	0.55	0.20	0.54	0.44
130	10	114666170	10509966	13697	CAAGACAGTCRCTATCTATGA	-	-	-	-	-	-	-	-	-	-	-	-
130	10	114685922	10509967	13698	GTGAAGAAAAMGACTACTGCT	0.12	0.00	0.00	0.37	0.53	0.55	0.61	0.00	0.37	0.56	0.54	0.62
130	10	114694771	17746916	13699	ATGTTAAATAYGCATCCAATT	-	-	-	-	-	-	-	-	-	-	-	-
130	10	114704715	2094406	13700	TTTAGCCGGGYAACTTCTCTT	0.06	0.19	0.19	0.62	0.99	1.06	1.77	0.18	0.59	0.97	1.07	1.74
130	10	114713640	2296783	13701	AGAAAATTGGYGGCTTTCTGG	-	-	-	-	-	-	-	-	-	-	-	-
130	10	114724086	11196174	13702	TGGAACTACCRGAAAGAAAAA	0.17	0.02	0.02	0.96	2.17	3.07	1.12	0.00	0.98	2.07	2.85	1.10
130	10	114733951	7895307	13703	CCTCCTTTTGRCTTGGGGAGC	0.55	0.63	0.63	1.42	2.69	1.39	1.83	0.58	1.49	2.50	1.35	1.80
130	10	114739724		13704	TTCATTGAGCRCTTCTGCGAA	0.78	0.33	0.30	3.62	2.32	1.99	1.80	0.28	3.77	2.16	1.90	1.75
130	10	114746031	4506565	13705	CCGAAGTGATWTGGGGCCCTT	1.10	1.42	1.42	1.82	3.88	2.52	1.66	1.36	1.95	3.42	2.27	1.65
130	10	114758599	6585200	13706	TCTGTTCCTARGCTCAGGGAT	1.60	1.05	1.05	0.73	1.52	2.54	1.84	1.02	0.71	1.46	2.34	1.71
130	10	114767714	10885406	13707	AGTGTATTAARAGGGCTGGAG	1.85	0.96	0.96	0.50	0.22	0.95	1.60	0.93	0.50	0.25	0.98	1.56
130	10	114777080	7907610	13708	TGTTTCATCARTGTCTTTTGG	1.97	1.00	1.00	0.29	0.22	0.12	0.68	0.97	0.26	0.22	0.13	0.70
130	10	114779067	7077039	13709	TCCTCTCTTAYCTTTCACAAG	1.65	1.01	1.10	0.14	0.14	0.30	0.45	1.07	0.13	0.12	0.31	0.50
130	10	114786038	7100927	13710	GAAGATTCTCRAGGATGAAGG	2.22	1.20	1.20	0.24	0.24	0.98	0.61	1.16	0.22	0.26	1.00	0.59
130	10	114798062	10885409	13711	TTTCTTGTCTYGCTGATTAAC	2.14	1.30	1.30	0.91	1.33	0.77	0.58	1.24	1.02	1.30	0.80	0.55
130	10	114814966	7919409	13712	ATGTTGTTTAYCAGGCAGCAA	0.49	0.60	0.60	1.75	1.10	0.49	0.43	0.57	1.77	1.09	0.45	0.46
130	10	114824488	7908486	13713	GCCATAGGCARATTTTCATAC	1.06	0.54	0.54	1.03	0.44	0.40	0.56	0.52	1.08	0.44	0.39	0.58
130	10	114840981		13714	ATACATTTCCRCATTTCTAGT	-	-	-	-	-	-	-	-	-	-	-	-
130	10	114849453	7085532	13715	TGCTTCTGCCRTGCGTTTTGC	0.65	0.20	0.23	0.11	0.41	0.68	0.19	0.19	0.11	0.43	0.71	0.18
130	10	114858152	17130188	13716	GCCGTTAAACYTGGGGCAATC	-	-	-	-	-	-	-	-	-	-	-	-
130	10	114864363	290474	13717	GTGAGTTAACYGACTCATTGA	0.44	0.63	0.63	0.63	0.36	0.54	0.26	0.57	0.64	0.36	0.52	0.26
130	10	114870541	12772424	13718	GTTTCAGAACWGTTTCTCAAC	1.16	1.13	1.13	0.71	0.39	0.39	0.36	1.07	0.82	0.43	0.41	0.35
130	10	114892980	17130192	13719	GCGACGCACGYGGTGCCCATT	0.96	1.50	1.69	0.47	0.12	0.34	0.35	1.61	0.49	0.13	0.35	0.33
130	10	114905204	290483	13720	TAAGTGTAGGKTTTATCCACT	0.04	0.02	0.02	0.41	0.06	0.01	0.12	0.00	0.41	0.06	0.00	0.12
130	10	114913815	290481	13721	TGTTATCAGCYATGGTTCTGA	1.03	0.58	0.65	0.08	0.01	0.15	0.02	0.60	0.05	0.01	0.17	0.01
130	10	114930492	12243558	13722	CAAATGAGAARTCAGCTTGGG	0.36	0.16	0.16	0.03	0.16	0.09	0.25	0.13	0.03	0.15	0.08	0.27
130	10	114937150	7922641	13723	AGGGGCACTAYACACACGGTT	0.25	0.15	0.15	0.03	0.28	0.20	0.09	0.11	0.00	0.28	0.24	0.07
131	10	126062195	11244635	13724	GGCCCTCTCCSGACTCAAGCA	0.08	0.07	0.07	0.30	1.11	0.65	0.21	0.05	0.30	1.10	0.64	0.22
131	10	126081804	2240882	13725	CTCACCAACTMTTTCCTTTGT	0.33	0.42	0.36	0.43	0.39	0.38	0.28	0.32	0.40	0.39	0.36	0.28
131	10	126094012	2491161	13726	TTAAGATGAAKTCTGGATATT	0.69	0.22	0.22	0.73	0.14	0.46	0.09	0.21	0.73	0.14	0.44	0.09
131	10	126158000	7099115	13727	GATGACAAGGKTTTGCTTCCT	-	-	-	-	-	-	-	-	-	-	-	-
131	10	126163530	2001516	13728	AGAGACATTARCAATTCCAGA	-	-	-	-	-	-	-	-	-	-	-	-
131	10	126168915	11245177	13729	GAGATTCTGGMTCCCCATGTG	1.37	1.91	1.91	0.47	0.46	0.10	0.30	1.80	0.48	0.46	0.09	0.32
131	10	126175608	3824810	13730	TCTGTCCCAARCTCTCTTCAG	0.22	0.49	0.49	1.27	0.78	0.45	1.25	0.45	1.32	0.81	0.47	1.19
131	10	126184239	11593207	13731	CTCACGGTTTMAGCTTCTGAA	-	-	-	-	-	-	-	-	-	-	-	-
131	10	126199125	17151960	13732	AATGTCAGACSTTTTGATTTG	0.55	0.51	0.60	0.67	0.66	1.97	1.30	0.49	0.76	0.67	1.88	1.28
131	10	126206317	11245261	13733	AACCTTGGACRTGATCTCTTT	0.03	0.14	0.17	0.92	0.67	1.22	1.04	0.16	0.98	0.68	1.19	1.06
131	10	126220868	7077436	13734	TTGAAGTTATMCAGCACTTAT	0.62	0.76	0.75	0.60	0.51	0.84	0.74	0.70	0.56	0.51	0.86	0.74
131	10	126228787	10901758	13735	CTCATACCCTSTCTCCTGACC	0.12	0.11	0.08	0.58	0.54	0.58	0.75	0.06	0.59	0.55	0.59	0.77
131	10	126238597	11245291	13736	TCTGGTTTGTMGCCTGTACCA	0.17	0.34	0.34	0.37	0.33	0.67	0.93	0.30	0.36	0.34	0.70	0.91
131	10	126247170	10901763	13737	GGAGGCTTACMGTGCTGGACC	0.26	0.53	0.71	0.51	1.00	0.72	0.43	0.66	0.51	1.00	0.72	0.43
132	11	20552900	16914839	13738	GTGATGTTGCRAAGAAGCTGG	0.15	0.34	0.34	0.84	1.10	1.05	1.14	0.33	0.89	1.10	1.02	1.10
132	11	20568845	7131598	13739	AGTAATCCCAYAGTTAGGAAC	1.84	1.31	1.30	1.48	1.21	1.00	0.90	1.29	1.53	1.17	0.98	0.90
132	11	20574611	16906511	13740	TGTTTTTCAGWAGGCTACCCC	1.02	0.72	0.72	0.74	1.79	1.26	1.33	0.67	0.74	1.73	1.25	1.34
132	11	20586413	10500882	13741	AGATGCTTCARATGTGAAATA	0.75	0.23	0.23	1.32	0.69	1.11	0.95	0.23	1.45	0.71	1.07	0.94
132	11	20596592	4922794	13742	TGAGCAATTASTTGGTAAGGG	0.84	1.06	1.07	0.44	0.84	0.97	0.85	1.04	0.41	0.86	0.98	0.85
132	11	20610197	1945771	13743	AGCAATGGCTMTCCCTGGTTG	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20621016	17298460	13744	CCAAACTGGCSCTGAAACCCA	0.22	0.46	0.49	0.42	0.47	1.22	1.72	0.46	0.40	0.46	1.20	1.67

132	11	20628245	7111588	13745	ATCACTTTTGSGCAGTTATTT	1.58	0.04	0.04	0.94	0.91	1.12	1.94	0.02	0.97	0.89	1.15	1.86
132	11	20636147	7122910	13746	TTTAATATGTRAGAAATGTAA	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20638148	12789398	13747	ATGCCCTCACRAGCTGATGCT	0.99	1.59	1.66	1.49	1.70	1.44	1.03	1.59	1.54	1.69	1.38	1.01
132	11	20651776		13748	TCAAGTGCCTYTGTGACATTG	1.11	1.09	1.09	2.08	1.27	1.76	0.69	0.93	2.27	1.22	1.67	0.64
132	11	20657351	951199	13749	CCATAGGCCASTTAACAGCTT	0.42	0.75	0.75	0.74	1.17	0.89	0.56	0.70	0.75	1.18	0.91	0.54
132	11	20664328	1715260	13750	GTGCTAGCCTRTTAATAATAT	0.15	0.38	0.38	0.17	0.53	0.83	1.05	0.34	0.16	0.55	0.81	1.01
132	11	20697654	7109431	13751	AACAGACATTWCAAGGATCCT	0.16	0.41	0.41	0.28	0.57	1.23	1.07	0.37	0.26	0.57	1.20	1.07
132	11	20703781	12295773	13752	GAGTTATACASCTTGTTAATT	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20711547	12282820	13753	TGAGCTCAAGMTGGACCATGC	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20722666	1519725	13754	TTTAAGTTGTYGGGCTTGGCT	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20732334	1554368	13755	TTCTGGACTARGTTATCTATT	0.34	0.54	0.54	0.50	1.59	0.94	1.30	0.50	0.51	1.54	0.90	1.30
132	11	20739458	1429795	13756	CAGTTCAAGGSTACCTGGCGT	0.18	0.11	0.11	0.82	0.97	1.62	0.95	0.07	0.79	0.98	1.56	0.93
132	11	20750221	1949523	13757	GGCCAATACARCATTTAAAAA	1.28	1.80	1.87	0.83	1.56	1.33	1.41	1.87	0.85	1.53	1.28	1.42
132	11	20758379	12804039	13758	TTAAGTGGGGSTGTCCTGCAA	0.81	1.10	1.10	2.23	1.08	1.22	0.97	1.08	2.34	1.10	1.20	0.98
132	11	20765840	1519736	13759	TGGGCATTATKAGATTCCTAG	3.07	3.74	3.72	1.78	2.73	1.40	1.25	3.67	1.83	2.51	1.33	1.21
132	11	20776327	16906806	13760	CAGAAAATGASGATGTTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20791637	11601634	13761	AGTTCTGCTCYGATTTGATTC	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20800564	378575	13762	TTGAATGAATRCGACAAACTT	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20809773	2680989	13763	CCTATGACACMGAGCCATCTC	0.30	0.16	0.16	3.14	2.84	2.02	0.78	0.14	3.32	2.51	1.92	0.76
132	11	20819832	4923100	13764	CAGTGAAGTTRCTCTGGTTAA	0.63	0.57	0.57	0.76	3.34	1.61	1.02	0.50	0.79	3.01	1.59	0.98
132	11	20831014	7121400	13765	TAAGTAACAGYACAAGGTAAG	0.04	0.04	0.10	1.46	1.28	1.83	1.16	0.06	1.52	1.29	1.70	1.09
132	11	20844238	10766732	13766	TGTAATGTACYGTGCACAAAG	0.08	0.15	0.17	0.35	0.79	0.43	0.70	0.16	0.32	0.78	0.45	0.70
132	11	20854966	10766739	13767	CCCCTGTCACRGTCAGTAAAC	0.01	0.07	0.02	0.10	0.02	0.15	0.10	0.00	0.08	0.02	0.16	0.11
132	11	20858495	7121209	13768	GACTAAGTGCSAAGGGCATGT	0.14	0.04	0.04	0.08	0.01	0.01	0.05	0.00	0.06	0.00	0.01	0.04
132	11	20896231	3740874	13769	CTGCCAAGAGYATGTGATTGC	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20907437	10833412	13770	ACAGTGGTCTRTCATTCTGCC	0.57	0.55	0.55	0.07	0.02	0.00	0.01	0.55	0.08	0.02	0.01	0.01
132	11	20914856	11025818	13771	GTTGCCTGCCSTTTAGTAACA	0.28	0.00	0.00	0.23	0.04	0.00	0.01	0.00	0.24	0.04	0.00	0.00
132	11	20921975	4922684	13772	AGAAGGATTGWTTGATCATTT	0.90	0.82	0.87	0.45	0.07	0.05	0.03	0.82	0.45	0.06	0.05	0.03
132	11	20935188	952696	13773	TGGAGTTGACRTTTGCCCTGA	-	-	-	-	-	-	-	-	-	-	-	-
132	11	20943671	2063913	13774	GGCACTAAGCSTAATAATGTA	0.23	0.10	0.10	0.10	0.34	0.15	0.28	0.05	0.10	0.35	0.15	0.31
132	11	20952147	10833420	13775	AATAAGTTTAYTTGTTTAGGC	0.61	0.13	0.12	0.70	0.18	0.50	0.89	0.11	0.74	0.19	0.48	0.91
132	11	20961155	17232890	13776	ACAGTGGAAARAGACCTTCAG	0.43	0.27	0.40	0.41	0.94	0.53	0.65	0.32	0.43	0.93	0.55	0.67
132	11	20971636	10500885	13777	TTAATGAATAYAGTAAAATGT	0.05	0.00	0.00	0.94	1.34	0.99	1.68	0.00	1.02	1.31	0.98	1.62
132	11	20978517	17232911	13778	TAATCTTTTCRGAACCCAGAG	0.41	0.76	0.89	1.32	0.88	1.54	1.10	0.83	1.38	0.92	1.48	1.05
132	11	20985160	1557434	13779	AAGCAAATGTYGGCTGACCCT	0.12	0.27	0.23	0.73	2.52	0.98	0.48	0.19	0.74	2.42	1.03	0.51
132	11	20993444	16907287	13780	AGCAGAGATTYGTCCTCGCCG	-	-	-	-	-	-	-	-	-	-	-	-
132	11	21008028	7126181	13781	ATTTTGATGGYAGGCGCATTA	0.36	0.35	0.43	0.91	1.43	0.65	0.24	0.38	0.95	1.34	0.62	0.24
132	11	21017772	7937542	13782	CTTCAATATTRTTATTGCCAA	-	-	-	-	-	-	-	-	-	-	-	-
132	11	21026120	940197	13783	TACACCCTTAYGCTGATGGCA	0.13	0.21	0.22	0.23	0.13	0.27	0.10	0.19	0.24	0.14	0.27	0.10
132	11	21031907	10833447	13784	TGGCAAAATTRCTTTTCTTTG	0.40	0.72	0.80	0.19	0.24	0.06	0.29	0.73	0.19	0.23	0.05	0.28
132	11	21037853	1516757	13785	ATGGGGATGARTAAACAGGTT	0.05	0.17	0.17	0.24	0.24	0.63	0.21	0.14	0.22	0.26	0.61	0.25
132	11	21051197	7936706	13786	GCTGGCATTGYAGGTGTCTCG	0.01	0.04	0.04	0.18	0.59	0.52	0.67	0.01	0.18	0.60	0.54	0.69
132	11	21057283	12225793	13787	AAAGAATTGTKAGTGACTAGA	0.27	0.06	0.06	0.49	0.72	0.64	0.31	0.04	0.52	0.74	0.63	0.32
132	11	21064416	12280903	13788	TGATTTTCAARCATTGAACCT	0.06	0.10	0.10	0.48	0.32	0.14	0.16	0.08	0.48	0.33	0.15	0.15
132	11	21071644		13789	AGCCTCCTGTRGCCATACAGC	0.06	0.15	0.15	0.54	0.14	0.38	0.12	0.13	0.55	0.14	0.39	0.12
132	11	21081184	1400377	13790	TGAGTACATTYAGCTGATCAT	0.01	0.02	0.02	0.33	0.31	0.44	0.21	0.00	0.32	0.34	0.45	0.21
132	11	21088360	10500891	13791	TATGCAAGAGSTGAAATTAAT	0.07	0.13	0.13	0.16	0.18	0.18	0.12	0.10	0.16	0.18	0.20	0.11
133	11	27543012	1565228	13792	GAGTACCACTSCATAAAAGGA	0.05	0.25	0.33	0.08	0.30	0.29	1.08	0.27	0.03	0.31	0.27	1.04
133	11	27550722	4923455	13793	GTTCTAGATCRTACTTGGCAT	-	-	-	-	-	-	-	-	-	-	-	-
133	11	27557911	10835196	13794	TCTGAACCCASCACATGGAAA	0.12	0.14	0.14	0.31	0.50	1.74	1.80	0.13	0.30	0.51	1.61	1.73
133	11	27569267		13795	ATACTCCTAAYCCTCTAGAGC	-	-	-	-	-	-	-	-	-	-	-	-
133	11	27577508	11030067	13796	AGTGAGGTGGYGCTATAGTAG	-	-	-	-	-	-	-	-	-	-	-	-
133	11	27583978	7936850	13797	GGTTCTTTTTRGTAGATGGTA	0.06	0.17	0.17	0.45	1.79	2.57	2.06	0.16	0.43	1.71	2.42	1.95
133	11	27589985	7939810	13798	ACACCTAACAYGATAATTAGT	0.52	0.77	0.81	2.56	3.47	2.47	1.94	0.75	2.70	3.18	2.31	1.87
133	11	27592147	12276167	13799	AAGGAAGGCTKGAAGCCAAAG	0.09	0.17	0.17	2.96	3.58	2.61	2.80	0.17	3.55	3.15	2.47	2.65
133	11	27619402	7130131	13800	ACTAGAGAGAYAGAAATAATG	1.78	2.19	2.19	1.17	3.07	3.50	2.66	2.07	1.34	2.86	3.14	2.48
133	11	27629076	4923463	13801	ACATACACACRGAGATGGGAA	0.35	0.14	0.14	1.05	0.63	1.73	2.34	0.12	1.15	0.67	1.65	2.20
133	11	27641093	11030104	13802	ACACTACCACRTACTAACTGT	0.35	0.14	0.14	0.07	0.40	0.38	0.98	0.11	0.04	0.40	0.35	0.92
133	11	27652894	12291186	13803	TCAAATACCAMCATATTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
133	11	27659764	6484320	13804	AGTTTTAGTCWTGTAAACTTT	0.13	0.12	0.12	0.01	0.02	0.22	0.53	0.10	0.02	0.02	0.21	0.54
134	11	31269473	2774402	13805	CTTCTCCTGTSACTAGAAGGA	0.63	0.95	0.95	0.48	0.09	0.02	0.01	0.91	0.50	0.10	0.01	0.00
134	11	31282996	2616821	13806	TAGCACTAGAYACCAAACTCT	0.12	0.33	0.33	0.24	0.05	0.03	0.00	0.29	0.22	0.04	0.04	0.00
134	11	31292456	11031352	13807	AATCTATTTAYATATCTAACC	0.01	0.01	0.20	0.03	0.10	0.03	0.01	0.09	0.03	0.11	0.03	0.00
134	11	31304246	17247682	13808	TGGTTTATCAKAATCAAAGTT	0.13	0.33	0.33	0.41	0.06	0.02	0.04	0.31	0.41	0.06	0.03	0.05
134	11	31319227	768734	13809	TGGAGAGCTASTAGGGAGGAG	0.84	1.09	1.09	0.39	0.09	0.05	0.15	1.08	0.38	0.09	0.05	0.17
134	11	31330512	17248064	13810	TGTTTTTACTWAACAAGTTCA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31339093	4922859	13811	CAGTACCAAGRTTATTAAATT	0.98	1.37	1.31	0.48	0.23	0.16	0.10	1.22	0.49	0.24	0.16	0.09
134	11	31347809	569385	13812	CTTCACAGTTYGGGAACTTAC	0.02	0.04	0.02	1.00	0.31	0.13	0.47	0.00	1.22	0.31	0.14	0.47
134	11	31354718	483534	13813	TGAAGGCTTASTTACAGTTAA	0.01	0.06	0.06	0.30	0.59	0.39	0.40	0.04	0.25	0.61	0.41	0.39
134	11	31360548	553074	13814	AATTTATCATYATCAGTAGAA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31361935	17248764	13815	AACAGAATGTRTCTCCTCTGC	0.00	0.00	0.00	0.04	0.96	0.46	0.71	0.00	0.01	0.96	0.45	0.71
134	11	31376410	2167299	13816	TTGACTTTCTSTCATCATTAG	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31386805	4922864	13817	GAATGATCCTYTATTTTTGTA	0.05	0.09	0.08	1.16	0.44	0.72	0.98	0.07	1.31	0.43	0.70	0.99
134	11	31395593	12295105	13818	AAAACCTTTGRGAGTAATAAT	1.84	1.84	1.87	0.82	0.83	0.65	0.53	1.79	0.84	0.82	0.67	0.57
134	11	31404103	7125445	13819	ACTGCTTACARAATAGAAGTC	1.96	2.05	2.05	0.80	1.04	0.59	0.37	1.98	0.82	1.04	0.64	0.37
134	11	31411551	3741028	13820	AGCTCAGAAARTAAACCTTAC	0.15	0.36	0.36	1.11	0.41	0.56	0.43	0.32	1.20	0.44	0.58	0.46
134	11	31421871	17633448	13821	ATCTACATCAYTGCTGGGAAC	1.73	1.87	1.76	0.91	0.34	0.13	0.56	1.69	0.94	0.34	0.13	0.59
134	11	31427076	1223118	13822	CCTCCGCAGTSAACTTCACTT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31435946	1237428	13823	TTTACAATGAYGATCTCTTGA	1.92	1.80	1.80	0.67	0.33	0.19	0.10	1.71	0.74	0.37	0.23	0.11
134	11	31451886	1223086	13824	AAGTTGTCCAYCTGATTGTTC	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31457414	2728921	13825	TCATCATCACMATCTCTTTAA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31463483	1223098	13826	CTTTCAATAAKCCTACAACTG	0.70	1.02	0.97	0.72	0.40	0.25	0.09	0.94	0.89	0.41	0.26	0.09
134	11	31468134	1223100	13827	GGAAATCTAAYCTCACATCTA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31483216	17634367	13828	CACAGACACARCAGTGATATG	0.09	0.26	0.32	0.98	0.64	0.20	0.09	0.30	1.12	0.69	0.22	0.08
134	11	31503803	502794	13829	TACCTACTTGKAGAATTCACA	0.58	0.93	0.93	1.19	0.61	0.19	0.10	0.86	1.34	0.62	0.20	0.11
134	11	31504508	475012	13830	ATCTCTAACGWCAAGTAGGCT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31540206	2996466	13831	GCTGGGACCTYGATAAGAAAT	1.88	1.89	1.89	0.75	0.42	0.15	0.04	1.83	0.83	0.43	0.13	0.04
134	11	31545775	2996464	13832	ATATAAAGGCRTACCTTGGAG	0.10	0.29	0.29	0.77	0.19	0.06	0.03	0.26	0.81	0.19	0.06	0.03
134	11	31559076		13833	TTAAGTGTGTRCATGATGACA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31572109	4922867	13834	ATATATAACASAGCACACGTT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31580865	11031427	13835	TGTCACTTAGRTAAGTATCTA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31583608	11031429	13836	CCCAGGTTCARAGTAAATTCT	2.13	2.25	2.05	0.57	0.14	0.04	0.02	1.95	0.55	0.14	0.03	0.01
134	11	31593626	6484516	13837	TTATAAGAAAYGTATTTTTAT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31599167	12803634	13838	CTTGTGAATARACTTCACGGT	-	-	-	-	-	-	-	-	-	-	-	-

134	11	31611385	2760085	13839	ATACAGCATAKATAGCAAATA	-	-	-	-	-	-	-	-	-	-	-
134	11	31621471	12363388	13840	TACTTGAGGCKTTGCATAAAT	1.76	2.01	2.01	0.71	0.15	0.02	0.00	1.93	0.70	0.15	0.02	0.00
134	11	31636249	11031440	13841	ATGCCCTAAGYTGTACTGCTA	1.65	1.97	1.94	0.69	0.17	0.01	0.00	1.86	0.86	0.16	0.00	0.00
134	11	31646982	11031445	13842	GGTGAGATCAMCCATAGCTGT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31652912	2862801	13843	CACTCATAAARTTAAACTTAT	1.76	2.01	2.01	0.70	0.14	0.02	0.00	1.94	0.92	0.14	0.02	0.01
134	11	31659092	10488689	13844	ATTAGCTGACKTATCAAAAAA	0.23	0.33	0.33	0.64	0.21	0.08	0.06	0.28	0.67	0.21	0.08	0.05
134	11	31669386	16922404	13845	TAATGCTTATYTTATGCAAAC	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31681826	16922410	13846	TGATTTCTCTRTTGGTGATCT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31698931	6484533	13847	CACCAGGGCAYAAGCAGATTC	1.95	2.23	2.23	0.73	0.23	0.29	0.25	2.15	0.70	0.25	0.31	0.24
134	11	31705388	12295846	13848	AACTGCTAACKAAAAATGTGT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31725460	7104512	13849	TAATTAGCTTMAGAGAACTTA	2.04	2.13	2.05	1.00	0.84	0.48	0.31	1.98	1.02	0.86	0.50	0.30
134	11	31731972	7948834	13850	TGATTCAAAAYTGTCCATGAG	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31741027	17716512	13851	CTGATACAGAYTTTATACCTT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31749627	10835818	13852	CTACAAGATCKGACCACTGCG	2.06	2.07	2.07	1.05	0.60	0.45	0.26	1.99	1.17	0.64	0.48	0.24
134	11	31757311	7950812	13853	GCTAAGGGTCRAAGTATACTA	0.52	0.82	0.82	1.13	0.29	0.06	0.24	0.74	1.22	0.31	0.08	0.26
134	11	31764100	3026401	13854	CTATATGGTAYTCATTTCTTA	1.31	1.23	1.25	0.64	0.20	0.10	0.10	1.20	0.64	0.21	0.11	0.09
134	11	31765351	3026398	13855	CTGAGCAGCCRCTTCTTCAGA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31790118	2071164	13856	AAGAAAGGGCSGGGAGAGCGG	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31813064	16922496	13857	ACTTCTGAGCRTACGGAAATA	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31827334	584762	13858	TGGATGTTGTKGCTGCCAAAT	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31842155	686699	13859	ATAACCAGACRTAATTAAACT	0.33	0.52	0.51	0.25	0.44	0.21	0.20	0.46	0.28	0.45	0.24	0.22
134	11	31847879	677874	13860	TCTGACTGTTKGGTCTGAGAT	0.12	0.13	0.13	0.65	0.65	0.73	0.56	0.08	0.66	0.66	0.73	0.54
134	11	31854004	11031501	13861	AATCAGTCCTWTATGTGTGTC	-	-	-	-	-	-	-	-	-	-	-	-
134	11	31865301	11031520	13862	AATGCCCAAGKTTGCCCTTAA	0.74	0.68	0.64	0.88	0.77	0.79	0.39	0.57	0.97	0.79	0.78	0.38
134	11	31871692	10767906	13863	GCACTAAGCCYCCGGACTTCT	0.75	0.70	0.76	0.47	1.03	0.45	0.27	0.68	0.46	1.04	0.45	0.29
134	11	31879151	683028	13864	TTTGCTGCCARGACCCTTGTT	0.51	0.28	0.28	0.38	0.46	0.59	0.21	0.25	0.42	0.51	0.62	0.19
134	11	31893920	689408	13865	TCATGGGGTTKTTTGGAATCA	0.65	1.13	1.13	0.60	0.38	0.34	0.67	1.08	0.62	0.38	0.33	0.66
134	11	31899347	10742260	13866	TGGTTTTACTSTTCTCTCAGG	0.66	1.08	1.08	0.63	0.49	0.51	0.46	1.03	0.63	0.51	0.54	0.47
134	11	31904703	7943160	13867	ATTTCCCATASCAGGATCTTT	0.67	1.05	1.01	0.86	0.49	0.45	0.44	0.92	0.93	0.53	0.48	0.46
135	11	62431179	4963323	13868	CTCACAACCCSGTAAGCTGTG	0.65	1.03	0.95	0.32	0.39	0.72	0.42	0.86	0.26	0.43	0.75	0.43
135	11	62441993	2186410	13869	TCCCCAGTTTRCAAAAGGCCT	0.15	0.11	0.11	0.57	0.58	0.44	0.62	0.08	0.57	0.57	0.46	0.63
135	11	62508234	10897312	13870	GGTCCTGACARCTGAGAGCAT	0.04	0.16	0.07	0.58	0.71	0.45	0.38	0.03	0.59	0.69	0.44	0.37
135	11	62515375	10792367	13871	TTTTGGAGCTSTTTGGTTACA	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62527337		13872	AAGGTGAAGAWCCAAACATTC	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62545711		13873	TGAGCTGTGAKGTCTCCTCCC	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62557724	1108539	13874	AAGTGTTCCTMTGACAAAATA	0.38	0.37	0.37	0.30	0.60	0.67	0.33	0.31	0.29	0.61	0.69	0.35
135	11	62571447	17157693	13875	ATGGTGGACARTGAAGCCATC	0.11	0.28	0.28	1.15	0.72	0.48	1.05	0.26	1.28	0.71	0.47	1.06
135	11	62595358	1944045	13876	ATAAGAGATTYCTGGTGCCAA	2.41	2.81	2.81	1.86	0.92	1.24	0.65	2.70	2.09	0.88	1.25	0.65
135	11	62607112	12418061	13877	TTGAGTAAGARCCCAAGTGCT	2.28	0.63	0.63	1.48	2.56	1.11	1.56	0.55	1.75	2.30	1.13	1.52
135	11	62640313	7111093	13878	TCTTTGTGATYAGGGTTTCTT	2.06	2.00	2.01	2.25	1.89	2.29	1.86	1.93	2.55	1.77	2.11	1.75
135	11	62643185	10897367	13879	TTCAAGGTCAWTTCAAGACAT	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62671995	2156571	13880	TCCATTTACAKTTTAACTCAA	0.41	0.75	0.75	2.45	2.84	2.28	1.75	0.71	2.80	2.58	2.16	1.69
135	11	62690350	2226866	13881	ATCTGTGGAASCTAAATCCTA	0.79	0.50	0.48	1.74	3.67	2.11	1.23	0.41	1.82	3.19	1.93	1.24
135	11	62706153	10897384	13882	CAGGAATAAGWCCACACACAT	1.83	1.86	1.92	1.87	1.06	1.67	1.08	1.83	2.22	1.05	1.61	1.09
135	11	62707082	1525071	13883	GTACCATTTGYGGCATACTAT	0.54	0.49	0.49	1.28	1.21	0.31	0.99	0.46	1.55	1.18	0.31	0.96
135	11	62744343	6591778	13884	ATCATGCTCCRGGCACAAGCC	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62753160	2510590	13885	CTGGCATTCARTAGAGAAGCA	0.70	0.53	0.56	0.37	0.80	0.57	0.35	0.50	0.32	0.80	0.56	0.36
135	11	62761789	1944090	13886	AGTGCTGACARGATAGCCCTC	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62770983	1193856	13887	AAGTATGGGAWGATAGTTGAA	1.89	1.10	1.10	0.56	0.09	0.46	0.51	1.04	0.59	0.06	0.50	0.53
135	11	62792962	722508	13888	AAATCCAAAGRAGAGGAAATT	1.54	0.87	0.84	0.42	0.26	0.09	0.30	0.82	0.42	0.26	0.07	0.31
135	11	62822101	524724	13889	ATGTGTAATGYTTTTCACTTT	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62828886	1201559	13890	TTCCTCCTACYAGAAACCAAG	0.72	0.19	0.19	0.42	0.39	0.09	-0.06	0.17	0.40	0.40	0.11	0.06
135	11	62861593	17158145	13891	GGGAGTGGAAKGTGTAGTATG	0.54	0.34	0.25	0.14	0.36	0.14	0.08	0.22	0.11	0.39	0.14	0.07
135	11	62866725	1525065	13892	CAAACCATAGYATTTACCTAT	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62876596	4963260	13893	ATTTATGATGMGTAAAACTGA	0.71	0.34	0.30	0.01	0.02	0.34	0.12	0.28	0.01	0.01	0.33	0.10
135	11	62886887	12283500	13894	ACACCAAGAGRTTCACTTATT	0.55	0.31	0.30	0.07	0.12	0.12	0.15	0.28	0.05	0.13	0.13	0.13
135	11	62900257	494608	13895	TTCTTCCATTYATGATACATT	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62905679	11605137	13896	AGTTATTCCTYATGGAAGCAT	0.51	0.15	0.15	0.68	0.26	0.04	0.04	0.13	0.70	0.26	0.04	0.04
135	11	62932376	7109920	13897	AAAATAAATCRTAACAGTCAT	0.56	0.94	0.94	0.50	0.34	0.09	0.05	0.87	0.53	0.34	0.10	0.06
135	11	62937884	17174203	13898	TCTTATGTCTRTGAAAAAAGA	-	-	-	-	-	-	-	-	-	-	-	-
135	11	62940407	17158280	13899	AAACACCTTCYGAGGGATCAA	0.36	0.35	0.35	0.21	0.20	0.34	0.11	0.26	0.21	0.22	0.34	0.09
136	11	68497528	752296	13900	GCCTCAGGTCRTGACAACTGG	0.04	0.17	0.17	0.20	0.52	0.62	0.23	0.11	0.22	0.50	0.62	0.25
136	11	68502904	10896389	13901	ACCTTCTGACRTGAAAAACAG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68516337	2846201	13902	CTCCATTTACWGGAACGACGT	0.20	0.41	0.41	1.25	0.57	0.11	0.19	0.32	1.37	0.61	0.11	0.20
136	11	68521012	1249586	13903	AGAGCCAGCTSAAGTCTAATG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68555242	11826557	13904	TGGTGCAAAASTAAAAAACTG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68561027	11228450	13905	TTTTTGCTTTYTTCCACGTGA	0.19	0.32	0.32	0.48	0.33	0.43	0.05	0.29	0.48	0.35	0.45	0.05
136	11	68575673	4930644	13906	CCGGATGCAGYATCTCAGCCC	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68594604	3829236	13907	ACCGATACACYCTGCTGCCTC	1.34	1.30	1.30	0.52	0.39	0.12	0.08	1.28	0.56	0.41	0.12	0.09
136	11	68614666	3168115	13908	GTAATGCTTTWTTCTCAAATA	0.81	1.00	0.97	0.48	0.31	0.11	0.03	0.90	0.49	0.34	0.11	0.02
136	11	68626681	2924536	13909	CGTCGGTGGCYACAGCGGGAA	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68646355	3019757	13910	TGGAGAGGGTRCAGCACAGAC	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68656782	4310622	13911	CTTCAATGTCRTTACTTTCAA	0.32	0.43	0.43	0.26	0.09	0.22	0.25	0.39	0.24	0.10	0.22	0.27
136	11	68666155	17149775	13912	GTTTACTTCTRATTTTGACTT	0.32	0.30	0.23	0.13	0.06	0.11	0.13	0.20	0.13	0.05	0.13	0.11
136	11	68676006	17309046	13913	GTCGGCTTTAYCTCTTGCAAA	0.10	0.10	0.00	0.07	0.02	0.67	0.28	0.00	0.02	0.02	0.69	0.28
136	11	68689617	17149785	13914	TGTGTCTCATYCAGAGATATC	0.12	0.11	0.11	0.02	1.31	0.72	0.27	0.06	0.00	1.29	0.73	0.31
136	11	68703434	12417953	13915	GCCTTTGCCGRTAAGAGTCCT	0.26	0.06	0.06	1.49	1.41	0.80	1.32	0.03	1.67	1.39	0.80	1.27
136	11	68738060	4268514	13916	ACTCGTCTGTSAGCCCAGAGA	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68750408	6591374	13917	AAGGCTTTCTRTTTTTTATTT	0.49	0.84	0.75	1.12	0.78	2.21	1.88	0.70	1.15	0.79	2.12	1.79
136	11	68763950	7104671	13918	TTCATGTGCTSCTATAGGAGG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68772447	7119988	13919	CCCAAGGTAARTCCTGGACGG	0.21	0.42	0.42	0.35	1.35	2.47	1.99	0.36	0.37	1.31	2.37	1.88
136	11	68796403	4930273	13920	TGCCATCTTCYCACCCCACTC	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68809258	4930673	13921	GAAATCGAGCYGCCACGGGGC	0.55	0.79	0.79	2.05	1.85	0.95	1.86	0.73	2.20	1.72	0.92	1.85
136	11	68825321	4619154	13922	TGCTGGGGCTYGCTCGGCTTC	2.81	3.28	3.32	2.54	1.91	1.52	0.66	3.24	2.62	1.75	1.48	0.66
136	11	68841126	7481709	13923	ACCCACCCCCYACACTCCTCT	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68857753	6606672	13924	TGGCAGGTCTRTGTGGGCACT	0.34	0.63	0.63	1.93	2.44	1.05	1.18	0.55	2.18	2.24	1.03	1.17
136	11	68870174	4584599	13925	CTAGTTGTTTKCTATGCACAT	0.15	0.08	0.12	1.62	1.40	1.14	1.08	0.08	1.80	1.35	1.14	1.04
136	11	68886319	7938650	13926	GGCCATGGTCRTGAAAAGGGT	0.83	0.36	0.34	0.18	1.27	0.93	0.72	0.32	0.16	1.23	0.96	0.70
136	11	68909864		13927	CGTGTAATCCSAGCAATTGTG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	68920400	3934535	13928	TTTAAACAGAYGCCCTCAGGT	0.43	0.72	0.74	0.25	0.09	0.78	0.73	0.73	0.24	0.10	0.80	0.75
136	11	68939602	7102236	13929	CCACAGAGCGYCAATGGGAGC	0.19	0.14	0.18	0.14	0.24	0.25	0.88	0.16	0.11	0.27	0.25	0.89
136	11	68943150	10160297	13930	AGACTCATTTYGGAGCCACTC	0.33	0.19	0.21	0.15	0.50	0.32	0.92	0.17	0.10	0.54	0.36	0.91
136	11	68962436	11263443	13931	TGTTTCCGCGYGGACGTGGAA	1.39	0.43	0.47	0.32	0.06	1.13	1.56	0.43	0.28	0.05	1.12	1.56
136	11	68978264	7396950	13932	ATATGCAAATMATGCTGCCAT	1.02	1.25	1.23	0.43	0.64	0.25	1.52	1.18	0.45	0.64	0.25	1.46

136	11	68985564	10796819	13933	TGGAACAATGKATTTGCAGCA	0.25	0.55	0.55	0.72	0.86	0.30	0.88	0.48	0.78	0.88	0.30	0.90
136	11	69003412	17136590	13934	GCAATCAACAKGTATTATTCT	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69015576	654829	13935	ATGCTAGCCCWGTGTTCTGTA	0.06	0.21	0.21	0.23	0.57	1.72	1.19	0.20	0.23	0.57	1.66	1.18
136	11	69028654	679146	13936	GAAAATAGTGMATGTCTAAAC	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69034292	567577	13937	GAGAGATTCCRGTTTTCAACT	0.66	0.28	0.24	0.75	1.16	1.74	1.82	0.20	0.73	1.12	1.65	1.73
136	11	69041441	559664	13938	ATGAATACTCRCTGAATTTTA	0.57	0.71	0.76	2.14	2.33	1.30	0.97	0.76	2.14	2.20	1.28	0.95
136	11	69048798	498931	13939	GAACCAAGTCRTGGCTTGCAA	1.18	1.17	1.15	0.69	1.59	1.59	0.86	1.08	0.68	1.51	1.52	0.89
136	11	69056078	1893721	13940	CTCATCCCACKCAGATAAAGA	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69060944	10908187	13941	GCTCTTCTTTWTACCCTTGAG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69069993	600523	13942	GCCATCCTCTRGAAGACAGGC	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69082765	9651783	13943	CACATCTGTCKGTTATCTGTC	1.04	1.46	1.46	0.89	0.39	0.76	1.13	1.36	1.01	0.42	0.75	1.10
136	11	69087917	12422135	13944	TATGGCAAAARTAGAAATAAG	1.47	1.70	1.70	0.70	0.45	0.29	0.82	1.60	0.74	0.51	0.30	0.83
136	11	69103572	7108090	13945	TTGGATCATGRCTTCATAACT	0.16	0.40	0.40	0.77	0.56	0.76	1.02	0.33	0.80	0.59	0.78	0.99
136	11	69109226	17318736	13946	CTTTGGCAGAYCTTACCTAGT	0.23	0.14	0.14	0.22	1.21	1.27	1.17	0.11	0.20	1.20	1.22	1.12
136	11	69115293	518418	13947	AGCCAACTATYTATAAATGTC	0.10	0.12	0.11	0.42	0.37	0.76	1.51	0.08	0.42	0.44	0.77	1.47
136	11	69122269	10737155	13948	ACATGGGTTCYGGGTCCCCAT	0.27	0.44	0.38	0.58	1.00	1.51	1.04	0.34	0.63	1.01	1.44	1.03
136	11	69129728	17136776	13949	GTGTTATTACYCATTCAGTGA	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69135877	7950525	13950	AGACCAAAGCRCCTATCACGA	0.14	0.38	0.38	0.31	2.45	1.21	1.19	0.36	0.30	2.27	1.20	1.19
136	11	69144411	3017614	13951	TCCAAATACARGCAGAGACTC	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69158965	2450254	13952	GCTTCTTTTTWAAATCAACAT	0.43	0.28	0.28	1.08	0.70	1.59	0.97	0.25	1.10	0.68	1.51	0.94
136	11	69174165	3212886	13953	GAAGCCCTAGYGTGGCTTCCT	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69199527	10796828	13954	ATTTTACCACKGCAGATAGAA	1.42	1.79	1.79	0.89	0.63	0.75	1.26	1.73	0.95	0.65	0.76	1.25
136	11	69211296	1192921	13955	GGTGCCTGCASTTCACTTACG	1.24	1.80	1.71	0.59	0.48	0.87	0.60	1.67	0.61	0.48	0.85	0.58
136	11	69221270	948995	13956	CAAATGCTCAYTTGGAATCAT	0.40	0.38	0.26	0.88	0.47	0.19	0.20	0.20	0.93	0.48	0.21	0.20
136	11	69234617	6606653	13957	TTGGGGTGGARATTGACCCTA	0.88	1.37	1.22	0.43	0.32	0.19	0.45	1.14	0.44	0.33	0.20	0.48
136	11	69246102	10908200	13958	GCTTCGCACTRCACAACTACA	0.96	1.46	1.35	0.52	0.25	0.54	0.49	1.28	0.54	0.27	0.55	0.47
136	11	69255910	4980685	13959	GTGACATGACMAGTGAGCCTG	-	-	-	-	-	-	-	-	-	-	-	-
136	11	69272914	7479018	13960	GGCCAGGCCTYGATCCTTCCT	0.27	0.48	0.48	0.67	0.91	0.41	0.43	0.43	0.68	0.93	0.44	0.44
137	11	92282045	10501799	13961	TCGAGCTTCAYTGTGGCCCCT	0.61	0.61	0.61	0.32	0.04	0.02	0.13	0.57	0.32	0.04	0.02	0.12
137	11	92288410	11020100	13962	TCGTGGCAGGYGGCTGGGCGG	0.24	0.52	0.55	0.26	0.04	0.21	0.12	0.53	0.25	0.02	0.22	0.13
137	11	92294628	1816939	13963	ATCTCCTGTTYATTTTGTGTG	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92301591	1158885	13964	AATATCTGTARTAAAACCAAT	0.42	0.40	0.40	0.15	0.92	0.43	0.27	0.37	0.14	0.89	0.44	0.25
137	11	92316121	1447348	13965	TGCTGCCTAASACTGTCATCA	0.30	0.15	0.12	0.08	0.37	0.56	0.47	0.09	0.09	0.37	0.60	0.47
137	11	92323970	7933855	13966	AGACTTGTCTRTGCCTTTGAC	0.59	0.28	0.30	0.44	0.19	0.46	0.57	0.26	0.44	0.21	0.51	0.60
137	11	92341244	4753426	13967	TAATCCATGCYGTTGTGTAGG	0.36	0.22	0.22	0.19	0.89	0.35	0.60	0.21	0.16	0.89	0.35	0.59
137	11	92346592	10765576	13968	CTGAGAGCAGRCACTTTCATT	0.37	0.02	0.04	0.15	0.33	0.90	0.19	0.01	0.16	0.36	0.89	0.20
137	11	92355564	12792653	13969	CTTGGTAACTRCAAGGGCCTC	0.47	0.14	0.17	0.08	0.24	0.24	0.25	0.14	0.06	0.26	0.27	0.25
137	11	92362409	1447352	13970	ACTGAGGGAARAGTAATAGAA	0.44	0.24	0.24	0.42	0.20	0.32	1.33	0.20	0.41	0.21	0.31	1.29
137	11	92380129	16918371	13971	GTTTGACCAARTTGCAATCAC	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92381970	1396374	13972	GGAGAGGGGTRTAAGCGGAAG	0.06	0.24	0.24	0.13	0.35	0.74	1.48	0.17	0.10	0.35	0.73	1.44
137	11	92406543	1348917	13973	CTTTTATTAAMCTTTCCAGAG	0.26	0.08	0.08	0.75	0.80	2.00	1.53	0.07	0.84	0.81	1.89	1.44
137	11	92415528	17547839	13974	TCAGCAACTGMCTTCAGGGTA	0.31	0.54	0.54	0.14	2.47	1.40	2.14	0.52	0.15	2.22	1.35	2.01
137	11	92423851	7931462	13975	TGAAGTGTCCRCCGTTTATAT	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92432802	16918463	13976	AGCAAGGGATRAAGAAAAAGG	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92440577	10765583	13977	TTTTACTTTCYAAAGCCTTAA	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92446435	471749	13978	CCTGCTTTTTYAGATTAGTCA	0.51	0.67	0.72	0.67	1.23	2.19	3.09	0.67	0.71	1.15	2.05	2.95
137	11	92453719	513407	13979	TTTGGTAACAYTGGCATTGCT	0.96	0.50	0.58	2.47	2.68	3.02	2.69	0.54	2.62	2.48	2.80	2.51
137	11	92460046	621724	13980	CAACCTTGCAMACTTCTCCAG	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92473846	614332	13981	ACTGATTGCAYATTTGGGTGA	0.20	0.33	0.33	3.45	4.85	3.72	2.80	0.31	3.51	4.20	3.36	2.64
137	11	92492545	10501802	13982	ACGTAGATATRTGTAGAGCTG	1.40	1.89	1.89	1.85	4.88	5.27	4.20	1.82	2.00	4.37	4.61	3.84
137	11	92504655	12576495	13983	CTAGGACATGYAACACTGCCA	0.39	0.24	0.24	2.13	3.19	5.36	5.49	0.23	2.34	2.86	4.87	4.96
137	11	92527289	10765587	13984	AATTCATTTTSACAAGACTGG	0.19	0.43	0.42	0.96	2.14	3.41	3.66	0.43	1.14	1.95	3.09	3.41
137	11	92533473	1508608	13985	CAAACCTTTCRATGTGAATGT	0.19	0.45	0.45	0.71	1.45	2.05	2.64	0.42	0.81	1.41	1.95	2.45
137	11	92543215	10830997	13986	TAGTACCCTAYATTTGTATCT	1.89	1.66	1.70	0.66	0.45	0.93	2.19	1.63	0.63	0.46	0.89	2.04
137	11	92554665	17631593	13987	ATAAAACCACYTCTTGAAATA	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92561089	1348871	13988	ATTTTAGCAGSCTCCATTAGC	0.17	0.41	0.45	0.86	0.33	0.42	0.75	0.41	0.91	0.36	0.45	0.78
137	11	92570294	2166583	13989	CGCAGGCTCTYGCGTCTTTGA	1.29	1.40	1.39	0.55	0.72	0.44	0.62	1.32	0.59	0.72	0.47	0.62
137	11	92575989	11020198	13990	TATTGACCCAYAAGAAATTGG	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92589095	4753439	13991	GGGTTCACACYCTCTCTTTTA	0.57	0.84	0.92	0.49	0.36	1.01	0.91	0.87	0.45	0.40	1.02	0.92
137	11	92596521	16918677	13992	AGATCATGTAYTTTATTGACA	1.65	0.83	0.87	0.23	0.59	1.18	0.64	0.77	0.20	0.63	1.14	0.64
137	11	92605911	11020212	13993	GTTTAATGACRTTGGACATTA	0.39	0.12	0.12	0.24	0.38	0.37	0.87	0.09	0.23	0.38	0.39	0.83
137	11	92614851	7110186	13994	GATTATAAGTKTCTTGAAGTC	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92625086	1446907	13995	AAGTCTTAAAYTTCACTTTTT	1.31	0.31	0.30	0.43	0.11	0.32	0.75	0.28	0.44	0.10	0.35	0.72
137	11	92631436	10831012	13996	AGGCACACACRGATCTCCTGA	1.08	0.17	0.17	0.70	0.56	0.26	0.70	0.16	0.82	0.57	0.30	0.68
137	11	92642358	7933645	13997	AATTCTATACRATCACAGCAC	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92648949	935450	13998	ACCAATCTCCYAGGACTGTTG	0.80	0.08	0.06	0.60	0.73	1.07	0.30	0.03	0.62	0.72	1.06	0.33
137	11	92664505	11825153	13999	AGGGCAGTTTYCTGAACTTAA	1.18	1.73	1.63	0.70	0.61	0.21	0.47	1.53	0.76	0.61	0.22	0.48
137	11	92671503	6483232	14000	TTTTTTAAATYCTAAATGGCT	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92699547	3020065	14001	CGAAACTCTARAAGTCCATAA	0.73	0.48	0.48	1.51	0.35	0.24	0.18	0.44	1.64	0.38	0.26	0.19
137	11	92708597	10831027	14002	TTAGGTCATAYCAAGTTTTTC	1.01	1.38	1.44	0.63	0.55	0.21	0.23	1.41	0.69	0.56	0.18	0.27
137	11	92716808	12416927	14003	CAAACACTAAYGATGACAGTA	-	-	-	-	-	-	-	-	-	-	-	-
137	11	92736858	975916	14004	TTAAGCTTTASTGCACTTTCT	0.13	0.36	0.33	0.54	0.30	0.26	0.27	0.30	0.58	0.30	0.27	0.25
138	11	95842433	7114658	14005	CCTTGGGAATKATTTCGCTTG	1.06	0.60	0.62	0.18	0.18	0.19	0.01	0.57	0.14	0.18	0.19	0.01
138	11	95854566	16923596	14006	CTCCTTGAGCRCTCCCTGATT	0.14	0.37	0.33	0.27	0.24	0.09	0.05	0.30	0.26	0.23	0.08	0.04
138	11	95868655	618929	14007	GTTTCTCAGARTGTGTCTCCA	-	-	-	-	-	-	-	-	-	-	-	-
138	11	95882778	564259	14008	AAAACCCTGCRGGGAAAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
138	11	95899268	10831534	14009	CCTGTACTTGYGAAACACTTG	-	-	-	-	-	-	-	-	-	-	-	-
138	11	95908847	1451329	14010	AATATACAGGSAATTATAGTA	-	-	-	-	-	-	-	-	-	-	-	-
138	11	95972342	4594032	14011	TAATGGTAATKGCTACTTGTC	2.23	0.06	0.06	0.38	0.14	0.11	0.13	0.04	0.41	0.12	0.13	0.13
138	11	95978625	10789966	14012	AAAAACACACRTGGGGGGCAC	-	-	-	-	-	-	-	-	-	-	-	-
138	11	95984270	3018648	14013	AGTAGGGTAGRCATGCTTTTG	0.78	0.39	0.39	0.12	0.12	0.14	0.05	0.35	0.08	0.13	0.14	0.04
138	11	95997753	17570993	14014	AAAATTAGAAYGTTACCAACA	-	-	-	-	-	-	-	-	-	-	-	-
138	11	96010408	7937263	14015	AGATTGAGATMAAGTGTTGCA	1.41	0.28	0.28	0.28	0.06	0.05	0.07	0.25	0.24	0.05	0.04	0.07
138	11	96021815	6590978	14016	ACTTCATCATRATACGGGAGT	0.03	0.11	0.10	0.26	0.06	0.11	0.03	0.06	0.25	0.04	0.12	0.02
138	11	96027660	7112811	14017	AATCACCCTCWTGATAAAGCA	0.88	0.48	0.50	0.22	0.27	0.10	0.25	0.45	0.22	0.29	0.10	0.29
138	11	96035910	754413	14018	GAATGACTATRGATCACTTAA	0.25	0.00	0.00	0.53	0.28	0.34	0.58	0.00	0.53	0.29	0.37	0.58
138	11	96043266	1439533	14019	GAAAAAGGAARGGAATCACAA	0.40	0.77	0.83	0.16	0.36	0.64	0.99	0.78	0.13	0.36	0.63	1.01
138	11	96056987	17129493	14020	TGTGACTACCRCCCTTAAAAC	0.40	0.77	0.77	0.83	0.79	0.78	0.52	0.67	0.90	0.80	0.82	0.52
138	11	96070313	7936111	14021	TCTCTAAACARCAAAGGTTTT	0.82	1.22	1.22	2.01	2.02	0.76	0.39	1.13	2.08	1.82	0.80	0.40
138	11	96077082	10890823	14022	TCAGCATACCYTTTTGCACTG	1.30	1.84	1.84	1.96	2.16	1.37	0.45	1.76	2.29	1.94	1.37	0.46
138	11	96083685	10890896	14023	CAAACTCTACSATAGTCAAAT	1.49	1.99	2.05	1.60	2.50	1.73	1.15	1.92	1.81	2.25	1.63	1.12
138	11	96093408	3018626	14024	GTATTAGGCTKTTGTGTGGAC	0.04	0.17	0.17	2.33	2.61	2.04	0.77	0.14	2.49	2.30	1.90	0.75
138	11	96108514	3019711	14025	ACCTTTGAAGKCCTTAGTGTG	0.24	0.18	0.20	1.14	1.94	1.13	0.87	0.18	1.22	1.80	1.10	0.84
138	11	96120495	17129576	14026	AAGATATTGTKCCATCTTTCC	-	-	-	-	-	-	-	-	-	-	-	-

138	11	96140274	11215007	14027	AATGTTTTCTYTCTTGTACTT	0.20	0.09	0.10	0.36	0.30	1.09	1.13	0.08	0.33	0.31	1.07	1.11
138	11	96142229	17129598	14028	TGAACTCTATSACTACACATA	-	-	-	-	-	-	-	-	-	-	-	-
138	11	96162329	10892015	14029	AAGTCTAGAAYTTAGTGAATT	0.12	0.08	0.08	0.30	0.11	0.51	0.83	0.05	0.31	0.11	0.55	0.86
138	11	96170227	10501862	14030	TCCTACAATAYTATCTTTCCC	0.06	0.04	0.04	0.02	0.04	0.07	0.45	0.02	0.01	0.04	0.06	0.44
138	11	96178231	12273087	14031	TTGTTTTTTAWACCTTCATTC	-	-	-	-	-	-	-	-	-	-	-	-
138	11	96184726		14032	TTGAATTGACWTTTTATTTAA	-	-	-	-	-	-	-	-	-	-	-	-
138	11	96193031	10790341	14033	TTTATTGATARCAGTGGTAGA	0.00	0.04	0.04	0.05	0.00	0.12	0.05	0.02	0.05	0.00	0.11	0.04
138	11	96198799	11217820	14034	ATTTTACTGTRATTGTGCACC	-	-	-	-	-	-	-	-	-	-	-	-
138	11	96207118	7119666	14035	TGAGCAGTCCRTGGTGAAACT	-	-	-	-	-	-	-	-	-	-	-	-
138	11	96214719	1452975	14036	AATGGACAAARCACAGGAATG	0.24	0.25	0.28	0.03	0.07	0.01	0.02	0.25	0.02	0.08	0.00	0.02
138	11	96230931	7120017	14037	AACATTGTCAYTTTGTTGGAA	0.12	0.19	0.19	0.14	0.04	0.01	0.00	0.17	0.12	0.03	0.01	0.00
138	11	96232767	1023849	14038	GGACCAGAAASAAGGCAGGGT	0.14	0.20	0.20	0.04	0.02	0.02	0.01	0.17	0.01	0.01	0.02	0.01
138	11	96257673	17129669	14039	CCTTTTAAGARCATTACACAG	0.14	0.36	0.36	0.24	0.04	0.01	0.14	0.32	0.20	0.02	0.01	0.13
138	11	96264630	17129681	14040	AAAGACATTTRCATTTGAAAT	0.06	0.18	0.19	0.45	0.04	0.23	0.35	0.17	0.47	0.02	0.25	0.36
138	11	96271128	17129694	14041	CCAATTCAAGSAGAAAATGTC	0.12	0.32	0.32	0.31	0.09	0.12	0.35	0.26	0.25	0.07	0.14	0.34
139	11	103578975	10895602	14042	CCATAGATCCRTGAAGGAAGA	0.35	0.65	0.65	1.35	1.32	0.64	0.27	0.60	1.61	1.24	0.65	0.29
139	11	103602301	11821446	14043	GATGTTTTCAYATTGAATTGC	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103605971	17102167	14044	GCATTCTGCARGTAGAGAGCA	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103617465	17102168	14045	GGCCCAAACARCTTCAACTAT	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103625932	17102203	14046	AATTTTTTAARTTGGCATTAT	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103632175	17102228	14047	GAGTTTTGGCRGCATTGCAGA	0.38	0.62	0.55	0.44	1.13	0.67	0.37	0.53	0.45	1.14	0.70	0.42
139	11	103667432	2130052	14048	GAGACATGAARGCTAACTAAT	0.46	0.72	0.72	1.38	1.13	0.57	0.92	0.67	1.72	1.12	0.61	0.89
139	11	103673925	10895635	14049	CTTCAGCCTCYATTCACATTT	0.72	1.11	1.11	1.36	1.29	1.25	1.42	1.05	1.59	1.31	1.18	1.34
139	11	103681012	4755020	14050	TAATAAAATAYGACCATGGAG	0.76	1.16	1.16	0.48	1.51	1.99	1.46	1.10	0.55	1.43	1.85	1.43
139	11	103688724	1906686	14051	GTTGCAAATTYAAAAGCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103694083	901949	14052	GGTAATGCGCRTTGCGACTTC	0.21	0.07	0.10	1.19	0.64	1.67	1.90	0.06	1.22	0.63	1.60	1.81
139	11	103699711	1488964	14053	CTATATTTCCYGCTTTCTCTC	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103707352	17344311	14054	TTACGATTTCRCATGTTTACA	1.81	2.48	2.49	1.31	0.97	1.04	1.67	2.44	1.37	0.95	1.07	1.58
139	11	103713704	11226307	14055	GTTCTGAGTASAAACATAGCT	2.25	2.89	2.89	1.78	1.31	1.11	0.88	2.79	2.07	1.31	1.13	0.88
139	11	103719675	7128172	14056	GTGTTGTTTAKTTGGACCCAT	1.30	1.88	1.88	1.80	1.38	1.25	1.03	1.83	2.03	1.32	1.21	1.00
139	11	103725167	10895658	14057	GAGGAAGTTAYGTGAAGGCAC	-	-	-	-	-	-	-	-	-	-	-	-
139	11	103745535	7110700	14058	ACAAGGCTGARCACTACACAT	0.60	1.01	1.05	1.09	2.19	1.38	1.45	0.96	1.19	1.98	1.31	1.39
139	11	103754464	12366084	14059	TAGACTGACTRTAAGCACAGA	0.31	0.55	0.54	0.91	1.26	2.47	1.14	0.51	1.06	1.18	2.22	1.11
139	11	103768020	12362748	14060	CAGCATATGGRTGAAAGGTGG	0.30	0.54	0.54	0.69	1.45	0.63	1.85	0.49	0.74	1.38	0.65	1.74
139	11	103800432	4754114	14061	TTAATTTTCARGAAAGCTAAA	0.32	0.57	0.64	0.81	0.90	1.55	0.69	0.60	0.97	0.90	1.45	0.67
139	11	103809638	17102463	14062	ATGAAATGTARCCGTCTACTG	0.40	0.64	0.64	0.75	1.30	1.06	1.50	0.62	0.92	1.22	1.06	1.41
139	11	103814624	10502034	14063	GCCCATTTTTRCAAAGTCCTG	1.44	1.51	1.41	0.91	1.06	1.25	0.83	1.38	0.97	1.04	1.22	0.85
139	11	103828805	1487712	14064	TAGCTCCACTRTATCCTTCTT	0.48	0.38	0.38	0.91	0.96	0.83	0.45	0.32	1.06	0.96	0.84	0.46
139	11	103836729	7946305	14065	ATGTTACTGCSTGTGGTGATC	0.49	0.51	0.51	0.96	0.78	0.31	0.65	0.48	1.18	0.75	0.32	0.63
139	11	103844029	2200615	14066	GCCCATAAACYTGGTCTTTGA	1.23	1.78	1.78	1.14	0.56	0.69	0.48	1.71	1.39	0.59	0.66	0.46
140	11	122348745	6589962	14067	TTATAGTGGARAAATGTAGAA	0.18	0.06	0.06	0.45	0.34	1.00	1.08	0.04	0.48	0.36	0.95	1.10
140	11	122356365	11218912	14068	ATGCGGACCTRGATTTACAAA	0.02	0.04	0.04	0.05	0.31	1.75	2.02	0.02	0.03	0.33	1.71	1.96
140	11	122378019	2045709	14069	TTGGCATTAGYCACTGTTTTT	0.24	0.39	0.39	0.42	1.45	1.81	1.97	0.33	0.45	1.43	1.77	1.86
140	11	122394689	17126992	14070	CTGAAGTCATYGGCCCAGTAC	0.51	0.50	0.50	1.19	1.27	1.80	1.69	0.32	1.23	1.22	1.75	1.63
140	11	122427286	17127018	14071	CCATACTATAWCCATATCCAT	-	-	-	-	-	-	-	-	-	-	-	-
140	11	122434085	4936770	14072	TGTGACCCTAYACTGAAATCC	0.74	1.11	1.11	0.43	1.13	1.66	3.36	1.02	0.44	1.14	1.59	3.11
140	11	122468110	7113273	14073	TGGGGCATACYGCTACCATAG	0.34	0.66	0.66	0.66	0.33	1.40	0.96	0.63	0.65	0.33	1.35	0.93
140	11	122476668	11218981	14074	TCCATCCATTRTGCCTGGGCT	0.33	0.00	0.00	0.39	0.30	0.14	0.23	0.00	0.41	0.32	0.14	0.21
141	12	16083756	4764242	14075	TGATTTTTTTWAAAGGTTGAA	0.39	0.73	0.77	0.13	0.47	0.35	0.11	0.77	0.12	0.47	0.34	0.10
141	12	16105879	10772892	14076	CCACTGGTTAKAAATTTCCCA	0.25	0.54	0.49	0.84	0.52	0.51	0.39	0.46	0.94	0.52	0.50	0.42
141	12	16117419	10505790	14077	GAAGTTTAGAWATGAAGGAGA	0.42	0.71	0.71	0.76	0.39	0.66	1.21	0.68	0.83	0.36	0.66	1.21
141	12	16124385	4763439	14078	TATAGTAATTYAGAAGCCATA	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16130385	7312983	14079	TTTAAAATCTKTACTTTGATC	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16134882	2598344	14080	ACTATATCTCRTGTGTTTCTT	0.34	0.10	0.10	0.44	0.81	1.18	0.77	0.09	0.43	0.80	1.21	0.79
141	12	16141980	2604259	14081	GCTATGGCCARCTGAGTCAAA	0.11	0.27	0.27	0.67	1.35	1.10	2.22	0.23	0.72	1.29	1.05	2.10
141	12	16164882	1671463	14082	GACCATTTTCYGTGTCCACAA	0.09	0.12	0.12	0.20	0.53	2.50	1.97	0.10	0.18	0.53	2.37	1.89
141	12	16171438	1799467	14083	TGATGAAGCTRCTCACCAACT	0.24	0.17	0.23	0.27	1.39	1.50	2.39	0.19	0.26	1.33	1.41	2.24
141	12	16176805	17352791	14084	ACCTTATACAYCAGGGCAATA	0.00	0.02	0.02	0.73	0.96	1.02	1.88	0.00	0.77	0.93	1.02	1.82
141	12	16186328	1799461	14085	CAGGTCAACTRCAGATTGTGG	0.52	0.79	0.79	1.21	1.48	0.73	0.80	0.71	1.20	1.44	0.73	0.78
141	12	16195480	961549	14086	GAGAAAGAATYCCCGAATCAA	0.23	0.16	0.16	1.62	0.59	1.05	1.59	0.11	1.66	0.62	1.04	1.60
141	12	16209096	12580015	14087	TCTGCTTGTCSTTTACCCGAC	0.30	0.49	0.44	0.25	1.45	1.39	1.03	0.39	0.23	1.45	1.35	1.00
141	12	16219962	17353923	14088	AGGCATAAAGYTGCAAGATGG	1.71	0.60	0.58	0.27	1.61	1.83	1.25	0.53	0.25	1.58	1.78	1.25
141	12	16226637	10505794	14089	CTCTACTTGCRGGAAAATTAG	0.32	0.65	0.74	1.64	1.16	1.75	2.60	0.69	1.68	1.11	1.71	2.45
141	12	16233095	17432911	14090	TTTCTGAATGYATCTGAATTG	0.97	1.47	1.47	1.24	1.15	2.28	2.80	1.41	1.26	1.10	2.13	2.66
141	12	16248681	10846308	14091	TGTGAAATTCMTCTAGAAGTA	1.75	2.02	2.02	1.02	1.54	2.77	1.86	1.94	1.09	1.49	2.54	1.75
141	12	16254589	3864922	14092	AATTGAACAGKACAACTGAAC	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16260504	11056826	14093	TTTACCAACAYGTGCAACCAA	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16273658	1527013	14094	TAAATTAGATMCCATAACATC	1.79	1.83	1.83	1.05	2.58	1.16	3.12	1.78	1.06	2.27	1.14	2.81
141	12	16283812	11056836	14095	ATAGCTAGTTYGGATCTTAGC	1.20	1.48	1.38	2.57	1.95	3.44	2.46	1.28	2.88	1.80	3.03	2.24
141	12	16292972	17434056	14096	AAAAGTCCATWATCATTACAG	1.22	1.78	1.77	2.16	3.84	3.49	2.27	1.74	2.65	3.32	3.16	2.09
141	12	16310672	3915237	14097	GTACTGAATAKGTATGTCTAG	0.90	1.28	1.28	1.43	3.19	2.34	3.01	1.22	1.52	2.81	2.21	2.76
141	12	16318581	1799507	14098	CTCCATGTTCRTTTTGCTCTT	0.10	0.30	0.31	1.49	1.64	2.07	2.69	0.26	1.51	1.57	1.94	2.53
141	12	16325555	4763443	14099	CTAGTTCTCAMTACAAAGTTC	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16332922	7304992	14100	AAAGCAAGGTRTAAAGAGCTA	0.16	0.21	0.21	1.34	1.67	1.49	3.14	0.21	1.44	1.61	1.43	2.94
141	12	16338780		14101	CCATTTAACAMCCAGAGAGCA	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16352770	7979961	14102	TTAAACTTGCYTTACTAAAGC	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16372216	12831514	14103	ATGTCAAGAAMCCAGATGTAG	0.86	0.92	0.92	1.44	2.24	3.28	2.13	0.90	1.54	1.99	2.94	1.99
141	12	16383782	6488840	14104	GTTCAAAAGAMTGAAAGCAGT	0.51	0.81	0.81	0.86	2.91	2.93	2.71	0.76	1.04	2.62	2.62	2.49
141	12	16391118	7970208	14105	AACATTTCTCRTATAAACCCA	0.68	0.71	0.71	0.27	0.78	1.93	2.16	0.68	0.25	0.82	1.85	2.07
141	12	16405457	2287152	14106	GTAGTTGTTCWCAGCCTGACA	1.06	0.61	0.58	0.78	0.39	2.74	2.71	0.55	0.74	0.41	2.60	2.53
141	12	16415437	7313177	14107	TTGACTCTATRAATTAGTTAG	1.04	0.98	0.98	1.33	1.50	1.78	3.98	0.96	1.35	1.46	1.74	3.67
141	12	16430035	1981752	14108	CTGCTTTTAAYACATACAGTT	0.50	0.82	0.82	0.78	1.46	1.76	3.52	0.76	0.79	1.39	1.75	3.28
141	12	16437965	991184	14109	TGGCCCAGAGRTATCTGCTAC	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16456431	7955298	14110	ATGAGTACAAYCTGAATCATA	0.15	0.04	0.04	0.85	0.99	1.58	1.29	0.02	0.98	0.96	1.55	1.24
141	12	16463806	11056933	14111	TTATTCTCTARTTAGTCAAAG	0.53	0.90	0.90	1.03	0.45	0.76	0.72	0.86	1.07	0.48	0.82	0.72
141	12	16470333	718481	14112	TGCTCAACAAMATGTCTCATT	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16483271	2417573	14113	AGAATCTCCARCTTCTTAGTG	0.28	0.32	0.32	0.50	0.69	0.25	0.42	0.27	0.52	0.67	0.26	0.42
141	12	16492251	993694	14114	ACACTGTACARGTTGTCGAGA	0.19	0.36	0.38	0.24	0.18	0.39	0.62	0.36	0.23	0.19	0.42	0.63
141	12	16500305	10772939	14115	GTTTCTGTTAYATGCCTGATA	0.11	0.09	0.08	0.19	0.20	0.83	0.71	0.05	0.14	0.21	0.86	0.67
141	12	16522889	16911964	14116	ATAAATTACARTATTAAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16527610	7294773	14117	TTCCAACCAAYGGTGTGAAAA	0.16	0.21	0.21	0.09	0.27	0.16	1.21	0.16	0.09	0.27	0.15	1.18
141	12	16536905	17668749	14118	TAAAGATTTTYTTAAAAAGGT	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16545580	7304507	14119	ACAGATTCTCRTTACATAAAA	0.77	0.32	0.31	0.41	0.15	0.66	0.45	0.26	0.36	0.16	0.69	0.48
141	12	16556513	17606144	14120	TTTCATAGGAYAATCTCATCT	0.49	0.86	0.80	0.41	0.36	0.33	0.37	0.78	0.40	0.35	0.35	0.37

141	12	16565329	10772943	14121	GTTATGGGCCRCCTACTTCAG	0.99	1.52	1.52	0.70	0.32	0.11	0.07	1.49	0.77	0.32	0.10	0.07
141	12	16572760	10082885	14122	TCAATTTATGRTGGCGTAATA	0.12	0.28	0.32	1.02	0.41	0.09	0.26	0.30	1.13	0.41	0.10	0.26
141	12	16578490	11056989	14123	ATGCACATTTKAGATAAAAGG	0.14	0.34	0.32	0.38	0.33	0.38	0.61	0.30	0.36	0.35	0.40	0.66
141	12	16587150	2193186	14124	TCAAGACTAARGGTAAATGTC	0.10	0.22	0.22	0.25	1.01	1.08	1.00	0.18	0.23	1.05	1.06	0.99
141	12	16599696	4763448	14125	ACTACCACTTRAGGTGTGTGG	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16606000	16912030	14126	GTGCAATGAAYGTTTATGCTC	0.32	0.13	0.13	1.35	1.37	1.43	1.37	0.11	1.39	1.34	1.39	1.36
141	12	16619342	16912040	14127	TAATCTAAACYTAACATTATG	-	-	-	-	-	-	-	-	-	-	-	-
141	12	16626906	2058796	14128	TTCCTAGGTAYGGTCCCTCAC	0.15	0.17	0.17	2.29	1.24	1.76	1.35	0.13	2.43	1.23	1.63	1.32
142	12	18197069	4457807	14129	CACCTCTGCCRTAATTCGATT	-	-	-	-	-	-	-	-	-	-	-	-
142	12	18202925	10770310	14130	AAATGGATTAYAGCAGCAAAA	-	-	-	-	-	-	-	-	-	-	-	-
142	12	18211004	6486890	14131	AATCACTGTCRTCATTTAAAT	-	-	-	-	-	-	-	-	-	-	-	-
142	12	18251388	10840972	14132	TTACCAAAACWGTGATGTAAA	0.08	0.04	0.04	0.20	0.46	1.57	1.53	0.02	0.17	0.46	1.48	1.49
142	12	18263391	16913970	14133	GCTTCCTTTARTAGATCTTTA	0.77	0.89	0.89	1.23	1.36	1.43	1.33	0.78	1.23	1.33	1.34	1.30
142	12	18269972	16914050	14134	TAAAGCAGATKAGCAGAAAGC	0.95	1.43	1.43	3.04	2.62	1.26	1.27	1.37	3.51	2.30	1.21	1.24
142	12	18290073	10505814	14135	ATTAGAGCACYTAAATATTTT	2.77	3.21	3.25	2.52	2.84	1.49	1.33	3.16	2.89	2.46	1.43	1.30
142	12	18296527	17473539	14136	GTCAGACAAAYTACTCTTCAC	0.62	1.00	1.00	2.41	2.42	2.71	2.00	0.90	2.60	2.17	2.40	1.89
142	12	18303311	7304954	14137	CACTCTATTARGCAACAGGGT	0.01	0.01	0.02	0.85	2.34	2.63	3.15	0.00	0.94	2.08	2.29	2.69
142	12	18312823	17408904	14138	TGTGCCTCCTRTGCAGTGAAT	1.09	1.59	1.58	0.86	0.94	2.37	2.51	1.49	0.90	0.94	2.06	2.26
142	12	18320816	11043995	14139	AATCCTACAARTAAAATGGAG	0.57	0.57	0.57	0.87	0.64	1.15	1.80	0.43	0.97	0.67	1.10	1.69
142	12	18326719	11044004	14140	ATTTTAGCTCYATCATTCACA	0.61	0.43	0.46	0.47	0.87	0.61	0.53	0.39	0.49	0.85	0.62	0.51
142	12	18334560	12230636	14141	GTAGTTGTGTRGTATCCAAAA	0.54	0.54	0.70	0.94	0.42	0.52	0.55	0.58	0.93	0.45	0.51	0.55
142	12	18354876	11044020	14142	AAGTAAAAATRTGTTTATGAA	-	-	-	-	-	-	-	-	-	-	-	-
142	12	18364996	11044026	14143	AAAAGGCTTAYATAGTTAAGG	-	-	-	-	-	-	-	-	-	-	-	-
142	12	18379331	12580062	14144	TCTGATCAGTRGGCATAGTTT	0.94	0.91	0.91	0.63	0.39	0.33	0.50	0.84	0.69	0.36	0.36	0.52
143	12	18959566	1490710	14145	TTGCTCAAGARGGAAGATAAA	0.13	0.20	0.20	0.55	2.23	0.89	0.75	0.18	0.58	1.98	0.91	0.75
143	12	18966506	11044357	14146	GCTGGGCACAYTGATTACACA	0.06	0.20	0.24	0.24	0.32	0.74	0.68	0.18	0.24	0.34	0.72	0.68
143	12	18979898	901802	14147	CCTAAAATCARAGAAATGCTC	-	-	-	-	-	-	-	-	-	-	-	-
143	12	18985602	10841116	14148	GCTGTTAAGASGTATGGGAAC	0.31	0.30	0.30	0.05	0.20	0.50	0.56	0.24	0.04	0.19	0.50	0.57
143	12	18992145	1490723	14149	GTTAGAAAAGYATTTTTGGTA	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19001732	4764439	14150	ACAAAAATTCYGTGAAAAAAG	0.43	0.46	0.47	0.59	0.18	0.12	0.60	0.43	0.65	0.17	0.13	0.60
143	12	19018286	17501677	14151	TATAAGAAACRGTCAAAAGAC	1.17	1.16	1.16	0.71	0.35	0.26	0.17	0.90	0.91	0.38	0.28	0.16
143	12	19027872	17429721	14152	AGTCCTTAATRTGTAGCTAAA	0.26	0.26	0.26	0.54	1.08	0.49	0.69	0.15	0.63	1.09	0.52	0.72
143	12	19036405	17429840	14153	CCTAATTTTGSAGTTAAATTG	0.39	0.39	0.39	0.52	0.76	0.94	0.99	0.24	0.47	0.82	0.92	1.00
143	12	19044559	17430253	14154	AGAGCCATTAYTGGGTCCTGG	0.16	0.16	0.16	0.58	0.37	0.43	1.05	0.07	0.47	0.39	0.48	1.05
143	12	19049616	17502533	14155	ACTCTGAACCRTAATACAGAA	0.51	0.50	0.39	0.42	0.27	0.62	0.44	0.25	0.36	0.28	0.66	0.48
143	12	19060615	17443238	14156	ACTCAACACAYTGTCTTATTT	0.30	0.29	0.29	0.15	0.62	0.34	0.97	0.18	0.15	0.62	0.40	0.92
143	12	19070627	7968997	14157	TTTCATCTTARAGCAATAATT	0.25	0.32	0.22	0.54	0.36	0.95	0.92	0.16	0.57	0.39	0.98	0.91
143	12	19082483	4764451	14158	TGGACTTATCRGAAACTTCTT	0.13	0.03	0.03	0.55	1.07	0.92	1.22	0.00	0.63	1.06	0.94	1.19
143	12	19084940	16915000	14159	CATATTTTTARAACCAATACT	0.81	0.65	0.59	0.92	1.21	1.32	1.23	0.55	1.05	1.18	1.23	1.20
143	12	19096918	1514839	14160	ATTTTATACCYGCTGCTTTTA	1.54	2.00	2.00	1.11	1.25	1.52	1.14	1.93	1.24	1.21	1.42	1.12
143	12	19109060	932103	14161	AAGATCCTCAYCCTGTGTGGT	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19115452	12815398	14162	CAAATGGTACKCAAAAGCAGA	0.95	0.85	0.84	1.85	1.73	1.08	0.99	0.77	1.91	1.66	1.03	0.99
143	12	19122465	7299781	14163	ACCTTTACACKAGTTTGCTAC	1.25	1.22	1.22	2.16	1.75	1.10	0.59	1.08	2.48	1.66	1.06	0.59
143	12	19131594	7308215	14164	TTTTCAGTGTYAGACATTTGT	2.29	2.62	2.62	2.04	1.46	0.56	0.37	2.52	2.20	1.35	0.57	0.39
143	12	19158982	4456315	14165	CGTGTTATCCRTATTACTTTA	1.31	1.20	1.20	1.92	1.26	0.62	0.69	1.13	2.28	1.26	0.63	0.72
143	12	19168111	954010	14166	TTTTAGGAAAYTTAACTTTGT	0.01	0.17	0.17	0.51	1.13	0.83	0.35	0.06	0.50	1.09	0.85	0.38
143	12	19178683	11044430	14167	ATTAAACTTTWAAAAAAACTA	1.36	1.37	1.40	1.10	0.63	0.50	0.65	1.33	1.16	0.64	0.53	0.68
143	12	19187948	16915121	14168	TTGATAATACYGTGTCAAATC	0.74	0.85	0.85	1.24	0.45	0.41	1.21	0.78	1.42	0.44	0.42	1.18
143	12	19200517	985692	14169	AGTGTGAAAAKTTGGTTTTTT	0.71	0.70	0.70	0.89	0.88	1.53	0.69	0.59	1.02	0.94	1.50	0.74
143	12	19203488	1399471	14170	ATCTGGATCCSAAAAGAAGTA	1.48	1.63	1.63	1.01	1.83	1.46	1.33	1.59	1.10	1.75	1.45	1.30
143	12	19239588		14171	GATATAAAGTRCGGGTGAGTG	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19246552	1388695	14172	TGAGACATTCYGTAAGTGCTA	0.05	0.14	0.14	1.65	1.96	1.64	2.10	0.09	1.88	1.88	1.56	1.99
143	12	19252852	1492127	14173	AGTTTTCTTTKCTGTAACCTA	0.11	0.20	0.26	1.27	1.70	2.27	2.14	0.19	1.43	1.61	2.11	1.99
143	12	19260960	10841183	14174	TATTAGGACAKGGAGAAAATG	0.06	0.25	0.20	1.61	1.44	1.62	1.62	0.14	1.69	1.36	1.53	1.55
143	12	19269576	11830213	14175	GAGGGTAGGAKTTTAATTTTC	0.47	0.93	1.02	0.47	1.80	1.44	1.73	0.91	0.48	1.72	1.36	1.66
143	12	19276915	981832	14176	TCCAGTTACTKTTTCTAAGAG	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19296487	7313162	14177	TCACCATACASAGCACATGTA	0.29	0.45	0.37	1.24	0.78	1.92	1.76	0.28	1.25	0.79	1.84	1.66
143	12	19306172	7965144	14178	TTAACCAACCSTATAAAATTG	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19316210	6486946	14179	ATTTTGCTGTRTGGCTCAAAT	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19322992	16915316	14180	AAGAGCAATTKGGTACCTTTC	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19328796	16915323	14181	AATGGAGATCRTGTTTTACTT	1.79	1.83	1.83	0.98	1.57	1.47	2.15	1.74	1.00	1.53	1.42	2.07
143	12	19341503	17271690	14182	TTCATGACAARTCAGTTTGCC	1.65	1.71	1.69	1.12	1.47	2.00	1.64	1.62	1.18	1.44	1.87	1.55
143	12	19350858	16915360	14183	ATAGGTGACTRATCTCCCCGG	0.39	0.57	0.68	1.18	1.18	1.61	1.61	0.58	1.25	1.19	1.55	1.54
143	12	19358527	10770473	14184	CTTTAATAAARTATGTGATTA	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19386339	4963532	14185	GCCAAAGAAARTATTGTTCTA	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19414336		14186	AATTTTGTTTMAGTCATTACA	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19420335	8601	14187	CAAATGTTACYGCTTATCTTT	1.15	1.61	1.61	1.64	1.86	1.35	1.28	1.57	1.79	1.76	1.27	1.24
143	12	19431361	2961370	14188	AAGCTGTCCARAAACTTGTTC	1.18	1.65	1.65	1.44	2.41	1.49	1.20	1.57	1.57	2.25	1.41	1.17
143	12	19442103	2565666	14189	AATTAGGCAAYGACCCATAAA	0.13	0.19	0.13	1.78	1.58	1.93	1.06	0.11	1.95	1.51	1.86	1.06
143	12	19455002	865316	14190	CTAAGAATTCKGGAGCAGGAA	0.62	0.10	0.10	1.71	1.82	1.16	1.34	0.07	1.90	1.75	1.13	1.29
143	12	19483209	2728781	14191	TTTGAGGACCYTGAACCAAGA	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19499661	16915302	14192	CTTCTCAGTCMTGGTAACATA	0.39	0.39	0.39	1.23	1.76	0.98	0.98	0.25	1.44	1.65	0.97	0.99
143	12	19509642	16915491	14193	TTTGATCAAASATAGGAGTCC	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19513612	1875467	14194	TTTGGACTTAMCACGTGTGCT	2.15	0.36	0.36	0.34	0.98	1.56	0.98	0.32	0.33	0.99	1.48	1.00
143	12	19532082	16915524	14195	CTAGAAGTTAMATATTAATGC	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19537833	16915544	14196	TTACTTGGCARCTTACTTCGT	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19551778	11044629	14197	GGAATGAGTGWTGTCCACCCT	0.07	0.20	0.20	0.30	0.09	1.57	0.82	0.19	0.33	0.07	1.46	0.79
143	12	19560722	7971277	14198	TTCTTATGCCRTATAGGAAGC	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19577611	16915591	14199	TATGCAATTTWTATCAGCTTA	0.70	0.49	0.49	0.31	0.39	0.48	1.17	0.41	0.31	0.37	0.49	1.15
143	12	19583978	2134135	14200	TCAGATGTTAMTTTATAATGT	0.84	0.63	0.63	0.69	0.39	0.69	0.30	0.53	0.65	0.42	0.68	0.32
143	12	19589435	3903219	14201	GCAATTGAGGRTCCCTAAGGA	1.01	1.10	1.10	0.59	1.15	0.45	0.23	0.99	0.63	1.09	0.45	0.22
143	12	19616798	6486969	14202	TTTCTTATAAMAGCCATTTCA	0.62	1.00	1.00	1.20	0.69	0.63	0.40	0.94	1.29	0.72	0.64	0.40
143	12	19627633	10841272	14203	AGCCCCAAGTYTCTGCAGCCT	-	-	-	-	-	-	-	-	-	-	-	-
143	12	19637854	7312615	14204	TATACTCTTTRTGAAGTCATA	1.03	1.51	1.51	0.89	0.72	0.57	0.35	1.41	0.95	0.73	0.52	0.33
143	12	19654084	6486979	14205	GATCTAGTAGMTTTTTAGACT	0.21	0.22	0.22	0.66	0.18	0.45	0.56	0.16	0.67	0.22	0.46	0.56
143	12	19668264	7313041	14206	CCTGGCCTTTRGTGTTCTGTA	0.79	0.47	0.47	0.07	0.32	0.17	0.40	0.41	0.06	0.35	0.18	0.39
144	12	23984329	17478946	14207	ATATTTCCCCRTAGTGTCTTG	0.33	0.13	0.13	0.31	0.16	0.34	0.11	0.13	0.30	0.17	0.38	0.12
144	12	23990929	17400846	14208	ACGGTAAAATRTAGAAGACTT	0.08	0.00	0.00	0.47	0.46	0.21	0.76	0.00	0.49	0.48	0.24	0.78
144	12	23997141	10505918	14209	ATAAACTGATMCTCCAGAATT	0.01	0.04	0.04	0.34	0.41	1.26	2.02	0.01	0.31	0.44	1.26	1.92
144	12	24022742	4281558	14210	CACCTTATAAWCATTATGCAG	0.51	0.92	0.92	0.35	0.32	2.10	1.78	0.90	0.35	0.36	2.05	1.71
144	12	24031096	10505921	14211	AAAGCTTAAARTTCTACTTCA	0.11	0.30	0.30	1.23	1.76	0.74	1.72	0.26	1.31	1.72	0.72	1.65
144	12	24039446	1566332	14212	ATATATACGTYTGACATTTAG	-	-	-	-	-	-	-	-	-	-	-	-
144	12	24050782	12422817	14213	TGGACCTGTGYCACTCCTTCC	1.27	1.43	1.43	1.21	1.78	1.49	0.92	1.37	1.29	1.64	1.44	0.93
144	12	24062373	11047211	14214	CCCAGCTTCCSTGACCACGTC	0.41	0.74	0.77	0.65	1.72	2.40	0.94	0.72	0.66	1.64	2.21	0.97

144	12	24072217	17482141	14215	TGCAATTCCTRGATTTCATCA	0.20	0.05	0.05	0.79	0.58	1.68	3.10	0.03	0.79	0.64	1.60	2.89
144	12	24079865	2418156	14216	CTCCTCTGGARCTTAAATGTA	0.41	0.61	0.61	0.39	0.78	0.82	2.60	0.57	0.36	0.76	0.85	2.48
144	12	24088917	16927079	14217	TGCATATTCCRTATCGAACTG	-	-	-	-	-	-	-	-	-	-	-	-
144	12	24094858	7961391	14218	AGAGAGGTACRGTTCTTTAAA	0.17	0.42	0.51	1.06	1.41	1.01	0.91	0.45	1.10	1.36	1.01	0.91
144	12	24101986	11047241	14219	TTGGAAAAAGYATGTCAATAG	-	-	-	-	-	-	-	-	-	-	-	-
144	12	24113698	7966621	14220	GAAGAACAGAYTTCAGCATTA	1.03	1.44	1.44	1.20	1.42	1.61	0.67	1.40	1.20	1.40	1.55	0.66
144	12	24127834	1021669	14221	CTTACCACAGYTATTGAGTAG	0.12	0.31	0.31	1.01	1.33	1.07	0.46	0.24	1.03	1.32	1.06	0.45
145	12	33041207	17623827	14222	ATGTGGGTGTRGCTAATTTTT	0.02	0.12	0.12	0.16	0.08	0.50	0.16	0.10	0.15	0.08	0.52	0.17
145	12	33051584	2173648	14223	CAAATTGGTTYAAATTTTTGG	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33071109	12810966	14224	AGGGTCTGCARGTATGGAAGG	0.24	0.30	0.30	0.13	0.34	0.10	0.10	0.27	0.14	0.34	0.09	0.11
145	12	33097905	11052413	14225	TCAAACTCTTKATTTCTAAAG	0.11	0.19	0.19	0.63	0.03	0.07	0.19	0.17	0.63	0.02	0.05	0.23
145	12	33105304	10506102	14226	GCCAAATTAASTACCTGAAAT	0.01	0.02	0.00	0.33	0.18	0.10	0.11	0.00	0.30	0.17	0.09	0.13
145	12	33125132	11052425	14227	TATTTTAAGCYCTTTTGATGG	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33136580	17624773	14228	CATTCCTGATRGAGCCTAAAG	1.16	0.17	0.16	0.25	0.21	0.21	0.04	0.12	0.21	0.23	0.21	0.03
145	12	33137627	17624942	14229	TGGAAAGGACWTATGCAGTTT	1.03	0.16	0.15	0.31	0.08	0.08	0.09	0.10	0.30	0.10	0.08	0.09
145	12	33161466	4931687	14230	TTTTACATGTYGGACAACACT	0.42	0.62	0.60	0.39	0.12	0.04	0.10	0.50	0.40	0.13	0.04	0.10
145	12	33171126	1445311	14231	TATCTGGAGTYTTTGGATAAT	0.64	0.46	0.46	0.46	0.21	0.11	0.04	0.37	0.43	0.19	0.12	0.03
145	12	33184655	17631348	14232	ATTTTCTCTGYTTTTCATTCT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33196682	11052480	14233	TGAGCCTATCRTTTTTCTAGG	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33207384	10506106	14234	AGACTTTTCCKTGTCTATTGT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33216932	10844489	14235	CTAAAATAATWAGGTTCTCAG	0.25	0.22	0.22	0.37	0.26	0.19	0.30	0.18	0.37	0.28	0.18	0.29
145	12	33225221	12297690	14236	TTTGCAGTTASTTTATGAATC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33228724	1840970	14237	CTGGGCAAAARTAAGATAACA	0.24	0.54	0.54	0.38	0.28	0.77	0.37	0.51	0.38	0.33	0.79	0.37
145	12	33253261	7972951	14238	TAGCTCTAAGSTTTCTCCTAT	0.59	0.62	0.62	0.50	0.66	0.75	0.52	0.60	0.48	0.68	0.76	0.49
145	12	33260949	4931708	14239	TTGTTCAAATYTTAACCTGCA	0.71	0.80	0.80	0.99	0.71	0.29	1.94	0.78	1.04	0.69	0.30	1.75
145	12	33269868	1457678	14240	AATAGTCCAAYATGCTTTGCC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33279529		14241	TTTACTGACARTTCAAGTACT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33283744	955063	14242	TAGAAGAGAARCTTGATGGTG	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33294675	16920728	14243	TTATCTATCAKAATGTTCAAT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33302609	7131991	14244	GCCCATAAGCRTTTTGGTTGT	0.15	0.33	0.33	0.95	0.55	1.73	1.78	0.28	1.01	0.61	1.66	1.69
145	12	33309428	10772058	14245	CCATTGGGAAYACAAAGGGGA	0.43	0.28	0.28	0.28	1.37	1.44	2.46	0.25	0.28	1.32	1.36	2.27
145	12	33317190	17633701	14246	ATTCCGTATAYTGTGGAGTCT	0.44	0.46	0.46	1.27	1.50	3.09	2.38	0.41	1.34	1.46	2.72	2.22
145	12	33331881	16920827	14247	TCACTCTTTGRAATGCCTAAG	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33337897	4142890	14248	AACCTCAAAGSTAGTGAGAAA	0.22	0.46	0.52	1.53	2.28	3.06	3.02	0.50	1.64	2.11	2.82	2.71
145	12	33348485	11052605	14249	ACGAGAGAATRGAAGGTCAGG	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33357140	16920840	14250	CTTTCTGGTCMCCATGGCAAA	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33362740		14251	TGCAATACTAYGGAAGATGCA	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33370194	7296465	14252	CCTGAAGGAGRTTTGAATAGA	1.19	1.73	1.73	1.66	3.71	3.25	2.96	1.65	1.77	3.26	2.92	2.66
145	12	33383533	10772067	14253	AATTTGTACCRCTTTCTAGAT	0.01	0.02	0.02	2.59	3.63	3.64	2.87	0.00	2.85	3.17	3.07	2.60
145	12	33388890	12321799	14254	TTTTTTCCTCKTGTAACATTA	2.63	3.51	3.51	2.43	3.35	2.96	1.93	3.39	2.94	2.64	2.67	1.79
145	12	33394821	12296290	14255	AATTTACATCKTTATATTTCT	0.00	0.00	0.00	2.71	2.56	1.55	1.08	0.00	3.14	2.21	1.48	1.12
145	12	33402536		14256	CACTCTGTGCSTGCATCTTTT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33422705	9888427	14257	AGTTGGAGACRTAGTGAACAG	3.00	3.18	3.46	2.47	1.72	0.91	0.48	3.37	2.64	1.60	0.91	0.51
145	12	33429446	11052670	14258	GCCCAGCCGTYGGTAGGTAAC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33435938	11829626	14259	ACAGTAGGTGYCAGAAAACAT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33438662	2892701	14260	CTTTAGGACAYGGAAGTAGCT	0.11	0.20	0.20	2.00	1.15	0.49	0.57	0.17	2.02	1.08	0.51	0.61
145	12	33447139	2389196	14261	GAGAGCCATGRCATTTACAAC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33454565	12299895	14262	AATTCAAAAARCACCATAAGA	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33465729	10844592	14263	CAGTGTTATCYCACCACTCAT	0.88	1.08	1.14	0.60	0.76	0.42	0.37	1.08	0.64	0.81	0.44	0.37
145	12	33472096	11052697	14264	ACTATGAGTTWGGATTTAATT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33480710	1482990	14265	TGTAAGTCTTSACCAATTTTA	0.89	1.31	1.31	0.69	0.28	0.46	0.26	1.22	0.68	0.30	0.44	0.29
145	12	33494943	10844612	14266	AACCACCCTTYTATATGGGCT	0.40	0.49	0.46	0.47	0.56	0.19	0.68	0.44	0.46	0.55	0.19	0.71
145	12	33516962	16921038	14267	TTTATTGGATYCACCTTTGTC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33530062	11052729	14268	TCTAAGACTAYGTTGGATATG	0.97	0.02	0.02	0.57	0.25	1.02	0.54	0.00	0.58	0.30	1.02	0.55
145	12	33562285	11052737	14269	AAGCTTAAAARGGCAAATTTC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33571076	1817500	14270	ATTTTTCTGAKCCTGCTGACT	0.09	0.02	0.02	0.70	0.47	0.40	1.70	0.00	0.70	0.47	0.41	1.61
145	12	33576567	7486521	14271	TTAGTCCTAAMAAACATCCCT	0.54	0.92	0.92	0.57	0.87	1.00	1.03	0.84	0.60	0.86	1.00	1.02
145	12	33582277	10844624	14272	CAAGCATAAGYTAGACACATG	0.29	0.11	0.13	0.80	0.76	1.52	0.90	0.10	0.87	0.77	1.42	0.90
145	12	33588363	10844629	14273	AAAGCAAGTGWTCAAAACAGA	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33599819	10506110	14274	TGCCAAGTCAMATCATTGGAT	0.18	0.02	0.02	0.51	0.92	0.87	0.79	0.00	0.51	0.93	0.88	0.81
145	12	33617726	815047	14275	ATAAAAGTCAYAAACCATTAC	0.46	0.42	0.42	0.76	0.94	0.88	0.77	0.39	0.78	0.93	0.87	0.74
145	12	33630081	815027	14276	ATGACAAATARAAATGATATC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33643911	7316684	14277	TTTGTAGGAGRTAAGAATCAC	0.12	0.05	0.05	0.84	0.80	0.77	0.90	0.03	0.91	0.80	0.76	0.89
145	12	33652893	11052780	14278	AGTAATGAGGKCCTCTTCCTC	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33666195	756448	14279	CAAAACTCAARCTCTGAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33674567	1386934	14280	TTTGGTGCACYCATATTTGTT	0.09	0.19	0.16	0.17	1.20	0.83	0.66	0.15	0.09	1.20	0.82	0.65
145	12	33680897	12425859	14281	AAAAAGCATCYCTTCTTCCTT	-	-	-	-	-	-	-	-	-	-	-	-
145	12	33694027	7962021	14282	TTCAGCCACTMATTTCCCAGA	0.43	0.04	0.04	0.20	0.22	0.89	0.68	0.02	0.08	0.21	0.89	0.71
146	12	40879703	712125	14283	TATGGTCCTAWCAGGAAACTT	0.15	0.20	0.17	0.11	0.17	0.92	1.50	0.14	0.06	0.18	0.92	1.40
146	12	40894268	10492388	14284	GCACTAGTCTYTGCTCAATGT	0.02	0.02	0.02	0.62	0.51	1.66	1.82	0.00	0.63	0.53	1.53	1.72
146	12	40899557	10459290	14285	TGAGAGTTCAKTAAGCTCATT	0.06	0.17	0.17	0.54	2.16	1.67	1.05	0.16	0.57	2.06	1.57	1.03
146	12	40922391	10785335	14286	ATACTATTCGRGTGTCTGCAC	-	-	-	-	-	-	-	-	-	-	-	-
146	12	40961474	2061191	14287	AGCCTAGGTARATGTGAAGAT	0.20	0.10	0.10	1.16	1.92	1.34	1.21	0.09	1.22	1.91	1.33	1.17
146	12	40972456	6582394	14288	AACATCCCAARGATTAAAAAA	0.10	0.25	0.28	0.11	1.13	0.99	1.47	0.24	0.09	1.12	0.99	1.44
146	12	40977266	17091052	14289	TGGAAACTGGMTGTGGCTATT	0.30	0.13	0.13	0.05	0.26	1.00	0.72	0.11	0.04	0.26	0.99	0.75
146	12	40991213		14290	GGGCATGTATRCGATACCACA	0.24	0.36	0.36	0.30	0.24	0.11	0.68	0.29	0.28	0.23	0.10	0.67
147	12	41341830	17569297	14291	CAGCAATTGAWCTTTTCTGTC	0.20	0.05	0.05	0.03	0.06	0.51	0.14	0.03	0.03	0.06	0.49	0.14
147	12	41352359	4131406	14292	TTTCCCAAGCRTGTTTTATCT	0.04	0.18	0.18	0.09	0.06	0.28	0.11	0.17	0.05	0.05	0.27	0.12
147	12	41359481	4768441	14293	CTGTCCCTGTWACTAGTCTTG	0.05	0.10	0.15	0.32	0.06	0.05	0.31	0.13	0.32	0.06	0.05	0.30
147	12	41365987	1400808	14294	TCAAGTACTAKTTTCAGGGCA	0.41	0.52	0.46	0.10	0.11	0.08	0.03	0.42	0.08	0.11	0.08	0.03
147	12	41373613	2731018	14295	CCATTTTAAARAGGAGATTAC	0.91	0.40	0.44	0.32	0.05	0.04	0.09	0.40	0.32	0.06	0.05	0.09
147	12	41384287	17091723	14296	TTGAATAATCRGAAAGCCTCT	0.05	0.00	0.00	0.32	0.06	0.08	0.01	0.00	0.36	0.05	0.07	0.02
147	12	41397957	10506214	14297	TCTCCATTAGYAGAAGCCAAG	0.76	0.20	0.21	0.05	0.08	0.01	0.04	0.15	0.02	0.07	0.01	0.03
147	12	41406358	868627	14298	CCCACTATTGKCTCCTTGAAA	0.44	0.51	0.49	0.08	0.01	0.05	1.16	0.44	0.08	0.00	0.04	1.19
147	12	41417475	10506217	14299	ATGTATTCTTYTGGAGTTATC	0.08	0.08	0.08	0.16	0.05	1.49	0.94	0.05	0.15	0.03	1.38	0.94
147	12	41428597	10880360	14300	GGTACTCCAGRAAAAAAAGGA	0.23	0.06	0.06	0.56	3.77	1.59	0.80	0.05	0.59	3.30	1.51	0.85
147	12	41435277	11181674	14301	TGCAAAGTAGWGCACATTTTA	0.79	0.81	0.81	5.23	4.31	2.25	0.71	0.75	5.74	3.80	2.06	0.73
147	12	41441029	12302566	14302	ACTTGGTGGARGAGAAAAGTG	0.19	0.05	0.02	4.66	4.18	2.49	0.99	0.00	5.34	3.41	2.30	0.97
147	12	41446468	12319782	14303	AGTCTGCAGARGAATTTGTGG	0.73	0.59	0.59	2.52	4.53	2.14	1.73	0.55	2.78	3.74	1.97	1.63
147	12	41451988	12297983	14304	TGATGGCAGCRTTTGAGCAGG	1.17	1.09	1.03	0.42	1.87	3.14	1.47	0.97	0.46	1.73	2.84	1.41
147	12	41459499	2255713	14305	TGTGCCTGCTKCAGGGAAACG	-	-	-	-	-	-	-	-	-	-	-	-
147	12	41467096	2730999	14306	CAGGAAACCTSAAGTTGTCCC	0.13	0.31	0.35	0.26	0.15	0.99	2.11	0.31	0.28	0.15	0.99	2.05
147	12	41473732	7963631	14307	AACAGTAATTSTTGGACAAGG	0.65	0.70	0.70	0.36	0.05	0.18	0.88	0.65	0.36	0.04	0.17	0.85
147	12	41480850	2468322	14308	ACTTTTCAGGSTGTACTTTTT	-	-	-	-	-	-	-	-	-	-	-	-

147	12	41487208	7138064	14309	ATATAGATAAYTGGTATCAAT	0.76	0.86	0.86	0.18	0.28	0.10	0.24	0.74	0.20	0.27	0.08	0.23
147	12	41494867	11181694	14310	TGGTATATTTYGAAACCCTTT	-	-	-	-	-	-	-	-	-	-	-	-
147	12	41500751	1914490	14311	GCCAACATCCRCTAAAATAAA	0.17	0.36	0.39	0.71	0.21	0.32	0.17	0.37	0.73	0.24	0.29	0.18
147	12	41510633	11613672	14312	GGCACCTATCYGCAGGCACCT	1.13	0.17	0.18	0.28	0.34	0.11	0.32	0.13	0.25	0.37	0.12	0.33
147	12	41530189	1474071	14313	AAAGTTTCTCRGGGCAGATTT	0.04	0.17	0.17	0.20	0.03	0.41	0.27	0.17	0.18	0.03	0.42	0.27
147	12	41539083	1033265	14314	TGTAAAACTGYCCAACTCTTT	0.15	0.39	0.41	0.19	0.18	0.19	0.24	0.38	0.17	0.17	0.21	0.25
147	12	41547318	10785390	14315	AGTGGCAATGSAGGCTGAAGA	0.61	0.40	0.32	0.26	0.38	0.06	0.07	0.26	0.22	0.41	0.05	0.06
147	12	41548186	17092200	14316	TGGGGGAGACKAAAGTTCCTG	0.14	0.37	0.32	0.44	0.18	0.12	0.11	0.30	0.44	0.21	0.13	0.11
148	12	41788288	1167100	14317	ATCAATACCARTCTCCTCTAA	0.24	0.43	0.44	0.27	0.08	1.20	1.32	0.41	0.21	0.07	1.15	1.29
148	12	41794923	1795920	14318	TTTTCTCAATSTCTAACAAAA	-	-	-	-	-	-	-	-	-	-	-	-
148	12	41801086	718914	14319	AGTCTTCTGTRTCACTCCCTG	-	-	-	-	-	-	-	-	-	-	-	-
148	12	41806820	1167152	14320	GTTTGCACATYTTGGGACTAA	0.33	0.47	0.47	0.50	2.22	1.92	1.85	0.48	0.61	1.99	1.78	1.68
148	12	41810488	1183241	14321	TTTATAGATGYGAAAGTGTCA	0.39	0.62	0.62	2.01	3.44	2.56	1.39	0.61	2.34	2.82	2.29	1.37
148	12	41831514		14322	AATAGCTCACYCAGTTATGCA	-	-	-	-	-	-	-	-	-	-	-	-
148	12	41837681	12099804	14323	GGCAACACCTRCTGAGAGGTT	2.88	3.54	3.54	2.06	2.69	2.22	1.78	3.46	2.19	2.39	2.00	1.66
148	12	41843669	11181896	14324	TATTAAATCARCCTCACTGAT	-	-	-	-	-	-	-	-	-	-	-	-
148	12	41849808	989033	14325	CTATTACTTARAAAGCTAAAT	-	-	-	-	-	-	-	-	-	-	-	-
148	12	41859463	17092798	14326	TCAGAAGAGARTTGGGGTTGA	0.37	0.73	0.73	2.68	1.71	2.18	1.51	0.67	3.30	1.58	1.96	1.45
148	12	41865983	12827899	14327	GATAGAGTTASTTTTACATGA	0.30	0.63	0.68	0.46	2.43	1.22	1.62	0.61	0.56	2.17	1.24	1.50
148	12	41891080	7979464	14328	AGATGAGATGRCTTTCCAAGA	0.22	0.34	0.34	0.99	0.68	1.73	0.76	0.29	0.99	0.67	1.66	0.75
148	12	41898954	1849777	14329	AGATTGATAGYAATGCTGAAT	0.54	0.69	0.66	0.31	0.79	0.41	0.35	0.61	0.25	0.82	0.41	0.38
149	12	58669336	9325169	14330	TATTTCCTGAMAATGTCATTT	0.09	0.28	0.28	0.26	0.28	0.63	0.59	0.23	0.24	0.26	0.66	0.60
149	12	58675856	10784017	14331	TCAAAGGCAGRAAGTATATAT	0.09	0.15	0.16	0.38	1.39	0.70	0.84	0.13	0.38	1.38	0.73	0.85
149	12	58693426	17575187	14332	TCTGGAGGAAYTGGGGCTTAC	0.57	0.64	0.66	0.44	0.80	1.25	1.16	0.64	0.50	0.83	1.18	1.12
149	12	58707175		14333	TGGTCAAATTMAATCTCTCCA	1.11	1.09	1.28	0.49	1.50	1.03	0.86	1.07	0.49	1.45	1.04	0.85
149	12	58710268	11173292	14334	AAATAGGTTAYAAATTGTGAA	0.61	0.66	0.66	2.26	1.81	1.13	0.69	0.60	2.53	1.72	1.11	0.66
149	12	58730430	11173303	14335	GTGATTTCTASTACATAAACA	2.20	1.61	1.61	0.68	1.77	1.20	0.65	1.53	0.73	1.63	1.16	0.68
149	12	58737092	10877389	14336	TTTTGTTTGASTAATAATATT	2.28	1.66	1.76	0.83	0.45	1.45	1.62	1.68	0.93	0.45	1.36	1.57
149	12	58745163	1389258	14337	TGTCTAATGCKCTCTTTCGTT	0.61	0.93	1.01	0.65	0.47	1.07	1.71	0.94	0.74	0.50	1.05	1.62
149	12	58747565	6581295	14338	CCAGAAAGAGRATTTGCTGTT	0.58	0.87	0.87	0.44	1.31	1.05	1.11	0.82	0.42	1.26	1.04	1.09
149	12	58763632	735926	14339	GTGGTTCTGGKGTCTGGAGCA	0.11	0.19	0.19	1.21	1.27	1.44	1.05	0.18	1.20	1.21	1.38	1.07
149	12	58775789	17593697	14340	TTTCTCTCTGYAGTGGATATC	0.74	0.81	0.81	0.59	1.85	1.43	0.67	0.73	0.59	1.67	1.41	0.65
149	12	58784955	17594045	14341	TCTACTTTAARGCCCCTCATT	0.89	0.25	0.24	0.37	0.43	0.89	0.91	0.20	0.38	0.46	0.88	0.94
150	12	85600523	981142	14342	GGGTCAGCCCKTTGGCTATGC	0.58	0.70	0.70	0.80	0.87	0.76	0.37	0.67	0.96	0.88	0.78	0.40
150	12	85623046	7314413	14343	GACAATCTAAMATTAATTTGA	0.70	0.81	0.86	0.71	1.20	0.59	0.27	0.80	0.78	1.15	0.59	0.26
150	12	85639955	2217237	14344	GCAAATCAATRTCCATCCCAG	0.50	0.53	0.53	0.75	0.58	0.55	0.55	0.53	0.73	0.58	0.60	0.60
150	12	85648042	17040810	14345	ACAAGCCTATYCTCCTTCAGC	0.64	0.43	0.40	0.36	0.31	0.14	0.40	0.41	0.35	0.31	0.14	0.42
150	12	85659181	977781	14346	TCAGATATCAYGTTATGACAC	0.49	0.51	0.53	0.39	0.15	0.23	0.26	0.50	0.36	0.16	0.23	0.26
150	12	85672636	10858479	14347	GGCTTAAATTYGTATAAATGT	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85680440	4583046	14348	TTGTTGCAACKATTCTTCCAC	0.06	0.19	0.22	0.41	0.50	0.45	0.21	0.18	0.45	0.50	0.48	0.22
150	12	85693923	4396350	14349	TCTAATTATTYGGGTAATTTA	0.38	0.15	0.18	0.42	0.68	0.44	0.32	0.17	0.38	0.71	0.49	0.33
150	12	85722557	2130177	14350	GCTTAGTTTAKGTCATGAGGT	0.06	0.11	0.11	0.00	0.33	0.39	1.15	0.11	0.00	0.36	0.39	1.14
150	12	85733477	11104120	14351	AATTTAAGGCSCTGTTCCTCA	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85745106	1387404	14352	CATGAGTATARTGATTAAAAT	0.01	0.02	0.02	0.30	0.26	1.55	0.92	0.00	0.30	0.31	1.48	0.91
150	12	85749440		14353	ACAGTCAAAASGCATAGTCCT	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85767860	11104164	14354	GATTGGGACCYGAACTCCATG	0.73	0.54	0.54	0.40	1.48	1.56	1.78	0.49	0.42	1.39	1.41	1.67
150	12	85776125	7957319	14355	TTTGTTGTTTKCTTTCTGCAG	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85784735	10858515	14356	GCATGCTTCTMCAGAGACTTT	0.49	0.66	0.62	1.54	1.94	1.77	1.08	0.60	1.77	1.76	1.66	1.02
150	12	85796598	7954947	14357	TAAGTTTTCTRTCTTGTTCCT	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85803961	10506937	14358	CCAACCGAACRTTACTGTAAG	0.54	0.93	0.93	2.27	3.22	1.41	0.87	0.88	2.54	2.78	1.34	0.86
150	12	85811365	10506938	14359	TTCAGGAGAARGTTTATACGT	0.34	0.19	0.19	1.54	2.60	1.78	1.01	0.16	1.84	2.26	1.61	1.01
150	12	85825238	17312379	14360	CTCTGTAAATSATATTTTAAG	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85841954		14361	CTATTGCTGARATGATAGTTT	0.24	0.38	0.38	1.34	1.53	1.73	1.35	0.32	1.45	1.44	1.64	1.30
150	12	85858541	1922750	14362	ACAGAAGTTAYAGCTATACCA	0.45	0.45	0.45	1.07	1.85	1.11	1.02	0.37	1.22	1.75	1.11	0.96
150	12	85864003	12311623	14363	GATTCTTCCTYCTCTTTATAA	0.67	0.94	0.94	0.86	0.89	0.97	0.61	0.89	0.95	0.88	0.98	0.61
150	12	85876565	17313148	14364	AATCTCCTTTWCAAAATCTCT	0.46	0.46	0.46	0.68	0.45	0.61	0.77	0.35	0.70	0.43	0.61	0.73
150	12	85888330	3861077	14365	GCATATAAATSTATGGTAAAT	0.59	0.29	0.25	0.07	0.44	0.20	0.26	0.23	0.07	0.48	0.19	0.25
150	12	85903714	2117017	14366	TAATCCTATAKTTTCAGAAGT	0.61	0.20	0.20	0.54	0.22	0.17	0.25	0.19	0.50	0.21	0.17	0.24
150	12	85923710	11104241	14367	CATGGAAGACYGAAAATAAAT	0.99	1.22	1.22	0.39	0.35	0.30	0.18	1.11	0.40	0.36	0.31	0.16
150	12	85932677	2117018	14368	ACCCTGAAAAKACTTGACTTG	0.92	0.14	0.10	0.82	0.23	0.08	0.12	0.07	0.86	0.25	0.08	0.12
150	12	85941632	17313674	14369	TTAACAATGARCATTTTGGAG	1.12	0.90	0.90	0.74	0.19	0.13	0.09	0.84	0.75	0.21	0.12	0.09
150	12	85954127	17014366	14370	CTAAAACAAARTATTCCAGAA	-	-	-	-	-	-	-	-	-	-	-	-
150	12	85962380	17314381	14371	AACTTCTTTARTAATTCTGCT	0.89	0.46	0.46	0.20	0.19	0.13	0.29	0.43	0.15	0.16	0.10	0.30
150	12	85980581	10858548	14372	TCCATTAATGMCATAAATTTC	1.08	0.50	0.46	0.05	0.26	0.27	0.56	0.40	0.05	0.23	0.26	0.59
150	12	85993220	1433330	14373	GTGCTACTTGRTACCCAGAGA	1.01	0.46	0.46	0.51	0.51	0.62	0.48	0.44	0.49	0.54	0.61	0.51
150	12	86007230	1541934	14374	CATTTCATTTYCCCCAAATTA	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86012640	11104293	14375	TCTGTTCACCWAATATCTTTC	0.47	0.06	0.06	1.04	1.27	0.84	0.47	0.06	1.24	1.23	0.85	0.49
150	12	86053941	17605515	14376	AGGCATAACARAAGTAAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86066313	1409597	14377	CCATTAGGCCYGAACAGGGTG	0.61	0.07	0.08	1.30	1.67	0.90	0.65	0.06	1.47	1.65	0.91	0.65
150	12	86075377	1409598	14378	CTCCAAAAAAMATAAGTAAGC	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86124724	2038951	14379	GAACTCTCTGYGCTTTTGCGT	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86130376	7484348	14380	GAAGTAATATYAGACTCCTGC	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86146673	10777025	14381	GGTTTTAGAAMACATTGTAGC	2.11	2.62	2.71	1.60	1.04	1.43	0.85	2.63	1.65	1.00	1.39	0.83
150	12	86156526	10506939	14382	TGTTACTTAAWAGCTCTGTAA	1.45	1.53	1.52	1.60	1.51	0.99	1.15	1.44	2.05	1.37	0.95	1.12
150	12	86163902	11104383	14383	ACAAAGTAAAMCATCAGAAAA	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86170493	17605650	14384	ATAAAGCTATYATCGTGGAAA	0.07	0.00	0.00	0.75	2.48	1.05	1.48	0.00	1.00	2.01	1.01	1.41
150	12	86176695	17577895	14385	TTGAATACATYAAATATCCTT	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86182913	17605785	14386	GCACTGTTGGRCAAGTTACCT	0.04	0.11	0.07	0.79	3.24	1.52	1.94	0.04	1.02	2.49	1.42	1.81
150	12	86201990	17014554	14387	TGGCAGCAGARACATGCTCAA	0.67	1.08	1.08	2.43	2.70	1.25	0.92	1.01	2.63	2.27	1.19	0.89
150	12	86208533	7296764	14388	TTGTAGGATAYTGGGTGACAA	1.70	2.25	2.32	2.03	1.56	1.25	1.06	2.25	2.35	1.44	1.18	1.03
150	12	86214644	10858579	14389	AGCGAAAAGAWGCATTCTGTG	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86217285	4640012	14390	TTTTGAAAAASGAATAAAATA	1.79	1.89	1.89	0.87	1.36	1.17	1.03	1.86	0.93	1.31	1.19	1.02
150	12	86234332	7967976	14391	GGGAAAAAAARTCCATTAAAA	0.26	0.30	0.34	0.60	1.03	1.26	0.87	0.29	0.59	1.02	1.21	0.88
150	12	86245413		14392	TGGCGTGAAGKTACCTACATA	0.52	0.90	0.90	0.39	0.65	0.71	1.01	0.84	0.39	0.67	0.71	0.99
150	12	86272799	4842565	14393	AAGGAAACATRGATGCTTCAA	0.31	0.62	0.62	0.32	0.08	0.45	0.49	0.57	0.29	0.07	0.45	0.51
150	12	86280067	17014724	14394	CTTAGGCAGCSAAGAGCCCTA	0.10	0.05	0.05	0.17	0.06	0.17	0.27	0.02	0.18	0.03	0.18	0.28
150	12	86288520	7964913	14395	GGGTGCCTCTRTTCCTATTTC	0.43	0.79	0.79	0.40	0.22	0.23	0.67	0.76	0.42	0.21	0.25	0.69
150	12	86296755	17325004	14396	CAAAGACGACSTTTCTTCCAC	0.39	0.73	0.73	0.44	0.44	1.12	0.84	0.68	0.45	0.47	1.09	0.86
150	12	86303034	4842457	14397	ACAAAGGAAAKACAACTAGAA	0.05	0.02	0.02	0.25	0.32	1.18	0.83	0.00	0.25	0.33	1.19	0.83
150	12	86310394	4442620	14398	GTTACAGATAYAAGAAAGCAT	0.34	0.16	0.17	0.05	0.30	0.29	1.45	0.15	0.05	0.32	0.29	1.40
150	12	86343785	7953581	14399	TGCTTATATTRCGTGTGGGTA	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86357443	4842462	14400	ATGAACAAGAYAGGAGTTATA	0.04	0.31	0.31	0.81	0.46	0.55	0.40	0.25	0.82	0.46	0.56	0.42
150	12	86365433	12231082	14401	AGACAAACCAYGTGGGCCTCT	0.58	0.93	0.93	0.90	1.57	0.51	0.55	0.84	0.98	1.43	0.51	0.56
150	12	86372557	4842464	14402	TACTTCATTAYTGATGTCTGG	0.80	1.22	1.22	1.41	1.36	0.74	0.64	1.18	1.61	1.34	0.73	0.67

150	12	86386121	17325685	14403	AATTAACATAYGTCCTATAAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86410068		14404	CATTTGCTTTYCATAAAAATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86419830		14405	ACATTATTTTYTAAAAGTCAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
150	12	86434281	11104543	14406	TGTTTTATGTYGCTTCTGGAT	1.05	1.54	1.54	1.35	0.77	0.79	0.67	1.41	1.51	0.75	0.80	0.67						
150	12	86464566	12423369	14407	ATAATTTCATMCTTTTAATGC	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86471242	790389	14408	ATGGCTCCTGMCCACTTGTGC	1.07	1.38	1.38	0.38	0.70	0.73	0.73	1.26	0.37	0.75	0.75	0.75						
150	12	86484163	2806311	14409	GATAAATGCTYCCTCTTTATA	0.19	0.04	0.04	0.86	0.38	0.64	0.68	0.01	0.98	0.43	0.65	0.72						
150	12	86493875	12425656	14410	AGATGCAGCASGTATTCAACA	1.03	1.67	1.67	1.04	0.65	0.47	0.58	1.48	1.25	0.65	0.48	0.60						
150	12	86499595	17326902	14411	CTGCACATTAYGATTTTTTTT	1.02	1.42	1.42	0.80	0.60	0.58	0.47	1.30	1.02	0.66	0.59	0.46						
150	12	86507732	790446	14412	TAATGGTATCRGGAGGTGCTA	0.99	1.26	1.26	0.95	0.89	0.60	0.47	1.19	1.09	0.91	0.64	0.48						
150	12	86525367	1398424	14413	ACTTGGTTTAYATGTACAAGA	0.81	1.42	1.42	0.97	1.08	0.67	0.47	1.30	0.96	1.10	0.72	0.52						
150	12	86534445	17386404	14414	CTGGTAAATASTTTTGCGTAT	0.81	1.42	1.42	1.16	0.72	0.86	0.68	1.31	1.40	0.76	0.87	0.67						
150	12	86540570	17327313	14415	GGTGAGTTACMCAAAGATAAG	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86547183	17015022	14416	CATAATACTGYTCCTTGGATG	0.94	1.28	1.54	0.89	1.10	0.72	0.66	1.39	1.16	1.15	0.76	0.69						
150	12	86555419	17386755	14417	TTCAAATGAAYATGCACAAGG	0.90	1.51	1.51	0.82	1.10	0.75	0.46	1.34	1.16	1.19	0.79	0.50						
150	12	86561449	17386977	14418	TTTACTTTAARAACACCAGAC	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86574612	17327943	14419	TCTTTGGAAARTCAGTGAAGA	0.92	1.54	1.54	0.82	0.75	0.62	0.62	1.44	1.18	0.77	0.64	0.65						
150	12	86581945	17015032	14420	TCTTTTTCACKCTAGGAAAAT	0.92	1.54	1.54	0.81	0.62	0.62	0.62	1.40	1.03	0.64	0.66	0.63						
150	12	86588851	17015038	14421	GTGGACTATASTCAATGATCA	0.46	0.92	1.02	0.74	0.79	0.62	0.38	0.97	0.83	0.83	0.67	0.42						
150	12	86618574	10858631	14422	TATGATGTAGYCAATAACTTT	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86624952	10506945	14423	TATTATCATCYGGGAAATTAG	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86637820	17329264	14424	CAGTCTAAAAYCCTCACTCTT	0.20	0.29	0.29	0.74	0.79	0.54	0.37	0.25	0.73	0.84	0.57	0.41						
150	12	86649100	17329285	14425	CACAAAGATGKTGAATGCCAT	0.20	0.29	0.29	0.29	0.46	0.53	0.20	0.28	0.23	0.49	0.58	0.18						
150	12	86655097	17389075	14426	CTGCTATATGMCAAATCAAGA	0.20	0.29	0.29	0.10	0.11	0.15	0.07	0.27	0.10	0.08	0.16	0.07						
150	12	86673108	2247050	14427	TTCCATTTCTYTTGACAGATA	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86683574	17389674	14428	TTGTTGAATARTTCTTATCTT	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86695773	17330765	14429	CAACAAAAGGRTACAAAAATG	-	-	-	-	-	-	-	-	-	-	-	-						
150	12	86709812	10506946	14430	TCACAGCCAAKAGTCAAATAT	0.13	0.09	0.09	0.16	0.05	0.01	0.05	0.06	0.09	0.05	0.00	0.06						
151	12	124113077	7307700	14431	GACATTTGTARAAGAATAAGC	0.24	0.52	0.52	0.29	0.08	0.20	0.60	0.51	0.28	0.08	0.24	0.60						
151	12	124151665	3751179	14432	GACACGCCAGSCAGTCTGACT	0.30	0.54	0.70	0.32	0.14	0.46	0.99	0.56	0.30	0.14	0.45	0.98						
151	12	124160965	1029075	14433	CATTCCCCAASCTCAGGTCAC	0.54	0.23	0.23	0.23	0.46	0.35	0.89	0.21	0.19	0.46	0.35	0.89						
151	12	124170678	4765223	14434	GGGGTGTCCTYGACACTGTCT	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124203697	6488991	14435	AACCCGTTGGKGGGGGGGTCT	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124228159	4765230	14436	TTGGGATGGGWAGGAGAGAGG	0.21	0.29	0.26	0.59	0.24	0.93	0.46	0.19	0.64	0.28	0.92	0.46						
151	12	124241020	4237993	14437	TTTTTTAGTGRTGGAACTCTT	0.63	0.88	0.88	0.45	1.75	1.09	0.44	0.86	0.46	1.59	1.07	0.45						
151	12	124254686	767355	14438	GTTCCCAGATSCCCCCCCAGG	0.72	0.84	0.80	1.78	2.27	1.01	0.84	0.75	2.04	2.07	1.03	0.85						
151	12	124263922	7963538	14439	TTAGTTTTCTRTCCATTAACC	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124281862	7300238	14440	ACTCCCTCTTYGGTCCAGCGA	3.06	3.02	3.02	2.41	1.75	1.37	1.11	2.84	2.92	1.62	1.30	1.09						
151	12	124295719	7958584	14441	TCTTCTGCCTYTGTGTGTCAG	0.17	0.28	0.31	2.58	1.85	1.73	2.82	0.25	3.24	1.76	1.70	2.68						
151	12	124306276	7956580	14442	GTTAGGGATTRCAGCAAAAGG	0.16	0.40	0.36	1.18	1.36	2.67	1.29	0.28	1.27	1.32	2.50	1.27						
151	12	124320871	326363	14443	GGTTGAAAACYCTGGCGTCAT	0.48	0.83	0.83	0.44	1.49	1.65	1.71	0.78	0.44	1.38	1.63	1.66						
151	12	124373302	1352871	14444	AATAGAAATAWTCATTAGAGG	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124397174	1388561	14445	CTGAGATGGAKAAACATCTGT	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124424975	3809261	14446	TTATCTTCACWCCTGCTGCCG	0.21	0.43	0.29	0.18	0.51	1.11	1.51	0.24	0.17	0.52	1.15	1.51						
151	12	124474900	1844915	14447	GTATCTAGAAWTGAACTGCTC	0.08	0.00	0.00	0.09	0.30	0.72	1.47	0.00	0.06	0.33	0.79	1.44						
151	12	124485669	7310566	14448	TTGCAGTGTCRTCCCTCCACC	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124523031	12578198	14449	GTTTGGGATAYAGTTTTCCTA	1.29	0.02	0.03	0.18	0.15	0.38	0.66	0.00	0.13	0.18	0.40	0.68						
151	12	124529455	2526738	14450	CAGGTAACTTRTGGATTGGAA	0.38	0.56	0.58	0.27	0.19	0.07	0.12	0.56	0.23	0.18	0.09	0.12						
151	12	124533120	11058221	14451	ATCTCTTCTCSCATGATCTGC	0.07	0.24	0.22	0.33	0.11	0.10	0.08	0.17	0.34	0.11	0.09	0.07						
151	12	124544606	10459109	14452	TTCATATTCTRTAACAGGCAT	0.34	0.22	0.22	0.11	0.05	0.11	0.58	0.19	0.08	0.02	0.11	0.57						
151	12	124554544	7136142	14453	AGGAGGCTCARTGTTAGTGGA	0.59	0.08	0.09	0.02	0.02	0.08	0.48	0.07	0.01	0.01	0.10	0.52						
151	12	124561404	12811466	14454	ATGACAAATGKTTTCTTTTCG	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124568003	10846917	14455	TATATCACTTYACAATGCAGA	0.73	0.21	0.21	0.04	0.02	0.06	0.09	0.20	0.02	0.01	0.08	0.09						
151	12	124578814	917058	14456	TTCAGTGCCCRTCACAGTGGC	0.71	0.22	0.21	0.13	0.06	0.01	0.01	0.18	0.09	0.06	0.01	0.00						
151	12	124583362	2189792	14457	ACTCCAACTTSTTTTTAACCA	-	-	-	-	-	-	-	-	-	-	-	-						
151	12	124595681	969791	14458	AAGGGAAAAAYGTGAATTTAG	0.18	0.27	0.27	0.34	0.11	0.00	0.01	0.23	0.34	0.11	0.01	0.01						
151	12	124604729	16919300	14459	TGTAGGCTAAWGGTGGAGCTT	0.29	0.50	0.39	0.05	0.03	0.03	0.01	0.29	0.04	0.03	0.03	0.01						
151	12	124615038	16919322	14460	TTAATTTTCARTGGGCGTCTG	0.19	0.28	0.28	0.04	0.01	0.05	0.11	0.23	0.01	0.00	0.05	0.13						
152	13	28993758	17660515	14461	AAATGCAATCRCGAAAGGAGG	0.51	0.50	0.50	0.19	0.61	0.41	0.51	0.37	0.14	0.67	0.47	0.51						
152	13	29002154	6490409	14462	GCACAAGTCARATGTCGGCGA	0.31	0.03	0.03	0.07	0.03	0.48	0.29	0.00	0.07	0.03	0.50	0.32						
152	13	29010971	914362	14463	TTCTCAATATYCCTTTTGGCA	0.04	0.04	0.04	0.01	0.06	0.02	0.19	0.00	0.00	0.06	0.01	0.19						
152	13	29012683	11617418	14464	GTGTGACGTTYTCACCTTGAA	0.01	0.03	0.08	0.00	0.01	0.06	0.04	0.05	0.00	0.00	0.04	0.04						
152	13	29023816	11616506	14465	TGGGGCGGCGYGGGGAAGAAT	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29036036	476506	14466	AGGCCATCTTKAGCCGGTGAG	0.04	0.03	0.04	0.03	0.05	0.05	0.15	0.00	0.00	0.05	0.04	0.13						
152	13	29048630	11839516	14467	CTCTCCCTACRTTCCAAAGGC	0.01	0.08	0.08	0.26	0.14	0.23	0.08	0.04	0.22	0.13	0.24	0.09						
152	13	29062630	7981502	14468	GTCACTGAGCRCAAGGTGCAT	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29070751	11618507	14469	AACATCTAAGKTTAAGGTTGA	0.16	0.25	0.25	0.51	0.46	0.18	0.09	0.20	0.50	0.49	0.18	0.10						
152	13	29085453	9506207	14470	AGGAGCAACCWGCACCAACAG	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29092288	280942	14471	CTTCCCATTCYTCTTTCTAAA	1.02	0.96	0.98	0.80	0.65	0.19	0.31	0.95	0.84	0.70	0.19	0.33						
152	13	29127665	538385	14472	TTCCGATCCAYAGGAAGAAGA	0.85	0.20	0.20	0.67	0.39	0.69	0.20	0.18	0.75	0.42	0.72	0.20						
152	13	29129038	9551714	14473	GATTTTGACAYGTCCTCTGAC	1.48	0.24	0.25	0.88	1.06	0.47	0.30	0.22	1.03	1.09	0.49	0.32						
152	13	29152578	12876062	14474	GATCACTTAARGTGGGCAAGA	1.01	1.22	1.22	1.13	1.13	0.76	0.97	1.17	1.14	1.12	0.79	0.97						
152	13	29164608	12184805	14475	GGGCTCTGGAYGTACCAAAGT	0.29	0.48	0.50	0.92	0.93	1.28	3.32	0.48	0.93	0.94	1.21	3.06						
152	13	29179760	17625129	14476	GGGCCTTGTCYGTACCTAGCT	0.58	0.66	0.66	1.36	0.83	2.82	3.39	0.61	1.45	0.86	2.69	3.10						
152	13	29188947	9551722	14477	CCCATCATGARCGATGGATTC	0.51	0.73	0.78	1.34	3.70	2.76	2.39	0.69	1.42	3.33	2.55	2.31						
152	13	29201509	12584812	14478	ATGTACATAGRTCATCAGCAA	0.13	0.12	0.12	2.17	3.30	2.90	1.93	0.10	2.23	2.96	2.65	1.83						
152	13	29207896	11147396	14479	GGTTACTCATYCCCGGAAACA	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29220170		14480	GAAGGGAAATRTGCCAAGGTG	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29231806	7331353	14481	TTATCTCATCKTTTTGTAAGC	2.24	1.40	1.40	3.85	2.36	2.76	2.78	1.32	3.95	2.20	2.48	2.48						
152	13	29238585	1058650	14482	CTAATATTTCYGCACAATAAT	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29245835	2892463	14483	CCTCTCCAGGKATCTAAAATT	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29252995	7992684	14484	ACAGCAGTTTRTAAGTTTATA	1.06	0.95	0.95	0.93	3.47	2.17	3.17	0.85	1.04	2.90	1.96	2.79						
152	13	29266798	17502694	14485	TAGTTTAGACYCTTATGACTA	0.00	0.02	0.02	0.33	0.42	3.36	2.13	0.00	0.32	0.44	2.87	1.93						
152	13	29277613	17073897	14486	GAAAGCATGGKCATCTCCACT	0.51	0.91	1.00	0.30	0.28	1.41	2.14	0.86	0.28	0.29	1.31	1.96						
152	13	29283510	1323931	14487	TCCTAAGAGTRTTTTAAAATG	0.14	0.32	0.36	0.44	1.25	1.09	0.84	0.28	0.45	1.20	1.06	0.85						
152	13	29294469	12872400	14488	CCTAGCAATAKGATAAAGTAC	0.89	0.34	0.34	1.44	1.39	0.84	0.54	0.30	1.46	1.34	0.84	0.55						
152	13	29308186		14489	TGAATCAAAGYAGAAGGATTA	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29318309	2182129	14490	GCAACATAAAKAAATAAATAC	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29335333	278048	14491	TACAAATAGTWTACTAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-						
152	13	29340944	17502944	14492	TATAGCACCAYGAGCGTGTTT	2.17	2.41	2.41	1.40	1.20	0.52	0.38	2.30	1.55	1.13	0.57	0.35						
152	13	29347608	1033930	14493	TGGAACCATGKGAGTGAGGAG	0.53	0.51	0.53	1.71	0.74	0.52	0.32	0.51	1.86	0.74	0.54	0.33						
152	13	29354114	11616444	14494	GAACTTGGAAYGGAGGATGCA	0.87	0.20	0.20	0.22	1.02	0.42	0.48	0.20	0.23	1.05	0.48	0.49						
152	13	29360712	9551767	14495	GTTCTGAAACYGACTCAACTA	0.64	0.96	0.96	0.57	0.75	0.92	0.32	0.91	0.57	0.71	0.93	0.34						
152	13	29366648	8000402	14496	CCGGGACCATRCAAGCAGGTA	0.71	0.91	0.95	1.27	0.96	0.39	0.33	0.92	1.23	0.96	0.39	0.31						

152	13	29373455	17503160	14497	AAGCATCCCAKTAATCCTTTT	0.65	1.01	1.01	1.26	0.52	0.37	0.34	0.95	1.28	0.53	0.41	0.33
152	13	29386370	11617065	14498	AGAATAATCARGGACTTGGCT	0.65	0.40	0.40	0.85	0.44	0.35	0.26	0.34	0.90	0.46	0.38	0.26
152	13	29393293	9508589	14499	GAGGCTCCCAKGTTGGCAGCT	0.30	0.36	0.36	0.24	0.55	0.30	0.42	0.32	0.21	0.56	0.30	0.40
152	13	29400315	7992473	14500	ACCACTTGCTYATGAAACTCA	0.68	0.32	0.28	0.29	0.01	0.44	0.51	0.23	0.28	0.01	0.44	0.50
152	13	29407719	17074063	14501	ATGCAGTGGCRGAGCAAGACG	-	-	-	-	-	-	-	-	-	-	-	-
152	13	29413610	646917	14502	GTAAATAATCYGCAGAGCTTG	0.05	0.17	0.17	0.21	0.24	0.11	0.59	0.17	0.19	0.24	0.10	0.62
152	13	29419992	503693	14503	CAGCAGAGCAMGGATTTTTTC	0.17	0.38	0.38	0.50	0.22	0.47	0.35	0.37	0.50	0.23	0.50	0.37
152	13	29425868	866019	14504	ATACCCTTACRTCAATATAGC	-	-	-	-	-	-	-	-	-	-	-	-
152	13	29433222	643508	14505	TCACAAATTCRTGCCAGTGGT	-	-	-	-	-	-	-	-	-	-	-	-
152	13	29439002	9579501	14506	TTACCTAAATYGGAAAATAAA	0.74	0.93	0.91	0.57	0.52	0.32	0.41	0.86	0.61	0.52	0.35	0.41
152	13	29452360		14507	AGAGCTCTTAYACAACACTTG	1.07	0.99	0.91	0.42	0.33	0.20	0.28	0.81	0.43	0.32	0.20	0.28
153	13	31737224	9534017	14508	TTAGACAAGTYCCTTTCCCAC	0.48	0.64	0.64	0.72	0.78	0.41	0.86	0.59	0.73	0.78	0.42	0.86
153	13	31745833	12877839	14509	AAATGCACAGWTTCCGTGCTG	-	-	-	-	-	-	-	-	-	-	-	-
153	13	31752998	17692070	14510	CTATTTCCCARACATTCCAAC	-	-	-	-	-	-	-	-	-	-	-	-
153	13	31763177	9595279	14511	GGTGGTTAGAYGTGAGGTCAG	0.08	0.20	0.20	0.51	0.21	0.68	1.70	0.18	0.48	0.22	0.70	1.64
153	13	31771953	762891	14512	AGACCTAAGAKTCACCCCAGG	0.02	0.13	0.13	0.11	0.39	1.88	2.44	0.11	0.08	0.40	1.81	2.34
153	13	31779775	2032471	14513	ATTAAAAAAAWTTCAAGCGAA	0.06	0.22	0.22	0.09	2.04	1.22	2.01	0.20	0.09	1.94	1.21	1.95
153	13	31786424	10492394	14514	GGATTACTGAYTATCAAACTA	0.43	0.42	0.42	1.69	1.52	1.14	1.04	0.34	1.71	1.49	1.13	0.99
153	13	31791791	9534174	14515	TATTTCTGCARGCTATCACAG	2.20	3.02	3.03	1.50	0.88	0.91	1.24	2.93	1.60	0.89	0.91	1.23
153	13	31798933	3752451	14516	CAAATACATTWAGTGGTAGTC	-	-	-	-	-	-	-	-	-	-	-	-
153	13	31804729	144848	14517	AAATGTAGCAMATCAGAAGCC	1.23	1.18	1.16	1.37	0.65	0.46	0.55	1.11	1.56	0.66	0.48	0.55
154	13	47287583	7992218	14518	AATTTTTCTTSCTAAATTCAT	0.88	1.09	0.95	0.65	0.40	0.40	0.31	0.89	0.65	0.42	0.43	0.35
154	13	47294709	12875794	14519	ACCTCAAGGCKTTGCTTACAA	0.10	0.26	0.26	0.24	0.63	0.36	0.38	0.23	0.21	0.67	0.38	0.39
154	13	47300251	9567925	14520	ACTATTCTACRCTCTATAGAA	0.10	0.10	0.00	0.18	0.16	0.61	0.52	0.00	0.09	0.17	0.64	0.55
154	13	47308847	753372	14521	TCGTCCTTAAYGAGTTTGACT	0.22	0.10	0.10	0.27	0.29	0.21	0.62	0.03	0.19	0.31	0.23	0.64
154	13	47314300	7990189	14522	GAAGGGAAATMCAACCTTGCA	0.10	0.11	0.11	0.21	0.16	0.98	0.53	0.07	0.16	0.20	0.99	0.51
154	13	47317020	4942705	14523	ATTTAGCTCTKATTATGTCTA	0.08	0.11	0.03	0.11	0.31	0.31	1.15	0.00	0.04	0.34	0.34	1.11
154	13	47331112	17070931	14524	ATATTCACATKTCAGAAGCCC	0.16	0.05	0.05	0.50	0.30	0.55	0.49	0.00	0.52	0.32	0.55	0.52
154	13	47337638		14525	TTACAATTGGYTTTTTTGGCT	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47351959	9567940	14526	TCTTACTTTTYGCATGCTATT	1.41	1.61	1.61	0.72	0.65	0.47	0.68	1.56	0.75	0.74	0.47	0.72
154	13	47365868	9534856	14527	TATAACAAACMTTGATCGAAT	0.08	0.23	0.23	1.06	0.56	0.74	0.91	0.21	1.41	0.60	0.70	0.90
154	13	47376038	9534860	14528	TCATGAAAAAYGGAGCATGCT	0.08	0.23	0.23	1.37	1.28	0.86	0.95	0.21	1.62	1.23	0.83	0.92
154	13	47404499		14529	AAGCATGAATKTTGGCAGCTT	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47411558	2094196	14530	GCAAGGTTAAYAGTCAAAATT	1.16	1.57	1.54	1.41	2.52	1.47	0.77	1.46	1.46	2.16	1.32	0.78
154	13	47416959	1326140	14531	CACATTAACTSGGTAAATTCA	0.71	1.16	1.20	1.39	1.89	2.54	1.82	1.11	1.64	1.71	2.10	1.63
154	13	47426008	7333821	14532	CACATCCCTTRTACTTTGATA	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47443619	7335962	14533	AATTTAATTCRATAGCAGCAT	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47457165	7981492	14534	AAGAAATCTARTTTAACAAAG	0.46	0.12	0.12	1.65	1.92	2.35	2.49	0.08	1.61	1.62	1.98	2.10
154	13	47483064	9526431	14535	AGTTAAGATAMGTTGATGAAG	2.22	2.48	2.60	1.67	1.74	1.21	1.69	2.51	1.65	1.58	1.20	1.50
154	13	47484300	9316343	14536	CTAATTCTTARAAGGACTGGA	0.79	1.23	1.23	1.69	1.48	1.15	1.53	1.19	1.91	1.36	1.14	1.41
154	13	47500961	840430	14537	TGGGCTGATGYTCCTTTCTTG	2.23	2.65	2.77	1.65	1.51	1.77	1.68	2.62	1.84	1.34	1.60	1.48
154	13	47510373	17071168	14538	GCAGCCCGATRTTGTCAGCTA	1.87	2.21	2.21	1.34	2.04	2.03	1.90	2.09	1.62	1.82	1.78	1.74
154	13	47522891	7997347	14539	TGTTTCAGACYGAACTTCCTC	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47528301	840437	14540	AATGTTTTGTMATATCCTTAA	1.80	2.06	2.06	2.19	2.42	2.28	1.96	1.94	2.42	2.11	2.01	1.77
154	13	47548684		14541	CCTACCTACAMTGACAGTATA	0.26	0.07	0.07	2.27	2.81	2.20	2.23	0.00	2.80	2.50	1.98	1.99
154	13	47556552	943067	14542	TAAACTGTTAKGAAGATGGAA	2.24	2.50	2.48	2.41	2.90	2.69	1.75	2.37	2.75	2.52	2.34	1.65
154	13	47565879	9567994	14543	TTAATTTCTGSTGTCTAGGTG	1.04	1.34	1.31	1.95	3.26	2.46	1.02	1.23	2.08	2.70	2.16	1.00
154	13	47574969	17429111	14544	AGAAGGTGGCKGGAATAAGTA	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47583917	1410116	14545	GCAAAAATGTMCCCTGTTGAC	2.17	2.41	2.41	1.99	1.80	1.48	0.57	2.29	2.30	1.69	1.39	0.55
154	13	47594325	9568005	14546	GGGAGATGCCYATATTGTCTG	1.36	1.85	1.80	1.81	1.30	0.49	1.21	1.72	2.01	1.26	0.48	1.15
154	13	47601583	9534964	14547	AACATGGCACYGCTCCTTGCT	0.17	0.01	0.03	0.43	0.93	0.84	0.74	0.00	0.43	0.93	0.84	0.79
154	13	47613754	7317685	14548	AAAGTGGTGCRAGGATATTTG	-	-	-	-	-	-	-	-	-	-	-	-
154	13	47624771	9526457	14549	TTTTGGAAGGRCACACCAAGA	0.03	0.16	0.16	0.00	0.58	1.15	0.58	0.15	0.00	0.61	1.10	0.61
154	13	47629504	2765074	14550	AGATCAGTCARTTAACTCTGG	0.17	0.12	0.12	0.10	0.07	0.32	0.82	0.10	0.07	0.07	0.37	0.80
154	13	47644365		14551	CCCTGAACCTKGACTATGCTA	0.05	0.05	0.05	0.08	0.06	0.05	0.29	0.03	0.02	0.07	0.04	0.26
155	13	50554432		14552	ATGGAATTTTKCAGGCTGTGT	0.45	0.57	0.57	0.96	1.05	0.43	0.35	0.50	0.95	1.03	0.45	0.35
155	13	50561252	7336329	14553	TTATATGGGCRTTTTGAAAAT	1.39	1.61	1.70	0.71	0.13	0.50	0.80	1.62	0.70	0.12	0.51	0.84
155	13	50577997	9316520	14554	AGTATGAGTTYCGACATGATA	-	-	-	-	-	-	-	-	-	-	-	-
155	13	50588385	8002769	14555	GAAGGGGCACRTCTGACAATG	0.02	0.08	0.08	0.66	0.36	0.41	0.49	0.06	0.65	0.37	0.43	0.52
155	13	50591509	9563026	14556	TCAGTGGGTGYGAATGGCTCA	0.13	0.05	0.05	0.44	1.32	0.37	0.14	0.03	0.40	1.28	0.36	0.13
155	13	50622936	1022960	14557	CATTAGCACTYGCTGAGGTAA	1.72	0.79	0.79	0.99	0.62	0.65	0.56	0.80	0.98	0.63	0.65	0.61
155	13	50639277	12560357	14558	AATATTTGTCRAGGGCTAAGA	1.52	1.20	1.20	0.88	0.56	1.07	0.73	1.17	0.86	0.62	1.07	0.75
155	13	50654440	12876228	14559	CTGCACTTTCYTATGAAAACC	-	-	-	-	-	-	-	-	-	-	-	-
155	13	50666777	9568542	14560	ACTTAAAAGAYTGGGACCTTA	0.07	0.26	0.26	0.25	0.82	1.23	0.78	0.22	0.23	0.83	1.21	0.79
155	13	50674737	17837200	14561	CTACAGGCTGRTGACCCAAGG	-	-	-	-	-	-	-	-	-	-	-	-
155	13	50680975	6561621	14562	TAAACCTCTCYGTTACCCGAT	0.13	0.36	0.34	1.23	0.78	0.33	0.56	0.31	1.31	0.78	0.32	0.56
155	13	50692556	4942974	14563	GTGATCACTTSAAGGTTCTTG	0.22	0.49	0.49	1.65	0.93	0.58	1.03	0.44	1.80	0.95	0.59	1.04
155	13	50706361	4942978	14564	CATTTGTTCCYGAGTTCACAG	0.50	0.32	0.32	0.78	1.52	2.41	1.13	0.27	0.82	1.47	2.18	1.11
155	13	50713442	9563038	14565	TCTCTGCGTCRTTTAGAATGT	0.84	1.20	1.20	0.27	2.65	1.55	1.16	1.12	0.24	2.41	1.52	1.17
155	13	50719963	2408302	14566	TGGAGTTACTSACTGGCAGAA	0.27	0.38	0.38	2.56	1.24	1.22	1.41	0.33	2.60	1.18	1.19	1.41
155	13	50726961	9568561	14567	GTTCTCCTTAYACGTTTTTGT	0.10	0.06	0.06	2.15	1.13	0.71	0.83	0.04	2.29	1.09	0.71	0.84
155	13	50733486	9535629	14568	CCGAGACCCTRAAGGAAATCG	0.27	0.33	0.33	0.40	1.83	0.11	0.10	0.29	0.40	1.73	0.10	0.10
155	13	50740514	9596491	14569	ATAATTTTATRAACTCTCTTA	-	-	-	-	-	-	-	-	-	-	-	-
155	13	50746378	751702	14570	CACAAGAGTCRCTACTGATAC	0.05	0.00	0.00	0.38	0.37	0.23	0.06	0.00	0.39	0.38	0.24	0.05
155	13	50748889	17194879	14571	CGTTGCCCAAYTTTCTTGAGA	-	-	-	-	-	-	-	-	-	-	-	-
155	13	50758644	7981566	14572	GCCCAAGAACYGGCCGGCTAG	0.79	0.27	0.27	0.42	0.06	0.15	0.24	0.22	0.44	0.05	0.17	0.23
155	13	50765291	2153512	14573	ACGGGCTCGCYGGCAGCCATA	0.14	0.34	0.31	0.06	0.10	0.03	0.11	0.27	0.06	0.08	0.03	0.10
155	13	50778896	6561632	14574	TAAAGTTTCTRTGGAAAAACA	-	-	-	-	-	-	-	-	-	-	-	-
155	13	50785140	9316533	14575	AATTCTGGTTRACAAAGTGAC	0.02	0.11	0.11	0.27	0.03	0.02	0.04	0.08	0.27	0.04	0.02	0.04
156	13	65187336	1343930	14576	CAACACCAACRTGAGTTCAAT	0.10	0.14	0.14	0.41	0.53	0.47	0.45	0.10	0.39	0.56	0.48	0.46
156	13	65195053	4589435	14577	AAATTAAGAAYGCTGGATGTA	0.55	0.97	0.97	0.44	0.27	0.62	0.72	0.90	0.42	0.26	0.58	0.72
156	13	65203759	17450679	14578	TTGTAAGCCAYGATGATTTTG	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65237874	4628840	14579	ACATACATTTYGGTGTATTTT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65253763	9540552	14580	AAAAGAACAGWAAGTAGCTTA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65262258	9630336	14581	TTTGACAGAAYGAAGGTGATA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65270936	17077670	14582	GAGAACAATTKTAAATACACC	0.99	0.03	0.03	0.67	0.70	0.46	0.50	0.00	0.64	0.70	0.49	0.49
156	13	65280392	1930769	14583	TCATTCTGACWCATCTGGGGC	0.56	0.94	0.90	0.79	0.80	0.35	0.37	0.83	0.77	0.80	0.37	0.39
156	13	65281726	9571482	14584	GTTAAAGAGCMCTGTGAAATT	0.20	0.38	0.37	1.21	0.68	0.58	0.28	0.34	1.33	0.71	0.60	0.30
156	13	65289506	9540562	14585	ATTAATATGTYCCTTCAGAGA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65300288	17549502	14586	ATAAATCCAGRGAAAATAAAA	0.67	1.03	1.08	0.58	0.81	0.41	0.36	1.03	0.63	0.85	0.40	0.33
156	13	65305727	9571490	14587	TCAAATTTTAYGTTATGTTTC	0.59	0.64	0.74	0.42	0.56	0.38	0.33	0.73	0.41	0.59	0.41	0.31
156	13	65319235	9571495	14588	GCCATTGTAARCTTCTAGAAT	0.84	1.09	1.09	0.51	0.26	0.42	0.32	1.05	0.47	0.28	0.47	0.33
156	13	65325758	17078344	14589	TTTGGCTGTGWGAGAAATAAA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65331750	9540570	14590	GAACATTCTGKGAACATATTC	-	-	-	-	-	-	-	-	-	-	-	-

156	13	65345215	1460658	14591	TTGCCTGATAKGGCCTATGCC	0.10	0.08	0.08	0.48	0.34	0.38	0.31	0.06	0.48	0.32	0.37	0.33
156	13	65351753	1460659	14592	AAGTACCAAGRTAATTGAACA	0.06	0.08	0.08	0.29	0.64	0.38	1.08	0.05	0.24	0.63	0.37	1.08
156	13	65358030	9571511	14593	AAGTTTTAGTYCCCTGCAGCA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65365114	9592437	14594	TAGCATGGAARTGATAGTCAC	0.32	0.64	0.63	0.45	0.46	0.94	1.18	0.57	0.45	0.47	0.94	1.18
156	13	65384389	9540604	14595	TATCACTGCTKTCATTTCTTT	0.13	0.14	0.14	0.94	0.98	1.55	1.25	0.12	1.00	0.98	1.50	1.23
156	13	65396244	17079605	14596	CCTAATATTTMCCCCACAAGA	0.29	0.56	0.56	1.47	2.58	1.66	1.44	0.52	1.68	2.34	1.57	1.43
156	13	65403169	11616834	14597	TCATTCCCTAWCATATCCCAG	0.50	0.79	0.79	3.01	2.04	1.95	1.69	0.74	3.18	1.89	1.80	1.61
156	13	65409806	7326862	14598	TATATATATTKGAAAGTCACC	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65415759	9529002	14599	TAATAGCACTRTAACTTTTAT	0.09	0.00	0.04	0.53	2.52	2.09	1.28	0.02	0.53	2.33	1.93	1.25
156	13	65421138	17079885	14600	AGATATGTACRTTTTTCAATG	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65434091	17837226	14601	CGATTCTCTAYAGTGTTTAGC	1.14	1.68	1.68	0.94	0.52	1.79	1.41	1.60	1.05	0.62	1.75	1.33
156	13	65438576	3843944	14602	TGGGGTTTACYACTGAAGCAT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65462424	7988764	14603	TTAATTAGCAYATCATGTTAC	1.01	1.53	1.53	1.32	0.53	0.45	1.47	1.46	1.77	0.56	0.48	1.43
156	13	65468454	11841425	14604	ACCTCTATTAYGTTACACCCT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65475125	17837232	14605	GTGGTAAGTGMAGTTTTATTC	1.07	1.61	1.61	1.05	1.26	0.48	0.25	1.54	1.17	1.21	0.48	0.27
156	13	65488880	17080582	14606	TTACTATTTTWAAAAATCTAT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65491884	9571528	14607	GATTCATCTCRTTTTAAATGT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65502471	2874734	14608	GAATACTTACRATTTTAGAAA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65511917	9317556	14609	CTTCCTTGTAYTTGTAATATA	0.83	0.88	0.88	0.98	0.94	0.79	0.29	0.86	1.12	0.95	0.83	0.29
156	13	65517740	2482974	14610	TAAGTAAAATMATCAATTAGC	0.68	0.64	0.64	0.76	0.71	0.58	0.56	0.61	0.88	0.78	0.57	0.60
156	13	65523553	17195090	14611	TTTATGCCAGRGAATGGATTA	0.34	0.54	0.55	0.61	0.52	0.51	0.70	0.53	0.68	0.56	0.55	0.72
156	13	65529714	17080638	14612	TGAAAATAATYGTTAAACTTC	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65540259	17080678	14613	TAAAAAATGTMGCAAACTAAT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65547028	17790947	14614	TAAGTGATGAYTTCTGAAGAG	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65558652	2779129	14615	AATACAACTTKATCTATTAGC	0.81	0.42	0.44	0.39	0.46	0.73	0.44	0.37	0.38	0.46	0.76	0.46
156	13	65566038		14616	TGTAAGTTATRTTAATGGATC	0.04	0.04	0.04	0.49	0.54	0.97	1.52	0.00	0.44	0.59	0.94	1.42
156	13	65576909	4433683	14617	TATTCTCTCTMAAATTCTGGC	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65592749		14618	TAAACAGGGGRTGGAGCAGAC	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65599024	17566918	14619	CTATGATTAAYGAGGCATCAC	0.19	0.41	0.41	0.60	1.05	1.21	1.10	0.36	0.63	1.02	1.11	1.08
156	13	65605741	3850042	14620	TTTTATATTCRAAGCTCAAAA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65612196	12869662	14621	TTTCAGCTTCYGTACCTAAGT	0.13	0.24	0.24	1.41	1.62	1.05	1.05	0.23	1.58	1.51	1.05	1.08
156	13	65621827	7984365	14622	TCACCTAACTKTATTCTTTTT	0.94	1.43	1.59	1.10	1.21	0.60	0.89	1.51	1.10	1.17	0.63	0.88
156	13	65631012	17080852	14623	TCTACTGGTASATCAGGGAAA	1.63	2.27	2.27	1.05	0.28	0.46	0.35	2.19	1.11	0.28	0.46	0.36
156	13	65636766	17080868	14624	CACTATGTCCRTGACGAGGAA	1.52	2.13	2.13	0.85	0.27	0.21	0.23	2.02	0.85	0.27	0.24	0.27
156	13	65643021	9317574	14625	CCTTTTTTGARTAGACTCTAA	1.43	2.06	2.12	0.79	0.43	0.24	0.35	2.04	0.92	0.46	0.26	0.33
156	13	65646338	9529031	14626	CTGCTTTGACRCAATTGGTGT	0.59	0.88	0.85	1.27	0.25	0.34	0.94	0.81	1.36	0.27	0.34	0.92
156	13	65659068	6562438	14627	CATAGTTTTAKTTCAGAATAC	0.07	0.30	0.30	0.39	0.76	1.12	0.88	0.23	0.35	0.73	1.09	0.90
156	13	65666979	10507733	14628	GTCACCACAASATTGGCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65673682	1322719	14629	ATGCCACACAYTTTGCTTGCC	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65683327	7982018	14630	ACAAGTAGTCMATGAAAGAAA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65696611	2183456	14631	ATTTTTGGTTKTGCTATAAAC	0.38	0.24	0.24	0.54	1.09	1.00	1.16	0.22	0.51	1.07	1.03	1.08
156	13	65710599	9599094	14632	ACGTTTGAAGWTAGAAGATGG	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65721667	4884662	14633	GTGATCACTARGAGTAACAGT	0.18	0.12	0.12	0.54	0.71	1.08	0.53	0.10	0.52	0.72	1.07	0.52
156	13	65733379	9599100	14634	GGCAAAAATAWCAAATCAATG	0.01	0.08	0.09	0.44	0.56	0.56	0.26	0.07	0.41	0.54	0.59	0.29
156	13	65742484	1322729	14635	TCACATCTATYCTTTCACATA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65765795	1200530	14636	TATCAATTTTRCGTCACAGGG	0.01	0.05	0.05	0.74	0.56	0.12	0.20	0.01	0.76	0.62	0.14	0.20
156	13	65778898	1334396	14637	TTCCTCTCACRTACCTCCAAT	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65789536	4145004	14638	GAATGTTCAARTGAAATTAAC	0.01	0.00	0.00	0.54	0.31	0.07	0.07	0.00	0.54	0.31	0.06	0.07
156	13	65800730	17081131	14639	GAGAGTTGACRTCCGTATGTC	0.06	0.14	0.14	0.18	0.23	0.38	0.22	0.12	0.16	0.26	0.43	0.22
156	13	65813902	7996220	14640	ACTTTTGTATWGCAATGGGCA	-	-	-	-	-	-	-	-	-	-	-	-
156	13	65819955	2875472	14641	TTCTCTCCTGWGCTGCGAGCT	0.22	0.30	0.30	0.16	0.18	0.50	0.51	0.28	0.13	0.17	0.55	0.57
156	13	65831413	17579852	14642	GTTTGAAAGARTATCAGCATT	0.27	0.22	0.24	0.09	0.32	0.45	0.13	0.22	0.03	0.34	0.48	0.12
157	13	68495875	9541728	14643	CCACTTCTCCKGAGCTTGAAT	0.16	0.12	0.12	1.32	1.20	0.55	0.80	0.08	1.50	1.14	0.54	0.82
157	13	68501543	17597133	14644	TGTTGAGAGARAGCAAATCAC	0.66	1.14	1.26	1.53	2.32	0.90	1.44	1.19	1.70	2.13	0.90	1.42
157	13	68512380	9599385	14645	AGAAGTAAAAWATCCTTTAAT	-	-	-	-	-	-	-	-	-	-	-	-
157	13	68518172	17084522	14646	TACTCCACACRTCCTCTACGC	1.03	1.54	1.47	1.74	1.82	2.75	1.10	1.37	1.77	1.70	2.45	1.05
157	13	68542973	9317764	14647	TGGCACTGTAKCTGATAAATT	0.53	0.69	0.69	1.80	2.35	3.20	2.26	0.68	1.79	2.21	2.90	2.14
157	13	68549638	9529506	14648	AATAGGCTTARTATGACCTTA	0.68	0.09	0.12	0.64	1.89	1.99	1.34	0.09	0.66	1.73	1.89	1.31
157	13	68556018	17598558	14649	GCTTATATCARCCCAAGAGTT	-	-	-	-	-	-	-	-	-	-	-	-
157	13	68562645	9599398	14650	GTAGATAAAGYGGACATTCAT	-	-	-	-	-	-	-	-	-	-	-	-
157	13	68569541	8002464	14651	TGAAAATTCARTCTGGGACAA	-	-	-	-	-	-	-	-	-	-	-	-
157	13	68573704	2875569	14652	TGTTGGTAAAKATCTTCTCCT	0.34	0.60	0.60	0.38	0.42	0.51	0.71	0.61	0.42	0.43	0.53	0.72
158	13	73768514	9318253	14653	ACTATCTCATYCAATCTACTG	0.39	0.38	0.34	0.35	1.14	1.17	0.69	0.29	0.32	1.09	1.17	0.69
158	13	73777615	2325607	14654	AAATAAAAATWGGAAAAAATA	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73794930	9543577	14655	TCATAAATGTRTCTATTCCTT	0.66	0.90	0.85	0.98	0.74	0.98	0.66	0.78	0.98	0.77	0.94	0.67
158	13	73801426	1556435	14656	TTCTGAAAGCYTATTTATTTC	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73808984	7332588	14657	TTCTTACTCCYCTTAAGTTAT	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73818335	9592989	14658	ATTTGAGAAAYTTTTGAATAG	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73825986	17062629	14659	CCCAGTGGCGRGCCCAGCTGT	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73834878	9600285	14660	TCCATTTTTTWAAAAATTTCT	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73840896	9318258	14661	CTCATGGCTTRTGCTCAGCCT	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73847826	1953318	14662	TTGCATGGAAYACTTGCAGAG	1.67	1.70	1.64	1.06	1.02	0.93	0.59	1.59	1.18	1.02	0.94	0.61
158	13	73848534	12585408	14663	AGTGGTTTACYCTAGGTCCCC	2.48	2.05	2.00	1.81	1.43	0.53	0.47	1.99	2.10	1.38	0.50	0.49
158	13	73864569	9600298	14664	TTAAAGGGTAWTAGACCACAA	0.20	0.12	0.10	1.59	0.84	0.71	0.30	0.11	1.97	0.84	0.72	0.30
158	13	73873575	9600309	14665	TATACCTAAAYTGGGTAGAAG	0.32	0.00	0.00	0.12	0.83	0.45	0.83	0.00	0.10	0.85	0.47	0.81
158	13	73876474		14666	AAGAAGTGACMCAAAGCTAGC	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73888917	17641985	14667	ATTGGTGCTAYGACAGTAATT	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73897991	6562823	14668	AAACATTTTGYTGTTGTTCTA	-	-	-	-	-	-	-	-	-	-	-	-
158	13	73904580	1931957	14669	TTTATGCCTTKAAATTGTTAT	0.09	0.30	0.30	0.23	0.22	0.99	0.27	0.23	0.21	0.23	0.95	0.30
158	13	73911046	9573384	14670	ATAACCTCCARCAACTATAAA	1.03	1.13	1.13	0.89	0.46	0.27	0.61	1.08	0.90	0.47	0.26	0.64
159	13	79755980	9545383	14671	CATGTGTGAAYGCCTTCTTCA	0.04	0.12	0.11	0.15	0.04	0.01	0.01	0.08	0.12	0.03	0.01	0.01
159	13	79767236	2988113	14672	AATTTTTTTGKGTGTATTTTT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79774400	12865196	14673	AAATCTGCTTSTATTTTTAGA	0.71	0.01	0.03	0.02	0.02	0.05	0.02	0.00	0.01	0.01	0.04	0.01
159	13	79782234	2988335	14674	AGCAAAGCTCRAGTGAAAGAG	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79799940	12876395	14675	TAACAGAGAARGGCATTTGCA	0.32	0.04	0.04	0.05	0.05	0.04	0.07	0.02	0.04	0.04	0.04	0.07
159	13	79810102	563692	14676	AATCCTGTGAYGTACAACAAT	0.07	0.15	0.15	0.02	0.02	0.07	0.33	0.12	0.02	0.02	0.07	0.36
159	13	79824658	9545411	14677	CATAGTGGCAKTTCTGGTTAA	0.34	0.00	0.00	0.06	0.02	0.28	0.29	0.00	0.04	0.01	0.29	0.32
159	13	79836288	7331081	14678	AAAAGACAGCRAGGAAAATTC	0.47	0.45	0.53	0.47	0.96	0.29	0.40	0.47	0.52	0.96	0.31	0.43
159	13	79853688	17072654	14679	TTTCCAACATKGGATTTTAGC	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79860561	552643	14680	TGAAATTCAARGTAGTCCAGT	0.32	0.60	0.60	0.31	0.20	0.94	0.35	0.59	0.32	0.24	0.94	0.40
159	13	79901845	477878	14681	GCCAAAACCTYTAATATTTTG	0.75	0.87	0.87	0.16	0.35	0.30	1.29	0.83	0.12	0.33	0.34	1.25
159	13	79907945	4885723	14682	ACTTTGAGCTRGAAGCCATAT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79919901	4885724	14683	CTCAAATTATYGGCATGACCT	0.30	0.51	0.51	0.22	0.41	0.49	0.68	0.51	0.18	0.42	0.49	0.67
159	13	79931263	9601389	14684	AGGTCACTATYCTCTTTATTC	0.27	0.33	0.33	0.25	0.63	0.58	0.46	0.31	0.24	0.68	0.61	0.51

159	13	79937882	7350644	14685	GATTTAATGCWGCAAGAGTCA	0.47	0.67	0.65	1.45	1.49	0.92	0.62	0.64	1.53	1.44	0.92	0.67
159	13	79944766	944751	14686	AATTGAATACYTGTTACCTTA	0.50	0.73	0.73	1.71	1.90	1.06	0.70	0.69	1.80	1.86	1.05	0.72
159	13	79955513	9545440	14687	AACCAACATCYGTCTTCCCTG	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79970135	17072760	14688	GAGAATTGTCMGTGACCCAAA	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79976607	1953080	14689	TTTCAAACTTYGAAAGAACTT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79982878	1930339	14690	TTGTTTTTCGYTGCTTTGAAC	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79984266	7994454	14691	TGACACACACRGGCAGTAATA	-	-	-	-	-	-	-	-	-	-	-	-
159	13	79997882	9574670	14692	ACTTACAAACRATTGCAATTT	0.63	0.77	0.95	1.42	1.86	1.80	0.97	0.91	1.59	1.77	1.69	0.95
159	13	80007597	17072803	14693	AATTTGGCGARACCACCATCC	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80015794	17072806	14694	TGCCATCTCARCTGCAGCATA	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80021202	7330316	14695	AATATATCCTYATTGCAGCTG	0.38	0.16	0.08	0.53	2.60	1.80	0.60	0.07	0.51	2.43	1.72	0.64
159	13	80028205	7995543	14696	CACAAAGAAGWTAAATACCAC	0.28	0.18	0.21	1.33	1.25	1.02	2.46	0.19	1.52	1.26	1.03	2.26
159	13	80035600	7325704	14697	AGCTTTTAAGYTCTCTTCTAA	1.14	1.14	1.03	1.86	0.98	2.45	2.17	0.96	2.19	0.95	2.25	2.03
159	13	80046307	9545484	14698	CCTCCTCATTSCATTTGTGTT	0.85	1.21	1.21	0.59	3.57	2.48	1.91	1.11	0.66	3.08	2.30	1.86
159	13	80059300	7317238	14699	AGATTTCATAKCAGATGTACA	0.04	0.15	0.20	0.55	2.85	3.09	1.57	0.17	0.56	2.54	2.87	1.54
159	13	80067462	9531095	14700	CCTTGAAGGGRACAACTAAAT	0.75	0.52	0.52	0.44	1.00	2.01	1.74	0.48	0.45	1.00	1.98	1.68
159	13	80074680	1984286	14701	TGAAAAGCATWGTTTGAAAAG	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80086805	1772575	14702	TCTATTACCTMCAGAATTAGC	0.93	1.30	1.30	0.81	0.49	0.97	1.41	1.27	0.89	0.50	0.96	1.43
159	13	80092373	17073072	14703	TAACAGTGGGRAAAATAGATT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80100649	1176300	14704	GGCACAACTTRAGTAGCAAAG	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80102779	1176293	14705	ATATCTCTCAYCATTAACACC	1.38	1.80	1.80	0.83	0.38	0.30	1.07	1.75	0.86	0.38	0.30	1.03
159	13	80119666	1176315	14706	CTACCAAAGAYCCCTAAAAAT	0.47	0.42	0.42	0.94	0.47	0.57	1.61	0.39	1.05	0.49	0.57	1.59
159	13	80126337	1417832	14707	AAGACAAATAYTAGGATCATT	0.68	0.38	0.38	0.18	1.14	0.59	0.59	0.37	0.12	1.10	0.59	0.63
159	13	80127654	7329522	14708	GAAGTTCATGRTACTGTTCCC	0.31	0.30	0.30	0.06	0.20	1.11	0.52	0.21	0.07	0.23	1.08	0.53
159	13	80190589	2794238	14709	GAAAGAAAAARCTTAAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80196246	9545540	14710	AGGAAGATTASAGCAGAGTTC	0.01	0.07	0.07	0.11	0.14	0.14	0.50	0.04	0.11	0.14	0.15	0.51
159	13	80201865	7981331	14711	AAAACTCAACSAAGTTAATAC	0.57	0.25	0.22	0.09	0.02	0.03	0.09	0.20	0.08	0.02	0.03	0.08
159	13	80207721	7321210	14712	CACCTCATTTMATTTATTGTA	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80216331	2765940	14713	TCATGTCAGGMCGTCCATGGG	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80223006	9545548	14714	TAATATTCATKCATCTTTGGG	0.02	0.04	0.02	0.01	0.01	0.02	0.20	0.00	0.02	0.01	0.02	0.21
159	13	80227579	9545549	14715	TAGCTGGAAARTGTCTTACAT	0.02	0.02	0.02	0.05	0.03	0.11	0.10	0.00	0.06	0.03	0.09	0.12
159	13	80237902	1322619	14716	CAACCAGAAGKCTGTGAATGT	0.72	0.52	0.52	0.18	0.08	0.13	0.13	0.47	0.18	0.09	0.13	0.12
159	13	80246416	17073282	14717	GTAAGCAGAGMCTCAGCAGGT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80253691	17073296	14718	TAGCACAGCCYGGAGTTGCCT	-	-	-	-	-	-	-	-	-	-	-	-
159	13	80261057	17073331	14719	CCTTTTGCTTYATAGGCTTTT	0.11	0.11	0.11	0.29	0.17	0.07	0.40	0.09	0.31	0.21	0.07	0.42
160	13	106243933	9555280	14720	CTCACTCTGGRAATTAAAGCA	0.17	0.41	0.41	0.16	0.18	0.57	0.33	0.38	0.15	0.19	0.57	0.35
160	13	106254768	4445765	14721	TGTATCAGTCRAAGTTATCTT	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106260832	10508180	14722	TTGTCAATGGRAATTGTGAAT	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106267787	287221	14723	ACCTTCTATCYAGCAATTAAT	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106274850	9587230	14724	CTGGCCATTTMTCTTCTTTTA	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106291948	9583131	14725	TCTCACTCGCRTCCAGGCTCG	0.40	0.38	0.39	0.69	0.59	0.36	0.57	0.35	0.70	0.64	0.37	0.59
160	13	106301233	288744	14726	GTTTTCCATAWTTTTTTTCAC	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106308987	9520221	14727	AGACAACTGCRTACACGTTTT	1.05	1.49	1.52	0.77	0.57	1.01	0.94	1.46	0.83	0.58	1.00	0.92
160	13	106318645	9520235	14728	TTTCCTTAACRCTCTGTAGTC	3.98	2.49	2.49	1.50	1.67	1.26	0.97	2.42	1.54	1.59	1.26	0.95
160	13	106332768	288698	14729	TACTGAGGACRTTACCTTCCC	2.61	2.87	2.80	1.25	0.97	1.38	0.60	2.73	1.36	0.92	1.37	0.58
160	13	106341752		14730	TTTTTTCTACRTTATATCCAT	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106353066	9301169	14731	GCTTACATAAYGTGGCAAGGT	0.06	0.07	0.09	1.90	0.90	0.31	0.28	0.06	1.93	0.87	0.33	0.28
160	13	106360377	9555295	14732	GGGATATTTAYAGGTCCTTGT	-	-	-	-	-	-	-	-	-	-	-	-
160	13	106373512	2774201	14733	GGAGGGAAGCYGGTCACCTCA	0.23	0.49	0.49	0.34	1.13	0.24	0.12	0.49	0.34	1.15	0.27	0.13
160	13	106377871	9583139	14734	GTGTGTACAGWTATCCCTGGC	0.13	0.17	0.17	0.41	0.11	0.44	0.08	0.14	0.38	0.11	0.46	0.09
161	14	23880999	8008406	14735	AGATGTCCCAYGCTTTTGGAG	0.70	1.22	1.24	0.81	0.86	0.96	1.34	1.20	0.82	0.87	0.97	1.31
161	14	23885591	4981507	14736	TGTGTTTCCARTATGAAGAAC	-	-	-	-	-	-	-	-	-	-	-	-
161	14	23900690	1950500	14737	TATAATATTCYTCTTTTGCTT	0.51	0.78	0.78	0.74	0.66	1.02	1.05	0.73	0.79	0.65	1.01	1.05
161	14	23913460	2295298	14738	TGGTACTGACYGGCTCCAACT	0.00	0.03	0.04	0.42	1.92	0.74	1.79	0.02	0.41	1.74	0.71	1.74
161	14	23919043	17199892	14739	CATCCACTCCRTCCCACAATG	0.03	0.03	0.00	0.47	0.49	3.10	0.86	0.00	0.51	0.48	2.82	0.86
161	14	23926042	10129213	14740	CCAAAGGTTCKGGGATTCATG	1.22	1.27	1.27	0.39	0.73	0.23	1.86	1.18	0.40	0.72	0.23	1.81
161	14	23939305	17795034	14741	ATCACAGTGCRCCTCTCTTGC	0.12	0.28	0.28	0.81	0.35	0.49	0.26	0.29	0.80	0.37	0.52	0.29
161	14	23945941	4982908	14742	TAAAGATGGCRAGTGTGTGCC	1.22	1.32	1.32	0.35	0.30	0.48	0.18	1.24	0.35	0.31	0.48	0.21
161	14	23952152	2273634	14743	TCGGTAAGATSGTCCCCAGAG	0.50	0.49	0.49	0.52	0.45	0.15	0.14	0.47	0.53	0.47	0.15	0.15
161	14	23958088	13841	14744	TGTTAACCCTRTCCAGAAAAA	0.13	0.24	0.20	0.12	0.12	0.12	0.19	0.18	0.12	0.12	0.10	0.21
161	14	23971273	17795094	14745	TCTGTGTCCAYCGTGAGCCTC	0.54	0.00	0.00	0.25	0.14	0.12	0.11	0.00	0.25	0.16	0.09	0.09
161	14	23981848	17184766	14746	TGCGTAAAGTYTAGAGTTTAC	1.31	1.73	1.73	0.74	0.39	0.10	0.08	1.69	0.73	0.43	0.09	0.08
161	14	23995185	12886673	14747	CAAGGGAATGRTGATGATGGG	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24003317	7142828	14748	TTTGCGATTTKATGATGCAAT	0.48	0.00	0.00	1.12	0.61	0.27	0.10	0.00	1.28	0.63	0.23	0.12
161	14	24011367	2332339	14749	GAAATGTCCASATGCAAAGGT	0.40	0.06	0.02	0.13	0.60	0.32	0.15	0.00	0.08	0.64	0.34	0.14
161	14	24017807	6573826	14750	TACTCATACARTTAGGATTTT	0.55	0.05	0.05	0.81	1.01	0.40	0.13	0.02	0.93	1.06	0.41	0.13
161	14	24037292	17184822	14751	ACAGGTAAATKATGAGTTCAC	0.99	1.44	1.44	1.31	0.56	0.73	0.26	1.35	1.53	0.56	0.77	0.28
161	14	24043723	12892955	14752	AGGCAGTCTTYTCTGCATATC	0.97	1.22	1.22	0.62	0.96	0.35	0.48	1.14	0.71	0.95	0.39	0.50
161	14	24050332	1956917	14753	CTGAGTTTCCRAACATTGTAT	1.00	1.42	1.42	1.06	0.39	0.61	0.32	1.37	1.22	0.42	0.60	0.37
161	14	24053479	4982956	14754	AGTCCTAGGAWGAGGGATGCA	1.03	1.47	1.47	0.83	0.55	0.65	0.92	1.43	0.92	0.54	0.66	0.95
161	14	24084765	7401983	14755	CCAGTCAGATRCGTAGTTTGC	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24099654	17257069	14756	ATTCAAGCCCRGATGGTGGGT	0.78	0.72	0.72	0.95	0.69	1.65	0.88	0.60	0.98	0.69	1.55	0.89
161	14	24115584	3759639	14757	GAACCCTCAAYCCATCAAATT	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24121355	17105431	14758	GATGAACTTGYGATTGCTTTA	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24139289		14759	TTATTCTGTTMTCTTGGGGTG	1.28	1.86	1.89	0.72	1.88	1.14	0.77	1.85	0.81	1.75	1.14	0.76
161	14	24148749		14760	GGATGGGTACWGTAAACTCAG	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24154521	11158813	14761	CTTTTGTTTCYGGTCCACTCA	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24155730	1951595	14762	CACTGCATGGKATTGTTTCTC	0.96	0.40	0.43	2.58	2.08	0.93	0.83	0.42	2.60	1.91	0.94	0.84
161	14	24173502	7144366	14763	ATGAAGTGAAYTGTAGGATGT	2.33	1.56	1.56	3.00	2.36	1.15	1.20	1.48	3.29	2.12	1.13	1.21
161	14	24179826	11626519	14764	CTATCTTACTRTATTACAAAG	1.34	1.41	1.41	1.51	2.42	1.45	1.96	1.32	1.61	2.27	1.40	1.91
161	14	24193605	12717544	14765	TTGATAACTAYAGTCACTGTA	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24201139	1951589	14766	GACTTTTTAARTTATTCCCCA	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24209714	17106805	14767	CTTTAAGTATKGCACACTGAA	1.34	1.85	1.59	1.06	2.69	2.38	2.57	1.52	1.18	2.48	2.27	2.44
161	14	24219679	8021801	14768	ACTGCTAGGTKTGGGAGCCAC	0.12	0.17	0.17	2.29	1.93	3.52	2.28	0.12	2.54	1.83	3.24	2.19
161	14	24232485	1951590	14769	CAGTATTTTTYAATGGTATTT	2.14	2.77	2.74	2.56	2.83	1.76	2.54	2.64	2.58	2.61	1.71	2.40
161	14	24237941	1957522	14770	TGGAGCCAGTKTGTAAATTGA	0.88	1.31	1.31	3.10	2.83	1.11	1.22	1.26	3.39	2.65	1.05	1.18
161	14	24248827	12895231	14771	GGGCTCTTGARCTATCATAAA	1.38	1.79	1.79	2.13	2.04	1.35	0.75	1.69	2.11	1.95	1.31	0.74
161	14	24264637	17200359	14772	ATGAACTGAAYTCCTTGTCCA	0.65	1.09	1.04	1.27	1.15	1.38	1.10	0.96	1.32	1.11	1.35	1.13
161	14	24274273	854408	14773	CTGGGCTGGCRAGTCCATTTC	0.38	0.17	0.17	0.62	0.90	1.07	0.78	0.15	0.57	0.86	1.08	0.78
161	14	24284414	1979339	14774	CAATGAACCAYGTTAACAAAA	0.07	0.22	0.22	0.56	0.27	0.46	0.67	0.17	0.58	0.26	0.48	0.67
161	14	24285362	1461653	14775	TAAGGGGTTASGGATATATAG	0.09	0.29	0.32	0.25	0.35	0.26	0.58	0.29	0.23	0.37	0.29	0.58
161	14	24297351	854435	14776	GGATGGAGAARTAGGTTAAGT	0.20	0.18	0.18	0.51	0.56	0.47	0.27	0.14	0.53	0.60	0.46	0.28
161	14	24307108	854416	14777	GGATGGCTACMATTCAGGAGA	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24314646	854345	14778	ATACTAGGGTRACGGAGGATT	0.79	0.33	0.34	0.23	0.83	0.43	0.43	0.29	0.16	0.86	0.44	0.42

161	14	24319662	11158905	14779	GTTAAAAGTGWCAATTCAGAA	0.02	0.06	0.06	0.73	0.52	0.53	0.94	0.04	0.77	0.54	0.56	0.93
161	14	24327620	17795538	14780	GCCTCAATTTRATTTTTTAAT	1.09	1.41	1.41	0.40	0.26	0.95	1.02	1.36	0.39	0.26	0.97	1.03
161	14	24335945	17200526	14781	GGAAAGGCTAWATATGAGGAG	0.26	0.34	0.34	0.62	0.21	0.43	1.18	0.31	0.62	0.24	0.45	1.12
161	14	24346289	17185158	14782	TTGCCTCATCSAACTATGTCC	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24354572	10133078	14783	CCTGTGCTCCKAAGACCCAGA	-	-	-	-	-	-	-	-	-	-	-	-
161	14	24361921	12879077	14784	AGTTTCACACRTATTTATTAA	0.49	0.34	0.33	0.14	0.29	0.21	0.38	0.27	0.14	0.33	0.21	0.40
162	14	33014942	17101323	14785	TGAGAAACTAMGTGATTTACT	0.14	0.38	0.38	0.36	0.09	0.14	1.12	0.33	0.34	0.07	0.13	1.13
162	14	33020606	7152665	14786	ACTCCTGTTCYAATTTGCACT	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33025960	1012023	14787	TTAAATTTGAMGAGGTGAAGA	0.44	0.43	0.43	0.07	0.33	0.54	0.12	0.29	0.07	0.33	0.57	0.12
162	14	33037860		14788	GATGGGCAGTKTTAAATGAAT	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33046626	1957315	14789	CCATGGAACAYGGAATTTCTA	0.36	0.49	0.49	0.42	0.60	0.40	0.28	0.47	0.44	0.63	0.41	0.31
162	14	33052891	17101420	14790	GAAGACTTGCRTGCCCAGGCT	0.47	0.68	0.68	0.92	0.26	0.39	0.53	0.64	0.98	0.27	0.41	0.53
162	14	33059625	2281628	14791	AGGAATAAAARCAACACAATT	0.44	0.06	0.04	0.71	0.50	0.36	0.56	0.01	0.76	0.52	0.37	0.55
162	14	33065343	8021131	14792	TTTGTTTTTARTAAAGGAAAA	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33072608	10134498	14793	CATTGTGGCAYTGCTTCTAAT	0.08	0.13	0.13	0.80	0.99	0.52	0.98	0.10	0.82	1.01	0.56	0.99
162	14	33073744	7159470	14794	AGACTTTGGARTTTCCTGGAA	0.14	0.29	0.29	1.03	0.72	1.23	0.85	0.24	1.20	0.72	1.23	0.85
162	14	33086522	1475067	14795	TACGGTCCACRCTCTCCCTGC	0.29	0.08	0.08	0.47	1.99	0.42	0.55	0.03	0.47	1.92	0.42	0.53
162	14	33096254	1888040	14796	AGCTGGTTCCRTGGGAAATAT	0.27	0.00	0.00	0.52	0.57	0.88	0.16	0.00	0.53	0.59	0.83	0.16
162	14	33105758	12432766	14797	ACATGTCAGTRTCTAACAATA	1.24	1.26	1.26	0.89	0.74	0.39	0.52	1.17	0.90	0.72	0.41	0.55
162	14	33111135	17101556	14798	TTCAGAGGTAKTATTATTCTA	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33118547	10134006	14799	CTATTAGTAAYGATAGAATTG	1.96	2.36	2.36	2.28	1.12	0.48	0.09	2.34	2.33	1.11	0.52	0.10
162	14	33124694	1958544	14800	TAATTTCTTTYAGTTTTCCGC	3.05	3.42	3.42	2.58	1.26	0.54	0.75	3.36	2.85	1.24	0.53	0.72
162	14	33130460	17101589	14801	ACTAAAGCCAYTGACTACCAT	0.16	0.00	0.00	1.87	1.13	1.49	2.25	0.00	2.17	1.07	1.48	2.17
162	14	33136550	17101598	14802	ACATATACCTKTGGAAACAAT	0.72	1.04	1.04	1.90	3.02	4.41	2.24	0.91	2.01	2.80	4.03	2.16
162	14	33150173	1952599	14803	AAATTAAATCWTTATGAAATA	2.62	3.13	3.13	2.32	4.27	4.30	2.19	3.08	2.40	3.82	3.91	2.07
162	14	33157821	4556706	14804	CAGACCTTCCRCAGTTGAAGA	0.01	0.07	0.06	3.86	3.89	3.02	3.52	0.02	4.42	3.44	2.86	3.31
162	14	33173262		14805	AGGTTGTTCARGGCCAAAGGA	0.37	0.72	0.72	2.70	3.62	3.22	3.01	0.65	2.88	3.33	2.99	2.85
162	14	33186743	7159875	14806	GTTCCCGTATRTAGTTGGTTT	1.79	2.17	2.10	1.61	2.41	2.79	2.48	2.04	1.69	2.23	2.64	2.36
162	14	33193123	4412895	14807	AGGGAATCCAYAATCCTGTGC	2.15	2.57	2.55	1.80	1.25	1.74	2.61	2.45	1.90	1.20	1.67	2.46
162	14	33200625	2183276	14808	CAAATAGTCAYCTACTCTGTT	0.81	0.75	0.75	1.56	1.77	1.16	1.73	0.74	1.65	1.70	1.16	1.65
162	14	33207984	11156808	14809	TGACAAATACKGAAACATGTA	0.40	0.75	0.75	0.55	0.95	0.72	1.26	0.71	0.56	0.97	0.71	1.21
162	14	33214581	2383522	14810	AAATCCCTCAYACGATTACAG	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33221257	17101697	14811	CTGACTTCTGYTAATACCCAG	0.79	1.12	1.12	0.69	0.45	0.56	0.92	1.05	0.71	0.47	0.56	0.92
162	14	33228529	12100738	14812	CAAATCGTAGYACCCAAAAGA	1.09	1.46	1.48	0.90	0.82	0.47	0.90	1.37	0.94	0.82	0.48	0.92
162	14	33238158	4462506	14813	TTTTTAATTGYTAGAAAATAT	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33249118	10498318	14814	GCGACTTGATKTAACAACTTT	0.82	0.42	0.42	1.10	0.64	1.53	0.62	0.37	1.09	0.63	1.47	0.64
162	14	33254537	1958055	14815	AGCTCTATACRTCTGTGTTGG	0.66	1.08	1.08	0.37	0.73	0.26	0.86	1.01	0.37	0.73	0.26	0.84
162	14	33260733	17101773	14816	ATAAGCACTAYGTATATGATC	0.46	0.71	0.71	0.42	0.20	0.67	0.41	0.66	0.42	0.21	0.70	0.39
162	14	33267366	9635158	14817	TGATTCACAASTTTCTAAACA	0.67	1.07	1.07	0.52	0.39	0.54	0.44	1.01	0.56	0.41	0.56	0.47
162	14	33272388		14818	GCTGACTGACWGTTCTGATCT	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33281123	8006749	14819	CGCAAGCACARGTCATTTTTC	0.39	0.38	0.38	0.80	0.76	0.35	0.13	0.31	0.90	0.79	0.36	0.14
162	14	33290737	8012590	14820	CTAATTATAGSAACCTTTGTA	0.47	0.45	0.45	0.34	0.42	0.48	0.10	0.39	0.35	0.42	0.50	0.10
162	14	33298904	17411590	14821	AATAAAATTGRGAAAAAATAT	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33305448	17101865	14822	TACCAGCCTTYGTTCCTAACT	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33316845	12895061	14823	AAAAGGGCCARGAGTGAAAGC	0.57	0.54	0.54	0.18	0.13	0.27	0.11	0.50	0.20	0.15	0.27	0.11
162	14	33322327	1958057	14824	TGGCTGGACTYTTCCCAGAGC	0.64	0.17	0.17	0.33	0.14	0.10	0.28	0.14	0.30	0.16	0.08	0.31
162	14	33330386	1958058	14825	CCCTAACAAAYGAGTGCTGGA	0.36	0.51	0.51	0.17	0.23	0.04	0.18	0.46	0.17	0.25	0.04	0.19
162	14	33344266	753239	14826	ATGGAACTGGYTGTGAGTGCA	-	-	-	-	-	-	-	-	-	-	-	-
162	14	33351066	1958035	14827	TGGCCAATAARCCAAAGACCC	0.55	0.94	0.99	0.25	0.02	0.33	0.14	0.96	0.22	0.03	0.35	0.14
163	14	36970890	7145671	14828	TCCCAGTTTCWTTCATATTTG	0.08	0.27	0.27	0.48	0.09	0.16	0.33	0.22	0.53	0.07	0.17	0.35
163	14	36975365	11156953	14829	CTTTTTCTTTSCATGACACAT	-	-	-	-	-	-	-	-	-	-	-	-
163	14	36987576	1955945	14830	CTGTATTCCA¥AGCATAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
163	14	36994871	1955943	14831	GCTCAGATTTMGTAAGTCTAT	0.01	0.05	0.04	0.13	0.50	0.26	0.68	0.03	0.11	0.50	0.26	0.67
163	14	37010210	7148547	14832	CCAAGAGAAAWCCCATCTTTT	0.08	0.27	0.27	0.90	0.43	0.68	0.35	0.25	0.92	0.41	0.70	0.37
163	14	37037616	1011818	14833	GGCACTACACWCTATTCTAAT	0.04	0.18	0.16	0.96	1.06	0.25	0.13	0.12	1.06	1.07	0.24	0.13
163	14	37038387	10143976	14834	ACAAGTAGAARATCAAGTAGA	-	-	-	-	-	-	-	-	-	-	-	-
163	14	37053842	2415404	14835	AAATAGACACRTAGGTATACT	-	-	-	-	-	-	-	-	-	-	-	-
163	14	37063074	2180609	14836	TTTGACTTTAYCTTACAAGCA	0.06	0.21	0.21	1.39	0.69	0.27	0.08	0.18	1.51	0.70	0.27	0.08
163	14	37069437	12881012	14837	GAGAATTTCTWTGGAATGATA	0.23	0.51	0.51	0.97	0.32	0.17	0.18	0.46	1.06	0.35	0.17	0.19
163	14	37075592	10133391	14838	AGTTTTTTCTYGCTCTCTCTA	-	-	-	-	-	-	-	-	-	-	-	-
163	14	37085795	10151200	14839	CTTTATCAGCSAGGACATTCT	0.07	0.19	0.19	0.05	0.43	0.46	1.34	0.17	0.04	0.45	0.51	1.33
163	14	37102609	11156962	14840	GTCAGTAAAAYCACACATTAA	0.07	0.24	0.24	0.06	0.02	1.11	1.51	0.22	0.01	0.02	1.09	1.48
163	14	37111646	11846416	14841	CCAGCATAGTKTACTGTCACT	0.05	0.21	0.21	0.10	0.66	0.63	0.73	0.18	0.09	0.67	0.65	0.74
163	14	37120786	12436923	14842	AGCTTTTGTGKTGGTTGTTTT	0.37	0.27	0.27	0.80	1.04	0.38	0.20	0.23	0.80	1.04	0.36	0.22
163	14	37145037	11627844	14843	GGGATCTGGARGGAAGCTTGG	0.39	0.57	0.57	0.18	0.50	0.23	0.07	0.52	0.18	0.52	0.25	0.07
164	14	43692035	12147686	14844	AGACTCTAAARTGAAAAGAGC	0.30	0.31	0.31	0.24	0.69	0.31	0.27	0.30	0.19	0.72	0.28	0.27
164	14	43700245	10484231	14845	CATTTCATTTKACAATCTGAT	0.08	0.06	0.06	0.46	0.18	0.40	0.14	0.03	0.48	0.18	0.40	0.14
164	14	43706681		14846	AGTGATCTCASTATAGCACTT	1.20	0.77	0.77	0.33	0.45	0.39	0.30	0.70	0.36	0.45	0.40	0.29
164	14	43711435	1040690	14847	TCAAGGATGAYTGGGAAAAAG	0.42	0.48	0.48	0.70	0.48	0.25	0.14	0.42	0.69	0.48	0.26	0.11
164	14	43722491	7148329	14848	ACATATTGCTSTAAAAGGCTT	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43732600	12433624	14849	ATGCCCAGAAYGATATGAGAT	0.16	0.42	0.42	0.34	0.43	0.16	0.18	0.39	0.32	0.46	0.15	0.20
164	14	43738700	1953479	14850	GCATTTGAATYTAGTATGCCT	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43745418	1959212	14851	TTAGGTATATMTAGCTCTCAG	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43746775	8012489	14852	TAGAGATTGTWCTAATCACAC	0.10	0.21	0.16	0.10	0.09	0.34	0.13	0.13	0.10	0.07	0.38	0.15
164	14	43766208	1953481	14853	TCTTTTCTCCRTTCCCATGTT	0.21	0.06	0.04	0.08	0.06	0.11	0.33	0.01	0.06	0.06	0.11	0.37
164	14	43785833	17648719	14854	AAACTCTTACMTGAGGAGAAG	0.05	0.01	0.05	0.02	0.08	0.07	0.65	0.02	0.02	0.08	0.07	0.63
164	14	43795701	1953456	14855	TACGTTCAACKTTCTATTGGT	0.51	0.42	0.30	0.07	0.00	0.34	0.37	0.26	0.06	0.00	0.35	0.38
164	14	43801795	17727693	14856	CAGATTTTCARTGGCCTCCAA	0.03	0.05	0.05	0.08	0.04	0.05	0.24	0.03	0.05	0.03	0.04	0.27
164	14	43812206	1959194	14857	CTGTGGTCCCRGCAGCACTTC	0.33	0.03	0.05	0.03	0.06	0.26	0.58	0.03	0.03	0.09	0.32	0.58
164	14	43822466	17654975	14858	TTATATGTTCYAAAATATCAA	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43848684	7154554	14859	TGTGAAGAGGYTGCTAATTAA	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43858726	12436820	14860	AGTACTTGTARTTATTTGGTC	0.16	0.08	0.04	0.19	0.26	1.14	0.94	0.02	0.19	0.29	1.14	0.98
164	14	43866630	8010583	14861	AGCTTGATTCSTATTCACAAA	0.06	0.22	0.22	0.42	2.31	1.50	1.30	0.16	0.41	2.13	1.43	1.27
164	14	43873003	17614700	14862	CCTGAAAAGAYGAAGTGGCTC	0.20	0.13	0.13	2.27	1.77	2.77	1.52	0.11	2.39	1.70	2.55	1.49
164	14	43883830	17543100	14863	TTGGTACCATRAAGCTATTCT	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43892659	10484180	14864	CATTTTAGTARGCCCAACAAT	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43899473	17543487	14865	TCCTGGGGAGYGTTTGTCTAG	0.05	0.17	0.21	2.41	2.14	1.53	1.43	0.18	2.82	1.96	1.48	1.41
164	14	43910304	950265	14866	CAGCAAAAAAYGGAGTCTGAC	0.16	0.09	0.13	3.01	3.23	1.29	0.64	0.11	3.29	2.84	1.26	0.65
164	14	43926887	4551953	14867	ATTTTAGAAARTCTGTAAATA	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43929685	12147597	14868	TTTTGAGTCTYTCTGCAACAT	0.06	0.19	0.19	0.47	2.70	2.53	1.82	0.17	0.47	2.49	2.40	1.68
164	14	43939568	1952573	14869	ATATTTTTTTWAAAAAAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43947540	8009199	14870	TTTGATACACRACCTTTATCA	0.02	0.10	0.10	0.47	1.07	3.08	4.01	0.06	0.47	1.06	2.85	3.57
164	14	43966684	10484177	14871	TCCTTAATCTKTATCCTCAGA	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43975942	10146815	14872	ACAGAGAATARTAACTAAGCA	1.53	1.35	1.35	0.47	1.49	2.51	3.50	1.24	0.47	1.38	2.36	3.16

164	14	43985837	17115012	14873	AATAACTGAGMACAAAACACT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
164	14	43992605	17545750	14874	ATCTGGCAAGSTGAGGAAATG	1.36	0.07	0.07	1.09	0.47	1.97	1.53	0.06	1.19	0.48	1.90	1.49	-	-	-	-	-	-
164	14	44005282	454761	14875	GATTTTATTTSTTCATAACTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
164	14	44015766	17628382	14876	GTACCCAGTGYTCCTTCTCCT	1.05	0.01	0.00	0.45	1.01	0.26	0.78	0.00	0.44	0.98	0.27	0.75	-	-	-	-	-	-
164	14	44030126	17115169	14877	GCAATATTTTYCAAAGGCTGG	0.31	0.31	0.31	0.20	0.37	0.49	0.30	0.18	0.08	0.42	0.52	0.31	-	-	-	-	-	-
164	14	44037304	12590651	14878	TAAACAAGTARCAATATCACT	0.47	0.46	0.46	0.32	0.07	0.02	0.30	0.33	0.25	0.07	0.01	0.29	-	-	-	-	-	-
164	14	44044672	3825632	14879	GAGGCTGAACWTCAGCAAGGG	0.17	0.04	0.04	0.14	0.03	0.00	0.03	0.01	0.13	0.03	0.00	0.02	-	-	-	-	-	-
164	14	44045586		14880	GGTATGTTTGRTGGAATTTCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
164	14	44070644	1953581	14881	TGTGGCTCTTYCAACTCAGAA	0.95	0.22	0.22	0.01	0.01	0.04	0.00	0.19	0.01	0.00	0.04	0.00	-	-	-	-	-	-
164	14	44077358	10149521	14882	CTTCTCTCCARTCTGTGTTCC	0.02	0.04	0.04	0.00	0.03	0.02	0.81	0.02	0.00	0.02	0.02	0.81	-	-	-	-	-	-
164	14	44090073	1953584	14883	GTTAACTGAGWTGGAAAAACA	0.07	0.22	0.22	0.02	0.00	0.89	0.62	0.18	0.02	0.00	0.88	0.63	-	-	-	-	-	-
164	14	44097440	17115281	14884	TTTTCTATAAWGAACTTGTGC	0.68	0.16	0.16	0.05	0.56	0.85	0.88	0.14	0.05	0.62	0.86	0.85	-	-	-	-	-	-
165	14	55009781	9323287	14885	GCATGGGTCAYTAAGAAAAGC	0.02	0.08	0.10	0.80	0.18	1.05	1.90	0.08	0.83	0.19	0.99	1.85	-	-	-	-	-	-
165	14	55016661		14886	GTAGGGAATCWGGGCTAAGAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55020961	17128515	14887	AGCCGAGCAAYTCTGAAGCTA	0.73	0.96	0.96	0.27	0.36	0.59	1.52	0.89	0.24	0.37	0.61	1.47	-	-	-	-	-	-
165	14	55040061	12880763	14888	TTAAATTGTTRCATATTTAGC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55051621	5022383	14889	TGCACAAATAMGAGTGCAAGT	0.18	0.12	0.12	0.73	1.15	0.72	0.17	0.10	0.73	1.09	0.75	0.17	-	-	-	-	-	-
165	14	55062619	7141027	14890	TTATACCTTTRTTCTTAAAAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55068100	17093174	14891	GTGGCAAAGTRAGTACTTTTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55080150	17128558	14892	GCTGTTTAAGYTGGCCCAGAG	0.60	0.97	0.94	1.28	1.09	0.39	0.39	0.92	1.33	1.09	0.41	0.39	-	-	-	-	-	-
165	14	55093575	942317	14893	TGGAGGTATGMAACAGAGCAG	1.69	1.78	1.78	0.47	0.42	0.49	0.57	1.74	0.49	0.43	0.46	0.57	-	-	-	-	-	-
165	14	55099286	10151664	14894	GTCACTGCAARGTCTTCTGGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55105332	8007832	14895	CTCTCTGAAGYTGTTGTGGGA	0.98	0.95	0.95	0.82	0.40	0.69	0.80	0.92	0.82	0.41	0.72	0.80	-	-	-	-	-	-
165	14	55110865	17683626	14896	AAGTATGCTGKTATTTAAAAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55127802	17128603	14897	ACTAGAGTGTRGATAGTTTTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55143888	17128614	14898	CCCGTGCATAYTCTTCAGGGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55149618	12891489	14899	TGAATAGTGCRTTTTCGAGGT	2.05	2.47	2.55	1.38	1.04	0.48	0.70	2.48	1.60	1.07	0.49	0.74	-	-	-	-	-	-
165	14	55162472	12895070	14900	TTTGGCATTCRGTAATTGTAC	1.19	1.63	1.63	1.87	1.46	0.99	0.67	1.57	2.18	1.47	1.01	0.66	-	-	-	-	-	-
165	14	55171632	10483644	14901	TAGTCTAAATRCTATGCCCTG	1.30	1.77	1.77	1.01	1.27	1.51	1.04	1.73	1.21	1.27	1.51	1.02	-	-	-	-	-	-
165	14	55173635	10483647	14902	AGGCAAAGAARGAGACCTCTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55181321	17128655	14903	AACTAAGCTGRGTCAGGTTTA	1.29	1.72	1.69	0.94	1.53	1.54	0.76	1.61	1.11	1.45	1.48	0.80	-	-	-	-	-	-
165	14	55190882		14904	TCTTTTGGCTRTGGTGTAACT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55206315	3783654	14905	TTGATAGTTTMCAGAGAATCC	1.19	1.15	1.14	1.31	1.50	0.86	0.55	1.09	1.46	1.46	0.86	0.58	-	-	-	-	-	-
165	14	55212233	3736877	14906	TTCATTCTTCRGTCCTAGAGG	1.30	1.40	1.40	0.92	0.81	0.60	0.45	1.32	0.96	0.82	0.61	0.45	-	-	-	-	-	-
165	14	55223060	6573053	14907	TCCTTGCCACYATCACAGTCA	1.40	1.49	1.49	1.02	0.63	0.51	0.44	1.43	1.02	0.62	0.50	0.47	-	-	-	-	-	-
165	14	55236868		14908	AGCCAAGGCCWGAAGCAGTAC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55243866		14909	TTGAGGAGCAKGCAGTACTGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55249852	10498477	14910	ACGATAATGARAATAAAACGG	0.15	0.05	0.05	0.83	0.47	0.40	0.17	0.02	0.92	0.50	0.42	0.16	-	-	-	-	-	-
165	14	55255787	1953354	14911	TTTTGATTGAMCTCTGCCTCC	0.65	0.80	0.91	0.60	0.65	0.17	0.37	0.86	0.63	0.69	0.20	0.39	-	-	-	-	-	-
165	14	55262547	17128756	14912	ACTATGACAARGCTGGACAGA	0.23	0.52	0.50	0.84	0.97	0.69	0.84	0.45	0.89	0.96	0.68	0.85	-	-	-	-	-	-
165	14	55270226	945270	14913	TCAATGTTCTSTTTACCATTT	0.44	0.73	0.73	0.50	0.93	1.53	1.91	0.69	0.46	0.92	1.48	1.84	-	-	-	-	-	-
165	14	55277667	945268	14914	ACTGGTCTACRGGAGTAAAGG	0.36	0.71	0.71	1.69	1.53	1.82	1.76	0.66	1.71	1.48	1.72	1.72	-	-	-	-	-	-
165	14	55284214	872187	14915	TAGTAAAGTARAAAAATGACT	0.51	0.82	0.79	0.94	1.96	1.86	1.27	0.74	0.95	1.85	1.77	1.27	-	-	-	-	-	-
165	14	55294742	8014382	14916	CTGATGTACTSTGCAAGCAAT	1.64	1.09	1.09	1.01	1.37	1.23	1.10	1.01	1.01	1.36	1.26	1.08	-	-	-	-	-	-
165	14	55302628	6573058	14917	GAAGGAGCCTYTCCCAGGCGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
165	14	55308828	12323643	14918	CAAAGATAAAYCGATACTTTT	1.15	0.08	0.08	0.63	0.85	1.39	1.04	0.05	0.62	0.84	1.36	1.00	-	-	-	-	-	-
166	14	82147133	7157219	14919	ATGAAGGCAGSAAGTAGCACA	0.50	0.61	0.88	0.57	0.65	0.33	0.48	0.78	0.60	0.66	0.37	0.48	-	-	-	-	-	-
166	14	82158119	2798379	14920	GCATTTATGAMAAATCTGGAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
166	14	82163891	1954374	14921	CTTTAGGGCAYGGAAAACACG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
166	14	82172499	997106	14922	AAACAAACTCRTGATAAGGTC	0.30	0.47	0.47	1.24	0.70	0.50	0.34	0.39	1.25	0.70	0.52	0.35	-	-	-	-	-	-
166	14	82179000	1632352	14923	AAATTCACTTYTGGTTTTAAC	2.03	2.39	2.39	1.69	1.74	0.54	0.12	2.34	1.81	1.58	0.54	0.13	-	-	-	-	-	-
166	14	82186231	17678072	14924	CAGACCTCTARAAAGGTTTGT	1.21	1.74	1.64	2.44	1.64	0.45	0.78	1.56	2.88	1.54	0.45	0.78	-	-	-	-	-	-
166	14	82195739	1777688	14925	GCGGTTTACTKTAACTAATGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
166	14	82202642	1756356	14926	AAATAACATGWCAATGGGCAA	0.60	0.93	0.96	0.74	1.18	1.49	0.80	0.87	0.79	1.13	1.47	0.83	-	-	-	-	-	-
166	14	82209290	1777695	14927	AAGAGCTAAARTAGAATTGCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
166	14	82225106	7149896	14928	CTAGATATTTKCCCCATTTCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
166	14	82226304	11851062	14929	TTATTTTTGCRTGGCATGTAG	0.29	0.04	0.04	0.33	0.80	1.53	0.83	0.02	0.34	0.82	1.49	0.81	-	-	-	-	-	-
167	14	86840424	1365524	14930	TGATGAATTGKTTGGATGTTG	0.00	0.02	0.02	0.26	0.23	0.16	0.23	0.00	0.27	0.23	0.16	0.22	-	-	-	-	-	-
167	14	86846426	1967048	14931	CATATTCCCTYGTTTTACAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86852776	9323803	14932	AATCTGTTAGYACCAAGCAAG	0.18	0.22	0.22	0.36	0.13	0.24	0.26	0.18	0.38	0.15	0.25	0.26	-	-	-	-	-	-
167	14	86865728	1430562	14933	AGAGACCCAAMAGAACAGCAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86872238	7148859	14934	ATATGCAATTSTAGAATTTTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86879690	877217	14935	CATCTCTTATMGTCCACCTGT	0.55	0.83	0.83	0.34	0.13	0.12	0.29	0.79	0.36	0.14	0.15	0.30	-	-	-	-	-	-
167	14	86888863		14936	TGGAATGTGTRCTGGAGAAGG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86897930	991407	14937	CCTTTTTAAAWATTTATTTCG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86906897	7158016	14938	CCAACACTAGYATACTACAAG	0.50	0.79	0.79	0.25	0.21	0.12	0.28	0.74	0.23	0.20	0.14	0.27	-	-	-	-	-	-
167	14	86915707	1426790	14939	ATTGATGAATYACTTAGTGCT	0.66	0.95	0.97	0.20	0.13	0.15	0.09	0.91	0.20	0.15	0.20	0.08	-	-	-	-	-	-
167	14	86921620	17672709	14940	TAAATATGCGRTGGGTAAATG	0.60	0.67	0.67	0.38	0.23	0.16	0.09	0.62	0.34	0.21	0.20	0.10	-	-	-	-	-	-
167	14	86929119	4904380	14941	CAAATTCTTASAAAGTTCATC	0.43	0.56	0.56	0.23	0.21	0.09	0.14	0.53	0.17	0.21	0.11	0.14	-	-	-	-	-	-
167	14	86935629	12432170	14942	CCTCAGAGGARACATTGATCT	0.46	0.79	0.79	0.19	0.20	0.16	0.35	0.73	0.16	0.20	0.16	0.36	-	-	-	-	-	-
167	14	86941994	7155212	14943	ATTTGGTCCCRTTATGAGAGC	0.55	0.83	0.83	0.42	0.30	0.34	0.78	0.79	0.44	0.33	0.38	0.80	-	-	-	-	-	-
167	14	86967392		14944	CAGAGTGTGGMACATGGGCCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86981302	11622162	14945	ATTGTGTTGTRTATTGTAAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	86995711	1009799	14946	CTGCTTAAACYGAATCTTCCT	0.89	0.24	0.24	0.91	0.72	0.86	1.06	0.20	1.03	0.79	0.87	1.06	-	-	-	-	-	-
167	14	87004779	11621042	14947	CTCTCTGTAGRAAGACTCGCA	0.74	0.72	0.72	0.47	1.53	1.39	0.76	0.61	0.54	1.44	1.34	0.77	-	-	-	-	-	-
167	14	87014094	12434979	14948	GATGCTATTCMAGAGGATGCC	0.12	0.19	0.19	2.22	1.86	1.18	1.32	0.15	2.43	1.66	1.14	1.26	-	-	-	-	-	-
167	14	87023484	4545736	14949	CGTGGTGCCCRTCTGTAAGTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87032174		14950	AATATACACAYACTGAGCAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87038552		14951	TCGATATTACYGTACTTAGGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87053009	4904384	14952	ATGGCAGAAASCCTAACACAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87061521	7153642	14953	TGACACAGGAMTTCCAAAGTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87072492	12883805	14954	TTGGAGTTCAYAGAAAAGTAA	1.55	2.07	2.14	1.08	2.41	1.95	1.27	2.09	1.28	2.09	1.78	1.24	-	-	-	-	-	-
167	14	87079104	174518	14955	CTATCACTTCYCCATTGGATA	1.67	2.21	2.20	1.22	1.65	2.53	1.53	2.16	1.38	1.56	2.19	1.47	-	-	-	-	-	-
167	14	87094077	10146188	14956	GTTTTCAAAGKGAGCCCTGAC	1.07	0.93	1.00	1.36	0.82	1.15	1.28	0.89	1.51	0.86	1.14	1.21	-	-	-	-	-	-
167	14	87104291	10467744	14957	TAGAGGGAATSTTGCAAAAGC	0.12	0.24	0.24	0.43	1.24	0.95	0.58	0.17	0.40	1.17	0.93	0.59	-	-	-	-	-	-
167	14	87109650	6574951	14958	AAATGCTCTCRAATGTACCCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87123598	1475407	14959	TAATTCATTTKCTTCTCATAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87139357	17123608	14960	AAATCAAGAGYACAGGCATAT	0.22	0.39	0.39	0.43	1.26	0.97	0.68	0.31	0.41	1.21	1.00	0.69	-	-	-	-	-	-
167	14	87152557	17123617	14961	AAAGCTGAATKTGCCTCTTCC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87162431		14962	CATTTGCAAGYACCACATCTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87177236	1958128	14963	AAGTCGCTGCYGGTTAAACAC	0.14	0.13	0.29	0.87	0.35	0.74	0.84	0.19	1.02	0.39	0.79	0.85	-	-	-	-	-	-
167	14	87191568	17123665	14964	TTCTTAATTTYGAGCGCTCGA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87193611	17123671	14965	GCCAACAAATRTGCTCAGATC	1.16	1.42	1.42	0.52	0.28	0.22	0.43	1.35	0.52	0.30	0.25	0.46	-	-	-	-	-	-
167	14	87204744	17123684	14966	TGAATACCATSAACTAAAAAG	0.81	1.18	1.25	0.52	0.31	0.13	0.07	1.18	0.51	0.30	0.12	0.06	-	-	-	-	-	-

167	14	87216295	17123693	14967	CTCCAAAAACRCTAGCGCTGA	0.16	0.16	0.16	0.61	0.28	0.09	0.85	0.07	0.67	0.33	0.09	0.86
167	14	87223882	12432131	14968	GATAAGCAAAYGGAGTGTTAA	0.52	0.48	0.48	0.11	0.18	1.29	1.56	0.39	0.12	0.18	1.26	1.46
167	14	87243310	17123713	14969	AGGAACCTGAYGACAATTCTT	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87243805		14970	AGTCACATCAYAGTCACAAAA	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87256973	17259751	14971	TGATAAACTAYGTAGGCACAC	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87268587	8010274	14972	CAAGTCGTACRGAAGGGCCCC	0.15	0.05	0.05	0.10	1.36	2.23	1.76	0.00	0.06	1.29	2.05	1.66
167	14	87282701	17259779	14973	CAATGCACAGKGGTCAACATG	0.06	0.38	0.38	1.64	1.91	1.43	1.25	0.31	1.88	1.75	1.37	1.21
167	14	87295330	17203279	14974	GCAAAATATGRATTCAGACAG	2.03	2.28	2.28	2.24	2.13	1.09	1.14	2.20	2.69	1.96	1.09	1.09
167	14	87303710	17797921	14975	CGAATCCCAGYAGCTTGAATA	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87311247		14976	ATTCTCACAAYAGCCCTTATA	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87328565		14977	TTGCCTTAAGSCACACTGTTT	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87337216	1017604	14978	TTATCTTCATYGTCCTGAACC	2.89	3.24	3.24	2.80	1.70	2.04	1.13	3.13	2.89	1.64	1.91	1.09
167	14	87345742	11849666	14979	TTGAGTGAACRTCAATAATCT	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87351123	4904396	14980	GAGTAGAGATKGAGGCAAATG	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87359052	8006648	14981	TTTAAATGGGYTTAACTGCTC	0.44	0.19	0.19	2.16	2.86	1.87	1.70	0.17	2.42	2.58	1.77	1.66
167	14	87372794	9323814	14982	CATGCCCATCRTACCTCTACT	1.82	2.45	2.45	2.71	2.89	2.11	1.29	2.36	3.10	2.54	2.01	1.26
167	14	87383870		14983	TCTGGCTACAWCTGGCTCACA	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87399449	1555556	14984	ATTATAGGAGRCAGTGAGAGC	0.23	0.26	0.26	2.05	2.80	1.81	1.63	0.23	2.24	2.48	1.72	1.59
167	14	87404811	17123862	14985	TGGGATATAAYGTTTTTGCTC	0.08	0.08	0.08	0.36	1.74	1.82	1.67	0.00	0.38	1.61	1.72	1.58
167	14	87412471	12432089	14986	TCAAAAGCCCRTTTAATCTGC	0.41	0.51	0.61	0.51	0.49	0.97	1.08	0.57	0.53	0.50	0.96	1.07
167	14	87418880	1450705	14987	ACCTGACCACMCAGTTGGAAC	0.60	0.15	0.16	0.57	0.36	0.23	0.85	0.15	0.64	0.42	0.25	0.88
167	14	87425350	4457933	14988	TGTAGCCCATSCCAAGGCAGC	0.40	0.17	0.17	0.66	0.29	0.38	0.20	0.14	0.67	0.34	0.39	0.20
167	14	87431836	17123888	14989	TGGTTCCCTCRTGAACATGGC	0.66	0.97	0.94	0.49	0.51	0.31	0.24	0.88	0.45	0.51	0.33	0.27
167	14	87438491	7153766	14990	TATTATGTATYTGTTGTATGG	0.10	0.16	0.16	0.37	0.37	0.52	0.32	0.12	0.37	0.38	0.53	0.36
167	14	87444793	7141307	14991	GGCACTTTCTYTCTTCAAAAC	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87453738	366788	14992	TGTTCTATACMCTCCATTTTT	-	-	-	-	-	-	-	-	-	-	-	-
167	14	87461086	12881373	14993	AGGGTCTAAARCACGATGATG	0.06	0.02	0.02	0.10	0.33	0.38	0.46	0.00	0.09	0.33	0.39	0.48
167	14	87470106	412915	14994	CCTGGAAAAAYGTTCACAGAG	0.30	0.08	0.10	0.17	0.12	0.36	0.22	0.07	0.11	0.11	0.36	0.22
167	14	87475652		14995	CAAAAATAAAYGCATATGGCT	0.02	0.08	0.08	0.00	0.13	0.06	0.24	0.05	0.01	0.14	0.07	0.26
167	14	87482935	450976	14996	TGTATTATAGYTGAGAGGACT	0.32	0.08	0.10	0.00	0.00	0.19	0.17	0.08	0.00	0.00	0.19	0.15
168	14	97942526	1542446	14997	CCAGGGCCAAYTGGAGAGGGC	1.08	1.21	1.24	1.18	1.30	0.52	0.75	1.15	1.19	1.26	0.53	0.76
168	14	97955481	1958802	14998	CAACACCTTGWATTCTGACTT	-	-	-	-	-	-	-	-	-	-	-	-
168	14	97968664	1350584	14999	ACTGACAATGWGCAAACTCAC	-	-	-	-	-	-	-	-	-	-	-	-
168	14	97980812	898194	15000	TTCTGAGTTAYGAACTGCTGT	0.98	1.15	1.42	1.32	0.84	1.17	0.70	1.31	1.41	0.85	1.19	0.70
168	14	97994662	973842	15001	GCAAAACCACRGGGACCGAGC	0.89	0.73	0.88	1.51	2.56	1.16	1.04	0.79	1.68	2.29	1.13	1.03
168	14	98006629	2753974	15002	ATTGAAATACRGTTGGATGTG	0.20	0.50	0.50	2.06	2.39	2.26	1.24	0.46	2.38	2.09	2.04	1.20
168	14	98017901	4243720	15003	TATTAACCTARATTTCCCTAT	1.08	1.67	1.67	1.34	1.89	1.89	1.92	1.62	1.69	1.66	1.74	1.78
168	14	98024879	1956847	15004	TAGATCATAGRTTTGAACTCA	0.27	0.61	0.60	1.69	0.66	1.26	1.08	0.54	1.94	0.66	1.24	1.04
168	14	98035383	17097046	15005	TGTAATGCAAYGTTCAGCTAC	1.76	1.54	1.54	0.87	1.03	0.48	2.40	1.40	0.94	1.05	0.49	2.29
168	14	98046050	17097078	15006	GGGTCACCGGRGACAAAAGAC	0.03	0.06	0.06	0.76	0.75	2.25	1.37	0.04	0.75	0.79	2.10	1.34
168	14	98057225	8022320	15007	TAAGTATCAARCTCGTTCAAT	0.18	0.19	0.19	0.17	2.45	1.32	1.39	0.16	0.16	2.27	1.33	1.35
168	14	98068763	1956856	15008	AATACTTAAARCATTTTAAAT	-	-	-	-	-	-	-	-	-	-	-	-
168	14	98076478	17595289	15009	GTGTCTGGAAYCCAGATGAGC	0.82	0.90	0.90	2.92	1.48	1.62	0.85	0.80	3.03	1.46	1.54	0.84
168	14	98084112	2400354	15010	TAACTTACCARGTGTTTAGAG	0.23	0.17	0.17	0.14	2.32	1.24	1.13	0.17	0.13	2.17	1.20	1.15
168	14	98090578	4505236	15011	GCTACCTCAAWTGAAAGTAAG	0.74	0.17	0.13	0.06	0.29	1.45	1.50	0.10	0.02	0.32	1.44	1.48
168	14	98097116	17097298	15012	TAATGACAAASAAGTTTAAGA	0.88	0.11	0.11	0.65	0.17	1.47	1.61	0.08	0.72	0.18	1.42	1.59
168	14	98104636	17097328	15013	AGCTAAGAGTYTCCTTTTCCC	0.82	1.29	1.19	0.66	2.42	1.09	0.92	1.12	0.65	2.24	1.05	0.92
168	14	98114191	17097366	15014	CTTCTGCAAAWATAACTGATT	-	-	-	-	-	-	-	-	-	-	-	-
168	14	98123359	8007003	15015	CCTGTGACTTYTGCATCCTCT	0.71	0.29	0.28	2.97	2.05	0.99	0.77	0.23	3.14	1.93	0.99	0.73
168	14	98130237	11627708	15016	GTCGGCGGTGRGCCTTAGATG	-	-	-	-	-	-	-	-	-	-	-	-
168	14	98137530	8016648	15017	TCTTCCCTTCYACAGAGGTCC	1.27	1.26	1.26	0.79	1.47	1.23	0.89	1.20	0.82	1.43	1.21	0.91
169	15	29084144	12913397	15018	ATTCACCATGYATGAGAAGTC	0.10	0.17	0.17	0.26	0.06	0.12	0.07	0.12	0.24	0.04	0.11	0.05
169	15	29100035	12901022	15019	CTTGCATCTTYGTTATTCCTG	0.17	0.33	0.33	0.09	0.24	0.16	0.02	0.28	0.06	0.26	0.17	0.02
169	15	29111823	2113945	15020	CTACAGTTGARATATGGTATG	1.06	0.22	0.22	0.59	0.14	0.03	0.04	0.19	0.61	0.13	0.04	0.04
169	15	29120612	2911849	15021	GATCCAGATTSAAATATTTGG	0.49	0.88	0.85	0.81	0.07	0.13	0.02	0.80	0.85	0.07	0.14	0.01
169	15	29130654	16956497	15022	TCAAGGGGAGWGTGTGCTCTA	-	-	-	-	-	-	-	-	-	-	-	-
169	15	29140680	2278133	15023	TAGGAGCTGARGCCCTCAATG	0.68	0.88	0.85	0.47	0.43	0.07	0.15	0.79	0.51	0.44	0.06	0.15
169	15	29149946	17815804	15024	ACATTGGATGRTTGCTCTTTC	0.45	0.81	0.63	1.02	0.28	0.53	0.38	0.58	1.05	0.30	0.51	0.36
169	15	29155896	2241494	15025	ATCTCTACTTRCATGACTTTA	0.23	0.41	0.41	0.29	1.00	0.37	0.62	0.38	0.25	1.02	0.39	0.63
169	15	29168484	12910440	15026	TTGGCTGATGSGCAGTTCTAG	0.68	0.28	0.28	1.27	0.96	0.64	0.15	0.27	1.22	0.99	0.66	0.13
169	15	29177180	17228136	15027	CCATTATGAAYTGAAAAAAAA	0.21	0.49	0.49	0.43	1.13	0.48	1.45	0.42	0.39	1.12	0.49	1.44
169	15	29185374	11635657	15028	ATTATGTGTCYAGTGAGCTGT	0.75	1.06	1.06	0.95	1.18	2.55	2.46	1.01	0.98	1.18	2.44	2.34
169	15	29208621	16956564	15029	TTCGTGTAGCRCTGTTTTTGG	0.02	0.01	0.06	1.32	3.26	1.88	1.20	0.04	1.37	3.02	1.87	1.23
169	15	29215548	803534	15030	TGTCAACAAAYCCCTGAACGT	0.39	0.54	0.53	2.08	1.95	1.23	1.01	0.52	2.22	1.83	1.17	0.98
169	15	29228600	1672409	15031	CACTCAAGTARCCTAATAGCC	0.21	0.50	0.50	0.64	0.75	0.83	0.57	0.46	0.64	0.76	0.84	0.54
169	15	29234640	1378847	15032	CCTATGTGAGYGTACATGAAA	-	-	-	-	-	-	-	-	-	-	-	-
169	15	29240203	12899902	15033	GTTGGACACCRTGGCAGGAAA	0.51	0.76	0.76	0.40	0.21	0.24	0.28	0.75	0.39	0.22	0.26	0.29
169	15	29256215	3096464	15034	TTGGCATGCTRTGTTCTCCGT	0.74	0.59	0.59	0.29	0.38	0.12	0.36	0.55	0.31	0.37	0.12	0.34
169	15	29257220	17228178	15035	CTATACTGCAYCATCTATACC	0.45	0.57	0.57	0.79	0.17	0.17	0.16	0.56	0.80	0.18	0.16	0.16
169	15	29277736		15036	AGCCACCAAGRGCGATGGACT	-	-	-	-	-	-	-	-	-	-	-	-
169	15	29282405	1863279	15037	GCCACGCTGTKTTGAGGACAC	-	-	-	-	-	-	-	-	-	-	-	-
169	15	29317050	12913460	15038	ACAGAAAAACYGCCCTTAAAG	-	-	-	-	-	-	-	-	-	-	-	-
170	15	40174495	2412657	15039	CGGGCTAGTGYATCCTCCTCA	0.44	0.47	0.47	0.51	0.73	0.74	0.86	0.45	0.57	0.73	0.75	0.82
170	15	40181660	17748355	15040	TGAGAATGTAMAGCACACAAC	0.79	1.10	1.10	0.24	1.50	0.75	1.53	1.05	0.25	1.42	0.75	1.50
170	15	40188056	675996	15041	TACTAATAGGYGATTGCTGTA	0.69	1.01	1.01	0.65	1.49	2.35	3.17	0.95	0.66	1.46	2.21	2.99
170	15	40201202	776714	15042	GCCTACTCCCRAAAGGGCTCA	1.17	0.00	0.00	0.76	1.92	5.09	3.67	0.00	0.79	1.84	4.55	3.38
170	15	40210922	17749181	15043	CCATGTGAAGSCACTCCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
170	15	40218074	16972725	15044	TTGTGAATGCYGAGCTGCATC	-	-	-	-	-	-	-	-	-	-	-	-
170	15	40224842	622083	15045	AGTCCTGCACMGAGTGGACCT	0.33	0.49	0.49	0.08	1.90	3.57	5.05	0.45	0.05	1.79	3.13	4.40
170	15	40232846	10220859	15046	CAAAGGATGAKGAATACATGG	0.53	0.37	0.37	0.54	1.52	1.68	2.97	0.30	0.51	1.47	1.62	2.64
170	15	40240570	1626437	15047	GCAAAACACAMGGCATATTAA	-	-	-	-	-	-	-	-	-	-	-	-
170	15	40246326	1619030	15048	GAGCCTTCTTYAGCACGTGCT	0.34	0.63	0.63	1.04	0.54	1.08	1.64	0.58	1.26	0.58	1.07	1.54
170	15	40252233	4924627	15049	GAGCTCCCTTYGTTTCCATCT	0.46	0.69	0.76	1.08	0.67	0.53	0.97	0.66	1.37	0.67	0.55	0.98
171	15	42022068	11853395	15050	AAGACAGCAAMAGACAGGGAG	0.34	0.33	0.40	0.11	0.13	0.15	0.25	0.34	0.10	0.13	0.16	0.26
171	15	42029750	8042714	15051	GATAGGTGAASGAAGGAGTAG	0.16	0.23	0.22	0.10	0.14	0.23	0.30	0.18	0.06	0.15	0.23	0.29
171	15	42036489	2930523	15052	CAGGTAGTTAWGTCAGCCTTT	0.53	0.51	0.51	0.26	0.14	0.39	0.25	0.46	0.25	0.14	0.44	0.25
171	15	42053984	2412845	15053	GTCCCATTCCYGCATCTACCT	1.05	1.04	1.04	0.55	0.30	0.24	0.31	0.87	0.57	0.35	0.26	0.34
171	15	42063847	2412849	15054	CGGAAACAAGSACTGTGTGCA	1.20	0.93	0.93	0.80	0.44	0.31	0.24	0.81	0.99	0.45	0.35	0.23
171	15	42091928	8035212	15055	TTCAAGTCTAYAGTAGAATAC	1.46	1.14	1.14	0.55	0.42	0.31	0.38	1.03	0.65	0.45	0.32	0.41
171	15	42108428	10518994	15056	TGTAAAGACAYTGACAAAGAA	1.04	0.80	0.79	0.54	0.27	0.51	0.50	0.67	0.56	0.31	0.57	0.50
171	15	42115404	4923971	15057	CTGAAGCCAAYTAACTAGAAT	1.86	0.22	0.22	0.32	0.62	0.53	0.40	0.21	0.28	0.67	0.58	0.43
171	15	42126211	1426658	15058	CAGTTCCTAAYCTTTTTACAT	1.04	0.80	0.89	0.39	0.56	0.47	0.32	0.78	0.49	0.60	0.51	0.37
171	15	42137357	958485	15059	CCAGCGCTTTRTGATCCTTAG	0.84	0.62	0.62	0.82	0.43	0.33	0.33	0.52	1.13	0.48	0.34	0.39
171	15	42146315	16959032	15060	CTGCTCTTTCWAGATTAAAAG	-	-	-	-	-	-	-	-	-	-	-	-

171	15	42154582	8038096	15061	TTGGCTCTGAMTAGTATAAAA	1.03	0.79	0.79	0.55	0.56	0.30	0.84	0.67	0.57	0.57	0.34	0.85
171	15	42167516	17583428	15062	TTCGTGAACAYCTACCATGTG	0.12	0.24	0.24	0.33	0.32	1.28	0.66	0.18	0.33	0.35	1.23	0.69
171	15	42174675		15063	CAAGCACCTCSAGGGGATTCA	0.17	0.16	0.16	0.28	1.49	1.22	1.36	0.10	0.27	1.39	1.18	1.30
171	15	42190577	2623017	15064	GTAAATATGASGTTCTCCTAT	1.06	0.81	0.70	1.41	1.17	1.54	1.28	0.60	1.68	1.12	1.43	1.22
171	15	42197162	2019074	15065	TGCTTCTTTGYATGCAATTCT	1.84	1.75	1.75	1.68	1.54	1.20	1.28	1.62	1.94	1.46	1.14	1.24
171	15	42203285	2615287	15066	GAGAAAATACWATGTTAGAAA	0.87	0.65	0.68	1.64	1.75	1.30	1.05	0.58	1.92	1.63	1.24	1.02
171	15	42213882	2042739	15067	AGTGAGGAGARTAAGGGTGTG	1.16	1.07	1.16	0.33	1.85	1.52	1.06	1.08	0.33	1.70	1.43	1.01
171	15	42224984	2733208	15068	AAGAGGATTTKGGGTTCTAAA	1.31	1.20	1.20	0.55	0.26	1.52	2.39	1.09	0.70	0.29	1.44	2.13
171	15	42238283	2555376	15069	GCTGAGTCCARTCATTTATTC	1.43	1.32	1.32	0.65	0.57	1.06	1.96	1.21	0.75	0.63	1.00	1.84
171	15	42250716	2733214	15070	AGAATAGTGASAATTTTAGAA	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42260464	17506480	15071	GAAAACATTCKATAGCAATTC	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42266186	2447334	15072	GTGGAGTGTCYGTATTGTCAG	1.18	1.40	1.40	1.05	1.07	1.25	0.51	1.27	1.03	1.08	1.18	0.54
171	15	42273531	2706465	15073	AACTAAACACSGGAGCATTGT	1.18	1.40	1.40	1.70	1.02	0.53	1.10	1.24	1.67	1.00	0.55	1.06
171	15	42280859	7178082	15074	TGAGAAATAGMCCAAAAAAAT	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42294695	2696082	15075	GCCACTTCATKAAAATATAGC	1.27	1.66	1.66	1.22	0.71	0.91	0.88	1.60	1.24	0.71	0.91	0.90
171	15	42300382	2615257	15076	ATTGCCTGACYTAAAAAACAT	1.35	1.85	1.85	0.58	1.01	1.03	0.95	1.80	0.63	1.00	1.04	0.92
171	15	42316154	2663994	15077	TTTTATGAAASGGTTTTTATG	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42355062		15078	AAAGCCACCAWGAGCTAGAAG	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42370178	8024461	15079	TGGCATGGTTRAGCATTACAA	1.45	1.75	1.75	1.25	0.90	1.06	1.02	1.68	1.34	0.86	1.05	1.02
171	15	42381118		15080	TGAGTCCTAARAAAAAGATCA	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42387972	8025727	15081	CACTTGAGTTSTTCCCCTCTT	0.51	0.29	0.29	1.21	1.49	0.87	1.12	0.20	1.49	1.35	0.88	1.09
171	15	42407463		15082	CTATGTTGGTWGTCGAATGTG	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42487755	905302	15083	ATGAAATCACSTAACCAAATC	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42515461	17586255	15084	TGATTTTTTTYCTTAGGTGAC	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42541526	8026945	15085	TTGACTTCCCRGCTCAGGTGA	0.22	0.06	0.06	0.41	1.28	1.18	0.62	0.00	0.41	1.21	1.11	0.62
171	15	42550890	7172106	15086	CATTTTTTTGRAGTGTAGAAG	0.30	0.13	0.13	0.29	0.17	0.26	1.45	0.05	0.27	0.19	0.30	1.43
171	15	42565931		15087	AATTAGCTTTYGTGAAGTATT	0.22	0.57	0.57	0.19	0.10	0.11	0.61	0.46	0.17	0.09	0.13	0.66
171	15	42581233		15088	ACTTTAATACKATTTAGTTAC	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42581784	16964417	15089	CAAATTTTTCMTCTGAAAGCC	-	-	-	-	-	-	-	-	-	-	-	-
171	15	42602452	4611428	15090	AAACTTTGGCRGGATGTAGTG	0.21	0.28	0.28	0.17	0.10	0.91	0.50	0.23	0.16	0.11	0.92	0.51
172	15	51163737	12593509	15091	GATGTCCCACRTTCACACAGA	0.16	0.35	0.35	0.29	0.62	0.69	0.47	0.31	0.28	0.63	0.69	0.49
172	15	51172430	608531	15092	GGCAAAAAAGWTTGATTTAAA	0.25	0.51	0.51	0.90	1.27	0.80	0.50	0.46	0.91	1.26	0.80	0.49
172	15	51186974	690275	15093	GTATATTTAGYTGGTTTATGT	-	-	-	-	-	-	-	-	-	-	-	-
172	15	51198813	627359	15094	CTGTCAATCTYCATTCAATTT	1.13	1.04	1.04	2.07	1.66	1.20	1.62	0.95	2.24	1.57	1.16	1.58
172	15	51205187	1155589	15095	GAGGAGAAAAKGATGAAACAT	0.55	0.83	0.81	0.78	2.33	2.34	1.89	0.74	0.87	2.10	2.17	1.79
172	15	51212254	12595250	15096	TTCCATGATTYTCTTTACCAC	0.16	0.36	0.49	0.45	1.97	3.11	1.95	0.40	0.47	1.74	2.75	1.87
172	15	51225655	16965587	15097	AATTTTCCCAKCAAGTAGCTG	0.52	0.82	0.82	0.33	0.81	1.71	1.93	0.78	0.36	0.81	1.59	1.86
172	15	51237241	1508030	15098	TCTTCATTCTRCTCTTCACCA	0.08	0.05	0.02	0.44	0.28	1.20	1.81	0.00	0.41	0.29	1.18	1.68
172	15	51245627	10518710	15099	TTAGCATCTTSGTCTTCTGCT	0.51	0.79	0.79	0.14	0.47	0.38	2.25	0.74	0.14	0.47	0.42	2.04
172	15	51256859	537047	15100	TCTTGAGACCKTGAGACAAGC	0.21	0.21	0.10	0.69	0.30	1.87	1.69	0.00	0.70	0.33	1.69	1.61
172	15	51268982	690133	15101	CAATGCATGGRCACTAATAAT	0.09	0.09	0.09	0.35	0.96	1.73	1.39	0.06	0.36	0.97	1.63	1.30
172	15	51277922	690399	15102	GCTTTCTGGCMACATTGATCC	0.30	0.54	0.59	1.11	1.31	0.77	1.36	0.55	1.40	1.23	0.75	1.28
172	15	51284586	566855	15103	GAAGAATAATKGGTGTTAGCG	0.22	0.19	0.14	1.17	1.07	0.95	0.23	0.12	1.43	1.02	0.96	0.25
173	15	58528133	17270146	15104	TAAACACAAGYTGCAAGACCC	0.92	1.09	1.09	0.27	0.92	0.50	1.73	1.01	0.22	0.94	0.53	1.63
173	15	58539068	17191421	15105	GAGAAGAAACKGTGGGCCAAA	0.82	1.09	1.09	0.57	0.28	2.88	1.60	1.04	0.59	0.30	2.49	1.52
173	15	58551368	11071537	15106	TAAAAGTAGCRTTTGGAAATG	0.67	0.92	0.92	0.73	2.12	2.10	2.13	0.88	0.80	1.97	1.97	2.02
173	15	58558097	16942593	15107	TGATCTCTCAYGTTCAGTACT	-	-	-	-	-	-	-	-	-	-	-	-
173	15	58564499	4775275	15108	TTTATAGCGCRTAAGTGTTCT	-	-	-	-	-	-	-	-	-	-	-	-
173	15	58583263		15109	TTAGCCCTGGRCCACGAAGAG	-	-	-	-	-	-	-	-	-	-	-	-
173	15	58587201	17270188	15110	CTCACTATATRAGGTCGTTTC	0.08	0.25	0.25	2.06	1.96	2.75	1.93	0.23	2.24	1.87	2.55	1.89
173	15	58609267	2033721	15111	ATAGCATGTTSTTAATTAATC	0.18	0.32	0.32	1.17	2.84	1.67	1.86	0.28	1.22	2.60	1.59	1.79
173	15	58618217	10519053	15112	GGCTTGTACGSTCTTGTCGGG	-	-	-	-	-	-	-	-	-	-	-	-
173	15	58628567	2028122	15113	TATGATATGTRGCAGCTCTTA	0.02	0.10	0.10	0.07	1.02	1.76	1.59	0.09	0.07	1.04	1.67	1.57
173	15	58636062	10431796	15114	CTTAGTTCTCRTGTTCACTCT	0.22	0.49	0.49	0.03	0.10	0.64	1.62	0.42	0.03	0.10	0.65	1.54
174	15	62303537	8034754	15115	TGCTCTGTAAYGTTTCTGAGG	0.97	0.63	0.63	0.28	0.78	0.55	0.64	0.56	0.27	0.80	0.57	0.62
174	15	62312033	8033972	15116	CAATGCCAGARAAATGGCTGT	0.01	0.00	0.00	0.56	0.40	0.83	0.81	0.00	0.66	0.42	0.87	0.80
174	15	62327248	1106912	15117	TGTCCAGTGAWTTATAAAATA	1.06	0.98	0.98	0.49	0.64	0.65	0.65	0.91	0.46	0.64	0.63	0.67
174	15	62328834	16947844	15118	TATGAGTCAAMAGTTGGCCTA	1.17	1.08	1.08	1.20	0.74	0.63	0.51	0.97	1.21	0.75	0.64	0.55
174	15	62346835	6494470	15119	CAAATCATCARGGAAATCAAG	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62384321	1018301	15120	CTTTTTTTTTWAAATTATGTT	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62404379		15121	GACATCTGGGYAGTGGACACT	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62415970	8034610	15122	CATTAGAGAGRAAGTTTACAG	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62424144	3843699	15123	AGAAACACAGYATTAACCAGA	1.88	1.29	1.29	1.22	1.35	0.67	0.40	1.20	1.21	1.27	0.68	0.43
174	15	62435239		15124	CGGGCAGATAYCTGGTCCAGC	0.11	0.29	0.29	1.04	1.45	1.12	0.71	0.25	1.09	1.37	1.07	0.74
174	15	62467444	16947927	15125	GGAAGACGCCMAATCTGTAAT	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62472260	1567985	15126	AAAGAATGCARTACATACGAT	0.90	1.22	1.18	0.66	0.98	1.54	0.98	1.09	0.72	0.99	1.40	1.00
174	15	62486451	9919981	15127	GTTGCTGACAKTGTAATCTTT	0.11	0.10	0.10	0.40	0.57	0.80	1.35	0.05	0.38	0.63	0.79	1.26
174	15	62493312	2046356	15128	ACCAATTGTTRCATCCTTTTG	0.87	1.18	1.18	1.04	0.44	0.53	1.43	1.10	1.26	0.51	0.54	1.31
174	15	62498227	7181518	15129	ACAAACTGAGYATAAAAAGGC	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62522580	936689	15130	CATGGAAGAARGAGGAGAGAT	1.00	1.36	1.36	0.97	1.01	1.09	0.95	1.31	1.05	1.01	1.04	0.94
174	15	62533333		15131	GGGCCTGTGGYATACTCAGCT	0.09	0.09	0.09	0.80	1.36	1.41	0.79	0.00	0.84	1.26	1.35	0.81
174	15	62548934	677561	15132	CCAACTTGCCRCATATATCTT	0.09	0.09	0.09	0.51	1.20	1.10	1.08	0.00	0.55	1.09	1.10	1.06
174	15	62562055	12593770	15133	TGGTAAGGAARGTCAGACCAA	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62572511	16953514	15134	GTTTTTGCCCYCTGAGCTGGG	1.56	1.51	1.51	1.24	0.95	0.95	1.14	1.35	1.51	0.96	0.92	1.11
174	15	62580670	576926	15135	AGTTTCTTCCRCTAATAATAC	1.00	1.36	1.36	1.26	1.27	0.99	0.99	1.28	1.44	1.21	0.96	0.99
174	15	62601640	16948030	15136	GATCTATACCKCATGAATCTC	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62607732	16948036	15137	GCTGAGCACARGGCACTTTAT	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62622459	16948044	15138	CTTAATTTTARGACACACAGC	0.00	0.00	0.04	1.02	1.69	1.33	0.99	0.00	1.02	1.50	1.19	0.99
174	15	62638185	500641	15139	GCAGGCCTTTYATCTGGACCT	1.00	1.36	1.36	0.95	1.08	1.71	1.13	1.26	1.08	1.10	1.49	1.11
174	15	62649963	563766	15140	TTCATGTTATKTTTTTTTGGA	1.14	1.55	1.46	1.00	1.08	1.26	1.45	1.33	1.30	1.05	1.17	1.35
174	15	62653382	547818	15141	TTGTGGCACTRCATTAGCCTT	0.23	0.23	0.16	0.91	1.47	1.33	1.34	0.10	0.97	1.36	1.22	1.30
174	15	62675098	592070	15142	TGGAAATCAGYCCTGCTCTCA	0.16	0.16	0.16	0.65	1.20	1.52	1.50	0.14	0.62	1.21	1.37	1.40
174	15	62683351	16948101	15143	CCTCTTTTGCRTTCTTTATGA	1.50	0.98	1.05	0.72	1.55	1.37	1.68	0.95	0.77	1.49	1.35	1.55
174	15	62701337	4777488	15144	CTGCTGTTGAYTGGCTTCTGG	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62714224	10519273	15145	GTTTATATACYTTTGTGGATT	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62728693	16948160	15146	GCTGGAAATTYGGGGAATCAC	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62737268	16948162	15147	AAAGGCAAAASTGACTGCACT	0.98	0.55	0.62	1.67	1.44	1.64	1.24	0.54	1.81	1.38	1.54	1.19
174	15	62754707	16948170	15148	CAAAGGACGCYGAACAGTTGG	2.00	1.84	1.84	1.19	2.03	1.48	2.43	1.72	1.35	1.78	1.39	2.19
174	15	62766435	16948182	15149	AGGGAAGGTGKGTGCTGCATC	2.00	1.90	1.90	1.36	2.11	2.15	2.58	1.82	1.86	1.91	1.96	2.35
174	15	62776035	16948187	15150	ATTTCACACAYTGACTACAGA	1.87	1.72	1.72	1.26	1.91	3.29	2.61	1.58	1.45	1.69	2.76	2.33
174	15	62808845	12904271	15151	TGCTTGAATTRCTTCCCGAGT	0.24	0.52	0.52	1.33	2.83	2.45	2.89	0.49	1.52	2.40	2.10	2.46
174	15	62823032	3935716	15152	AAGATACACCRGAAAGCAAGC	0.54	0.80	0.75	1.93	2.16	2.41	0.93	0.63	2.27	1.91	2.13	0.93
174	15	62832344	7403350	15153	CCATAGCTTASATCCATTCAA	1.06	1.42	1.42	2.47	2.51	0.74	0.51	1.31	2.96	2.12	0.74	0.56
174	15	62846704	1008917	15154	AGTTCAGTTCYGGGTAATCTT	-	-	-	-	-	-	-	-	-	-	-	-

174	15	62860213	11071809	15155	TCTGTAAAATSGGAATACTAG	0.10	0.10	0.05	1.21	1.67	0.58	0.23	0.00	1.31	1.53	0.60	0.25
174	15	62866644	4238460	15156	AGTTAGGCGTMTCTCATCCCT	0.23	0.22	0.16	0.13	0.45	0.75	0.16	0.12	0.06	0.49	0.77	0.17
174	15	62886703		15157	CCCTGCTTGCYTTCTCCACAA	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62895557	17802279	15158	GGCTCAGAGGWTTGGGTCCAT	0.07	0.17	0.19	0.25	0.31	0.16	0.53	0.20	0.25	0.31	0.16	0.56
174	15	62936982	1107529	15159	ATTTCTGCTTYTCACAAGGGA	-	-	-	-	-	-	-	-	-	-	-	-
174	15	62944535	2010875	15160	GAGTGCAGAAYCGTCCCAGGC	1.22	1.52	1.52	0.59	0.18	0.38	0.13	1.44	0.65	0.19	0.39	0.11
174	15	62957490	871447	15161	GTCGCCTAACYTCTGCTCTTC	0.32	0.01	0.02	0.60	0.77	0.19	0.31	0.00	0.64	0.74	0.20	0.34
174	15	62963661	1719265	15162	GCTAACAGTGRGGAAAGGCCT	1.22	1.33	1.33	1.34	0.85	0.36	0.26	1.27	1.60	0.88	0.37	0.27
174	15	62975956	2630502	15163	CTCAGAGTGTRAGTTTCTGGC	0.63	0.54	0.54	1.43	0.69	0.49	0.32	0.49	1.68	0.72	0.49	0.32
174	15	63003839	11630459	15164	GCTGTTTATGWAGCTCTACCT	0.82	0.55	0.55	0.12	0.37	0.23	0.26	0.52	0.12	0.39	0.26	0.28
174	15	63015237	10851743	15165	TATGCTGGTAYTACAAACTGA	0.82	0.54	0.54	0.04	0.03	0.17	0.30	0.49	0.03	0.03	0.17	0.33
174	15	63028788	11637964	15166	TCATGGTACCMCAACGATGAA	0.24	0.22	0.22	0.21	0.05	0.04	0.49	0.17	0.20	0.04	0.03	0.46
175	15	63570070	1865421	15167	TAGGGGACATRTAACTCTCTT	0.09	0.27	0.27	2.02	0.76	0.91	0.61	0.27	2.41	0.75	0.91	0.62
175	15	63579892	11071846	15168	CTTTGTTGGTRGGTAAACTGA	0.37	0.64	0.67	1.09	1.27	0.60	0.66	0.63	1.13	1.21	0.60	0.65
175	15	63587909	3784448	15169	AAGATATGAAYCAAAGAAAAC	0.18	0.12	0.05	0.22	0.74	0.88	0.47	0.02	0.14	0.73	0.89	0.47
175	15	63592442	352476	15170	GTAATAAAATYGTCAAAAATA	0.55	0.75	0.75	1.71	1.09	0.57	1.12	0.72	1.86	1.07	0.58	1.11
175	15	63633104	421442	15171	CTGTCCTACCKTAAGGAATTT	2.12	2.90	2.90	1.97	1.86	2.22	1.38	2.75	2.15	1.67	2.08	1.36
175	15	63638524	10519294	15172	TGTGGTTGTCMGCCTGAAAGA	0.10	0.28	0.28	2.18	3.17	2.97	2.25	0.27	2.41	2.66	2.64	2.10
175	15	63650039	16948832	15173	GAAATGGCCTYTAACCCAATT	-	-	-	-	-	-	-	-	-	-	-	-
175	15	63657183	11539010	15174	CAAGAACTTCRGGGTGAACAC	0.10	0.28	0.28	0.29	2.14	2.98	2.57	0.23	0.29	1.92	2.56	2.36
175	15	63665258	16948859	15175	TGGACCAACAYTTCCTTTGTC	0.14	0.38	0.38	0.28	0.13	1.27	2.85	0.36	0.28	0.13	1.20	2.56
175	15	63668546	16948867	15176	AAACCATCACRATAGTCTAGT	0.06	0.21	0.21	0.15	1.47	1.80	2.07	0.19	0.15	1.43	1.72	1.94
175	15	63676303	17809330	15177	TTTGCTGTCCRTACCTCCCTT	-	-	-	-	-	-	-	-	-	-	-	-
175	15	63685187	16948871	15178	ATATAGCAATWCTCTAAATTT	0.14	0.29	0.29	1.65	1.80	2.29	2.29	0.24	1.73	1.73	2.13	2.15
175	15	63703580	3743171	15179	CATCGGTTCTWCTTATCAGCA	-	-	-	-	-	-	-	-	-	-	-	-
175	15	63717937	16948889	15180	TATAAAAGCCRGATTACCTAT	0.16	0.38	0.38	1.85	1.53	2.29	2.29	0.34	1.97	1.49	2.10	2.11
175	15	63719658	16948897	15181	CCAAAGGACAYCCTGGAAACT	0.13	0.21	0.21	1.82	2.36	1.99	2.32	0.18	1.92	2.08	1.87	2.13
175	15	63731602	8035639	15182	TCTAAAAGGCYGAGATTAGGG	0.34	0.46	0.46	0.48	2.44	2.30	2.01	0.41	0.59	2.05	2.10	1.87
175	15	63742226	8027260	15183	AAGGCTTGTTKGAGTTGAGTC	0.45	0.60	0.56	0.57	2.49	2.38	2.29	0.54	0.61	2.11	2.08	2.14
175	15	63746783	12591647	15184	ATTAGGAATAYGCAAACATTA	0.08	0.21	0.21	0.60	0.63	2.45	2.22	0.17	0.59	0.63	2.16	2.07
176	15	88573386	7167139	15185	AGCTTGGGCTSCGTGCGTTCT	0.09	0.09	0.09	0.06	0.09	0.29	0.24	0.00	0.05	0.10	0.29	0.23
176	15	88575263	1044813	15186	CAGGATCTGGSAAAGGGAGAG	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88600286	1996179	15187	CTCCAGGAAGRGCATGGACTA	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88610637	9635390	15188	CAGATACGGTRAGACTCAGGA	0.09	0.30	0.20	0.17	0.13	0.14	0.20	0.13	0.18	0.14	0.14	0.21
176	15	88617343	1059495	15189	ATGGCTACTCYGAATTTAAAT	0.43	0.56	0.52	0.17	0.08	0.09	0.32	0.48	0.15	0.08	0.08	0.30
176	15	88626437	16944127	15190	AAGATTTTCARCCATATCTGT	0.01	0.05	0.05	0.22	0.14	0.38	0.16	0.03	0.23	0.14	0.37	0.18
176	15	88639959	16944134	15191	TCTGCATGCCWTTCTTTTCGA	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88651377	16944150	15192	ATGAGATGGTYCTCCAAGAGC	0.24	0.34	0.34	0.22	0.51	0.11	0.14	0.27	0.20	0.52	0.09	0.12
176	15	88654431	8040697	15193	GCTTTGGTCCMCTCATCTCTG	0.21	0.31	0.34	0.49	0.24	0.22	0.07	0.29	0.53	0.25	0.22	0.05
176	15	88666202	9920226	15194	ATACCAATCTRTTGTCTGCTA	0.83	1.25	1.25	0.21	0.20	0.28	0.17	1.18	0.22	0.19	0.31	0.16
176	15	88677812	7163411	15195	AATGCTGAATYGGATAGAACA	0.16	0.32	0.32	0.65	0.25	0.17	0.45	0.30	0.70	0.26	0.17	0.46
176	15	88683405	2123212	15196	TAAACAAAAAYGGTACATTCA	0.14	0.35	0.38	0.36	0.63	0.56	0.50	0.34	0.34	0.63	0.60	0.50
176	15	88688964	16944209	15197	TAATAGGAACMCCAGAGAGGT	0.65	0.05	0.05	0.53	1.61	1.13	0.48	0.03	0.51	1.52	1.12	0.49
176	15	88696363	2589971	15198	TTGAGGTCTTSCTCGGGACTA	0.21	0.44	0.44	1.11	1.92	1.62	1.11	0.36	1.16	1.75	1.50	1.14
176	15	88704315	2589957	15199	AATCAGGACARTTCTGAAACA	0.71	1.11	1.10	0.54	1.68	1.87	1.84	1.03	0.56	1.50	1.73	1.72
176	15	88709938	2601165	15200	TAGATATTCTSAGGGTTATCA	0.06	0.23	0.27	0.73	0.88	1.48	2.34	0.23	0.87	0.87	1.45	2.18
176	15	88717391	2589960	15201	TTGAAGCCAGRAGCTTGCTTT	0.24	0.42	0.42	0.77	1.13	2.22	3.22	0.37	0.99	1.12	2.02	2.79
176	15	88726725	2601183	15202	GAGCTGATGAKGTAAGGATAC	0.17	0.42	0.47	1.08	2.59	3.38	2.28	0.41	1.28	2.33	2.98	2.09
176	15	88738055	2601194	15203	GGTGTTTTTTWGTTGAGTGCT	0.89	1.37	1.37	2.05	3.69	3.20	3.02	1.32	2.21	3.17	2.81	2.71
176	15	88749621	2657948	15204	TAAAGTTGGCRTTGAGAAAAC	0.14	0.38	0.36	2.76	2.64	3.36	4.08	0.34	3.11	2.41	2.97	3.55
176	15	88756019	2589949	15205	ATGCTCCATGRTAAGTGGTAA	0.18	0.24	0.24	2.06	3.51	4.34	3.46	0.20	2.46	2.99	3.75	3.07
176	15	88763630	2526000	15206	ATGAGTCATTYTATGTTACTT	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88769981	2657947	15207	ACAGTTGAAAYGGTGGCTTCA	0.45	0.75	0.75	1.17	2.39	3.44	4.14	0.73	1.34	2.14	2.98	3.51
176	15	88780414	2238321	15208	GATAAGACCCYAGTTTTCCAT	1.83	2.38	2.38	1.24	1.16	3.01	3.95	2.32	1.37	1.13	2.56	3.23
176	15	88786746	2238322	15209	GTTGATGACARAACGAAGACA	0.57	0.22	0.22	1.25	1.70	1.72	2.82	0.18	1.45	1.57	1.60	2.36
176	15	88793691	2301829	15210	ACTTATGACTRTGGCTCTCTC	0.10	0.25	0.27	0.32	1.35	1.48	1.14	0.23	0.27	1.23	1.39	1.12
176	15	88800132	3213649	15211	AAAAATCCTCMTCGCTTTTAA	0.29	0.39	0.39	0.34	0.30	0.97	0.58	0.33	0.40	0.35	0.97	0.59
176	15	88807993	2238324	15212	CTCTTAGAATYGTAAGGCCAG	0.29	0.39	0.39	0.28	0.96	0.67	0.42	0.36	0.28	0.99	0.68	0.46
176	15	88816905	16974212	15213	GTGAGAACAAYCTAGTCCTAA	0.39	0.22	0.22	1.19	0.76	0.52	0.48	0.19	1.17	0.78	0.56	0.49
176	15	88824604	16944485	15214	CCACCATACAMGTAGCAAACT	1.60	2.11	2.11	1.05	0.67	0.52	0.17	2.03	1.10	0.70	0.57	0.17
176	15	88832052	16974215	15215	AATCATTGTGYCCATCCCGTA	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88837980	1978149	15216	GGGATGAAAARCAGGCCCACC	0.33	0.56	0.59	1.05	0.64	0.22	1.40	0.58	1.16	0.69	0.23	1.33
176	15	88843925	2107436	15217	TGTGTGTGGCWATTGAACATG	0.20	0.31	0.31	0.64	0.41	1.78	0.75	0.26	0.70	0.42	1.67	0.74
176	15	88879807	17263706	15218	ACTTGTGTTGMGGAACCAGAG	0.22	0.45	0.45	0.35	2.25	1.12	1.07	0.43	0.34	2.10	1.12	1.06
176	15	88885636	3862437	15219	GAGTGCTGATRGGAACTCCAA	0.25	0.36	0.36	0.71	1.20	1.19	0.96	0.32	0.77	1.23	1.16	0.95
176	15	88895068	4349125	15220	GGAAAGGGGAYCAGAAACGGG	0.65	0.63	0.63	0.67	0.31	1.31	1.18	0.60	0.67	0.33	1.29	1.15
176	15	88908798	16944572	15221	CCCCGAGACTMGTCCCTGCAG	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88925410	16944584	15222	TTGGCTGGCCYGGAAGATCAT	-	-	-	-	-	-	-	-	-	-	-	-
176	15	88936415	6416553	15223	AAAAACATTGYGTCACAGGAT	0.23	0.45	0.45	0.21	0.65	0.55	1.09	0.42	0.18	0.66	0.55	1.05
176	15	88942179	7175350	15224	AGGGACAAAARGAAGTAGAAT	0.15	0.24	0.24	0.20	0.12	0.39	0.68	0.19	0.15	0.13	0.42	0.67
176	15	88948516	1104880	15225	ACTCTTGCAGRGCGAGGTGAG	0.49	0.02	0.02	0.12	0.03	0.13	0.29	0.00	0.08	0.02	0.14	0.28
176	15	88954944	7183485	15226	CATTTCACACWTACATGCAGA	0.56	0.39	0.39	0.03	0.12	0.12	0.10	0.32	0.05	0.13	0.14	0.10
176	15	88975419	16944683	15227	ATTGGTCACTSTTTACCAATT	0.06	0.11	0.16	0.12	0.10	0.16	0.65	0.13	0.08	0.11	0.17	0.65
176	15	88982493	7165170	15228	TGAATGGAACMTGCTTTGTGG	0.09	0.16	0.16	0.10	0.21	0.67	0.50	0.14	0.06	0.23	0.69	0.51
176	15	88993717	16944699	15229	CAGTGGGCCTSACATCAAGGC	0.07	0.23	0.23	0.14	0.48	0.53	0.51	0.21	0.12	0.48	0.56	0.52
177	16	20859599	11649212	15230	GCTTAGAACCRTATCTGTCCC	0.01	0.04	0.04	0.15	0.36	1.89	1.68	0.03	0.12	0.40	1.82	1.62
177	16	20871819	12051478	15231	ATGACCACTCRTATTTCCAAG	0.17	0.33	0.29	0.01	1.08	1.72	2.16	0.24	0.01	1.07	1.66	2.11
177	16	20896562	3115440	15232	GAGATGGTAAYGATACTTTCT	0.03	0.12	0.12	1.32	1.12	1.06	1.95	0.09	1.37	1.11	1.03	1.87
177	16	20916191	3115446	15233	TTGTGTCTTTYTTGTCAAACC	1.09	1.54	1.54	1.09	0.77	1.37	1.72	1.47	1.14	0.78	1.35	1.69
177	16	20943133	330134	15234	TCAGCTTCCAYAGAGAACATT	1.20	1.66	1.66	0.76	1.30	1.63	2.97	1.64	0.81	1.24	1.58	2.77
177	16	20951302	16970821	15235	TCCTTCAAAGYAGGGAAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
177	16	20958710	330150	15236	AGTAGAGGGASATTTCTCCAA	0.05	0.00	0.00	1.12	0.49	1.14	1.59	0.00	1.22	0.51	1.16	1.51
177	16	20971699	9938279	15237	GAAGGAAGCCSGAGAATCCAT	1.44	1.75	1.75	1.44	0.84	1.01	0.79	1.67	1.57	0.85	1.02	0.81
177	16	20985943	858212	15238	TAAGTAAAGAYGGTGAAGCCA	0.64	0.79	0.79	0.76	1.19	0.91	1.03	0.71	0.83	1.14	0.91	1.01
178	16	25578533	12930907	15239	GTTGTGATTGMAGATAAAAGG	0.18	0.42	0.42	0.52	0.42	1.09	1.53	0.35	0.52	0.46	1.10	1.49
178	16	25601780	2966227	15240	CACTGCACCCRCCCATAAGCT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25606680	17703943	15241	AATCTTTCATYTATCTACTTT	0.47	0.45	0.45	0.09	0.51	0.90	0.82	0.39	0.07	0.51	0.90	0.84
178	16	25620576	17703961	15242	CATGGCCAGCSATCTGAAAGA	0.14	0.37	0.37	0.34	0.35	0.53	0.41	0.33	0.36	0.37	0.55	0.40
178	16	25628376	16975134	15243	GAGGTTCCACYGGCTTGCATG	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25664744	17774701	15244	GATGTTACGTYTGGCAAATAT	0.24	0.37	0.37	0.28	0.30	0.22	0.09	0.28	0.27	0.34	0.23	0.09
178	16	25671015	10852292	15245	CACTAATTACRCCAACTAATT	0.08	0.23	0.23	0.19	0.22	0.19	0.31	0.18	0.16	0.24	0.23	0.30
178	16	25680046	6497885	15246	ATCACCATGCRTCATTACACA	0.10	0.25	0.26	0.43	0.21	0.37	0.16	0.23	0.44	0.24	0.36	0.14
178	16	25689143		15247	GTAAAATAGCYAGCAGTTACC	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25704578	4319768	15248	TACAGCTTCCRGTAACCCAAA	0.09	0.07	0.06	0.20	0.53	0.04	0.25	0.05	0.21	0.54	0.04	0.23

178	16	25714802	16975223	15249	GATTTCTTAGYCTTCTCCCCT	-	-	-	-	-	-	-	-	-	-	-
178	16	25758889	4787767	15250	CAGTGGAAACYAAAATGTTCT	0.53	0.06	0.06	0.40	0.02	0.07	0.12	0.04	0.38	0.02	0.05	0.10
178	16	25766868	4496146	15251	TAATCACAGTRAAGTACAGAT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25783639	8044051	15252	TCCATTGTATRTATATTTATA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25797928	4620963	15253	CACATAGCAGRCCTTTAGAGG	0.20	0.03	0.03	0.15	0.09	0.05	0.07	0.00	0.14	0.09	0.04	0.08
178	16	25810187	4592663	15254	TTTAGGAGGGYGTCTCTGCTT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25820663	4787781	15255	TTCCATTACARAATTCTCCCA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25849214	8056908	15256	AAATTCAATCYCAAAACCCAT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25857102	8051001	15257	AGCTGGGAGASAGTTGGAGGA	0.17	0.12	0.14	0.17	0.11	0.15	0.09	0.12	0.18	0.12	0.16	0.09
178	16	25875940	4238929	15258	TGGTGAAGGCRGGAAGAGGCT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25888946	4787792	15259	CTTCTCCAATYATTTATACAG	0.32	0.59	0.59	0.54	0.24	0.05	1.01	0.51	0.57	0.24	0.05	1.04
178	16	25901182	4335774	15260	TTTGTTAAAAYGCCTTGAGTC	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25909019	7196918	15261	TTGGCAATTARTGCTTTAGCT	0.78	1.20	1.20	0.39	0.07	0.28	1.19	1.13	0.39	0.06	0.27	1.19
178	16	25920812	4620960	15262	GGGCAAGGAARATGAACAAGC	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25967078	6497912	15263	AACAAATGAAYGTAGGAACAA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	25992075	7200234	15264	ACATTGGATAYTAGTGTCAAT	0.41	0.40	0.40	0.23	0.70	1.56	1.72	0.37	0.21	0.68	1.55	1.67
178	16	26002801	8049952	15265	TGTCAAATACWAGGGTCCTGA	0.18	0.08	0.08	1.57	1.15	1.21	1.08	0.06	1.62	1.15	1.18	1.04
178	16	26011243	7185420	15266	GCCCAAAGGTRTATACCTGAT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26031718	4787814	15267	AAGCATTTTGKAAAACAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26042623	17413310	15268	TCCACTTAGAWTAATGACTTC	1.52	1.96	1.97	2.31	1.89	1.03	0.57	1.87	2.34	1.82	1.03	0.62
178	16	26067217	6497930	15269	TACCAAGAAGMGTAACAACTA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26078831	7192683	15270	ATCAGTGGTCRGTTATTACAT	0.26	0.27	0.25	1.00	1.45	0.56	2.29	0.22	1.12	1.35	0.57	2.25
178	16	26094704	7204296	15271	ACTCAGTAAAYATCTGGCTGA	0.45	0.52	0.52	0.44	0.91	4.80	2.82	0.46	0.43	0.92	4.39	2.68
178	16	26113764	17774978	15272	TTCTTATCCTYTCCACTACCC	0.00	0.02	0.02	0.18	4.73	4.46	3.96	0.00	0.15	4.17	3.95	3.65
178	16	26124641		15273	AAACTGTCGGRCTGGGCTGAC	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26135788	889785	15274	TAGATCTTACSTGGAGCCAAA	0.39	0.56	0.56	3.84	4.34	2.99	2.71	0.50	4.15	3.80	2.71	2.48
178	16	26146585	1895545	15275	GATTATCGTTYGTCTTTCCTT	3.13	3.74	3.74	2.20	2.85	3.83	2.15	3.67	2.28	2.60	3.34	2.02
178	16	26150812	17626198	15276	ATTTATGCCARCTGTTGTACC	0.96	1.41	1.41	2.03	1.72	2.21	2.33	1.35	2.26	1.65	1.99	2.16
178	16	26170740	1424220	15277	GGAAAGACTTKCCTTGCTTTG	0.12	0.27	0.27	1.08	1.75	1.15	1.29	0.24	1.19	1.65	1.13	1.27
178	16	26177938	1541708	15278	GCCTGGCTTTRCATCAGCCTC	2.07	2.68	2.68	1.62	1.45	0.46	0.52	2.64	1.68	1.44	0.46	0.52
178	16	26184700	9807000	15279	AAATCACACCKTAGCTTCCCC	1.06	0.57	0.57	2.32	1.24	0.87	0.27	0.49	2.54	1.22	0.91	0.27
178	16	26192254	12928231	15280	TGAATATCCASTGACAATGAA	0.78	1.14	1.14	0.22	1.19	0.86	0.58	1.05	0.22	1.15	0.87	0.58
178	16	26200785	4530142	15281	CCTCTGGAATRTGTGATATAA	0.01	0.06	0.06	0.59	0.40	1.23	0.72	0.03	0.61	0.42	1.26	0.68
178	16	26201987	7202159	15282	CTCTAAAGAARGCCCTGGACT	0.59	0.88	0.88	1.04	1.60	1.52	1.12	0.83	1.07	1.55	1.41	1.12
178	16	26214430	4787827	15283	CCTCCTTCTGKTTCTCTTTGG	0.73	1.18	1.18	1.72	2.79	1.19	0.96	1.10	1.70	2.61	1.15	0.94
178	16	26226003	9937183	15284	GCTAGTTTGTRGAACAATGCA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26236156	1154722	15285	GTGATCCTCTSTCTGCTCCCA	1.02	0.92	0.92	1.90	1.08	1.36	1.59	0.90	2.16	1.07	1.33	1.53
178	16	26241106	3803710	15286	CCAGTGGTGASAGAATGGAAG	0.80	1.17	1.17	1.64	0.96	0.74	1.53	1.11	2.13	0.96	0.76	1.50
178	16	26255281	4787367	15287	AGAAATGTGTKTATGTCATCA	0.45	0.76	0.76	1.05	1.75	1.43	0.40	0.77	1.15	1.64	1.39	0.40
178	16	26265221	17503574	15288	AAAATAATAGRATTTGTGGAT	1.26	1.77	1.77	1.49	1.88	0.99	0.88	1.72	1.56	1.73	1.00	0.87
178	16	26278433	9931576	15289	CACCAAGGCCRCAGGTAGTTA	0.18	0.31	0.31	1.23	0.84	0.97	0.40	0.26	1.42	0.86	0.96	0.41
178	16	26291884	16975812	15290	TCTATTAAGCKCTAAGCCTCA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26297554	2881409	15291	AGGAAGCCAARCCCACAGCTC	0.38	0.40	0.40	0.30	0.86	0.30	0.46	0.39	0.28	0.90	0.30	0.47
178	16	26305116	2214030	15292	TGTCTCTGCTKGGTGTCAACA	0.61	0.71	0.71	0.22	0.13	0.22	0.18	0.60	0.22	0.14	0.21	0.17
178	16	26314435	1157804	15293	TGGTCTCTACYTCCCAGGGAT	0.22	0.49	0.50	0.13	0.01	0.03	0.30	0.46	0.13	0.01	0.03	0.29
178	16	26318745	1029376	15294	CTGAGAAAATRGGTTTAAGTC	0.04	0.02	0.02	0.04	0.02	0.10	0.26	0.00	0.05	0.01	0.08	0.28
178	16	26334893	16975842	15295	GAAATACTCAYGAGACTTGCT	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26354075	7196027	15296	GAATCATGGCRCAGAAAGATA	0.00	0.02	0.02	0.05	0.34	0.08	0.61	0.00	0.02	0.35	0.08	0.63
178	16	26363940	11643516	15297	TATCTATCATYTAACCATAAC	0.01	0.08	0.08	0.83	0.40	0.47	0.16	0.05	0.89	0.43	0.45	0.17
178	16	26373581	7188924	15298	CTCTGGCAGCYGGAAGCAGGC	1.22	1.64	1.64	0.92	0.99	0.55	0.73	1.55	1.02	1.00	0.53	0.74
178	16	26381711	8064084	15299	GTGGCAGTCAKTATATTTATT	0.00	0.02	0.02	1.39	1.31	0.49	0.30	0.00	1.53	1.29	0.50	0.31
178	16	26406959	16975887	15300	ACAGATTGAGRAGTTCTACAC	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26414030	1858860	15301	TGTCCCATGARACTGTGGCTC	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26420768	16975911	15302	AGATGAAGACYGTGAGACCAG	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26425212	16975928	15303	CACTTGATTTYTCTTGTTACA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26438412	4787847	15304	TGTGAGACTGYAAATTAATGA	-	-	-	-	-	-	-	-	-	-	-	-
178	16	26460770	17775884	15305	TTTTCAAAATRTCTTCCCCTG	0.50	0.81	0.72	0.25	1.11	0.69	0.45	0.62	0.25	1.12	0.68	0.46
179	16	27529217	916763	15306	GGAGAGACCTWCCTAGGGATC	0.21	0.31	0.31	0.53	0.38	0.27	0.16	0.27	0.58	0.39	0.29	0.15
179	16	27540876	718965	15307	CACCCCACTAMATTGTGCAGT	0.19	0.45	0.48	0.59	0.51	0.16	0.16	0.42	0.61	0.55	0.17	0.15
179	16	27564142	233466	15308	TTCATGAGTGSTGTCTTAACA	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27571941	233468	15309	ACTAAAAATGRCATATTTCAT	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27586241	16952081	15310	GGTCCAGGCARATTAATAATA	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27600870	8048175	15311	ATGAGAGTGAYTTTCTGATTC	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27610271	12929432	15312	TAGATCCACCRTCCTCTAGGT	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27617625	12925331	15313	TGCAAACTGGYGGGTCAGTGA	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27619789	963999	15314	CAGAGATTCCRGGGACTAAAA	0.17	0.39	0.39	0.07	0.33	0.23	0.48	0.36	0.03	0.36	0.23	0.50
179	16	27629342	12919365	15315	TCAGCTTCATYCACAATTATC	0.25	0.43	0.43	0.24	0.06	0.83	0.24	0.39	0.20	0.06	0.84	0.24
179	16	27640930	8043889	15316	GACTCATCTGYGGGATCTTGC	0.03	0.00	0.00	0.29	0.71	0.16	0.16	0.00	0.31	0.72	0.18	0.17
179	16	27649057	9938187	15317	GTAGACTTCCRCTGGATCACA	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27661631		15318	CTATGCAAAGSCAAGGCATGC	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27670373	17514997	15319	CTTATGGTCCRTGCATTCCAT	0.34	0.34	0.34	0.91	0.34	0.14	0.17	0.24	0.96	0.37	0.14	0.19
179	16	27687879	1038189	15320	GACTTTGAAAYTGACCAGTAG	0.10	0.16	0.16	0.06	0.27	0.27	0.22	0.11	0.03	0.28	0.28	0.24
179	16	27707178	745604	15321	GTGCCCATAGYTGCGGTGATC	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27726752	1559167	15322	TACATTGAAAKGCACAGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27735359	4787993	15323	GATGGGAAAGKTGAAGCGAAG	0.12	0.30	0.30	0.31	0.27	0.26	0.74	0.28	0.31	0.30	0.29	0.72
179	16	27746355	772973	15324	CTGGCCCATARGAGCAGTTCT	0.75	0.82	0.82	0.40	0.35	0.47	1.37	0.76	0.38	0.37	0.44	1.38
179	16	27758715	1709795	15325	GGCTAATTGTKTGGCTTTCAA	0.53	0.27	0.27	0.38	1.20	1.49	0.63	0.26	0.38	1.17	1.47	0.64
179	16	27772260	10438534	15326	AAATCTTTCCMGCTCCAATTT	0.37	0.34	0.34	1.86	2.69	1.22	0.68	0.28	2.06	2.46	1.22	0.68
179	16	27778015	8053229	15327	CTCTGCAGGCYCTTGGTCTTC	2.32	2.88	2.88	3.77	2.30	1.30	0.54	2.83	4.02	2.12	1.26	0.54
179	16	27783523	754132	15328	ATGAGACCCARCAGGCTTTGA	3.50	4.08	4.25	3.08	2.66	1.26	1.90	4.16	3.22	2.47	1.26	1.80
179	16	27799488	1645363	15329	TAGAAACTTTSAGAACCCCTT	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27808998	1423045	15330	AGATATTCTCYGGAGTCCCAA	0.82	1.28	1.26	2.25	2.10	3.37	1.42	1.21	2.40	2.02	3.09	1.34
179	16	27816756	11644117	15331	CCTCTGTAAAYGGCAGCCTAT	0.49	0.62	0.62	1.06	4.57	1.93	1.72	0.53	1.07	4.12	1.83	1.69
179	16	27826754	12708705	15332	ACCTTGGCAAYTGCATCTGCA	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27837681	2052544	15333	ACCATGAAATKCTATGGGAGA	0.48	0.32	0.32	2.34	1.98	2.95	1.23	0.28	2.50	1.86	2.62	1.19
179	16	27844106	876081	15334	GGCAGGGCCARCATTTCAGGC	2.13	2.76	2.76	1.47	1.47	2.23	1.33	2.68	1.61	1.39	2.06	1.32
179	16	27851671	7193702	15335	CCATAAGAATRTCCCCTGGTG	0.09	0.15	0.13	1.30	1.61	1.83	2.17	0.10	1.71	1.56	1.73	2.09
179	16	27852854	11861542	15336	TTAAAGAGGCRTTGATGAGAA	0.09	0.20	0.19	0.10	2.16	2.79	2.51	0.16	0.10	1.93	2.55	2.32
179	16	27865626	7193224	15337	CGCAAACTGARTTATTCCAAG	0.07	0.19	0.19	0.47	0.82	3.07	1.55	0.16	0.47	0.79	2.74	1.52
179	16	27874886	7194904	15338	CCAATAATTTRCAAAAAGGAT	0.65	0.36	0.36	0.53	1.03	0.96	1.08	0.32	0.55	0.99	0.98	1.06
179	16	27886219	9941164	15339	AAGAATCACAMGGCCACAGAT	0.29	0.59	0.59	0.26	0.76	1.35	0.48	0.56	0.24	0.77	1.31	0.47
179	16	27893462	8045501	15340	CCTCACCATCRCACACCATTG	0.09	0.29	0.29	0.26	0.25	0.40	0.47	0.26	0.22	0.26	0.41	0.46
179	16	27900129	8054996	15341	ACTTGCTGGGYGGGCAGAGAA	0.02	0.07	0.07	0.39	0.32	0.36	0.25	0.06	0.37	0.35	0.38	0.28
179	16	27922061	11640841	15342	GGAGGCTGAGYGGCTGCAAAA	0.95	0.87	0.83	0.26	0.19	0.50	0.18	0.78	0.24	0.18	0.53	0.19

179	16	27930557	11074888	15343	GAGCAACTGTYTAGAGGGATT	0.21	0.37	0.37	0.32	0.18	0.18	0.47	0.32	0.30	0.18	0.17	0.45
179	16	27947087	205383	15344	TACATGAGAARTGCCTAGACC	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27967543	205402	15345	ACTCATAGGAYATGGCTAAAG	-	-	-	-	-	-	-	-	-	-	-	-
179	16	27969482	47666	15346	CTCCATCACCRTTAGAGAAAA	0.87	0.79	0.79	0.11	0.19	0.12	0.15	0.76	0.12	0.19	0.11	0.16
179	16	27991410	4788035	15347	AAAGTGTCATYGAAGAATCTT	0.28	0.13	0.14	0.08	0.02	0.08	0.04	0.12	0.07	0.02	0.08	0.03
179	16	28012030	205355	15348	ACAGAAATTCYTCACTGAAGA	0.01	0.01	0.02	0.10	0.06	0.02	0.11	0.00	0.08	0.05	0.03	0.13
179	16	28027257	16939824	15349	GACCCTCATCMATCTGGGAGA	0.48	0.47	0.38	0.07	0.08	0.08	0.01	0.26	0.08	0.09	0.09	0.01
180	16	50178482	17340527	15350	AAAAGTTGTAYTTGGATTGTG	0.63	0.60	0.67	0.13	0.04	0.31	0.24	0.57	0.09	0.04	0.32	0.27
180	16	50187872	16950107	15351	GTCATGTGATRGGCATCCCTT	-	-	-	-	-	-	-	-	-	-	-	-
180	16	50200614	1498766	15352	AATTAAGAAGYGTGTTTTTAA	-	-	-	-	-	-	-	-	-	-	-	-
180	16	50212580	1498767	15353	ATAGTGGTTAYGTATTTTTAT	0.11	0.18	0.18	0.45	0.86	0.34	0.39	0.16	0.44	0.84	0.35	0.39
180	16	50223747	2647970	15354	TATGTTTGTARTGTCTTAGGG	0.10	0.30	0.30	1.80	1.91	0.70	0.36	0.26	1.90	1.76	0.69	0.37
180	16	50258599	10521243	15355	CCTTTTTTTCRTGTAGCCTGA	-	-	-	-	-	-	-	-	-	-	-	-
180	16	50271614	11859590	15356	CTATTTGCCARAAATGGTGTC	1.47	1.05	1.05	2.24	1.52	1.18	0.90	1.02	2.42	1.47	1.16	0.92
180	16	50279920	1461927	15357	AAACCTTTAGYTCAAGAAACA	1.56	1.10	1.10	0.57	2.87	1.96	0.82	1.01	0.64	2.42	1.77	0.87
180	16	50291776		15358	TGATAGTGGGRGAGTACAGTC	0.03	0.15	0.15	0.93	0.66	1.44	1.07	0.13	0.92	0.66	1.36	1.05
180	16	50300556	1870821	15359	AGAAGAGGATRCTAGCAGACC	0.80	1.26	1.26	0.88	0.31	0.23	1.06	1.18	0.93	0.30	0.24	1.03
180	16	50323508	4784633	15360	AGTGAGTAGARAATGAAAACA	-	-	-	-	-	-	-	-	-	-	-	-
180	16	50331612	4784639	15361	GCAAAATTACRGGGGACACTG	-	-	-	-	-	-	-	-	-	-	-	-
180	16	50340590	1461940	15362	CTTTTCCTTCYGAATTTCCTT	0.66	0.74	0.72	0.90	0.29	0.25	0.34	0.68	0.98	0.33	0.30	0.29
181	16	57771254	4511520	15363	TAGTGGACAGYGAACAGATAC	0.03	0.13	0.13	0.42	1.50	0.98	1.90	0.06	0.42	1.43	0.98	1.79
181	16	57794417	4427788	15364	AAGCATTCCARGCTCTTCTTG	-	-	-	-	-	-	-	-	-	-	-	-
181	16	57827293	1000100	15365	TTTAACATACWGGTTTTCTAA	0.18	0.25	0.25	2.78	1.86	1.62	1.42	0.23	3.03	1.77	1.53	1.35
181	16	57837122	6500027	15366	TATTATTTTTWAAATGTGGTA	0.36	0.31	0.31	1.04	3.83	2.30	2.32	0.29	1.18	3.16	2.14	2.16
181	16	57848243	8047595	15367	ATATGTAAGARACTGTTTGTT	-	-	-	-	-	-	-	-	-	-	-	-
181	16	57860255	9934151	15368	CTCCTCTGAARTGACTTGTTA	0.17	0.28	0.28	1.17	2.01	3.51	2.98	0.23	1.42	1.83	3.06	2.77
181	16	57866980	17258073	15369	TTTAAATCAARCAGAAAATAT	0.66	0.79	0.98	1.20	0.85	2.67	3.31	0.90	1.63	0.84	2.42	2.94
181	16	57879327	1117306	15370	AAGACATATCRTATGCTCTCT	0.23	0.22	0.28	1.00	1.40	1.10	2.32	0.21	1.14	1.33	1.09	2.18
181	16	57885832	1593112	15371	CAAAGGGAATYGGTGGCAGAA	0.48	0.40	0.40	0.65	1.32	1.27	0.72	0.38	0.69	1.28	1.23	0.75
181	16	57892785	4784075	15372	AGATCGCAGTMGCTTATAGCA	0.40	0.70	0.71	0.47	0.67	0.57	0.49	0.65	0.49	0.69	0.60	0.52
182	16	65329111	7204805	15373	CTGCCTAACAMAAGAAAGGGT	0.53	0.92	0.92	0.63	0.05	0.97	0.86	0.87	0.66	0.05	0.98	0.85
182	16	65350727	363157	15374	TATGTGTAGAYGTCACAAAAT	0.12	0.33	0.31	0.34	1.73	0.90	0.67	0.30	0.32	1.64	0.92	0.68
182	16	65355355	8061964	15375	GTGAAAAAGCRTAGTATTCAG	0.59	1.01	1.01	2.84	2.04	1.06	0.92	0.94	3.27	1.93	1.04	0.93
182	16	65363457		15376	CTACTTTTTAMAAATCTTTTA	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65372261	16956948	15377	TAGAGATACAWCCTTTGCATG	0.95	0.68	0.42	2.65	2.66	1.69	0.93	0.33	2.92	2.36	1.59	0.92
182	16	65386956	12931266	15378	AATCTAAAGASTTAAAATGGA	0.65	1.10	1.10	2.99	2.51	1.73	1.48	1.05	3.53	2.26	1.60	1.47
182	16	65395918	543419	15379	TGCATTTACAYTTTGAACACT	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65405159	16957014	15380	CCAAAGTTTTWGCAGCAATGT	0.78	1.02	1.10	0.53	3.08	2.16	2.63	1.01	0.54	2.53	1.95	2.37
182	16	65411630	363173	15381	AGTAAAAATGYTTTCTTGAGT	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65424134	422945	15382	ACCTATGGACKTCATGAAAGG	0.16	0.21	0.22	0.40	0.21	3.25	3.69	0.21	0.41	0.24	2.73	3.08
182	16	65440620	185042	15383	CTCACTGGGTRTCAAGGCAAG	0.52	0.83	0.83	0.46	1.93	1.93	4.14	0.79	0.46	1.73	1.72	3.24
182	16	65448584	467130	15384	GCTGCTGCTGYTGCAAAGGCT	0.25	0.56	0.56	2.05	1.88	2.37	1.86	0.52	2.15	1.70	2.07	1.72
182	16	65467586	7190459	15385	TAAATTGAAAKAAGTAGAATT	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65472947	17700154	15386	GGAGGCAGATRTGAAGCTTTT	2.68	2.62	2.62	1.90	2.05	1.78	1.09	2.45	2.16	1.86	1.74	1.02
182	16	65478450	10153119	15387	AAGTTTCTCTRAATCCTTTCC	1.49	1.44	1.44	2.07	1.93	0.95	0.80	1.32	2.54	1.81	0.94	0.84
182	16	65485864		15388	GGGCTTTTGGSTATTCTTGTT	0.67	0.66	0.66	1.44	1.33	0.76	0.67	0.46	1.59	1.28	0.76	0.68
182	16	65491654	3843712	15389	TAACCTTTTCYACCCTTATGG	0.10	0.20	0.20	0.21	0.97	0.78	1.11	0.17	0.22	0.89	0.81	1.05
182	16	65504788		15390	TCTTCGGGGCYCTTTCCCACT	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65521692	17767961	15391	CCTACAGTCTRTCCAGGTGAC	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65543407	6499106	15392	TCTGTTAGGCRATTTTCCATC	0.24	0.15	0.17	1.14	1.00	1.37	1.28	0.13	1.17	1.00	1.32	1.24
182	16	65557047		15393	GAGATTTTCTSAACCACAGAC	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65567798	12446329	15394	TCTCCACGTGYCACTGAAGTC	0.94	0.92	0.93	0.51	1.21	1.38	1.01	0.80	0.51	1.18	1.32	1.01
182	16	65597836	3848290	15395	TGAGCACCACRCTCGTGGAAT	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65639794	13337006	15396	GACCAGGGGARAGAATTGAGC	-	-	-	-	-	-	-	-	-	-	-	-
182	16	65645146		15397	ACTGAAACCAYTGCTCACCGT	0.36	0.36	0.36	1.97	1.03	0.69	1.25	0.27	2.32	1.05	0.73	1.26
183	17	19381812	8080953	15398	CTATTTGACAYTGACTTGTTC	1.36	1.34	1.34	0.69	0.66	0.60	0.46	1.15	0.72	0.68	0.60	0.45
183	17	19384037	2453584	15399	TTGTATCCGASACATCTAATG	0.01	0.04	0.04	0.90	1.03	1.79	0.92	0.02	0.93	1.04	1.74	0.92
183	17	19399564	16960203	15400	TCTACATCCTYGGGAAAAAAC	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19405783	8065082	15401	TTCTTAGTATYGGCCAAAGTG	1.05	1.21	1.16	0.82	0.53	1.04	2.11	1.09	0.84	0.52	1.00	2.01
183	17	19417507	2440158	15402	ACTGCACCCTYTACATCTTGG	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19429443	2453589	15403	GTGTTTATCARGCCAGAGTCG	0.63	0.79	0.79	0.85	1.08	0.81	1.65	0.74	0.92	1.06	0.83	1.63
183	17	19439840	2440162	15404	GGTAAGAACTYGGGTGAGACT	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19459213	2453608	15405	CCACCAAAAAYGAGGTATTGT	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19486426	8074500	15406	TGGGCTAACTYCTCCGCCCCC	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19496568	1004491	15407	CTCCAACATAYGTGTTTACTG	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19506537	2108971	15408	TGGAACAGTGRACTAAGGTTT	0.80	1.30	1.30	1.70	1.71	1.77	0.83	1.25	1.79	1.56	1.73	0.83
183	17	19516313	2072331	15409	AGGTGAAGGCRAGAACTCTGG	1.13	1.38	1.28	0.88	3.27	2.02	1.01	1.25	1.09	2.88	1.95	0.98
183	17	19524677	12937179	15410	GTTCAGACTARTTTGAGTTCT	1.03	1.22	1.22	1.44	2.26	2.30	1.12	1.16	1.56	2.07	2.18	1.11
183	17	19549365	4925042	15411	TGGCCACCTCRTAGATGACAG	0.18	0.14	0.14	1.37	2.14	2.53	1.50	0.11	1.40	2.00	2.36	1.49
183	17	19563235	11656096	15412	CAGTAGAAACRAACTGGGATC	1.62	1.51	1.55	1.06	1.37	1.48	2.15	1.48	1.09	1.34	1.44	2.05
183	17	19569055	7222877	15413	CACAACCTCASTGTCTTCATA	1.49	2.10	2.05	0.93	0.63	1.27	1.32	1.97	0.99	0.66	1.21	1.27
183	17	19575299	2016823	15414	TCAGGGGCCCRTGCCCTACCT	0.98	1.49	1.49	1.60	0.83	0.65	1.93	1.40	1.78	0.81	0.65	1.87
183	17	19581913	1042183	15415	AAATTGTATTYGTCTCTTTAT	1.22	1.78	1.78	1.57	1.84	1.27	1.00	1.68	1.95	1.73	1.22	0.97
183	17	19589841	4646787	15416	CATCCCAAAGRTCCGAAAGAA	1.27	1.74	1.74	1.46	2.62	2.11	1.29	1.67	1.69	2.32	1.93	1.27
183	17	19593167	3760487	15417	GCACAATGCTRTCGTCTTCCT	0.82	1.27	1.27	1.24	2.19	2.76	1.48	1.24	1.44	1.87	2.29	1.41
183	17	19604339	8067794	15418	CTGCACCGACYTTTTCTTCCA	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19615696	205111	15419	ACCTGCCAAAYTGAGTTGCAG	1.06	1.04	1.04	1.11	1.69	1.42	1.21	0.92	1.40	1.46	1.32	1.16
183	17	19627899	205090	15420	AACCTGCTGARGTGACAAAGG	0.89	0.87	0.87	0.93	1.07	0.92	0.99	0.74	1.24	1.05	0.90	0.94
183	17	19641940	157387	15421	TTGAACAGGAWGATTGTTACT	1.16	1.40	1.13	0.66	1.75	1.22	0.88	1.00	0.68	1.52	1.12	0.87
183	17	19654798	157407	15422	CTCTAGTTCCRTAAAATGTCG	0.08	0.44	0.44	1.21	1.76	1.96	0.95	0.36	1.41	1.59	1.80	0.92
183	17	19663067	16960456	15423	TAATTCAACAWAACCCACTCT	1.66	1.92	1.99	1.22	1.96	1.54	1.25	1.92	1.37	1.81	1.41	1.22
183	17	19670087	157397	15424	GGCTAAAAAAYGCTTCTGTAA	1.20	1.17	1.17	2.31	1.44	1.25	0.69	1.02	2.71	1.37	1.23	0.69
183	17	19692076	281346	15425	AAACTTTAGAMAAAGGCTTTG	2.12	2.07	2.07	1.20	2.37	0.56	0.56	1.89	1.46	2.09	0.60	0.58
183	17	19702371	8066134	15426	TCCTGTAAGASTTCCACAATG	-	-	-	-	-	-	-	-	-	-	-	-
183	17	19709773	281342	15427	ATACCATTCCRCATAAATAAC	1.58	1.55	1.55	1.14	0.53	0.87	0.23	1.38	1.33	0.54	0.89	0.24
183	17	19728534	281365	15428	AAACAGTATTYATCCTTGAGG	1.13	1.10	1.46	0.74	0.42	0.28	0.38	1.30	0.79	0.42	0.29	0.40
184	17	28595673	1553040	15429	TGTTTACGCARACACAAAGCT	0.52	0.00	0.00	0.22	0.17	0.27	0.17	0.00	0.17	0.19	0.30	0.17
184	17	28606834	1995100	15430	TAAATTCTCARAAATCAAATA	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28615256	17248888	15431	CAATCAATCTKCAGAGGCACA	0.54	0.51	0.48	0.17	0.16	0.26	0.66	0.47	0.15	0.16	0.26	0.66
184	17	28624412	1002317	15432	GGAGTGGAGARTTAAAAAGTT	0.46	0.09	0.09	0.30	0.32	0.20	0.37	0.07	0.32	0.35	0.21	0.41
184	17	28631983	1532457	15433	TTATGGATGTRAGTTCACAGT	0.39	0.13	0.13	0.46	0.42	0.28	0.14	0.11	0.48	0.42	0.29	0.15
184	17	28648529	4795764	15434	TTGCTTCAGGRATTTCATGGA	0.80	1.26	1.26	0.68	0.31	0.30	0.25	1.15	0.69	0.36	0.35	0.26
184	17	28655588	8074585	15435	AAAGTGTTCTYACTGTAATAG	1.12	0.64	0.68	0.79	0.42	0.12	0.34	0.61	0.91	0.46	0.11	0.34
184	17	28662692	6505334	15436	CTGCTAATTCYTCATGTACCT	0.95	0.53	0.53	0.31	0.38	0.22	0.31	0.51	0.28	0.41	0.21	0.30

184	17	28663615	1391077	15437	TGGCAGACATYAGAGAGGACC	0.96	0.68	0.68	0.49	0.05	0.19	0.25	0.62	0.50	0.03	0.17	0.26
184	17	28676435		15438	TGACCTAAACWGGTTTGGGAT	0.60	0.31	0.31	0.25	0.09	0.12	0.05	0.26	0.26	0.10	0.12	0.06
184	17	28682496		15439	GCTCAAAGATRTTAAGATGTT	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28693656	1875873	15440	GCTAGGGCCTSTCTTCTTGCC	0.33	0.25	0.25	0.01	0.26	0.11	0.69	0.21	0.00	0.29	0.13	0.74
184	17	28701273	439783	15441	ATTCTACCTGYTCCTTTTTAT	0.53	0.12	0.10	0.53	0.08	0.90	1.14	0.08	0.56	0.09	0.90	1.13
184	17	28706773	7224450	15442	CTCTGTTCCCRTAACAACCCT	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28712566	10512443	15443	ACCAAATAGCYTTATGCACCT	0.65	1.13	1.13	0.49	1.81	1.76	1.03	1.04	0.47	1.70	1.71	0.98
184	17	28718074	1007035	15444	TGGCAAATAGKTTCACTTTCA	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28727436	2347154	15445	GGGGTGCTCCYTTGAATCACA	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28733779	7207801	15446	TCCCTGTAACRTGAGTTTGAC	0.48	0.73	0.73	2.14	1.96	1.37	1.48	0.68	2.24	1.87	1.33	1.43
184	17	28752847	9898140	15447	ATCTTTGTTCRCTTCCCAGGA	0.54	0.52	0.59	2.73	2.05	1.54	0.81	0.55	2.94	1.98	1.51	0.84
184	17	28759358	6505339	15448	AATAACCAACSTTTGTTGCAT	0.41	0.52	0.43	1.70	2.97	1.64	0.46	0.40	1.68	2.64	1.58	0.50
184	17	28764852	16968315	15449	TTCATTAGATYCCACTCACTC	1.27	1.55	1.55	1.06	1.56	1.81	0.80	1.46	1.03	1.50	1.69	0.78
184	17	28772713	16968324	15450	AGCAAGTTGCRTTGACTTATT	1.27	1.55	1.55	1.26	0.44	2.58	1.48	1.48	1.32	0.43	2.38	1.44
184	17	28779746	1504576	15451	TGGCCTCATTRGAGGGAAGAA	0.18	0.44	0.44	0.83	1.51	1.26	1.66	0.38	0.86	1.44	1.27	1.58
184	17	28782990	12453053	15452	AGTGAAAGTAYACCAGTAAGA	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28797566	12602581	15453	TCCTCAGGCCRTTAGCTAAAT	0.18	0.43	0.43	1.37	1.02	0.73	1.37	0.37	1.49	1.03	0.79	1.37
184	17	28805492	11651843	15454	AAGGACTCAAYTCAGAAACAG	1.28	1.77	1.77	1.18	0.68	1.11	1.51	1.74	1.20	0.70	1.11	1.48
184	17	28814076	869097	15455	GATTTGGGCCRCCTGTCCCTC	0.06	0.23	0.23	1.22	2.25	1.49	1.39	0.22	1.35	2.11	1.48	1.36
184	17	28820633	1857737	15456	AAGAGGAACAYGGAGGTACAG	0.57	0.65	0.65	1.20	1.96	2.31	0.94	0.56	1.24	1.79	2.23	0.92
184	17	28826890	9901123	15457	GGAAAGCAAGYGGCCTTATCT	0.74	1.14	1.14	1.22	1.58	1.36	1.31	1.08	1.26	1.57	1.32	1.30
184	17	28834683	12452593	15458	TGTGAGCTCAYACACGTTACT	0.32	0.35	0.35	1.12	0.72	0.69	1.07	0.32	1.16	0.74	0.71	1.07
184	17	28875052	17191673	15459	TCATCCATAGYATAGCCTCAG	0.03	0.08	0.08	0.06	0.47	0.45	0.59	0.07	0.05	0.49	0.44	0.63
184	17	28882982	2117389	15460	TCGTGAGCAGRAATGATCACA	0.30	0.39	0.39	0.50	0.16	0.36	0.86	0.37	0.49	0.14	0.40	0.85
184	17	28890180	9903859	15461	GGCACAGACARGGAACACAAT	0.72	1.14	1.14	0.35	0.09	0.22	0.45	1.05	0.30	0.08	0.21	0.49
184	17	28905871	7215028	15462	ACATACAGTCMTCACCACCAG	0.27	0.24	0.24	0.34	0.71	0.28	0.13	0.14	0.34	0.75	0.30	0.12
184	17	28912992	1369109	15463	AATAGATGCAYGTCTTAGTTC	0.40	0.56	0.55	0.92	0.48	0.29	0.32	0.51	0.94	0.50	0.28	0.36
184	17	28920672	1434588	15464	GATGTTAAGCRTCAGAACGGC	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28928643	4795811	15465	CTAGACCCAGWGCTTCCCAAC	0.92	1.42	1.42	0.71	0.44	0.43	1.51	1.40	0.72	0.48	0.46	1.50
184	17	28936456	1369104	15466	TGGGAACTTASATGCCTTCCC	0.58	0.96	0.96	0.59	0.64	1.23	1.09	0.88	0.73	0.65	1.20	1.07
184	17	28945062	12452523	15467	TCAATATTCARGGAGTTTTAA	-	-	-	-	-	-	-	-	-	-	-	-
184	17	28955705	1369112	15468	ATCCAGGAACKTTTGGTCCAA	0.43	0.78	0.78	0.48	2.25	1.32	0.97	0.77	0.51	2.00	1.29	0.95
185	17	58581369	17745579	15469	GATTCAACTARTACTTTGTGC	1.38	0.42	0.42	1.96	2.13	1.07	1.34	0.40	2.32	1.97	1.06	1.32
185	17	58591931	17683399	15470	TTTAAAATTTRTGTGTGTTTG	1.05	1.57	1.57	0.84	1.39	1.90	2.14	1.52	1.01	1.30	1.79	2.03
185	17	58599333	6504154	15471	TAGTTTCGGARGAGAGGTAGA	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58614495	10491185	15472	TAATGCATTCRTCGTAATACA	1.25	0.35	0.35	1.71	2.56	3.03	2.41	0.27	2.18	2.19	2.75	2.29
185	17	58624704	2447454	15473	ATTTTTGTAAWGTCCTTTAAA	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58642205	10506519	15474	TCTACTTTTCRTCTTGTTCTT	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58656201	10506520	15475	TTAATTTCATSTCCCTCTCAC	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58669004	2460111	15476	AACCTTGGCARTCTCAAAAAT	1.56	2.19	2.20	1.79	4.10	3.04	2.40	2.12	2.00	3.56	2.76	2.34
185	17	58677144	2460109	15477	CCTGTTGTCTYTGCAGAAGGA	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58695046	10506521	15478	AAACTATACGRAAATATAACA	1.61	0.20	0.15	2.66	2.30	2.88	2.45	0.11	2.89	2.30	2.71	2.30
185	17	58703983	2920443	15479	GTGACAAGCCMTGCATTGATT	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58711264	17202291	15480	TCCACTTGCCYAGGGTAATAG	1.33	0.50	0.50	1.24	2.02	1.76	2.29	0.47	1.35	1.98	1.75	2.22
185	17	58726543	17797070	15481	ATTAGCATTASTCATATTCAT	1.36	0.52	0.50	1.10	2.23	1.81	1.45	0.47	1.31	2.13	1.73	1.44
185	17	58740187	2907466	15482	TTTAATGTCTRTGTAATTTTT	1.29	1.87	2.00	0.86	0.76	1.47	0.85	1.98	0.88	0.75	1.43	0.87
185	17	58746777	2429426	15483	GTGTGAGATARTAGTAGTTAC	1.06	1.59	1.59	1.21	0.48	0.26	0.77	1.51	1.24	0.49	0.25	0.79
185	17	58754089	9908094	15484	AACATTGTATSAGAAGTAGCC	1.13	1.39	1.39	1.21	0.46	0.19	0.09	1.32	1.35	0.47	0.22	0.10
185	17	58762537		15485	ATTGTGCCCAYGAAGTGGACT	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58771614	1015760	15486	AGTAACTACTMCTTCCTCTTT	1.56	2.20	2.20	0.86	0.54	0.20	0.10	2.15	0.87	0.58	0.22	0.09
185	17	58785486	3809721	15487	TTCTAAGCCAKTCTTTGAATC	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58799097	9902439	15488	TTGGGCTACTWATTAAGAGGT	1.63	2.26	2.26	0.95	0.52	0.25	0.19	- 2.14	1.18	0.50	0.25	0.21
185	17	58811999	16946897	15489	ACCAAAAATGRCCTTACTTAG	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58818462	7219930	15490	GACCCTGAACYCTCTATGGGA	1.71	2.33	2.33	0.91	0.79	0.42	1.02	2.30	1.07	0.80	0.45	1.01
185	17	58826552	17760841	15491	CTCAGGAAGAYGAAGCTCAAA	0.66	0.51	0.51	1.42	1.29	1.38	0.83	0.49	1.66	1.26	1.32	0.82
185	17	58833422	16946910	15492	AGGACATATCWCCATTGTGCA	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58842307	13342595	15493	CACATCCATTYGGCCAAAGTG	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58855317	17549181	15494	TCCCCAGGGTSTCTCAGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
185	17	58872498	4968775	15495	ACAAGCGACASGCCCCCAAAT	0.83	1.30	1.30	1.69	1.79	1.91	1.41	1.27	1.84	1.70	1.78	1.34
186	18	17660599	8089787	15496	AAATTTTTGTYATAATGTGGT	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17680634	16947345	15497	GTGTCCATCCYGGTTCTAGCC	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17682026	12458857	15498	ATCTCTTTGGWATCTGTGCAT	1.78	1.45	1.50	0.72	0.44	0.13	0.06	1.41	0.70	0.44	0.14	0.07
186	18	17716667	8097660	15499	CCTAATCTATYTACATTTAAT	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17735453	16948167	15500	TCTCTCCTGCMTCTGAGCTCT	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17741964	6508699	15501	GGTGTCAGAGRTGTCAATGCA	1.78	0.82	0.82	0.47	0.21	0.18	0.10	0.72	0.47	0.20	0.16	0.11
186	18	17759002	6508709	15502	ACTATTTTTAYATAATTTCAG	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17777576	9948997	15503	TGATTGCTTCWTGTCGTTGGA	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17794465	10163732	15504	TGACTGTGCGRTAACTTAAAG	0.66	0.47	0.47	0.41	0.61	0.19	0.11	0.40	0.40	0.59	0.20	0.11
186	18	17804306		15505	TTTCCCCTGGMACTTTCATTT	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17811090	9961451	15506	AACCTGTCAGRGAATACAATA	1.17	1.34	1.41	0.78	0.52	0.59	0.57	1.33	0.84	0.53	0.62	0.56
186	18	17824618	4800342	15507	ATGATGTGAAMTGCCCAGTGG	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17835971	9947423	15508	CGGGCACCAGYTCACACGCTC	0.72	0.95	0.92	1.30	0.63	0.66	0.71	0.89	1.44	0.64	0.68	0.71
186	18	17840823	7229372	15509	GCCAATGAGGRATTTTAGAGC	0.81	1.04	1.04	1.17	0.66	0.79	1.43	0.98	1.43	0.66	0.78	1.41
186	18	17853740	4800103	15510	AGAACCAGTARGGTGTAGTTC	0.58	0.75	0.77	0.39	1.29	2.00	1.35	0.75	0.35	1.22	1.88	1.31
186	18	17857497	2891770	15511	TTTCTCGGCCRTCTTAGCTGT	1.82	1.55	1.31	1.12	1.75	1.84	1.52	1.27	1.24	1.66	1.78	1.48
186	18	17868324	12955789	15512	TGATAATCCARGAAGTAAATT	1.16	1.60	1.60	0.81	1.61	1.45	1.93	1.53	0.95	1.59	1.38	1.77
186	18	17875644	11664821	15513	GTCAGTTAACRGCATCACAGG	1.38	1.45	1.45	1.92	1.57	1.85	2.05	1.39	2.04	1.46	1.72	1.91
186	18	17882971	16962602	15514	TGGGAAAAGAYGCTGGCCTTT	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17883237	16962606	15515	TTTGATTAAGYGAGCCAGGCT	1.71	2.10	2.13	1.38	2.38	2.40	2.07	2.05	1.59	2.05	2.12	1.88
186	18	17895626	9960339	15516	CAGTTCTCTGYGGCCTGTCCT	0.50	0.71	0.62	1.68	2.09	2.07	1.40	0.58	2.13	1.83	1.91	1.36
186	18	17908432	1479915	15517	CTTACCATAARCCATCAAGCT	0.49	0.69	0.69	1.57	1.69	0.96	1.83	0.65	1.98	1.53	0.96	1.74
186	18	17918096	9953528	15518	TCAGTGCCTARTTGTGTTATA	2.17	2.58	2.59	1.67	1.18	0.80	0.92	2.48	1.70	1.17	0.77	0.91
186	18	17927767	8097782	15519	TTGGGTTGAASTTCTAAGCTG	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17940725		15520	GTGTTTAATAYTCACTGGCTA	-	-	-	-	-	-	-	-	-	-	-	-
186	18	17948381	12373329	15521	TTCTTTCTGAYGCCAAACTCC	1.18	1.68	1.68	1.14	0.78	0.83	0.97	1.56	1.19	0.78	0.87	0.96
186	18	17971699	8099745	15522	ACTTCCTTTTYTCACTGACAA	0.26	0.32	0.32	0.57	0.41	0.86	0.98	0.29	0.57	0.41	0.85	0.98
187	18	23189662	10502490	15523	GACAATCCTGWTGGTGCCACT	0.94	0.69	0.86	0.17	0.11	0.11	0.36	0.81	0.15	0.11	0.11	0.34
187	18	23202749	10502491	15524	CATGAAAAAGWGCAAAAAATT	0.06	0.14	0.16	0.23	0.12	0.85	0.90	0.12	0.22	0.11	0.85	0.89
187	18	23210271	1519143	15525	CCTTACCTGARAGCCTGAATG	0.06	0.07	0.07	0.23	2.88	1.83	1.85	0.04	0.17	2.56	1.77	1.78
187	18	23215939	10502492	15526	TTAGAGAAAASTTAAGATGAG	1.17	0.51	0.47	1.15	1.65	4.00	1.62	0.37	1.13	1.56	3.47	1.59
187	18	23231527	1401466	15527	TTATTCCTGCKGCCAGAGCTG	0.55	0.56	0.56	1.17	2.04	1.13	1.42	0.54	1.24	1.90	1.08	1.37
187	18	23245216	1401462	15528	TAATTCCAGGYGGCATACTAA	0.90	1.40	1.38	2.10	1.18	0.57	0.63	1.33	2.38	1.15	0.58	0.62
187	18	23253013	6508486	15529	CTGGAGAGCCRCTTGAGAGTA	-	-	-	-	-	-	-	-	-	-	-	-
187	18	23258373	9956638	15530	CATTCTAGCCYACCCCATGAA	1.03	1.39	1.39	0.91	1.49	1.04	0.38	1.34	0.97	1.45	1.05	0.37

188	18	39397135	2622796	15531	AGAAGAAAGARTGATCCTGTT	0.08	0.04	0.04	0.22	0.08	0.53	0.52	0.01	0.23	0.06	0.53	0.53
188	18	39404662	7237317	15532	AGGAATTTCCMGGCTTCTCAT	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39406786	16881	15533	AATACTATTAWTAAGTTGATC	0.40	0.72	0.72	0.20	0.44	0.24	0.89	0.67	0.17	0.48	0.28	0.87
188	18	39420553	1918358	15534	GGAGATGTCAWTGTCAGACCT	0.03	0.06	0.02	0.52	0.24	0.83	0.96	0.00	0.54	0.25	0.83	0.97
188	18	39427547	756051	15535	AAGAATGTTGMCACTATTACT	1.25	1.53	1.53	0.44	1.07	0.84	1.50	1.49	0.47	1.07	0.86	1.48
188	18	39443487	1405725	15536	GCTGATTTGGSTGACAACAGC	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39456247	16977608	15537	AAACCTACCCRGAGAGCTATT	0.21	0.12	0.14	0.52	0.87	1.60	1.31	0.12	0.50	0.85	1.61	1.32
188	18	39462517	12459000	15538	CAGGAGATGARGCAGATCCAA	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39468657		15539	TTATCTCTAAYGCTCTTTTTC	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39475145	1440206	15540	GAGTAGGATTMGTCAAATTAG	0.32	0.08	0.11	0.19	0.84	0.83	1.32	0.09	0.17	0.83	0.85	1.25
188	18	39481721	1918362	15541	CCTAAGCTTTYAAGTTTGACA	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39491276	7231543	15542	TTCAGAAAGAYGACGGTAATT	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39500663	12960735	15543	GGAATGGAAGKCATCATTGGG	0.68	0.43	0.43	0.07	0.21	0.49	2.24	0.41	0.09	0.20	0.50	2.13
188	18	39507451	12458538	15544	CTTAAAATAGYAAAGTCCTGC	-	-	-	-	-	-	-	-	-	-	-	-
188	18	39532306	2359238	15545	AAAAGAAGTARTAGCAAACAC	2.06	0.71	0.71	0.31	0.06	1.01	1.61	0.67	0.29	0.05	0.98	1.55
189	18	44810722	11082725	15546	GACTCAGCCCRTTCCTCTCTC	0.60	1.03	1.03	0.15	0.56	0.41	0.23	0.95	0.14	0.57	0.41	0.25
189	18	44821750	833521	15547	TTCCATCTGAWCACACGATGA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	44829492	357854	15548	TGATCATTATYTCCATAGAAG	0.20	0.02	0.00	0.50	0.13	0.38	0.38	0.00	0.53	0.13	0.39	0.39
189	18	44838182	357897	15549	AAATTCAAGAYGTCTGGATTT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	44842474	11659241	15550	CCAGATTAAGYAAGCTGTCTG	0.40	0.71	0.70	0.26	0.37	0.39	0.46	0.65	0.22	0.41	0.42	0.49
189	18	44856962	10520770	15551	TTGTACATTCYGCTTTAAAAC	0.63	1.05	1.05	0.29	0.31	0.76	0.33	0.99	0.28	0.32	0.79	0.36
189	18	44865840		15552	AACATGCTGGKAGTGATTTTC	-	-	-	-	-	-	-	-	-	-	-	-
189	18	44872826	7239949	15553	CCATTCATTTKACACGCAGCG	0.12	0.36	0.36	0.81	0.40	0.19	0.89	0.32	0.82	0.43	0.19	0.88
189	18	44881039	9284426	15554	TGTCAAAACCRAAGGAAACAA	0.08	0.06	0.06	1.28	0.64	0.40	0.27	0.03	1.33	0.66	0.41	0.29
189	18	44899816	10502897	15555	CATAAAATAGYTGCCAAACAG	0.66	0.70	0.70	0.97	1.85	0.71	0.61	0.65	1.14	1.78	0.71	0.62
189	18	44907378	7236575	15556	AAAACTAACCRTATTTCCTCA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	44917618	11082735	15557	AATAACACACYCAGTACAGGC	0.46	0.72	0.72	1.39	1.96	2.08	1.26	0.67	1.58	1.81	1.94	1.22
189	18	44932715	17196970	15558	CTCCAACTCARTATTGTCCTT	1.89	2.50	2.54	1.44	1.73	2.11	2.17	2.47	1.79	1.59	1.92	1.92
189	18	44949547	1943000	15559	AGTCAGGTGARAAAGGACGTG	1.15	1.51	1.51	1.56	2.46	1.97	1.46	1.46	1.78	2.06	1.68	1.40
189	18	44955409		15560	CCCAAGCTTTYTTTCTCTATC	-	-	-	-	-	-	-	-	-	-	-	-
189	18	44966106	1893527	15561	CCTCGTTTAAWCCTGGCCTCA	2.02	2.53	2.53	1.99	3.11	1.68	1.00	2.43	2.36	2.44	1.50	0.96
189	18	44974759	2032252	15562	CCTTCACCAAYGCAATCTACA	0.64	1.05	1.05	2.15	1.47	1.61	1.09	1.02	2.67	1.45	1.50	1.05
189	18	44994117	4483916	15563	CTTCCCTCCTYTCCTTCCTTT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45008660	16950454	15564	ACAATTTAGGMTGGGCTGGGA	0.95	1.42	1.42	1.11	2.07	1.25	1.95	1.29	1.37	1.92	1.22	1.80
189	18	45017811	16950465	15565	AGTAGAAAATYATCTAGAGTG	1.02	1.45	1.48	1.22	1.69	2.21	2.07	1.43	1.40	1.58	1.96	1.86
189	18	45024184	11661691	15566	GGTCTCTGATKGGCTTATGTA	1.89	2.47	2.47	1.18	1.82	1.94	1.56	2.40	1.39	1.71	1.81	1.49
189	18	45034882	7229796	15567	ACAATCTAAAYGCTCTCAAAT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45052895	8087374	15568	TCTCTTAAGGYCTAACCAACA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45068791		15569	GAAGACCATAYGAGATCTGAA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45083464	9789092	15570	GAAACAGTTGSTAGTCCAAAA	0.12	0.29	0.29	1.77	1.93	1.46	1.33	0.25	2.00	1.74	1.44	1.31
189	18	45089717	522324	15571	TAACTAACTTYTCAGGCTGGA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45096185	577979	15572	CATCTCAGTGRTAACCATATA	0.02	0.09	0.07	0.53	1.71	1.25	1.27	0.04	0.57	1.59	1.23	1.26
189	18	45103669		15573	GTGGTTTAAGRTAATGACTAG	0.83	0.82	0.82	0.79	0.49	1.42	1.45	0.66	0.76	0.51	1.37	1.39
189	18	45156065	4939864	15574	TCGGATTGAARGATGCAAAGT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45174609	4939579	15575	CTTTATGTCTKAATTTCCTCA	0.54	0.86	0.74	0.72	0.58	0.47	0.94	0.71	0.73	0.59	0.50	0.92
189	18	45189003	6507906	15576	TATGTGATGAYAGTAAGCAAG	0.01	0.09	0.09	0.84	0.76	0.26	0.51	0.07	0.92	0.78	0.27	0.51
189	18	45211316	7407441	15577	ACAAAAATCCRAATCTATATT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45227629	17725438	15578	AGCATAAGAGRCCAGAAAGTA	1.21	1.78	1.78	1.04	0.48	0.67	0.35	1.66	1.01	0.54	0.73	0.35
189	18	45241638	16950548	15579	ATTAAGGCCTYTGTTAATTGC	0.27	0.53	0.53	0.87	0.76	0.58	1.24	0.46	0.96	0.74	0.60	1.19
189	18	45253512	6417104	15580	CTTGAAGTACMGGCACTTTCT	0.28	0.27	0.30	0.15	0.51	0.38	0.80	0.26	0.12	0.53	0.39	0.79
189	18	45261593	9957337	15581	AATCAGTGACYTGACCAGCCA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45271818	1943676	15582	TGCATGCTAGRAAATAAAACG	0.28	0.49	0.49	0.27	0.09	0.66	0.37	0.44	0.30	0.09	0.65	0.40
189	18	45280734	11082758	15583	CGGATGTCAASTGGGCCCTGC	0.03	0.02	0.02	0.17	0.32	0.16	0.58	0.00	0.14	0.34	0.16	0.57
189	18	45289849	17712538	15584	GCAATAAATGRTGGTTCAGCT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45305484		15585	GCCTCCATCARTTACTACCTT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45317541	9962108	15586	CTATATGCTARTGAAATCCTT	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45332909	12962061	15587	TTCAGTTTCCYCTAGATGTCT	0.55	0.31	0.35	0.39	0.31	0.37	1.09	0.26	0.39	0.30	0.39	1.07
189	18	45341116	3829632	15588	CGGTTTCCTCRCACAGGTCTC	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45370673	17798937	15589	AAGTGCATCTRTGGCTTGTCA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45377761	4939585	15590	AGAGAGGTGTYGGTGCCCTCT	0.00	0.04	0.04	0.26	0.74	1.42	0.71	0.01	0.24	0.74	1.43	0.72
189	18	45384340	17712928	15591	GCTGGAATGCRCTTATCAGAA	0.01	0.04	0.04	0.86	0.47	1.01	1.50	0.02	0.97	0.45	0.97	1.49
189	18	45389970	7231795	15592	GGTGGGCAGAYGTTCTGGATG	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45397977	1016562	15593	CTTGGTGGGTRGAGCAGAGAT	1.18	1.31	1.31	0.71	0.60	0.35	1.43	1.24	0.66	0.66	0.36	1.40
189	18	45400164	11661190	15594	GGCTGTGATCYGTGGTGGAAT	0.37	0.73	0.72	0.82	0.46	0.38	0.10	0.66	0.84	0.49	0.41	0.12
189	18	45413088	7240405	15595	AGCTAAGTGCRCGGTAAGGGA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45420253	948931	15596	CCTCTGGTCAYGTTCTGATGT	0.19	0.47	0.59	0.32	0.27	0.18	0.84	0.55	0.32	0.28	0.19	0.82
189	18	45436676	1540036	15597	TGATAAGCCTWATCCCTCACA	0.31	0.56	0.58	0.61	0.31	0.60	1.01	0.57	0.62	0.30	0.62	0.96
189	18	45449763		15598	ACCATTGTCARATCCCTTTCC	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45456496	12455122	15599	GTGTAGTGCASTGGTTCAGAG	0.60	0.58	0.38	0.19	1.02	0.39	0.32	0.31	0.16	1.00	0.36	0.33
189	18	45467085	6507943	15600	GACTATCACCRTCCAAAACTC	0.71	0.71	0.71	1.43	0.96	0.68	1.05	0.72	1.69	0.95	0.67	1.09
189	18	45475489	11082773	15601	GTGGCCCGCGRTCTGGCTGTT	0.71	1.16	1.12	1.07	1.02	0.73	1.24	1.03	1.11	1.04	0.73	1.24
189	18	45484429	948932	15602	TGAGCCTTCAMAAAGCCCAAC	0.87	1.26	1.27	0.51	1.05	2.95	2.37	1.18	0.52	1.01	2.70	2.20
189	18	45514562	4084206	15603	GGACTGGAGGSACTTCATGAC	0.08	0.26	0.26	1.38	3.50	2.66	2.05	0.23	1.43	3.21	2.46	1.93
189	18	45523744	7228406	15604	CTGAGGGCCAYAGTAGGGACA	0.01	0.02	0.02	0.14	3.02	2.51	2.49	0.00	0.12	2.70	2.31	2.31
189	18	45540045	8096273	15605	ACTGGGAGGGRTGTGTTGAGA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45561988	561726	15606	AAGTCCTTAARAAAACTAAGA	0.12	0.30	0.30	0.15	0.06	1.73	2.06	0.27	0.16	0.05	1.63	1.94
189	18	45572501	10502901	15607	TTCAAGCTAAWCTGTGTGGTG	0.54	0.51	0.43	0.07	0.02	0.06	1.40	0.33	0.07	0.02	0.05	1.35
189	18	45584997	7506023	15608	CCCTTAGAATRTAAGAATATA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45591834		15609	TCGAGCGAAAMCCTCCTGCCA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45605966	17726873	15610	TTCATATTGAYTTGTTTGGTT	0.71	0.50	0.50	0.08	0.01	0.02	0.13	0.46	0.09	0.01	0.02	0.14
189	18	45617007	621101	15611	TAACCACCAAYGAGAACAGAC	0.41	0.42	0.42	0.23	0.08	0.06	0.02	0.40	0.16	0.08	0.06	0.02
189	18	45624286	12454607	15612	CTCTGGCCCAWCAGTTCAGGA	0.53	0.49	0.49	0.35	0.34	0.16	0.02	0.42	0.35	0.38	0.15	0.02
189	18	45631749	1942419	15613	TGTGCTAAGGRGAATTATATA	0.02	0.11	0.11	0.56	0.36	0.12	0.05	0.06	0.58	0.41	0.14	0.05
189	18	45640542	515811	15614	GGGTAGAAGTKGACAGGAATC	0.62	0.75	0.67	0.42	0.19	0.12	0.11	0.64	0.42	0.19	0.13	0.13
189	18	45648929	613674	15615	TGGCCGTAAGSAGGGTCTGTC	1.28	0.42	0.38	0.42	0.16	0.15	0.22	0.32	0.43	0.17	0.15	0.21
189	18	45658007	4939907	15616	GCTCTTGAGAWTTAGCCCCTG	0.07	0.05	0.05	0.06	0.35	0.13	0.69	0.02	0.07	0.36	0.13	0.67
189	18	45668900	2027705	15617	GGTTTGGGAAKGTGAAGAGTT	0.55	0.51	0.51	0.26	0.13	0.81	0.66	0.45	0.23	0.13	0.84	0.66
189	18	45675973	1612142	15618	GCACAAAGAGYTGCAATCTAA	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45683020	2298624	15619	CACGTTGAGAYGTTTCAGATG	-	-	-	-	-	-	-	-	-	-	-	-
189	18	45689548	17727982	15620	TTCTCGATACRAAGTCCCAGG	0.06	0.14	0.08	0.20	0.23	1.20	0.92	0.05	0.18	0.24	1.16	0.95
190	18	45866536	16951490	15621	CTGTTTAACGKATTTATGGCC	0.07	0.21	0.21	0.88	1.08	0.25	0.10	0.17	1.05	1.09	0.30	0.06
190	18	45880146	16951520	15622	GTATCTTGTASTTATGTTCCC	0.03	0.14	0.14	0.94	0.77	0.28	0.20	0.10	1.21	0.75	0.29	0.18
190	18	45886488	17716413	15623	CCCAAAAATGMACCCTGGACA	0.81	1.25	1.25	0.55	0.49	0.58	0.14	1.18	0.56	0.52	0.63	0.15
190	18	45895399	9952908	15624	GGACAGCACCYTTCTGATTCC	-	-	-	-	-	-	-	-	-	-	-	-

190	18	45904693	1790445	15625	CATTTTCCTCRACATGTGGCT	0.07	0.24	0.24	0.44	0.23	0.13	0.52	0.22	0.46	0.25	0.13	0.53
190	18	45910839	4939948	15626	CCTGAGATGTRCACACATGCG	0.91	1.46	1.46	0.43	0.20	0.32	0.11	1.39	0.45	0.21	0.36	0.12
190	18	45917467	16951581	15627	TTGAAATGAGYTAATTCAAGT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	45928041	10502906	15628	CGGTAGCATASAAGACCGTTC	0.11	0.31	0.31	0.65	0.40	0.14	0.03	0.29	0.60	0.39	0.14	0.02
190	18	45935533	1705509	15629	TAGTAGCTGCMACCACTCCAG	0.76	1.25	1.25	0.24	0.49	0.21	0.04	1.20	0.23	0.49	0.19	0.04
190	18	45943290	11082806	15630	CCAAGCTACTSGGAGCCACAC	0.29	0.13	0.13	0.53	0.30	0.21	0.46	0.10	0.50	0.30	0.19	0.50
190	18	45955763	1705521	15631	CCTCCCACCAYTAAATAACCA	1.07	1.53	1.53	0.51	0.21	0.65	0.86	1.49	0.49	0.23	0.64	0.83
190	18	45966244	7242498	15632	GAAAAGATAGYCATAGATTAA	0.88	1.06	1.06	0.42	1.16	1.13	1.09	0.99	0.40	1.16	1.13	1.03
190	18	45977941	12455907	15633	AATCTAATTCYAACCTTACTC	0.98	0.96	0.96	0.64	0.58	0.52	1.34	0.93	0.62	0.55	0.54	1.30
190	18	45986967	17660567	15634	ATGACGAAAAMAAACACAAAT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	45994936	729964	15635	ACCACTCTGCRAGAAAAAAAT	0.94	1.26	1.19	0.96	0.61	0.96	1.18	1.16	1.06	0.62	0.93	1.15
190	18	46000432	7245013	15636	CAAGCCTTAAMGGGCATATTG	0.51	0.91	0.91	1.02	1.74	1.37	2.37	0.81	1.07	1.59	1.33	2.29
190	18	46007489	894771	15637	TGTCAGCAAAYGGAGCTAGTC	1.40	0.78	0.68	1.15	1.07	4.18	3.00	0.67	1.17	1.04	3.83	2.81
190	18	46034348	1470326	15638	ATTTAAAAAGRAATTTCATAA	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46054419	140689	15639	TCATTAAGCCWAGAACAATGT	0.81	0.93	0.93	1.16	3.36	3.57	3.61	0.92	1.22	2.97	3.27	3.42
190	18	46060955	12957023	15640	GTGTTACAACYTCGACTTCCT	0.66	0.51	0.52	0.57	2.32	3.29	3.45	0.47	0.55	2.11	2.97	3.13
190	18	46067833	3753067	15641	CATAGACTCCYGCCGTTCAGT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46073566	8095785	15642	CCAAATAGTGYCATGCGGTAA	0.13	0.30	0.30	0.34	0.63	2.60	2.39	0.27	0.33	0.62	2.35	2.21
190	18	46081941	12019102	15643	CCAGGAGACTRTCTTTTGGTC	1.11	0.99	0.99	0.74	0.51	0.39	2.70	0.92	0.89	0.51	0.38	2.49
190	18	46088575	746263	15644	AGTTGCAGGGWGTGTTGCTAG	1.30	0.99	0.99	0.40	0.41	0.66	0.95	0.91	0.40	0.42	0.68	0.95
190	18	46097564	1036934	15645	AAAACTACCASAATGAAATTT	1.09	0.93	0.93	0.58	0.25	0.59	0.58	0.90	0.63	0.24	0.60	0.58
190	18	46106634	16951751	15646	ATATTTTTCTRGATTTGGATT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46112551		15647	TGCAAATGGGMAAAATCAATA	0.71	1.04	1.04	0.30	0.24	0.44	0.44	0.99	0.30	0.26	0.47	0.48
190	18	46113324	1561698	15648	TCCTACAGTCYTTGCATCTAA	0.02	0.08	0.08	0.27	0.46	0.53	0.19	0.04	0.23	0.45	0.56	0.20
190	18	46152002	12955772	15649	CTATGACTGCYTGTGAGAATT	0.06	0.17	0.17	0.28	0.43	0.22	0.15	0.16	0.27	0.45	0.26	0.15
190	18	46157832	4939979	15650	TTATTACTCTRTATCACTGGG	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46163517	8095350	15651	TCTGCTTTTTSCCCGAGGCCC	0.07	0.15	0.15	1.16	0.79	0.19	0.18	0.13	1.25	0.80	0.20	0.17
190	18	46170228	16951852	15652	ATGCTTCCATRAAGAGCTATT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46176195	17741080	15653	TGGAGCACACWTTCTACTTGT	1.37	1.52	1.52	1.01	0.75	0.62	0.28	1.44	1.02	0.72	0.65	0.30
190	18	46203000	9963208	15654	GCTGGCTTCTMCCTTAGAGAG	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46209674	17741164	15655	AAAATTTAAAYGGTGGGTAAC	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46215506	2969992	15656	ACAACTCATCRCTAGACGTAG	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46221902	2969966	15657	CATCCTCTTAWCTGGTGGCTT	0.95	1.46	1.46	1.03	0.93	0.89	0.69	1.39	1.05	0.92	0.90	0.74
190	18	46228688	3017260	15658	GGGTCTATTCSTTGTCATCAC	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46234687	2919768	15659	AAGATACAGCRAGGCCAGCTT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46242949	8098594	15660	CCATCTCTGCRTTCCCTGAAC	1.30	0.47	0.47	0.89	0.51	0.61	1.02	0.39	0.91	0.53	0.62	1.00
190	18	46249556	17803514	15661	ACAGTGCTTCYGGGAATTTTG	1.43	0.71	0.68	0.31	0.59	0.64	0.38	0.64	0.29	0.65	0.67	0.44
190	18	46255800	1348147	15662	TTTGATATATYCTCATGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
190	18	46264502	1441300	15663	TTAAAAGATCSTCAAATAGAC	1.38	0.58	0.58	0.23	0.60	0.41	0.43	0.53	0.18	0.64	0.42	0.47
190	18	46276258	2958011	15664	CTAAAGTACCRTCCAAATGCA	1.23	0.63	0.63	0.71	0.24	0.40	0.42	0.56	0.92	0.26	0.45	0.44
190	18	46287571	2970002	15665	CTCACAGTTGYCACCTATTTG	0.42	0.29	0.29	0.37	0.59	0.38	0.26	0.24	0.37	0.68	0.40	0.26
190	18	46293912	2958001	15666	ATGTAAAGACWCATTTTGTAA	0.72	0.38	0.38	0.87	0.61	0.38	0.22	0.33	0.93	0.63	0.45	0.25
190	18	46304219	2957997	15667	ACTTATGGATMCCCAGGAACT	0.55	0.39	0.39	0.10	0.47	0.28	0.25	0.36	0.07	0.53	0.30	0.27
190	18	46310991	16952113	15668	TCAAATGAGAYGAGTGAAAAG	0.37	0.22	0.22	0.31	0.11	0.31	0.17	0.14	0.31	0.11	0.31	0.18
190	18	46330718	2969961	15669	GTCTTTGCCASAATTGGGCAG	0.48	0.14	0.16	0.03	0.12	0.05	0.20	0.12	0.03	0.13	0.05	0.21
190	18	46338558	16952149	15670	GCCATCGTACRGTAATGGGCA	0.05	0.06	0.06	0.10	0.04	0.06	0.19	0.04	0.02	0.02	0.04	0.17
191	18	52559917	1558941	15671	TCCACCAACTYTTCTCCAGTT	0.03	0.18	0.18	0.04	0.14	0.20	0.10	0.12	0.03	0.12	0.21	0.09
191	18	52570059	9945889	15672	AAGAAAATATMAAGCACAGTG	0.46	0.33	0.36	0.08	0.31	0.19	0.25	0.29	0.07	0.34	0.18	0.25
191	18	52586782	8097197	15673	TGTCTAGTCGRTAACATGAAC	0.46	0.74	0.66	0.56	0.16	0.27	0.24	0.60	0.59	0.15	0.28	0.26
191	18	52599776	2302845	15674	GAGAAGCCGCRCAGGCCCTGC	0.75	0.74	0.74	0.36	0.28	0.23	0.35	0.70	0.32	0.30	0.23	0.38
191	18	52607026		15675	TAATAGTTGTSTTATAGTGTT	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52615287	17750277	15676	GCACCTTGGCRGAATCATGTG	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52625153	17090358	15677	TATTGGCAATRCCAGCCTCTC	0.58	0.33	0.33	0.45	0.24	0.46	0.31	0.28	0.49	0.26	0.48	0.31
191	18	52636307	17090367	15678	GTGTTTGTTCMGTTTTCACTG	0.20	0.05	0.03	0.35	0.39	0.18	0.22	0.00	0.30	0.42	0.19	0.23
191	18	52642214	12326572	15679	ACCCTTCACCMTCATTAACAG	0.78	0.38	0.38	0.70	0.30	0.09	0.04	0.33	0.76	0.30	0.08	0.03
191	18	52649483	8095415	15680	TTCCCTGTGARTGTGTATAGA	1.01	1.52	1.52	0.40	0.13	0.06	0.13	1.44	0.37	0.14	0.05	0.16
191	18	52656352	2909366	15681	TTATGATGATWTATAAAAGAC	0.98	1.44	1.44	0.37	0.08	0.27	0.38	1.39	0.37	0.09	0.28	0.36
191	18	52663508	11659890	15682	GCAAAGCTCTRTAGTGTTTCT	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52671762	1214044	15683	AAATATATTTYGTTTAATCAG	0.66	0.95	0.95	0.49	0.43	0.39	0.48	0.91	0.48	0.46	0.35	0.51
191	18	52682781	2543161	15684	AAAAATTACCKTGACCATCAA	0.98	1.46	1.46	1.19	1.19	0.83	1.27	1.41	1.39	1.17	0.87	1.24
191	18	52694410	8092563	15685	ATACCAAAAARTATTCAGAGA	1.53	2.11	2.19	1.72	1.47	1.69	1.73	2.09	1.81	1.38	1.63	1.67
191	18	52699802	4800953	15686	AAAGGGCTTARTGACTAATAT	2.47	3.01	3.01	2.22	1.98	1.88	1.29	2.93	2.41	1.88	1.76	1.27
191	18	52706612	7233975	15687	TATCCCTCTGSGTTGCAGAAT	1.12	1.15	1.15	2.30	2.33	1.49	0.95	1.11	2.56	2.11	1.46	0.89
191	18	52718757	2083020	15688	CAGAGATACTRTGTGCAAAAT	0.21	0.38	0.38	0.68	1.70	0.96	0.97	0.37	0.76	1.60	0.98	0.96
191	18	52728143	12455664	15689	GTATGAGGCAWCTAATTGCTT	0.81	1.18	1.18	0.96	0.42	1.33	1.00	1.11	1.04	0.44	1.31	0.99
191	18	52741713		15690	CCATCCTTCAYTGCAACGCGC	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52751015	17090444	15691	GGAAACTATCYACTTGTCACT	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52766826	17090451	15692	TTAAGCAGTGWCCTTACTGCA	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52777227	1657426	15693	ATATCTCAATRGTGATGGACA	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52794679	17090456	15694	CATTTCATCTRCAAAGTAATA	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52800709	1657415	15695	GAAAATTTTCRTCAAGGAAAT	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52807023	1657418	15696	GGATGTTTGGKTTAGGAAATT	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52814203	1787479	15697	ACATTTGGTASCTGGGCCACT	0.09	0.28	0.31	0.91	0.96	0.43	0.83	0.29	0.95	0.95	0.42	0.84
191	18	52820517	994660	15698	TGACTGTACTRTAATTTTCTT	0.12	0.11	0.15	0.99	0.69	0.40	0.23	0.12	1.07	0.68	0.43	0.24
191	18	52825978	1437068	15699	ACAATGTGTAMAATGAGCCCA	0.10	0.31	0.31	1.46	0.37	0.28	0.24	0.28	1.58	0.37	0.31	0.23
191	18	52834578	17684110	15700	TGGTATTTATSATAGGGAAAT	0.26	0.54	0.54	0.27	0.54	0.20	0.20	0.45	0.28	0.55	0.20	0.21
191	18	52843208		15701	GACCAAAGGCRTTTATCAAAG	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52857409	10084025	15702	TGAGCAGTGAYGGAAACAAGG	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52864560	1787483	15703	TATGTGAGAAYGATTGTGAGG	-	-	-	-	-	-	-	-	-	-	-	-
191	18	52871776	1942344	15704	CTTTATTAGCRCAGAAACTTG	0.31	0.52	0.47	0.19	0.18	0.34	0.25	0.46	0.18	0.19	0.37	0.26
191	18	52877271	4801077	15705	CTGTCTTTAGYTAGCAGGGTG	0.02	0.08	0.08	0.06	0.15	0.34	0.42	0.07	0.06	0.14	0.34	0.40
191	18	52882841	9949774	15706	CATCTTGGGTSATTTTCCTCC	0.20	0.35	0.35	0.19	0.16	0.30	0.60	0.32	0.20	0.17	0.29	0.58
191	18	52896047	11661250	15707	TAGGAGCCGTKGCAGAGGTGT	0.07	0.18	0.16	0.34	0.13	0.18	0.77	0.13	0.30	0.11	0.19	0.79
192	18	54839050	17761781	15708	ACAATGTGTCYTGCCACCAAG	1.24	0.00	0.02	1.36	0.60	0.53	0.56	0.00	1.43	0.64	0.54	0.56
192	18	54853925	17695181	15709	TTTTCTTGGCMGAAGAATGTG	0.13	0.31	0.31	0.62	0.86	0.69	1.02	0.25	0.64	0.88	0.71	1.03
192	18	54860262	17761829	15710	GCCTTCTGATYATCTTGAAGA	0.24	0.03	0.02	0.20	0.12	0.65	0.46	0.00	0.20	0.14	0.63	0.50
192	18	54874907	8097047	15711	GGTTTCATAGRTGACAAGGGA	0.05	0.20	0.20	0.13	0.35	0.25	0.34	0.16	0.14	0.38	0.25	0.34
192	18	54887527	12608217	15712	TGTAATTTGGSTTATGAAGCT	-	-	-	-	-	-	-	-	-	-	-	-
192	18	54898702	11874612	15713	TGGCTTTGATYCATGACCCCA	0.02	0.03	0.04	0.22	0.19	0.23	0.24	0.02	0.25	0.19	0.25	0.26
192	18	54905030	8097066	15714	ATACTTTTCCRTTCATAGTGG	-	-	-	-	-	-	-	-	-	-	-	-
192	18	54911056	9944697	15715	TTGGTCATCAMTGAAAAAGGC	0.14	0.29	0.19	0.12	0.13	0.38	0.20	0.19	0.10	0.14	0.40	0.21
192	18	54918651	9961653	15716	GAGATGACAAYGAAAGAACAG	-	-	-	-	-	-	-	-	-	-	-	-
192	18	54925367	1458932	15717	AAGCAGACTGYTGATTCAAGA	0.28	0.50	0.50	0.28	0.14	0.11	0.15	0.43	0.25	0.16	0.10	0.15
192	18	54929121	17835341	15718	ATGGACCAAARTAGCCCCAGT	-	-	-	-	-	-	-	-	-	-	-	-

192	18	54938955	9675436	15719	ACTAATGCCTYTTTACTGTTC	0.47	0.13	0.13	0.44	0.43	0.12	0.20	0.09	0.43	0.45	0.12	0.20
192	18	54945353	17768362	15720	ATTGTGACTTSCTGGAGGGTG	0.27	0.54	0.56	0.18	0.16	0.40	0.50	0.51	0.15	0.16	0.43	0.52
192	18	54953669	4940843	15721	TGTTTCATGTRGTCCTCAGTG	0.36	0.36	0.39	0.19	0.28	0.42	0.64	0.34	0.17	0.28	0.44	0.63
192	18	54961900	8090894	15722	TTGTTTTATCRTTTGGTGAGA	0.28	0.56	0.58	0.37	0.62	0.89	1.43	0.53	0.36	0.65	0.91	1.41
192	18	54970100	4940847	15723	CTTTGAATCCRCCAAAGATTT	-	-	-	-	-	-	-	-	-	-	-	-
192	18	54978535	12605870	15724	CCGCTGGGAAYAGCTTGCCCT	0.24	0.52	0.57	1.27	1.39	2.45	3.32	0.47	1.39	1.34	2.32	3.02
192	18	54983755	10503023	15725	GAAAGTCATARTTTACAAAGG	0.15	0.02	0.02	1.89	3.12	2.54	3.61	0.00	2.02	2.85	2.39	3.34
192	18	54995399	3903299	15726	TCTTGACCAGKTATTCACTTG	-	-	-	-	-	-	-	-	-	-	-	-
192	18	55002156	1979302	15727	CCCAAAATTCRGAACTTGAAC	1.00	0.76	0.83	2.53	2.70	3.05	1.64	0.70	2.64	2.56	2.81	1.64
192	18	55017020	1517038	15728	ATGATAAATAWGTGGCAATTT	-	-	-	-	-	-	-	-	-	-	-	-
192	18	55030807	9319943	15729	ACGGCCAACAYTAGTTTCAAC	2.82	3.46	3.46	1.68	2.19	1.69	1.62	3.35	1.72	2.04	1.66	1.57
192	18	55042364	1563713	15730	GTTAGAAGACRTTGCCAAGCA	2.43	0.59	0.56	2.19	1.64	1.52	1.34	0.50	2.33	1.56	1.47	1.30
192	18	55046817	17065649	15731	TGCTCGACCAYGGAAACAGCT	0.06	0.06	0.06	0.42	2.36	0.77	0.89	0.00	0.45	2.11	0.78	0.90
192	18	55057941	7231030	15732	ACATTGTAGAMAGAGTTTTGC	0.27	0.27	0.27	0.97	0.18	0.98	0.47	0.26	1.02	0.17	0.96	0.50
192	18	55069460	10221422	15733	AGTTTTGTCTYGTTTTTAACA	-	-	-	-	-	-	-	-	-	-	-	-
192	18	55071538	8094537	15734	TCCATAGGCCRTAAGAAATTG	0.20	0.16	0.24	0.60	0.12	0.21	0.29	0.21	0.63	0.12	0.23	0.29
192	18	55095993	12964217	15735	CCAGCAGATAMATTAAAGCAA	-	-	-	-	-	-	-	-	-	-	-	-
192	18	55105194	9973180	15736	TCTTCAAGGGYTTCTGAAATG	0.02	0.11	0.11	0.07	0.34	0.03	0.13	0.09	0.07	0.41	0.03	0.15
192	18	55113665	1914321	15737	TACATGAAACWTTTTGTACAA	0.68	0.21	0.21	0.49	0.07	0.25	0.20	0.17	0.48	0.06	0.25	0.20
192	18	55120972	473567	15738	CTTCTTGGACYTGGATAAACT	0.16	0.37	0.49	0.05	0.23	0.40	0.25	0.42	0.04	0.24	0.43	0.25
192	18	55131547	609209	15739	CCAATTTAGGYACGGTATTTT	0.40	0.08	0.08	0.07	0.32	0.08	0.21	0.06	0.03	0.34	0.08	0.22
192	18	55156635	10515978	15740	TGGTCCCCTAYTTGTAAAATG	0.11	0.19	0.19	0.06	0.19	0.15	0.14	0.18	0.02	0.20	0.16	0.14
192	18	55163556	1444488	15741	AGCACACTCAMGTTCTTAATA	0.04	0.16	0.16	0.33	0.10	0.33	0.10	0.15	0.29	0.11	0.31	0.12
192	18	55169902	12963340	15742	TGGGGAGTACRTTTTGCAAGG	0.15	0.22	0.22	0.87	0.41	0.06	0.51	0.19	1.00	0.44	0.07	0.52
192	18	55183906	12964312	15743	ATAACATTTCMTTCATAGAAC	-	-	-	-	-	-	-	-	-	-	-	-
192	18	55191422	9948377	15744	TTGTGGCCTGRCCTCACTCTG	0.06	0.22	0.22	0.23	0.46	0.40	0.18	0.20	0.22	0.49	0.42	0.19
193	19	18310238	9636202	15745	AAAGTGGAACRGGCTATCAGT	0.12	0.36	0.47	0.60	0.31	0.42	0.88	0.41	0.64	0.27	0.43	0.89
193	19	18316679	2112176	15746	CAATTAAACAMTCTTTGGAAA	-	-	-	-	-	-	-	-	-	-	-	-
193	19	18328886	7248363	15747	ATTTTAACACYTGCATAGCAG	-	-	-	-	-	-	-	-	-	-	-	-
193	19	18335705	3746183	15748	CCATGAGCTGMGATACCACGG	1.28	1.82	1.82	1.00	1.30	1.21	0.72	1.75	1.08	1.25	1.20	0.77
193	19	18343358	17725099	15749	ATATCTGGGTRGTCTTTCCCA	0.27	0.00	0.00	1.91	3.16	1.87	0.66	0.00	1.93	2.90	1.83	0.67
193	19	18357495	12459782	15750	GTCTCAGTCCYTTTTTTCCTG	0.15	0.38	0.38	0.32	0.75	2.03	1.60	0.36	0.32	0.73	1.97	1.54
193	19	18386701	7258891	15751	CTAGGTTCAAWCCCAGGCCCA	0.15	0.40	0.38	0.12	0.45	0.81	1.63	0.35	0.14	0.46	0.80	1.58
193	19	18418673	2303693	15752	TGGCACCGGTYGGCAGGAAGC	0.30	0.58	0.58	0.44	0.26	0.32	0.77	0.52	0.48	0.30	0.31	0.78
194	20	947784	6056637	15753	AGATGTTCAGYATTATAGAAT	1.09	0.60	0.60	0.69	0.96	0.55	0.03	0.56	0.69	0.97	0.53	0.03
194	20	957788	879012	15754	ACAGGATAGTYGTTCCCTGTG	0.07	0.06	0.06	0.84	1.08	0.55	0.44	0.02	0.84	1.06	0.53	0.44
194	20	968318	6056801	15755	AGACCTTGAGYGTGGACTAGA	-	-	-	-	-	-	-	-	-	-	-	-
194	20	978416	6118731	15756	CCATTCTCCTMACCTAAAATC	0.15	0.24	0.24	0.56	1.02	1.19	0.90	0.20	0.57	1.00	1.15	0.87
194	20	991243	733595	15757	AACCAGGATTSCATGCTGCCA	-	-	-	-	-	-	-	-	-	-	-	-
194	20	994045	4813904	15758	TGCAATACATRTGTATCAAGA	-	-	-	-	-	-	-	-	-	-	-	-
194	20	1012980	6039731	15759	AAAAAAGCATYTTGTGAGCAA	-	-	-	-	-	-	-	-	-	-	-	-
194	20	1018829	11699986	15760	TGGAAAAATGMATCGACTGGG	0.82	0.60	0.53	0.21	1.13	1.28	1.62	0.45	0.19	1.12	1.26	1.57
194	20	1025097	4813923	15761	TTTTTTTCACRTATTCCCCAC	0.00	0.02	0.05	1.03	0.88	2.03	1.37	0.02	1.19	0.89	1.91	1.34
194	20	1035124	16991645	15762	GCATCTTCACRCAACCAGGGA	0.35	0.57	0.60	0.73	1.69	0.53	2.98	0.54	0.81	1.58	0.51	2.75
194	20	1046954	7348188	15763	GTAGCAAGCASGGCGAACGTG	1.70	0.03	0.03	0.53	0.66	0.94	0.40	0.00	0.57	0.70	0.93	0.42
195	20	10313407	6039899	15764	GTAATAATACRCTCTTCACAG	0.73	0.67	0.67	0.90	0.89	1.18	1.35	0.62	0.89	0.89	1.16	1.36
195	20	10339628	6133912	15765	ATGGTTTCTAYGGGAAAATGT	0.18	0.44	0.44	0.38	0.50	0.98	0.17	0.43	0.43	0.53	1.00	0.19
195	20	10350591	16991555	15766	TGCTATGAACYTGGCTCAATT	0.14	0.04	0.04	0.67	0.81	0.36	0.29	0.00	0.82	0.80	0.36	0.31
195	20	10358080	6133929	15767	TGCATCCACTYTGGCTCTCAC	1.18	1.41	1.41	0.80	0.32	0.49	0.41	1.32	0.83	0.34	0.51	0.44
195	20	10365492	2327294	15768	CAATATACTTWTATGTAATTT	-	-	-	-	-	-	-	-	-	-	-	-
195	20	10371753	6032879	15769	TAACTGAAGTRTTATTTATTT	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16842293	17690253	15770	TAGCTCAAGAKGATATTAATG	0.79	0.02	0.02	0.63	0.20	0.26	0.17	0.00	0.75	0.19	0.28	0.18
196	20	16851953	4814572	15771	GATGTTTTTAYCAGCAGCTTT	1.24	1.63	1.47	0.49	0.66	0.28	0.61	1.39	0.48	0.68	0.28	0.59
196	20	16853329	6080493	15772	AAACCATCCCYGACTTCGCCA	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16875987	2424005	15773	TGGGGAGGTTKTAGGTACACA	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16886784	6080506	15774	ATTCATCTGCYAGACGTTTGT	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16894871	17769782	15775	ACAGATATTTYTTAAAGTGTT	0.30	0.29	0.29	0.84	0.72	1.16	0.48	0.21	0.95	0.73	1.11	0.46
196	20	16902096	2424025	15776	TTTTTGGTTTYATGCTTACTT	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16910793	1118599	15777	GAACGTTTCTKGATGTATTGA	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16917569	4814578	15778	TGCAAAATGAYCAGAGTTATA	0.49	0.77	0.76	0.56	1.54	0.95	0.88	0.68	0.57	1.48	0.93	0.88
196	20	16930918	6044565	15779	CGGAGATATCRAATCTATTGA	0.16	0.10	0.10	1.25	0.79	0.91	1.27	0.07	1.32	0.82	0.92	1.24
196	20	16943788	16998578	15780	GTGTTTATTASAGCCTGCATT	0.60	0.54	0.54	0.66	0.59	1.20	1.04	0.49	0.70	0.60	1.19	0.99
196	20	16951406	16998590	15781	AGCAATGCACRCTCAGCTAAG	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16958754	982281	15782	ATGCATCACTRATTATCTTTG	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16968974	10485566	15783	CTTCCTTTACRTCAATGGAAC	0.10	0.10	0.10	0.83	1.33	0.97	1.34	0.09	0.91	1.31	0.96	1.32
196	20	16979201	2057	15784	GATATTTATCYGAATTGCTGT	0.07	0.13	0.07	1.34	1.67	2.00	0.89	0.05	1.53	1.59	1.90	0.84
196	20	16987959	6080544	15785	GTGCAGACATYAAAGAAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
196	20	16994284	17772083	15786	TAGTCACTTCWTCTTGACCAC	2.03	2.28	2.28	1.81	1.48	1.37	1.65	2.12	1.85	1.41	1.33	1.57
196	20	17001777	4396776	15787	CACATGGGATMCTTAGGAGCA	0.12	0.24	0.24	1.98	1.27	1.21	0.59	0.20	2.00	1.22	1.19	0.57
196	20	17008650	6131896	15788	TTGATAGTCARTGCTGTAAGT	0.29	0.46	0.46	1.51	1.78	0.51	0.58	0.40	1.57	1.61	0.53	0.59
196	20	17015215	7268410	15789	AGGTCCATGTKGCCCCCTGGT	1.96	1.91	1.94	1.43	0.74	1.17	0.92	1.85	1.85	0.74	1.16	0.90
196	20	17021176	7269653	15790	TGGTCATTAGWTGCACAAATA	1.86	1.94	1.94	1.03	1.29	1.14	0.78	1.87	1.27	1.25	1.10	0.79
196	20	17027009	16998735	15791	TCTACAACAGRAAAGTTACTT	-	-	-	-	-	-	-	-	-	-	-	-
196	20	17034287	6135975	15792	TGTGGAAATGYGTAATGGAAA	-	-	-	-	-	-	-	-	-	-	-	-
196	20	17037380	13042936	15793	AAGATATGTGYTGGCTTAGAC	-	-	-	-	-	-	-	-	-	-	-	-
196	20	17059967	1033807	15794	ATTCACATCCRATTGACAAGA	0.37	0.26	0.26	1.54	1.06	1.29	0.82	0.24	1.63	1.04	1.23	0.81
197	21	14572877	2822539	15795	TTCTAGCTTCMGAATTTTTTA	0.10	0.10	0.10	0.17	0.50	0.58	0.53	0.05	0.15	0.53	0.60	0.57
197	21	14578559	2822550	15796	AGTCAAAATTMTCTCTAAGAT	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14585162	2822554	15797	GACTATCAGCYGAGATACTTG	0.65	0.51	0.58	0.22	0.46	0.74	0.66	0.55	0.19	0.47	0.77	0.68
197	21	14592539	1153310	15798	TGGGAATTTTRAATGGAGGAA	0.08	0.06	0.06	0.22	0.40	0.45	0.37	0.04	0.19	0.43	0.49	0.39
197	21	14598028	980267	15799	AGGTAATAGGYAGAAGTGAGA	0.01	0.01	0.04	0.49	0.36	0.16	0.34	0.02	0.54	0.38	0.18	0.32
197	21	14604204	2822563	15800	CACCACTATTKTTAAGCCTTA	0.47	0.81	0.79	0.50	0.16	0.25	0.67	0.73	0.52	0.16	0.25	0.69
197	21	14609904	2822566	15801	CTTAGAGTTGWACTTTTGCCA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14619114	2245589	15802	TATCAGATTTRGCTGACTCCG	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14628202	2822578	15803	TGGATTTCATRGCATTTTATG	0.03	0.07	0.07	0.36	0.32	0.56	0.72	0.03	0.33	0.35	0.59	0.74
197	21	14637995	2822601	15804	CAGAAAAATAKTGACACAAGC	0.56	0.98	1.13	0.69	1.21	0.26	0.20	1.05	0.74	1.15	0.26	0.20
197	21	14644155	2822616	15805	TTTCTGTGTGSAGCATTCTCT	0.17	0.41	0.41	1.44	0.50	0.57	0.25	0.35	1.49	0.53	0.60	0.25
197	21	14650445	2822620	15806	TGCTCATGAAWCTGAGGAACA	1.56	1.74	1.78	0.39	0.69	0.38	1.06	1.74	0.40	0.72	0.40	1.06
197	21	14656191	2822630	15807	ATGAAGTCCAYTGTTGAAATT	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14663291	2822636	15808	CATTGAATTARGTTCTGATGA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14670057	2822642	15809	AGGATGCGATMAAGTAATCTC	0.23	0.49	0.45	0.86	0.31	1.20	1.82	0.44	0.90	0.32	1.16	1.74
197	21	14676857	1882881	15810	CAAACCCGATKTGATGGAAAA	0.89	0.67	0.67	0.36	0.79	1.58	2.94	0.67	0.34	0.78	1.53	2.76
197	21	14688525	2822655	15811	GAATTTAAAAYTAGATCCGTC	0.67	0.91	0.91	1.30	1.69	1.53	1.21	0.86	1.37	1.61	1.48	1.23
197	21	14696600	2822657	15812	ATTTCCACCAYGAACATTTCC	2.03	2.32	2.32	2.68	2.19	1.61	0.97	2.23	2.84	2.05	1.56	0.99

197	21	14709609	2822661	15813	GTTTTAAGATRCAAACAAAGA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14740509	7283911	15814	AAGTGTTGGAYCCAGAACTTA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14746713	2822666	15815	CTTTTATTAARAAGTTCGTTA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14752966	2822670	15816	CAAGAGTGTTYGGTAAGCCAT	0.19	0.42	0.42	2.73	2.63	1.93	1.99	0.38	2.94	2.50	1.86	1.88
197	21	14760831	9978450	15817	GTCTTTTCTGYGCTTGTGCAC	1.35	1.87	1.87	1.90	1.65	2.42	1.10	1.77	2.04	1.62	2.26	1.12
197	21	14767822	2822680	15818	AACCTGATAGYTATTGGCTAG	0.60	0.43	0.28	0.55	0.78	0.36	0.59	0.23	0.57	0.79	0.35	0.60
197	21	14773971	2822686	15819	TTTCATTGTAYGCTACCAAAA	0.84	0.84	0.82	0.27	0.49	0.28	0.42	0.80	0.29	0.53	0.27	0.39
197	21	14780568	2822695	15820	TGAACTTCCCKCATCAGCAAA	0.72	1.11	1.11	0.41	0.31	0.19	0.07	1.01	0.41	0.35	0.20	0.08
197	21	14791464	2822707	15821	GAGCACATATRTTTTAAAAAT	0.12	0.14	0.14	0.51	0.24	0.17	0.29	0.14	0.53	0.24	0.18	0.30
197	21	14796330	2822709	15822	TGCTGCTCTGRGAATGTGTGT	0.11	0.32	0.32	0.10	0.26	0.46	0.15	0.30	0.10	0.26	0.46	0.15
197	21	14808487	2822711	15823	GCATTTCCTGYCATAAATCTG	0.10	0.10	0.10	0.30	0.32	0.39	0.77	0.08	0.31	0.30	0.43	0.79
197	21	14819910	2822733	15824	ATTAGCTGGAYGGTGGCTATA	0.25	0.47	0.47	0.39	0.26	0.24	0.37	0.43	0.35	0.28	0.26	0.34
197	21	14832438	1980955	15825	TTTTATATCAYGTATTTTATT	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14838005	2822761	15826	CACAAATTCTRAGAGTATAGT	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14844910	2822767	15827	GGGAGAATCTRAATTCATTTT	0.65	0.10	0.10	0.44	0.12	0.05	0.11	0.08	0.45	0.12	0.04	0.10
197	21	14858760	7275386	15828	CCAAACCTGTYATGCAGAATA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14864087	1974155	15829	TCTTGCAGATRGTAGGCCTAA	-	-	-	-	-	-	-	-	-	-	-	-
197	21	14873578	2822778	15830	AAATATGACTRTTGTGTATTT	0.34	0.10	0.10	0.00	0.19	0.43	0.32	0.08	0.01	0.20	0.44	0.33
197	21	14884234	455221	15831	CTAAGTTTTCYGGTCTTATGA	0.02	0.12	0.12	0.02	0.05	0.37	0.34	0.07	0.01	0.06	0.38	0.37
198	21	18675802	2824788	15832	TACATTTGTGRTACTAATTCT	0.07	0.14	0.10	0.01	0.09	0.14	0.54	0.08	0.00	0.10	0.16	0.55
198	21	18684231	2824797	15833	GCCCTCAATGYCAGCTCTATT	0.31	0.08	0.08	0.07	0.16	0.33	0.37	0.04	0.10	0.17	0.31	0.37
198	21	18693121	2824806	15834	TAGAATGCTGKAGAAAATAGA	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18706732	2252042	15835	TTTTAGCCACYATCCAAATAA	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18712156	2824815	15836	CAAGGAATTTSTTCAAAAAAA	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18718381	2824820	15837	TTTAAGCTTAYATTTACCTCA	0.31	0.63	0.59	0.10	0.34	0.31	0.41	0.59	0.07	0.37	0.34	0.40
198	21	18729277	2824830	15838	AATTTTTTTTMCAAAAGATAA	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18737308	2824834	15839	CTAGCCCCGAWTAAATAGTGC	0.04	0.15	0.15	0.39	0.56	0.48	0.71	0.13	0.38	0.57	0.52	0.71
198	21	18745201	2824837	15840	AATCCACAATYAATCACTGGC	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18746350	2824839	15841	ATGGCACCTGMGAGTACATAG	0.45	0.75	0.75	0.31	0.67	0.64	1.49	0.70	0.29	0.69	0.64	1.44
198	21	18767176	2824843	15842	TTTGTATCCARATGAATTCCA	0.52	0.87	0.87	0.33	0.39	0.38	0.42	0.83	0.31	0.42	0.38	0.40
198	21	18775552	2824848	15843	ATTATTATTAYTCAGTAGGTT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18784648	2824851	15844	GTACACTAGGMTTTGATGTCT	0.36	0.36	0.36	0.37	0.21	0.29	0.22	0.27	0.36	0.24	0.26	0.22
198	21	18793849	2824860	15845	TTAACAAATCRTCTCATATAT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18802094	2824867	15846	TTGGAAATCTSTCTTTGAATG	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18810326	2245939	15847	CATTCATTCAYTCAAATACAT	0.09	0.15	0.15	0.07	0.17	0.39	0.50	0.11	0.08	0.19	0.43	0.51
198	21	18820035	2824902	15848	CAGAAGCCTCYAGCACTAGCC	0.10	0.14	0.14	0.01	0.36	1.03	0.36	0.13	0.00	0.37	1.01	0.39
198	21	18829403	2824906	15849	GAGTTATAGGYATTGATTGTA	0.16	0.08	0.08	0.61	0.95	0.52	0.51	0.04	0.64	0.94	0.57	0.50
198	21	18841285	2824907	15850	GTAGTTTTTTMAAAAGGAAAA	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18848364	983475	15851	ACTGACTTTCMTCATGCTGCA	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18854528	2824910	15852	AGTTTAATATRTACCAGTTTT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18864576	2824916	15853	GTGGAAGCTGYGGGAGCGAGA	1.54	1.57	1.55	1.97	1.33	0.46	0.36	1.51	2.35	1.28	0.49	0.39
198	21	18871561	1735791	15854	TGGAATGTATMTACGCATATG	1.10	0.61	0.61	1.84	1.40	0.91	0.33	0.58	2.02	1.38	0.91	0.35
198	21	18881089	1740167	15855	CTTTCTTAATRTTTCCATTCA	0.25	0.25	0.24	0.17	1.66	0.97	0.47	0.14	0.13	1.52	0.98	0.47
198	21	18888864	2178982	15856	CTATAAGGTAYCATTGGTTCC	0.81	0.51	0.48	0.40	1.68	0.81	0.43	0.43	0.41	1.52	0.80	0.42
198	21	18895085	2824943	15857	ATAAATGCACKTTTGATCATC	0.87	0.48	0.48	2.05	1.54	0.54	0.25	0.43	2.14	1.45	0.58	0.25
198	21	18901237	2824951	15858	TGTATTCAATYGCAAGTAGGT	3.73	3.33	3.13	1.47	0.83	0.63	0.40	3.05	1.56	0.86	0.65	0.41
198	21	18909107	1556297	15859	ACAACACTGAYTAAAAACTGC	1.11	0.53	0.53	1.13	0.79	0.48	0.48	0.50	1.42	0.80	0.48	0.47
198	21	18914694	2824957	15860	ATCATCCTGTYGAAAGGGCTC	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18920528	2205478	15861	CTCCTAACTGMAGGGTTTTAT	0.95	0.53	0.53	1.13	0.82	0.46	0.40	0.50	1.40	0.85	0.49	0.37
198	21	18926884	2824968	15862	AGGGTATTTARCTGCAGGATT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18934242	2824969	15863	AATGGTTTTCWTCCTGTTTCC	-	-	-	-	-	-	-	-	-	-	-	-
198	21	18940866	2824972	15864	ATGATTGTGGWGGAACTGGAA	2.68	2.92	2.92	1.29	0.80	0.69	0.47	2.85	1.34	0.80	0.69	0.46
198	21	18948707	2824976	15865	TTGATTTGATKTTTATGTCCC	1.89	2.25	2.30	1.49	1.08	0.75	0.32	2.20	1.90	1.07	0.77	0.34
198	21	18956769	2824981	15866	TTAGGCATCTRTTGCAAAGGA	1.70	2.27	2.27	1.42	1.30	0.36	0.39	2.23	1.73	1.23	0.37	0.40
198	21	18964301	2824984	15867	GAACCCTTATKGCATTTGTGT	1.52	2.07	2.07	1.43	0.57	0.77	0.81	2.03	1.56	0.59	0.77	0.82
198	21	18973225	2824988	15868	GGAAATTATGYTTTTTTATTG	2.01	2.66	2.66	1.01	1.22	1.12	0.55	2.58	1.05	1.21	1.12	0.59
198	21	18981497	1041409	15869	GTCCCCATGTRATTCTATTCC	0.06	0.10	0.10	1.97	1.88	1.06	0.66	0.07	2.00	1.79	1.07	0.66
198	21	18995502	2825000	15870	TATATATTTCYCACTCTTTAA	0.87	0.63	0.63	0.81	1.96	1.22	0.70	0.56	0.87	1.89	1.20	0.71
198	21	19005042	2825020	15871	GACACTGGGARATGTTTCAAA	0.13	0.34	0.34	0.21	0.60	1.21	1.36	0.32	0.20	0.57	1.20	1.38
198	21	19011363	2825024	15872	TAATACATGCYCAATAAACAT	0.15	0.28	0.28	0.21	0.30	0.95	1.22	0.26	0.18	0.31	0.94	1.20
198	21	19018063	2825041	15873	ATATCACTTCWTAAATAGCCA	1.02	0.82	0.82	0.41	0.34	0.72	0.90	0.77	0.44	0.36	0.72	0.92
198	21	19024400	2825051	15874	TATAATGTTTWTCCTTGTCTT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	19031172	2156200	15875	TTGATGAAAAYGTGAATAGTT	0.20	0.10	0.10	0.72	0.92	0.71	0.19	0.06	0.81	0.91	0.74	0.18
198	21	19040670	2825067	15876	ATATTAAAGTRCCAATCAGCT	1.16	0.88	0.88	0.23	0.87	0.15	0.26	0.78	0.20	0.89	0.15	0.25
198	21	19046370	2825071	15877	TGCAAAGACCYGAGGCTCTGT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	19060612	2825074	15878	GCTCTCATCARAAAAAGGCCT	0.26	0.56	0.56	0.21	0.04	0.29	0.20	0.52	0.20	0.03	0.28	0.19
198	21	19070893	12329876	15879	TGAAATGTTTYATTATACAAT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	19082377	2825121	15880	TGACTTAAATKTTTTTTGAAT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	19090538	2825124	15881	AGATCATTATSGTTTAATATT	0.03	0.10	0.10	0.16	1.11	0.48	0.27	0.06	0.13	1.08	0.53	0.28
198	21	19096373	2825129	15882	ACCTTAAAATKCCTGATTGTT	-	-	-	-	-	-	-	-	-	-	-	-
198	21	19102114	2825149	15883	ATAGGCATTGRCAAGAGAAAG	-	-	-	-	-	-	-	-	-	-	-	-
198	21	19109902	1893507	15884	TACAAAGAGASGAATGGAAAC	0.06	0.23	0.23	0.91	0.71	0.64	0.42	0.21	0.96	0.72	0.64	0.44
199	21	36165999	4447684	15885	ATCTGCACTGMAAATAACCAT	0.19	0.32	0.40	0.57	0.42	0.53	1.20	0.31	0.55	0.44	0.56	1.20
199	21	36179508	8129502	15886	AAAAATACACRCAAATATATG	-	-	-	-	-	-	-	-	-	-	-	-
199	21	36180839	2835156	15887	AAGGTTACTCRACTCAAGCTA	-	-	-	-	-	-	-	-	-	-	-	-
199	21	36203455	438540	15888	CTCATAAGTTWACCATGCTAG	1.03	1.50	1.50	0.98	0.59	1.08	0.59	1.43	0.99	0.63	1.07	0.61
199	21	36214925	2835158	15889	AGAGTCCTTGYGCTCAACCTC	1.10	1.26	1.26	0.53	0.50	0.89	0.48	1.20	0.54	0.51	0.86	0.48
199	21	36223400	2835162	15890	GCAAATGTTARTCAGATGGTT	0.34	0.66	0.62	0.77	0.41	0.31	0.60	0.59	0.80	0.44	0.30	0.58
199	21	36232226	2835165	15891	ACTTTTTCTGYGAGTTAGGAA	1.20	1.76	1.76	0.67	0.44	0.19	0.60	1.69	0.70	0.46	0.19	0.61
199	21	36239509	2178810	15892	CCAGCAAGCTSATCCATAGAG	1.38	1.94	1.94	0.78	0.71	0.82	0.55	1.87	0.81	0.72	0.82	0.57
199	21	36245282	2251046	15893	GCCACTGATAYCCCCAGTTCT	0.21	0.49	0.49	1.22	0.77	0.80	0.79	0.47	1.32	0.75	0.81	0.81
199	21	36252957	2835185	15894	TATGCCAGCTYTTGAATCATA	1.71	2.32	2.32	0.93	1.24	0.70	0.81	2.26	1.06	1.19	0.69	0.85
199	21	36261732	2243634	15895	AAAGTCATGTRAAGTCCTTTC	0.47	0.84	0.84	1.22	0.88	1.30	0.43	0.85	1.50	0.84	1.26	0.45
199	21	36270350	972641	15896	CTCAATGCACYATGGGAAACT	0.66	0.98	0.98	0.96	0.96	0.67	1.19	0.94	1.05	0.91	0.70	1.18
199	21	36276189	867223	15897	AGATGCAACCRTTTCTCTGTG	0.96	1.50	1.50	1.11	0.87	1.29	0.77	1.39	1.23	0.87	1.23	0.79
199	21	36284588	2835215	15898	AGTTTCAAATMGATACAGCAC	0.72	0.82	0.82	0.77	1.00	1.16	1.76	0.74	0.76	0.94	1.13	1.64
199	21	36293010	2835225	15899	GTATGAATAARCTGAAATCAC	-	-	-	-	-	-	-	-	-	-	-	-
199	21	36309272	743420	15900	CATCCCGAAARTCTCAAATCT	0.23	0.22	0.22	0.63	0.74	1.72	2.13	0.21	0.70	0.75	1.62	1.93
199	21	36319470	2835235	15901	CCAGGACAGGRCTAAAGGGAT	1.06	0.98	0.98	0.17	3.05	2.13	1.55	0.89	0.16	2.68	1.96	1.47
199	21	36327722	2835236	15902	GAAAGATGATSGAGGAATGCC	-	-	-	-	-	-	-	-	-	-	-	-
199	21	36334622	2255858	15903	CTCCAATGTAYGACATCCCTT	0.05	0.10	0.10	3.26	2.73	2.53	1.46	0.10	3.49	2.50	2.28	1.43
199	21	36341714	2835255	15904	TGGAAGAGAASAGGCTACTAT	2.95	3.72	3.72	3.23	3.58	2.39	1.56	3.65	3.50	3.00	2.23	1.51
199	21	36349153	2835260	15905	AGTTGGATTTKATGAGTCCCA	0.67	1.07	1.07	3.23	3.39	2.13	1.00	0.99	3.42	2.99	2.02	1.02
199	21	36352115	2835263	15906	GATTTACATARGACTTTCCAG	0.06	0.10	0.10	1.01	2.02	1.37	1.54	0.08	1.05	1.94	1.33	1.49

199	21	36366566	2835265	15907	CACCTCTCTAYGGGATTGTTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
199	21	36372453	2835270	15908	CATTCGGAACYGCCCAGTCCT	0.65	0.87	0.87	0.94	0.64	1.41	1.01	0.84	0.92	0.64	1.38	1.01	0.87	0.64	1.38	1.01	0.87	0.64	1.38	1.01
199	21	36381871	2835275	15909	ACAGTTGCCAYCATACCTCAG	0.46	0.24	0.22	0.86	1.33	0.66	1.29	0.17	0.89	1.31	0.69	1.27	0.24	1.33	0.66	1.29	0.24	1.33	0.66	1.29
199	21	36404139	2009849	15910	TAAACTTCCTYGTAACGCAAA	0.16	0.13	0.10	0.96	1.48	1.96	2.06	0.07	1.06	1.39	1.86	1.98	0.13	1.48	1.96	2.06	0.13	1.48	1.96	2.06
199	21	36412525	2835283	15911	TCTGTGCGTAYCTGCAAACAG	1.02	1.58	1.58	1.34	2.47	2.81	2.80	1.50	1.42	2.24	2.54	2.60	1.58	2.47	2.81	2.80	1.58	2.47	2.81	2.80
199	21	36415880	2226827	15912	TTCATGTAGARTCAATTGTGA	0.08	0.22	0.21	0.62	0.91	2.36	2.03	0.19	0.68	0.91	2.20	1.89	0.22	0.91	2.36	2.03	0.22	0.91	2.36	2.03
199	21	36429637	2835285	15913	CAACGCGGCCRTCGCCTTCAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
199	21	36440232	2835286	15914	TATATTTATCRTTCTGTTTCA	0.10	0.08	0.08	0.03	0.42	0.46	0.96	0.04	0.00	0.44	0.47	0.96	0.08	0.42	0.46	0.96	0.08	0.42	0.46	0.96
199	21	36447699	2835288	15915	CAGCAACAAGSATTGTGACAG	0.08	0.14	0.14	0.58	0.40	0.08	0.12	0.07	0.64	0.42	0.09	0.11	0.14	0.40	0.08	0.12	0.14	0.40	0.08	0.12
199	21	36457767	2835289	15916	CGTTCACTCAYGTTTAACTAT	0.62	1.09	1.09	0.39	0.07	0.09	0.07	1.04	0.39	0.07	0.09	0.07	1.09	0.07	0.09	0.07	1.09	0.07	0.09	0.07
200	22	29573887	2413001	15917	CTGACTCTTTYATCATAATGA	0.38	0.45	0.45	0.53	0.07	0.02	0.01	0.38	0.55	0.07	0.02	0.01	0.45	0.07	0.02	0.01	0.45	0.07	0.02	0.01
200	22	29586310	5749182	15918	CGGGTGGTTAYCATCCTTCCC	0.45	0.74	0.70	0.35	0.20	0.03	0.02	0.66	0.37	0.20	0.04	0.02	0.74	0.20	0.03	0.02	0.74	0.20	0.03	0.02
200	22	29597838	12167141	15919	CTTGAATTACWGTTTTGGGTA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
200	22	29610234	5749186	15920	TTTCCTGTGCRTGGATGAGCA	0.20	0.22	0.22	0.81	0.28	0.34	0.02	0.21	0.87	0.29	0.30	0.03	0.22	0.28	0.34	0.02	0.22	0.28	0.34	0.02
200	22	29626787	3804085	15921	AGAGGCTGGAYCCGCTGACCG	0.64	0.96	0.96	0.98	1.31	0.23	0.15	0.89	1.14	1.26	0.21	0.15	0.96	1.31	0.23	0.15	0.96	1.31	0.23	0.15
200	22	29629762	5749194	15922	TGGGGACACAMAGCTTCCTTT	0.05	0.17	0.17	1.96	1.33	0.73	0.06	0.14	2.48	1.28	0.75	0.05	0.17	1.33	0.73	0.06	0.17	1.33	0.73	0.06
200	22	29635500	5753388	15923	TCACTTGTAAYGGTACAATTC	0.20	0.36	0.30	2.06	1.08	0.42	0.18	0.27	2.52	1.08	0.42	0.19	0.36	1.08	0.42	0.18	0.36	1.08	0.42	0.18
200	22	29648454	5753394	15924	GAGAACCATASATTCCTGTGA	0.67	1.02	1.02	0.80	1.04	0.25	0.07	0.93	0.79	1.00	0.25	0.06	1.02	1.04	0.25	0.07	1.02	1.04	0.25	0.07
200	22	29658185	3747151	15925	GCTCACTGGAYGGGGGCTGGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
200	22	29664853	11089484	15926	CTTCACAGCCRTCCCAGGTGA	0.60	0.91	0.91	0.92	0.14	0.19	0.14	0.87	0.96	0.13	0.19	0.13	0.91	0.14	0.19	0.14	0.91	0.14	0.19	0.14
200	22	29671306	1003480	15927	CCTTCTGCTCRCTCCACCTGG	0.25	0.36	0.36	0.64	0.10	0.07	0.25	0.31	0.71	0.10	0.07	0.24	0.36	0.10	0.07	0.25	0.36	0.10	0.07	0.25
200	22	29678379	3827330	15928	ATAAGTTTATKGTATACACAG	0.50	0.84	0.86	0.91	0.40	0.19	0.13	0.86	0.99	0.40	0.19	0.14	0.84	0.40	0.19	0.13	0.84	0.40	0.19	0.13
200	22	29685146	2240182	15929	GTAACAGCATRAAACTCCTTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
200	22	29704798	5997830	15930	AATGACAGATYCAGGACTAAT	0.63	0.97	0.97	0.33	0.98	0.46	0.15	0.94	0.32	1.00	0.46	0.15	0.97	0.98	0.46	0.15	0.97	0.98	0.46	0.15
200	22	29707320	3948685	15931	TATTAGTTGCSCTCTGAGTTT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
200	22	29720379	5997835	15932	CAATTTTTAAYAATAATAAAT	0.58	0.87	0.87	0.82	0.28	0.43	0.43	0.82	0.84	0.26	0.43	0.41	0.87	0.28	0.43	0.43	0.87	0.28	0.43	0.43
201	X	13760724	17215742	15933	TTTTGTCACAYTCTCACCTAA	-	-	0.15	0.39	0.08	0.11	0.11	0.12	0.33	0.05	0.11	0.11	-	-	0.15	0.39	0.08	0.11	0.11	0.12
201	X	13771022	17215756	15934	CTGGCTCTTCYCCATGCTTCT	-	-	0.25	0.19	0.19	0.22	0.68	0.22	0.12	0.22	0.27	0.67	-	-	0.25	0.19	0.19	0.22	0.68	0.22
201	X	13776638	16979382	15935	GTCTAGCACTRTAACACATAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13797029	1003829	15936	ATAATAGGGARAGAAGCATTT	-	-	0.21	0.19	0.22	1.56	1.11	0.17	0.13	0.23	1.42	1.09	-	-	0.21	0.19	0.22	1.56	1.11	0.17
201	X	13804200	16979387	15937	TAAACACTGAMGAGGCCTATA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13818318	12006779	15938	ACAGAATAGCYGTATATGTGA	-	-	0.21	0.20	1.65	1.22	1.19	0.18	0.07	1.53	1.19	1.12	-	-	0.21	0.20	1.65	1.22	1.19	0.18
201	X	13824455		15939	GTGCAAACCTRCTGTGTGCTT	-	-	0.08	1.69	1.60	1.25	1.05	0.09	1.88	1.46	1.21	1.04	-	-	0.08	1.69	1.60	1.25	1.05	0.09
201	X	13832787	16996926	15940	GACATGCTAARAAATGGGAAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13840940		15941	TGCTTGGTGARCAAACTATTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13860240	6653507	15942	TTAGCTATAAMATTTTGCATC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13878848	5935702	15943	TCCCACTCTCYACCTTCAAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13887898	6653686	15944	GTAAGCACTARGATTTATAGA	-	-	2.99	1.35	1.60	1.34	0.68	2.97	1.49	1.52	1.28	0.70	-	-	2.99	1.35	1.60	1.34	0.68	2.97
201	X	13904093	4574997	15945	AGGCACTTTGYGTGATTCACT	-	-	2.39	1.59	1.25	0.83	0.52	2.34	1.85	1.19	0.84	0.53	-	-	2.39	1.59	1.25	0.83	0.52	2.34
201	X	13917476	5935713	15946	CGGGTCAGAARCAGTGGCTCT	-	-	2.45	1.39	1.21	0.51	0.57	2.41	1.65	1.16	0.51	0.57	-	-	2.45	1.39	1.21	0.51	0.57	2.41
201	X	13927337	4333771	15947	GCTAAAGCCAYCTCCACCAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
201	X	13957057		15948	TGTTTCCTTGSGATGATTATT	-	-	0.57	1.29	1.18	1.12	0.57	0.55	1.46	1.13	1.10	0.55	-	-	0.57	1.29	1.18	1.12	0.57	0.55
201	X	13961488		15949	CTATATGCCTRTTTGAAATAC	-	-	0.04	0.25	1.12	0.82	0.57	0.05	0.22	1.10	0.86	0.60	-	-	0.04	0.25	1.12	0.82	0.57	0.05
201	X	13971625	7051988	15950	CAAAACAATAYTCTGTGTCCA	-	-	0.10	0.29	0.12	0.48	0.34	0.08	0.21	0.09	0.51	0.35	-	-	0.10	0.29	0.12	0.48	0.34	0.08
202	X	24252580	7062675	15951	CGTCTTTTCASAAAACTAAAT	-	-	0.32	0.59	0.25	0.19	0.44	0.30	0.62	0.28	0.20	0.47	-	-	0.32	0.59	0.25	0.19	0.44	0.30
202	X	24260285	5986463	15952	TTTAAACCTAYGCTCTTTTCA	-	-	0.36	0.36	1.64	1.39	0.33	0.34	0.41	1.46	1.37	0.30	-	-	0.36	0.36	1.64	1.39	0.33	0.34
202	X	24265910	5986480	15953	GTTATCAGCCRCTATGTAAAC	-	-	0.48	1.14	2.77	2.15	0.49	0.45	1.45	2.20	1.77	0.51	-	-	0.48	1.14	2.77	2.15	0.49	0.45
202	X	24272853	2269912	15954	AGTTGTTTTARTGAAAATGCT	-	-	0.39	2.10	2.24	0.67	0.62	0.38	2.47	1.82	0.73	0.63	-	-	0.39	2.10	2.24	0.67	0.62	0.38
202	X	24278342	5986510	15955	TGTGCTTGACSATAGCAATAA	-	-	0.27	0.72	0.82	0.46	0.41	0.25	0.89	0.81	0.45	0.39	-	-	0.27	0.72	0.82	0.46	0.41	0.25
202	X	24289796	5986549	15956	GTGCATCTTGYGTAGCATTAA	-	-	0.35	0.45	0.31	0.44	0.45	0.35	0.47	0.32	0.46	0.50	-	-	0.35	0.45	0.31	0.44	0.45	0.35
203	X	39060851	2130442	15957	CCAAACATCCRCAGAGCCCCA	-	-	0.25	0.94	2.67	2.17	1.76	0.25	0.97	2.40	2.01	1.69	-	-	0.25	0.94	2.67	2.17	1.76	0.25
203	X	39071264	17145397	15958	CTTAGCATCGMGTCTGCTCCG	-	-	1.74	1.59	1.42	2.54	1.69	1.76	1.66	1.39	2.31	1.61	-	-	1.74	1.59	1.42	2.54	1.69	1.76
203	X	39084763	902254	15959	TGGACCAAGGYTCTGCCCAAG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
203	X	39090481	4827157	15960	TCACCAGGAGRTAGCACAGTC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
203	X	39101590	1318833	15961	AAACTATGAGSTCCCTTTACC	-	-	0.26	2.14	1.94	1.54	2.59	0.22	2.19	1.85	1.45	2.39	-	-	0.26	2.14	1.94	1.54	2.59	0.22
203	X	39110837	5963663	15962	AAAAGGAGGAYCACAGGTACA	-	-	0.26	0.78	2.36	2.70	2.46	0.25	0.83	2.08	2.41	2.19	-	-	0.26	0.78	2.36	2.70	2.46	0.25
203	X	39120863	5917839	15963	TGGTTCACTGYTCTATAATGG	-	-	0.73	0.62	2.03	4.07	3.04	0.72	0.67	1.83	3.49	2.62	-	-	0.73	0.62	2.03	4.07	3.04	0.72
203	X	39128734	11266258	15964	TGCTGTACTTYGGTCATCCAG	-	-	0.22	1.94	2.03	1.70	3.54	0.22	2.06	1.84	1.59	3.23	-	-	0.22	1.94	2.03	1.70	3.54	0.22
203	X	39141263	17145430	15965	GTTTATAGCCRATTCTGCACC	-	-	1.47	1.70	1.90	1.66	1.93	1.53	1.70	1.77	1.59	1.77	-	-	1.47	1.70	1.90	1.66	1.93	1.53
203	X	39155287	12014916	15966	CTGGGTCTACYGGGACCTTTG	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
203	X	39171907	7059737	15967	ACATGTGTGCRGTTTCATGGA	-	-	1.47	0.95	1.58	2.10	0.97	1.54	0.92	1.52	1.96	0.97	-	-	1.47	0.95	1.58	2.10	0.97	1.54
203	X	39179436	2168227	15968	TCAGCTGGGARACAAGACATA	-	-	0.13	1.60	1.69	1.23	0.59	0.13	1.62	1.60	1.22	0.63	-	-	0.13	1.60	1.69	1.23	0.59	0.13
203	X	39192293	12013781	15969	TGCTGCCTTGYTCCCAAGGTG	-	-	2.27	1.72	1.14	0.74	0.59	2.17	1.87	1.12	0.76	0.59	-	-	2.27	1.72	1.14	0.74	0.59	2.17
203	X	39198036	12009148	15970	GGAGAGAACCMTAACGGAGCT	-	-	1.47	1.51	0.76	0.78	0.69	1.41	1.62	0.77	0.80	0.67	-	-	1.47	1.51	0.76	0.78	0.69	1.41
203	X	39207992	5963671	15971	ATTTATGAAASTTAAGAACCC	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
203	X	39231187	6610305	15972	ACGATTTGCARAAATTATAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
203	X	39235645	4434756	15973	CTGTGCTAACSTTTGTGGTTC	-	-	0.84	0.53	1.13	0.67	0.65	0.79	0.53	1.14	0.68	0.65	-	-	0.84	0.53	1.13	0.67	0.65	0.79
204	X	84892457	5968697	15974	GAAGAGCAGAYATATTATTGT	-	-	0.25	0.20	0.17	0.29	0.46	0.22	0.18	0.20	0.28	0.46	-	-	0.25	0.20	0.17	0.29	0.46	0.22
204	X	84900913	6524586	15975	GGAACTGAGAWAATTTTCAGA	-	-	0.20	0.45	0.25	0.36	0.61	0.20	0.45	0.24	0.35	0.59	-	-	0.20	0.45	0.25	0.36	0.61	0.20
204	X	84914983	12392458	15976	TAGACAAAAAYAACTGGCATG	-	-	0.13	0.42	0.48	0.70	0.53	0.14	0.39	0.49	0.71	0.55	-	-	0.13	0.42	0.48	0.70	0.53	0.14
204	X	84929024		15977	TTCTTGGACAYGCCAATTACT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
204	X	84947192		15978	AAACATTTCARCATCATAATT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
204	X	84954511	719988	15979	AAGTGAAAGARCAGGTAAAGT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
204	X	84963956	16980334	15980	TCATTAAACAYCAATCTCTAT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
204	X	84983252	12559759	15981	ACACATGTTCRTGCACTATAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
204	X	84993285	11092732	15982	CTTCCAGGGGKAGCAAACTGC	-	-	0.41	0.43	0.89	0.86	0.71	0.48	0.43	0.87	0.86	0.72	-	-	0.41	0.43	0.89	0.86	0.71	0.48
204	X	85000776	1018368	15983	TATGAAGGTGYGGAATGGTGC	-	-	0.04	0.26	0.81	0.90	1.19	0.03	0.20	0.79	0.90	1.14	-	-	0.04	0.26	0.81	0.90	1.19	0.03
204	X	85009182	5968730	15984	AAATGCCCTCYTTTAACAAAA	-	-	0.03	0.37	0.28	1.45	1.30	0.02	0.35	0.30	1.42	1.28	-	-	0.03	0.37	0.28	1.45	1.30	0.02
204	X	85025166	10217950	15985	TTTTCTGCAGYGCACCAGCTT	-	-	0.06	0.52	0.68	0.51	2.00	0.05	0.40	0.71	0.55	1.90	-	-	0.06	0.52	0.68	0.51	2.00	0.05
204	X	85029184	2411872	15986	TCTTACCCAAYACGACTTGCT	-	-	0.06	0.68	0.57	0.97	0.86	0.05	0.66	0.64	0.98	0.86	-	-	0.06	0.68	0.57	0.97	0.86	0.05
204	X	85038880	12861027	15987	AATATCTAGTSAGCTGTACCT	-	-	0.88	0.50	0.90	0.61	0.33	0.88	0.53	0.91	0.67	0.33	-	-	0.88	0.50	0.90	0.61	0.33	0.88
204	X	85060846	5968768	15988	TCACGTGTCCRCAGCTCATTA	-	-	0.06	0.99	0.54	0.26	0.17	0.04	1.00	0.53	0.28	0.20	-	-	0.06	0.99	0.54	0.26	0.17	0.04
204	X	85070402	12853262	15989	ATATGGTCAAYGATATACATC	-	-	1.15	0.56	0.26	0.14	0.08	1.09	0.56	0.27	0.14	0.08	-	-	1.15	0.56	0.26	0.14	0.08	1.09
204	X	85087905	5923428	15990	TTTTTTTATAYTGTAGCATTC	-	-	0.72	0.53	0.17	0.08	0.13	0.79	0.52	0.17	0.09	0.14	-	-	0.72	0.53	0.17	0.08	0.13	0.79
204	X	85100464		15991	TCCATGTGTARAACTTTTTCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
204	X	85107122	1883796	15992	GTTCATAGCARCTACAACCAG	-	-	0.18	0.34	0.21	0.18	0.09	0.20	0.33	0.19	0.17	0.09	-	-	0.18	0.34	0.21	0.18	0.09	0.20
205	X	95234712	4969668	15993	AAGTGTGAATRATGCTGAATG	-	-	0.11	0.86	0.63	0.65	0.37	0.11	0.86	0.64	0.69	0.36	-	-	0.11	0.86	0.63	0.65	0.37	0.11
205	X	95241371	12013487	15994	GTTCTAGAAAYAGCCGATTCT	-	-	0.96	0.75	1.89	1.18	0.53	0.97	0.83	1.65	1.17	0.51	-	-	0.96	0.75	1.89	1.18	0.53	0.97
205	X	95252986	4969669	15995	ACTCATTCATKTATGTACTTA	-	-	0.07	1.37	1.89	1.73	0.89	0.03	1.60	1.64	1.54	0.89	-	-	0.07	1.37	1.89	1.73	0.89	0.03
205	X	95271298	1883399	15996	CAGAAATAAGYTGGTGGCCCT	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
205	X	95283829	1206604	15997	TGGCAACATAYGGATTTAGCT	-	-	1.31	1.67	1.73	1.63	2.10	1.27	2.09	1.50	1.44	1.85	-	-	1.31	1.67	1.73	1.63	2.10	1.27
205	X	95303430	1150267	15998	AAAGTGTTGARAAATATACAG	-	-	1.24	0.65	1.87	2.11	2.10	1.18	0.81	1.58	1.86	1.83	-	-	1.24	0.65	1.87	2.11	2.10	1.18
205	X	95308858	1937297	15999	CTCCAAACCCRGCAGGAAATA	-	-	1.10	1.29	2.01	2.55	2.69	1.01	1.43	1.79	2.14	2.27	-	-	1.10	1.29	2.01	2.55	2.69	1.01
205	X	95320857		16000	ACATGTTTGAKAGCATGAAAA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

205	X	95324895	1150280	16001	GGTCACAATCKTGAAAGTTTA	-	-	1.84	1.94	2.50	2.91	3.20	1.72	2.21	2.16	2.33	2.50
205	X	95347362	5949820	16002	TACCTAAAACSGTCTCTTGTA	-	-	0.49	1.68	3.05	3.15	3.23	0.46	2.05	2.45	2.46	2.53
205	X	95356811	1150293	16003	TAGGGTGTAGWTTAAGACCAC	-	-	1.76	1.30	2.25	3.41	3.26	1.83	1.63	1.75	2.66	2.66
205	X	95374935	1150304	16004	TTCACAGAAAYTTCATAAATG	-	-	-	-	-	-	-	-	-	-	-	-
205	X	95385858	9887355	16005	TTGAGGAAAARGCTATGTCAC	-	-	0.30	0.93	2.31	2.36	2.79	0.35	1.19	1.89	1.93	2.28
205	X	95396191	10218318	16006	AGCTCATTATRCCATCCTAAC	-	-	0.30	0.23	1.09	3.14	2.42	0.40	0.17	1.08	2.55	2.06
205	X	95405525	17337632	16007	GATTCTATATYTCACCAAATT	-	-	0.38	1.11	1.44	1.04	1.99	0.37	1.15	1.34	1.04	1.79
205	X	95426353	16982129	16008	AACCTAATGCRTGGTTGATAT	-	-	1.84	1.29	1.26	1.36	0.95	1.92	1.54	1.22	1.27	0.98
205	X	95439763	1933402	16009	GCAGAATCCCRTGAACCACTT	-	-	0.02	1.25	1.55	1.15	1.12	0.00	1.50	1.44	1.10	1.11
205	X	95448794	2225920	16010	CTCCAACACASTTAGATTTCC	-	-	0.12	0.37	1.05	1.25	1.45	0.13	0.40	1.00	1.26	1.44
205	X	95459008	5949835	16011	CCCCATCTGCYCAATCCACAG	-	-	0.32	0.81	0.44	1.39	1.62	0.33	0.84	0.47	1.32	1.52
205	X	95464845	5990203	16012	AATACAGGAARGTAATTAGTT	-	-	0.39	0.89	0.47	0.90	1.46	0.34	0.96	0.51	0.87	1.38
205	X	95478145	5990206	16013	TAGCTTCTCGKTAAATAGACA	-	-	0.02	0.74	1.03	0.74	0.95	0.00	0.84	1.02	0.76	0.94
206	X	110155224	5985318	16014	ACTGAAAACCRTCACTCTACC	-	-	0.82	1.15	0.57	0.65	0.92	0.76	1.47	0.63	0.65	0.91
206	X	110161338	4243372	16015	GCATGTGCTTYCTGTCTCTTG	-	-	-	-	-	-	-	-	-	-	-	-
206	X	110170703	5942721	16016	TCTCCCGTTCRAATCAAAATC	-	-	0.12	1.31	1.81	1.07	1.62	0.07	1.64	1.64	1.05	1.53
206	X	110177597	5943137	16017	TGCAGTGCTGYGTAATGGACT	-	-	0.07	1.12	1.86	3.31	1.52	0.00	1.55	1.69	2.73	1.45
206	X	110186485	16986378	16018	GAGCCAAAGTMCTCAATGGAG	-	-	0.09	0.94	2.98	2.80	1.93	0.08	1.15	2.56	2.40	1.72
206	X	110203072	12116264	16019	CAGTAGATCTYCTTTAGTTGT	-	-	-	-	-	-	-	-	-	-	-	-
206	X	110209121	1884552	16020	AGCCCAGTTGWTATGGCTAAA	-	-	0.06	1.12	1.68	2.09	2.02	0.00	1.25	1.72	1.86	1.83
206	X	110219841	16986393	16021	ATTATGTTGTMTACTAGCCCA	-	-	0.39	1.14	0.52	1.38	2.02	0.39	1.27	0.55	1.29	1.85
206	X	110227586	10521534	16022	GTCATCTCTCRTATGAATCAC	-	-	0.15	0.18	0.60	0.64	1.21	0.09	0.16	0.61	0.68	1.19
206	X	110237476	16986417	16023	ATTTGTCGCARTTTTATACCA	-	-	-	-	-	-	-	-	-	-	-	-
206	X	110249921	16986424	16024	TGTGGGTTAGYCCTCCATGGA	-	-	-	-	-	-	-	-	-	-	-	-
206	X	110259372	7884588	16025	CAGTTGCACAYCAGTGTCAGT	-	-	-	-	-	-	-	-	-	-	-	-
206	X	110269647	16986440	16026	TATCTTAATTMAAAAGGGCTG	-	-	0.53	0.18	0.34	0.81	0.63	0.50	0.15	0.35	0.79	0.65
207	X	146042507	5905023	16027	AAAAAGCTACKCAATGTTTTC	-	-	0.44	0.24	0.36	0.80	0.83	0.44	0.24	0.36	0.81	0.82
207	X	146060287	12008050	16028	GAGAATTTAARGTGACTGTGG	-	-	0.70	0.52	1.01	1.10	1.29	0.70	0.54	1.03	1.11	1.28
207	X	146065815	17273595	16029	AAAGAACTACYATCTGTTGGG	-	-	0.58	1.57	1.16	1.74	1.92	0.74	1.66	1.15	1.68	1.82
207	X	146074651	5905034	16030	CTCAGTATATRTGAATGGTAC	-	-	1.70	1.73	2.21	2.23	1.96	1.64	1.95	1.96	2.09	1.83
207	X	146090115	16994068	16031	TGATTCTCATRTATATTTACT	-	-	0.59	1.62	3.16	2.35	2.36	0.56	1.74	2.76	2.06	2.19
207	X	146101256	16994075	16032	GGTGTTGAAAYGGAGGACATT	-	-	-	-	-	-	-	-	-	-	-	-
207	X	146109117	16994086	16033	TAAACCTTTASACCGTTCTGC	-	-	1.42	1.28	2.26	3.63	4.03	1.38	1.52	2.06	3.15	3.61
207	X	146117168		16034	ATAACCAGAGKATTCATTGCA	-	-	1.30	1.45	2.14	4.78	5.11	1.24	1.71	1.97	4.15	4.35
207	X	146127914	5951961	16035	GAAAGGCTTASTGTACATTCT	-	-	0.77	1.57	2.40	2.66	4.52	0.72	1.62	2.24	2.38	3.96
207	X	146150694	7889464	16036	GATTCAGTGTYAGAACTAGAA	-	-	1.26	2.39	2.21	1.99	1.73	1.23	2.48	2.02	1.92	1.64
207	X	146156919	7066569	16037	CTTATTTGCAYGAAAGTTCTT	-	-	1.97	1.71	2.50	1.35	1.90	1.91	2.08	2.23	1.29	1.75
207	X	146169387	16994102	16038	CCCATGCATAWTGTACAGCAG	-	-	1.64	1.14	2.94	2.87	1.58	1.72	1.44	2.73	2.51	1.52
207	X	146172444	16994106	16039	TAAAAATGGTRAGCAGATATA	-	-	-	-	-	-	-	-	-	-	-	-
207	X	146189014	4824292	16040	AAACATACTAYGCATGACTAC	-	-	0.91	1.04	1.13	3.15	2.39	0.89	1.00	1.11	2.62	2.19
207	X	146206642	4824297	16041	CTGGTGTGTARAAGAGTTGGT	-	-	0.17	0.58	2.03	1.85	2.47	0.13	0.63	1.84	1.67	2.17
207	X	146210157	11797394	16042	AAAACGGGATKCCTGGGTCAA	-	-	0.02	0.57	1.71	1.72	1.73	0.00	0.61	1.56	1.61	1.59
208	X	147481778	5936223	16043	AAAAATTACTYGATTAACCTT	-	-	1.01	0.22	0.91	1.17	1.35	0.93	0.21	0.91	1.13	1.31
208	X	147486681	5936418	16044	ATAATGATGAWCTTTCACTCA	-	-	0.73	1.11	1.08	1.73	0.87	0.68	1.17	1.08	1.61	0.88
208	X	147509886	241086	16045	ACTGCCCCAAYGTGTGTCATG	-	-	0.26	1.61	2.93	1.07	0.97	0.31	1.65	2.49	1.04	0.97
208	X	147522461		16046	CATGAAGACTRTGTTGGAACA	-	-	-	-	-	-	-	-	-	-	-	-
208	X	147531140	16994697	16047	TTACGTTATAKGCCGAAAGAA	-	-	-	-	-	-	-	-	-	-	-	-
208	X	147544525	5936225	16048	AAATACAATTKAAAGCACCGT	-	-	0.74	1.31	1.77	1.79	1.04	0.68	1.54	1.65	1.67	0.99
208	X	147555839	16994713	16049	CAGAAAGTTAYGAGGACATGT	-	-	-	-	-	-	-	-	-	-	-	-
208	X	147561806	10521876	16050	TTTGTTTCTTYGGGCTCAGAT	-	-	0.56	0.55	1.32	1.80	1.33	0.52	0.57	1.28	1.66	1.28
208	X	147573026	5936435	16051	GACTCACTTCRTACCCAGGTC	-	-	0.21	0.06	0.38	0.77	1.51	0.21	0.05	0.36	0.82	1.46
208	X	147576685	2007875	16052	AATAAATAGASAGGTATGGTC	-	-	0.22	0.14	0.02	0.41	- 0.92	0.21	0.14	0.00	0.44	0.93

Table 3. List of significantly associated haplotypes based on the Crohn's Disease genome wide scan results using the Quebec Founder Population (QFP). Individual haplotypes with associated relative risks are presented in each row of the table; these values were extracted from the associated marker haplotype window with the most significant p value for each SNP in Table 2. The first column lists the region ID as presented in Table 1. The Haplotype column lists the specific nucleotides for the individual SNP alleles contributing to the haplotype reported. The Case and Control columns correspond to the numbers of cases and controls, respectively, containing the haplotype variant noted in the Haplotype column. The Total Case and Total Control columns list the total numbers of cases and controls for which genotype data was available for the haplotype in question. The RR, column gives to the relative risk for each particular haplotype.
The remainder of the columns lists the SeqIDs for the SNPs contributing to the haplotype and their relative location with respect to the central marker. The Central marker (0) column lists the SeqID for the central marker on which the haplotype is based. Flanking markers are identified by minus (-) or plus (+) signs to indicate the relative location of flanking SNPs.

Region ID	Haplotype	Case	Control	Total Case	Total Control	RR	Central marker (-4)	Central marker (-3)	Central marker (-2)	Central marker (-1)	Central marker (0)	Central marker (+1)	Central marker (+2)	Central marker (+3)	Central marker (+4)
1	CAGCGTATC	42	21	754	754	2.059	8964	8965	8966	8967	8968	8969	8972	8973	8974
1	GGACTTGGC	64	38	754	754	1.748	8964	8965	8966	8967	8968	8969	8972	8973	8974
1	CAGCGCGGT	9	24	754	754	0.367	8964	8965	8966	8967	8968	8969	8972	8973	8974
1	GCGTATC	42	21	754	754	2.059		8965	8966	8967	8968	8969	8972	8973	8974
1	ACTTGGC	64	38	754	754	1.748		8965	8966	8967	8968	8969	8972	8973	8974
1	GCGCGGT	9	24	754	754	0.367		8965	8966	8967	8968	8969	8972	8973	8974
1	TTGGC	64	38	754	754	1.748			8966	8967	8968	8969	8972	8973	8974
1	GCGGT	9	24	754	754	0.367			8966	8967	8968	8969	8972	8973	8974
2	TTGCT	11	24	754	754	0.450			8976	8979	8980	8981	8982		
2	TTTGCTGCT	8	21	754	754	0.374	8977	8978	8979	8980	8981	8982	8983	8984	8990
2	A	202	300	754	754	0.606					8983				
2	G	402	454	754	754	1.241					8983				
2	TACCA	247	284	754	754	0.806			8982	8983	8984	8990	8992		
2	TGCTG	6	20	754	754	0.304			8982	8983	8984	8990	8992		
2	CCA	414	456	754	754	0.700				8984	8990	8992			
2	CTA	188	152	754	754	1.316				8984	8990	8992			
2	CTG	8	21	754	754	0.374				8990	8992	8993			
2	CAC	453	496	754	754	0.774				8990	8992	8993			
2	TAA	288	231	754	754	1.399				8990	8992	8993			
2	TGC	8	21	754	754	0.374					8993				
2	C	465	522	754	754	0.715					8993				
2	A	280	232	754	754	1.308				8993	8997	8999			
2	AGC	237	172	752	752	1.552				8997	8999	9000	9001	9002	9003
2	TAAGCCAGG	75	47	750	750	1.662	8990	8992	8993	8997	8999	9000	9001	9002	9003
2	TGCGCTTAG	7	19	750	750	0.362	8990	8992	8993	8997	8999	9000	9001	9002	9003
2	CACGCTTAG	11	26	750	750	0.432	8990	8992	8993	8997	8999	9000	9001	9002	9003
2	AGCCAGG	75	47	750	750	1.662		8993	8997	8999	9000	9001	9002	9003	
2	CGCTTAG	18	44	750	750	0.396		8993	8997	8999	9000	9001	9002	9003	
2	AGCCAAGGC	69	48	750	750	1.482	8993	8997	8999	9000	9001	9002	9003	9007	9008
2	AGCCAGGGC	75	47	750	750	1.662	8993	8997	8999	9000	9001	9002	9003	9007	9008
2	CGCTTAGAC	7	18	750	750	0.383	8993	8997	8999	9000	9001	9002	9003	9007	9008
2	CGCTTAGGC	2	10	750	750	0.108	8993	8997	8999	9000	9001	9002	9003	9007	9008
2	GCCAGGGCA	95	60	750	750	1.668	8997	8999	9000	9001	9002	9003	9007	9008	9009
2	GCTTAGACA	6	18	750	750	0.328	8997	8999	9000	9001	9002	9003	9007	9008	9009
2	CCAGGGCAG	53	28	750	750	1.961	8999	9000	9001	9002	9003	9007	9008	9009	9010
2	CTTAGACAA	8	20	750	750	0.394	8999	9000	9001	9002	9003	9007	9008	9009	9010
2	GGC	248	209	754	754	1.278				9003	9007	9008			
2	GCA	244	205	754	754	1.281				9007	9008	9009			
2	ACCGATT	67	91	754	754	0.711		9007	9008	9009	9010	9012	9014	9015	
2	GCCGGTC	1	8	754	754	0.124		9007	9008	9009	9010	9012	9014	9015	
2	GCCGGTCCG	1	8	754	754	0.124	9007	9008	9009	9010	9012	9014	9015	9018	9019
3	CGCTTAGGG	3	15	754	754	0.197	9023	9024	9025	9028	9029	9032	9033	9034	9038
3	CATTGGCAA	17	6	754	754	2.870	9023	9024	9025	9028	9029	9032	9033	9034	9038
3	CATTTGCGA	16	4	754	754	4.065	9023	9024	9025	9028	9029	9032	9033	9034	9038
3	CACTGAGGG	6	16	754	754	0.370	9023	9024	9025	9028	9029	9032	9033	9034	9038
3	ATTTGCGAC	15	3	754	754	5.081	9024	9025	9028	9029	9032	9033	9034	9038	9040
3	ACTGAGGGC	4	14	754	754	0.282	9024	9025	9028	9029	9032	9033	9034	9038	9040
3	ATGTGCAGT	2	11	754	754	0.180	9024	9025	9028	9029	9032	9033	9034	9038	9040
3	TGGCAAT	17	4	754	754	4.325		9025	9028	9029	9032	9033	9034	9038	
3	TTGCGAC	17	3	754	754	5.774		9025	9028	9029	9032	9033	9034	9038	
3	CAA	59	40	754	754	1.515					9033				
3	CGA	49	20	754	754	2.551					9033				
3	G	638	688	754	754	0.528									
3	A	116	60	754	754	1.895									
3	ACA	68	37	754	754	1.021					9038	9040	9041		
3	ATA	12	3	754	754	4.049					9038	9040	9041		
3	ACATG	53	23	754	754	2.403				9038	9040	9041	9043	9044	
3	GACATGATG	19	4	754	754	4.847	9034	9038	9040	9041	9043	9044	9046	9047	9049
3	GGCACGATG	8	21	754	754	0.374	9034	9038	9040	9041	9043	9044	9046	9047	9049
3	GACATGACA	19	7	754	754	2.759	9034	9038	9040	9041	9043	9044	9046	9047	9049
4	C	477	520	754	754	0.775					9056				
4	T	277	234	754	754	1.290					9056				
4	TAT	276	234	754	754	1.283				9056	9058	9059			
4	GCA	160	211	754	754	0.743				9058	9059	9060			
4	ATG	276	234	754	754	1.283				9058	9059	9060			
4	A	169	216	754	754	0.720					9060				
4	G	585	538	754	754	1.300					9060				
4	C	477	517	754	754	0.789					9062				
4	A	277	237	754	754	1.267					9062				
4	C	477	519	754	754	0.780					9063				
4	T	277	235	754	754	1.283					9063				
4	G	475	512	754	754	0.805					9064				
4	A	279	242	754	754	1.243					9064				
4	AAT	275	232	752	752	1.292				9064	9066	9067			
4	G	476	517	752	752	0.784					9067				
4	T	276	235	752	752	1.276					9067				
5	GGCGATCTA	65	41	754	754	1.641	9070	9073	9075	9078	9079	9081	9082	9083	
5	CGATCTA	76	47	754	754	1.668		9075	9076	9078	9079	9081	9082	9083	
5	GATCTAC	74	45	754	754	1.715		9076	9076	9079	9081	9082	9083	9085	
5	TCTAC	103	73	754	754	1.476			9079	9081	9082	9083	9085		
5	C	628	680	754	754	0.710					9083				
5	A	126	94	754	754	1.400					9083				
5	TCCCGGG	11	28	754	754	0.384		9081	9082	9083	9085	9087	9088	9090	
5	CTACGAG	51	30	754	754	1.751		9081	9082	9083	9085	9087	9088	9090	
5	CTCCAAG	3	11	754	754	0.270		9081	9082	9083	9085	9087	9088	9090	
5	TCCCGGGCC	10	20	754	754	0.370	9081	9082	9083	9085	9087	9088	9090	9091	9092
5	CTACGAGGG	34	16	754	754	2.178	9081	9082	9083	9085	9087	9088	9090	9091	9092
5	TCCCGGACG	3	13	754	754	0.228	9081	9082	9083	9085	9087	9088	9090	9091	9092
5	TCCCGAGCC	23	11	754	754	2.125	9081	9082	9083	9085	9087	9088	9090	9091	9092
5	CTCCAAGCC	3	11	754	754	0.270	9081	9082	9083	9085	9087	9088	9090	9091	9092
5	CCCGGGCCC	6	19	754	754	0.310	9082	9083	9085	9087	9088	9090	9091	9092	9094
5	TACGAGGGC	34	16	754	754	2.178	9082	9083	9085	9087	9088	9090	9091	9092	9094
5	CCCGGACCC	27	10	754	754	2.703	9082	9083	9085	9087	9088	9090	9091	9092	9094
5	CCCGGACGC	2	13	754	754	0.152	9082	9083	9085	9087	9088	9090	9091	9092	9094
5	CCCGAGCCA	14	4	754	754	3.547	9082	9083	9085	9087	9088	9090	9091	9092	9094
5	GGACG	8	20	754	754	0.394			9085	9087	9088	9090	9091	9092	
5	ACG	9	27	754	754	0.325					9090	9091	9092		
5	ACGCG	8	26	754	754	0.300				9090	9091	9092	9094	9095	
5	CGCGC	10	23	754	754	0.427				9091	9092	9094	9095	9096	
5	GCCCAATAC	91	63	754	754	1.505	9090	9091	9092	9094	9095	9096	9097	9098	9099
5	ACGCGCCAT	3	14	754	754	0.211	9090	9091	9092	9094	9095	9096	9097	9098	9099
5	GCCAGCCAC	12	3	754	754	4.049	9090	9091	9092	9094	9095	9096	9097	9098	9099
5	CCCGACGCC	82	59	754	754	1.437	9091	9092	9094	9095	9096	9097	9098	9099	9100
5	CCAGCCGCC	140	172	754	754	0.772	9091	9092	9094	9095	9096	9097	9098	9099	9100
5	CCCAATACT	65	61	754	754	1.443	9091	9092	9094	9095	9096	9097	9098	9099	9100
5	CGCGCCATC	3	14	754	754	0.211	9091	9092	9094	9095	9096	9097	9098	9099	9100
5	CCCGACGCT	18	33	754	754	0.534	9091	9092	9094	9095	9096	9097	9098	9099	9100
5	CCAGCCACT	13	4	754	754	3.289	9091	9092	9094	9095	9096	9097	9098	9099	9100
5	CGACGCC	82	59	754	754	1.437		9092	9094	9095	9096	9097	9098	9099	9100
5	AGCCGCC	140	173	754	754	0.766		9092	9094	9095	9096	9097	9098	9099	9100
5	AAACACT	5	14	754	754	0.353		9092	9094	9095	9096	9097	9098	9099	9100
5	CGCCATC	3	16	754	754	0.184		9092	9094	9095	9096	9097	9098	9099	9100
5	CGACGCT	18	34	754	754	0.518		9092	9094	9095	9096	9097	9098	9099	9100
5	AGCCACT	13	4	754	754	3.289		9092	9094	9095	9096	9097	9098	9099	9100
5	CCGCC	144	170	754	754	0.758				9095	9096	9097	9098	9099	
5	CCACT	44	24	754	754	1.885				9096	9097	9098	9099	9100	
5	ACGCT	35	56	754	754	0.607				9096	9097	9098	9099	9100	

5	CCATC	3	16	754	754	0.184			0096	0097	0098	0099	0100		
5	CCGCCAG	125	101	754	754	0 732		0096	0097	0098	0099	0100	0101	0104	
5	ATACTGA	35	17	754	754	2.110		0096	0097	0098	0099	0100	0101	0104	
5	CCATCGG	3	16	754	754	0 184		0096	0097	0098	0099	0100	0101	0104	
5	ACGCTGA	12	26	754	754	0.453		0096	0097	0098	0099	0100	0101	0104	
5	CCACTGA	30	15	754	754	2.041		0096	0097	0098	0099	0100	0101	0104	
5	ATACTGACC	27	13	754	754	2.117	0096	0097	0098	0099	0100	0101	0104	0105	0108
5	ACACTGACC	6	16	754	754	0.370	0096	0097	0098	0099	0100	0101	0104	0105	0108
5	CCATCGGAC	3	13	754	754	0.228	0096	0097	0098	0099	0100	0101	0104	0105	0108
5	CCACTGACC	26	11	754	754	2.412	0096	0097	0098	0099	0100	0101	0104	0105	0108
6	CATGGGAGA	32	18	754	754	1 612	0118	0119	0121	0122	0123	0124	0125	0126	0127
6	GAG	118	85	754	754	1.460				0124	0125	0126			
6	GGGAGATAG	114	78	754	754	1.544	0122	0123	0124	0125	0126	0127	0128	0129	0130
6	TAAAAATAG	163	128	754	754	1.349	0122	0123	0124	0125	0126	0127	0128	0129	0130
6	GAGATAG	115	78	754	754	1.500		0124	0125	0126	0127	0128	0129	0130	
6	GATAG	125	84	754	754	1.585			0126	0127	0128	0129	0130		
6	GATTA	14	20	754	754	0.473			0126	0127	0128	0129	0130		
6	TAG	373	313	754	754	1.370				0128	0129	0130			
6	TTA	186	232	754	754	0.747				0128	0129	0130			
6	TAA	3	12	754	754	0 247				0128	0129	0130			
6	TAA	185	227	754	754	0 755				0129	0130	0131			
6	AGC	110	91	754	754	1.365				0129	0130	0131			
6	AAA	1	10	754	754	0.000				0129	0130	0131			
6	TAACT	184	226	754	754	0.754			0129	0130	0131	0132	0133		
6	AGCCG	116	82	754	754	1.490			0129	0130	0131	0132	0133		
6	TAACTAG	184	226	754	754	0 754		0129	0130	0131	0132	0133	0134	0135	
6	AGCCGGG	40	20	754	754	2.050		0129	0130	0131	0132	0133	0134	0135	
6	AACTAGT	183	222	754	754	0 708		0130	0131	0132	0133	0134	0135	0136	
6	GCCGGGT	40	20	754	754	2.050		0130	0131	0132	0133	0134	0135	0136	
6	AACTAGC	1	10	754	754	0 000		0130	0131	0132	0133	0134	0135	0136	
6	A	634	666	754	754	0.698					0134				
6	G	120	88	754	754	1.432					0134				
6	GGT	41	21	754	754	2.007				0134	0135	0136			
6	GTG	86	60	754	754	1.480				0135	0136	0137			
6	C	589	627	754	754	0.723					0137				
6	G	105	127	754	754	1 383					0137				
6	CAA	186	223	754	754	0.780				0137	0138	0140			
6	GAC	165	126	754	754	1,300				0137	0139	0140			
6	C	568	529	754	754	1.209					0140				
6	A	186	225	754	754	0,770					0140				
6	AACCG	185	222	754	754	0.770			0139	0140	0141	0143	0144		
6	ACCCG	203	161	754	754	1.357			0139	0140	0141	0143	0144		
6	CAACCGCGG	65	101	754	754	0 610	0137	0139	0140	0141	0143	0144	0145	0146	0147
6	GACCCGCGG	10	7	754	754	2.750	0137	0139	0140	0141	0143	0144	0145	0146	0147
6	CACCCACTG	7	20	754	754	0.344	0137	0139	0140	0141	0143	0144	0145	0146	0147
6	ACCGCGG	65	102	754	754	0.603		0140	0141	0143	0144	0145	0146	0147	
6	CCCACTG	7	20	754	754	0.344		0140	0141	0143	0144	0145	0146	0147	
6	ACCGCGGGG	59	80	754	754	0.634	0140	0141	0143	0144	0145	0146	0147	0148	0149
6	CCCGCGGGG	57	38	754	754	1.541	0140	0141	0143	0144	0145	0146	0147	0148	0149
6	CCCACTGGG	7	20	754	754	0.344	0140	0141	0143	0144	0145	0146	0147	0148	0149
6	ACCGCGGCG	3	11	754	754	0.270	0140	0141	0143	0144	0145	0146	0147	0148	0149
6	CGCTACGGC	28	13	754	754	2.198	0143	0144	0145	0146	0147	0148	0149	0152	0153
6	CACTGGGGC	7	10	754	754	0.363	0143	0144	0145	0146	0147	0148	0149	0152	0153
7	CAA	13	2	754	754	6.596				0154	0155	0158			
7	GAG	281	242	754	754	1 257				0155	0158	0159			
7	AAA	15	2	754	754	7.632				0155	0158	0159			
7	GAGTG	270	237	754	754	1.281			0155	0158	0159	0160	0161		
7	AAACA	14	2	754	754	7.114			0155	0158	0159	0160	0161		
7	GAACACA	87	126	754	754	0 650		0155	0158	0159	0160	0161	0162	0165	
7	GAGTGAG	220	173	754	754	1.384		0155	0158	0159	0160	0161	0162	0165	
7	AAACACA	13	2	754	754	6 596		0155	0158	0159	0160	0161	0162	0165	
7	GAACACAAC	31	50	754	754	0.604	0155	0158	0159	0160	0161	0162	0165	0169	0170
7	GAGTGAGGC	214	162	754	754	1.448	0155	0158	0159	0160	0161	0162	0165	0169	0170
7	ACA	355	406	754	754	0,763				0161	0162	0165			
7	GAG	222	176	754	754	1 370				0161	0162	0165			
7	A	414	472	754	754	0 727					0165				
7	G	340	282	754	754	1,375					0165				
7	GGC	201	199	754	754	1.477				0165	0169	0170			
8	T	221	281	754	754	0,783					0181				
8	C	533	493	754	754	1.277					0181				
8	GTAAT	209	245	754	754	0.707			0179	0181	0184	0185	0186		
8	GTAATGA	204	243	754	754	0 780		0179	0181	0184	0185	0186	0187	0191	
8	TGA	230	272	754	754	0 778				0186	0187	0191			
8	GAG	231	273	754	754	0.778				0187	0191	0192			
8	AGC	233	270	754	754	0.802				0191	0192	0193			
8	G	207	245	754	754	0,786					0194				
8	A	547	500	754	754	1,272					0194				
8	GCG	206	244	754	754	0 786				0194	0195	0197			
8	G	205	243	754	754	0 785					0198				
8	C	540	511	754	754	1.274					0198				
8	CGT	147	114	754	754	1.300				0198	0199	0203			
8	GGA	87	115	754	754	0.725				0198	0199	0203			
9	G	274	230	754	754	1 301					0206				
9	T	480	524	754	754	0 709					0206				
9	C	274	220	754	754	1.300					0207				
9	T	480	525	754	754	0,764					0207				
9	A	271	231	754	754	1.270					0208				
9	G	483	523	754	754	0.787					0208				
9	GGG	341	300	754	754	1.250				0211	0212	0215			
9	GCCGATCAT	4	13	754	754	0.304	0208	0209	0211	0212	0215	0216	0217	0218	0219
9	CGGGCCGAA	27	12	754	754	2.206	0209	0211	0212	0215	0216	0217	0218	0219	0220
9	CCGATCATG	4	13	754	754	0.304	0209	0211	0212	0215	0216	0217	0218	0219	0220
9	GGGCCGAAT	17	7	754	754	2.402	0211	0212	0215	0216	0217	0218	0219	0220	0221
9	GCCGAAT	22	8	754	754	2.803		0215	0216	0217	0218	0219	0220	0221	
9	CCGAATC	22	8	754	754	2.803		0216	0217	0218	0219	0220	0221	0222	
9	AAT	30	10	754	754	3.083				0219	0220	0221			
9	AATCG	20	10	754	754	2.976			0219	0220	0221	0222	0223		
9	AATCGTT	13	3	754	754	4 392		0219	0220	0221	0222	0223	0225	0226	
9	ATCGTTT	14	3	754	754	4.736		0220	0221	0222	0223	0225	0226	0228	
9	ACT	32	51	754	754	0 611				0223	0225	0226			
9	CGTTTAG	19	4	754	754	4.847		0222	0223	0225	0226	0228	0230	0231	
9	TATTGGG	5	14	754	754	0,353		0222	0223	0225	0226	0228	0230	0231	
9	GTTTAGG	37	20	754	754	1.604		0223	0225	0226	0228	0230	0231	0232	
9	TTAGG	70	46	754	754	1 575			0226	0228	0230	0231	0232		
9	TTAAA	31	52	754	754	0 579			0226	0228	0230	0231	0232		
9	GTGGGTC	76	48	754	754	1.649		0226	0228	0230	0231	0232	0233	0234	
9	TTGGGTG	9	20	754	754	0.443		0226	0228	0230	0231	0232	0233	0234	
9	TTAGGTC	40	24	754	754	1 704		0226	0228	0230	0231	0232	0233	0234	
10	T	142	184	754	754	0.710					0244				
10	C	612	570	754	754	1.391					0244				
10	TCA	125	161	754	754	0,732				0244	0246	0247			
10	CCA	509	457	754	754	1.350				0244	0246	0247			
10	CCAAT	280	243	754	754	1,242			0244	0246	0247	0248	0249		
10	CCCAGATGT	32	16	754	754	2 044	0243	0244	0246	0247	0248	0249	0252	0254	0255
10	CCAGATGTT	18	6	754	754	3 040	0244	0246	0247	0248	0249	0252	0254	0255	0257
10	CCAATCGTC	23	10	754	754	2.341	0244	0246	0247	0248	0249	0252	0254	0255	0257
10	CAATCGTCT	22	9	754	754	2.488	0246	0247	0248	0249	0252	0254	0255	0257	0258
10	CAGATGTTT	18	7	754	754	2 610	0246	0247	0248	0249	0252	0254	0255	0257	0258
10	GATGTTT	18	7	754	754	2 610		0248	0249	0252	0254	0255	0257	0258	
10	CGTCT	24	12	754	754	2.033			0252	0254	0255	0257	0259		
10	TGTTT	25	12	754	754	2.120			0252	0254	0255	0257	0258		
10	TGTTTGA	24	9	754	754	2 721		0252	0254	0255	0257	0258	0259	0260	
10	CGGCTGA	66	114	754	754	0.723		0252	0254	0255	0257	0258	0259	0260	
10	TGTTTGAAA	19	4	754	754	4 847	0252	0254	0255	0257	0258	0259	0260	0261	0262
10	CGGCTGAAG	32	67	754	754	0.454	0252	0254	0255	0257	0258	0259	0260	0261	0262
10	TTTGAAA	36	20	754	754	1.840		0255	0257	0258	0259	0260	0261	0262	
10	GCTGAAG	33	66	754	754	0.402		0255	0257	0258	0259	0260	0261	0262	
10	TGGGG	28	47	754	754	0,580			0258	0259	0260	0261	0262		

10	TGAAG	89	139	754	754	0 592			9258	9259	9260	9261	9262					
10	TGAAGGG	60	108	754	754	0 603	9258		9259	9260	9261	9262	9264	9265				
10	GAC	304	252	754	754	1 346				9261	9262	9264						
10	AGG	83	125	754	754	0 622				9261	9262	9264						
10	AAC	82	57	754	754	1.492				9261	9262	9264						
10	C	504	426	754	754	1.552					9264							
10	G	250	328	754	754	0.644					9264							
10	CGC	355	299	754	754	1 354				9264	9265	9266						
10	GGC	247	322	754	754	0.654				9264	9265	9266						
10	CAT	42	25	754	754	1.720				9264	9265	9266						
10	CGCCC	281	232	754	754	1.337			9264	9265	9266	9268	9269					
10	GGCCC	148	197	754	754	0 691			9264	9265	9266	9268	9269					
10	CATCC	33	17	754	754	1.984			9264	9265	9266	9268	9269					
10	CGCCCTA	184	152	754	754	1.278	9264		9265	9266	9268	9269	9270	9271				
10	GGCCCCG	75	110	754	754	0.047	9264		9265	9266	9268	9269	9270	9271				
10	CGCCACG	26	10	754	754	2 057	9264		9265	9266	9268	9269	9270	9271				
10	CATCCTA	29	15	754	754	1.071	9264		9265	9266	9268	9269	9270	9271				
10	CGTCACG	11	2	754	754	5.567	9264		9265	9266	9268	9269	9270	9271				
10	CCACG	34	17	754	754	2.047			9265	9266	9268	9269	9270	9271				
10	TCCTA	30	22	754	754	1.815			9266	9268	9269	9270	9271					
10	CCTAT	204	226	754	754	1.259			9268	9269	9270	9271	9272					
10	CACGT	46	21	754	754	2 268				9269	9270	9271	9272					
10	CCCATGG	20	14	754	754	2.114		9268		9269	9270	9271	9272	9273	9274			
10	CACGTAA	20	6	754	754	3.397		9268		9269	9270	9271	9272	9273	9274			
10	CCCGTGG	26	44	754	754	0.576		9268		9269	9270	9271	9272	9273	9274			
10	CACATAA	4	15	754	754	0 263		9268		9269	9270	9271	9272	9273	9274			
10	ACGTAAG	43	26	754	754	1 093		9269		9270	9271	9272	9273	9274	9275			
10	ACATAAG	4	15	754	754	0 263		9269		9270	9271	9272	9273	9274	9275			
10	CCATGGA	14	5	754	754	2 834		9269		9270	9271	9272	9273	9274	9275			
10	CGTGGAC	12	25	754	754	0.472		9270		9271	9272	9273	9274	9275	9276			
10	CATAAGT	10	24	754	754	0.400		9270		9271	9272	9273	9274	9275	9276			
10	CGTGGACTC	12	24	754	754	0 492	9270	9271		9272	9273	9274	9275	9276	9277	9278		
10	CATAAGTCT	10	23	754	754	0.427	9270	9271		9272	9273	9274	9275	9276	9277	9278		
10	GTGGACTCC	12	24	754	754	0.492	9271	9272		9273	9274	9275	9276	9277	9278	9279		
10	ATAAGTCTC	14	27	754	754	0 509	9271	9272		9273	9277	9278	9283	9284	9290	9292		
10	GTCTCATAA	19	7	754	754	2.759	9275	9270		9270	9278	9283	9284	9290	9292			
10	CATAA	20	7	754	754	2.908					9283	9284	9290	9292				
10	CAA	7	21	754	754	0.327					9284	9290	9292					
10	TAA	20	7	754	754	2.908					9284	9290	9292					
10	CATGTGGCG	35	19	754	754	1.883	9270		9283	9284	9290	9292	9293	9294	9295	9297		
10	CACGAACGA	17	35	754	754	0.474	9270		9283	9284	9290	9292	9293	9294	9295	9297		
10	TGTGGCG	35	19	754	754	1.883			9284	9290	9292	9293	9294	9295	9297			
10	CGAACGA	19	37	754	754	0.501			9284	9290	9292	9293	9294	9295	9297			
10	CAAACGA	3	12	754	754	0 247					9292	9293	9294	9295				
10	ACG	77	108	754	754	0.680					9293	9294	9295					
10	CGA	87	127	754	754	0.644					9294	9295	9297					
10	CGT	155	124	754	754	1.315					9295	9297	9298					
10	GAC	25	53	754	754	0.454					9295	9297	9298					
10	GACGA	22	51	754	754	0.414			9295		9297	9298	9299	9301				
10	CACGAAC	42	26	754	754	1.652		9295	9297		9298	9299	9301	9302	9303			
10	GACGAGG	10	25	754	754	0.392		9295	9297		9298	9299	9301	9302	9303			
10	CACGAACAC	42	26	754	754	1 652	9295	9297	9298		9299	9301	9302	9303	9305	9307		
10	GACGAAGCT	7	18	754	754	0 383	9295	9297	9298		9299	9301	9302	9303	9305	9307		
10	GACGAGGAT	10	25	754	754	0 392	9295	9297	9298		9299	9301	9302	9303	9305	9307		
10	A	660	630	754	754	1 382						9302						
10	G	94	124	754	754	0 724						9302						
10	GGA	87	115	754	754	0 725					9302	9303	9305					
10	GATAA	77	104	754	754	0.711			9303		9305	9307	9308	9310				
10	ATAAG	73	100	754	754	0 701			9303		9305	9307	9308	9310	9312			
10	C	675	648	754	754	1.398							9310					
10	A	70	100	754	754	0.715							9310					
10	AGG	66	90	752	752	0.708					9310	9312	9313					
10	A	653	617	752	752	1.443							9313					
10	G	90	135	752	752	0 603							9313					
10	GGA	37	71	752	752	0 496					9313	9315	9316					
10	GGAGA	16	37	752	752	0.420			9313		9315	9316	9317	9318				
10	GGT	2	10	754	754	0 198					9317	9318	9319					
11	GTA	73	100	754	754	0.655					9331	9332	9334					
12	TGTCGTGGA	12	26	754	754	0.453	9337	9338	9339		9340	9341	9342	9344	9346	9347	9350	
12	GTTGTAGGA	32	17	754	754	1.921	9338	9339	9340		9341	9342	9344	9346	9347	9350		
12	GGA	16	32	754	754	0.480					9344	9346	9347					
12	GGAGC	16	30	754	754	0.523			9344		9346	9347	9350	9352				
12	AGGAA	33	16	754	754	2.111			9344		9346	9347	9350	9352				
12	G	612	647	754	754	0 713						9350						
12	A	142	107	754	754	1 403						9350						
12	AAA	140	101	754	754	1.474					9350	9352	9354					
12	A	383	341	754	754	1.250						9354						
12	G	371	413	754	754	0.800						9354						
12	G	208	160	754	754	1 310						9356						
12	C	546	585	754	754	0.758						9356						
12	CGC	546	581	754	754	0.782					9356	9357	9358					
12	GCC	505	626	754	754	0.705					9357	9358	9360					
12	GCT	48	28	754	754	1 703					9357	9358	9360					
12	T	158	123	754	754	1 300						9360						
12	C	506	631	754	754	0.735						9360						
12	C	709	730	754	754	0 518						9361						
12	T	45	24	754	754	1.931						9361						
12	CCCCAGT	9	27	752	752	0.325		9358	9360		9361	9364	9365	9367	9369			
12	CCCCAAT	113	144	752	752	0.747		9358	9360		9361	9364	9365	9367	9369			
12	CTTCGAT	37	22	752	752	1.717		9358	9360		9361	9364	9365	9367	9369			
12	CCAGT	9	27	752	752	0.325			9361		9364	9365	9367	9369				
12	CCAAT	115	145	752	752	0 750			9361		9364	9365	9367	9369				
12	TCGAT	40	22	752	752	1 804			9361		9364	9365	9367	9369				
12	GAT	215	167	752	752	1 403					9365	9367	9369					
12	AGT	10	27	752	752	0 302					9365	9367	9369					
12	CGATCTA	68	41	752	752	1.724		9364	9365		9367	9369	9370	9372	9374			
12	CAGTCTA	7	18	752	752	0.383		9364	9365		9367	9369	9370	9372	9374			
12	CAAACTG	4	13	752	752	0 304		9364	9365		9367	9369	9370	9372	9374			
12	ATCTA	150	125	752	752	1.345			9365		9367	9369	9370	9372	9374			
12	GTCTA	7	18	752	752	0.383			9365		9367	9369	9370	9372	9374			
12	AACTG	4	13	752	752	0.304			9365		9367	9369	9370	9372	9374			
12	GTCTAAA	6	16	752	752	0.370		9367	9369		9369	9370	9372	9374	9375	9378		
12	AACTGAA	3	13	752	752	0.228		9367	9369		9369	9370	9372	9374	9375	9378		
12	GTCTAAAGA	4	13	752	752	0 304	9367	9369	9370		9370	9372	9374	9375	9378	9379	9380	
12	AACTGAAGC	3	12	752	752	0.247	9367	9369	9370		9370	9372	9374	9375	9378	9379	9380	
12	GAAGCCGAT	31	50	752	752	0.004	9374	9375	9378		9378	9379	9380	9381	9382	9383	9386	
12	AAAAC	40	62	752	752	0.625			9378		9380	9381	9382	9383	9386			
12	CCGGT	14	28	752	752	0.491			9378		9380	9381	9382	9383	9386			
12	GGT	14	28	752	752	0 491						9381	9382	9383				
13	CCC	203	241	754	754	0 784						9380	9382	9384				
13	TCC	512	455	754	754	1.390						9382	9384	9386				
13	CCT	201	239	754	754	0 783						9382	9384	9386				
13	CCG	454	392	754	754	1.398						9384	9386	9387				
13	CTA	204	243	754	754	0 780						9384	9386	9387				
13	G	456	399	754	754	1.361							9387					
13	A	208	365	754	754	0.735							9387					
13	A	457	402	754	754	1 347							9389					
13	G	297	352	754	754	0 742							9389					
13	ATT	313	268	754	754	1 287						9389	9402	9403				
13	GTC	291	339	754	754	0.769						9389	9402	9403				
13	T	458	408	754	754	1.312							9403					
13	C	290	340	754	754	0.762							9403					
14	GCCCC	2	22	754	754	0 088						9404	9405	9406	9407	9408		
14	CCCCC	1	18	754	754	0 054						9405	9406	9407	9408	9409		
14	CCC	1	18	754	754	0 054							9407	9408	9409			
14	CCT	1	17	754	754	0 058							9408	9409	9411			
14	TCTCT	33	16	754	754	2.111						9408	9409	9411	9414	9416		
14	CCTCA	1	17	754	754	0 058						9408	9409	9411	9414	9416		

14	TCTCTCC	33	16	754	754	2.111		0408	0409	0411	0414	0416	0417	0420		
14	CCTCATT	1	16	754	754	0.061		0408	0409	0411	0414	0416	0417	0420		
15	G	713	687	754	754	1.606					0435					
15	A	41	67	754	754	0.590					0435					
15	ATA	143	178	754	754	0.757				0441	0442	0443				
15	G	605	569	754	754	1.320					0443					
15	A	140	185	754	754	0.757					0443					
15	ATT	148	184	754	754	0.757				0443	0444	0445				
15	CCT	196	161	754	754	1.204				0444	0445	0449				
15	TGCCTTCCG	150	107	754	754	1.502	0442	0443	0444	0445	0449	0450	0451	0453	0454	
15	TATTCCACA	82	107	754	754	0.542	0442	0443	0444	0445	0449	0450	0451	0453	0454	
15	GCCTTCCGC	128	97	754	754	1.385	0443	0444	0445	0445	0449	0450	0451	0453	0454	0455
15	ATTCCACAC	82	107	754	754	0.542	0443	0444	0445	0445	0449	0450	0451	0453	0454	0455
15	GCCTTCCGT	22	10	754	754	2.230	0443	0444	0445	0445	0449	0450	0451	0453	0454	0455
15	CCACA	121	155	754	754	0.739				0449	0450	0451	0453	0454		
15	TTCCG	151	109	754	754	1.482				0449	0450	0451	0453	0454		
15	CCACG	22	7	754	754	3.207				0449	0450	0451	0453	0454		
15	TCCGC	211	173	754	754	1.305				0450	0450	0451	0453	0454		
15	CACAC	121	155	754	754	0.739				0450	0450	0451	0453	0454		
15	CACGC	22	7	754	754	3.207				0450	0450	0451	0453	0454		
15	TCCGT	22	10	754	754	2.230				0450	0450	0451	0453	0454		
15	G	277	209	754	754	1.514					0451					
15	A	477	545	754	754	0.660					0451					
15	GCT	254	198	754	754	1.427					0451					
15	ACA	400	450	754	754	0.763				0454	0454	0454	0454	0454	0455	
15	GTT	22	10	754	754	2.230				0454	0454	0454	0454	0455		
15	T	353	303	754	754	1.310				0454	0454	0454	0454	0455		
15	A	401	451	754	754	0.763					0455					
15	CACAATTTG	109	240	754	754	0.727	0453	0454	0455	0456	0456	0456	0456	0456		
15	CGTTACGTG	20	0	754	754	2.256	0453	0454	0455	0456	0456	0456	0456	0456		
15	ACG	255	202	754	754	1.306				0456	0456					
15	ATT	247	287	754	754	0.793				0458	0458					
15	G	426	382	754	754	1.205					0458					
15	T	328	372	754	754	0.701					0459					
15	CGTGG	203	155	754	754	1.424				0459	0459	0459	0459	0459	0460	
15	CGTGGAC	182	138	754	754	1.420				0459	0459	0459	0459	0459	0460	
15	TTTGAGT	199	238	754	754	0.777		0459	0459	0461	0461	0461	0461			
15	G	296	245	754	754	1.343		0459			0461					
15	A	458	509	754	754	0.745					0461					
15	A	261	214	754	754	1.336					0461					
15	G	403	540	754	754	0.749					0461					
15	C	280	214	754	754	1.328					0461					
15	T	404	540	754	754	0.753					0461					
15	T	470	437	754	754	1.264					0461					
15	C	275	317	754	754	0.701					0461					
15	CAGGA	215	253	754	754	0.700					0465					
15	TAGGG	103	160	754	754	1.277					0465					
15	CAA	101	71	754	754	1.488					0465					
15	GGA	218	257	754	754	0.787					0466					
15	GGG	223	188	754	754	1.264					0466					
15	GGGCC	40	30	752	752	1.677					0466					
15	GGATT	22	40	752	752	0.536					0466					
15	GAATC	6	18	752	752	0.328					0466					
15	GCC	40	31	752	752	1.621					0466					
15	T	301	355	752	752	0.746					0466					
15	C	451	397	752	752	1.340					0466					
15	GATTCCGGA	9	20	752	752	0.443	0461	0462	0463	0466	0466					
15	GACTCCGAA	8	1	752	752	8.075	0461	0462	0463	0466	0466					
15	GGCCCCGAA	8	1	752	752	8.075	0461	0462	0463	0466	0466					
15	AATCCCAGC	1	9	752	752	0.110	0461	0462	0463	0466	0466					
15	TTCGAAC	94	125	752	752	0.717		0462	0463	0466	0466					
15	TCGAACT	87	116	752	752	0.717		0462	0463	0466	0466					
15	TCGAACTTC	86	114	750	750	0.723	0467	0468	0469	0470	0471					
15	CTCCCGT	12	25	752	752	0.472		0468	0469	0470	0471					
15	C	540	513	754	754	1.258					0471					
15	T	205	241	754	754	0.705					0471					
10	GTG	59	31	754	754	1.980					0477					
10	C	605	722	754	754	0.522					0477					
10	G	59	32	754	754	1.915					0477					
10	CGT	209	252	754	754	0.764					0479	0481	0482			
10	GGG	26	12	754	754	2.208					0479	0481	0482			
10	CGTTC	206	248	754	754	0.767					0479	0481	0482			
10	CGTTCGG	128	169	754	754	0.708					0481	0482	0483	0486		
10	CGTTCGGTA	84	113	754	754	0.711	0502	0502	0502	0502	0503	0506				
10	GCAGGTG	213	177	754	754	1.283		0503	0503	0502	0503	0506				
10	GCCGGCA	41	22	754	754	1.913		0506	0506	0503	0506	0506				
10	TTCCACATA	30	14	754	754	2.190	0506	0507	0507	0506	0507	0508	0509	0510		
10	GCCGGCATA	40	22	754	754	1.804	0506	0507	0507	0507	0508	0508	0509	0510	0511	0512
10	GTA	344	305	754	754	0.703				0508	0508					
10	GTC	268	230	754	754	1.250					0508					
10	GTATA	231	269	754	754	0.700					0509					
10	ACATA	30	16	754	754	1.911					0509					
10	GTATATG	219	261	754	754	0.773					0509					
10	GCATATT	22	10	754	754	2.230		0510	0510	0510	0510	0510	0511	0512		
10	ATATG	256	296	754	754	0.705		0510	0510	0510	0510	0511	0512	0513		
10	ATATT	57	31	754	754	1.907					0511					
10	ATT	62	33	754	754	1.958					0511					
10	ATATTGGCC	57	20	754	754	2.044	0512	0513	0513	0513	0513	0517	0518	0520		
10	ATATGGATT	70	95	754	754	0.710	0512	0513	0517	0517	0517	0517	0518	0520		
10	TATTGGCCT	62	31	754	754	2.000	0513	0517	0518	0518	0518	0518	0520			
17	TCAAGAA	2	12	754	754	0.164		0535	0536	0536	0536	0536	0520			
17	AAGAA	2	12	754	754	0.164				0537	0537	0537	0522	0523	0525	0529
17	GAGAGTC	9	20	754	754	0.443		0537	0537	0538	0538	0538	0523	0525	0529	0529
17	AAGAACC	2	12	754	754	0.164				0538	0538	0538	0525	0529	0529	0533
17	G	751	734	754	754	0.821					0539					
17	A	3	20	754	754	0.147					0539					
17	GCC	688	648	754	754	1.705					0539					
17	ACC	3	20	754	754	0.147					0539					
17	ACCGG	3	17	754	754	0.173					0539					
17	ACCGGAA	2	15	754	754	0.131					0539					
17	ACCGGAACC	1	9	754	754	0.110					0539					
17	CCGGAACCC	16	32	754	754	0.480					0539					
17	CCGAAACCT	26	13	754	754	2.030					0539					
17	GGAACCC	21	43	754	754	0.474					0539					
17	GAAACCC	19	36	754	754	0.516					0539					
17	GAAACCT	26	13	754	754	2.030					0539					
17	AACCC	40	70	754	754	0.479					0539					
17	CCC	99	140	754	754	0.663					0539					
17	CAT	7	18	754	754	0.383					0539					
17	CTC	496	448	754	754	1.313					0539					
17	CCC	29	52	754	754	0.540					0539					
17	ATC	7	22	754	754	0.312					0539					
17	CCCCT	28	50	754	754	0.543					0539					
17	ATCCG	6	17	754	754	0.348					0539					
17	CTCCGGT	117	80	754	754	1.372					0539					
17	CCCCTGT	27	45	754	754	0.585					0539					
17	ACGCGAC	20	8	754	754	2.541					0539					
17	ATCCGAC	1	10	754	754	0.000					0539					
18	GGTAGTC	3	13	754	754	0.228					0539					
18	TAGTC	4	15	754	754	0.263					0539					
18	AGTCC	9	21	754	754	0.422					0539					
18	TCC	9	23	754	754	0.384					0539					
18	TCCGA	3	14	754	754	0.211					0539					
18	GCGCG	67	46	754	754	1.501					0539					
18	GTCCGAGTG	2	12	754	754	0.164	0575	0576	0580	0580	0580	0580	0580	0580	0587	
18	AGCGCGGTG	13	4	754	754	3.289	0575	0576	0580	0580	0580	0580	0580	0586	0587	
18	GTTCGAGTG	20	16	754	754	1.071	0575	0576	0580	0581	0582	0583	0585	0586	0587	
18	TCCGAGTGA	1	12	754	754	0.082	0576	0580	0581	0582	0583	0585	0586	0587	0588	

18	GCGCGGTGA	10	2	754	754	5.054	9576	9580	9581	9582	9583	9585	9586	9587	9588
18	CCGAGTGAT	1	12	754	754	0.082	9580	9581	9582	9583	9585	9586	9587	9588	9590
18	CGCGGCGGC	3	14	754	754	0.211	9580	9581	9582	9583	9585	9586	9587	9588	9590
18	TCCGGCGGC	3	11	754	754	0.270	9580	9581	9582	9583	9585	9586	9587	9588	9590
18	CGGCGGC	7	28	754	754	0.243									
18	GCGGC	7	30	754	754	0.226									
18	GGC	7	30	754	754	0.226									
18	T	740	724	754	754	3.804									
18	C	8	30	754	754	0.259									
18	CTT	8	30	752	752	0.259									
18	CTTCA	8	30	750	750	0.259									
18	TGCGGCT	133	167	750	750	0.753									
18	CTTCACT	7	26	750	750	0.262									
18	TGCGGGC	15	5	750	750	3.041									
18	CTTCACTCA	6	25	750	750	0.234									
18	TGCGGCGA	14	4	750	750	3.548									
18	CGGTCATCT	8	22	750	750	0.357									
18	GGGCGAATT	13	3	750	750	4.302									
18	GTCATCTAA	15	20	754	754	0.507									
18	CGAATTAGT	23	10	754	754	2.341									
18	AATTAGT	81	57	754	754	1.472									
18	TTAGT	91	66	754	754	1.431									
18	AGT	152	119	754	754	1.347									
18	AAC	4	13	754	754	0.304									
18	T	745	733	754	754	2.372									
18	C	9	21	754	754	0.422									
18	CCA	9	20	754	754	0.443									
18	TCAGA	178	141	754	754	1.344									
18	TCAGAAGAG	23	8	754	754	2.934									
18	AGAAGAG	23	8	754	754	2.934	9608	9609	9610	9611	9612	9613	9615	9616	9619
18	TAACAGGGT	7	24	754	754	0.285									
18	TACGAAAAA	2	10	754	754	0.108	9611	9612	9613	9615	9616	9619	9620	9622	9623
18	AGAGGGT	12	29	754	754	0.404	9611	9612	9613	9615	9616	9619	9620	9622	9623
18	CGAAAAA	4	14	754	754	0.282									
18	AGGGT	14	31	754	754	0.441									
19	ATG	713	693	754	754	1.531									
19	ATGACTC	89	126	754	754	0.667									
19	ATGACTG	190	162	754	754	1.284									
19	ATGACTCAT	88	125	754	754	0.665	9627	9628	9629	9630	9632	9633	9635	9636	9638
19	ATGACTGAT	150	120	754	754	1.312	9627	9628	9629	9630	9632	9633	9635	9636	9638
19	GTGACTGAC	16	30	754	754	0.523	9627	9628	9629	9630	9632	9633	9635	9636	9638
19	ATGGCTGGC	20	14	754	754	2.114	9627	9628	9629	9630	9632	9633	9635	9636	9638
19	CTG	431	388	754	754	1.259									
19	CTC	105	145	754	754	0.680									
19	G	553	495	754	754	1.440									
19	C	201	259	754	754	0.605									
19	GAT	426	369	754	754	1.355									
19	CAT	199	258	754	754	0.689									
19	GAC	42	62	754	754	0.658									
19	GGC	79	57	754	754	1.431									
19	ATA	293	250	754	754	1.281									
19	ATG	332	377	754	754	0.787									
19	GCA	54	35	754	754	1.585									
19	A	396	316	754	754	1.307									
19	G	388	438	754	754	0.765									
19	AAG	329	279	754	754	1.318									
19	GAG	50	78	754	754	0.605									
19	AAGGCTA	310	265	754	754	1.288									
19	GGCTA	376	331	754	754	1.271	9641	9644	9645	9646	9652	9653	9654	9655	9656
20	GGGTC	76	101	754	754	0.725									
20	GAACT	11	3	754	754	3.706									
20	CTG	263	225	754	754	1.259									
20	TGC	264	225	754	754	1.267									
20	ACTGCAATT	103	150	754	754	1.386	9653	9654	9655	9656	9657	9659	9661	9662	9663
20	ACTGCAATC	3	12	754	754	0.247	9653	9654	9655	9656	9657	9659	9661	9662	9663
20	A	433	392	754	754	1.246									
20	T	321	382	754	754	0.803									
20	CAATTTC	241	185	754	754	1.445									
20	CAATCCC	20	50	754	754	0.563									
20	ATTTCAGAA	76	51	754	754	1.590									
20	TCCCTTCAA	6	17	754	754	0.348									
20	ATTTCACGG	27	14	754	754	1.063									
20	TTTCAGAAG	76	52	754	754	1.513									
20	CCCTTCAAG	6	16	754	754	0.370									
20	TTTCACAAA	11	1	754	754	11.148									
20	TTCAGAAGC	59	39	754	754	1.556									
20	CCTTGGAGT	49	71	754	754	0.669									
20	TTCACAAAC	11	1	754	754	11.148									
20	CTTGGGGTA	46	29	754	754	1.624									
20	CTTGGAGTA	48	71	754	754	0.654									
20	TCACAAACA	11	1	754	754	11.148									
20	CTTCAAGCG	2	11	754	754	0.180									
20	TGGGGTA	51	31	754	754	1.692									
20	ACGAGCG	17	31	754	754	0.538									
20	TGGAGTA	53	75	754	754	0.684									
20	AGGAGCG	2	10	754	754	0.198									
20	ACAAACA	11	1	754	754	11.148									
20	TCAAGCG	2	12	754	754	0.164									
20	AGGGGCGGG	23	11	754	754	2.125	9666	9667	9669	9671	9672	9674	9675	9676	9678
20	ACGAGCGGG	17	31	754	754	0.538	9666	9667	9669	9671	9672	9674	9675	9676	9678
20	ACAAACAGG	11	1	754	754	11.148	9666	9667	9669	9671	9672	9674	9675	9676	9678
20	TCAAGCGGG	2	11	754	754	0.160									
20	AAACAGG	15	3	754	754	5.081	9669	9671	9672	9674	9675	9676	9678	9679	9681
20	AAACAGGGC	15	3	754	754	5.081	9669	9671	9672	9674	9675	9676	9678	9679	9681
20	AACAGGGCT	15	4	754	754	3.666									
20	CCCGG	30	14	754	754	2.190									
20	CCCGGAA	30	13	754	754	2.362									
20	TTCGGAG	12	3	754	754	4.049									
20	CCCGGAATT	27	9	754	754	3.074	9682	9683	9684	9685	9686	9687	9689	9690	9692
20	TCGGGATTG	88	64	754	754	1.425	9683	9684	9685	9686	9687	9689	9690	9692	9694
20	CGGAATCGG	12	20	754	754	0.453	9684	9685	9686	9687	9689	9690	9692	9694	9695
20	CGGAATTTG	30	15	754	754	2.041	9684	9685	9686	9687	9689	9690	9692	9694	9695
20	GGAATCGGG	12	25	754	754	0.472	9685	9686	9687	9689	9690	9692	9694	9695	9696
20	GGAATTTGC	20	15	754	754	1.071	9685	9686	9687	9689	9690	9692	9694	9695	9696
20	GGAATTGAC	124	96	754	754	1.349	9685	9686	9687	9689	9690	9692	9694	9695	9696
20	GGAGTTGGG	0	1	754	754	0.007									
20	T	509	458	754	754	1.343									
20	C	245	296	754	754	0.745									
20	TCGGG	34	65	754	754	0.501									
20	TTGAC	150	120	754	754	1.332									
20	TTGACCC	157	120	754	754	1.311									
20	TCGGGTC	9	28	754	754	0.313									
20	TTGACCCGA	154	124	754	754	1.304	9690	9692	9694	9695	9696	9697	9698	9699	9701
20	TCGGGTCAT	9	28	754	754	0.313	9690	9692	9694	9695	9696	9697	9698	9699	9701
20	TTGCCCATA	37	22	754	754	1.717	9692	9694	9695	9696	9697	9698	9699	9701	9704
20	CGGGTCATA	31	55	754	754	0.545	9692	9694	9695	9696	9697	9698	9699	9701	9704
20	GGGTGAAAC	66	45	754	754	1.511	9694	9695	9696	9697	9698	9699	9701	9704	9707
20	CCCATATTC	27	14	754	754	1.063	9695	9696	9697	9698	9699	9701	9704	9707	9708
20	CCCGAATCC	25	42	754	754	0.581	9696	9697	9698	9699	9701	9704	9707	9708	9709
20	GTGAAACTC	16	6	754	754	2.703	9696	9697	9698	9699	9701	9704	9707	9708	9709
20	CCATATTCC	24	12	754	754	2.033	9697	9698	9699	9701	9704	9707	9708	9709	9710
21	TCGTTCA	194	159	754	754	1.290									
21	TTT	385	433	754	754	0.773									
21	T	499	538	754	754	0.780									
21	C	255	216	754	754	1.273									
21	TTTAGTT	313	357	754	754	0.769									
21	TTCAAGT	183	151	754	754	1.374									
21	G	528	573	754	754	0.738									

21	A	220	181	754	754	1.355					0727				
21	AGTTA	457	405	754	754	0.805			0726	0727	0729	0731	0732		
21	AAGTA	222	177	754	754	1.360			0726	0727	0729	0731	0732		
21	AAGTATG	219	175	754	754	1.354		0726	0727	0729	0731	0732	0733	0735	
21	ACGGCGG	15	29	754	754	0.507		0732	0733	0735	0737	0739	0741	0742	
21	CGGCGAAGG	30	15	754	754	2.470	0733	0735	0737	0739	0741	0742	0744	0746	0747
21	CGGCGGAGA	5	15	754	754	0.320	0733	0735	0737	0739	0741	0742	0744	0746	0747
21	TGGCTAAAA	10	3	754	754	5.427	0733	0735	0737	0739	0741	0742	0744	0746	0747
21	GCTAAAA	24	9	754	754	2.721		0737	0739	0741	0742	0744	0746	0747	
21	GCGAAAGCG	41	62	754	754	0.642	0737	0739	0741	0742	0744	0746	0747	0748	0749
21	GCTAAAATG	20	6	754	754	2.541	0737	0739	0741	0742	0744	0746	0747	0748	0749
21	GCGGAAACG	27	44	754	754	0.590	0737	0739	0741	0742	0744	0746	0747	0748	0749
21	CGAAAGCAA	30	10	754	754	1.011	0739	0741	0742	0744	0746	0747	0748	0749	0750
21	CGAAAGCGG	70	108	754	754	0.700	0739	0741	0742	0744	0746	0747	0748	0749	0750
21	TAAAACGGC	11	3	754	754	3.700	0741	0742	0744	0746	0747	0748	0749	0750	0751
21	GAAAGCAAG	30	10	754	754	1.011	0741	0742	0744	0746	0747	0748	0749	0750	0751
21	GAAAGCGGG	74	102	754	754	0.696	0741	0742	0744	0746	0747	0748	0749	0750	0751
21	AAAACGGCT	14	5	754	754	2.834	0742	0744	0746	0747	0748	0749	0750	0751	0752
21	AAAGCGGGG	71	97	754	754	0.704	0742	0744	0746	0747	0748	0749	0750	0751	0752
21	AAG	104	100	754	754	1.286				0749	0750	0751			
21	GGG	315	370	754	754	0.745				0749	0750	0751			
21	GGG	91	123	754	754	0.704				0750	0751	0752			
21	T	663	630	754	754	1.434					0752				
21	G	91	124	754	754	0.697					0752				
21	AAGTCACGA	144	113	754	754	1.330	0749	0750	0751	0752	0755	0756	0757	0759	0762
21	GGGGCGCGA	40	64	754	754	0.604	0749	0750	0751	0752	0755	0756	0757	0759	0762
21	GGCGCGA	40	64	754	754	0.604		0751	0752	0755	0756	0757	0759	0762	
21	CGCGA	47	75	754	754	0.602			0755	0756	0757	0759	0762		
21	CGCGATC	44	64	754	754	0.668		0755	0756	0757	0759	0762	0763	0766	
21	CACGAGT	8	1	754	754	8.075		0755	0756	0757	0759	0762	0763	0766	
21	CGAGT	9	1	754	754	9.097			0757	0759	0762	0763	0766		
21	GTC	40	27	754	754	1.740				0762	0763	0766			
21	AGT	12	2	754	754	6.081				0762	0763	0766			
21	GGTCGTT	43	24	754	754	1.840		0759	0762	0763	0766	0767	0769	0770	
21	CATTGCC	17	5	754	754	3.455		0759	0762	0763	0766	0767	0769	0770	
21	GTCGTTG	42	24	754	754	1.704		0762	0763	0766	0767	0769	0770	0771	
21	ATTGCCG	17	4	754	754	4.325		0762	0763	0766	0767	0769	0770	0771	
21	ATTGTCA	4	16	754	754	0.246		0762	0763	0766	0767	0769	0770	0771	
21	TCGTTGA	67	44	754	754	1.574		0763	0766	0767	0769	0770	0771	0772	
21	TTGTCAA	4	13	754	754	0.304		0763	0766	0767	0769	0770	0771	0772	
21	TTGCCGA	13	3	754	754	4.392		0763	0766	0767	0769	0770	0771	0772	
21	CCG	17	4	754	754	4.325				0769	0770	0771			
21	CCA	2	10	754	754	0.198				0769	0770	0771			
21	CTTTGGTTC	7	16	754	754	0.383	0766	0767	0769	0770	0771	0772	0773	0774	0775
21	TGCTGGTAC	5	16	754	754	0.308	0766	0767	0769	0770	0771	0772	0773	0774	0775
21	TGCCGACTT	11	2	754	754	5.567	0766	0767	0769	0770	0771	0772	0773	0774	0775
21	CGTTGACTT	9	1	754	754	9.097	0766	0767	0769	0770	0771	0772	0773	0774	0775
21	TTGACTT	20	9	754	754	2.250		0769	0770	0771	0772	0773	0774	0775	
21	TTGGTTC	11	25	754	754	0.432		0769	0770	0771	0772	0773	0774	0775	
21	CTGGTAC	5	16	754	754	0.308		0769	0770	0771	0772	0773	0774	0775	
21	CCGACTT	11	2	754	754	5.567		0769	0770	0771	0772	0773	0774	0775	
21	CTT	107	81	754	754	1.374				0773	0774	0775			
21	TTC	54	76	754	754	0.688				0773	0774	0775			
21	TTCACGGGG	7	18	752	752	0.383	0773	0774	0775	0776	0777	0778	0779	0780	0783
21	CACGAAG	47	72	752	752	0.630		0775	0776	0777	0778	0779	0780	0783	
22	AATCAGC	60	94	754	754	0.697		0784	0785	0786	0787	0788	0792	0794	
22	TCAGC	60	96	754	754	0.593			0786	0787	0788	0792	0794		
22	CAGCC	59	94	754	754	0.596			0787	0788	0792	0794	0795		
22	CAGCCTCGC	42	74	754	754	0.542	0787	0788	0792	0794	0795	0798	0802	0803	0805
22	CCTCG	363	408	754	754	0.787			0794	0795	0798	0802	0803		
22	GCCTCGCGT	180	245	754	754	0.651	0792	0794	0795	0798	0802	0803	0805	0806	0807
22	GCCTCGTAT	3	12	754	754	0.247	0792	0794	0795	0798	0802	0803	0805	0806	0807
22	G	457	503	754	754	0.768					0803				
22	A	297	251	754	754	1.302					0803				
22	TCGCGTC	233	263	754	754	0.704		0798	0802	0803	0805	0806	0807	0808	
22	TCGTAGG	21	8	754	754	2.672		0798	0802	0803	0805	0806	0807	0808	
22	TCGTATC	3	13	754	754	0.228		0798	0802	0803	0805	0806	0807	0808	
22	GCGTC	238	300	754	754	0.698			0803	0805	0806	0807	0808		
22	GTAGG	21	8	754	754	2.672			0803	0805	0806	0807	0808		
22	GTATC	3	13	754	754	0.228			0803	0805	0806	0807	0808		
22	T	345	404	754	754	0.731					0807				
22	G	409	350	754	754	1.308					0807				
22	C	467	523	754	754	0.710					0808				
22	G	287	231	754	754	1.301					0808				
22	CCA	440	498	754	754	0.720				0808	0810	0811			
22	GCA	113	85	754	754	1.387				0808	0810	0811			
22	CAG	389	454	754	754	0.704				0810	0811	0814			
22	CAC	164	129	754	754	1.347				0810	0811	0814			
22	AGC	303	344	754	754	0.801				0811	0814	0817			
22	ACA	163	130	754	754	1.324				0811	0814	0817			
22	C	314	352	754	754	0.815					0817				
22	A	440	402	754	754	1.227					0817				
22	AGA	159	128	754	754	1.307				0817	0818	0822			
22	T	305	455	754	754	0.723					0822				
22	A	359	290	754	754	1.383					0822				
22	G	309	460	754	754	0.718					0823				
22	T	355	294	754	754	1.392					0823				
22	G	309	450	754	754	0.722					0824				
22	C	355	295	754	754	1.384					0824				
22	G	308	460	754	754	0.715					0825				
22	A	356	294	754	754	1.400					0825				
22	A	308	459	754	754	0.710					0826				
22	G	356	295	754	754	1.392					0826				
22	T	307	460	754	754	0.711					0827				
22	C	357	294	754	754	1.407					0827				
22	TGC	376	439	754	754	0.714				0827	0828	0829			
22	CGC	304	257	754	754	1.306				0827	0828	0829			
22	TGCCT	361	423	754	754	0.710			0827	0828	0829	0830	0831		
22	CGCCT	298	240	754	754	1.325			0827	0828	0829	0830	0831		
22	GTA	37	21	754	754	1.801				0829	0830	0831			
22	CGCCTAACT	166	132	754	754	1.330	0827	0828	0829	0830	0831	0833	0834	0835	0836
22	TGCCTAACT	61	103	754	754	0.550	0827	0828	0829	0830	0831	0833	0834	0835	0836
23	CCGAGAC	101	75	752	752	1.400		0841	0844	0845	0847	0848	0849	0851	
23	TTACGGC	1	9	752	752	0.110		0841	0844	0845	0847	0848	0849	0851	
23	TTACGGCCG	1	8	752	752	0.124	0841	0844	0845	0847	0848	0849	0851	0855	0856
23	CCAAAGGTG	1	8	752	752	0.124	0841	0844	0845	0847	0848	0849	0851	0855	0856
23	AAAGGTG	1	8	752	752	0.124		0845	0847	0848	0849	0851	0855	0856	
23	AGGTGCC	1	9	752	752	0.110		0846	0849	0851	0855	0856	0857	0858	
23	CCGCC	504	540	752	752	0.708			0851	0855	0856	0857	0858		
23	GTGCC	1	9	752	752	0.110			0851	0855	0856	0857	0858		
23	ACCGCCGGC	3	11	752	752	0.270	0849	0851	0855	0856	0857	0858	0859	0861	0864
23	GGTGCCGAC	1	8	752	752	0.124	0849	0851	0855	0856	0857	0858	0859	0861	0864
23	ACCGCCAAG	10	6	752	752	3.223	0849	0851	0855	0856	0857	0858	0859	0861	0864
23	CCGCCAACA	234	275	752	752	0.784	0851	0855	0856	0857	0858	0859	0861	0864	0865
23	GTGCCGACA	1	8	752	752	0.124	0851	0855	0856	0857	0858	0859	0861	0864	0865
23	CCGCCAAGA	10	6	752	752	3.223	0851	0855	0856	0857	0858	0859	0861	0864	0865
23	GCCAAGA	20	6	754	754	3.307		0856	0857	0858	0859	0861	0864	0865	
23	CAAGA	20	6	754	754	3.307			0858	0859	0861	0864	0865		
23	CCGACACTG	1	8	754	754	0.124	0857	0858	0859	0861	0864	0865	0866	0867	0868
23	CCAAGACCG	20	6	754	754	3.307	0857	0858	0859	0861	0864	0865	0866	0867	0868
23	CGGCATTTT	29	11	754	754	2.702	0858	0859	0861	0864	0865	0866	0867	0868	0871
23	CGACACTGT	1	8	754	754	0.124	0858	0859	0861	0864	0865	0866	0867	0868	0871
23	CAAGACCGC	16	6	754	754	2.703	0858	0859	0861	0864	0865	0866	0867	0868	0871
23	GGCATTTTT	20	9	754	754	2.250	0859	0861	0864	0865	0866	0867	0868	0871	0872
23	GACACTGTT	1	8	754	754	0.124	0859	0861	0864	0865	0866	0867	0868	0871	0872
23	AAGACCGCC	16	6	754	754	2.703	0859	0861	0864	0865	0866	0867	0868	0871	0872
23	ATTTT	30	13	754	754	2.302			0865	0866	0867	0868	0871		
23	ACCGC	36	21	754	754	1.652			0865	0866	0867	0868	0871		

23	ACTGT	18	34	754	754	0.518			9865	9866	9867	9868	9871		
23	CGCTGCCGT	53	35	754	754	1.553	9864	9865	9866	9867	9868	9871	9872	9873	9874
23	GACCGCCGT	26	11	754	754	2.412	9864	9865	9866	9867	9868	9871	9872	9873	9874
23	GCTGCCGTC	53	35	754	754	1.553	9865	9866	9867	9868	9871	9872	9873	9874	9875
23	ACCGCCGTC	35	16	754	754	2.245	9865	9866	9867	9868	9871	9872	9873	9874	9875
23	ACTGTTGCC	15	28	754	754	0.526	9865	9866	9867	9868	9871	9872	9873	9874	9875
23	TTTTTGCCA	18	7	754	754	2.610	9866	9867	9868	9871	9872	9873	9874	9875	9876
23	CCGCCGTCA	35	16	754	754	2.245	9866	9867	9868	9871	9872	9873	9874	9875	9876
23	CTGTTGCCG	3	12	754	754	0.247	9866	9867	9868	9871	9872	9873	9874	9875	9876
23	TGT	1	12	754	754	0.082				9872	9873	9874			
23	TGTCA	1	12	754	754	0.082			9872	9873	9874	9875	9876		
23	TGCCG	5	14	754	754	0.353			9872	9873	9874	9875	9876		
23	TGCCACT	130	101	754	754	1.347		9872	9873	9874	9875	9876	9878	9879	
23	TGCCGTT	5	14	754	754	0.353		9872	9873	9874	9875	9876	9878	9879	
23	CGCCACT	8	1	754	754	8.075		9872	9873	9874	9875	9876	9878	9879	
23	A	740	738	754	754	3.248					9876				
23	G	5	16	754	754	0.308					9876				
24	C	696	671	754	754	1.484					9883				
24	T	58	83	754	754	0.674					9883				
24	AGG	241	278	754	754	0.804				9890	9891	9892			
24	GAGCTCCGA	245	280	754	754	0.774	9892	9893	9894	9895	9897	9898	9899	9901	9902
24	GCTCCGA	245	280	754	754	0.774		9894	9895	9897	9898	9899	9901	9902	
24	GCTCCGAGG	243	286	754	754	0.778	9894	9895	9897	9898	9899	9901	9902	9903	9904
24	CCG	280	248	754	754	1.208				9899	9901	9902			
24	CGA	240	300	754	754	0.746				9899	9901	9902			
24	G	304	201	754	754	1.276					9902				
24	A	450	403	754	754	0.784					9902				
24	C	304	201	754	754	1.276					9903				
24	G	450	403	754	754	0.784					9903				
24	CGCAAAC	249	202	754	754	1.347		9901	9902	9903	9904	9906	9908	9909	
24	GAGGGAG	193	235	754	754	0.700		9901	9902	9903	9904	9906	9908	9909	
24	GAGGGAC	5	20	754	754	0.245		9901	9902	9903	9904	9906	9908	9909	
24	CAAAC	252	205	754	754	1.344			9903	9904	9906	9908	9909		
24	GGGAG	194	230	754	754	0.700			9903	9904	9906	9908	9909		
24	GGGAC	5	20	754	754	0.245			9903	9904	9906	9908	9909		
24	AAC	260	215	754	754	1.367				9906	9908	9909			
24	GAG	212	250	754	754	0.789				9906	9908	9909			
24	GAC	5	21	754	754	0.233				9906	9908	9909			
24	AACCC	206	214	754	754	1.375			9906	9908	9909	9910	9911		
24	GAGTC	102	240	754	754	0.732			9906	9908	9909	9910	9911		
24	GACCC	5	21	754	754	0.233			9906	9908	9909	9910	9911		
24	AACCCGG	228	170	754	754	1.302		9906	9908	9909	9910	9911	9913	9916	
24	GAGTCAG	171	221	754	754	0.707		9906	9908	9909	9910	9911	9913	9916	
24	GACCCGG	5	20	754	754	0.245		9906	9908	9909	9910	9911	9913	9916	
24	AACCCGGCT	210	165	754	754	1.378	9906	9908	9909	9910	9911	9913	9916	9917	9918
24	GAGTCAGCT	153	208	754	754	0.608	9906	9908	9909	9910	9911	9913	9916	9917	9918
24	GACCCGGCT	4	10	754	754	0.206	9906	9908	9909	9910	9911	9913	9916	9917	9918
24	AGTCAGCTT	155	211	754	754	0.666	9908	9909	9910	9911	9913	9916	9917	9918	9920
24	CAGCT	231	202	754	754	0.609			9911	9913	9916	9917	9918		
24	TAGTA	24	12	754	754	2.033			9911	9913	9916	9917	9918		
24	C	626	651	754	754	0.732					9917				
24	T	134	103	754	754	1.306					9917				
24	T	618	648	754	754	0.743					9920				
24	C	136	106	754	754	1.345					9920				
24	A	621	650	754	754	0.747					9922				
24	G	133	104	754	754	1.330					9922				
24	A	618	640	754	754	0.735					9923				
24	G	136	105	754	754	1.360					9923				
24	CGGGACAAA	25	12	754	754	2.120	9920	9921	9922	9923	9925	9927	9928	9929	9933
24	GGGACAAAT	25	12	754	754	2.120	9921	9922	9923	9925	9927	9928	9929	9933	9936
24	GACAAAT	25	12	754	754	2.120		9923	9925	9927	9928	9929	9933	9936	
24	GACAAATGC	22	10	754	754	2.236	9923	9925	9927	9928	9929	9933	9936	9937	9938
24	CAAATGC	23	10	754	754	2.341		9927	9928	9929	9933	9936	9937	9938	
25	T	633	660	754	754	0.745					9939				
25	C	121	94	754	754	1.342					9939				
25	CATAACC	116	86	754	754	1.412		9939	9940	9941	9942	9945	9946	9948	
25	TTTGACC	26	42	754	754	0.605		9939	9940	9941	9942	9945	9946	9948	
25	TGACC	26	43	754	754	0.591			9941	9942	9945	9946	9948		
25	GACCA	26	43	754	754	0.591			9942	9945	9946	9948	9951		
25	TGACCACGT	2	10	754	754	0.198	9941	9942	9945	9946	9948	9951	9952	9953	9955
25	ATG	12	24	754	754	0.492				9951	9952	9953			
25	T	585	542	754	754	1.354					9953				
25	G	169	212	754	754	0.730					9953				
25	C	671	642	754	754	1.410					9955				
25	T	83	112	754	754	0.700					9955				
25	A	570	537	754	754	1.327					9956				
25	G	176	217	754	754	0.754					9956				
25	TCACAGC	370	338	754	754	1.244		9953	9955	9956	9957	9958	9959	9961	
25	GTGTCCC	79	108	754	754	0.700		9953	9955	9956	9957	9958	9959	9961	
25	GTCCC	124	171	754	754	0.671			9956	9957	9958	9959	9961		
25	G	530	492	754	754	1.335					9959				
25	C	215	262	754	754	0.740					9959				
25	CCT	155	204	754	754	0.698				9959	9961	9962			
25	GCCAG	380	347	754	754	1.230			9959	9961	9962	9963	9968		
25	CCTAA	120	168	754	754	0.660			9959	9961	9962	9963	9968		
25	CCTAACG	40	76	754	754	0.500		9959	9961	9962	9963	9968	9969	9971	
25	C	659	623	754	754	1.459					9972				
25	G	95	131	754	754	0.686					9972				
25	CGC	659	622	754	754	1.472				9972	9973	9974			
25	GGC	6	19	754	754	0.310				9972	9973	9974			
25	GATCCCA	11	23	754	754	0.471		9972	9973	9974	9975	9976	9978	9979	
25	CCC	15	32	754	754	0.458				9975	9976	9978			
25	CCA	14	29	754	754	0.473				9976	9976	9979			
25	CCCGAGAAC	24	10	754	754	2.446	9974	9975	9976	9978	9979	9980	9981	9983	9986
25	TCCCAGAAT	10	23	754	754	0.427	9974	9975	9976	9978	9979	9980	9981	9983	9986
25	CCCGAGAAT	2	10	754	754	0.198	9974	9975	9976	9978	9979	9980	9981	9983	9986
25	CGAGAAC	46	28	754	754	1.703		9976	9978	9979	9980	9981	9983	9986	
25	CCAGAAT	11	27	754	754	0.390		9976	9978	9979	9980	9981	9983	9986	
25	CGAGAAT	2	11	754	754	0.180		9976	9978	9979	9980	9981	9983	9986	
25	AGAAC	55	33	754	754	1.719			9979	9980	9981	9983	9986		
25	AGAAT	26	53	754	754	0.472			9979	9980	9981	9983	9986		
25	AGAACGT	55	33	754	754	1.710		9979	9980	9981	9983	9986	9988	9990	
25	AGAATAA	14	39	754	754	0.347		9979	9980	9981	9983	9986	9988	9990	
25	AGAACGTGG	55	32	754	754	1.775	9979	9980	9981	9983	9986	9988	9990	9991	9993
25	AGAATAAGA	11	28	754	754	0.384	9979	9980	9981	9983	9986	9988	9990	9991	9993
25	AGAATAAAA	3	11	754	754	0.270	9979	9980	9981	9983	9986	9988	9990	9991	9993
25	AACGTGG	78	46	754	754	1.776		9981	9983	9986	9986	9990	9991	9993	
25	AATAAGA	25	44	754	754	0.563		9981	9983	9986	9988	9990	9991	9993	
25	CGTGG	78	46	754	754	1.776			9986	9988	9990	9991	9993		
25	TAAGA	25	44	754	754	0.553			9986	9988	9990	9991	9993		
25	GTGGA	78	46	754	754	1.776			9988	9990	9991	9993	9994		
25	AAGAG	25	42	754	754	0.581			9988	9990	9991	9993	9994		
25	GGA	78	46	754	754	1.776				9991	9993	9994			
25	GAG	25	42	754	754	0.581				9991	9993	9994			
25	GAG	74	44	754	754	1.756				9993	9994	9995			
25	AGG	24	43	754	754	0.544				9993	9994	9995			
25	GAGAT	57	35	754	754	1.686			9993	9994	9995	9998	10000		
25	GAGAA	17	7	754	754	2.402			9993	9994	9995	9998	10000		
25	AGGAA	24	40	754	754	0.587			9993	9994	9995	9998	10000		
25	GAGATGG	57	35	754	754	1.686		9993	9994	9995	9998	10000	10001	10002	
25	GAGAAAC	17	7	754	754	2.402		9993	9994	9995	9998	10000	10001	10002	
25	AGGAAAC	24	40	754	754	0.587		9993	9994	9995	9998	10000	10001	10002	
25	GAGAAACAA	17	7	754	754	2.402	9993	9994	9995	9998	10000	10001	10002	10003	10005
25	AGGAAACAA	24	40	754	754	0.587	9993	9994	9995	9998	10000	10001	10002	10003	10005
25	A	692	712	754	754	0.658					10003				
25	G	62	42	754	754	1.510					10003				
25	G	698	717	754	754	0.643					10007				
25	A	56	37	754	754	1.555					10007				

25	C	690	711	754	754	0.652					10006									
25	T	64	43	754	754	1.534					10006									
25	TCA	63	43	754	754	1.508			10008		10011	10012								
26	CCCTG	410	375	752	752	1.245		10015	10016		10018	10019	10020							
26	CTGTA	258	303	752	752	0.774		10015	10016		10018	10019	10020							
26	CTG	410	370	752	752	1.238			10018		10019	10020								
26	GTA	265	310	752	752	0.770			10018		10019	10020								
26	G	484	440	752	752	1.281					10020									
26	A	268	312	752	752	0.781					10020									
26	GCC	457	406	752	752	1.320			10020		10024	10025								
26	ACG	259	299	752	752	0.809			10020		10024	10025								
26	C	407	424	754	754	1.266					10025									
26	G	287	330	754	754	0.790					10025									
26	T	490	452	754	754	1.240					10026									
26	C	294	302	754	754	0.806					10026									
26	C	723	705	752	752	1.662					10027									
26	T	20	47	752	752	0.602					10027									
26	C	466	421	754	754	1.294					10028									
26	T	286	333	754	754	0.773					10028									
26	TAC	252	299	754	754	0.803			10028		10029	10030								
26	CGC	22	0	754	754	2.488			10028		10029	10030								
26	GCG	18	0	754	754	3.040			10029		10030	10031								
26	G	465	420	754	754	1.230					10031									
26	A	289	328	754	754	0.807					10031									
26	CGGGT	18	5	754	754	3.664			10030	10031	10033	10034	10035							
27	TTGCA	182	220	754	754	0.772			10038	10039	10040	10042	10043							
27	TGCAC	182	221	754	754	0.767			10039	10040	10042	10043	10044							
27	CACAGAGAG	255	309	754	754	0.773	10042	10043	10044	10045	10046	10047	10049	10051	10053					
27	CAGAGAG	332	372	754	754	0.808		10044	10045	10046	10047	10049	10051	10053						
27	ATC	413	370	754	754	1.257				10049	10051	10053								
27	ATCTG	413	369	754	754	1.264			10049	10051	10053	10055	10056							
27	CTG	413	369	754	754	1.264				10053	10055	10056								
27	G	413	373	754	754	1.237					10056									
27	A	341	381	754	754	0.808					10056									
27	A	413	373	754	754	1.237					10057									
27	G	341	381	754	754	0.808					10057									
27	C	412	367	754	754	1.270					10059									
27	T	342	387	754	754	0.787					10059									
27	C	519	483	754	754	1.230					10060									
27	G	235	271	754	754	0.807					10060									
27	G	453	414	754	754	1.236					10065									
27	T	301	340	754	754	0.809					10065									
27	TGG	88	122	754	754	0.684				10065	10068	10070								
27	A	666	630	754	754	1.490					10070									
27	G	88	124	754	754	0.671					10070									
27	ACT	447	408	752	752	1.236				10070	10071	10072								
27	GCG	88	123	752	752	0.678				10070	10071	10072								
27	CGGATTA	191	236	752	752	0.744		10071	10072	10074	10076	10079	10080	10081						
27	CGGATCA	37	21	752	752	1.801		10071	10072	10074	10076	10079	10080	10081						
27	GATTA	192	240	754	754	0.732			10074	10076	10079	10080	10081							
27	GATCA	37	21	754	754	1.801			10074	10076	10079	10080	10081							
27	GATTATA	191	239	754	754	0.731		10074	10076	10079	10080	10081	10082	10083						
27	GATCAAC	36	20	754	754	1.840		10074	10076	10079	10080	10081	10082	10083						
28	GTG	237	202	754	754	1.253				10084	10086	10087								
28	TGA	229	191	754	754	1.286				10086	10087	10088								
28	T	522	558	754	754	0.790					10088									
28	A	232	196	754	754	1.265					10088									
28	A	522	557	754	754	0.790					10090									
28	C	232	197	754	754	1.257					10090									
28	CCC	230	194	754	754	1.267				10090	10091	10092								
28	A	522	560	754	754	0.779					10095									
28	G	232	194	754	754	1.283					10095									
28	C	522	557	754	754	0.790					10096									
28	T	232	197	754	754	1.257					10096									
28	TAT	231	193	754	754	1.284				10096	10097	10099								
28	TATAA	227	186	754	754	1.315			10096	10097	10099	10102	10103							
28	TAA	227	187	754	754	1.306				10099	10102	10103								
28	TAATT	225	183	754	754	1.327			10099	10102	10103	10105	10106							
28	ATT	226	184	754	754	1.326				10103	10105	10106								
28	A	521	556	754	754	0.796					10106									
28	T	233	198	754	754	1.256					10106									
28	GTAGG	226	187	752	752	1.298			10107	10108	10109	10110	10111							
28	AGG	228	189	754	754	1.296				10108	10109	10110	10111							
28	T	523	564	754	754	0.763					10110									
28	G	231	190	754	754	1.311					10111									
28	GGA	229	188	754	754	1.313					10111									
28	GAT	229	189	754	754	1.314				10111	10113	10114								
28	GATGA	215	172	754	754	1.350			10113	10114	10114	10115	10116	10117						
28	AGCAA	3	15	754	754	0.197			10113	10114	10115	10116	10117							
28	TGA	217	174	754	754	1.347				10114	10115	10116	10117							
28	CAA	5	18	754	754	0.273				10115	10116	10117	10118							
28	GAT	213	165	754	754	1.405				10115	10116	10117	10118							
28	AAT	4	13	754	754	0.304				10116	10117	10118	10121	10122	10128	10129				
28	GATATTA	46	27	754	754	1.749	10116	10117		10118	10121	10122	10128	10129						
28	ATT	87	57	754	754	1.505				10121	10122	10128	10129	10130	10131					
28	TAA	392	433	754	754	0.803				10122	10128	10129	10130	10131						
28	TTA	91	62	754	754	1.532				10122	10128	10129	10130	10131						
28	TAT	91	61	754	754	1.550				10128	10129	10130	10131							
28	ATA	88	61	754	754	1.501				10129	10130	10131								
28	C	665	603	754	754	0.658					10131									
28	A	89	61	754	754	1.520					10131									
28	ACC	88	59	754	754	1.517				10131	10132	10133								
28	T	661	665	754	754	0.716					10133									
28	C	93	69	754	754	1.307					10133									
28	CTTTA	73	103	754	754	0.678			10132	10133	10135	10136	10138							
28	CCCTG	61	36	754	754	1.756			10132	10133	10135	10136	10138							
28	CTG	89	63	754	754	1.408				10135	10136	10138								
28	TTA	73	103	754	754	0.678				10135	10136	10138								
28	A	613	650	754	754	0.696					10138									
28	G	141	104	754	754	1.438					10138									
28	C	620	669	754	754	0.621					10139									
28	T	128	85	754	754	1.609					10139									
28	ACAAT	68	110	754	754	0.580			10138	10139	10141	10142	10143							
28	GTAAC	67	41	754	754	1.600			10138	10139	10141	10142	10143							
28	GTAGT	8	1	754	754	8.075			10138	10139	10141	10142	10143							
28	CAATG	47	76	754	754	0.593			10139	10141	10142	10143	10144							
28	CAATC	21	36	754	754	0.571			10139	10141	10142	10143	10144							
28	TAACC	67	41	754	754	1.600			10139	10141	10142	10143	10144							
28	TAGTG	8	1	754	754	8.075			10139	10141	10142	10143	10144							
28	GTAACCTAA	67	40	754	754	1.741	10138	10139	10141	10142	10143	10144	10145	10148	10150					
28	ACAATGCGT	32	55	754	754	0.583	10138	10139	10141	10142	10143	10144	10145	10148	10150					
28	ACAACGTGT	20	12	754	754	2.473	10138	10139	10141	10142	10143	10144	10145	10148	10150					
28	GTAGTGCAA	8	1	754	754	8.075	10138	10139	10141	10142	10143	10144	10145	10148	10150	10152				
28	TAACCTAAG	64	37	754	754	1.707	10139	10141	10142	10143	10144	10145	10148	10150	10152					
28	CAATGCGTG	32	50	754	754	0.552	10139	10141	10142	10143	10144	10145	10148	10150	10152					
28	CAACCTGTG	20	12	754	754	2.473	10139	10141	10142	10143	10144	10145	10148	10150	10152					
28	ATCTAAG	28	44	754	754	0.576		10142	10143	10144	10145	10148	10150	10152						
28	ATGCGTG	35	57	754	754	0.595		10142	10143	10144	10145	10148	10150	10152						
28	ACCTGTG	29	12	754	754	2.473		10142	10143	10144	10145	10148	10150	10152						
28	TGT	37	20	754	754	1.804				10145	10148	10150								
28	CCTAAGTTA	314	275	754	754	1.243	10143	10144	10145	10148	10150	10152	10153	10154	10155					
28	TGCGTGCTA	36	58	754	754	0.637	10143	10144	10145	10148	10150	10152	10153	10154	10155					
28	CCTGTGCTA	29	12	754	754	2.473	10143	10144	10145	10148	10150	10152	10153	10154	10155					
28	TGTGCTA	37	19	754	754	1.990		10145	10148	10150	10152	10153	10154	10155						
28	TGACCGCTT	54	23	754	754	2.452	10150	10158	10160	10163	10167	10168	10169	10170	10171					
28	TGACTTTTC	40	78	754	754	0.563	10150	10158	10160	10163	10167	10168	10169	10170	10171					
28	ACCGCTT	54	23	754	754	2.452		10158	10160	10163	10167	10168	10169	10170	10171					
28	ACTTTTC	40	78	754	754	0.563		10160	10163	10167	10168	10169	10170	10171						

29	CTCTC	9	20	754	754	0.443			10167	10168	10169	10170	10171			
29	CGCTT	54	23	754	754	2.452			10167	10168	10169	10170	10171			
29	TTTTC	46	80	754	754	0.547			10167	10168	10169	10170	10171			
29	CGCTTAC	54	23	754	754	2.452		10167	10168	10168	10169	10170	10171	10172	10173	
29	TTTTCGC	43	73	754	754	0.564		10167	10168	10168	10169	10170	10171	10172	10173	
29	GTA	7	17	754	754	0.400					10170	10171	10172			
29	TCG	87	130	754	754	0.626					10170	10171	10172			
29	TCGCG	76	125	754	754	0.564			10170	10170	10171	10172	10173			
30	CTCGCTTCG	2	10	754	754	0.198	10175	10177	10170	10170	10180	10181	10182	10183	10184	10185
30	CGCTTCG	2	10	754	754	0.198		10170		10180		10181	10182	10183	10184	10185
31	GCT	203	239	754	754	0.794						10197	10198	10200		
31	C	551	515	754	754	1.200							10200	10200		
31	T	203	239	754	754	0.794				10198			10200	10202		
31	CCAGG	110	70	754	754	1.600							10202	10203		
31	AGG	110	70	754	754	1.600							10202	10203		
31	AGC	45	65	754	754	0.073								10203		
31	G	225	182	754	754	1.337								10207		
31	C	520	572	754	754	0.748								10207		
31	CAGGCCTCA	57	31	754	754	1.907	10200	10202	10203	10207	10207	10209	10211	10212	10213	10214
31	CGCCCCCTA	18	6	754	754	3.040	10200	10202	10203	10207	10207	10209	10211	10212	10213	10214
31	AGGCCTCAT	54	31	754	754	1.709	10202	10203	10207	10207	10209	10211	10212	10213	10214	10215
31	GCCCCCTAT	21	6	754	754	3.572	10202	10203	10207	10207	10209	10211	10212	10213	10214	10215
31	CCCGTCATG	6	10	754	754	0.310	10203	10207	10207	10209	10211	10212	10213	10214	10215	10216
31	CCCCCTCCG	11	20	754	754	0.370	10203	10207	10207	10209	10211	10212	10213	10214	10215	10216
31	GGCCTCACC	11	2	754	754	5.567	10203	10207	10207	10209	10211	10212	10213	10214	10215	10216
31	CCCCCTATC	21	6	754	754	3.572	10203	10207	10207	10209	10211	10212	10213	10214	10215	10216
31	CCCTCATCC	105	70	754	754	1.382	10207	10209	10209	10211	10212	10213	10214	10215	10216	10217
31	CCCTCATGC	6	10	754	754	0.310	10207	10209	10209	10211	10212	10213	10214	10215	10216	10217
31	CCCCTCCGC	12	32	754	754	0.365	10207	10209	10209	10211	10212	10213	10214	10215	10216	10217
31	GCCTCACCC	11	2	754	754	5.567	10207	10209	10209	10211	10212	10213	10214	10215	10216	10217
31	CCCCTATCC	22	6	754	754	3.747	10207	10209	10209	10211	10212	10213	10214	10215	10216	10217
31	TAC	211	251	754	754	0.779						10213	10214	10215		
31	TAT	58	35	754	754	1.712						10213	10214	10215		
31	CAC	23	9	754	754	2.604						10213	10214	10215		
31	CTCCGCG	18	34	754	754	0.518		10212	10213	10214	10214	10215	10216	10217	10218	
31	TCACCCG	21	9	754	754	2.372		10212	10213	10214	10214	10215	10216	10217	10218	
31	CTATCCG	27	12	754	754	2.298		10212	10213	10214	10214	10215	10216	10217	10218	
31	CTCCGCGCC	18	33	754	754	0.534	10212	10213	10214	10215	10215	10216	10217	10218	10219	10220
31	CTATCCGCC	27	12	754	754	2.298	10212	10213	10214	10215	10215	10216	10217	10218	10219	10220
31	CCG	645	606	754	754	1.445					10216	10217	10218			
31	CCGCC	631	592	754	754	1.404				10216	10217	10218	10219	10220		
31	CCGCCAC	577	505	754	754	1.607		10216	10217	10217	10218	10218	10219	10220	10224	10227
31	CCGCCAG	42	78	754	754	0.511		10216	10217	10218	10218	10219	10220	10224	10227	10227
31	CGCCAGA	46	82	754	754	0.532		10217	10218	10218	10219	10220	10224	10227	10228	10228
31	CGCCACG	370	318	754	754	1.386		10217	10218	10219	10220	10224	10227	10228		
31	CCAGA	47	85	754	754	0.523			10218	10219	10220	10224	10227	10228		
31	CCACG	384	324	754	754	1.377			10218	10219	10220	10224	10227	10228		
31	G	51	94	754	754	0.509				10219			10227			
31	C	703	660	754	754	1.063				10219			10227			
31	GAG	48	80	754	754	0.573					10227	10227	10228	10231		
31	CAA	15	32	754	754	0.458					10227	10227	10228	10231		
31	GAGGG	38	65	754	754	0.563				10227	10228	10228	10231	10235	10236	
31	CAAGG	13	28	754	754	0.455				10227	10228	10228	10231	10235	10236	
31	GAGGGGT	27	47	754	754	0.559		10227	10228	10228	10231	10231	10235	10236	10237	10238
31	CAGGGGT	127	98	754	754	1.356		10227	10228	10228	10231	10231	10235	10236	10237	10238
31	CAAGGGT	12	27	754	754	0.435		10227	10228	10228	10231	10231	10235	10236	10237	10238
31	CAGGAGT	18	5	754	754	3.004		10227	10228	10228	10231	10231	10235	10236	10237	10238
31	GGAGT	26	10	754	754	2.057				10231		10235	10236	10237	10238	
31	AGT	20	10	754	754	2.057						10236	10237	10238		
31	GCGTCGTAG	43	24	754	754	1.840	10237	10238	10239	10241	10241	10243	10244	10246	10249	10250
31	GCGTCGTAA	23	46	754	754	0.463	10237	10238	10239	10241	10243	10244	10246	10249	10250	10252
31	CGTCGTAGC	41	23	754	754	1.828	10238	10239	10241	10241	10243	10244	10246	10249	10250	10252
31	CGTCGTAAC	21	48	754	754	0.421	10238	10239		10243	10244	10246	10249	10250		
31	CGTAG	50	28	754	754	1.842					10244	10246	10249	10250		
31	CGTAA	27	50	754	754	0.523					10244	10246	10249	10250		
31	CTGTAACGT	13	20	754	754	0.491	10241	10243	10244	10246	10246	10249	10250	10252	10254	10255
31	TCGTAACGT	20	37	754	754	0.526	10241	10243	10244	10246	10246	10249	10250	10252	10254	10255
31	TTGTAACGT	16	32	754	754	0.489	10241	10243	10244	10246	10246	10249	10250	10252	10254	10255
31	TCGTAACGC	3	13	754	754	0.228	10241	10243	10244	10246	10246	10249	10250	10252	10254	10255
31	TTGTAGCGC	11	2	754	754	5.567	10241	10243	10244	10246	10246	10249	10250	10252	10254	10255
31	TGTAACGTT	29	58	754	754	0.480	10243	10244	10246	10246	10249	10250	10252	10254	10255	10256
31	CGTAACGTT	22	37	754	754	0.582	10243	10244	10246	10246	10249	10250	10252	10254	10255	10256
31	TAACGTT	97	147	754	754	0.610		10244	10246	10246	10249	10250	10252	10254	10255	10256
31	TAGCGCT	73	46	754	754	1.650		10246	10246	10249	10250	10252	10254	10255	10256	
31	AACGTTC	89	139	754	754	0.502		10246	10249	10249	10250	10252	10254	10255	10256	
31	AGCGCTG	35	18	754	754	1.990		10249	10249	10250	10252	10254	10255	10256	10258	
31	AACGTTCAG	47	71	754	754	0.640	10249	10250	10250	10252	10254	10255	10256	10258	10259	10260
31	AACGTTCGC	34	56	754	754	0.589	10249	10250	10250	10252	10254	10255	10256	10258	10259	10260
31	AACGCTCAG	2	13	754	754	0.152	10249	10250	10250	10252	10254	10255	10256	10258	10259	10260
31	AGCGCTCAC	6	1	754	754	6.075	10249	10250	10250	10252	10254	10255	10256	10258	10259	10260
31	AGCGCTGGC	14	4	754	754	3.547	10249	10250	10250	10252	10254	10255	10256	10258	10259	10260
31	CAG	259	299	754	754	0.796					10254	10255	10256			
31	CAC	65	41	754	754	1.641					10258	10255	10260			
31	ACA	67	42	754	754	1.653					10258	10259	10260			
31	ACATA	42	25	754	754	1.720				10259	10260	10260	10261			
31	GGACG	18	32	754	754	0.552				10259	10260	10261	10263	10264		
31	GGACGCG	13	26	754	754	0.491		10259	10260	10260	10261	10263	10264	10266	10268	
31	ACATACA	13	4	754	754	3.280		10259	10260	10260	10261	10263	10264	10266	10268	
32	G	431	474	754	754	0.788						10263	10273			
32	A	323	280	754	754	1.209						10263	10273			
32	ATGGCGCTT	7	17	752	752	0.400	10270	10272	10273	10275	10276	10277	10278	10279	10281	
33	GTCAGGCAC	192	220	752	752	0.783	10283	10284	10280	10293	10295	10296	10300	10301	10302	
33	ACCGGACAC	1	8	752	752	0.124	10283	10284	10280	10293	10295	10296	10300	10301	10302	
33	CAGGCAC	201	241	754	754	0.774		10284	10280	10293	10295	10296	10300	10301	10302	
33	CGGACAC	6	19	754	754	0.310		10289	10293	10295	10296	10300	10301	10302		
33	ACC	322	283	754	754	1.241					10296	10300	10301			
33	ACA	12	25	754	754	0.472						10300	10301			
33	A	345	393	754	754	0.775						10301				
33	C	469	381	754	754	1.201						10301				
33	C	526	561	754	754	0.704						10302				
33	T	228	193	754	754	1.200						10302				
33	TCT	152	118	754	754	1.361					10302	10304	10305			
33	A	391	439	754	754	0.773						10305				
33	T	383	315	754	754	1.204						10305				
34	CGCTCGT	2	10	754	754	0.198		10314	10315	10317	10319	10320	10321	10322		
34	CTTGT	1	0	754	754	0.110			10317	10319	10320	10321	10322			
34	CTCGT	2	10	754	754	0.198			10317	10319	10320	10321	10322			
34	TGT	1	9	754	754	0.110					10320	10321				
34	CGT	2	10	754	754	0.198					10320	10321				
34	C	750	734	754	754	5.109						10322				
34	T	4	20	754	754	0.196						10322				
34	CGCCGACCC	28	13	754	754	2.198	10320	10321	10322	10324	10325	10327	10328	10331	10332	
34	TGCCGACTC	51	27	754	754	1.953	10320	10321	10322	10324	10325	10327	10328	10331	10332	
34	CGCCAGCCT	7	21	754	754	0.327	10320	10321	10322	10324	10325	10327	10328	10331	10332	
34	CCGACTC	138	106	754	754	1.370		10322	10324		10327	10328	10331	10332		
34	CTC	139	110	754	754	1.323					10331	10332				
34	T	451	490	754	754	0.802					10332					
34	C	503	204	754	754	1.247					10332					
34	C	450	486	754	754	0.607					10335					
34	A	304	266	754	754	1.230					10335					
35	TCC	242	207	754	754	1.240				10345	10346	10347				
35	CAGCGGC	93	125	754	754	0.708		10347	10348	10349	10350	10352	10353	10354		
35	AGCGGCT	81	116	754	754	0.662		10348	10349	10350	10352	10354	10355	10356	10357	
35	CGGCTCA	69	99	754	754	0.666		10350	10352	10353	10353	10354	10355	10356	10357	
35	CGACTTG	26	12	754	754	2.208		10350	10352	10353	10353	10354	10355	10356	10357	
35	CGGCTTA	4	13	754	754	0.304		10350	10352	10353	10353	10354	10355	10356	10357	
35	CGGCTCACT	41	67	754	754	0.690	10350	10352	10353	10354	10354	10355	10356	10357	10358	10360
35	CGACTTGCA	20	11	754	754	2.412	10350	10352	10353	10354	10355	10355	10356	10357	10358	10360

35	CGGCTTACA	1	10	754	754	0.699	10350	10352	10353	10354	10355	10356	10357	10358	10360
35	GGCTCACTC	38	63	754	754	0.582	10352	10353	10354	10355	10356	10357	10358	10360	10361
35	GACTTGCAC	26	11	754	754	2.412	10352	10353	10354	10355	10356	10357	10358	10360	10361
35	GGCTTACAC	1	10	754	754	0.000	10352	10353	10354	10355	10356	10357	10358	10360	10361
35	CTCACTC	111	149	754	754	0.701		10354	10355	10356	10356	10357	10358	10361	
35	CTTACAC	9	21	754	754	0.422		10354	10355	10356	10356	10357	10358	10361	
35	CTCACTCGC	109	145	754	754	0.710	10354	10355	10356	10356	10357	10358	10360	10361	10362	10363
35	CTTACACGC	7	10	754	754	0.303	10354	10355	10356	10357	10358	10360	10361	10362	10363
35	T	392	440	754	754	0.773					10358	10360			
35	A	382	314	754	754	1.204					10360	10360			
35	TCG	202	243	754	754	0.770				10360	10361	10361	10362		
35	ACG	360	311	754	754	1.302				10360	10361	10362	10362		
35	CGA	165	129	754	754	1.357				10361		10362	10363		
35	C	580	624	754	754	0.744						10363			
35	A	165	130	754	754	1.345						10363			
35	ACGATCCAA	144	112	754	754	1.353	10360	10361	10362	10363	10365	10368	10367	10368	10369
35	CCAAATCCA	78	51	754	754	1.600	10360	10367	10368	10369	10370	10371	10373	10374	10375
35	CAAACGGTG	27	47	754	754	0.550	10367	10368	10369	10370	10371	10373	10374	10375	10377
35	CAAATCCAA	12	3	754	754	4.049	10367	10368	10369	10370	10371	10373	10374	10375	10377
35	G	558	601	754	754	0.785					10373				
35	C	100	103	754	754	1.274					10373				
35	CCA	81	58	754	754	1.444				10373	10374	10375			
35	GTG	34	53	754	754	0.625				10374	10375	10377			
35	CAA	12	3	754	754	4.049				10374	10375	10377			
37	AGG	82	59	754	754	1.437				10403	10407	10408			
37	GGATC	81	53	754	754	1.502			10407	10408	10409	10410	10412		
37	AGGATCTCT	40	24	754	754	1.704	10403	10407	10408	10409	10410	10412	10414	10416	10417
37	CGTCTCTCG	8	1	754	754	6.075	10408	10409	10410	10412	10414	10416	10417	10418	10420
37	ATCCTCTGT	29	15	754	754	1.971	10409	10410	10412	10414	10416	10417	10418	10420	10421
37	TCTGT	63	39	754	754	1.671			10416	10417	10418	10420	10421		
37	CTTCT	11	23	754	754	0.471			10416	10417	10418	10420	10421		
37	G	739	722	754	754	2.184					10418				
37	C	15	32	754	754	0.456					10420				
37	GTG	280	216	754	754	1.311				10420	10421	10423			
37	CTA	15	29	754	754	0.507				10420	10421	10423			
37	TGTGTCT	204	171	754	754	1.205		10418	10420	10421	10423	10424	10426	10427	
37	CGTATCT	4	13	754	754	0.304		10418	10420	10421	10423	10424	10426	10427	
37	TGTATCT	53	35	754	754	1.553		10418	10420	10421	10423	10424	10426	10427	
37	GTCTA	262	223	754	754	1.208			10423	10424	10426	10427	10428		
37	TCTAT	266	228	754	754	1.258			10424	10426	10427	10428	10429		
37	TCTGT	42	64	754	754	0.636			10424	10426	10427	10428	10429		
37	A	325	270	754	754	1.200					10428				
37	G	420	475	754	754	0.775					10428				
37	ATG	324	270	754	754	1.283				10426	10428	10429	10430		
37	GTG	170	223	754	754	0.693				10426	10428	10429	10430		
37	TGA	312	269	754	754	1.273				10426	10428	10429	10430		
37	TGG	182	233	754	754	0.711				10426	10428	10429	10430		
37	A	315	271	754	754	1.279					10429		10432		
37	G	439	483	754	754	0.782					10429		10432		
37	TGAACAA	198	151	754	754	1.422		10428	10430	10432	10434	10436	10437	10441	
37	TGGAGAA	16	30	754	754	0.523		10428	10430	10432	10434	10436	10437	10441	
37	TGGGCAC	13	36	754	754	0.350		10428	10430	10432	10434	10436	10437	10441	
37	AACAA	201	152	754	754	1.440			10430	10432	10434	10436	10437	10441	
37	GGCAC	15	39	754	754	0.372			10430	10432	10434	10436	10437	10441	
37	ACAAC	184	128	754	754	1.579			10430	10434	10436	10437	10441	10443	
37	AGAAT	46	70	754	754	0.635			10430	10434	10436	10437	10441	10443	
37	GCACT	14	34	754	754	0.401			10430	10434	10436	10437	10441	10443	
37	AACAACCCT	148	104	754	754	1.501	10432	10434	10436	10437	10441	10443	10444	10445	10446
37	GAGAATTTT	44	66	754	754	0.646	10432	10434	10436	10437	10441	10443	10444	10445	10446
37	GGCACTTTT	13	32	754	754	0.396	10432	10434	10436	10437	10441	10443	10444	10445	10446
37	AACACTTTG	16	6	754	754	2.703	10432	10434	10436	10437	10441	10443	10444	10445	10446
37	C	377	335	754	754	1.251					10443				
37	T	377	419	754	754	0.800					10443				
37	C	363	324	754	754	1.232					10444				
37	T	391	430	754	754	0.812					10444				
37	CCT	355	314	754	754	1.247				10444	10445	10446			
37	TTT	347	386	754	754	0.813				10444	10445	10446			
37	CCTTC	345	299	754	754	1.284			10444	10445	10446	10449	10450		
37	CTTCT	343	299	754	754	1.291			10444	10445	10446	10449	10450	10453	
37	TTTTT	10	24	754	754	0.400			10445	10446	10449	10450	10453		
37	TTT	12	33	754	754	0.353				10446	10449	10450	10453		
37	TCTAT	301	253	754	754	1.316			10444	10445	10446	10449	10450	10453	10454	10457	
37	TTTAT	7	23	754	754	0.298			10444	10445	10446	10449	10450	10453	10454	10457	
37	TCTATGG	300	250	754	754	1.332		10446	10449	10450	10453	10454	10457	10458	10459		
37	TTTATGG	7	23	754	754	0.298		10446	10449	10450	10453	10454	10457	10458	10459		
37	TCTATGGCT	206	240	754	754	1.311	10446	10449	10450	10453	10454	10457	10458	10459	10460	10461	
37	TTTATGGCT	6	18	754	754	0.328	10446	10449	10450	10453	10454	10457	10458	10459	10460	10461	
37	CTATGGCTC	254	209	754	754	1.325	10446	10449	10450	10453	10454	10457	10458	10459	10460	10461	10463
37	TTATGGCTC	6	18	754	754	0.328	10446	10449	10450	10453	10454	10457	10458	10459	10460	10461	10463
37	ACAAGCTAT	39	60	754	754	0.631	10449	10450	10453	10454	10457	10458	10459	10460	10461	10463	10464
38	A	714	731	754	754	0.562					10459						
38	G	40	23	754	754	1.781					10460	10461	10463	10464	10466		
38	AATTAAGTC	313	300	754	754	0.777	10469	10471	10473	10474	10475	10478	10479	10481	10482
38	CGACAGACT	37	20	754	754	1.604	10469	10471	10473	10474	10475	10478	10479	10481	10482
38	AATTGGATT	16	5	754	754	3.248	10469	10471	10473	10474	10475	10478	10479	10481	10482
38	A	569	607	754	754	0.745					10478				
38	G	185	147	754	754	1.343					10478				
38	A	422	373	754	754	1.208					10479				
38	G	332	381	754	754	0.770					10479				
38	GTC	332	378	754	754	0.783				10479	10481	10482			
38	ACT	43	23	754	754	1.022				10479	10481	10482			
38	GTCTT	316	371	754	754	0.745			10479	10481	10482	10483	10486		
38	ACTTT	43	23	754	754	1.922			10479	10481	10482	10483	10486	10487	
38	TCTTA	316	370	754	754	0.749			10481	10482	10483	10486	10487		
38	CTTTA	43	23	754	754	1.922			10481	10482	10483	10486	10487		
38	TCTGG	14	3	754	754	4.736			10482	10483	10486	10487	10489		
38	CTTAG	314	367	754	754	0.753			10482	10483	10486	10487	10489		
38	TTTAG	77	54	754	754	1.474			10482	10483	10486	10487	10489		
38	CTGGA	14	3	754	754	4.736				10483	10486	10487	10489		
38	TCTTAGGAG	305	349	754	754	0.788	10481	10482	10483	10486	10487	10489	10490	10492	10493
38	CTTTAGGAG	40	20	754	754	2.050	10481	10482	10483	10486	10487	10489	10490	10492	10493
38	TCTGGAAAG	14	3	754	754	4.736	10481	10482	10483	10486	10487	10489	10490	10492	10493
38	CTTAGGAGA	305	348	754	754	0.793	10482	10483	10486	10487	10489	10490	10492	10493	10495
38	TTTAGGAGA	74	51	754	754	1.500	10482	10483	10486	10487	10489	10490	10492	10493	10495
38	CTGGAAAGG	14	3	754	754	4.736	10482	10483	10486	10487	10489	10490	10492	10493	10495
38	AAA	330	292	754	754	1.231				10489	10490	10492			
38	AAG	317	274	754	754	1.271				10490	10492	10493			
38	AGG	317	276	754	754	1.256				10492	10493	10495			
39	CAA	123	170	754	754	0.670				10496	10497	10498			
39	AAG	125	171	754	754	0.678				10497	10498	10500			
39	AGT	101	130	754	754	0.742				10498	10500	10501			
39	AGTGT	6	16	754	754	0.370			10498	10500	10501	10502	10504		
39	GGAAC	20	9	754	754	2.250			10498	10500	10501	10502	10504		
39	GTACA	173	142	754	754	1.283			10500	10501	10502	10504	10505		
39	GTATG	51	83	754	754	0.586			10500	10501	10502	10504	10505		
39	GAACA	24	12	754	754	2.033			10500	10501	10502	10504	10505		
39	ACA	203	217	754	754	1.320				10501	10502	10504	10505		
39	ATG	52	88	754	754	0.561				10502	10504	10505			
39	GTATGCTTA	9	21	754	754	0.422	10500	10501	10502	10504	10505	10507	10508	10510	10512
39	TATGCTTAT	7	20	754	754	0.344	10501	10502	10504	10505	10507	10508	10510	10512	10513
39	TATGTTCAG	20	39	754	754	0.500	10501	10502	10504	10505	10507	10508	10510	10512	10513
39	ACTCA	23	11	754	754	2.125			10504	10505	10507	10508	10510	10512	
39	TATTCAGAG	28	15	754	754	1.900	10504	10505	10507	10508	10510	10512	10513	10514	10515
39	CATTCAGAC	24	42	754	754	0.557	10504	10505	10507	10508	10510	10512	10513	10514	10515
39	ATTCAGAGT	151	120	754	754	1.323	10505	10507	10508	10510	10512	10513	10514	10515	10517
39	ACTCAGAGT	9	1	754	754	9.097	10505	10507	10508	10510	10512	10513	10514	10515	10517
39	ATTCAGACT	19	36	754	754	0.516	10505	10507	10508	10510	10512	10513	10514	10515	10517
39	TGCATACTA	92	119	754	754	0.742	10507	10508	10510	10512	10513	10514	10515	10517	10518

30	TTCAGACTA	24	52	754	754	0.444	10507	10508	10510	10512	10513	10514	10515	10517	10518	
30	CTCAGAGTA	11	2	754	754	5.567	10507	10508	10510	10512	10513	10514	10515	10517	10518	
30	TTATACTGT	18	32	754	754	0.552	10508	10510	10512	10513	10514	10515	10517	10518	10520	
30	GCATACTAT	71	105	754	754	0.643	10508	10510	10512	10513	10514	10515	10517	10518	10520	
30	TCAGACTAC	20	41	754	754	0.474	10508	10510	10512	10513	10514	10515	10517	10518	10520	
30	ATAGTAT	12	25	754	754	0.472		10512	10513	10514	10515	10517	10518	10520		
30	ATACTAT	81	117	754	754	0.655		10512	10513	10514	10515	10517	10518	10520		
30	AGACTAC	22	42	754	754	0.509		10512	10513	10514	10515	10517	10518	10520		
30	ATAGTATCA	10	23	754	754	0.427	10512	10513	10514	10515	10517	10518	10520	10522	10523	
30	ATACTATCA	77	112	754	754	0.652	10512	10513	10514	10515	10517	10518	10520	10522	10523	
30	AGACTACTG	22	41	754	754	0.523	10512	10513	10514	10515	10517	10518	10520	10522	10523	
30	TAGTATCAT	10	23	754	754	0.427	10513	10514	10515	10517	10518	10520	10522	10523	10524	
30	TACTATCAT	81	120	754	754	0.630	10513	10514	10515	10517	10518	10520	10522	10523	10524	
30	GACTACTGC	13	26	754	754	0.455	10513	10514	10515	10517	10518	10520	10522	10523	10524	
30	TATCA	120	174	754	754	0.688			10515	10517	10518	10520	10522	10523		
30	TGCTG	30	13	754	754	2.302			10517	10517	10518	10520	10522	10523		
30	GTATCATGT	9	22	754	754	0.402	10515	10517	10518	10518	10520	10522	10523	10524	10525	10526
30	CTATCATGT	22	48	754	754	0.442	10515	10517	10518	10518	10520	10522	10523	10524	10525	10526
30	GTACTGTGG	38	22	754	754	1.706	10515	10517	10518	10518	10520	10522	10523	10524	10525	10526
30	TATCATGTG	27	57	754	754	0.454	10517	10518	10518	10520	10522	10522	10523	10524	10525	10526
30	TGCTGCGGA	23	10	754	754	2.341	10517	10518	10518	10520	10520	10522	10523	10524	10525	10526
30	TGTTGTGGA	90	65	754	754	1.437	10517	10518	10518	10520	10520	10522	10523	10524	10525	10526
30	TATCATGTA	4	13	754	754	0.304	10517	10518	10518	10520	10520	10522	10523	10524	10525	10526
30	ATCATGTGC	27	57	754	754	0.454	10518	10520	10522	10522	10523	10523	10524	10525	10526	10527
30	GCTGCGGAT	23	10	754	754	2.341	10518	10520	10522	10522	10523	10523	10524	10525	10526	10527
30	GTTGTGGAT	35	19	754	754	1.883	10518	10520	10522	10522	10523	10523	10524	10525	10526	10527
30	ATGTG	35	65	754	754	0.516			10522	10523	10524	10524	10525	10526	10527	
30	GTGGA	166	126	754	754	1.407			10523		10525	10525	10526	10527		
30	GGA	481	428	754	754	1.342					10526	10526	10527			
30	GTG	66	106	754	754	0.586						10527				
30	A	686	640	754	754	1.707										
30	G	68	114	754	754	0.556										
30	TGCGA	64	105	754	754	0.573				10526	10527	10529	10530	10531		
30	GACAC	28	47	754	754	0.580				10526	10527	10529	10530	10531		
30	GCGAC	64	106	754	754	0.567				10527	10529	10530	10531	10532		
30	ACACC	28	47	754	754	0.580				10527	10529	10530	10531	10532		
30	CGACT	171	222	754	754	0.703				10529	10530	10530	10531	10532	10533	
30	CACCG	29	47	754	754	0.602				10529	10530	10530	10531	10532	10533	
30	ACT	173	223	754	754	0.709						10531	10532	10533		
30	ACG	200	245	754	754	1.208						10531	10532	10533		
30	CCG	29	48	754	754	0.588							10532	10533		
30	G	577	530	754	754	1.378							10532			
30	T	177	224	754	754	0.726							10533			
39	ACTTGGG	165	211	752	752	0.721		10531	10532	10533			10534	10535	10536	10537
39	TTGGG	169	211	752	752	0.743			10533				10535	10536	10537	
39	GGG	172	219	754	754	0.722								10537		
39	A	580	524	754	754	1.463										
39	G	174	230	754	754	0.683										
39	AAA	380	332	754	754	1.347							10537			
39	GAA	87	110	754	754	0.571							10537			
39	GGGAAATGG	54	94	754	754	0.542	10535	10536	10537	10538	10539	10540	10541	10542	10543	
39	AAAACATGG	15	31	754	754	0.473	10535	10536	10537	10538	10539	10540	10541	10542	10543	
39	GGAAATGGA	56	95	754	754	0.557	10536	10537	10538	10539	10540	10541	10542	10543	10544	
39	AAACATGGT	30	13	754	754	2.302	10536	10537	10538	10539	10540	10541	10542	10543	10544	
39	GAAATGGAA	56	97	754	754	0.543	10537	10538	10539	10540	10541	10542	10543	10544	10546	
39	AACATGGTA	30	13	754	754	2.302	10537	10538	10539	10540	10541	10542	10543	10544	10546	10550
39	AAATGGAAC	38	68	754	754	0.535	10538	10539	10540	10541	10542	10543	10544	10546	10550	
39	ACATGGTAG	37	19	754	754	1.996	10538	10539	10540	10541	10542	10543	10544	10546	10550	
39	ATGGAAC	120	180	754	754	0.658		10540	10541	10542	10543	10544	10546	10550		
39	ATGGTAG	51	28	754	754	1.681		10540	10541	10542	10543	10544	10546	10550		
39	GGAAC	172	221	754	754	0.713			10542	10543	10544	10546	10550			
39	GGTAG	63	40	754	754	1.627						10546	10550			
39	AAC	180	231	754	754	0.710						10550				
39	C	473	516	754	754	0.776										
39	G	281	238	754	754	1.288										
40	C	483	424	754	754	1.387										
40	T	271	330	754	754	0.721										
40	GCCGG	398	335	754	754	1.398			10550	10551	10552	10554	10558			
40	GTTAA	143	202	754	754	0.640			10550	10551	10552	10554	10558			
40	CCGGC	393	330	754	754	1.333			10551	10552	10554	10558	10559			
40	TTAAC	143	202	754	754	0.640			10551	10552	10554	10558	10559			
40	G	603	529	754	754	1.567					10558	10558				
40	A	161	225	754	754	0.638					10558	10559	10570			
40	GCA	518	468	754	754	1.341					10559	10559	10570			
40	ACA	169	225	754	754	0.633					10559	10570	10571	10572		
40	ACAGA	155	216	754	754	0.645					10570	10571	10572	10573	10574	
40	ACAGAAC	148	203	754	754	0.663		10568			10571	10572	10573	10574	10575	
40	CAGAACA	107	216	754	754	0.709		10569			10572	10573	10574	10575		
40	TGGAAAG	20	15	754	754	1.971		10569			10572	10573	10574	10575		
40	CAGAAAA	3	13	754	754	0.228		10569			10573	10574				
40	AAC	174	221	754	754	0.724					10574					
40	A	579	532	754	754	1.381					10574					
40	C	175	222	754	754	0.724					10575					
40	A	549	583	754	754	0.780					10575					
40	G	205	171	754	754	1.273					10576	10577				
40	AGT	172	224	754	754	0.699				10575	10585	10587	10588			
41	GTCCC	89	124	754	754	0.680			10584	10585	10586	10587				
41	CCC	90	124	754	754	0.689				10586		10588				
41	T	604	630	754	754	1.452										
41	C	90	124	754	754	0.689				10588	10588	10589	10590			
41	CTC	90	124	754	754	0.689			10588	10588	10589	10590	10591	10592		
41	CTCCG	89	124	754	754	0.680				10589	10590	10594				
42	A	240	199	754	754	1.351				10590	10594	10595	10596			
42	G	508	555	754	754	0.740				10594	10595	10596				
42	AAG	240	199	754	754	1.351				10595	10596	10597	10598			
42	GGGTGCAAG	5	14	754	754	0.353	10594	10595	10596	10597	10598	10601	10603	10605	10607	
42	GGG	25	41	754	754	0.596				10596	10597	10598	10601	10603	10605	
42	GGGGAGGAG	14	29	754	754	0.473	10601	10603	10605	10597	10598	10601	10603	10605		
42	AGA	338	297	754	754	1.250				10598	10601	10603	10605			
42	T	343	304	754	754	1.235				10601	10603	10605				
42	G	411	450	754	754	0.800				10603	10605					
42	GTA	97	127	754	754	0.729				10605						
43	TTTCT	5	17	754	754	0.289										
44	T	630	591	754	754	1.401										
44	C	124	163	754	754	0.714										
44	CGC	38	59	754	754	0.625										
44	CGA	49	71	754	754	0.669										
44	ACGAGGA	27	50	754	754	0.523										
44	CCGCGAG	16	37	754	754	0.474										
44	ACGAGGAAG	10	37	754	754	0.501										
44	CCGCGAGAG	18	37	754	754	0.474										
44	GCGAGAGCG	117	150	754	754	0.740										
44	GAAAG	473	415	754	754	1.375										
44	AAG	475	415	754	754	1.301										
44	AAGCG	347	294	754	754	1.334										
44	AGCGC	331	286	754	754	1.280										
44	G	522	485	754	754	1.246										
44	C	232	269	754	754	0.801										
45	TTC	22	7	752	752	3.207										
45	CCG	100	62	752	752	1.826										
45	CTC	15	29	752	752	0.507										
46	C	521	571	752	752	0.715										
46	T	231	181	752	752	1.309										
46	CGG	215	282	752	752	0.667										
46	TTG	81	53	752	752	1.592										
46	GGT	123	164	752	752	0.701										
46	GAC	310	266	752	752	1.281										
46	GAT	7	19	752	752	0.362										

DEMANDE OU BREVET VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVET COMPREND PLUS D'UN TOME.

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JUMBO APPLICATIONS/PATENTS

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NOTE POUR LE TOME / VOLUME NOTE:

WE CLAIM:

1. A method of constructing a GeneMap for Crohn's disease comprising identifying at least two chromosomal loci associated with Crohn's disease, wherein said at least two chromosomal loci are selected from the genomic regions listed in Table 1.

2. The method of claim 1, wherein said population is a general population.

3. The method of claim 1, wherein said population is a founder population.

4. The method of claim 3, wherein said founder population is the population of Quebec.

5. The method of claim 1, wherein said at least two chromosomal regions are selected from the genes in Table 8, 9 or 10.

6. The method of claim 5, wherein said genes are used to construct gene networks based on the functional relationship of gene products interactions.

7. The method of claim 6, wherein the interactions are direct, indirect, or a combination thereof.

8. The method of claim 1, wherein the identifying comprises screening for the presence or absence of at least one single nucleotide polymorphisms (SNPs) from Tables 2, 3, 4, 5, 6 and 7, in at least one sample.

9. The method of claim 8, wherein the screening comprises the steps of: (a) obtaining biological samples from at least one disease patient; (b) screening for the presence or absence of at least one SNP or a group of SNPs from Tables 2, 3, 4, 5, 6 and 7 within each biological sample; and (c) evaluating whether said SNP or a group of SNPs shows a

statistically significant skewed genotype distribution between a group of patients compared to a control.

10. The method of claim 9, wherein said biological samples are fluid, serum, tissue or buccal swabs, saliva, mucus, urine, stools, spermatozoids, vaginal secretions, lymph, amiotic liquid, pleural liquid or tears.

11. The method of claim 9, wherein said patients and controls are from a human population.

12. The method of claim 11, wherein said patients and controls are recruited independently according to specific phenotypic criteria.

13. The method of claim 11, wherein said patients and controls are recruited in the form of trios comprising two parents and one child or one parent and two children.

14. The method of claim 8, wherein said screening is performed by a method selected from the group consisting of an allele-specific hybridization assay, an oligonucleotide ligation assay, an allele-specific elongation/ligation assay, an allele-specific amplification assay, a single-base extension assay, a molecular inversion probe assay, an invasive cleavage assay, a selective termination assay, RFLP, a sequencing assay, SSCP, a mismatch-cleaving assay, and denaturing gradient gel electrophoresis.

15. The method of claim 8, wherein said screening is carried out on each individual of a cohort at each of at least one SNP or a group of SNPs from Tables 2, 3, 4, 5, 6 and 7.

16. The method of claim 8, wherein said screening is carried out on pools of patients and pools of controls.

17. The method of claim 8, wherein the genotype distribution is compared one SNP at a time.

18. The method of claim 8, wherein the genotype distribution is compared with a group of markers from Tables 2, 3, 4, 5, 6 and 7 forming a haplotype.

19. The method of claim 17, wherein the genotype distribution is compared using the allelic frequencies between the patient pools and control pools.

20. The method of claim 1, wherein the GeneMap comprises all of the genes of Table 2, 3, 4, 5, 6 and 7.

21. A method of diagnosing Crohn's disease, the predisposition to Crohn's disease, or the progression or prognostication of Crohn's disease, comprising determining the amount and/or concentration of at least one polypeptide from Table 8, 9 or 10 and/or at least one nucleic acid encoding the polypeptide present in said biological sample

22. The method of claim 21, wherein the diagnosing comprises the steps of: (a) obtaining a biological sample of mammalian body fluid or tissue to be diagnosed; (b) comparing the amount and/or concentration of said polypeptide and/or nucleic acid encoding the polypeptide determine in said biological sample with the amount and/or concentration of said polypeptide and/or nucleic acid encoding the polypeptide as determined in a control sample, wherein the difference in the amount of said polypeptide and/or nucleic acid encoding the polypeptide is indicative of Crohn's disease or the stage of Crohn's disease.

23. The method of claim 21, wherein a nucleic acid probe is used for determining the amount and/or concentration of at least one nucleic acid sequence from Table 8, 9 or 10 encoding the polypeptide.

24. The method of claim 23, wherein said nucleic acid probe is selected from the nucleic acid sequences designated as SEQ ID NO: 1 to 16984.

25. The method of claim 23, wherein said nucleic acid probe comprises nucleic acids hybridizing to the nucleic acid sequences designated as SEQ ID NO: 1 to 16984, and/or fragments thereof.

26. The method of claim 23, wherein said nucleic acid probe comprises nucleic acids hybridizing to at least five nucleic acid sequences from Table 8, 9 or 10.

27. The method of claim 23, wherein said nucleic acid probe specifically hybridizes to at least 10 nucleic acid sequences from Table 8, 9 or 10.

28. The method of claim 23, wherein said nucleic acid probe specifically hybridizes to at least 20 nucleic acid sequences from Table 8, 9 or 10.

29. The method of claim 23, wherein said nucleic acid probe specifically hybridizes to at least 50 nucleic acid sequences from Table 8, 9 or 10.

30. The method of claim 23, wherein said nucleic acid probe specifically hybridizes to at least 100 nucleic acid sequences from Table 8, 9 or 10.

31. The method of claim 23, wherein said nucleic acid probe specifically hybridizes to at least 100 nucleic acid sequences from Table 8, 9 or 10.

32. The method of claim 23, wherein said nucleic acid probe is at least about 10 nucleotides in length.

33. The method of claim 23, wherein said nucleic acid probe is at least about 30 nucleotides in length.

34. The method of claim 23, wherein said nucleic acid probe is at least about 50 nucleotides in length.

35. The method of claim 23, wherein a PCR technique is used for determining the amount and/or concentration of at least one nucleic acid from Table 8, 9 or 10.

36. The method of claim 21, wherein a specific antibody is used for determining the amount and/or concentration of at least one polypeptide from Table 8, 9 or 10.

37. The method of claim 36 wherein said antibody is selected from the group comprising polyclonal antiserum, polyclonal antibody, monoclonal antibody, antibody fragments, single chain antibodies and diabodies.

38. The method of claim 21, wherein the amounts and/or concentrations of at least five polypeptides or nucleic acids are determined.

39. A method of detecting susceptibility to Crohn's disease comprising detecting at least one mutation or polymorphism in the nucleic acid molecule selected from Table 8, 9 or 10 in a patient.

40. The method of claim 39, wherein said method comprises hybridizing a probe to said patient's sample of DNA or RNA under stringent conditions which allow hybridization of said probe to nucleic acid comprising said mutation or polymorphism, wherein the presence of a hybridization signal indicates the presence of said mutation or polymorphism in at least one gene from Table 8, 9 or 10.

41. The method of claim 39, wherein the patient's DNA or RNA has been amplified and said amplified DNA or RNA is hybridized.

42. The method of claim 39, wherein said method comprises using a single-stranded conformation polymorphism technique to assay for said mutation.

43. The method of claim 39, wherein said method comprises sequencing at least one gene from Table 8, 9 or 10 in a sample of RNA or DNA from a patient.

44. The method of claim 39, wherein said method comprises determining the sequence of at least one gene from Table 8, 9 or 10 by preparing cDNA from RNA taken from said patient and sequencing said cDNA to determine the presence or absence of a mutation.

45. The method of claim 39, wherein said method comprises performing an RNAse assay.

46. The method of claim 39, wherein said probe is attached to a microarray or a bead.

47. The method of claim 39, wherein said probes are oligonucleotides.

48. The method of claim 40, wherein said sample is selected from the group consisting of blood, normal tissue and tumor tissue.

49. The method of claim 39, wherein the mutation is selected from the group consisting of at least one of the SNPs from Tables 2, 3, 4, 5, 6 and 7, alone or in combination.

50. The method of claim 21, further comprising comparing the level of expression or activity of a polypeptide of Table 8, 9 or 10 in a test sample from a patient with the level of expression or activity of the same polypeptide in a control sample wherein a difference in the level of expression or activity between the test sample and control sample is indicative of Crohn's disease.

51. A method of treatment of Crohn's disease in a mammal in need thereof, comprising the steps of: performing steps a) to c) according to claim 22; and treating the mammal in need of said treatment; wherein said medical treatment is based on the stage of the disease.

52. A method of diagnosing susceptibility to Crohn's disease in an individual, comprising screening for an at-risk haplotype of at least one gene or gene region from Table 8, 9 or 10, that is more frequently present in an individual susceptible to Crohn's disease compared to a control individual, wherein the presence of the at-risk haplotype is indicative of a susceptibility to Crohn's disease.

53. The method of claim 52 wherein the at-risk haplotype is indicative of increased risk for Crohn's disease.

54. The method of claim 53, wherein the risk is increased at least about 20%.

55. The method of claim 52, wherein the at-risk haplotype is characterized by the presence of at least one single nucleotide polymorphism from Tables 2, 3, 4, 5, 6 and 7.

56. The method of claim 52, wherein screening for the presence of an at-risk haplotype in at least one gene from Table 8, 9 or 10, comprises enzymatic amplification of nucleic acid from said individual or amplification using universal oligos on elongation/ligation products.

57. The method of claim 56, wherein the nucleic acid is DNA.

58. The method of claim 57, wherein the DNA is human DNA.

59. The method of claim 52, wherein screening for the presence of an at-risk haplotype in at least one gene from Table 8, 9 or 10 comprises: (a) obtaining material containing nucleic acid from the individual; (b) amplifying said nucleic acid; and (c) determining the presence or absence of an at-risk haplotype in said amplified nucleic acid.

60. The method of claim 59, wherein determining the presence of an at-risk haplotype is performed by electrophoretic analysis.

61. The method of claim 59, wherein determining the presence of an at-risk haplotype is performed by restriction length polymorphism analysis.

62. The method of claim 59, wherein determining the presence of an at-risk haplotype is performed by sequence analysis.

63. The method of claim 59, wherein determining the presence of an at-risk haplotype is performed by hybridization analysis.

64. A method of diagnosing a susceptibility to Crohn's disease, comprising detecting an alteration in the expression or composition of a polypeptide encoded by at least one gene from Table 8, 9 or 10 in a test sample, in comparison with the expression or composition of a polypeptide encoded by said gene in a control sample, wherein the presence of an alteration in expression or composition of the polypeptide in the test sample is indicative of a susceptibility to Crohn's Disease.

65. The method of claim 64, wherein the alteration in the expression or composition of a polypeptide encoded by said gene comprises expression of a splicing variant polypeptide in a test sample that differs from a splicing variant polypeptide expressed in a control sample.

66. A drug screening assay comprising: a)administering a test compound to an animal having Crohn's disease, or a cell population isolated therefrom; and (b) comparing the level of gene expression of at least one gene from Table 8, 9 or 10 in the presence of the test compound with the level of said gene expression in normal cells; wherein test compounds which provide the level of expression of one or more genes from Table 8, 9 or 10 similar to that of the normal cells are candidates for drugs to treat Crohn's disease.

67. A pharmaceutical preparation for treating an animal having Crohn's disease comprising a compound identified by the assay of claim 66 and a pharmaceutically acceptable excipient.

68. A method for treating an animal having Crohn's disease comprising administering a compound identified by the assay of claim 66.

69. A method for predicting the efficacy of a drug for treating Crohn's disease in a human patient, comprising: (a) obtaining a sample of cells from the patient; (b) obtaining a gene expression profile from the sample in the absence and presence of the drug ; the gene expression profile comprising one or more genes from Table 8, 9 or 10; and (c) comparing the gene expression profile of the sample with a reference gene expression profile, wherein similarity between the sample expression profile and the reference expression profile predicts the efficacy of the drug for treating Crohn's disease in the patient.

70. The method of claim 69, further comprising exposing the sample to the drug for treating Crohn's disease prior to obtaining the gene expression profile of the sample.

71. The method of claim 69, wherein the sample of cells is derived from a tissue selected from the group consisting of: the jujenum, ileum, mucosa, submucosa, cecum, inner and outer intestinal coatings, muscle and nervous tissue.

72. The method of claim 71, wherein the cells are selected from the group consisting of: smooth muscle cell, neutrophil, dentric cell, T cell, mast cell, CD4+ lymphocyte, monocyte, macrophage, dendritic cell, synovial cell, glial cell, villous intestinal cell, neutrophilic granulocyte, eosinophilic granulocyte, keranocyte, lamina propria lymphocyte, intraephitelial lymphocyte and epithelial cell.

73. The method of claim 69, wherein the sample is obtained via small bowel or colon biopsy.

74. The method of claim 69, wherein the gene expression profile comprises expression values for all of the genes listed in Table 8, 9 or 10.

75. The method of claim 74, wherein the gene expression profile of the sample is obtained by detecting the protein products of said genes.

76. The method of claim 69, wherein the gene expression profile of the sample is obtained using a hybridization assay to oligonucleotides contained in a microarray.

77. The method of claim 76, wherein the oligonucleotides comprises nucleic acid molecules at least 95% identical to the gene sequences from Tables 8, 9 and 10.

78. The method of claim 69, wherein the reference expression profile is that of cells derived from patients that do not have Crohn's disease.

79. The method of claim 69, wherein the drug is selected from the group consisting of symptom relievers and anti-inflammatory drugs for an inflammatory disease condition.

80. The method of claim 69, wherein said patient's sample of DNA has been amplified or cloned.

81. A method for predicting the efficacy of a drug for treating Crohn's disease in a human patient, comprising: a) obtaining a sample of cells from the patient; b) obtaining a set of genotypes from the sample, wherein the set of genotypes comprises genotypes of one or more polymorphic loci from Tables 2, 3, 4, 5, 6, 7, 8, 9 and 10; and c) comparing the set of genotypes of the sample with a set of genotypes associated with efficacy of the drug, wherein similarity between the set of genotypes of the sample and the set of genotypes associated with efficacy of the drug predicts the efficacy of the drug for treating Crohn's disease in the patient.

82. The method of claim 81, wherein the sample of cells is derived from a tissue selected from the group consisting of: the scalp, GI track, muscle, sebaceous gland, nerve, blood, dermis, epidermis and other

skin cells, cutaneous surfaces, intertrigious areas, genitalia, vessels and endothelium.

83. The method of claim 82, wherein the cells are selected from the group consisting of: melanocytes, hair follicle cells, muscle cells, nerve cells, keratinocytes, monocytes, neutrophils, langerhans cells, CD4+ and CD8+ T cells and lymphocytes.

84. The method of claim 81, wherein the sample is obtained via biopsy.

85. The method of claim 81, wherein the set of genotypes from the sample comprises genotypes of at least two of the polymorphic loci listed in Tables 2, 3, 4, 5, 6, 7, 8, 9 and 10.

86. The method of claim 81 wherein the set of genotypes from the sample is obtained by hybridization to allele-specific oligonucleotides complementary to the polymorphic loci from Tables 2, 3, 4, 5, 6, 7, 8, 9 and 10, wherein said allele-specific oligonucleotides are contained on a microarray.

87. The method of claim 86, wherein the oligonucleotides comprise nucleic acid molecules at least 95% identical to SEQ ID from Tables 2, 3, 4, 5, 6, 7, 8, 9 and 10.

88. The method of claim 81 wherein the set of genotypes from the sample is obtained by sequencing said polymorphic loci in said sample.

89. The method of claim 81, wherein the drug is selected from the group consisting of symptom relievers and drugs for Crohn's disease.

90. A method of treating Crohn's disease in a patient in need thereof, comprising expressing *in vivo* at least one gene from Tables 8, 9, or 10 in an amount sufficient to treat the disease.

91. The method of claim 90, comprising: (a) administering to a patient a vector comprising a gene selected from Table 8, 9 or 10 that encodes

the protein; and (b) allowing said protein to be expressed from said gene in said patient in an amount sufficient to treat the disease.

92. The method of claim 91, wherein said vector is selected from the group consisting of an adenoviral vector, and a lentiviral vector.

93. The method of claim 91, wherein said vector is administered by a route selected from the group consisting of: topical administration, intraocular administration, parenteral administration, intranasal administration, intratracheal administration, intrabronchial administration and subcutaneous administration.

94. The method of claim 91, wherein said vector is a replication-defective viral vector.

95. The method of claim 91, wherein said gene encodes a human protein.

96. A method of treating Crohn's disease in a patient in need thereof, comprising administering an agent that regulates the expression, activity or physical state of at least one gene or its encoding RNA from Table 8, 9 or 10 in the patient.

97. The method of claim 96, wherein the encoded protein from said gene comprises an alteration.

98. The method of claim 96, wherein said gene comprises a mutation that modulates the expression of the encoded protein.

99. The method of claim 96, wherein said agent is selected from the group consisting of chemical compounds, oligonucleotides, peptides and antibodies.

100. The method of claim 99, wherein said agent is an antisense molecule or interfering RNA.

101. The method of claim 99, wherein said agent is an expression modulator.

102. The method of claim 101, wherein said modulator is an activator.

103. The method of claim 101, wherein said modulator is a repressor.

104. The method of claim 96, wherein said gene comprises a mutation that modifies at least one property or function of the encoded protein.

105. The method of claim 96, wherein the agent modulates at least one property or function of said gene.

106. A method of treating Crohn's disease in a patient in need thereof, comprising administering an agent that regulates the expression, activity or physical state of at least one polypeptide encoded by a gene from Table 8, 9 or 10 in the patient.

107. The method of claim 106, wherein the encoded protein from said gene comprises an alteration, wherein said alteration is encoded by a polymorphic locus in said gene.

108. The method of claim 106, wherein said gene comprises an associated allele, a particular allele of a polymorphic locus, or the like that modulates the expression of the encoded protein.

109. The method of claim 106, wherein said agent is selected from the group consisting of chemical compounds, oligonucleotides, peptides and antibodies.

110. The method of claim 106, wherein said agent is an antisense molecule or interfering RNA.

111. The method of claim 106, wherein said agent is an expression modulator.

112. The method of claim 111, wherein said modulator is an activator.

113. The method of claim 111, wherein said modulator is a repressor.

114. The method of claim 106, wherein said gene comprises an associated allele, a particular allele of a polymorphic locus, or the like that modifies at least one property or function of the encoded protein.

115. A method for preventing the occurrence of Crohn's disease in an individual in need thereof, comprising regulating the level of at least one gene from Table 8, 9 or 10 compared to a control.

116. The method of claim 115, wherein said level is regulated by regulating expression of at least one gene from Table 8, 9 or 10 by a binding agent, a receptor to said gene, a peptidomimetic, a fusion protein, a prodrug, an antibody or a ribozyme.

117. The method of claim 115, wherein said level is controlled by genetically altering the expression level of at least one gene from Table 8, 9 or 10, whereby the regulated level of said gene mimics the level in a healthy individual.

118. A method for identifying a gene that regulates drug response in Crohn's disease, comprising: (a) obtaining a gene expression profile for at least one gene from Table 8, 9 or 10 in a resident tissue cell induced for a pro-inflammatory like state in the presence of the candidate drug; and (b) comparing the expression profile of said gene to a reference expression profile for said gene in a cell induced for the pro-inflammatory like state in the absence of the candidate drug, wherein genes whose expression relative to the reference expression profile is altered by the drug may identifies the gene as a gene that regulates drug response in Crohn's disease.

119. A method for identifying an agent that alters the level of activity or expression of a polypeptide of Table 8, 9 or 10 for use in diagnostics, prognostics, prevention, treatment, or study of Crohn's disease, comprising: (a) contacting a cell, cell lysate, or the polypeptide, with an agent to be tested; (b) assessing a level of activity or expression of the polypeptide; and (c) comparing the level of activity or expression of the

polypeptide with a control sample in an absence of the agent, wherein if the level of activity or expression of the polypeptide in the presence of the agent differs by an amount that is statistically significant from the level in the absence of the agent then the agent alters the activity or expression of the polypeptide.

120. A kit for diagnosing susceptibility to Crohn's disease in an individual comprising: primers for nucleic acid amplification of a region of at least one gene from Table 8, 9 or 10.

121. The kit of claim 120, wherein the primers comprise a segment of nucleic acids of length suitable for nucleic acid amplification of a target sequence, selected from the group consisting of: single nucleotide polymorphism from Tables 2, 3, 4, 5, 6 and 7, and combinations thereof.

122. A kit for assessing a patient's risk of having or developing Crohn's disease, comprising: (a) detection means for detecting the differential expression, relative to a normal cell, of at least one gene shown in Table 4 or the gene product thereof; and (b) instructions for correlating the differential expression of said gene or gene product with a patient's risk of having or developing Crohn's disease.

123. The kit of claim 122, wherein the detection means includes nucleic acid probes for detecting the level of mRNA of said genes.

124. A kit for assessing a patients risk of having or developing Crohn's disease, comprising: (a) at least one means for amplifying or detecting a sequence of at least one gene in Table 8, 9 or 10, wherein the detection means includes nucleic acid probes or primers for detecting the presence or absence of mutations or changes to at least one sequence of Table 8, 9 or 10.

125. The kit of claim 124, wherein the detection means includes an immunoassay for detecting the level of at least one gene product from Table 8, 9 or 10.

126. A kit for assessing a patient's risk of having or developing Crohn's disease, comprising: a) a detection means for detecting the genotype of at least one polymorphic locus shown in Tables 2, 3, 4, 5, 6, 7, 8, 9 or 10; and b) instructions for correlating the genotype of said at least one polymorphic locus with a patient's risk of having or developing Crohn's disease.

127. The kit of claim 126, wherein the detection means includes nucleic acid probes for detecting the genotype of said at least one polymorphic locus.

128. A diagnostic composition for diagnosing or detecting susceptibility to Crohn's disease comprising a set of oligonucleotide probes that specifically hybridizes to at least two geneonic regions listed in Table 1.

129. The composition of claim 128, wherein said set of oligonucleotide probes specifically hybridize to sequences of at least two genes selected from the genes in Table 8, 9 or 10.

130. The composition of claim 128, wherein the oligonucleotide probes are detectably labeled with an agent selected from the group consisting of a fluorescent dye, a radioisotope, a bioluminescent compound, a chemiluminescent compound, a fluorescent compound, a metal chelate and an enzyme.

131. The composition of claim 130, wherein the oligonucleotide probes are labeled with different fluorescent compounds.

132. The composition of claim 128, wherein the set of oligonucleotide probes hybridizes in situ.

133. The composition of claim 128, wherein the set of oligonucleotide probes hybridizes at a gradually changing temperature.

134. The composition of claim 128, wherein the oligonucleotide probes are between 2 to 100 bases.

135. The composition of claim 128, wherein the oligonucleotide probes are between 3 to 50 bases.

136. The composition of claim 128, wherein the oligonucleotide probes are between 8 to 25 bases.

137. A method of assessing a patient's risk of having or developing Crohn's disease, comprising: (a) determining the level of expression of at least one gene from Table 8, 9 or 10 or gene products thereof, and comparing the level of expression to a normal cell; and (b) assessing a patient's risk of having or developing Crohn's disease by determining the correlation between the differential expression of said genes or gene products with known changes in expression of said genes measured in at least one patent suffering from Crohn's disease.

138. A method of assessing a patient's risk of having or developing Crohn's disease, comprising (a) determining a genotype for at least one polymorphic locus from Tables 2, 3, 4, 5, 6, 7, 8, 9 or 10 in a patient; (b) comparing said genotype of (a) to a genotype for at least one polymorphic locus from Tables 2, 3, 4, 5, 6, 7, 8, 9or 10 that is associated with Crohn's disease; and (c) assessing the patient's risk of having or developing Crohn's disease, wherein said patient has a higher risk of having or developing Crohn's disease if the genotype for at least one polymorphic locus from Tables 2, 3, 4, 5, 6, 7, 8, 9 or 10 in said patient is the same as said genotype for at least one polymorphic locus from Tables 2, 3, 4, 5, 6, 7, 8, 9 or 10 that is associated with Crohn's disease.

139. A method for assaying the presence of a nucleic acid associated with resistance or susceptibility to Crohn's disease in a sample, comprising: contacting said sample with a nucleic acid recited in claim 5 under stringent hybridization conditions; and detecting a presence of a hybridization complex.

140. A method for assaying the presence or amount of a polypeptide encoded by a gene of Tables 8, 9 or 10 for use in diagnostics, prognostics, prevention, treatment, or study of Crohn's disease, comprising: contacting a sample with an antibody that specifically binds to a gene of Tables 8, 9 or 10 under conditions appropriate for binding; and assessing the sample for the presence or amount of binding of the antibody to the polypeptide.