

DNA METHYLATION STATUS AS A BIOMARKER OF ALCOHOL USE AND ABSTINENCE

CROSS REFERENCE TO RELATED APPLICATIONS

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2014. This disclosure of the prior application is considered part of (and is incorporated by
reference in) the disclosure of this application.

FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

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invention.

BACKGROUND

Alcoholism has a profound socio-economic and personal impact on tens of millions
of individuals throughout the world. Unfortunately, the ability make the diagnosis is often
hindered by the reliance on self-reporting, while the ability to monitor treatment response is
challenged by the absence of robust and reliable biomarkers.

SUMMARY

This disclosure provides for methods and materials that can be used to determine
whether or not an individual is using alcohol, and also to determine whether or not the
individual has stopped using alcohol.

In one aspect, a method of determining whether or not an individual uses alcohol is
provided. Such a method typically includes determining the methylation status of at least
one CpG dinucleotide in a biological sample from the individual; and correlating the
methylation status of the at least one CpG dinucleotide to determine whether or not the
individual uses alcohol.

In some embodiments, the at least one CpG dinucleotide comprises position
71389896 of chromosome 10. For example, demethylation at position 71389896 of

chromosome 10 is indicative of previous or current alcohol use; and remethylation at position 71389896 of chromosome 10 is indicative of less or no alcohol use (e.g., abstinence).

In some embodiments, the at least one CpG dinucleotide comprises position 54677008 of chromosome 12. For example, demethylation at position 54677008 of chromosome 12 is indicative of previous or current alcohol use; and remethylation at position 54677008 of chromosome 12 is indicative of less or no alcohol use (e.g., abstinence).

In some embodiments, the at least one CpG dinucleotide comprises position 75262522 of chromosome 8. For example, demethylation at position 75262522 of chromosome 8 is indicative of previous or current alcohol use; and remethylation at position 75262522 of chromosome 8 is indicative of less or no alcohol use (e.g., abstinence).

In some embodiments, the at least one CpG dinucleotide comprises position 92137791 of chromosome 9. For example, demethylation at position 92137791 of chromosome 9 is indicative of previous or current alcohol use; and remethylation at position 92137791 of chromosome 9 is indicative of less or no alcohol use (e.g., abstinence).

In some embodiments, the determining step includes contacting DNA in the biological sample with bisulfite under alkaline conditions to produce bisulfite-treated DNA; optionally, amplifying the bisulfite-treated DNA to produce amplified bisulfite-treated DNA; contacting the bisulfite-treated DNA or the amplified bisulfite-treated DNA with at least one oligonucleotide that is complementary to a sequence comprising the at least one CpG dinucleotide; and detecting the methylation status of the at least one CpG dinucleotide.

In some embodiments, the at least one oligonucleotide detects the CpG dinucleotide in the bisulfite-treated DNA in the unmethylated state. In some embodiments, the at least one oligonucleotide detects the CpG dinucleotide in the bisulfite-treated DNA in the methylated state. Representative biological samples include, without limitation, peripheral blood, lymphocytes, urine, saliva, and buccal cells. In some embodiments, the methylation status of the at least one CpG dinucleotide is determined using bi-sulfite treated DNA. In some embodiments, such a method further includes obtaining self-report data from the individual regarding whether or not the individual is user of alcohol.

In another aspect, a computer implemented method for determining whether or not an individual uses alcohol is provided. Such a method typically includes obtaining measured data associated with the user, the measured data comprising one or more measured CpG

methylation status; generating a predictive score based on the obtained measured data; and providing a likelihood of alcohol use by the user based on the predictive score.

In some embodiments, such a method further includes determining the CpG methylation status for the user, wherein a change in methylation status is an indicator of alcohol use. In some embodiments, such a method further includes outputting a predicted level of alcohol use based on the predictive score.

In one aspect, a kit for determining the methylation status of at least one CpG dinucleotide is provided. Such a kit typically includes at least one first nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence that includes at least one CpG dinucleotide, where the at least one first nucleic acid primer detects the methylated CpG dinucleotide. In some embodiments, the kit further includes at least one second nucleic acid primer at least 8 nucleotides in length that is complementary to a bisulfite-converted nucleic acid sequence that includes the at least one CpG dinucleotide, where the at least one second nucleic acid primer detects the unmethylated CpG dinucleotide.

In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes a methylated CpG dinucleotide at position 71389896 of chromosome 10. In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes an unmethylated CpG dinucleotide at position 71389896 of chromosome 10. In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes a methylated CpG dinucleotide at position 54677008 of chromosome 12. In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes an unmethylated CpG dinucleotide at position 54677008 of chromosome 12. In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes a methylated CpG dinucleotide at position 75262522 of chromosome 8. In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes an unmethylated CpG dinucleotide at position 75262522 of chromosome 8. In some embodiments, the first nucleic acid primer is complementary to a bisulfite-converted sequence that includes a methylated CpG dinucleotide at position 92137791 of chromosome 9. In some embodiments, the first nucleic acid primer is

complementary to a bisulfite-converted sequence that includes an unmethylated CpG dinucleotide at position 92137791 of chromosome 9.

In some embodiments, a kit as described herein can include at least a third nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence upstream of the CpG dinucleotide. In some embodiments, a kit as described herein can include at least a fourth nucleic acid primer at least 8 nucleotides in length that is complementary to a nucleic acid sequence downstream of the CpG dinucleotide. In some embodiments, the at least third nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence. In some embodiments, the at least fourth nucleic acid primer is complementary to a bisulfite-converted nucleic acid sequence.

In some embodiments, the at least one first nucleic acid primer, the at least one second nucleic acid primer, the at least one third nucleic acid primer, and/or the at least one fourth nucleic acid primer includes one or more nucleotide analogs. In some embodiments, the at least one first nucleic acid primer, the at least one second nucleic acid primer, the at least one third nucleic acid primer, and/or the at least one fourth nucleic acid primer includes one or more synthetic or non-natural nucleotides.

In some embodiments, the kit further includes a solid substrate to which the at least one first nucleic acid primer is bound. Representative solid substrates include, without limitation, polymers, glass, semiconductors, papers, metals, gels and/or hydrogels. In some embodiments, the solid substrate is a microarray or microfluidics card. In some embodiments, the kit further includes a detectable label. In some embodiments, such a kit further includes instructions for correlating a change in methylation status at one or more CpG positions with alcohol use.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the methods and compositions of matter belong. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the methods and compositions of matter, suitable methods and materials are described below. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. All publications,

patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety.

DESCRIPTION OF DRAWINGS

Figure 1 is a graph showing Quantile-Quantile (QQ) plots of the comparison between the methylation status of DNA from the 32 case subjects (at time T1) and the methylation status of DNA from the 33 abstinent controls.

Figure 2 is a graph showing QQ plots of the comparison between the methylation status of DNA from 25 case subjects at time T1 and the methylation status of DNA from the same 25 case subjects at time T2.

DETAILED DESCRIPTION

Using a genome wide approach, this disclosure shows that, as compared to abstinent controls, alcohol use is associated with widespread changes in DNA methylation. This disclosure also shows that the changes in DNA methylation have a tendency to revert as a function of abstinence. Thus, DNA methylation can be used clinically to assess alcohol use status and/or to monitor alcohol treatment response.

Methylation of Nucleic Acids and Determining the Methylation Status of Nucleic Acids

CpG islands are stretches of DNA in which the frequency of the CpG sequence is higher than other regions. The “p” in the term CpG designates the phosphodiester bond that binds the cysteine (“C”) nucleotide and the guanine (“G”) nucleotide. CpG islands are often located around promoters and are often involved in regulating the expression of a gene (e.g., housekeeping genes). Generally, CpG islands are not methylated when a sequence is expressed, and methylated to suppress expression (or “inactivate” the gene).

The methylation status of one or more CpG dinucleotides in genomic DNA or in a particular nucleic acid sequence (e.g., a CpG island) can be determined using any number of biological samples, such as blood, urine (e.g., cells from the bladder and/or urethra contained within the urine), saliva, or buccal cells. In certain embodiments, a particular cell type, e.g., lymphocytes, basophils, or monocytes, can be obtained (e.g., from a blood sample) and the DNA evaluated for its methylation status.

The methylation status of genomic DNA, of a CpG island, or of one or more specific CpG dinucleotides can be determined by the skilled artisan using any number of methods. The most common method for evaluating the methylation status of DNA begins with a bisulfite-based reaction on the DNA (see, for example, Frommer et al., 1992, *PNAS USA*, 89(5):1827-31). Commercial kits are available for bisulfite-modifying DNA. See, for example, EpiTect Bisulfite or EpiTect Plus Bisulfite Kits (Qiagen).

Following bisulfite modification, the nucleic acid can be amplified. Since treating DNA with bisulfite deaminates unmethylated cytosine nucleotides to uracil, and since uracil pairs with adenosine, thymidines are incorporated into DNA strands in positions of unmethylated cytosine nucleotides during subsequent PCR amplifications.

In some embodiments, the methylation status of DNA can be determined using one or more nucleic acid-based methods. For example, an amplification product of bisulfite-treated DNA can be cloned and directly sequenced using recombinant molecular biology techniques routine in the art. Software programs are available to assist in determining the original sequence, which includes the methylation status of one or more nucleotides, of a bisulfite-treated DNA (e.g., CpG Viewer (Carr et al., 2007, *Nucl. Acids Res.*, 35:e79)). Also for example, amplification products of bisulfite-treated DNA can be hybridized with one or more oligonucleotides that, for example, are specific for the methylated, bisulfite-treated DNA sequence, or specific for the unmethylated, bisulfite-treated DNA sequence.

In some embodiments, the methylation status of DNA can be determined using a non-nucleic acid-based method. A representative non-nucleic acid-based method relies upon sequence-specific cleavage of bisulfite-treated DNA followed by mass spectrometry (e.g., MALDI-TOF MS) to determine the methylation ratio (methyl CpG/total CpG) (see, for example, Ehrich et al., 2005, *PNAS USA*, 102:15785-90). Such a method is commercially available (e.g., MassARRAY Quantitative Methylation Analysis (Sequenom, San Diego, CA)).

Nucleic Acid Sequences in Which the Methylation Status is Associated with Alcohol Use

The methylation status of certain genomic DNA has been shown to be altered in individuals that use alcohol (relative to non-users). See, for example, Philibert et al. (2008, *Am. J. Med. Genet. B Neuropsychiatr. Genet.*, 147B:565-70); Philibert et al. (2008, *Am. J.*

Med. Genet. B Neuropsychiatr. Genet., 147B:543-9); Philibert et al. (2009, *Psychiatr. Genet.*, 19:91-8); Philibert et al. (2012, *Front Genet.*, 3:54); and also in U.S. Patent No. 8,637,652, each of which are incorporated herein by reference in its entirety.

The present disclosure describes additional changes in the methylation status of one or more CpG islands and/or particular CpG dinucleotides that are correlated with alcohol use (e.g., heavy alcohol use). See, for example, Table II, which shows the top 30 probes that were most-significantly associated with changes in the methylation status of alcohol users compared to non-drinkers; and Table III, which show the top 30 differentially regulated gene pathways between alcohol users and non-drinkers. Any one or more of the CpG dinucleotides in which methylation status has been associated with alcohol use can be used in the methods herein to determine the predictive value (e.g., representing the likelihood of alcohol use). It would be understood that, particularly for determining alcohol use, the more CpG dinucleotides (i.e., CpG dinucleotides in which methylation status has been associated with alcohol use) are evaluated, the more accurate the predictive value will be.

In addition, it would be appreciated that the methylation status of one or more neighboring CpG dinucleotides can be in linkage disequilibrium with the methylation status of a CpG dinucleotide having significance with alcohol use (see, for example, Philibert et al., 2009, *Am. J. Med. Genet. B. Neuropsychiatr. Genet.*, 153B:619-28) and, therefore, the methylation status of those neighboring CpG dinucleotides (e.g., about 200 nucleotides upstream and/or downstream of a CpG dinucleotide having significance with alcohol use (e.g., about 100 nucleotides upstream and/or downstream; about 50 nucleotides upstream and/or downstream; about 25 nucleotides upstream and/or downstream; about 20 nucleotides upstream and/or downstream; about 10 nucleotides upstream and/or downstream; or about 5 nucleotides upstream and/or downstream)) can be used in the methods described herein.

Further, it would be appreciated that, in some instances, the greater (or more significant) the changes in the methylation status, the greater the alcohol use. See, for example, Philibert et al., 2012, *Epigenetics*, 7:1-8.

Nucleic Acids and Methods Related Thereto

As used herein, nucleic acids can include DNA and RNA, and includes nucleic acids that contain one or more nucleotide analogs or backbone modifications. A nucleic acid can be single stranded or double stranded, which usually depends upon its intended use.

As used herein, an “isolated” nucleic acid molecule is a nucleic acid molecule that is free of sequences that naturally flank one or both ends of the nucleic acid in the genome of the organism from which the isolated nucleic acid molecule is derived (e.g., a cDNA or genomic DNA fragment produced by PCR or restriction endonuclease digestion). Such an isolated nucleic acid molecule is generally introduced into a vector (e.g., a cloning vector, or an expression vector) for convenience of manipulation or to generate a fusion nucleic acid molecule, discussed in more detail below. In addition, an isolated nucleic acid molecule can include an engineered nucleic acid molecule such as a recombinant or a synthetic nucleic acid molecule.

Nucleic acids can be isolated using techniques routine in the art. For example, nucleic acids can be isolated using any method including, without limitation, recombinant nucleic acid technology, and/or the polymerase chain reaction (PCR). General PCR techniques are described, for example in PCR Primer: A Laboratory Manual, Dieffenbach & Dveksler, Eds., Cold Spring Harbor Laboratory Press, 1995. Recombinant nucleic acid techniques include, for example, restriction enzyme digestion and ligation, which can be used to isolate a nucleic acid. Isolated nucleic acids also can be chemically synthesized, either as a single nucleic acid molecule or as a series of oligonucleotides.

A vector containing a nucleic acid (e.g., a nucleic acid that encodes a polypeptide) also is provided. Vectors, including expression vectors, are commercially available or can be produced by recombinant DNA techniques routine in the art. A vector containing a nucleic acid can have expression elements operably linked to such a nucleic acid, and further can include sequences such as those encoding a selectable marker (e.g., an antibiotic resistance gene). A vector containing a nucleic acid can encode a chimeric or fusion polypeptide (i.e., a polypeptide operatively linked to a heterologous polypeptide, which can be at either the N-terminus or C-terminus of the polypeptide). Representative heterologous polypeptides are those that can be used in purification of the encoded polypeptide (e.g., 6xHis tag, glutathione S-transferase (GST))

Expression elements include nucleic acid sequences that direct and regulate expression of nucleic acid coding sequences. One example of an expression element is a promoter sequence. Expression elements also can include introns, enhancer sequences, response elements, or inducible elements that modulate expression of a nucleic acid.

5 Expression elements can be of bacterial, yeast, insect, mammalian, or viral origin, and vectors can contain a combination of elements from different origins. As used herein, operably linked means that a promoter or other expression element(s) are positioned in a vector relative to a nucleic acid in such a way as to direct or regulate expression of the nucleic acid (e.g., in-frame). Many methods for introducing nucleic acids into host cells, 10 both *in vivo* and *in vitro*, are well known to those skilled in the art and include, without limitation, electroporation, calcium phosphate precipitation, polyethylene glycol (PEG) transformation, heat shock, lipofection, microinjection, and viral-mediated nucleic acid transfer.

Vectors as described herein can be introduced into a host cell. As used herein, “host 15 cell” refers to the particular cell into which the nucleic acid is introduced and also includes the progeny or potential progeny of such a cell. A host cell can be any prokaryotic or eukaryotic cell. For example, nucleic acids can be expressed in bacterial cells such as *E. coli*, or in insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

20 Oligonucleotides for amplification or hybridization can be designed using, for example, a computer program such as OLIGO (Molecular Biology Insights, Inc., Cascade, CO). Important features when designing oligonucleotides to be used as amplification primers include, but are not limited to, an appropriate size amplification product to facilitate detection (e.g., by electrophoresis), similar melting temperatures for the members of a pair of 25 primers, and the length of each primer (i.e., the primers need to be long enough to anneal with sequence-specificity and to initiate synthesis but not so long that fidelity is reduced during oligonucleotide synthesis). Typically, oligonucleotide primers are 15 to 30 (e.g., 16, 18, 20, 21, 22, 23, 24, or 25) nucleotides in length. Designing oligonucleotides to be used as hybridization probes can be performed in a manner similar to the design of amplification 30 primers. In some embodiments, hybridization probes can be designed to distinguish between

to targets that contain different sequences (e.g., a polymorphism or mutation, e.g., the methylated vs. non-methylated sequence in the bisulfite-treated DNA).

Hybridization between nucleic acids is discussed in detail in Sambrook et al. (1989, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; Sections 7.37-7.57, 9.47-9.57, 11.7-11.8, and 11.45-11.57).

Sambrook et al. discloses suitable Southern blot conditions for oligonucleotide probes less than about 100 nucleotides (Sections 11.45-11.46). The T_m between a sequence that is less than 100 nucleotides in length and a second sequence can be calculated using the formula provided in Section 11.46. Sambrook et al. additionally discloses Southern blot conditions for oligonucleotide probes greater than about 100 nucleotides (see Sections 9.47-9.54). The T_m between a sequence greater than 100 nucleotides in length and a second sequence can be calculated using the formula provided in Sections 9.50-9.51 of Sambrook et al.

The conditions under which membranes containing nucleic acids are prehybridized and hybridized, as well as the conditions under which membranes containing nucleic acids are washed to remove excess and non-specifically bound probe, can play a significant role in the stringency of the hybridization. Such hybridizations and washes can be performed, where appropriate, under moderate or high stringency conditions. For example, washing conditions can be made more stringent by decreasing the salt concentration in the wash solutions and/or by increasing the temperature at which the washes are performed. Simply by way of example, high stringency conditions typically include a wash of the membranes in 0.2X SSC at 65°C.

In addition, interpreting the amount of hybridization can be affected, for example, by the specific activity of the labeled oligonucleotide probe, by the number of probe-binding sites on the template nucleic acid to which the probe has hybridized, and by the amount of exposure of an autoradiograph or other detection medium. It will be readily appreciated by those of ordinary skill in the art that although any number of hybridization and washing conditions can be used to examine hybridization of a probe nucleic acid molecule to immobilized target nucleic acids, it is more important to examine hybridization of a probe to target nucleic acids under identical hybridization, washing, and exposure conditions.

Preferably, the target nucleic acids are on the same membrane.

A nucleic acid molecule is deemed to hybridize to a nucleic acid but not to another nucleic acid if hybridization to a nucleic acid is at least 5-fold (e.g., at least 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 50-fold, or 100-fold) greater than hybridization to another nucleic acid. The amount of hybridization can be quantitated directly on a membrane or from an autoradiograph using, for example, a PhosphorImager or a Densitometer (Molecular Dynamics, Sunnyvale, CA).

A nucleic acid sequence, or a polypeptide sequence, can be compared to one or more related nucleic acid sequences or polypeptide sequences, respectively, using percent sequence identity. In calculating percent sequence identity, two sequences are aligned and the number of identical matches of nucleotides or amino acid residues between the two sequences is determined. The number of identical matches is divided by the length of the aligned region (i.e., the number of aligned nucleotides or amino acid residues) and multiplied by 100 to arrive at a percent sequence identity value. It will be appreciated that the length of the aligned region can be a portion of one or both sequences up to the full-length size of the shortest sequence. It also will be appreciated that a single sequence can align with more than one other sequence and hence, can have different percent sequence identity values over each aligned region.

The alignment of two or more sequences to determine percent sequence identity can be performed using the computer program ClustalW and default parameters, which allows alignments of nucleic acid or polypeptide sequences to be carried out across their entire length (global alignment). Chenna et al., 2003, *Nucleic Acids Res.*, 31(13):3497-500. ClustalW calculates the best match between a query and one or more subject sequences, and aligns them so that identities, similarities and differences can be determined. Gaps of one or more residues can be inserted into a query sequence, a subject sequence, or both, to maximize sequence alignments. For fast pairwise alignment of nucleic acid sequences, the default parameters can be used (i.e., word size: 2; window size: 4; scoring method: percentage; number of top diagonals: 4; and gap penalty: 5); for an alignment of multiple nucleic acid sequences, the following parameters can be used: gap opening penalty: 10.0; gap extension penalty: 5.0; and weight transitions: yes. For fast pairwise alignment of polypeptide sequences, the following parameters can be used: word size: 1; window size: 5; scoring method: percentage; number of top diagonals: 5; and gap penalty: 3. For multiple

alignment of polypeptide sequences, the following parameters can be used: weight matrix: blosum; gap opening penalty: 10.0; gap extension penalty: 0.05; hydrophilic gaps: on; hydrophilic residues: Gly, Pro, Ser, Asn, Asp, Gln, Glu, Arg, and Lys; and residue-specific gap penalties: on. ClustalW can be run, for example, at the Baylor College of Medicine Search Launcher website or at the European Bioinformatics Institute website on the World Wide Web.

Changes can be introduced into nucleic acid coding sequences using, for example, mutagenesis (e.g., site-directed mutagenesis, PCR-mediated mutagenesis) or by chemically synthesizing a nucleic acid molecule having such changes. Such nucleic acid changes can lead to conservative and/or non-conservative amino acid substitutions at one or more amino acid residues. A “conservative amino acid substitution” is one in which one amino acid residue is replaced with a different amino acid residue having a similar side chain (see, for example, Dayhoff et al. (1978, in *Atlas of Protein Sequence and Structure*, 5(Suppl. 3):345-352), which provides frequency tables for amino acid substitutions), and a non-conservative substitution is one in which an amino acid residue is replaced with an amino acid residue that does not have a similar side chain.

Nucleic acids can be detected using any number of amplification techniques (see, e.g., *PCR Primer: A Laboratory Manual*, 1995, Dieffenbach & Dveksler, Eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; and U.S. Patent Nos. 4,683,195; 4,683,202; 4,800,159; and 4,965,188) with an appropriate pair of oligonucleotides (e.g., primers). A number of modifications to the original PCR have been developed and can be used to detect a nucleic acid. Detection (e.g., of an amplification product, a hybridization complex, or a polypeptide) is usually accomplished using detectable labels. The term “label” is intended to encompass the use of direct labels as well as indirect labels. Detectable labels include enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials.

Articles of Manufacture or Kits

This disclosure also provides for articles of manufacture that can be used to determine the methylation status of one or more CpG dinucleotides and/or CpG islands. An article of manufacture as provided herein can include one or more oligonucleotides for determining the

methylation status of one or more CpG dinucleotides and/or CpG islands, together with suitable packaging materials. The one or more oligonucleotides can detect the CpG dinucleotide in the bisulfite-treated DNA in the unmethylated state or in the methylated state.

Articles of manufacture may additionally include reagents (e.g., buffers, enzymes, co-factors) for carrying out the methods disclosed herein (e.g., bisulfite-treating DNA, amplification, sequencing, hybridization). Articles of manufacture provided herein also can contain a package insert or package label having instructions thereon for using the components within the article of manufacture to determine the methylation status of one or more CpG dinucleotides and/or one or more CpG islands in a biological sample.

In accordance with the present invention, there may be employed conventional molecular biology, microbiology, biochemical, and recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. The invention will be further described in the following examples, which do not limit the scope of the methods and compositions of matter described in the claims.

EXAMPLES

Example 1—Materials and Methods

All protocols and procedures used in this study were approved by the University of Iowa Institutional Review Board and full details are available from the inventors upon request. The case subjects described herein were recruited from the University of Iowa hospitals and clinics or two alcohol treatment centers in the State of Iowa. In brief, after admission to a hospital or alcohol treatment center and achievement of both sobriety and absence of significant cognitive impairment, potential subjects were approached by facility personnel as to their potential interest in participating in the current study. If interested, this information was relayed to the research team with the potential subjects then being contacted by a member of the research team who provided detailed information and screened the individuals for suitability for the study. Inclusion criteria included the ability to consent, an absence of significant active substance use disorders other than tobacco, an absence of medications hypothesized to affect DNA methylation, the absence of medical disorders including cancer, gastrointestinal disorders, diabetes, chronic obstructive pulmonary disease

or severe cardiac disease, and in general, otherwise overall general good health. If not excluded and still willing to participate, subjects were consented and the study procedure initiated.

At the index intake (Time 1, or T1), which could occur up to seven days after admission, all case subjects were interviewed with a modified version of the Semi-Structured Assessment for the Genetics of Alcoholism, Version 2 (SSAGA-II; Bucholz et al., 1994, *J. Stud. Alcohol*, 55:149-58), which included specific items to assess use of substances over the past six months. In addition, subjects were phlebotomized to provide biomaterial for the current study. Then, approximately 4 weeks later (Time 2, or T2), the same subjects were once again interviewed to assess for changes in medical status and phlebotomized.

Control subjects were recruited from the Iowa City region. Inclusion criteria for the study were similar to those of the case subjects and included good overall general health, a complete abstinence from alcohol for at least six months, an absence of medications hypothesized to influence DNA methylation, and an absence of significant substance use other than tobacco. All control subjects were interviewed with the same instruments as the case subjects and phlebotomized to provide biomaterial for the current study.

Sera and mononuclear cell (i.e. lymphocyte) pellets were prepared as previously described (Philibert et al., 2012, *Epigenetics*, 7:1331-8). As part of an effort to assess self-report reliability, cotinine and tetrahydrocannabinol levels were assessed in sera using an enzyme linked immunoassay (ELISA) kits supplied by Abnova (Taiwan) according to manufacturer's directions and previous protocols (Philibert et al., 2013, *Epigenetics*, 5:19-26). DNA was prepared from the lymphocyte cell pellets using a QiaAmp kit (Qiagen, Germany) according to manufacturer's directions.

Genome wide DNA methylation was assessed using the Illumina (San Diego, CA) HumanMethylation450 Beadchip by the University of Minnesota Genome Center (Minneapolis, MN) using the protocol specified by the manufacturer as previously described (Monick et al., 2012, *Am. J. Med. Genet., Part B Neuropsychiatric Genet.*, 159:141-51). This chip contains 485,577 probes recognizing at least 20216 transcripts, potential transcripts or CpG islands (from the Genome Reference Consortium human genome build 37 (GRCh37)).

The resulting data were inspected for complete bisulfite conversion and average beta values were determined for each targeted CpG residue determined using the Illumina Genome Studio Methylation Module, Version 3.2. The resulting data were then cleaned using a PERL-based algorithm to remove those beta values whose detection *p*-values, an index of the likelihood that the observed sequence represents random noise, were greater than 0.05. Then, data from arrays with < 99.5% complete assessment success were removed.

The surviving data was imported into MethLAB (Kilaru et al., 2012, *Epigenetics*, 7:225-9) and analyzed with respect to alcohol use status using standard general linear models approach controlling for chip and batch variables. The resulting *p*-values were corrected for genome wide comparisons using either False Discovery Rate or Bonferroni correction methods (Benjamini et al., 1995, *J. Royal Stat. Soc. Series B, Method.*, 57:289-300).

Essentially, a genome wide linear regression was used; in this case, a t-test that accounts for batch and slide co-variables. “Batch” is a term in DNA methylation that refers to the grouping with respect to bisulfite conversion (e.g., “batch” takes into account the degree of bisulfite conversion or lack thereof). “Slide” refers to the individual chip(s) or array(s) on which the hybridizations are performed, since, for example, there can be slide to slide variation with respect to the degree of hybridization of the same sample. It would be understood that accounting for batch and slide variation usually results in a greater degree of significance.

Example 2—Experimental Results

The clinical and demographic characteristics of the case and control subjects included in the study are described in Table 1. In brief, in keeping with the population of Iowa and overall referral characteristics of patients referred for alcohol treatment, the subjects tended to be in their 40’s and were primarily white males. The case subjects were extremely heavy alcohol users, with the typical subject describing the average consumption of a fifth of vodka or 12 pack of beer for at least the past week prior to admission. The delay between the time of phlebotomy and their last drink averaged four days and varied between one and eight days. Not surprisingly, the case subjects were enriched for tobacco use disorders, with 85% of them being daily smokers. They also tended to have a higher rate of THC use, with 10 subjects having either marginal or markedly positive hydroxy-THC levels. In each and every

case, the results of the serum cotinine and THC ELISA tests were consistent with self-report data. Of the 41 case Time 1 (T1) subjects ascertained during the time period leading up to this study, only 26 completed the Time 2 (T2) assessments. The reasons for the failure varied. In some cases, the subject had already left treatment and had begun to drink, while in other cases, the subject had already left treatment and was either unavailable or unwilling to complete the second stage of assessment.

Table I. Clinical and demographic characteristics of study subjects

	Case Subjects	Control Subjects
N=	33	33
Age	45.5 7.8	46.7 7.8
Ethnicity		
White	30	31
African American	2	1
Hispanic	0	1
Gender		
Male	25	25
Female	8	8
Days since last drink	4.0 1.8	
Average daily drink consumption prior to admission by self report		
Past week		0
Past month		0
Past 6 months		0
Smoking Status		
Current daily	27	1
Positive cotinine	28	1
Cannabis Use Status		
Use in past year by self report	11	0
Positive hydroxyl-THC	9	1

In contrast, though similar in age, gender and ethnicity, the 33 control subjects had lower rates of both tobacco and cannabis use. In fact, only one of the control subjects was a current daily smoker and all control subjects denied cannabis use in the past year. In contrast to the results from the case subjects, one discrepancy in the serum ELISA testing was observed (i.e., there was one positive test for THC).

Genome wide methylation data was successfully obtained (measurements for >99.5% of all probes) for 95 samples, including two lymphoblast DNA standards and one internal replicate. This included 33 controls, 33 case subjects at T1 and 26 case subjects at T2. The correlation between the internal replicate was greater than 0.998. The average beta value for the controls, and the subjects at T1 and T2 was 0.4788, 0.4800 and 0.4833, respectively.

The results from these experiments and the CpG residues, regions and gene claimed in this application are given in Appendix A. The data contained in Appendix A provides the Illumina probe ID, the sequences of which are publicly available, and the identity of the CpG in question denoted by sequence information and mapping information. Finally, the p-value for the t-test comparing methylation of the alcoholic subjects to that for the controls is provided. A $p < 0.05$ is considered significant, and complete annotation files for the probes listed in Appendix A are publically available.

Specifically, Column A, "Probe Name": the Illumina designation for the probe. Column B, "Target Region": the genomic sequence of the region; the center of the region, the CpG residue, is denoted by brackets (e.g. [CG]). Column C, "CHR": the chromosome on which the target region is found. Column D, "Map Info": the base pair at which the CpG residue is found in the GRCH37 assembly; note that the since the cytosine and guanine nucleotides are complementary, the CpG residue is found on both the sense and anti-sense strand. Column E, "UCSC Ref Gene Name": the generally accepted gene names, when present, in which the CpG residue is found. Column F, "p-value": the significance of the t-test comparing methylation of the alcoholic cases to that of the controls.

The list of the 30 most significant results from the comparison of the methylation status of the DNA from the 32 T1 subjects and the 33 healthy abstinent controls are listed in Table II. Overall, after genome wide correction using false discovery rate (FDR) method, a total of 8636 probes were differentially methylated while, when using more conservative Bonferroni correction, only 56 comparisons were statistically significant. Examination of the QQ plot for the comparison reveals the basis for these observed differences is significant with positive skewing (greater numbers of more significant p values) being markedly prominent (Figure 1).

Table II. The 30 Most Significantly Associated Probes in Case and Control Analysis

Probe ID	GENE	Placement	Island Status	Average Beta Values		T-test	Corrected P-value
				Case	Control		
cg23193759	C10orf35	TSS200	Island	0.128	0.168	4.66E-12	2.26E-06
cg02583484	HNRNPA1	Body	S Shelf	0.250	0.319	1.42E-11	3.46E-06
cg23779890	GDAP1	TSS200	Island	0.194	0.243	1.30E-10	2.10E-05
cg13415831				0.073	0.098	3.18E-10	3.87E-05
cg09935388	GFI1	Body	Island	0.647	0.799	1.35E-09	0.0001
cg01432120			Island	0.660	0.720	1.86E-09	0.0002
cg12655542				0.225	0.282	2.18E-09	0.0002
cg11832281	CUGBP2	Body	S Shelf	0.070	0.097	4.20E-09	0.0003
cg06126421				0.643	0.750	5.34E-09	0.0003
cg12895631	C11orf75	5'UTR		0.161	0.192	7.07E-09	0.0003
cg25998745				0.588	0.666	8.43E-09	0.0003
cg08352774	TMEM181	Body	S Shelf	0.110	0.149	8.46E-09	0.0003
cg19939077	PPIF	Body	S Shore	0.147	0.184	8.85E-09	0.0003
cg13126206			S Shelf	0.468	0.521	1.11E-08	0.0004
cg22888484	SNHG11	TSS200	N Shore	0.043	0.056	1.21E-08	0.0004
cg00159243	SELPLG	5'UTR		0.397	0.474	1.76E-08	0.0005
cg24046474	RPL12	Body	N Shore	0.221	0.296	1.89E-08	0.0005
cg00957665	TRIM8	Body	S Shore	0.097	0.125	1.93E-08	0.0005
cg06093152				0.572	0.654	2.03E-08	0.0005
cg12126344				0.795	0.835	2.13E-08	0.0005
cg17485265	FAM50B	TSS1500	N Shore	0.677	0.744	2.29E-08	0.0005
cg16854826	ZMIZ1	5'UTR		0.603	0.654	2.42E-08	0.0005
cg23028436	STK38L	TSS200	Island	0.064	0.094	2.89E-08	0.0006
cg00690082	STAT5A	TSS1500	N Shore	0.309	0.376	3.00E-08	0.0006
cg06285727	ATG16L2	TSS1500	N Shore	0.152	0.216	3.68E-08	0.0007

A frequent concern in high-risk cohorts such as these case subjects is the effect of co-morbid substances. In particular, this is a concern for the current results because smoking has profound effects on DNA methylation (see, for example, Dogan et al., 2014, *BMC Genomics*, 15:151), and 27 of the 33 case subjects were active smokers. In this regard, cg05575921, which has been shown to correlate strongly with tobacco use (see, for example, Dogan et al., 2014, *BMC Genomics*, 15:151), was the 31st ranked probe. However, overall, there was no significant overlap between the signal for alcohol consumption and the signal for smoking. Only 22 of the 910 probes that attained genome wide significance with respect to smoking in Dogan et al. (2014, *BMC Genomics*, 15:151) were ranked among the top 10,000 most highly associated probes in the current study. Conversely, the overall rank of the 10,000 most highly associated probes with respect to smoking in Dogan et al. was 302,264 (of 485,577), with the median of the distribution being 318,258th. Hence, there appears to be little overlap in the methylation signatures between subjects that use alcohol and subjects that use tobacco.

As the next step of the analyses, the differential distribution of the 1000 most significantly associated probes were analyzed using the GoMiner™ algorithm (Zeeberg et al., 2003, *Genome Biol.*, 4:R28). The results, shown in Table III, demonstrated a marked enrichment of the most highly associated probes for pathways involved in programmed cell death (apoptosis) or GTPase signaling.

Whereas the primary goal of many biomarker studies is to determine whether a given marker can be used to differentiate pathological states from control states, a secondary goal of the present study was to determine whether DNA methylation could be used to monitor alcohol abstinence. As a first step in that assessment, the genome wide DNA methylation patterns of 25 subjects for whom we successfully obtained both T1 and T2 data were compared. The average length of time between the T1 and T2 draws for these 25 individuals was 25 days. No single probe crossed the threshold of genome-wide significance with the best observed uncorrected p -value being only 5×10^{-6} with QQ plots of the analysis demonstrating significant negative skewing was prominent (Figure 2).

Table III. The Top 30 Most Differentially Regulated Gene Ontology Pathways

GO Category	Category Name	Genes		Log10		FDR
		Total	Changed	P-Value		
GO:0005515	protein binding	6815	286	-7.37		0
GO:0005737	cytoplasm	7845	312	-5.75		0
GO:0008219	cell death	1392	78	-5.69		0
GO:0016265	death	1395	78	-5.66		0
GO:0005829	cytosol	1884	98	-5.63		0
GO:0012501	programmed cell death	1278	72	-5.36		0
GO:0007264	small GTPase mediated signal transduction	566	40	-5.33		0
GO:0043067	regulation of programmed cell death	981	59	-5.30		0
GO:0010941	regulation of cell death	989	59	-5.20		0
GO:0006915	apoptosis	1271	71	-5.16		0
GO:0042981	regulation of apoptosis	974	57	-4.79		0
GO:0023033	signaling pathway	2812	130	-4.73		0
GO:0019899	enzyme binding	671	43	-4.63		0
GO:0048523	negative regulation of cellular process	2069	101	-4.61		0
GO:0002376	immune system process	1256	68	-4.52		0
GO:0023034	intracellular signaling pathway	1707	86	-4.44		0.01
GO:0023052	signaling	3787	164	-4.36		0.01
GO:0065007	biological regulation	7226	283	-4.33		0.01
GO:0048519	negative regulation of biological process	2235	106	-4.31		0.01
GO:0035556	intracellular signal transduction	1454	75	-4.24		0.01
GO:0005622	intracellular	11231	411	-4.22		0.01
GO:0060548	negative regulation of cell death	441	31	-4.21		0.01
GO:0044464	cell part	14663	511	-4.14		0.02
GO:0005623	cell	14664	511	-4.13		0.01
GO:0035466	regulation of signaling pathway	1158	62	-4.02		0.02
GO:0009987	cellular process	11702	424	-3.98		0.02
GO:0043069	negative regulation of cell death	434	30	-3.96		0.02

GO:0007265	Ras protein signal transduction	335	25	-3.91	0.02
GO:0051056	regulation of GTPase signal transduction	339	25	-3.83	0.03
GO:0050794	regulation of cellular process	6319	249	-3.81	0.03

FDR=false discovery rate.

Secondary analysis of the T1 and T2 proved highly interesting. Since exposure to ethanol is stressful to cells, and biological systems tend to revert to their homeostatic means after perturbation, we next asked which methylation assessment for the ethanol-imbibing subjects, T1 or T2, was more similar to that of the controls for the 8636 FDR-significant probes identified. Remarkably, the average methylation of these CpG residues for all 25 subjects was more similar to the control subjects at the T2 draw time than it was at the T1 draw time at 7360 of 8636 probes (Chi Square $p < 0.0001$) including all 30 of those listed in Table II. Unfortunately, the average version to the mean of the controls was rather modest at each locus, with the overall change in the beta value being approximately 0.005 (i.e. 0.5%).

Example 3—Summary

The experiments herein demonstrate that alcohol use is associated with significant and widespread changes in DNA methylation as compared to controls that do not use alcohol. The experiments herein also demonstrate that the degree of the changes in methylation tends to diminish after approximately one month of abstinence. Thus, the DNA methylation signature can be used to infer recent alcohol use status. The results reported herein likely will impact the choice of settings in which alcohol treatment is conducted and monitored.

As would be expected with alcohol use, the magnitude of the changes in DNA methylation due to alcohol use are not as strong as those observed with, for example, tobacco use. In contrast to that of smoking, for example, where the differences of methylation at cg05575921 between chronic smokers (~60%) and non-smokers (92%) can exceed 30%, the average differences at any one point in the current alcohol use study tend to be around 5% to 10%.

It is to be understood that, while the methods and compositions of matter have been described herein in conjunction with a number of different aspects, the foregoing description of the various aspects is intended to illustrate and not limit the scope of the methods and compositions of matter. Other aspects, advantages, and modifications are within the scope of the following claims.

Disclosed are methods and compositions that can be used for, can be used in conjunction with, can be used in preparation for, or are products of the disclosed methods and compositions. These and other materials are disclosed herein, and it is understood that combinations, subsets, interactions, groups, etc. of these methods and compositions are disclosed. That is, while specific reference to each various individual and collective combinations and permutations of these compositions and methods may not be explicitly disclosed, each is specifically contemplated and described herein. For example, if a particular composition of matter or a particular method is disclosed and discussed and a number of compositions or methods are discussed, each and every combination and permutation of the compositions and the methods are specifically contemplated unless specifically indicated to the contrary. Likewise, any subset or combination of these is also specifically contemplated and disclosed.

[illegible]

[illegible]

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[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

cg12548759	CGGAGGCTGGGCTGCAAGAGAGCTTGGCTGGTTC[CG]AGACCATCTGGTTCGCGTCAGAGCTGCTGGAGTGG	12	6647682		1.10E-05
cg02856842	AACTAAAGGAGAGGAGTGGTCACTGCTCACTGCTGCTCA[CG]GAGTAACTAGGAGAGAGCTAGCTATCTGCTGATG	1	249105687	SH3BP5L	1.11E-05
cg02445807	AATGGAAGAGCTTGGAGAGCTGGCTGCTGGAGAGAGCT[CG]GAGAGAGAGCTTCTTGGAGAGCTTGGAGAGAGCTTGG	6	36294404	CGorf22	1.11E-05
cg24670552	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	13	110436780	IRS2	1.12E-05
cg13683800	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	10	115066103		1.13E-05
cg14039246	ACCAAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	1	53365446	ECHDC2	1.12E-05
cg01055562	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	1	230777685	COG2,COG1	1.12E-05
cg04894537	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	11	2763171	KCNH1,KCNH1	1.12E-05
cg24019248	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	8	160548849	MIR599,VP513B,VP513B	1.13E-05
cg20847766	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	13	111840490	ARHGEP7,ARHGEP7,ARHG	1.13E-05
cg07622001	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	5	158758903	EF7,ARHGEP7,ARHGEP7	1.13E-05
cg05573626	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	16	49673687	ZNF423	1.13E-05
cg08607108	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	7	2105890	MAD1L1,MAD1L1,MAD1L1	1.13E-05
cg18887769	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	14	23945181		1.13E-05
cg02184700	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	4	8698168	S100P	1.14E-05
cg01122755	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	6	44281249	AAR52	1.14E-05
cg05249766	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	11	12332182		1.14E-05
cg17232357	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	15	67012832	SMAD6,SMAD6,SMAD6	1.14E-05
cg11051295	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	4	185876283		1.15E-05
cg26367031	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	3	178984747	KCNH3,KCNH3,KCNH3	1.15E-05
cg01418188	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	11	3145609	OSBP1,OSBP1,OSBP1	1.15E-05
cg06004033	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	12	104173675	NT5DC3	1.15E-05
cg17230002	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	12	54689504	NFE2L3,NFE2L3,NFE2	1.16E-05
cg12352399	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	3	2689774	TOP2B	1.16E-05
cg03331914	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	1	208038413		1.16E-05
cg07046436	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	16	30663252	PRR14	1.16E-05
cg25213452	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	1	206630385	SRGAP2,SRGAP2	1.16E-05
cg18780288	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	10	111659903	XPPEP1,XPPEP1,XPPEP1	1.17E-05
cg04334723	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	19	13054427	CAIR	1.17E-05
cg05155595	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	2	70008161	ANKA4	1.17E-05
cg06351477	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	2	3382031	TTC15,TTC15	1.17E-05
cg05496814	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	5	111484415		1.17E-05
cg11422864	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	16	4802786	ZNF500	1.17E-05
cg18786374	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	3	203315532	TRAK2	1.17E-05
cg20741040	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	1	230566509		1.18E-05
cg05404236	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	13	110437093	IRS2	1.18E-05
cg05655930	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	3	50397494	HYAL1,HYAL1,HYAL1	1.18E-05
cg06553114	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	10	69970751	MYPH	1.18E-05
cg06679494	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	17	6921295	MIR497,MIR195	1.18E-05
cg059394035	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	9	104131758		1.18E-05
cg27081745	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	5	67627382		1.19E-05
cg23348703	AGAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGCT[CG]GAGAGAGCTGGAGAGAGCTGGAGAGAGCTGGAG	17	42928238	BTBD2,BTBD2	1.19E-05

cg07433769	ACACGACATCAAGAGGAGGATTAAGTTTCTGAAAG[CG]GGACACAGGAGAAAGAGCTGAGGTTTCTGAGAGAC	18	13620827	C18orf1,C18orf1,C18orf1,C18orf1	1.19E-05
cg20671781	CGGACGCTGGGCTACATGCTAGGCTGTCAGAGGCT[CG]CGGATGAGGCGGACAGGCTGAGGCGGCGCTG	10	43628471		1.20E-05
cg26028440	TGAAAGGAGAGGCTGAGGAGTACCTTAATTTTGGT[CG]GAGTGGGCTGAGGCTTATAGGAGGCTGGGCTTA	1	27982716		1.20E-05
cg02010481	GGACAGGAGATTTGCTGAGGAGAGAGATTTGGGAG[CG]TTTGGGAGGATGATGCTGCTGAGGAGGAGGCTG	7	26218924	JAZF1	1.20E-05
cg14322343	AGGCTTGAGGCTTCAGAGCTCAGAGCTTAAGAGTC[CG]CAGCTGGAGGAGAGGCTGAGGAGGAGGAGGAGG	9	93863472		1.20E-05
cg07092111	TGTGTGCGGAGGAGGAGGCTGGGAGGAGGAGTAA[CG]TGAGCTTCAGAGTGGGTTGAGGAGGAGGAGTGG	10	32621403	EPCL	1.20E-05
cg12349571	AGAGGCTCGGAGGAGGAGGAGGCTGAGGCTGCTG[CG]TATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	15	70364359	TLE3,TLE3,TLE3	1.20E-05
cg12729639	AGGAGGCTTATGCTGAGGCTGAGGCTGAGGCTGAG[CG]AGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG	12	12519119	MLXIP	1.21E-05
cg04465154	CGGAGGCTTATGCTGAGGCTGAGGCTGAGGCTGAG[CG]AGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG	8	9045558		1.21E-05
cg23045991	CGGAGGCTTATGCTGAGGCTGAGGCTGAGGCTGAG[CG]AGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG	7	101943095	94282	1.21E-05
cg20470975	GTACCGAGGCTTATGAGGAGGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG	8	138101307		1.21E-05
cg06512663	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	5	30709867	CDKAL1	1.21E-05
cg11302401	GGGCTGATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	6	6888947		1.21E-05
cg011132064	TGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	11	46383562	DGKZ,DGKZ,DGKZ,DGKZ	1.22E-05
cg24448013	AGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	1	24128076	GALE,GALE,GALE	1.22E-05
cg05117308	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	17	40438312	STAT3	1.23E-05
cg06397161	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	22	59760059	SYNGR1,SYNGR1,SYNGR1	1.23E-05
cg04275040	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	17	78935628	RPTOR,RPTOR	1.23E-05
cg22507772	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	6	67598931		1.23E-05
cg22084410	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	3	51987688		1.23E-05
cg22983370	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	4	13303880	IGHG,IGHG,IGHG	1.24E-05
cg01973676	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	7	101556404	CUX1,CUX1,CUX1	1.24E-05
cg23144225	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	15	62123643		1.24E-05
cg12506121	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	12	50238076	BCDIN3D	1.25E-05
cg18616534	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	5	158385443	EBF1	1.25E-05
cg07943111	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	17	1492285	SIC3A2	1.25E-05
cg01687189	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	12	10225365	GNPTAB	1.26E-05
cg22881435	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	8	37732086	RAB11FIP1,RAB11FIP1,RA	1.26E-05
cg05003559	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	11	3175625	OSBP1,OSBP1,OSBP1	1.26E-05
cg08685085	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	12	57114435	NACA,NACA,NACA,NACA	1.26E-05
cg21055554	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	12	113652889	IQCD	1.27E-05
cg01415837	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	1	10134620	UBE4B,UBE4B	1.27E-05
cg05754958	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	1	202130692	PTPN7	1.27E-05
cg00115638	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	17	54701692		1.27E-05
cg00443094	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	4	1771149		1.28E-05
cg09020113	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	13	114810036	RASA3	1.28E-05
cg05860789	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	9	11351571	BLK,BLK	1.28E-05
cg02995045	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	1	6419906	ACD17,ACD17,ACD17,AC	1.29E-05
cg14016363	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	7	100486297		1.29E-05
cg07582825	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	3	152769889		1.29E-05
cg14114297	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	5	81084231		1.29E-05
cg11389756	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	6	28873354	PRIM2	1.29E-05
cg01702089	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	6	42863762	PTCRA,PTCRA	1.30E-05
cg27009044	AGGAGGCTTATGAGGCTGAGGCTGAGGCTGAGGCTGAG[CG]TGTGAGGCTGAGGCTGAGGCTGAGGCTGAG	17	74721842	C17orf95,IMD6,IMD6	1.30E-05

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cg00578614	TAATCTTAAATTTTCACAAATGTTGTTCTGCGGAGG	CG	CAGAGAGAGAGTCTGTTCAATGAGTGGTGGTGGAGG	5	30070403		5.46E-05
cg009457350	ATCAGAGAAATTTAAGAGATGGAGCTTAAAGAGAGA	CG	AGTATATGATAATACACAGCTGAGAAATCTGACAGAG	3	171894094	FNDC3B:FNDC3B	5.46E-05
cg19486804	CGGCTCCATCTCGAGATCTGGACATGCGCCGAGG	CG	AGCAGCTGAGTGTGAGGCTGAGGAGAGAGAGAGAG	7	1345819	C7orf50:C7orf50	5.46E-05
cg10341466	AAATCTGAGAGTGGAGAGGTTAGAGGCTATGAGG	CG	CTCTGACAGATGTCATGAGAGAGAGAGAGAGAGAG	1	11345263		5.47E-05
cg20438687	GGAGCTCAGAGTGAATGCTGTGAAATGAGAGAG	CG	ATAAAGCAAGAGTGAAGAGAGAGAGAGAGAGAG	17	4761644	MINK1:MINK1	5.47E-05
cg25708790	GCAGCTGCGCAGAGCTGAGAGAGCTGAGAGAGAG	CG	GTCAGAGAGCTGAGAGAGAGAGAGAGAGAGAG	13	132549361	EP400	5.48E-05
cg10787197	GGATCCGCGAGTTGCTATCTGAGTAACTGAGTCT	CG	AGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAG	6	11779941	G6orf105:G6orf105	5.48E-05
cg21201109	ATATGAGAGATCTAGAGAGTGGAGCTTATGAGGCT	CG	TTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG	19	11307090	KANK2	5.48E-05
cg14685356	AGAAATGATACAGAGAGAGAGAGAGAGAGAGAG	CG	TTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG	6	153639548	SYNE1:SYNE1	5.48E-05
cg04928129	GAGTAAAGCTGGGTCAGAGAGAGAGAGAGAGAG	CG	GGGTCAGAGAGAGAGAGAGAGAGAGAGAGAG	16	1429051	UNKL	5.49E-05
cg17480764	ACATTAAGAGATATGACTCTGAGCTTTTTCAGCA	CG	TGACTATGAGATGAGAGAGAGAGAGAGAGAG	1	206971195	IL19	5.49E-05
cg03989987	TCTCTCTTCTGTTGATGAGAGAGAGAGAGAGAG	CG	AGGTCGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	113885277	IL1RN:IL1RN	5.50E-05
cg2120078	CAACAGATATCTATCTCCAGAGAGAGAGAGAGAG	CG	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	13386904	HSPA4	5.50E-05
cg19880751	TGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	GGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	72362618	PRF1:PRF1	5.51E-05
cg07817400	ACGAGCTGAAGAGAGAGAGAGAGAGAGAGAGAG	CG	CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	33173817	HSD17B8	5.52E-05
cg14236443	CAAGATTAATACAGAGAGAGAGAGAGAGAGAGAG	CG	CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	37	943270	ABR:ABR	5.52E-05
cg06984156	CTGAGAGATCTGAGAGAGAGAGAGAGAGAGAGAG	CG	TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	20929649	CDA	5.53E-05
cg25978218	TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	15759732	BPHD2	5.54E-05
cg19825437	GAGAGATGAGAGAGAGAGAGAGAGAGAGAGAG	CG	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	169383292		5.58E-05
cg03579641	CAAAATTAATACAGAGAGAGAGAGAGAGAGAGAG	CG	CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	134963543	TACC2:TACC2	5.58E-05
cg05296619	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	13	114834683	RASA3	5.59E-05
cg09735827	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	7	106407970		5.60E-05
cg15225315	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	5	176921820	POLM7:POLM7	5.60E-05
cg20589553	ATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	6	33219392	VP52	5.60E-05
cg06206827	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	6	30709045	PLOT1	5.60E-05
cg14183540	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	11	3175007	OSBP1:OSBP1	5.61E-05
cg05756251	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	17	37024760	LASP1	5.61E-05
cg23689615	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	15	74238839	LOX1	5.62E-05
cg03001333	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	1	2805560	PRKZ:PRKZ	5.63E-05
cg26482164	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	30	56830240	C2orf197	5.63E-05
cg20762729	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	21	30451398	C2orf7	5.63E-05
cg07639982	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	10	12555079	CAMK1D:CAMK1D	5.63E-05
cg19873021	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	19	6738068	GPR108:GPR108	5.64E-05
cg25900943	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	8	103820614		5.64E-05
cg24636368	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	17	46388447	SKAP1:SKAP1	5.64E-05
cg05173058	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	15	93573145		5.65E-05
cg08086511	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	16	48413428	SHAH1	5.66E-05
cg17222829	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	11	70433293	SHANK2:SHANK2	5.66E-05
cg10604530	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	5	43001210		5.67E-05
cg06574869	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	17	80351150	C1orf101:C1orf101	5.67E-05
cg27553947	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	1	9819767	CLSTN1:CLSTN1	5.67E-05
cg14279856	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	6	30851086	DDRL1:DDRL1	5.68E-05
cg06468347	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	17	3705875	ITGAE	5.68E-05
cg24517899	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	10	126290093	LHPF:LHPF	5.68E-05
cg26182859	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	1	153762281		5.68E-05
cg08092230	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	CG	ATATTCCTATGAGAGAGAGAGAGAGAGAGAGAG	7	5457225	TNRC18	5.69E-05

qg17126924	CAAGGTAACAGACAGAGGAAATTTGAAACATGATATTTGGTCTTAAATGAAGTTATTTGGAATGAGTGGTGAATTCGGA	17	25773641			5.69E-05
qg14646977	CTGGATGAGAGAGATTTGGGAGAGAGAGGCTGGAGAGAGCTGGAGAGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	30636667	NRMKIA1949		5.69E-05
qg18412721	GGAAATCAGAGGAGAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	53421269			5.69E-05
qg20146909	AGCAATTTGATCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	90289611	UBRCX1.URRC80		5.70E-05
qg18697143	CGGATCCAGCAATTCCTGCTTCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	118227831	ETV6		5.70E-05
qg3078586	CTCAGATAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	49469953	FTL		5.70E-05
qg25137372	CTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	96390059	BALHAL		5.70E-05
qg06595162	ACGTCTTAATTCAGTTAATAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	21	40141040	NCRNAD0114.NCRNAD011		5.71E-05
qg26684776	GAACACCTGATCTCCAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	90085550	RPAGD		5.71E-05
qg11895549	CACTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	116996871	MAPIL1.C82		5.72E-05
qg14651616	CTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	64563992	MAPAK2		5.72E-05
qg09076077	ATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	59630315	C20orf097		5.73E-05
qg03341503	AGCCGCAACAGACAGATGTTAATCACTCTTAAAGCGCTTTCTCTCAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAG	30	45947123	ZMYND8.L0C100131496.Z		5.74E-05
qg0606703	TCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	773998	MYND8.ZMYND8		5.78E-05
qg24324441	ATGAGCTCTTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	158519002	MESD1.MFSD1		5.76E-05
qg26233369	AAATACATGCAAAATTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	173286135			5.77E-05
qg04902833	TGCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	76153421	C17orf59		5.77E-05
qg12864859	CTTCCCAAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	43224132	HEXIM1		5.78E-05
qg17445891	GGAGAGATTAATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	2082352	PRKC2.PRKC2.PRKC2		5.78E-05
qg03899510	TAACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	170581690			5.78E-05
qg13785883	CCCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	73407670	CT62.CT62		5.79E-05
qg00716579	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	13984990	MIR181C.MIR181D		5.79E-05
qg15700582	AGATATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	68960655	ARMGAP25.ARMGAP25		5.81E-05
qg02099017	AGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	54805345	ITGA5		5.82E-05
qg03116466	GGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	2116512	MAD1L1.MAD1L1.MAD1L1		5.82E-05
qg06526741	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	31549929	LTB1.LT8		5.82E-05
qg13483399	ACTGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	22	26876075	HP54.HP54		5.82E-05
qg27618318	GGCTCTTGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	63355027	TPM1.TPM1.TPM1.TPM1		5.82E-05
qg9641323	AGATATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	134157797	TPM1.TPM1.TPM1		5.83E-05
qg04206284	CAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	64127515	ZNF107.ZNF107		5.84E-05
qg10533990	CAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	73846713	FOLR3		5.84E-05
qg10299697	GGTATCGGATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	138069423	MRA5.MRA5		5.84E-05
qg25236277	AGATTTGATCTCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAAT	3	119076999	CDGAP		5.86E-05
qg17231565	AGTATGATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAATCTGATTAAT	1	44444305	BAGAL7		5.87E-05
qg00246989	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	99159655	STK24.STK24		5.87E-05
qg10506318	TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	60239580	PRCCS.NDUFAF2		5.88E-05
qg038224029	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	29570008	GABBR1.GABBR1.GABBR1		5.89E-05
qg0776647	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	125359265	NDUF58		5.90E-05
qg14070987	AGAATGCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	67804005	C10orf99		5.90E-05
qg25526001	CTATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	85939451	SH3PXD2A		5.90E-05
qg063722808	GAATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	105595043	HDAC3		5.91E-05
qg28849931	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	140104062			5.91E-05
qg00376392	CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	16802505			5.92E-05
qg04460609	GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	16532808	LDK2.LDB2		5.92E-05

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cg19679155	CGGCGGCTTGGCTGGGCTGGAGCGGACCGACCTGAG[CG]GGAGAGAGAGGTAATGAGGACTGAGAGCTGGCCCA	10	72995181	UNC5B	6.89E-05
cg22110158	AGCTGAGAGATCTGGACAGACTGGCTGUAAGAGCTG[CG]CTGAGGAGAAATGAGAGCTGAGGCTGAGAGGCTCAG	11	130036342	ST14	6.90E-05
cg23051272	AGCCTAGTGTGAAAGGCGGAGGCTGAGAACAGAGAA[CG]CTGAGAAATGCTTCTGCGAGAAAGGCGAGGCTGAG	17	17589471	RAI1	6.90E-05
cg23264829	ATCTGGAGCACTGGGCTGTTCTGATGAGATCTATTA[CG]GTCTGGAGAGAGGTAAGAGAGAGGAGAGAGC	10	90642003	STAM8P11	6.91E-05
cg15701612	GGGAGCAATGTGAAAGAGAGAGAGAGGAGAGGAG[CG]TTTAAATATCTAGACATATAAGAGAGAGAGAGAGAG	11	130253770		6.91E-05
cg05178291	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]ATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	18287689	SAA1-5A41	6.91E-05
cg07016556	AGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	78393532	BAHCL1	6.92E-05
cg07493362	CTCTTTCTCTGAGCTCTGAGAGAGAGAGAGAGAG[CG]TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	78244468	WWOX-1WVOR	6.92E-05
cg04186460	CACTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	154942910	SHC1-5HCL1SHC1	6.92E-05
cg15823461	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	50639566	TMEM132A, TMEM132A	6.93E-05
cg07297967	CGGAGCTTATTAAGAGAGAGAGAGAGAGAGAGAG[CG]AGAAATAAATATGATATATGATATATGAGAGAGAG	8	57473034		6.94E-05
cg22803510	TTTGAAGTATGAGGCTAGAGAGAGAGAGAGAGAG[CG]CGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	94017621	FNBP1L, FNBP1L	6.94E-05
cg01416295	CAATATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	156710278	MRP124, MRP124	6.94E-05
cg20179907	GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	72336908	PDE2A, PDE2A, PDE2A, PDE	6.95E-05
cg22111527	ATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	89260136		6.95E-05
cg02032125	GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGGCTTTTCTGAGAGAGAGAGAGAGAGAGAGAG	14	101000136		6.95E-05
cg14315430	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	57913618	MBD6, DDX3	6.96E-05
cg20227511	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	28670602	FLT3	6.96E-05
cg15015109	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	63136480	HELZ	6.97E-05
cg08928938	TCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGGTTTGGTGAAGAGAGAGAGAGAGAGAGAGAG	5	149178783	PPARGC1B	6.97E-05
cg24866700	GGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	2235103	MIR1227, PLEKH1	6.97E-05
cg25518868	AAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	140984057	DIAPH1, DIAPH1	6.98E-05
cg01475110	CTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	90332983		6.98E-05
cg19573490	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	79870317	PCYT2, SIRT7	6.98E-05
cg19240637	AGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	7172297	RNF144A	6.98E-05
cg11831182	TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	156104614	LMNA, LMNA, LMNA	7.00E-05
cg00207226	AAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	125407180	ELN45D6, ELN45D6	7.00E-05
cg00106282	CTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	845047		7.01E-05
cg14728864	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	48794276		7.01E-05
cg05236399	CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	7660950	SORCS2	7.02E-05
cg13541353	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	9	32426330	ACO1	7.02E-05
cg26106532	AAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	6105656	IL2RA	7.03E-05
cg07495704	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	14	104091493		7.03E-05
cg18749675	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	43041125		7.04E-05
cg01438296	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	249200039	PGSD2, PGSD2	7.04E-05
cg00734567	CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	86172782	ZNHT6, ZNHT6	7.04E-05
cg24395503	CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	14	103046330		7.05E-05
cg07800426	AGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	27838209		7.05E-05
cg15491247	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	4330424	PRDM15, PRDM15	7.05E-05
cg13575139	CTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	58456976		7.05E-05
cg09122442	CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	6894410		7.05E-05
cg26917899	TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	15239600		7.07E-05
cg00405190	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	175545838	WIPF1	7.07E-05
cg23481246	GGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	731772	STU8L, MBD8	7.07E-05
cg09094921	TTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	136215608	DCPS	7.07E-05
cg08091439	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	110546703	AHCY1	7.08E-05

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g01992734	TCCTTTCCAGATTTCGATTCGAACTTCGATATCTGACG	3	50376409	RASSF1-RASSF1-RASSF1	8.23E-05
g22436583	AGAGCAACCTGATTTGCAATGAGAGTCGCGGAGAAAG	12	98233359		9.24E-05
g04871472	CGAATTTGGAATCGAGAGACGACGACGAGGAGAGAG	2	70268913		8.24E-05
g07912723	AGAGAGACGAGAGATGATGATGAGAGAGAGAGAGAG	1	2032058	PRKC2-PRKC2	8.24E-05
g11901722	GGACACCTTTGAGAGAAAGGATGATATGAGGAGATTT	5	175974973	PCDH24	8.26E-05
g11603299	TTGATGATGAACTTGGAGAGTCGAGAGAGATCTGTTG	19	55918225	UBE25	8.26E-05
g09376756	CTCTGATGAGATCTGAGAGATGAGAGAGATCTGTTG	14	24568943	PKC2-PCK2	8.27E-05
g07986469	AGCACTAATGGAGGAGATGAGAGATGAGAGATGAGAG	10	129795003	PTPRE	8.28E-05
g032111593	GCAGAGAGATGAGAGAGATGAGAGATGAGAGATGAG	11	44731693		8.29E-05
g087893514	ATTTAGATGATGAGATGAGATGAGATGAGATGAGATG	15	63772233		8.30E-05
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g11051139	TTGGATTTAGAGATGAGATGAGATGAGATGAGATGAG	12	52580428	KR180-KR180	8.31E-05
g223551120	TGAGAGATGAGATGAGATGAGATGAGATGAGATGAG	13	113375848	ATP11A-ATP11A	8.31E-05
g21850879	TTGAGATGAGATGAGATGAGATGAGATGAGATGAG	17	28621943	REF5-OMG1NF1	8.32E-05
g116234747	AGATGATGAGATGAGATGAGATGAGATGAGATGAG	22	44573802	PARVG-PARVG-PARVG-PA	9.33E-05
g20942867	CTCTAGAGATGAGATGAGATGAGATGAGATGAGATG	1	27426144	SLC9A1	9.33E-05
g17569736	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	8	140843235	KCNK9	8.33E-05
g30304848	AGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	16	89994953	CBFA2T3-CBFA2T3	9.34E-05
g26601047	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	12	58210715	AVIL	8.34E-05
g14422498	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	9	100639423		9.34E-05
g223668631	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	17	3796936	CAMKK1-CAMKK1	8.35E-05
g20618826	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	10	81148896	ZCCHC24	9.35E-05
g20602900	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	15	40846077	C15orf57-C15orf57-C15orf	8.36E-05
g16618104	TGAGATGAGATGAGATGAGATGAGATGAGATGAGAT	12	104853100	C43T11	8.41E-05
g03010763	ATTTAGATGAGATGAGATGAGATGAGATGAGATGAG	15	61044829	RORA	8.42E-05
g25758828	TACTAGATGAGATGAGATGAGATGAGATGAGATGAG	2	113976143	PAX8-PAX8-PAX8-PA	9.42E-05
g13693136	TCGATGATGAGATGAGATGAGATGAGATGAGATGAG	1	228666638	XSLCC40839	8.43E-05
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g19373099	GAGATGATGATGAGATGAGATGAGATGAGATGAGAT	2	210008092		8.44E-05
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g24657756	TTGATGATGATGAGATGAGATGAGATGAGATGAGAT	17	78698822	RPTOR-RPTOR	8.45E-05
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g13237068	CTGATGATGATGATGAGATGAGATGAGATGAGATGAG	13	25485381	CEMP1	9.48E-05
g09287773	TTGATGATGATGATGAGATGAGATGAGATGAGATGAG	5	139594619	C5orf32	8.49E-05
g11467506	TTGATGATGATGATGAGATGAGATGAGATGAGATGAG	7	33357047		9.49E-05
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g16436562	GTATGATGATGATGATGAGATGAGATGAGATGAGATG	11	94307971	PRH14	8.50E-05
g14082893	CTGATGATGATGATGAGATGAGATGAGATGAGATGAG	15	73400931		8.51E-05
g06250921	TGAGATGATGATGATGAGATGAGATGAGATGAGATGAG	16	83111009		8.52E-05
g14022913	ATATGATGATGATGATGAGATGAGATGAGATGAGATG	4	178229651	NEIL3	9.53E-05

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g25576997	AGCCATCTGACACATGTTCTTATCTAGGATGCTGCGCTTTCTGTCGACAGAGTCTTATTAAGAGGAAGTTTTT	14	56257750	C146434_C146434	0.000107316
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g11120551	GAACAAAGGTGACTTCTCAACACGAGGCGCAACCGAGGAGGCTGACACATGATAGAGAGAGAGAGATTA	1	346713986	CHD1L	0.000107386
g10271819	GTCAATGAGAGAAATGAGCTGAGTAAAGAAAGAGAGCGAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	139476030	HPK2.HPK2	0.000107444
g101406317	GGTGGAAATATATAAATCTCTGAGAGCTGAGCACAACGTCGACCAATTTGGGTAAATGATATTTCTGTGAGAG	16	4397791	Magnas	0.000107481
g10838410	ACATGCGAAGCTCTCAATAGACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	5659524	IFPO1.IFPO1.IFPO1	0.00010749
g11626175	CGATCTGAGAGATGATGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	15365074	JARID2	0.000107536
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g161317479	CTTGAGTAAAGATCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	39070179		0.000107982
g11040575	CATGCGCCGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	89213465	MIR437.MIR195	0.000108018
g133330678	TAAGAGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	73416233	SEF19.SEF19.SEF19	0.000108019
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g14293576	GATTCGCAATGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	23604302		0.000108126
g13090982	AGGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	109634248	TMEM167B	0.000108142
g10220544	CTCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	60171693	FGG7.FGG7	0.000108143
g21768523	ACAGAGACTTTGGGTGGGTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	113544348	IL1A	0.000108195
g1436628	ATTATATATGCTACTTAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	26290463		0.000108294
g1519096	TTATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	24833311	HCAN3	0.000108391
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g1713689	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	74809552	FAM161B	0.000108593
g10920316	CAGGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	14	137946599		0.000108603
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g27679940	GAAGGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	71097650	HK1.HK1.HK1.HK1.HK1	0.000108812
g107363330	TAGGATTTATCTGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATAT	5	55148493	IL31RA	0.000108813
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g10912202	TCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	1476661	C1orf70	0.000108947
g140493339	TTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	28875356	TRIM27	0.000109054
g17812664	TTCTGCTTTCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	104957217		0.000109072
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g105057534	TGTTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	28497659	BRE.BRE.BRE.BRE.BRE	0.000109101
g11442676	GGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	117695591	FXYD2.FXYD2.FXYD2	0.000109107
g10227272	CTTCTGCTTTCTGATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	131130459	PTPN18	0.000109263
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g14488957	CGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	1244644	ACAF3.PUSL1	0.00010957
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g13709271	TCCTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	45966142	MARCH8.MARCH8.MARCH8	0.00010987
g25451702	TACAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	225440987	CUL3	0.000109927

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cg01299932	AAAGCTCTGTCAGAGCTGCTGGGAGTTCTTGAAG[CG]AAGGCTGTGGCTTCACTGAGTGGCTGCTGAGCTGG	5	79406275		0.00011995
cg26874367	TGGTCTGATGTCATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT	2	129381792		0.000120061
cg13377486	AAAGGAAADACTTGAAGTGGGCAAGAGCTTAAG[CG]CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	10	304211236	C30orf95;C10orf95	0.000120093
cg18524934	TAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	97164073	NEURL3	0.000120104
cg03353699	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	30644693	KIAA1949;KIAA1949	0.000120164
cg13454216	TGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	10	3823758	KLF6;KLF6;KLF6;KLF6	0.000120188
cg26482585	TGACAGGATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	31463768		0.00012036
cg09868299	AGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	59259957		0.000120294
cg17071578	AGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	36852463	STK40	0.00012035
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cg272337438	GGGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	19	54327437	NLRP12;NLRP12	0.000120457
cg02561912	CCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	50158202	NEAT2;NEAT2;NEAT2	0.000120463
cg10131879	TGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	8011594	GLCCH	0.000120542
cg15246895	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	17672475	RAI1	0.000120637
cg23410501	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	12937954		0.000120644
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cg05223292	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	2647927	ICE1;ICE1	0.000120673
cg14501219	CCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	62775713	LOC146880;LOC146880	0.000120806
cg07434244	DACAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	209847729	GOS2	0.000120853
cg20618842	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	114521572	OLFM13	0.000120971
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cg28611765	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	27199915		0.000122078
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cg05154518	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	86245702	AKAP13;AKAP13;AKAP13	0.00012218
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cg15462879	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	X	133930034	FAM122B;FAM122B;FAM122B	0.000122915
				22C;FAM122B;FAM122B	
cg11854981	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	42219847	TRPF1	0.000123038
cg15118447	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	159220343	E2F4;E2F4	0.000123042
cg10482632	TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	201476606	CSRPI;CSRPI	0.000123103
cg19097880	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	128160637		0.000123144
cg09628887	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	16255619	CENPV	0.000123192
cg14609407	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	42883172	SLPI	0.000123271
cg09860281	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	8	21882397	NPM2;NPM2	0.000123328
cg09843054	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	8211214	C3AR1	0.000123399

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cg07104958	CGGCTGGTGAAGACCCAGCAGCATCTTTTCAGAG[CG]CTTGATTTCTGGAGATTAGGAGATAGAGCAAGAGCG	10	46166351	ANURLIJANURLI	0.000178329
cg18911856	CAGACTCGTAACCTGTCTGGTAACTATATCTCTG[CG]CTTTGCTCTGTCAGCTTGGGAGACAATACTAAGA	14	21483641		0.000178536
cg05804846	AATTTGCAAGATTTCGACACACACAGAGAGAGATTTCTG[CG]CACAGAGATTTGGTATTTGATTTGAGGAGAGG	11	9775858		0.000378701
cg12121103	GTCAGCTGTGAGCTGAGCTCTTAGAGAGGAGAGATTA[CG]AAATCTGGAGAGAGATTAAGGAGATTTCTTAAGAGGA	17	48231729		0.000178783
cg18168845	GAGAGATTTATTTACTATATACATATAGAAATGAGAG[CG]ACTGCTTTATCTGTADAAGAGATGAGATTTCTGCCA	13	41173440	FOXO1	0.000178879
cg08439276	TAAAGAGAGAGACATTTACACAGAGTAAAGATAGTA[CG]GAGTTGATTTATATTTATATATATATATATATATAT	2	58937224		0.000179091
cg07532955	TAAATCTCAAGATTTGATTAAGATTAAGATTAAGATTA[CG]GAGTTGATTTATATTTATATATATATATATATAT	10	29346742		0.000179412
cg05249744	CTCTGCAGCTGTGCTGATTTCTGATGATGATG[CG]GAGAGCTGGTGGCTTTCTCTCTCAGAGAGAGGAGAGG	17	78834710	RPTOR,RPTOR	0.000179419
cg18412107	TACTCTTAATTTGAAGAACATCTCTGTGTTCTGGAAT[CG]TAGTCATTTCTACTAACAGGCTCTATCTCTTAGATAT	6	134288301	TBP1	0.000179437
cg13210395	SAGCTTTTAGAGAGATTTCTCTCTAGATTTGATTA[CG]GTTTAGAGAGAGTAACTCTTCTGATGAGAGAGAGGCT	15	57802103	ZGNL1	0.000179505
cg13617811	CAAAGCCTTTGTATAGAGAGAGAGAGAGAGAGAGAG[CG]GAGCTCAAGATTTGATTTCTCTCTCTCTCTCTCT	12	48170484	SLC4A41	0.000179522
cg27016107	AGCTCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG[CG]CAATCTGGCTCTCTCTCTCTCTCTCTCTCTCTCT	17	47329321		0.000179568
cg24911485	GATGCTATATCTCCATTTAGAGAGAGAGAGAGAGAG[CG]ATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	18	7653597		0.000179615
cg295672711	CAGCTGCTACATAGAGCTGTGCTCTCTCTCTCTCT[CG]ATGATCTAGATTAAGAGAGAGAGAGAGAGAGAGAG	3	110965888		0.000179717
cg314412620	CTCTAGAGTAAAGATTTAGAGAGAGAGAGAGAGAG[CG]GAGTTTGTGATCTCTCTCTCTCTCTCTCTCTCTCT	19	3163885	ANKRD27	0.000179856
cg05779219	GTGGCTCTAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	23092166		0.000179926
cg23444667	CAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	238610221	LRRFP1,LRRFP1,LRRFP1, LRRFP1,LRRFP1	0.000179945
cg02463948	CCCTGCTAGAGAGATTTCTCTCTCTCTCTCTCTCT[CG]AGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	122612858	UBASH3B	0.00017996
cg08852979	CTTCTGCAAGCTGATCAGAGAGAGAGAGAGAGAG[CG]GAGCTGTGATTTGATTTCTCTCTCTCTCTCTCTCT	17	76134717	TMC8	0.000179989
cg04478251	CAGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	998431	ABR-ABR-ABR	0.000180008
cg13048350	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]AGTATTTATATATTTCTCTCTCTCTCTCTCTCT	6	33256165	PFDNG,WDR46,WDR46	0.0001801
cg17811213	TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	101636912		0.000180247
cg12976582	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	50359593	HVAL2,HVAL2	0.000180354
cg18739433	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	150086159	ZNFR75	0.000180532
cg03575483	CTTCTGCAAGCTGATCAGAGAGAGAGAGAGAGAG[CG]AGTATTTATATATTTCTCTCTCTCTCTCTCTCT	6	117826786	DCBLD1	0.000180579
cg04582938	CGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGTATTTATATATTTCTCTCTCTCTCTCTCTCT	9	139971429	IAP1L1	0.000180595
cg07067577	AGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	17	43508829	SH3D30	0.000180652
cg07438246	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]AGTATTTATATATTTCTCTCTCTCTCTCTCTCT	3	14496645	SLC6A6,SLC6A6,SLC6A6	0.000180806
cg01813757	TGATCTATCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	19	13031108	SYCE2	0.000180823
cg04011829	TAACTAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGTATTTATATATTTCTCTCTCTCTCTCTCTCT	20	51275033	SLCO4A1	0.000181303
cg25909064	AAGAGCCTCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]AGTATTTATATATTTCTCTCTCTCTCTCTCTCT	11	130082895	OAF	0.000181303
cg033027822	AAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	99928067	CJUTF28	0.000181305
cg06711744	CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]ATATAGATTTCTCTCTCTCTCTCTCTCTCTCTCT	10	75389185		0.000181355
cg25596754	AGHTATTTATTTTCTCTCTCTCTCTCTCTCTCT[CG]CATCATATATATATATATATATATATATATATAT	6	32026610	TNRB	0.000181438
cg15922057	TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	25784714		0.000181631
cg27504328	CAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	160519425	CD84	0.000181718
cg02452552	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	150618048		0.000181732
cg23779651	CGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]TGGTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	4	164415027	C4orf43	0.000181758
cg24222546	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT[CG]CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	15	74501771	STRAG,STRAG,STRAG	0.0001818

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g13104939	g07677AGGCGAGATCCAGCTGCAAGCTTGGAGGCTTTCCGCGCGTCAACGAGCTGGGCTAAGGCGCGCTGGGGAGAGCTTCCCG	11	843956	TSPAN4;TSPAN4;TSPAN4;TSPAN4;TSPAN4;POLR2L;TSPAN4
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cg17313269	CTTCGAAAGTCTAAGATTAACAGAGTGAAGGACCGTGTGTGCTGGTGTGATGATATTTCTTGTGAGTTAACT	6	25965330	TRIM38	0.000258954
cg22854009	ACGGCTTATCTCTCTGAGGTCTAGAGAGAGAGCGCGTACCTCTGGTGGTCCGAGAGAGGAGGATGATACAT	19	58111128	ZNF530	0.000259011
cg06499205	GGAAAGACAGAGCAGGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	19	45927594	ERCCLERCCLERCCL	0.000259039
cg01620611	GGAGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	71306145	CDC42EP4	0.000259048
cg22893755	GGCAAGAGAGAGATTCATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	30021145		0.000259108
cg17806418	CTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	6	29599319	GABBR1-GABBR1	0.000259238
cg15726814	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	17859499	ADAMTS2-ADAMTS2	0.000259328
cg13804488	GGAGCTTGAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	17	73760363	GALK1	0.000259476
cg13613748	GGAGCTTGAAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	18	61090281	VPS4B	0.000259496
cg07377178	GAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	6	3825064		0.000259519
cg26529303	TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	19	570438	BSG	0.000259522
cg08125959	GAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	16	3632556	BTBD12	0.000259721
cg01674036	ACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	74058002		0.000259796
cg226053795	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	14	103373907		0.000259818
cg32240252	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	47931591		0.00026
cg157204703	TCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	3509710		0.000260088
cg00145118	TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	141391931	GNPDA1	0.0002600327
cg17344091	TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	28885444	TRIM27	0.000260288
cg07526439	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	39929751	ZHX3	0.000260481
cg08984797	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	227058941	PSEN2-PSEN2	0.000260486
cg13799986	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	9	139686745	TMEM141	0.000260505
cg099864921	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	21	35865767		0.000260509
cg11357670	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	114143948	DCUNID2-TMCO3	0.000260661
cg25129485	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	82189257		0.000260689
cg06126721	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	14780965	SLC43A2	0.000261113
cg26730763	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	38205189	XPO6	0.000261172
cg227313519	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	18385724	KIAA1583-KIAA1583-RIA	0.000261356
cg07241680	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	69259335		0.000261396
cg01674274	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	892585	FAM195A	0.000261408
cg12836863	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	32889023	BRC42	0.000261507
cg21835197	ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	38038514	TFAP2E	0.000261525
cg25185585	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	177052687	HOMD1	0.000261975
cg04563996	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	5709519	ARHGAP3-SPA1A12	0.000261991
cg10442325	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	3	48401953		0.000262052
cg22501942	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	11799278	AGTRAP-AGTRAP-AGTRAP	0.000262226
cg04849030	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	77810309	AGTRAP-AGTRAP	
cg24880546	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	170864648	CBX4	0.000262614
cg27143204	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	54539373	CCNO	0.000262803
cg24620905	GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1	149908781	MTMR11-MTMR11-MTMR	0.000262807

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cg01803759	TCAGCTCAGAGAGGCGCTCCAGACCTGABAG[CG]AGTCGAGATGAGGAGCTGCAAGCTCCAGACGAC	1	27883295			0.00027357
cg22328837	KAAAAATTCACACACAGATGAAATGAGCTTT[CG]TAGATAGAGATTTGGGCAADAAGACTGACGAGGAA	6	45422120		RUNK2:RUNK2-RUNX2	0.000273572
cg03219197	CCGCGCAGGAAATTCGCTGAGCTCTGAGAAATC[CG]TCTATATTTCTTATCTGATGCTCCAAAGAGGAGCTCAAA	2	128175390		PROC	0.000273585
cg02110858	GCAGACTGCTAGGTTACAGAGCGGATACAGAG[CG]CTGAGAGAGAGAGAGCTCTGATCTGAGAGAGCTCCAG	8	145028222		PLEC1:PLEC1-LEC1	0.000273688
cg06033824	ATGGTGGGCAAGCTGGAGGCACTGAGG[CG]GATGAGG[CG]ATGCGAGGCTGAGGAGGAGGAGGAGGAGGAGG	5	172110579		NEURLB	0.0002737
cg045866126	GGGCTCTGCGCGCTGAGAGAGCTGCTGCTGAG[CG]GAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5	176734633		MXO3:MXO3	0.000273794
cg08792777	AGATGAGCTTCTGAGAGGCTGCACTGAGCTGAGT[CG]CTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	14	186322429			0.000274006
cg08437984	ATGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	8	146078724		COMMD5:COMMD5-COM	0.000274036
cg04007328	AGTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	1	13372138			0.000274074
cg25983531	CCGTAATTAACACTCCAGGCAAGCTGAGGATAT[CG]ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	7	36765142		AOAH	0.000274235
cg03708045	GTTCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	8	48595620		KIAA0146	0.000274257
cg20477147	TGCAAAATTCCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	20	57265991			0.000274316
cg06419312	AGCGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	16	89161567		ACSF3:ACSF3-ACSF3	0.000274547
cg14255417	ACAGCAAGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10	104417977		TRM48	0.000274726
cg25153741	AGGCAATTCGTAATTAACACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5	177913458		COL23A1	0.000274811
cg16962257	AGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT	4	153587387		TIME154	0.000274841
cg19770381	AGAGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3	132261993			0.000274948
cg06033796	CGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	20	62367805		LIME1	0.000275256
cg22046301	AGAGTGTGATTAAGTCTGCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1	64213080			0.000275281
cg15815339	GCAGAGTGGAAATCTGCTGTAACAGCTGAGCT[CG]GGTTCAGCTACACAGAGGAGGAGGAGGAGGAGGAG	10	10828105		SFTA3P	0.000275306
cg18560092	AAATTAAGGCTTCTGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	15	71183869		THAP10:LRRC49	0.000275332
cg11019305	TACCTTTCTGAAACTCAAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5	172708836		UBID2	0.000275395
cg20536248	AGAGCAAGAACTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	10	121439845			0.000275402
cg03679544	GGTAACCGAGGCTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	6	155537972		TIAM2:TIAM2	0.000275402
cg03471150	ATTTCTGTTGTTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	201797198		IPG9	0.000275408
cg00026033	CGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	12	56414490		KZ4	0.000275424
cg24575128	AAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3	52502445		NISCH	0.000275437
cg0488015	GGGCGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	17	1494272		SLC3A2	0.000275657
cg10589689	TGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	11	63677197		MARK2:MARK2-MARK2-M	0.00027572
					ARK2:MARR2	
cg01257799	AGAGTTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	11	118753476		CXCR5	0.000275759
cg27044455	CTGGCTTTGTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5	149878183			0.000276022
cg07539190	CTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	9	22459182		CBorf58	0.000276048
cg07110356	CGGTTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	17	58353431		MPO	0.000276053
cg17086398	AGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	31896392		SEBNC2	0.000276088
cg23940612	CTGCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2	218898788			0.000276154
cg20272648	TGCAAGCTTACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	8	37660108		GPR124	0.000276371
cg21877464	CTGCGTAAAGCTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5	151056339		SPARC	0.000276279
cg00446046	AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	3	187686919			0.000276295
cg27241845	TAGTATCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2	233250370			0.000276329
cg08090407	CGATTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	7	7139271			0.000276489
cg19180056	CAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	11	133821072		IGSF9B	0.000276603
cg24790689	AGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	21023823		KIF17:KIF17	0.00027679
cg17996914	CGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	15	11406993		ISPAN16	0.000277041
cg27166581	GGGTTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1	155044322			0.000277078
cg00593607	GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	17	93530780			0.000277216

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g007888994	GCTATCTCTCTGGGTTCTCTGTCCCAAGATTCTTG[CG]AGAAGTGTGTGGAGGTCCTCTGCTGGTCTGAGG	20	6266005	PRPF5	0.000414475
g027510257	TGGGTGTGAAGAACACACTTCCACAGAGAGCTCTGA[CG]CTCCAGACTTATCTGAAAGAGATTTCACTTGACC	13	111305893	CARS2	0.000414517
g007263632	GATTGACATCATCTGTGCAGAAAGAGAGAGAGCTGG[CG]TCTCAGAGAAGAGAGAGAGAGAGAGAGAGAGAG	6	50675674		0.000414753
g005278955	TGAGTGTGTAAGAAAACATAGTATCTGTGTTATG[CG]TACATCTGTGTGAAAGATTAGTATTACTGTGACATAT	5	76381538	ZBED3LOC718713	0.000414811
g027017580	TGCTGTGAGTGTCTGGAGAGAGCTGAGAGAGCTAT[CG]AGTGAAGTGGAGAGAGAGAGAGAGAGAGAGAGAG	14	105717038	BPF1B18D6	0.000414849
g027586417	TGTGCTCTCTCATATGACATCTCTGTGGTGTGAGAG[CG]GGAGATGTATCTCACAGATCTCTGAGATGTGAGAGADA	16	85577809		0.000414967
g026426486	AATTCTTGTGGCAGAGAGCTGAGAGAGCTAAGAG[CG]AAAAATTTCTGTGTGAGAGATGTATGAGATGTGAGAGAG	7	100461644	SIC1A9	0.000415281
g01852476	TCAAGTGCAGAGAGCTGTGAGAGAGAGAGAGAGAG[CG]GACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	2232063	SKI	0.000415366
g000791074	AGAAATGTTTATGCTTATATTTCTAAATTTAGAG[CG]ATTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	151166159	MTHFD1L	0.000415383
g01778567	GAGGTCGTGAGAGAGAGAGTGTGTGAGAGAGAG[CG]TGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	32605782	HILA-DOA1	0.000415622
g017582074	AGCAGAGATGAC TGAGAGTGAGAGAGAGAGAGAG[CG]TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	81818641		0.000415772
g018755846	TTGAGTGTGAGAGATCTGCTTTCTGAGAGATATG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	115157993		0.00041584
g016476991	CATAAGGAATCAAAGATCTGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	114831404	RASA3	0.000416332
g026059316	AATGCCATTTGCGAGCGATGATGTTCTGCTGCTG[CG]CCGAGCTGGGCGCGGCTCTGAGAGAGAGAGAGAG	10	102808232		0.000416417
g00719439	PACTTTTGAAGGAGTGGCGATGAGAGAGAGAGAG[CG]GATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	30	30403325	MYLK2	0.000416564
g00035871	CTCTCTCTGTGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	62539047	DNAK5	0.000416592
g004353288	GTGTGCTGTGGGAGAGAGAGAGAGAGAGAGAG[CG]CTGTGATATACAGAGAGAGAGAGAGAGAGAGAG	16	87958407	CASA	0.000416722
g017078393	GGGACAGGTAAAGAGAGAGCTGTGATTTGGAGAGAG[CG]CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	32717002	LCK	0.000416739
g007471203	GGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	64280911	TM7SF2	0.000417155
g024312537	GTGATAGATCTGAGAGAGAGAGAGAGAGAGAG[CG]GATCTGATTTTATGAGAGAGAGAGAGAGAGAGAG	8	38831332	HTRA4-PIERHA2	0.000417184
g005944840	AGGAGGCTGAGAGAGAGAGAGAGAGAGAGAG[CG]ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	89401631	ANKRD11	0.000417256
g00424276	AGGAGGCTTTATCTGAGAGAGAGAGAGAGAGAG[CG]GATCTGATTTTATGAGAGAGAGAGAGAGAGAG	7	105221180	EFCAB10	0.000417541
g005830220	PACTTTTGAAGAGAGAGAGAGAGAGAGAGAG[CG]ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	87757033	KLHDC4	0.000417625
g003236222	CGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]ATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	9	132245490		0.000417729
g008942183	TTAGGCTTAAATTAATTAACAAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	46522607	HOXB2	0.000417918
g007091220	TATGCTTGAGAAATGAGAGAGAGAGAGAGAGAG[CG]TATATACAGAGAGAGAGAGAGAGAGAGAG	4	146752115	ZNFR27	0.000417958
g015378097	AAATGCTCAGAGAGAGAGAGAGAGAGAGAGAG[CG]CCCTTTTAAAGAGAGAGAGAGAGAGAGAGAG	11	118135270	MPZ2-MPZ1	0.000417984
g01644741	CTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAG[CG]ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	47896888	MIR1259-SNORD138-C206	0.000418067
g024344970	AAATATTTGAGAGAGAGAGAGAGAGAGAGAG[CG]CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	160708987	SLAMF7	0.000418244
g003126058	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATCTGATTTTATGAGAGAGAGAGAGAGAGAG	1	3282757	PRDM16;PRDM16	0.000418247
g01066209	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	2382352	FIS2-NUDT1-NUDT1-NUD1	0.000418254
g01093026	AGGCTTTGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	89749080	T1-NUDT3-NUDT3-NUDT3	0.000418285
g025151803	GGCTCTTGAAGAGAGAGAGAGAGAGAGAGAG[CG]CCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	242677058	DJHEDH	0.000418288
g016896911	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	32895690	PEPD;PEPD;PEPD	0.000418354
g016659510	TTTATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	87998870	BANP-BANP	0.000418396
g015177211	ACAGATCTGAGAGAGAGAGAGAGAGAGAGAG[CG]TATATGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	75567469	POR	0.000418632
g006287548	TGAGATTTATCTGAGAGAGAGAGAGAGAGAGAG[CG]TATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG	21	347773372		0.000419773
g027072545	CGACATGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	31799575		0.00041888
g006000053	CGAGAGAGAGAGAGAGAGAGAG	17	86092975	KPNA2	0.000419021
g01805480	CAGATATGCTGCTGGAAGAGAGAGAGAGAGAG[CG]TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	133137879	FBRSL1	0.000419648
g012359904	TGACTTCTTGAGGTGTAATGAGAGAGAGAGAGAG[CG]ACACTCTTTGAGAGAGAGAGAGAGAGAGAGAG	3	156048454		0.000420059
g014328115	ACCAATTGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	2554562	KCNJ3-KCNJ3	0.000420204
g000174992	ACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	169659121	NOSTRIN-NOSTRIN-NOSTRIN	0.000420205

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cg0381767	TTGCGAATGAGACAGAGGAGTTCAGACTT[CG]AGAGCTGGAGATCTCCAGAGCGGTTGCGAGG	13	97646778	OXGR1	0.000512578
cg00686823	ATTACATATCTCTATCCAGCATTAATGGCCAC[CG]CTGTGAGGCTTCTGAGGCTGAGGCTGAGGCT	3	127311038	TPRA1	0.000512615
cg16527057	CGGCGCTAGGAGACGCTTGAGGAGGAGGAGGAG[CG]GCGAGGAGGCTGAGGAGGAGGAGGAGGAG	1	157069242	ETV3L	0.000512683
cg26368228	GAGGCTGGGAGGCTTCTGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	171770825		0.000512991
cg21368578	ATTGAGGCTGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	22	38029473	GGAI1GGA1	0.00051354
cg25134567	CTGAGGCTTGAAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	17	64782369	PRKCA-MIR634	0.000513936
cg16555909	TGTAAGGCTTCTGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	23721285	TCEA3	0.000513562
cg09499413	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	11	9780133		0.000513994
cg07347461	TGTAAGGCTTCTGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	16	85668905		0.000514262
cg13493766	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	9	97365869	FBP1-FBP1	0.00051435
cg01704474	TGTAAGGCTTCTGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	11	304918	RNH1-RNH1, RNH1-RNH1, R	0.000514744
cg19867924	TGTAAGGCTTCTGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2	148234430	ARHGAP15	0.000514828
cg16931707	ATTACATATCTCTATCCAGCATTAATGGCCAC[CG]CTGTGAGGCTTCTGAGGCTGAGGCTGAGGCT	12	42873702	PRICKLE1, PRICKLE1, PRICK	0.000515097
cg03916225	TGTAAGGCTTCTGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	111768837	IF1, PRICKLE1	0.000515275
cg24586978	TGTAAGGCTTCTGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	13	98613723	CHB12, CHB12	0.000515331
cg08116137	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2	73870653	DOCK9, DOCK9, DOCK9, DO	0.000515334
cg12740380	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	7516366	NAT5, NAT5IP	0.000515619
cg21554588	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5	138720378	CAMTA1	0.000515638
cg26444741	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	7	102921054	SIC23A1, SIC23A1	0.000515642
cg08409451	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	16	2273123	DPY19L2P2, DPY19L2P2	0.000515883
cg16398451	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	12	53593265	E4F1	0.000516214
cg08110363	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	19	13984735	POU6F1, POU6F1	0.000516649
cg07786220	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	17	78683082	MIR181C, MIR181D	0.000516687
cg08509155	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	36616028	RPTOR, RPTOR	0.000516722
cg05037688	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	9	139556554	TRAPPC3	0.000517063
cg11690666	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	17	80415469	EGFL7, EGFL7	0.000517145
cg08220966	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	10	88717364	NARE, NARE, NARE, NARE	0.000517238
cg16164260	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3	187454439	MIRN2, SNCG, MIRN2	0.000517312
cg08582438	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	7	142920396	BC16, BC16	0.000517498
cg08133616	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	16	67867224	TAS2R40	0.000517752
cg01530082	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	6	32784327	CENPT	0.00051781
cg13483882	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3	128212476	HUA, DOB	0.000517906
cg21545857	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2	242710824	GATA2	0.000517947
cg24681612	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	233356952		0.000518036
cg18278894	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	179945973	PCW12	0.000518256
cg02187759	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2	16804452	CEP350	0.000518273
cg25135019	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	154435948	PAM49A	0.00051919
cg26433561	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	110426090	IL6R1LR	0.000519299
cg15552491	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	11	119037285		0.000519643
cg111942936	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	10	77169689		0.000519678
cg125866150	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	6	2840792	SERPINE1	0.000519707
cg21687740	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	157164556		0.000519894
cg09563216	GAGGCTAGGAGGAGGAGGAGGAGGAGGAG[CG]GAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1	150255241	C1orf51, C1orf51	0.00052009

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g038837313	AGAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	11	57195350	SIC43A3_SIC43A3_SIC43A	0.00067755
g038837314	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	13	42184765	RUA0564	0.000677886
g038837318	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	3	328914658		0.000677916
g038837319	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	2	240020152	HOAC4	0.000677995
g038837327	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	17	43340243	LOC100133951:LOC10013	0.000678022
g038837328	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT				
g038837329	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	21	40124277	3991_C17orf46	0.000678089
g038837330	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT			4NCBNA000134	
g038837331	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	5	149865757		0.00067825
g038837332	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	1	181109487		0.000678631
g038837333	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	7	3078786	MAD1L:MAD1L:MAD1L	0.000678759
g038837334	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	1	82319602	INADL	0.000678825
g038837335	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	6	31540121	LTA1:TA1:TA	0.000679034
g038837336	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	10	181370592	SIC25A28	0.000679124
g038837337	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	6	151258520	MTHFDL	0.00067948
g038837338	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	22	37256947	NCF4:NCF4	0.000679513
g038837339	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	12	116581414	MED13L	0.000679615
g038837340	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	19	3361374	NFIC	0.000680021
g038837341	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	5	3605558		0.000680207
g038837342	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	17	48047917		0.000680351
g038837343	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	6	32905190	HLA-DMB	0.000680369
g038837344	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	17	72359213	BTBD17	0.000681067
g038837345	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	7	180464553	TRIP6:SIC12A9	0.000681124
g038837346	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	8	11059241	KR6	0.000681142
g038837347	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	6	155517944	TIAM2:TIAM2	0.000681291
g038837348	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	9	179468985		0.00068135
g038837349	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	17	38077870	GRMDL3	0.000681868
g038837350	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	15	68682927	HGA11	0.000682012
g038837351	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	16	21664231	METTL9:IGSF5:METTL9	0.000682046
g038837352	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	6	166856094	RP56KA2:RP56KA2	0.000682199
g038837353	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	15	83501699	WHAMM	0.000682346
g038837354	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	5	33171158	GOLPH3	0.000682407
g038837355	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	19	18920396		0.0006828
g038837356	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	12	113535352	DTX1	0.000682968
g038837357	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	15	98030316	RHC6	0.000683126
g038837358	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	11	134085593	VPS28	0.000683284
g038837359	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	21	35570815		0.000683635
g038837360	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	15	69076089	ANP32A	0.000683996
g038837361	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	7	127774154		0.000684265
g038837362	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	19	9753024	SH2D3A	0.000684481
g038837363	GAGCAGAGGCTTACATACCTTCCAGCCGAGAGCA[CG]TGAGGCTGACGCTCTCTTCTGAGCTCTCTGAGGCTCTT	7	633445	PRKAR1B:PRKAR	

cg09265392	GGGACGCTGAAACATGCAAGTGGGATCCAGAGAG[CG]CGAGTGGCGGAGACGCGTGCTGCACTGCGCTGCT	15	48910215		0.000685624
cg12483797	CTGCGCTTCGCTCAGTCACTTADACAAACATGAGT[CG]CGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	9	132431581	PRRX2	0.000685933
cg18101284	GCATGCGGGTGCACACATATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1	67595214	C3orf141	0.000686263
cg20795401	CAGTCTGAGAGAGCTGCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT	2	173291908	ITGAB,ITGAB	0.000686282
cg26014335	CACCTTACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT	8	6384320	AGPAT5	0.000686668
cg27316818	TAAATTTACCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT	10	104436518	ARL3	0.000686943
cg10619379	CGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT	17	27452684	PHF12,PHF12	0.000686962
cg17342247	TTGAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	17	3540594	CTNS,SHPK,CTNS	0.000687207
cg04944800	TAGAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6	149775853	ZC3H12D	0.000687335
cg09152866	TAAAGAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5	11714562	C6orf105,C6orf105	0.000687575
cg22173949	TGGCTGAGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1	117210557	IGSF3,IGSF3	0.000687629
cg03736958	ACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3	52099548	C3orf74	0.000687792
cg01052838	AGGACGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	30	3075251		0.000688063
cg04709771	GATGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16	846395	RAB40C	0.000688196
cg09903452	ACAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	17	75315244	SEP19,SEP19,SEP19	0.000688239
cg06261052	AGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	10	13545875	BEND7,BEND7	0.000688337
cg12526374	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	7	140097579	SLC37A3,SLC37A3	0.000688362
cg18125371	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	11	44332719	ALX4	0.000688787
cg17674640	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	13	52586589	ALG11,ATP7B,ATP7B	0.000688911
cg06477069	ACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	20	35493378	C20orf117	0.000689198
cg13895650	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	9	84228185	TLC1	0.000689311
cg06001524	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	17	9364709	STX8	0.000689435
cg27031754	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5	54185940		0.000689679
cg06635946	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	22	46470016		0.000689716
cg00145079	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	15	58112888		0.000689728
cg00900817	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1	8272081		0.000689811
cg00592460	AGGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5	9343256		0.000689839
cg11291003	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5	134576241		0.000689865
cg23976388	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	11	61510081	DAGLA	0.000689995
cg04352938	AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16	88101013	BAMP,BAMP	0.000689999
cg18148314	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1	8425319	ACOT7,ACOT7	0.000690185
cg18182566	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	14	105888161	MTA1	0.000690254
cg00369658	AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	11	57365088	SERPING1,SERPING1,SERP	0.000690628
cg18062140	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	30	53967678	RBM38,RBM38	0.000690945
cg00479827	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	7	21036986	RCRMA00185	0.000691972
cg00830393	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	3	66553063	URIG1	0.000692001
cg20916427	AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	18	44627440	KATNAL2	0.000692027
cg02335251	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	2	66801399		0.000692309
cg03132773	AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	16	22824877	HS3ST2	0.000693147
cg11091844	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	11	85460604	SYTL2,SYTL2,SYTL2	0.000693589
cg26474127	CTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	13	28562619	PHOXNB	0.000693654
cg04188920	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	10	3138534	PKP	0.000694343
cg14045860	AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	11	36158283		0.000694829
cg00774102	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5	31590870	BAT1,SNORA36	0.000695078
cg05891054	CGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	17	40380254	STAT5B	0.000695241
cg13826055	AGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	9	117259143	DRNB31,DRNB31	0.000695554

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cg02447879	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	17	79593682	BAHCC1	0.000788963
cg03128268	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	18	48432179	BSM3	0.0007891
cg19735804	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	7	342421812		0.00078914
cg16166160	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	6	108479144		0.000789207
cg22354583	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	1	33588590	HPCA	0.00078952
cg27561350	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	15	55583094	RA027A	0.000789851
cg14184780	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	9	95475751	BICD2, BICD2	0.000790366
cg07727594	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	20	45187423	SIC13A3, SIC13A3	0.000790729
cg02753670	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	1	6762231	DNAC11	0.00079154
cg09298313	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	14	55569859		0.000791599
cg07601475	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	16	89941916	ICF25	0.000791661
cg02343628	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	15	93790914		0.000791819
cg01985390	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	2	27529881	TRIM54, TRIM54	0.000791922
cg24152603	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	3	127945838	EFSEC	0.000791924
cg10640764	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	19	11216364	IDL1	0.000792115
cg16486502	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	6	39882954	USP45	0.000792489
cg26209169	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	3	1316164		0.000792642
cg11200462	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	15	86786368	SNAPC5	0.00079279
cg20427486	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	2	162849137	OPP4	0.000792981
cg10275766	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	2	173591150	LOC91149	0.000793664
cg01057573	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	5	118683890	TNFAIP8	0.000793834
cg04326356	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	7	48328294	UPP1, UPP3	0.000794037
cg11982471	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	6	31130167	ICF19, ICF19	0.000795415
cg27640054	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	7	47623863	FOXK1	0.000795456
cg09744840	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	10	74463027	CCDC109A	0.000795556
cg18255315	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	7	73897230	GTF2IRD1, GTF2IRD1	0.000795678
cg01594488	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	4	1580172		0.000795717
cg02313366	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	8	13469021	ST3GAL1, ST3GAL1	0.000796565
cg06553052	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	19	1275167	C19orf24	0.000796642
cg22961402	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	17	27913793	GHI1, GHI1	0.000796851
cg01338023	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	5	138555698	TNEM173	0.000797117
cg20107506	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	4	100874826		0.00079712
cg27494647	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	7	150038898	RARRS2	0.000797481
cg08290675	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	11	23423025		0.000797692
cg05301682	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	6	2988723	DKFZP686I5217, DKFZP68	0.000797715
cg14763104	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	11	811317		
cg0025625	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	11	2406384	CD81	0.000797834
cg25444092	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	16	25608058		0.000798041
cg10136168	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	13	102520143	FGF14, FGF14	0.000798397
cg04884267	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	14	77783447	POMT2	0.000798908
cg14043316	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	19	58694502	ZNF274, ZNF274; ZNF274; ZNF274	0.000798956
cg1832395	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	22	30743429	PLKRB2	0.000799052
cg14093936	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	5	17805785		0.000799709
cg14191024	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	15	74726614	SEMA7A, SEMA7A; SEMA7	0.000799844
	CGTCTGCGGCGTCACTAATCAAAACAAAGGCTCG	CGCTGCGGCGTCACTAATCAAAACAAAGGCTCG	11	110070509		0.000800487

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qg02354389	AAAGTTTGTGATGAAAGATACCTTTCTGTCGTCGCTGCTGATCTTTCTCAATACAGAGTGAATCGG	4	185362534	IR72	0.001059962
qg18644093	CAGAGCTGCTCTCTGAGAGGATGATGCTGCGCGCTGGAGCTTATATATTAATATTTGAGATCAAGATAGAA	5	150521257	ANVAG;ANKA6	0.001059974
qg25941075	GGGAAAGAGAAAGACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	73729854		0.001060031
qg24360269	CTGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	148527081		0.001060034
qg23801028	CACGCTTTGATACAGAGATATCTCGCTCTCTCTGTCGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	10	96791308	CRFAC1	0.001060109
qg06010514	CAGAGAGGAGATCTGACAGAGATGAGTACAGTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	16	18271105	SPB3	0.001060158
qg21822573	GGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	31812336	G12orf72;C12orf	0.001060372
qg12201380	CTAGCTGCTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	123717181	NSMCE4A;NSMCE4A	0.001060547
qg25136988	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	31645623	LV6G5C	0.001060769
qg13542542	CTGAGAGCTGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	19	42821106	TMRM145	0.001061142
qg21610834	CTAGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1	1582359914	CDIC	0.001062529
qg01751802	AGCATATACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	19	11509639	KANK2	0.001062684
qg20618651	CTGTGAGAGTGTAAATCTCAGAGAGATTAAGCTTTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	56718365	EXOC1;EXOC1;EXOC1	0.001062839
qg26424817	AGCTGAGAGATGAGAGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1	59424096		0.001063136
qg13720971	GAAGAAATGCTGAGAAATGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	19	895642	PRSS11	0.001063237
qg09959259	GGCAGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	3	122291975	PARP9;PARP9;DIXAL;PARP	0.001064058
				9;PARP9;PARP9;PARP9	
qg25741215	GAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2	63287682		0.001064184
qg18024065	GGAGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	11	94278603	FUT4	0.001064328
qg17785202	TTCTGCTGTAAATCTGAGAGAGATCACTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1	14870226		0.001064337
qg0178728	GAAGCAATCTTTAAATCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	22516158	GPR125	0.001064477
qg05593716	AGCATCAATCTTAAAGATTCATCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	8	317950454	CBorf55	0.001065087
ch.137472519R	CTCATAGAGAGATGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	2	37615915		0.001065338
qg25741790	TTTGAGAGAGAGATGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	7	127295153	SMD1	0.001065858
qg12191432	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	312631258	LOC282997;PDCD4;PDCD4	0.001065911
qg00853979	CTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1	37681368	DCDC2B	0.001066009
qg12619347	CTCTAGAGAGAGATGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	11	52280909	SLC43A1	0.001065836
qg07788665	GGAGAGAGAGATGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	10	30101042		0.00106722
qg04755604	ATTATATCTGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	11	13011184		0.001067773
qg0587385	CTTTATATCTGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	15	26337648		0.00106792
qg24705939	CGAGAGAGAGATGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	8	30413864	RBPMS;RBPMS;RBPMS	0.001068142
qg11080652	CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1	8556722	REPERERE	0.001068143
qg06390187	TTCTAGTGGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	15	41233838		0.00106841
qg03302036	CCGAGCTTCATCTGATCTGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	1	182574639	RGS15	0.001068499
qg13827779	GGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAG	14	103524999	CD42BPB	0.001068937
qg03796324	CTCACTCTGAGCTTTGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAG	6	30383625	RBPMS;RBPMS;RBPMS;R6	0.001068865
qg21805115	CTGAGAGAGAGATTTGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAG	6	106539937	PRDM1	0.001068901
qg27332104	GATGCTAGAGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAGATTTGAGAGAG	15	52386161		0.001068903
qg23894905	GCATCTGATTAATCTTATTCAGAGTATAGTATAG[OH]TGGCAGAGATGATATATTTGTTTATTTGAGAGAG	19	41983773	MGA;MGA;MRK26	0.001069295
qg13424029	SACATCGAGAGAGAGCTAGAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	10	101297508		0.001069351
qg21335378	TCGAAAGAGATGGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	173150101		0.001069538
qg24512005	CGGAGAGAGCTGTGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	3014291	NAP114	0.001069561
qg04896607	CAGAGCTCACAGAGAGAGAGATATATATATAT[OH]ATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	66262214	HMGAS;HMGAS2	0.001069991
qg15647311	AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	12897519		0.001070039

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cg1574277	CGTCTCTATTAATGCTTACCAACGTCAGAAATAG[CG]TGGTCTGCTCTGGTGAAGAGCTCAGAGGATCTGAG	2	5539218		0.001080707
cg17838016	TGAGGAAAGGCTCGGACAGAAACAAACAAATCTGTA[CG]CTCTCCCTGAAACATCTCTGAGACAGACCTGAGTG	19	50832861	KCMC3	0.001081045
cg13359071	AGAAATAGGAGATAGCGAAACATCTTTATTAATAAA[CG]AGGAGGAGCTGAGATCTCAAGATCGAGACATGAGAC	7	134134721	ANR181	0.001081119
cg21491308	GTGGCTTATGATCTCTATATAGCTGGGAAATAGATGATGAG[CG]TGGATCTCTGAAAGAAATATGTTATGAGGATTTGATG	19	43892826	TEX101:TEX101	0.001082011
cg1362778	TGAGGATCGAGAGGAGAGCTGAGATGAAATGAGAGGCTGAG[CG]TACAGAGAGAGAGAGGCTCTGCTGAGGATGAGAGCTGAG	12	54779312	ZNF385A:ZNF385A:ZNF38	0.001082036
				5A:ZNF385A	
cg08615050	GCCTTCCTGAGAGCTGACATATGCTGCTTATGAGGAT[CG]AGATATATCTTGGGCTATGAGGAGATATGACAGCTGAG	11	67049363	ADR6K1	0.001082251
cg01369689	ATTAAGCTCTGAGGCTTCTAGGCTAGAGTATGAGGAGAGG[CG]CAGCGAATATGAGGAGAGGCTTTTATGAGCTGAGAGC	16	30786529	RNF40	0.001082295
cg25778076	CATATCTCGAGGCTGCTGAGGATGAGAGAGAGAGAGG[CG]GTGATGAGGATGAGGAGAGAGGATGAGGAGAGAGG	22	34915573	IGL11:IGL11	0.00108262
cg17012126	CTCTTCAAGAGGCTGCTTGGCTGGCTGAGAGAGAGG[CG]GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	54784859	SNK15:SNK15	0.001082897
cg12699599	CGAGATTAAGGATTAAGCTATGCTCTTATATCTCT[CG]AGCTCTCTGATCTGAGAGAGAGAGAGAGAGAGAGAG	15	40643142	PHGR1	0.001083359
cg13299822	TGGAATGTATGACAGAGAGAGAGAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	73738087	KCMC5:KCMC5:KCMC5:KC	0.001083525
				NQS:KCMC5	
cg14919455	AGCAATGTATGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	7167468	RREB1:RREB1:RREB1:RREB	0.00108416
cg09001777	GAGGAAATGTGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TGTACATCTGAGAGAGAGAGAGAGAGAGAGAGAG	19	5851504	FUT3:FUT3:FUT3:FUT3	0.001084277
cg22836174	ATCTGGGCTGAGGAGAGAGAGAGAGAGAGAGAGAG[CG]GTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	228231970	TMM5F20	0.001085064
cg18706831	TTTATGATCTGAGATCTGAGAGAGAGAGAGAGAG[CG]TGGCTGATTTTCTGAGATTTTCTGAGAGATTTTCTG	6	26204823	HIST1H4E	0.001085369
cg05555434	ATGATGATCTGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	17660838	RBP1:RBP1	0.001085789
cg09698634	CTCTATGAGGCTCTGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	31	14981080	ROTE1	0.001087384
cg12368890	AGAGCTTTGAGGCTGAGGATTTGATAGAGAGAGAG[CG]GTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	20	1712153		0.001087503
cg01115058	AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGATGATCTGAGAGAGAGAGAGAGAGAGAGAGAG	8	145733180	MFSD3	0.001087618
cg08426377	CATATGAGATCTGAGAGAGAGAGAGAGAGAGAG[CG]CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	36785939	C10orf113:C10orf113	0.00108777
cg00057663	CATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	105945629	IGFBRAP1:IGFBRAP1	0.001087781
cg24640577	CATATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	246939216		0.001088284
cg07723510	CGATTTATGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	30228063	HLA-L	0.001088557
cg18689392	GTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	114637656	TEX5:TEX5:TEX5:TEX5	0.001088923
cg14942952	ATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGATGATGAGAGAGAGAGAGAGAGAGAGAGAG	22	44576168	PARVG:PARVG:PARVG:PA	0.001089099
				RVG:PARVG:PARVG	
cg28751120	TGAGGATGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	113496053	DTX1	0.00108924
cg12516954	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	134714252	H2AFYH2AFYH2AFYH2A	0.001089346
cg07148591	CTGACATAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	15	59457701	MIR548H4:GLCE	0.001089614
cg03019090	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAG	15	58812960	UFC	0.001089688
cg19040012	ATATCTGATGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGATGAGAGAGAGAGAGAGAGAGAGAGAG	6	35185397	SCUB3	0.001090403
cg04231636	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGATGAGAGAGAGAGAGAGAGAGAGAGAG	6	18188411	KDM1B	0.001090617
cg14814714	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]CTGATGAGAGAGAGAGAGAGAGAGAGAGAG	20	57000	DEFB125	0.001091661
cg27563650	AGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	18	74826769	MBP:MBP	0.001091761
cg10257521	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	1363828	USP1:USP1:USP1:USP1	0.001092223
cg08916411	TTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	4	94054319	GRID2	0.001092403
cg23729449	GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	15621840	BEAP	0.001092558
cg03776506	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	30581384	ZNF688:ZNF688	0.001093353
cg26796095	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	5625046	SAFB	0.001093775
cg05494417	TTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	21	43933482	SIC37A1	0.001094349
cg20872937	GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	74981969	GALR1	0.001094469
cg05598919	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	45128053	NACAD	0.001094476
cg1697872	CTGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]GATGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	64008132	FKBP2:FKBP2:FKBP2	0.001095766
cg23599820	TGATGAGAGAGAGAGAGAGAGAGAGAGAGAG[CG]TAAAGAGAGAGAGAGAGAGAGAGAGAGAG	17	73456199	NIAA195	0.001094227

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cg04075726	CGAAGTACGCTTGAAGAGTGGAGAGTGTGGTAC[CG]TTATGCAACACATGAAAGGACATGACACACATCTA	2	88499425		0.001107466
cg21186443	TTCAGATGAGGACGGAAGTGCCTCTTCAAGATG[CG]CTGTATATCTGCAATCTGTCGCTGAGCTGGGG	3	68057322	FAM19A1	0.001107751
cg14328641	TTCGGTACCTGG[CG]CTCTTCTCTTTCCTGATCA[CG]TCTGCACTGACCTCTCTGTCTGTAGAGATGAGAC	11	58822727	MS4A3.MS4A3.MS4A3	0.001107755
cg11009233	GAGAGAGAGGATTTGTGGAATGACTGATGAG[CG]GAGTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAG	5	1174646		0.001107756
cg12229555	TCTCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	80360329		0.001108305
cg10787704	CAGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	13	59948751		0.001108882
cg07068683	AGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	9	131941454	HERSL	0.001109769
cg03924164	AGTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	88515063		0.001110227
cg0646736	TATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	84140893	MEI	0.001110342
cg1146414	GCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	4671731		0.001110489
cg1147471	AGAGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	135087686		0.001110648
cg11573840	GTTCGCTATGCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	47092156	IGF2BP1.IGF2BP1	0.00111068
cg04240553	GAAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	6188614	TRADD	0.001111
cg21830849	GAATCAGCTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	129283486	SLC15A4	0.0011112
cg21462732	CGGAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	136871881	MAP7	0.00111135
cg14009467	CTCTGCTCTCTGAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	13052719	CAIR	0.0011113491
cg09980626	CTCTCTCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	30123405	LOC100271231.GDPD3	0.001111331
cg11359912	TGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	145421667	SH3BP2	0.001112107
cg04310806	CTTTTACTGTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	87504597	DBP4.SLC25A40	0.001112322
cg14299369	CAATAGCATATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	15	43560165	TGMS.TGMS	0.001112578
cg03043696	TAATGAGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	1820656	GNB1	0.001112746
cg13489137	TAGAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	2	161290449	RBMS1.RBMS1	0.001112792
cg1146178	TTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	92666247		0.001112832
cg08434569	TAATGAGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	12	54970794	ATF7.ATF7.ATF7	0.001112978
cg1075731	CTGAGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	17	72527627	COX30L8.COX30L8	0.001113576
cg26578983	AGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	16	80073249	RIAA0513	0.001113716
cg01952989	AGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	7	1986334	MAD1L1.MAD1L1.MAD1L1	0.001113777
cg18067134	TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3	71084634	FOX1	0.001113952
cg04257984	GTAGTTTGAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	171568984	LOC40925	0.001114751
cg2A98814	AGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2	1516240	TFD.TFD.TFD.TPD	0.001115037
cg08553292	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	58920029	FAM111A.FAM111A.FAM111A	0.001115087
cg25875049	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	15	43531947	TGMS.TGMS	0.001115396
cg17291836	TAATGAGTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	30	45319455	TP53BK	0.001115593
cg08553572	GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	19	947765	ARD3A	0.001115785
cg14909495	CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	7	150649472	ABP1	0.001116097
cg10880485	TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	14	60974394		0.001116325
cg12042808	TTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	17	11924852	MAP2K4	0.001116361
cg09389149	CAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	16	87359115		0.001116398
cg00892368	AGAGGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	6	32847704	PFF182P1	0.001116319
cg02889001	AAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	16	1519785	CLCN7.CLIN7	0.001116639
cg10798725	ATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	11	448822	PTD52	0.001116894
cg14547028	TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	9	139617537	FAM69B	0.001117341
cg21578207	AGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	1	44870088	RNF20	0.001117353
cg17633988	GCATATTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1	144928806	PDK4NP.PDK4NP.PDK4NP	0.001117531
cg15530916	CTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5	20046086		0.001117806

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WHAT IS CLAIMED IS:

1. A method of determining whether or not an individual uses alcohol, comprising the steps of:
determining the methylation status of at least one CpG dinucleotide in a biological sample from the individual; and
correlating the methylation status of the at least one CpG dinucleotide to determine whether or not the individual uses alcohol.
2. The method of claim 1, wherein the at least one CpG dinucleotide comprises position 71389896 of chromosome 10.
3. The method of claim 2, wherein demethylation at position 71389896 of chromosome 10 is indicative of previous or current alcohol use.
4. The method of claim 3, wherein remethylation at position 71389896 of chromosome 10 is indicative of less or no alcohol use.
5. The method of claim 1, wherein the at least one CpG dinucleotide comprises position 54677008 of chromosome 12.
6. The method of claim 5, wherein demethylation at position 54677008 of chromosome 12 is indicative of previous or current alcohol use.
7. The method of claim 6, wherein remethylation at position 54677008 of chromosome 12 is indicative of less or no alcohol use.
8. The method of claim 1, wherein the at least one CpG dinucleotide comprises position 75262522 of chromosome 8.

9. The method of claim 8, wherein demethylation at position 75262522 of chromosome 8 is indicative of previous or current alcohol use.
10. The method of claim 9, wherein remethylation at position 75262522 of chromosome 8 is indicative of less or no alcohol use.
11. The method of claim 1, wherein the at least one CpG dinucleotide comprises position 92137791 of chromosome 9.
12. The method of claim 11, wherein demethylation at position 92137791 of chromosome 9 is indicative of previous or current alcohol use.
13. The method of claim 12, wherein remethylation at position 92137791 of chromosome 9 is indicative of less or no alcohol use.
14. The method of claim 1, wherein the determining step comprises:
 - contacting DNA in the biological sample with bisulfite under alkaline conditions to produce bisulfite-treated DNA;
 - optionally, amplifying the bisulfite-treated DNA to produce amplified bisulfite-treated DNA;
 - contacting the bisulfite-treated DNA with at least one oligonucleotide that is complementary to a sequence comprising the at least one CpG dinucleotide; and
 - detecting the methylation status of the at least one CpG dinucleotide.
15. The method of claim 14, wherein the at least one oligonucleotide detects the CpG dinucleotide in the bisulfite-treated DNA in the unmethylated state.
16. The method of claim 14, wherein the at least one oligonucleotide detects the CpG dinucleotide in the bisulfite-treated DNA in the methylated state.

17. The method of claim 1, wherein the biological sample is selected from the group consisting of peripheral blood, lymphocytes, urine, saliva, and buccal cells.

18. The method of claim 1, wherein the methylation status of the at least one CpG dinucleotide is determined using bi-sulfite treated DNA.

19. The method of claim 1, further comprising obtaining self-report data from the individual regarding whether or not the individual is user of alcohol.

20. A computer implemented method for determining whether or not an individual uses alcohol, the method comprising:

obtaining measured data associated with the user, the measured data comprising one or more measured CpG methylation status;
generating a predictive score based on the obtained measured data; and
providing a likelihood of alcohol use by the user based on the predictive score.

21. The method of claim 20, further comprising:
determining the CpG methylation status for the user, wherein a change in methylation status is an indicator of alcohol use.

22. The method of claim 20, further comprising:
outputting a predicted level of alcohol use based on the predictive score.