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(54) **Title:** METHODS AND COMPOSITIONS FOR CANCER DIAGNOSIS AND TREATMENT BASED ON NUCLEIC ACID METHYLATION

(57) **Abstract:** The present invention provides evidence that PRC2 target methylation is present in multiple forms of cancer. In six out of seven tumor types, hypermethylated genes were found to have promoters that are enriched for PRC2 targets. Thus, featured herein are compositions and methods for treating cancer. In one aspect, methods are provided for blocking the binding of all or part of a PRC2 complex to a nucleic acid target gene region that comprises one or more PRC2 binding sites.

METHODS AND COMPOSITIONS FOR CANCER DIAGNOSIS AND TREATMENT BASED ON NUCLEIC ACID METHYLATION

RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application No. 60/890,822 filed February 20, 2007, entitled "METHODS AND COMPOSITIONS FOR CANCER DIAGNOSIS AND TREATMENT BASED ON NUCLEIC ACID METHYLATION," naming Mathias Ehrich and Dirk van den Boom as inventors, and bearing attorney docket no. SEQ-6006-PV. This application also claims the benefit of U.S. Provisional Patent Application No. 60/890,825 filed February 20, 2007, entitled "METHODS AND COMPOSITIONS FOR CANCER DIAGNOSIS AND TREATMENT BASED ON NUCLEIC ACID METHYLATION," naming Mathias Ehrich, Dirk van den Boom and Aaron Scalia as inventors, and bearing attorney docket no. SEQ-6007-PV. This application is also related to U.S. Patent Application No. 10/888,359 filed July 9, 2004, entitled "Methods and Compositions for Phenotype Identification Based on Nucleic Acid Methylation," naming Dirk van den Boom & Mathias Ehrich as inventors, and bearing attorney docket no. SEQ.001.P; and PCT Patent Application No. PCT/US2006/030256 filed August 2, 2006, entitled "Methods and Compositions for Disease Prognosis Based on Nucleic Acid Methylation," naming Dirk van den Boom & Mathias Ehrich as inventors, and bearing attorney docket no. SEQ-4098-PC. This application also is related to International Patent Application No. PCT/US2005/009929 filed March 24, 2005 (attorney docket no. SEQ-2080-PC), U.S. Patent Application No. 11/089,805 filed March 24, 2005 (attorney docket no. SEQ-2080-UT) and U.S. Provisional Patent Application No. 60/556,632 filed March 26, 2004 (attorney docket no. SEQ-2080-PV), each entitled "Base Specific Cleavage Of Methylation-Specific Amplification Products In Combination With Mass Analysis" and each naming Mathias Ehrich and Dirk van den Boom as inventors. These applications are related to subject matter in U.S. Application No. 10/272,665 filed October 15, 2002, entitled "Methods For Generating Databases And Databases For Identifying Polymorphic Genetic Markers" and naming Andreas Braun, Christian Jurinke and Dirk van den Boom as inventors. Each of the foregoing patent applications is incorporated herein by reference in its entirety in jurisdictions allowing incorporation by reference.

FIELD OF THE INVENTION

The present invention relates to therapeutic applications in the field of medicine and biotechnology. More specifically, the invention relates to novel therapeutic targets and methods for treating cancer.

BACKGROUND

Genetic information is stored not only in the sequential arrangement of nucleotide bases, but also in covalent modification of selected bases (*see, e.g.*, Robertson *et al.*, *Nature Rev. Genet.* 1:11-19 (2000)). One of these covalent modifications is methylation of cytosine nucleotides, particularly cytosines adjacent to guanine nucleotides in "CpG" dinucleotides. Covalent addition of methyl groups to cytosine within CpG dinucleotides is catalyzed by proteins from the DNA methyltransferase (DNMT) family (Amir *et al.*, *Nature Genet.* 23:185-88 (1999); Okano *et al., Cell* 99:247-57 (1999)). In the human genome, CpG dinucleotides are generally under represented, and many of the CpG dinucleotides occur in distinct areas called CpG islands. A large proportion of these CpG islands can be found in promoter regions of genes. The conversion of cytosine to 5'-methylcytosine in promoter associated CpG islands has been linked to changes in chromatin structure and often results in transcriptional silencing of the associated gene. Transcriptional silencing by DNA methylation has been linked to mammalian development, imprinting and X-Chromosome inactivation, suppression of parasitic DNA and numerous cancer types (*see, e.g.,* Li *et al., Cell* 69:915-*26* (1992); Okano *et al., Cell* 99:247-57 (1999)).

DNA methylation has become increasingly important in the field of cancer research. Methylation changes have been associated with the occurrence of cancer, and these changes may serve as markers for the early detection of neoplastic events (Costello *et al.*, Nature Genet. 24:132-38 (2000)). The best known methylation changes refer to promoter specific hypermethylation with correlated downregulation of the corresponding transcription product (Laird, P.W. *Nat Rev Cancer* 3, 253-66 (2003)). Another frequent methylation change is global hypomethylation of repetitive elements within the genome (Rollins, R.A. et al. *Genome Res* 16, 157-63 (2006)). Together, studying these changes offer a powerful tool for cancer research, in terms of diagnostics, prognostics and treatment.

SUMMARY

In embryonic stem cells a distinct set of developmental regulator genes is silenced through epigenetic modifications to maintain pluripotency. These genes have binding sites for the polycomb

repressive complex 2 (PRC2) in their promoter region. Subunits of the PRC2 complex are able to recruit DNA methyltransferases (DNMTs) and initiate *de-novo* methylation. Provided herein is evidence that PRC2 target methylation is present in multiple forms of cancer. A cell line model was used for discovery and a subset of the results were further validated using clinical specimens. In six out of seven tumor types, hypermethylated genes were found to have promoters that are enriched for PRC2 targets.

Thus, featured herein are compositions and methods for treating cancer. In one aspect, methods are provided for treating cancer which comprise blocking the binding of all or part of a PRC2 complex to a nucleic acid target gene region that comprises one or more PRC2 binding sites. In one embodiment, the invention includes in part nucleic acid probes that bind specifically to the PRC2 binding sites of the target genes and block the binding of the PRC2 complex to the target genes. In another embodiment, DNA methyltransferase inhibitors are administered to a subject found to be at an increased risk for cancer. Examples of DNA methyltransferase inhibitors include, but are not limited to, azacitidine and decitabine. See Silverman et al. *Nat Clin Pract Oncol.* 2005 Dec;2 Suppl 1:S12-23, which is hereby incorporated by reference. In yet another embodiment, an S-adenosylhomocysteine hydrolase inhibitor is administered to a subject found to be at an increased risk for cancer. An example of an S-adenosylhomocysteine hydrolase inhibitor includes, but is not limited to, 3-Deazaneplanocin A (DZNep). See Tan et al. Genes Dev. 2007 May 1;21(9):1050-63, which is hereby incorporated by reference. In another therapeutic embodiment, a histone deacetylase (HDACs) inhibitor, or more specifically a hydroxamate histone deacetylase inhibitor, is administered to a subject found to be at an increased risk for cancer. An example of a histone deacetylase inhibitor is vorinostat. In another example, Fiskus et al. Mol Cancer Ther 2006;5(12), which is hereby incorporated by reference, determined that treatment with the hydroxamate histone deacetylase inhibitor LBH589 or LAQ824 depleted the protein levels of EZH2, SUZ12, and EED in the cultured (K562, U937, and HL-60) and primary human acute leukemia cells.

The invention in part provides methods for identifying candidate therapeutic molecules for treating cancer and related disorders, as well as methods for treating cancer in a subject by diagnosing breast cancer in the subject and treating the subject with a suitable treatment, such as administering a therapeutic molecule. In a related embodiment, the cancer therapeutic is a molecule or compound that disrupts or otherwise blocks the binding of a PRC2 complex to a nucleic acid target gene region of the invention. Examples of said molecules include, but are not limited to, nucleic acid oligonucleotides that bind to a portion of the nucleic acid target gene region, thereby disrupting the binding of a PRC2 complex.

In a related embodiment, the invention provides in part methods for identifying a subject at risk of cancer, which comprises determining the methylation status of one or more nucleic acid target gene regions described herein in a human nucleic acid sample, wherein the methylation status is associated with the occurrence of cancer.

The methods described herein have been practiced using a novel approach for DNA methylation analysis. This method employs MALDI-TOF analysis to overcome the limitations of previous large scale methylation analysis methods. Using a combination of four base specific cleavage reactions, each CpG of a target region can be analyzed individually and is represented by multiple indicative mass signals. The acquired information about the methylation status of the examined region is based on numerous independent observations. The redundancy of this information can be leveraged to achieve higher confidence in qualitative analysis, and to obtain highly accurate averages in quantitative analysis with small standard deviations. The present methods may be customized to meet individual needs in DNA methylation analysis. For example, discovery of methylation in large stretches of genomic DNA with a single cleavage reaction, methylation ratio analysis, where fractions of methylated DNA are as low as 5% may be detected in mixtures of methylated and non-methylated template, and methylation pattern analysis, where the methylation status of each CpG within a target region can be determined as a group or independently. The general applicability of these methods have been demonstrated by reconstructing the described methylation sites for IGF2/ H19 using cloned DNA as well as genomic DNA (see Examples 1-7). The semi-quantitative assessment of methylation in larger target regions spanning multiple CpG sites was demonstrated and was able to accurately analyze methylation down to ratios of approximately 5%. The large-scale analysis of methylation in AML is a first implementation of the method for quantitative assessment of methylation ratios in a high-throughput format to predict AML patient outcome.

In some embodiments, the number of target gene regions is 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 147, 150 or more.

In certain embodiments, the comparison of methylation states or characteristic methylation states is made by use of a classification algorithm.

In particular embodiments, the reagent that modifies unmethylated cytosine to produce uracil is bisulfite. In certain embodiments, the methylated or unmethylated nucleic acid base is cytosine. In another embodiment, a non-bisulfite reagent modifies unmethylated cytosine to produce uracil.

In selected embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies

nucleotides of the target nucleic acid molecule as a function of the methylation state of the target nucleic acid molecule, amplifying treated target nucleic acid molecule, fragmenting amplified target nucleic acid molecule, and detecting one or more amplified target nucleic acid molecule fragments, and based upon the fragments, such as size and/or number thereof, identifying the methylation state of a target nucleic acid molecule, or a nucleotide locus in the nucleic acid molecule, or identifying the nucleic acid molecule or a nucleotide locus therein as methylated or unmethylated.

Fragmentation can be performed, for example, by treating amplified products under base specific cleavage conditions. Detection of the fragments can be effected by measuring or detecting a mass of one or more amplified target nucleic acid molecule fragments, for example, by mass spectrometry such as MALDI-TOF mass spectrometry. Detection also can be affected, for example, by comparing the measured mass of one or more target nucleic acid molecule fragments to the measured mass of one or more reference nucleic acid, such as measured mass for fragments of untreated nucleic acid molecules. In an exemplary method, the reagent modifies unmethylated nucleotides, and following modification, the resulting modified target is specifically amplified.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different nucleotide; contacting the treated target nucleic acid molecule with a primer containing one or more nucleotides complementary to the selected nucleotide, or one or more nucleotides complementary to the different nucleotide; treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, whereby nucleotides are synthesized onto primers hybridized to the target nucleic acid molecule; treating the synthesized products under base specific cleavage conditions; and detecting the products of the cleavage treatment, where a target nucleic acid molecule containing one or more methylated or unmethylated selected nucleotides is determined according to the number of cleavage products or according to a comparison between one or more cleavage products and one or more references.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different nucleotide; amplifying the treated target nucleic acid molecule to form an amplification product; contacting the treated target nucleic acid molecule with a primer containing one or more nucleotides complementary to a nucleotide complementary to the selected nucleotide, or one or more nucleotides

complementary to a nucleotide complementary to the different nucleotide; treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, whereby nucleotides are synthesized onto primers hybridized to the target nucleic acid molecule; treating the synthesized products under base specific cleavage conditions; and detecting the products of the cleavage treatment, where a target nucleic acid molecule containing one or more methylated or unmethylated selected nucleotides is determined according to the number of cleavage products or according to a comparison between one or more cleavage products and one or more references.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent selected from among a reagent that modifies an unmethylated selected nucleotide to produce a different nucleotide, and a reagent that modifies a methylated selected nucleotide to produce a different nucleotide; specifically amplifying the treated target nucleic acid molecule by a method selected from: (i) contacting the treated target nucleic acid molecule with a primer that specifically hybridizes to a target nucleic acid region containing one or more of the selected nucleotides or one or more of the different nucleotides, and treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, and (ii) amplifying the treated target nucleic acid molecule to form an amplification product, contacting the amplification product with a primer that specifically hybridizes to a target nucleic acid region containing one or more of the selected nucleotides, or one or more of the different nucleotides, and treating the contacted amplification product under nucleic acid synthesis conditions; treating the amplified products with base specific cleavage conditions; and detecting the products of the cleavage treatment, where a target nucleic acid molecule containing one or more methylated or unmethylated selected nucleotides is indicated by an observation selected from among: the presence of two or more cleavage products, the presence of only a single cleavage product, the presence of one or more cleavage products greater than the number of reference nucleic acid molecules, the presence of one or more cleavage products fewer than the number of reference nucleic acid molecules, the presence of the same number of cleavage products as reference nucleic acid molecules, a change in the mass of one or more cleavage products compared to a reference nucleic acid molecule mass, and one or more cleavage products that are the same mass as a reference nucleic acid molecule mass.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies unmethylated cytosine to produce uracil; specifically amplifying the treated target nucleic acid molecule with a primer that contains one or more guanine nucleotides; base specifically cleaving the amplified

products; and detecting the cleaved products, where the presence of two or more fragments indicates that the target nucleic acid molecule contains one or more methylated cytosines. Another example includes a method of identifying an unmethylated nucleic acid molecule, by treating a target nucleic acid molecule with a reagent that modifies unmethylated cytosine to produce uracil; specifically amplifying the treated target nucleic acid molecule with a primer that contains one or more adenine nucleotides; base specifically cleaving the amplified products; and detecting the cleaved products, where the presence of two or more fragments indicates that the target nucleic acid molecule contains one or more unmethylated cytosines.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies unmethylated cytosine to produce uracil; specifically amplifying the treated target nucleic acid molecule with a primer that contains one or more guanine nucleotides; base specifically cleaving the amplified products; and detecting the mass of the cleaved products, where: a change in mass of one or more cleaved products compared to a reference mass indicates that a nucleotide locus in a target is methylated. A similar exemplary method includes a method for identifying the nucleotide locus of an unmethylated nucleotide in a nucleic acid, by treating a target nucleic acid molecule with a reagent that modifies unmethylated cytosine to produce uracil; specifically amplifying the treated target nucleic acid molecule with a primer that contains one or more adenine nucleotides; base specifically cleaving the amplified products; and detecting the mass of the cleaved products, where: a change in mass of one or more cleaved products compared to a reference mass indicates that a nucleotide locus in a target is methylated.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule to deaminate unmethylated cytosine nucleotides; specifically amplifying the treated target nucleic acid molecule with a primer that specifically hybridizes to a pre-determined first region in the target nucleic acid molecule containing one or more cytosine nucleotides; base specifically cleaving the amplified products; and detecting the mass of the cleaved products, where: a change in mass of one or more cleaved products compared to a reference mass indicates that a nucleotide locus in a second region in a target is methylated, where the first region and second region do not overlap.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies unmethylated cytosine to produce uracil; specifically amplifying the treated target nucleic acid molecule with a primer that contains one or more guanine nucleotides; base specifically cleaving the amplified

products; and cleaving or simulating cleavage of a reference nucleic acid with the same cleavage reagent(s); detecting the mass of the cleaved products; determining differences in the mass signals between the target nucleic acid molecule fragments and the reference fragments; and determining a reduced set of sequence variation candidates from the differences in the mass signals and thereby determining sequence variations in the target compared to the reference nucleic acid, where methylation of a nucleotide locus is indicated by the nucleotide locus of a sequence variation. In another example of the methods, combinations and kits provided herein, a method, combination and kit is provided for identifying the nucleotide locus of a methylated nucleotide in a nucleic acid, by treating a target nucleic acid molecule with a reagent that modifies unmethylated cytosine to produce uracil; amplifying the treated target nucleic acid molecule to form a first amplification product; specifically amplifying the first amplification product with a primer that contains one or more cytosine nucleotides to form a second amplification product; base specifically cleaving the second amplification products; cleaving or simulating cleavage of a reference nucleic acid with the same cleavage reagent(s); detecting the mass of the cleaved products; determining differences in the mass signals between the target nucleic acid molecule fragments and the reference fragments; and determining a reduced set of sequence variation candidates from the differences in the mass signals and thereby determining sequence variations in the target compared to the reference nucleic acid, where methylation of a nucleotide locus is indicated by the nucleotide locus of a sequence variation.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating two or more different target nucleic acid molecules with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different nucleotide; contacting the treated target nucleic acid molecules with a primer containing one or more nucleotides complementary to the selected nucleotide, or one or more nucleotides complementary to the different nucleotide; treating the contacted target nucleic acid molecules under nucleic acid synthesis conditions, whereby nucleotides are synthesized onto primers hybridized to the target nucleic acid molecules; treating the synthesized products under base specific cleavage conditions; and detecting the products of the cleavage treatment, where target nucleic acid molecules containing one or more methylated or unmethylated selected nucleotides are determined according to a comparison between one or more cleavage products and one or more references.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different

nucleotide; contacting the treated target nucleic acid molecule with a primer containing one or more nucleotides complementary to the selected nucleotide, or one or more nucleotides complementary to the different nucleotide; treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, whereby nucleotides are synthesized onto primers hybridized to the target nucleic acid molecules; treating the synthesized products under fragmentation conditions; and detecting the products of the fragmentation treatment by mass spectrometry, where target nucleic acid molecules containing one or more methylated or unmethylated selected nucleotides are determined according to the number of fragmentation products or according to a comparison between one or more fragmentation products and one or more references. Similarly, methods are provided for identifying one or more methylated or unmethylated nucleotides in a nucleic acid, by treating a target nucleic acid molecule with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different nucleotide; contacting the treated target nucleic acid molecule with a blocking oligonucleotide containing one or more nucleotides complementary to the selected nucleotide, or one or more nucleotides complementary to the different nucleotide; treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, where nucleotide synthesis is inhibited when the blocking oligonucleotide is hybridized to a target nucleic acid molecule; treating the synthesized products under base specific cleavage conditions; and detecting the products of the cleavage treatment, where a target nucleic acid molecule containing one or more methylated or unmethylated selected nucleotides are determined according to the number of cleavage products or according to a comparison between one or more cleavage products and one or more references.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include treating a target nucleic acid molecule with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different nucleotide; contacting the target nucleic acid molecule with a cleavage reagent that selectively cleaves the target nucleic acid at a site containing one or more methylated selected nucleotides or one or more unmethylated selected nucleotides, or with a cleavage reagent that selectively cleaves the treated target nucleic acid at a site containing one or more selected nucleotides or one or more different nucleotides; treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, where a target nucleic acid molecule not cleaved is amplified; treating the amplified products under base specific cleavage conditions; and detecting the products of the cleavage treatment, where a target nucleic acid molecule containing one or more methylated or unmethylated selected nucleotides are determined

according to the number of cleavage products or according to a comparison between one or more cleavage products and one or more references.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include contacting the target nucleic acid molecule with a primer and treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions, where a strand complementary to the target nucleic acid molecule is synthesized; contacting the target nucleic acid-synthesized product duplex with a methyltransferase reagent whereby methylation in a CpG sequence of the target nucleic acid also is present in the complementary CpG sequence of the synthesized product; repeating the primer and methyltransferase reagent contacting steps to form a second synthesized product having the same sequence of nucleotides and methylation state of CpG nucleotides as present in the target nucleic acid molecule; treating synthesized products with a reagent that modifies a selected nucleotide as a function of the methylation state of the selected nucleotide to produce a different nucleotide; treating the reagent-treated products under base specific cleavage conditions; and detecting the products of the cleavage treatment, where a target nucleic acid molecule containing one or more methylated or unmethylated selected nucleotides are determined according to the number of cleavage products or according to a comparison between one or more cleavage products and one or more references.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include identifying one or more methylated or unmethylated nucleotides in a nucleic acid, where the amplified products are cleaved by base specific cleavage conditions selected from chemical conditions, physical conditions, enzymatic base specific cleavage conditions, and combinations thereof. For example, the amplified products can be cleaved by an RNase, a DNase, an alkaline compound, piperidine formate, piperidine, dimethyl sulfate, hydrazine, sodium chloride, and combinations thereof.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may include identifying one or more methylated or unmethylated nucleotides in a nucleic acid, where the amplifying step includes transcription. In such methods, the nucleoside triphosphates incorporated into the transcript can include three rNTPs and one dNTP. For example, the one dNTP can be selected from dCTP, dTTP, dATP and dGTP. In another example, the one dNTP can be selected from dCTP and dTTP, and the transcript can be cleaved by RNase A.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may include identifying one or more methylated or unmethylated nucleotides in a nucleic acid, where the intensity of one or more sample measured masses is compared to the intensity of one or

more reference masses. Similarly, also provided herein are methods of identifying one or more methylated or unmethylated nucleotides in a nucleic acid, where two or more nucleic acid samples are pooled, and the intensity of one or more sample measured masses is compared to the intensity of one or more reference masses. In such methods an incompletely converted target nucleic acid molecule can be distinguished from a methylated target nucleic acid molecule.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may be used for distinguishing between a false positive methylation specific amplification and a true methylation specific amplification, by, for example, treating a target nucleic acid molecule with a reagent that modifies an unmethylated selected nucleotide to produce a different nucleotide; contacting the treated target nucleic acid molecule with a methylation state specific primer complementary to a first target nucleic acid region containing one or more of the selected nucleotides; treating the contacted target nucleic acid molecule under nucleic acid synthesis conditions; treating the synthesized products under base specific cleavage conditions; and detecting the mass of the cleaved products, where: a change in mass of one or more cleaved products compared to a reference mass indicates that a nucleotide locus in a second region in a target is methylated, where the second region does not overlap with the first region, whereby presence of one or more methylated loci in the second region confirms true methylation specific amplification.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may be used for identifying methylated nucleotides and thereby identify methylation patterns, which can be correlated with a disease, disease outcome, or outcome of a treatment regimen, by, for example, identifying methylated or unmethylated nucleotides, in accordance with the method of any of methods provided herein, in one or more nucleic acid molecules from one or more samples collected from one or more subjects having a known disease, disease outcome, or outcome of a treatment regimen; identifying methylated or unmethylated nucleotides, in accordance with the method of any of methods provided herein, in one or more nucleic acid molecules from one or more samples collected from one or more normal subjects; and identifying the differently methylated or unmethylated nucleotides between the one or more nucleic acid molecules of step (a) and the one or more nucleic acid molecules of step (b); whereby the differently methylated or unmethylated nucleotides identify methylation correlated with a disease, disease outcome, or outcome of a treatment regimen.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may be used for identifying therapeutic targets, deciding upon a treatment regimen, or determining a disease outcome in a subject, by, for example, identifying one or more methylated or

unmethylated nucleotides in one or more nucleic acid molecules from one or more samples collected from a subject; and comparing the methylated or unmethylated nucleotides in the one or more nucleic acid molecules with one or more reference nucleic acid molecules correlated with a known disease, disease outcome, or outcome of a treatment regimen; whereby methylated or unmethylated nucleotides that are the same as the reference nucleic acid molecules identify the disease, disease outcome, or outcome of a treatment regimen in the subject. The methods, combinations and kits provided herein also can be used in deciding upon a treatment regimen, or determining a disease outcome in a subject, by, for example, identifying one or more methylated or unmethylated nucleotides in one or more nucleic acid molecules from one or more samples collected from a subject; and comparing the methylated or unmethylated nucleotides in the one or more nucleic acid molecules with one or more reference nucleic acid molecules correlated with a known disease, disease outcome, or outcome of a treatment regimen; whereby methylated or unmethylated nucleotides that are different from the reference nucleic acid molecules identify the disease, disease outcome, or outcome of a treatment regimen in the subject.

In certain embodiments, the methods for determining the methylation state of (one or more) target gene regions may be used in determining a methylation state at one or more nucleotide loci correlated with an allele, by, for example, pooling nucleic acid molecules containing a known allele; identifying one or more methylated or unmethylated nucleotide loci in the nucleic acid molecules containing the known allele; identifying the methylation state of the corresponding nucleotide loci in nucleic acid molecules that do not contain the allele; and comparing the methylation state of the nucleotide loci in allele-containing nucleic acid molecules to the methylation state of nucleotide loci in allele-lacking nucleic acid molecules, whereby differences in methylation state frequency at one or more loci identify the different loci as correlated with the allele. Similarly, the methods, combinations and kits provided herein can be used for determining an allele correlated with a methylation state at one or more nucleotide loci, by forming a first pool of nucleic acid molecules containing one or more known methylated or unmethylated nucleotide loci, which loci were identified in accordance with the methods provided herein; identifying the frequency at which one or more alleles are present in the pooled nucleic acid samples; identifying the allele frequency at which one or more alleles are present in a second pool of nucleic acid molecules having nucleotide loci with different methylation state relative to the first pooled nucleic acid molecules; and comparing the allelic frequency in the first pool of nucleic acid molecules to the allelic frequency in the second pool of nucleic acid molecules, whereby differences in allelic frequency identify the one or more loci as correlated with the allele.

In some embodiments, the methods for determining the methylation state of (one or more) target gene regions may be used for determining the probable identity of one or more alleles, by, for example, identifying one or more methylated or unmethylated nucleotides a nucleic acid molecule; and determining the frequency of presence of one or more alleles with the presence of one or more methylated or unmethylated nucleotides where the probable identity of the allele is determined.

Also provided herein are combinations and kits for determining the methylation state of a target nucleic acid molecule. Kits can include a reagent that modifies one or more nucleotides of the target nucleic acid molecule as a function of the methylation state of the target nucleic acid molecule, one or more methylation specific primers capable of specifically hybridizing to a treated target nucleic acid molecule, and one or more compounds capable of fragmenting an amplified target nucleic acid molecule. The one or more compounds capable of fragmenting amplified nucleic acid products can include an RNase, a DNase, an alkaline compound, piperidine formate, piperidine, dimethyl sulfate, hydrazine, sodium chloride, and combinations thereof. For example, kits provided herein can include one or more RNases

In some embodiments, the methylation state is determined by mass spectrometry.

In some embodiments, the methylation state is determined by multiplexed hME assays, fluorescence-based real-time PCR, methylation-sensitive single nucleotide primer extension, methylated CpG island amplification, methylation-specific PCR, restriction landmark genomic scanning, methylation-sensitive-representational difference analysis (MS-RDA), methylation-specific AP-PCR (MS-AP-PCR) methyl-CpG binding domain column/segregation of partly melted molecules (MBD/SPM), or bisulphite sequencing direct. Specific methods for determining the methylation state may include combined bisulfite restriction analysis (COBRA), PyroMeth or MethyLight.

In some embodiments, the cancer diagnosis for the subject in the preceding embodiments is combined with another cancer diagnosis based on morphology, cytochemistry, immunophenotype, cytogenetics or other molecular techniques to provide a more accurate diagnosis for the subject. In a related embodiment, the molecular technique is a gene expression profile. In a further related embodiment, the gene expression profile consists of one or more target gene regions and/or genes regulated by one or more target gene regions.

In other embodiments, the invention provides a method for identifying a subject at risk of cancer and then prescribing to the subject a cancer detection procedure, prevention procedure and/or a treatment procedure.

In some embodiments, the method for determining the susceptibility to cancer of a subject further comprises administering a cancer treatment procedure or preventative procedure based upon the cancer diagnosis. In a further related embodiment, the cancer treatment is selected from the group consisting of administering a a non-standard, non-aggressive or experimental chemotherapy agent chemotherapy agent, administering a novel therapy, administering palliative care, and combinations of the foregoing. A "novel therapy" as used herein refers to an investigational treatment (e.g., monoclonal antibodies, new consolidation chemotherapy regimens, multiple drug resistance inhibitors, biological modifier therapies, and demethylating agents). In another related embodiment, the cancer treatment is a standard cancer treatment course. Standard cancer treatment are well known in the art and often varying depending on the type of cancer. Typically cancer treatment comprises radiation therapy, chemotherapy and/or surgery. In another related embodiment, a subject found to be at an increased risk for cancer may undergo more frequent cancer exams for the detection of cancer.

In certain embodiments, the methods described herein may be utilized to detect the presence or absence of a disease in a tissue or cell that correlates with changes in the methylation state of the tissue or cell, or classify the susceptibility of a tissue or cell to a disease where the disease is correlated with changes in the methylation state of the tissue or cell. In another embodiment, the methods described herein may be utilized for the early detection of cancer before the cancer is otherwise detectable by current diagnostic methods known in the art. For example, the methods described herein may be utilized to detect an altered methylation state associated with the presence of an oncogenic event before physical indicators manifest (*e.g.*, the presence of a detectable tumor).

In some embodiments, the nucleic acid target gene represents a therapeutic target. In a related embodiment, the nucleic acid target gene is one or one or more of ACSL6, ATP10A, BCL6, BCR, CA3, CCND1, CCND2, CD38, CDKN1C, CHGA, COL5A1, EGFR, ESR1, FLI1, FLJ32447, FLT3, FLT4, FRAT1, GABRB3, GAS7, GNAS, GPC3, HEAB, HIST1H4I, HOXA1, HOXA10, HOXA2, HOXA6, HOXA7, HOXA9, HOXC13, IL10RA, IRF4, KIT, LCK, LEP, LMO2, LYL1, MLLT6, MYH11, MYOD1, NFKB2, OLIG2, PAX5, PAX7, PAX8, PEG3, PHOX2B, PLOD1, PON1, PSIP1, PTPRN2, REL, RET, RUNX1T1, SBDS, SET, SLC22A3, SLC38A4, SNRPN, TAL1, TCL1A, TLX1, TLX3, TMPRSS2, TSPYL5, WDR66, WT1, ZIM2, ZNF198 or ZNF331, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene comprises one or more PRC2 binding sites, wherein the nucleic acid target gene is one or one or more of CA3, CD38, EGFR, ESR1, FLI1, FLJ32447, FLT3, FRAT1, GAS7, GNAS, GPC3, HIST1H4I, HOXA1, HOXA10, HOXA2, HOXA6, HOXA7, HOXA9, HOXC13, IL10RA, IRF4,

MYOD1, OLIG2, PAX5, PAX7, PAX8, PHOX2B, PTPRN2, SLC22A3, TAL1, TLX1, TLX3 and WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

In a related embodiment, the disease state is cancer. In a further related embodiment, the cancer is present in a blood, breast, CNS, colon, lung, ovarian, prostate, renal, or skin cell or tissue. As used herein, a target gene may be associated with one or more cancers. See Tables 6 and 7. For example, the following gene targets were found to be hypermethylated in 5 cancer types: TSPYL, PAX8, LEP, PHOX2B, TMPRSS2. The following gene target was found to be hypermethylated in 6 cancer types: MYOD1, and the following gene target was found to be hypermethylated in 8 cancer types: PAX5.

When the cancer is cancer of the blood, it is preferably a blood-related carcinoma. In one embodiment, the blood-related carcinoma is myeloid leukemia, acute myeloid leukemia (AML), chronic myeloid leukemia (CML), acute lymphoblastic leukemia (ALL), chronic lymphocytic leukemia (CLL), blood myeloproliferative diseases, blood multiple myeloma, blood myelodysplasic syndrome, Hodgkin's disease or non-Hodgkin's lymphoma. The hematologic cancer often is acute myeloid leukemia. In one embodiment, the nucleic acid target gene associated with a blood-related carcinoma is one or one or more of CCND1, GNAS, MYOD1 or TSPYL5, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a blood-related carcinoma comprises one or more PRC2 binding sites and is either GNAS or MYOD1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is cancer found in breast cells, it is preferably a breast carcinoma. Breast cancer is typically described as the uncontrolled growth of malignant breast tissue. Breast cancers arise most commonly in the lining of the milk ducts of the breast (ductal carcinoma), or in the lobules where breast milk is produced (lobular carcinoma). Other forms of breast cancer include Inflammatory Breast Cancer and Recurrent Breast Cancer. In one embodiment, the nucleic acid target gene associated with a breast carcinoma is one or one or more of GNAS, HOXA6, LEP, LYL1, MYOD1, PAX5, PAX8, PTPRN2, TSPYL5 or ZIM2, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a breast carcinoma comprises one or more PRC2 binding sites and is one or more of GNAS, HOXA6, MYOD1, PAX5, PAX8 or PTPRN2, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is a cancer of the nervous system, it is preferably a glioma. In one embodiment, the glioma is skull osteoma, skull hemangioma, skull granuloma, skull xanthoma, skull osteitis, skull

defomians, meningioma, meningiosarcoma, bliomatosis, brain astrocytoma, brain medulloblastoma, brain glioma, brain ependymoma, brain germinoma, brain glioblastoma multiform, brain oligodendroglioma, brain schwannoma, brain retinoblastoma, brain congenital tumors, spinal cord neurofibroma, spinal cord memingioma, spinal cord glioma, or spinal cord sarcoma. In one embodiment, the nucleic acid target gene associated with a glioma is one or one or more of BCR, HOXA2, HOXA6, HOXA9, IRF4, LCK, LEP, LYL1, MLLT6, MYOD1, PAX5, PAX8, PHOX2B, SET, SLC22A3, SLC38A4, TLX3, TMPRSS2, WDR66 or ZNF198, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a glioma comprises one or more PRC2 binding sites and is one or more of HOXA2, HOXA6, HOXA9, IRF4, MYOD1, PAX5, PAX8, PHOX2B, SLC22A3, SLC38A4 or TLX3, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is a cancer of the colon, it is preferably a colorectal carcinoma. In one embodiment, the nucleic acid target gene associated with a colorectal carcinoma is one or one or more of ACSL6, ATP10A, CA3, CD38, CDKN1C, CHGA, COL5A1, EGFR, ESR1, FLI1, FLJ32447, FLT3, FLT4, GABRB3, GNAS, GPC3, HOXA2, HOXC13, IRF4, LEP, LMO2, MYH11, MYOD1, OLIG2, PAX5, PAX7, PAX8, PEG3, PHOX2B, PON1, PTPRN2, RET, RUNX1T1, SNRPN, TAL1, TCL1A, TLX3, TSPYL5, WT1, ZIM2 or ZNF331, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a colorectal carcinoma comprises one or more PRC2 binding sites and is one or more of CA3, CD38, EGFR, ESR1, FLI1, FLJ32447, FLT3, GNAS, GPC3, HOXA2, HOXC13, IRF4, MYOD1, OLIG2, PAX5, PAX7, PAX8, PHOX2B, PTPRN2, TAL1, TLX3 or WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is a lung cancer, it is preferably a lung carcinoma. In one embodiment, the lung carcinoma is lung squamous cell carcinoma, lung undifferentiated small cell carcinoma, lung undifferentiated large cell carcinoma, lung adenocarcinoma, alveolar carcinoma, bronchial adenoma, lung sarcoma, lung lymphoma, lung chondromatous hanlartoma, lung bronchoalveolar carcinoma or lung inesothelioma. In one embodiment, the nucleic acid target gene associated with a lung carcinoma is one or one or more of BCR, CA3, CCND2, FLI1, FLJ32447, GPC3, HIST1H4I, HOXA10, HOXA6, HOXA7, HOXA9, MYOD1, OLIG2, PAX5, PAX7, PAX8, PHOX2B, PLOD1, PON1, PTPRN2, SBDS, SLC38A4, TCL1A, TLX3, TMPRSS2 or WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a lung carcinoma comprises one or more PRC2 binding sites and is one or more of CA3,

FLI1, FLJ32447, GPC3, HIST1H4I, HOXA10, HOXA6, HOXA7, HOXA9, MYOD1, OLIG2, PAX5, PAX7, PAX8, PHOX2B, PTPRN2, TLX3 or WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is an ovarian cancer, it is preferably an ovarian carcinoma. In one embodiment, the ovarian carcinoma is a uterus endometrial carcinoma, cervical carcinoma, pre-tumor cervical dysphasia, ovarian carcinoma, serous cystadenocarcinoma, mucinous cystadenocarcinoma, unclassified ovarian carcinoma, ovarian granulosa-thecal cell tumors, SertoliLeydig tumors, ovarian dysgerminoma, ovarian malignant teratoma, vulva squamous cell carcinoma, vulva intaepithelial carcinoma, vulva adenocarcinoma, vulva fibrosarcoma, vulva melanoma, vagina clear cell carcinoma, vagina squamous cell carcinoma, botryoid sarcoma, or fallopian tube carcinoma. In one embodiment, the nucleic acid target gene associated with an ovarian carcinoma is one or one or more of BCL6, CA3, FLJ32447, GNAS, GPC3, HOXA10, HOXA7, HOXA9, IRF4, LEP, LYL1, PAX5, PAX7, PHOX2B, SBDS, TMPRSS2, WT1 or ZIM2, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with an ovarian carcinoma comprises one or more PRC2 binding sites and is one or more of CA3, FLJ32447, GNAS, GPC3, HOXA10, HOXA7, HOXA9, IRF4, PAX5, PAX7, PHOX2B or WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is a cancer of the prostate, it is preferably prostate carcinoma. In one embodiment, the nucleic acid target gene associated with an prostate carcinoma is one or one or more of CDKN1C, HIST1H4I, HOXA1, IL10RA, NFKB2, PAX5 or PAX8, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a prostate carcinoma comprises one or more PRC2 binding sites and is one or more of HIST1H4I, HOXA1, IL10RA, PAX5 or PAX8, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is a cancer of the kidney, it is preferably a renal cell carcinoma. In one embodiment, the nucleic acid target gene associated with renal cell carcinoma is one or one or more of BCR, CA3, CDKN1C, CHGA, FLJ32447, FRAT1, GAS7, HOXC13, LEP, LYL1, MYOD1, PAX5, PAX7, PEG3, PHOX2B, PON1, RET, SLC22A3, TLX3, TMPRSS2, TSPYL5 or WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with a renal cell carcinoma comprises one or more PRC2 binding sites and is one or more of CA3, FLJ32447, FRAT1, GAS7, HOXC13, MYOD1, PAX5,

PAX7, PHOX2B, SLC22A3, TLX3 or WT1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

When the cancer is a skin cancer, it is preferably a melanoma, skin basal cell carcinoma, skin squamous cell carcinoma, skin Karposi's sarcoma, skin moles dysplasic nevi, skin lipoma, skin angioma, dematofibroma or skin keloids, psoriasis. In one embodiment, the nucleic acid target gene associated with a melanoma is one or one or more of BCR, CCND2, FLI1, FRAT1, HEAB, HOXA10, HOXA2, HOXA6, HOXA7, HOXA9, KIT, PAX5, PLOD1, PON1, PSIP1, REL, SBDS, TLX1, TMPRSS2, TSPYL5 or WDR66, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer. In a related embodiment, the nucleic acid target gene associated with melanoma comprises one or more PRC2 binding sites and is one or more of FLI1, FRAT1, HOXA10, HOXA2, HOXA6, HOXA7, HOXA9, PAX5 or TLX1, wherein hypermethylation of the nucleic acid target gene is associated with the occurrence of cancer.

In another embodiment of the invention, the nucleic acid target region is one or more of TCL1A, SLC22A2, TRPM5, KCNQ1, IGF2, PEG3 or DLK1, wherein hypomethylation of the nucleic acid target gene is associated with the occurrence of cancer.

In one embodiment of the invention, the methods of the present invention are combined with known methods of diagnosing cancer such as transcriptional profiling (Staunton, J.E. et al. *Proc Natl Acad Sci U S A* 98, 10787-92 (2001)); and Wang, H. et al. *BMC Genomics* 7, 166 (2006)), spectral karyotyping (Roschke, A.V. et al. *Cancer Res* 63, 8634-47 (2003)) or proteomic profiling (Nishizuka, S. et al. *Proc Natl Acad Sci U S A* 100, 14229-34 (2003)). All of the above references are hereby incorporated by reference.

In certain embodiments the primer sequence further comprises a promoter sequence. In an embodiment the promoter sequence is obtained from a T7 promoter, a SP6 promoter or a T3 promoter. If the promoter is a T7 promoter it may have the sequence: 5'-CAGTAATACGACTCACTATAGGGAGA-3' (SEQ ID NO.:)

In some embodiments, a method is provided for identifying at least one CpG island region in a nucleic acid having a characteristic methylation state that correlates with an unknown disease outcome of an organism, tissue or cell comprising the steps of providing a first CpG island region of the nucleic acid; identifying or discovering at least a second CpG island region within a region spanning about 5 Kb 5' of the first CpG island region and about 5Kb 3' of the first CpG island region in the nucleic acid including the first CpG island region; and determining if at least one of the at least a second CpG island region has a

characteristic methylation state that correlates with the unknown disease outcome of the organism, tissue or cell.

In the preceding embodiments, the methylation state of 50 or more gene target regions in the nucleic acid of the subject is determined in 24 hours or less. In some embodiments the methylation state of 50 or more gene target regions in the nucleic acid of the subject is determined in 12 hours or less, 8 hours or less, 6 hours or less, 5 hours or less, 4 hours or less, 3 hours or less, 2 hours or less, or less than 1 hour. In some embodiments the methylation state of 100 or more gene target regions in the nucleic acid of the subject is determined in 24 hours or less. In some embodiments the methylation state of 100 or more gene target regions in the nucleic acid of the subject is determined in 12 hours or less, 8 hours or less, 6 hours or less, 5 hours or less, 4 hours or less, 3 hours or less, 2 hours or less, or less than 1 hour. In some embodiments the methylation state of 150 or more gene target regions in the nucleic acid of the subject is determined in 24 hours or less. In some embodiments the methylation state of 150 or more gene target regions in the nucleic acid of the subject is determined in 12 hours or less, 8 hours or less, 6 hours or less, 5 hours or less, 4 hours or less, 3 hours or less, 2 hours or less, or less than 1 hour. In some embodiments the methylation state of 20 or more gene target regions in the nucleic acid of the subject is determined in 24 hours or less. In some embodiments the methylation state of 20 or more gene target regions in the nucleic acid of the subject is determined in 12 hours or less, 8 hours or less, 6 hours or less, 5 hours or less, 4 hours or less, 3 hours or less, 2 hours or less, or less than 1 hour.

The methods, combinations and kits provided herein can be performed or used in conjunction with any of a variety of other procedures including, but not limited to, any procedures for modifying the target nucleic acid molecule according to the methylation state of the target nucleic acid molecule, any procedures for amplifying a target nucleic acid molecule, any procedures for fragmenting a target nucleic acid molecule, and any procedures for detecting target nucleic acid molecule fragments.

BRIEF DECRIPTION OF THE DRAWINGS

Figure 1A displays mass signals generated by cytosine specific cleavage of the forward transcript of the IGF2/H19 region (upper spectral analysis is the methylated template; lower spectral analysis is the non-methylated template). Figure 1B shows the IGF2/H19 RNA transcript sequence wherein each CpG sequence is methylated (upper sequence) and the same RNA transcript sequence where none of the CpG sequence is methylated (lower seqeunce).

Figure 2 is an overlay of mass signal patterns generated by cytosine specific cleavage of the forward transcript of the IGF2/H19 region.

Figure 3 is an overlay of mass spectra generated by uracil specific cleavage of the reverse transcript of the IGF2/H19 region.

Figure 4 depicts mass spectra representing all four base-specific cleavage reactions of the IGF2/H19 amplicon. Numbers correspond to the CpG positions within this target region. Arrows point at the mass signals that indicate the presence of a methylated Cytosine at the marked position. All methylated CpG's in the selected region can be identified by one or more mass signals.

Figure 5 depicts mass spectra generated by uracil specific cleavage of the reverse transcript of the IGF2/H19 region. Genomic DNA was used for amplification. Dotted lines mark the position of mass signals representing non-methylated CpG's. Signals with 16 Dalton shift (or a multitude thereof) represent methylation events. The area-under-the-curve ratio of methylated versus non-methylated template approximates to 1, as one expects for hemi-methylated target regions.

Figures 6A-6E provide descriptive analysis of methylation data for normal and tumor cell line samples. (a) A scatterplot depicts the results from a replicate analysis of ERBB2 using two different primer designs. The quantitative measurements are highly concordant. (b) Relationship between CpG density and mean methylation levels in cancer and normal samples. CpG density of amplicons was calculated as the fraction of CpG nucleotides within the total amplicon sequence. The mean methylation value for each amplicon was generated using all individual CpG sites methylation values. Amplicons with more than 10% CpG content are likely to have lower methylation values in normal tissues. In cancer cell lines DNA methylation is observed more frequently in these amplicons. (c) Amplicons were binned based on their average methylation values. Each bin contained amplicons within a 5% range of methylation values. Bins from 15% to 85% average methylation contain more amplicons in the set of cancer cell lines. (d) Histogram of methylation differences. For each amplicon the difference in mean methylation was calculated between the group of normal samples and the group of tumor cell lines. Positive values translate to hypermethylation in cancer cell lines; whereas negative values indicate that the mean methylation was higher in the group of normal samples. The distribution of methylation differences is skewed towards hypermethylated changes. (e) DNA methylation in relation to the closest 5'-UTR. The distance from the 5'UTR was calculated for every individual CpG site. Each data point contains 1770 individual methylation values for the cancer cell lines and 180 values for the normal samples. It is necessary to adjust the number of datapoints in each group because of the difference in sample numbers in the two sets. A window of 1kbp around the 5'-UTR shows low methylation values in the normal and the cancer cell line samples. Methylation values in the cancer cell line samples are generally elevated.

Figure 7 is a two-way hierarchical cluster analysis of 59 tumor cell line samples and 6 samples from normal tissues (rows) and DNA-methylation of CpG Units in 531 promoter regions (columns). DNA-methylation values are depicted in this false color image on a continous scale from red (non-methylated) to yellow (100% methylated). Poor quality data is annotated in gray. Samples are color-coded according to their cell line tissue origin (legend depicted upper left) to simplify identification of potential sample clusters. Strong sample cluster formation is observed for the group of normal samples, the group of colon cancer samples (brown), Melanoma samples (green) and CNS tumors (yellow). Less dominant clustering is observed in lung cancers (black), renal carcinoma (orange) and ovarian cancer. The cell line samples derived from breast cancer (pink), leukemia (red) and prostate cancer (grey) do not form obvious clusters. The normal samples are characterized by consistent low methylation levels. The cell line samples show more variable methylation patterns.

Figure 8 shows the group of significantly differentially methylated genes in cancer. The genes are divided into subsets according to their number of PCR2 marks. A box whisker plot reveals that genes with a higher number of PRC2 marks tend to be connected altered in more tumor types, while genes with no PRC2 marks are most connected to one or two tumor types.

Figure 9 shows therapeutic options available to a subject diagnosed with AML.

Throughout the document and in the Figures, CpG sites are referenced according to their CpG ID. The CpG ID's refer to the specific CpG location within the particular genomic region. For example, each CpG ID follows the general schema: databaseID_GeneName_ AmpliconID_CPG_CPGposition in the amplicon. "GeneName" is the refseq gene name of the analysed promoter region, or in the case of intragenic regions, the nearest gene is identified. "AmpliconID" is the particular amplicon analyzed within the gene or region, especially relevant if multiple amplicons were analyzed for this gene. "CPG" is a constant text string. "CPGposition in the amplicon" indicates which CpG Sites are enclosed in the measured CpG Unit. The numbers given refer to the CpG sites as counted from the 5' end of the analyzed amplicon sequence. The amplicon sequences are provided in Table 10.

DETAILED DESCRIPTION OF THE INVENTION

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the invention(s) belong. All patents, patent applications, published applications and publications, GENBANK sequences, websites and other published materials referred to throughout the entire disclosure herein, unless noted otherwise, are incorporated by reference in their entirety. In the event that there are a plurality of definitions for terms

herein, those in this section prevail. Where reference is made to a URL or other such identifier or address, it is understood that such identifiers can change and particular information on the internet can come and go, but equivalent information is known and can be readily accessed, such as by searching the internet and/or appropriate databases. Reference thereto evidences the availability and public dissemination of such information.

As used herein, a "nucleic acid target gene region" is a nucleic acid molecule that is examined using the methods disclosed herein. For the purposes of the application, "nucleic acid target gene region", "target gene", "target region", "region" and "gene" may be used interchangeably. A nucleic acid target gene region includes genomic DNA or a fragment thereof, which may or may not be part of a gene, a segment of mitochondrial DNA of a gene or RNA of a gene and a segment of RNA of a gene. A nucleic target gene region may be further defined by its chromosome position range. The chromosome position ranges provided herein were gathered from the March 2006 human reference sequence (NCBI Build 36.1), which was produced by the International Human Genome Sequencing Consortium and can be accessed at World Wide Web URL genome.ucsc.edu/cgi-bin/hgGateway. Information about a particular target gene (*e.g.*, genomic sequence, cDNA sequence, peptide sequence, expression profile, etc.) can be easily obtained by methods well known in the art, for example, by visiting the World Wide Web URL genecards.org/index.shtml.

In the context of methods for treating cancer, the invention provides methods for identifying nucleic acid target gene region that serve as therapeutic targets. A nucleic acid target gene region can also refer to an amplified product of a nucleic acid target gene region, including an amplified product of a treated nucleic acid target gene region, where the nucleotide sequence of such an amplified product reflects the methylation state of the nucleic acid target gene region. One skilled in the art would recognize that the size or length of the nucleic acid target gene region may vary depending on the limitation, or limitations, of the equipment used to perform the analysis. The nucleic acid target gene region may comprise intragenic nucleic acid, a gene of interest, more than one gene of interest, at least one gene of interest or a portion of a gene of interest. Correspondingly a sequential or non-sequential series of nucleic acid target gene regions may be analyzed and exploited to map an entire gene or genome. The intended target will be clear from the context or will be specified.

As used herein, a "nucleic acid target gene molecule" is a molecule comprising a nucleic acid sequence of the nucleic acid target gene region. The nucleic acid target gene molecule may contain less than 10%, less than 20%, less than 30%, less than 40%, less than 50%, greater than 50%, greater than

60%, greater than 70% greater than 80%, greater than 90% or up to 100% of the sequence of the nucleic acid target gene region. A "target peptide" refers to a peptide encoded by a nucleic acid target gene.

As used herein, the "methylation state" or "methylation status" of a nucleic acid target gene region refers to the presence or absence of one or more methylated nucleotide bases or the ratio of methylated cytosine to unmethylated cytosine for a methylation site in a nucleic acid target gene region. For example, a nucleic acid target gene region containing at least one methylated cytosine is considered methylated (*i.e.* the methylation state of the nucleic acid target gene region is methylated). A nucleic acid target gene region that does not contain any methylated nucleotides is considered unmethylated. Similarly, the methylation state of a nucleotide locus in a nucleic acid target gene region refers to the presence or absence of a methylated nucleotide at a particular locus in the nucleic acid target gene region. For example, the methylation state of a cytosine at the 7th nucleotide in a nucleic acid target gene region is methylated when the nucleotide present at the 7^{th} nucleotide in the nucleic acid target gene region is 5-methylcytosine. Similarly, the methylation state of a cytosine at the 7th nucleotide in a nucleic acid target gene region is unmethylated when the nucleotide present at the 7th nucleotide in the nucleic acid target gene region is cytosine (and not 5-methylcytosine). Correspondingly the ratio of methylated cytosine to unmethylated cytosine for a methylation site or sites can provide a methylation state of a nucleic acid target gene region. In certain embodiments the methylation state or status may be expressed as a percentage of methylateable nucleotides (e.g., cytosine) in a nucleic acid (e.g., amplicon or gene region) that are methylated (e.g., about 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95% or about 100% methylated; greater than 80% methylated, between 20% to 80% methylated, or less than 20% methylated). A nucleic acid may be "hypermethylated," which refers to the nucleic acid having a greater number of methylateable nucleotides that are methylated relative to a control, and in some embodiments refers to greater than 80% of the methylatable nucleotides being methylated. A nucleic acid may be "hypomethylated," which refers to the nucleic acid having a smaller number of methylateable nucleotides that are methylated relative to a control, and in some embodiments refers to less than 20% of the methylatable nucleotides being methylated. The methylation status or state is determined in a CpG island in certain embodiments.

As used herein, a "characteristic methylation state" refers to a unique, or specific data set comprising the location of at least one, a portion of the total or all of the methylation sites of a nucleic acid, a nucleic acid target gene region, a gene or a group of genes of a sample obtained from an organism, a tissue or a cell.

As used herein, “methylation ratio” refers to the number of instances in which a molecule or locus is methylated relative to the number of instances the molecule or locus is unmethylated. Methylation ratio can be used to describe a population of individuals or a sample from a single individual. For example, a nucleotide locus having a methylation ratio of 50% is methylated in 50% of instances and unmethylated in 50% of instances. Such a ratio can be used, for example, to describe the degree to which a nucleotide locus or nucleic acid region is methylated in a population of individuals. Thus, when methylation in a first population or pool of nucleic acid molecules is different from methylation in a second population or pool of nucleic acid molecules, the methylation ratio of the first population or pool will be different from the methylation ratio of the second population or pool. Such a ratio also can be used, for example, to describe the degree to which a nucleotide locus or nucleic acid region is methylated in a single individual. For example, such a ratio can be used to describe the degree to which a nucleic acid target gene region of a group of cells from a tissue sample are methylated or unmethylated at a nucleotide locus or methylation site.

As used herein, a “methylated nucleotide” or a "methylated nucleotide base" refers to the presence of a methyl moiety on a nucleotide base, where the methyl moiety is not present in a recognized typical nucleotide base. For example, cytosine does not contain a methyl moiety on its pyrimidine ring, but 5-methylcytosine contains a methyl moiety at position 5 of its pyrimidine ring. Therefore, cytosine is not a methylated nucleotide and 5-methylcytosine is a methylated nucleotide. In another example, thymine contains a methyl moiety at position 5 of its pyrimidine ring, however, for purposes herein, thymine is not considered a methylated nucleotide when present in DNA since thymine is a typical nucleotide base of DNA. Typical nucleoside bases for DNA are thymine, adenine, cytosine and guanine. Typical bases for RNA are uracil, adenine, cytosine and guanine. Correspondingly a "methylation site" is the location in the target gene nucliec acid region where methylation has, or has the possibility of occuring. For example a location containing CpG is a methylation site wherein the cytosine may or may not be methylated.

As used herein, a "methylation site" is a nucleotide within a nucleic acid, nucleic acid target gene region or gene that is susceptible to methylation either by natural occurring events *in vivo* or by an event instituted to chemically methylate the nucleotide *in vitro*.

As used herein, a “methylated nucleic acid molecule” refers to a nucleic acid molecule that contains one or more methylated nucleotides that is/are methylated.

As used herein “CpG island” refers to a G:C-rich region of genomic DNA containing a greater number of CpG dinucleotides relative to total genomic DNA. A CpG island may be about 200 base pairs

in length, where the G:C content of the region is at least 50% and the ratio of observed CpG frequency over expected frequency is 0.6; typically a CpG island can be at least 500 base pairs in length, where the G:C content of the region is at least 55% and the ratio of observed CpG frequency over expected frequency is 0.65. The observed CpG frequency over expected frequency can be calculated according to the method provided in Gardiner-Garden *et al., J. Mol. Biol.* 196:261-281 (1987). For example, the observed CpG frequency over expected frequency could be calculated according to the formula:

R = (AxB)/(CxD)

where R is the ratio of observed CpG frequency over expected frequency, A is the number of CpG dinucleotides in an analyzed sequence, B is the total number of nucleotides in the analyzed sequence, C is the total number of C nucleotides in the analyzed sequence, and D is the total number of G nucleotides in the analyzed sequence.

As used herein, a first nucleotide that is "complementary" to a second nucleotide refers to a first nucleotide that base-pairs, under high stringency conditions to a second nucleotide. An example of complementarity is Watson-Crick base pairing in DNA (*e.g.,* A to T and C to G) and RNA (*e.g.,* A to U and C to G). Thus, for example, G base-pairs, under high stringency conditions, with higher affinity to C than G base-pairs to G, A or T, and, therefore, when C is the selected nucleotide, G is a nucleotide complementary to the selected nucleotide.

As used herein, "treat", "treating" or grammatical variations thereof, refers to the process of exposing an analyte, typically a nucleic acid molecule, to conditions under which physical or chemical analyte modification or other chemical reactions (including enzymatic reactions) can occur. For example, treating a nucleic acid target gene molecule with a reagent that modifies the nucleic acid target gene molecule as a function of its methylation state may include adding a reagent such as bisulfite or an enzyme such as cytosine deaminase to a solution containing the nucleic acid target gene region. In treating the nucleic acid target gene with bisulfite any unmethylated nucleotide, such as any unmethylated C nucleotide, present in the nucleic acid target gene molecule can be chemically modified, such as deaminated; however, if the nucleic acid target gene molecule contains no unmethylated selected nucleotide, such as no unmethylated C nucleotide, then a nucleic acid target gene molecule treated with such a reagent may not be chemically modified. In another example, treating a nucleic acid target gene molecule under fragmentation or cleavage conditions can include adding a cleavage reagent such as RNase T1, such that in selected nucleic acid target gene molecules, such as nucleic acid target gene molecules containing G nucleotides, cleavage can occur. Cleavage, however, need not occur, such as with nucleic acid target gene molecules not containing G nucleotides, cleavage with RNase T1 may not occur.

In another example, treating a nucleic acid target gene molecule under nucleic acid synthesis conditions can include adding a DNA or RNA polymerase and NTPs, such that nucleic acid synthesis can occur if, for example, a primer is hybridized to a nucleic acid target gene molecule, however, no nucleic acid synthesis is necessary if, for example, no primer is hybridized to a nucleic acid target gene molecule.

As used herein, the phrase "hybridizing" or grammatical variations thereof, refers to binding of a first nucleic acid molecule to a second nucleic acid molecule under low, medium or high stringency conditions, or under nucleic acid synthesis conditions. Hybridizing can include instances where a first nucleic acid molecule binds to a second nucleic acid molecule, where the first and second nucleic acid molecules are complementary.

As used herein, "specifically hybridizes" refers to preferential hybridization under nucleic acid synthesis conditions of a probe, or primer, to a nucleic acid molecule having a sequence complementary to the probe or primer compared to hybridization to a nucleic acid molecule not having a complementary sequence. For example, specific hybridization includes the hybridization of a probe to a target nucleic acid sequence that is complementary to the probe.

As used herein, "nucleotide synthesis conditions" in the context of primer hybridization refer to conditions in which a primer anneals to the nucleic acid molecule to be amplified. Exemplary nucleotide synthesis conditions are 10 mM TrisHCl pH 8.3, 1.5 mM MgCl, 50 mM KCl, 62°C. Other exemplary nucleotide synthesis conditions are 16.6 mM ammonium sulfate, 67 mM Tris pH 8.8, 6.7 mM MgCl, 10 mM 2-mercaptoethanol, 60°C. Those of skill in the art are familiar with parameters that affect hybridization; such as temperature, probe or primer length and composition, buffer composition and pH, and salt concentration can readily adjust these parameters to achieve specific hybridization of a nucleic acid to a target sequence.

As used herein, "complementary base pairs" refer to Watson-Crick base pairs (*e.g.,* G to C and A to T in DNA and G to C and A to U in RNA) or the equivalent thereof when non-natural or atypical nucleotides are used. Two nucleic acid strands that are complementary contain complementary base pairing. A probe is not complementary when mismatches such as G-T, G-A, C-T or C-A arise when a probe or primer hybridizes to a nucleic acid target gene molecule.

As used herein "substantially complementary" refers to primers that are sufficiently complementary to hybridize with nucleic acid target gene molecules having a desired sequence under nucleic acid synthesis conditions. Primers should have sufficient complementarity to hybridize to a desired nucleic acid target gene molecule and permit amplification of the nucleic acid target gene molecule. For example, a primer used in the methods disclosed herein can be 100% complementary with

the nucleic acid target gene molecule desired to be amplified. In another example, a primer can have 1, 2, 3, or more mismatches, provided that the primer can be used to amplify at least one nucleic acid target gene molecule desired to be amplified. For example, a nucleic acid target gene molecule can have three cytosine nucleotides in the region with which a primer hybridizes; when only one of the three C nucleotides are methylated, treatment with bisulfite can convert the two unmethylated C nucleotides to U nucleotides, and a primer 100% complementary to a nucleic acid target gene molecule having three C nucleotides can still hybridize to a nucleic acid target gene molecule having only one C nucleotide, such that the nucleic acid target gene molecule having only one C nucleotide can still be amplified.

As used herein "nucleic acid" refers to polynucleotides such as deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). The term also includes, as equivalents, derivatives, variants and analogs of either RNA or DNA made from nucleotide analogs, single-stranded ("sense" or "antisense", "plus" strand or "minus" strand, "forward" reading frame or "reverse" reading frame) and double-stranded polynucleotides. Deoxyribonucleotides include deoxyadenosine, deoxycytidine, deoxyguanosine and deoxythymidine. For RNA, the base cytosine is replaced with uracil.

As used herein, "mass spectrometry" encompasses any suitable mass spectrometric format known to those of skill in the art. Such formats include, but are not limited to, Matrix-Assisted Laser Desorption/Ionization, Time-of-Flight (MALDI-TOF), Electrospray (ES), IR-MALDI (see, *e.g.*, published International PCT application No.99/57318 and U.S. Patent No. 5,118,937), Ion Cyclotron Resonance (ICR), Fourier Transform and combinations thereof.

As used herein, the phrase "mass spectrometric analysis" refers to the determination of the mass to charge ratio of atoms, molecules or molecule fragments.

As used herein, a "reference nucleic acid molecule" refers to a nucleic acid molecule known to be methylated or unmethylated, or a nucleic acid molecule in which the methylation state of one or more nucleotide loci of the nucleic acid molecule is known. A reference nucleic acid can be used to calculate or experimentally derive reference masses. A reference nucleic acid used to calculate reference masses is typically a nucleic acid containing a known sequence with known methylated nucleotide loci. A reference nucleic acid used to experimentally derive reference masses can have, but is not required to have, a known sequence or known methylated nucleotide loci; methods such as those disclosed herein or otherwise known in the art can be used to identify a reference nucleic acid as methylated even when the reference nucleic acid does not have a known sequence.

As used herein, a "correlation" between a nucleic acid target gene molecule and a reference, including a "correlation" between a nucleotide locus in a nucleic acid target gene molecule and a

nucleotide locus in a reference, refers to a similarity or identity of the methylation state of a nucleic acid target gene molecule or nucleotide locus to that of a reference, such that the nucleic acid target gene molecule and the reference are expected to have at least one undefined locus with the same methylation state. For example, when the methylation state of fewer than all nucleotide loci of a nucleic acid target gene molecule have been identified, and when there is a correlation between a reference nucleic acid and a nucleic acid target gene, one or more of the unidentified loci of the nucleic acid target gene molecule can be expected to have the same methylation state as the corresponding nucleotide locus in the reference.

As used herein, the term "correlates" as between a specific diagnosis or a therapeutic outcome of a sample or of an individual and the changes in methylation state of a nucleic acid target gene region refers to an identifiable connection between a particular diagnosis or therapy of a sample or of an individual and its methylation state.

As used herein, "nucleic acid synthesis" refers to a chemical or biochemical reaction in which a phosphodiester bond is formed between one nucleotide and a second nucleotide or an oligonucleotide. Nucleic acid synthesis can include enzymatic reactions such as DNA replication reactions such as PCR or transcription, or chemical reactions such as solid phase synthesis. Nucleic acid synthesis conditions refers to conditions of a nucleic acid molecule-containing solution in which nucleotide phosphodiester bond formation is possible. For example, a nucleic acid target gene molecule can be contacted with a primer, and can be treated under nucleic acid synthesis reactions, which can include, for example, PCR or transcription conditions, and, when the primer hybridizes to the nucleic acid target gene molecule, nucleotides can be synthesized onto the primer, that is, nucleotides can be enzymatically added via phosphodiester linkage to the 3' end of primer, however, when no primer is hybridized to the nucleic acid target gene molecule, it is possible that no nucleotides are synthesized onto the primer.

As used herein, "amplifying" refers to increasing the amount of a nucleic acid molecule or a number of nucleic acid molecules. Amplification may be performed by one or more cycles of polymerase chain reaction (PCR). Based on the 5' and 3' primers that are chosen the region or regions of the nucleic acid molecule or nucleic acid molecules to be amplified may be selected. Amplification can be by any means known to those skilled in the art, including use of the PCR, transcription, and other such methods.

As used herein, "specifically amplifying" refers to increasing the amount of a particular nucleic acid molecule based on one or more properties of the molecule. For example, a nucleic acid molecule can be specifically amplified using specific hybridization of one or more primers to one or more regions of the nucleic acid molecule in PCR. Typically, specifically amplifying includes nucleic acid synthesis of a

nucleic acid target gene molecule where a primer hybridizes with complete complementarity to a nucleotide sequence in the nucleic acid target gene molecule.

As used herein a “primer” is a polynucleotide such as DNA or RNA that because of its specific nucleotide sequence is able to hybridize to a template nucleic acid, whereupon an enzyme can catalyze addition of one or more nucleotides to the 3' hydroxyl group of the primer thorough formation of a phosphoester or phosphodiester bond in a nucleotide synethesis reaction such as transcription or DNA replication.

As used herein, a “methylation specific primer” or “methylation state specific primer” refers to a primer that can specifically hybridize with a nucleic acid target gene region or a methylation-specific reagent-treated nucleic acid target gene molecule in accordance with the methylation state of the nucleic acid target gene molecule. For example, a nucleic acid target gene molecule can be treated with a methylation-specific reagent, resulting in a change in the nucleotide sequence of the nucleic acid target gene molecule as a function of the methylation state of the nucleic acid target gene molecule; and a methylation state specific primer can specifically hybridize to the treated methylated nucleic acid target gene molecule, without hybridizing to a treated unmethylated nucleic acid target gene molecule or without hybridizing to a treated, differently methylated nucleic acid target gene molecule. In another example, a nucleic acid target gene molecule can be treated with a methylation-specific reagent, resulting in a change in the nucleotide sequence of the nucleic acid target gene molecule as a function of the methylation state of the nucleic acid target gene molecule and a methylation state specific primer can specifically hybridize to the treated unmethylated nucleic acid target gene molecule, without hybridizing to a treated methylated nucleic acid target gene molecule or without hybridizing to a treated, differently unmethylated nucleic acid target gene molecule. Methylation specific primers that hybridize to a nucleic acid target gene molecule then can serve as primers for subsequent nucleotide synthesis reactions, such as PCR.

As used herein, an “amplified product” or "amplified nucleic acid" is any product of a nucleotide synthesis reaction using a nucleic acid target gene molecule as the template. Thus, a single-stranded nucleic acid molecule complementary to the treated nucleic acid target gene molecule and formed in the first amplification step is an amplified product. In addition, products of subsequent nucleotide synthesis reactions, which contain the same sequence as the treated nucleic acid target gene molecule, or the complement thereof, are amplification products. An amplification product can be a single-stranded nucleic acid molecule or a double-stranded nucleic acid molecule.

As used herein, "fragmentation" or "cleavage" refers to a procedure or conditions in which a nucleic acid molecule, such as a nucleic acid target gene molecule or amplified product thereof, is severed into two or more smaller nucleic acid molecules. Such fragmentation or cleavage can be sequence specific, base specific, or nonspecific, and can be accomplished by any of a variety of methods, reagents or conditions, including, for example, chemical, enzymatic, physical fragmentation.

As used herein, "fragment*s*", "cleavage product*s*", "cleaved products" or grammatical variants thereof, refers to nucleic acid molecules resultant from a fragmentation or cleavage of a nucleic acid target gene molecule or amplified product thereof. While such fragments or cleaved products can refer to all nucleic acid molecules resultant from a cleavage reaction, typically such fragments or cleaved products refer only to nucleic acid molecules resultant from a fragmentation or cleavage of a nucleic acid target gene molecule or the portion of an amplified product thereof containing the corresponding nucleotide sequence of a nucleic acid target gene molecule. For example, it is within the scope of the present methods, compounds and compositions, that an amplified product can contain one or more nucleotides more than the amplified nucleotide region of the nucleic acid target gene sequence (*e.g.,* a primer can contain "extra" nucleotides such as a transcriptional initiation sequence, in addition to nucleotides complementary to a nucleic acid target gene molecule, resulting in an amplified product containing "extra" nucleotides or nucleotides not corresponding to the amplified nucleotide region of the nucleic acid target gene molecule). In such an example, the fragments or cleaved products corresponding to the nucleotides not arising from the nucleic acid target gene molecule will typically not provide any information regarding methylation in the nucleic acid target gene molecule. One skilled in the art can therefore understand that the fragments of an amplified product used to provide methylation information in the methods provided herein are fragments containing one or more nucleotides arising from the nucleic acid target gene molecule, and not fragments containing nucleotides arising solely from a sequence other than that in the nucleic acid target gene molecule. Accordingly, one skilled in the art will understand the fragments arising from methods, compounds and compositions provided herein to include fragments arising from portions of amplified nucleic acid molecules containing, at least in part, nucleotide sequence information from or based on the representative nucleic acid target gene molecule.

As used herein, "base specific cleavage" refers to selective cleavage of a nucleic acid at the site of a particular base *(e.g.,* A, C, U or G in RNA or A, C, T or G in DNA) or of a particular base type *(e.g.,* purine or pyrimidine). For example, C-specific cleavage refers to cleavage of a nucleic acid at every C nucleotide in the nucleic acid.

As used herein, the phrase "non-specifically cleaved", in the context of nucleic acid cleavage, refers to the cleavage of nucleic acid target gene molecule at random locations throughout, such that various cleaved fragments of different size and nucleotide sequence content are randomly generated. Cleavage at random locations, as used herein, does not require absolute mathematical randomness, but instead only a lack of sequence-based preference in cleavage. For example, cleavage by irradiative or shearing means can cleave DNA at nearly any position, however, such methods can result in cleavage at some locations with slightly more frequency than other locations. Nevertheless, cleavage at nearly all positions with only a slight sequence preference is still random for purposes herein. Non-specific cleavage using the methods described herein can result in the generation of overlapping nucleotide fragments.

As used herein, the phrase "statistically range in size" refers to the size range for a majority of the fragments generated using cleavage methods known in the art or disclosed herein, such that some of the fragments can be substantially smaller or larger than most of the other fragments within the particular size range. An example of such a statistical range in sizes of fragments is a Poisson distribution. For example, the statistical size range of 12-30 bases also can include some oligonucleotides as small as 1 nucleotide or as large as 300 nucleotides or more, but these particular sizes statistically occur relatively rarely. In some embodiments, there is no limit to the statistical range of fragments. In other embodiments, a statistical range of fragments can specify a range such that 10% of the fragments are within the specified size range, where 20% of the fragments are within the specified size range, where 30% of the fragments are within the specified size range, where 40% of the fragments are within the specified size range, where 50% of the fragments are within the specified size range, where 60% or more of the fragments are within the specified size range, where 70% or more of the fragments are within the specified size range, where 80% or more of the fragments are within the specified size range, where 90% or more of the fragments are within the specified size range, or where 95% or more of the fragments are within the specified size range.

As used herein, the phrase "set of mass signals" or a "mass peak pattern" refers to two or more mass determinations made for each of two or more nucleic acid fragments of a nucleic acid molecule. A "mass pattern" refers to two or more masses corresponding to two or more nucleic acid fragments of a nucleic acid molecule.

As used herein, a "subject" includes, but is not limited to, an animal, plant, bacterium, virus, parasite and any other organism or entity that has nucleic acid. Among animal subjects are mammals,

including primates, such as humans. As used herein, "subject" may be used interchangeably with "patient" or "individual".

As used herein, "normal", when referring to a nucleic acid molecule or sample source, such as an individual or group of individuals, refers to a nucleic acid molecule or sample source that was not selected according to any particular criterion, and generally refers to a typical nucleotide sequence of a nucleic acid molecule or health condition of a sample source (*e.g.,* one or more healthy subjects or one or more subjects that do not a disease). For example, a normal methylation state of a particular nucleotide locus can be the wild type methylation state of the nucleotide locus. In another example, a group of normal subjects can be a group of subjects not having a particular phenotype (such as a disease).

As used herein, a "phenotype" refers to a set of parameters that includes any distinguishable trait of an organism. A phenotype can be physical traits and/or mental traits, such as emotional traits. A phenotype may also include a subject's disease diagnosis, prognosis or therapeutic response.

As used herein, a "methylation" or "methylation state" correlated with a disease, disease outcome or outcome of a treatment regimen refers to a methylation state of a nucleic acid target gene region or nucleotide locus that is present or absent more frequently in subjects with a known disease, disease outcome or outcome of a treatment regimen, relative to the methylation state of a nucleic acid target gene region or nucleotide locus than otherwise occur in a larger population of individuals (*e.g.,* a population of all individuals).

As used herein, a "plurality of genes" or a "plurality of nucleic acid target gene molecules" includes at least two, five, 10, 25, 50, 100, 250, 500, 1000, 2,500, 5,000, 10,000, 100,000, 1,000,000 or more genes or nucleic acid target gene molecules. A plurality of genes or nucleic acid target gene molecules can include complete or partial genomes of an organism or even a plurality thereof. Selecting the organism type determines the genome from among which the gene or nucleic acid target gene molecules are selected.

As used herein, "sample" refers to a composition containing a material to be detected. Samples include "biological samples", which refer to any material obtained from a living source, for example, an animal such as a human or other mammal, a plant, a bacterium, a fungus, a protist or a virus or a processed form, such as amplified or isolated material. The biological sample can be in any form, including a solid material such as a tissue, cells, a cell pellet, a cell extract, a biopsy, or feces, or a biological fluid such as urine, whole blood, plasma, serum, interstitial fluid, peritoneal fluid, lymph fluid, ascites, sweat, saliva, follicular fluid, breast milk, non-milk breast secretions, cerebral spinal fluid, seminal fluid, lung sputum, amniotic fluid, exudate from a region of infection or inflammation, a mouth

wash containing buccal cells, synovial fluid, or any other fluid sample produced by the subject. In addition, the sample can be solid samples of tissues or organs, such as collected tissues, including bone marrow, epithelium, stomach, prostate, kidney, bladder, breast, colon, lung, pancreas, endometrium, neuron, muscle, and other tissues. Samples can include organs, and pathological samples such as a formalin- fixed sample embedded in paraffin. If desired, solid materials can be mixed with a fluid or purified or amplified or otherwise treated. Samples examined using the methods described herein can be treated in one or more purification steps in order to increase the purity of the desired cells or nucleic acid in the sample, Samples also can be examined using the methods described herein without any purification steps to increase the purity of desired cells or nucleic acid. In particular, herein, the samples include a mixture of matrix used for mass spectrometric analyses and a biopolymer, such as a nucleic acid.

As used herein, "array" refers to a collection of elements, such as nucleic acids. Typically an array contains three or more members. An addressable array is one in which the members of the array are identifiable, typically by position on a solid support. Hence, in general the members of the array will be immobilized to discrete identifiable loci on the surface of a solid phase. Arrays include a collection on elements on a single solid phase surface, such as a collection of nucleotides on a chip.

As use herein, the term "data set" refers to numerical values obtained from the analysis, such as by mass spectral analysis of the nucleic acid target gene region. These numerical values associated with analysis may be values such as peak height, area under the curve and molecular mass for example in the case of mass spectral analysis.

As used herein the term "data structure" refers to a combination of two or more data sets, applying one or more mathematical manipulations to one or more data sets to obtain one or more new data sets, or manipulating two or more data sets into a form that provides a visual illustration of the data in a new way. An example of a data structure prepared from manipulation of two or more data sets would be a hierarchical cluster.

As used herein, the term "breast cancer" refers to a condition characterized by anomalous rapid proliferation of abnormal cells in one or both breasts of a subject. The abnormal cells often are referred to as "neoplastic cells," which are transformed cells that can form a solid tumor. The term "tumor" refers to an abnormal mass or population of cells (*i.e.* two or more cells) that result from excessive or abnormal cell division, whether malignant or benign, and pre-cancerous and cancerous cells. Malignant tumors are distinguished from benign growths or tumors in that, in addition to uncontrolled cellular proliferation, they can invade surrounding tissues and can metastasize. In breast cancer, neoplastic cells may be identified in one or both breasts only and not in another tissue or organ, in one or both breasts and one or

more adjacent tissues or organs (e.g. lymph node), or in a breast and one or more non-adjacent tissues or organs to which the breast cancer cells have metastasized.

The term "invasion" as used herein refers to the spread of cancerous cells to adjacent surrounding tissues. The term "invasion" often is used synonymously with the term "metastasis," which as used herein refers to a process in which cancer cells travel from one organ or tissue to another non-adjacent organ or tissue.

In the case of breast cancer, cancer cells in the breast(s) can spread to tissues and organs of a subject, and conversely, cancer cells from other organs or tissue can invade or metastasize to a breast. Cancerous cells from the breast(s) may invade or metastasize to any other organ or tissue of the body. Breast cancer cells often invade lymph node cells and/or metastasize to the liver, brain and/or bone and spread cancer in these tissues and organs. Breast cancers can spread to other organs and tissues and cause lung cancer, prostate cancer, colon cancer, ovarian cancer, cervical cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, bladder cancer, hepatoma, colorectal cancer, uterine cervical cancer, endometrial carcinoma, salivary gland carcinoma, kidney cancer, vulval cancer, thyroid cancer, hepatic carcinoma, skin cancer, melanoma, ovarian cancer, neuroblastoma, myeloma, various types of head and neck cancer, acute lymphoblastic leukemia, acute myeloid leukemia, Ewing sarcoma and peripheral neuroepithelioma, and other carcinomas, lymphomas, blastomas, sarcomas, and leukemias.

The present invention also provides a method for identifying an unknown phenotype of a tissue or cell that correlates with changes in the methylation state of the tissue or cell comprising; treating a nucleic acid sample from said tissue or cell with a reagent that modifies unmethylated cytosine to produce uracil; amplifying a nucleic acid target gene region using at least one primer that hybridizes to a strand of the nucleic acid target gene region producing amplified nucleic acids; determining the characteristic methylation state of the nucleic acid target gene region by base specific cleavage and identification of methylation sites of the amplified nucleic acids; and comparing the ratio of methylated cytosine to unmethylated cytosine for each of the methylation sites of the characteristic methylation state of the sample from the tissue or cell nucleic acid to the ratio of methylated cytosine to unmethylated cytosine for each of the methylation sites of a tissue or cell nucleic acid sample of the same type having a known phenotype thereby identifying the unknown phenotype.

In one preferred aspect of the present invention analysis of the DNA methylation of a nucleic acid target gene region is obtained by MALDI-TOF MS analysis of base-specific cleavage products derived from amplified nucleic acid target gene molecules. In general, a PCR amplification product is generated from bisulfite treated DNA, which is transcribed *in vitro* into a single stranded RNA molecule and

subsequently cleaved base-specifically by an endoribonuclease. The conversion of cytosine to uracil during bisulfite treatment generates different base specific cleavage patterns that can be readily analysed by MALDI-TOF MS. These spectral analyses may be used to determine the ratio of methylated versus non-methylated nucleotide at each methylation site of the nucleic acid target gene region. One skilled in the art will recognise that the methylation state of any nucleic acid, nucleic acid target gene region or gene of interest may be determined using the methods of the present invention. In addition, one skilled in the art would recognise the importance of the location of CpG islands in identifying novel, unique or specific methylation states for diagnostic purposes. Correspondingly, the location of a CpG island in a nucleic acid of interest may indicate other CpG islands of significance located in and around, or in close proximity to, the initially identified CpG island. Consequently it would be reasonable that one skilled in the art would look to other areas in proximity to initially identified CpG island to locate other CpG islands of interest.

The Polycomb repressive complex (PRC2)

The invention provides in part evidence of *de-novo* DNA methylation moderated through genes in the polycomb group family. The Polycomb repressive complex 2 (PRC2) comprises histone deacetylases and methyltransferases and is involved in the initiation of genes silencing through chromatin silencing. PRC2 institutes methylation of Hisytone H3 lysine 27, which can be recognized by polycomb repressive complex 1 (PRC1) to maintain gene silencing (Valk-Lingbeek, M.E., Bruggeman, S.W. & van Lohuizen, M. *Cell* 118, 409-18 (2004)). PRC2 is of particular interest because of its ability to initiate gene silencing. PRC2 recruits DNA methyltransferases to establish cytosine methylation on the bases of H3K27 markings (Vire, E. et al. *Nature* 439, 871-4 (2006)) and (Schlesinger, Y. et al. *Nat Genet* 39, 232-6 (2007)). Thus, in one embodiment of the invention, DNA methyltransferase inhibitors are administered to a subject found to be at an increased risk to cancer. Hypermethylation of PRC2 target genes in colon cancer has been reported, but it remains unclear how frequent this biological mechanism is employed in other types of cancer such as breast cancer, ovarian cancer, brain cancer, prostate cancer, colon cancer, lung cancer, kidney cancer, leukemias and melanoma.

Acute Myeloid Leukemia (AML)

Acute myelogenous leukemia (AML) is the most common form of leukemia with more than 10,000 people diagnosed each year, according to National Cancer Institute estimates.

Etiology

Heredity, radiation, chemical and other occupational exposures, and drugs have been implicated in the development of AML. There is no direct evidence of a viral etiology in AML.

Heredity: Certain syndromes with somatic cell chromosome aneuploidy, *e.g.*, Down Syndrome, are associated with an increased incidence of AML. Inherited diseases with excessive chromatin fragility, *e.g.*, ataxia telangiectasia, are also associated with AML.

Chemical and Other Exposures: Exposure to benzene, which is used as a solvent in the chemical, plastic, rubber, and pharmaceutical industries, is associated with an increased incidence of AML. Smoking and exposure to petroleum products, paint, embalming fluids, ethylene oxide, herbicides, pesticides, and electromagnetic fields have also been associated with an increased risk of AML.

Drugs: Antineoplastic drugs are the leading cause of drug-related (or treatment-associated) AML. Alkylating agent-associated leukemia occurs on average 48-72 months after exposure and demonstrates aberrations in chromosomes 5 and 7. Topoisomerase II inhibitor-associated leukemias occur 1-3 years after exposure and usually have aberrations involving chromosome band 11q23. Similarly, chloramphenicol, phenylbutazone, and less commonly chloroquine and methoxypsoralen have been reported to result in bone marrow failure that may evolve into AML.

Classification

Currently, the categorization of acute leukemia into biologically distinct groups is based on morphology, cytochemistry and immunophenotype as well as cytogenetic and molecular techniques. See Table 1 below:

TABLE 1: French-American-British (FAB) Classification of AML

FAB subtype	% of Cases	Morphology	Cytochemistry		Flow Cytometry	Cytogenetic Association
			Peroxidase / Sudan Black	Nonspecific Esterase		
M0: Minimally differentiated leukemia	2-3	Immature morphology	-	-	CD13 or 33	
M1: Myeloblastic leukemia without maturation	20	Few blasts with azurophilic granules, Auer rods, or both	3% or more	-	CD13, 33, 34, HLA-DR+	
M2: Myeloblastic leukemia with maturation	25-30	Azurophilic granules, Auer rods are often present	+	-	CD13, 15,33, 34, HLA-DR+	T(8;21) (q22;q22)[e]
M3: Hypergranular promyelocytic leukemia	8-15	Hypergranular promyelocytes with multiple Auer rods; Variant: hypogranular	+	-	CD13, 15, 33, HLA-DR-	T(15;17) (q22;q11-12)
M4: Myelomonocytic	20-25	Granulocytic and	+/-	+	CD11b, 13,	M4Eo: inv(16

FAB subtype	% of Cases	Morphology	Cytochemistry		Flow Cytometry	Cytogenetic Association
			Peroxidase / Sudan Black	Nonspecific Esterase		
leukemia		monocytic blasts; Variant: M4Eo: increase in abnormal marrow eosinophils			14f, 15, 33, HLA-DR+	(p13q22)
M5: Monocytic leukemia	20-25	M5a undifferentiated; M5b differentiated	-	+	CD11b, 13, 14f, 15, 33, HLA-DR+	11q23 translocation
M6: Erythroleukemia (Di Gugielmo's disease	5	Erythroblasts >50% of nucleated cells, myeloblasts >30% of nonerythroid cells	+/-	-	CD33, HLA-DR+	
M7: Megakaryoblastic leukemia	1-2	Megakaryoblasts >30% of all nucleated cells	-	-	CD33	

Source: BD Cheson et al, *J Clin Oncol* 8:813, 1990.

Morphologic and Cytochemical Classification: The diagnosis of AML is established by the presence of at least 20% myeloblasts in blood and/or bone marrow according to the World Health Organization classification. Once diagnosed, AML is classified based on morphology and cytochemistry according the FAB schema (see Table 1), which includes eight major subtypes, M0-M7.

Immunophenotypic Classification: The phenotype of human myeloid leukemia cells can be studied by multiparameter flow cytometry following labeling with monoclonal antibodies to cell-surface antigens. While results are useful for both diagnosis and prognosis, the process is complicated, time consuming and expensive. For example, M7 can often be diagnosed only by expression of the platelet-specific antigen cluster designation (CD) 41 or by electron-microscopic demonstration of myeloperoxidase.

Chromosomal Classification: Chromosomal analysis of the leukemic cell currently provides the most important pretreatment prognostic information for AML, but suffers from resolution limitations especially among those AML patients that fall into an "intermediate" risk group. Therefore, any improvement of existing AML classification methods (in terms of accuracy, speed and cost) has tremendous utility within the AML diagnostic, prognostic and therapeutic area. Two cytogenetic abnormalities have been invariably associated with a specific FAB group: T(15;17)(q22;q12) with M3 and inv(16)(p13q22) with M4Eo, and many chromosomal abnormalities have been associated primarily with one FAB group, including t(8;21)(q22;q22) with M2. Many of the recurring chromosomal abnormalities in AML have been associated with specific clinical characteristics. Changes in chromosomes in leukemia cells can be identified in 80% of children with AML. More commonly associated with younger age onset are t(8;21) and t(15;17), and with older age onset, del(5q) and del(7q). With currently available treatments, 30-50% of children with AML are cured. It is important to identify

those children who can be cured with standard treatments and those who should receive more individualized treatment or more aggressive treatment. The distinct type of chromosomal abnormality present at diagnosis has been shown to help identify patients with a "good" or "bad" outcome.

For example, in one Pediatric Oncology Group study, outcomes of 478 children with AML were reported. They found that children with an inverted 16th chromosome had a survival rate without relapse of 58%, those with a translocation of chromosomes 8 and 21 had a survival rate without relapse of 45% and patients with no chromosomal abnormalities had a survival rate without relapse of 45%. Children with translocation of chromosomes 15 and 17 had a survival rate without relapse of 20% and children with 11q23 abnormalities had a survival rate of 24%. This study demonstrates the benefit of using clinical data to decide which treatment regimen is best suited for patients suffering from AML.

Molecular Classification: Molecular studies of many recurring cytogenetic abnormalities have revealed genes that may by involved in leukogenesis. The 15;17 translocation encodes a chimeric protein, Pml/Rarα, which is formed by the fusion of the retinoic acid receptor-α (RARα) gene from chromosome 17 and the promyelocytic leukemia (PML) gene from chromosome 15. The Pml-Rarα fusion protein tends to suppress gene transcription and blocks differentiation of the cells. Pharmacologic doses of the Rarα ligand, all-*trans*-retinoic acid (tretinoin), relieve the block and promote differentiation.

Similar translocations resulting in molecular aberrations involved in leukogenesis include inv(16), t(8;21), and 11q23, all of which are increasingly being used for diagnosis and detection of residual disease after treatment. Molecular aberrations are also being identified that are useful for classifying risk of relapse in patients without cytogenetic abnormalities. A partial tandem duplication (PTD) of the MLL gene is found in 5-10% of patients with normal cytogenetics and results in short remission duration.

Recently, more wide-scale gene expression profiling has been used in to improve the molecular AML classification. Initial studies have provided useful results identifying novel AML subgroups and prognostic gene expression signatures (Bullinger L. et al. *N Engl J Med* 350:1605-16 (2004)) and (Valk PJ et al. *N Engl J Med* 350:1617-28 (2004)). In addition, Bullinger *et al* observed differential expression of DNA methylation enzymes (regulators) DNMT3A and DNMT3B in AML patients. DNA methylation is recognized as a key regulatory element of gene expression (Feinberg, AP *Nat Genet* 27:9-10 (2001), therefore these findings point to a potential pathogenic role of aberrant DNA methylation patterns in subgroups of AML patients resulting in distinct gene expression signatures. In particular, aberrant promoter hypermethylation represents an important mechanism in the initiation and progression of human

cancer. Aberrant methylation patterns have also been described in AML by Toyota, M. et al (Blood 97:2823-9 (2001)) and Issa JP (Nat Rev Cancer 4:988-93 (2004)).

Thus, in an embodiment of the invention, the methods described herein may be used alone or in combination with currently used morphology (*e.g.*, the percent of myeloblasts in blood and/or bone marrow), cytochemistry, immunophenotype (*e.g.*, platelet-specific antigen cluster designation) as well as cytogenetic and molecular techniques (*e.g.*, gene expression) to provide a better means to stratify AML patients into different risk groups and accordingly administer the proper treatment regimen as determined by one skilled in the art.

Clinical Presentation

Symptoms: Patients with AML most often present with nonspecific symptoms that begin gradually or abruptly and are the consequence of anemia, leukocytosis, leukopenia or leukocyte dysfunction, or thrombocytopenia. Nearly half have had symptoms for greater than three months before the leukemia was diagnosed.

Half of leukemia patients mention fatigue as the first symptom, but most complain of fatigue or weakness at the time of first diagnosis. Anorexia and weight loss are common. Fever with or without an identifiable infection is the initial symptom in ~10% of patients. Signs of abnormal hemostasis are noted in 5% of patients. On occasion, bone pain, lymphaderiopathy, non-specific cough, headache, or diaphoresis is the presenting symptom.

Physical Findings: Fever, splenomegaly, hepatomegaly, lymphadenopathy, sternal tenderness, and evidence of infection and hemorrhage are often found at diagnosis. Significant gastrointestinal bleeding, intrapulmonary hemorrhage, or intracranial hemorrhage occur most often in acute promyelocytic leukemia (APL). Retinal hemorrhages are detected in 15% of patients.

Hematologic Findings: Anemia is usually present at diagnosis and can be severe. The degree varies considerably irrespective of other hematologic findings, splenomegaly, or the duration of symptoms. Decreased erythropoiesis often results in a reduced reticulocyte count, and erythrocyte survival is decreased by accelerated destruction. Active blood loss also contributes to the anemia.

The median presenting leukocyte count is about 15,000/μl. Between 25 and 40% of patients have counts <5,000/μl, and 20% have counts >100,000/μl. Fewer than 5% have no detectable leukemic cells in the blood. Poor neutrophil function may be noted functionally by impaired phagocytosis and migration and morphologically by abnormal lobulation and deficient granulation.

Platelet counts <100,000/μl are found at diagnosis in ~75% of patients, and about 25% have counts <25,000/μl.

Pretreatment Evaluation: Once the diagnosis of AML is suspected, a rapid evaluation and initiation of appropriate therapy should follow. Factors that have prognostic significance, for example, for achieving complete remission (CR), for predicting the duration of CR or for predicting survivability, should also be assessed before initiating treatment.

Prognostic Factors

Although 70-80% of younger AML patients achieve complete remission (CR) with current chemotherapy induction regimens, more than half of these patients relapse and die of their disease. More intensive consolidation treatments, such as allogeneic stem cell transplantation, often prevent relapse, but are themselves associated with high treatment-related mortality (Giles, F.J. et al. Acute myeloid leukemia. *Hematology (Am Soc Hematol Educ Program)*, 73-110 (2002)). Therefore, it is crucial to stratify patients by risk in order to prescribe the appropriate treatment regimen that matches their risk profile. For example, a patient with a poor prognosis (*i.e.*, high risk) may be more willing to assume the risks associated with intensive consolidation treatments, such as allogeneic stem cell transplantation.

Many factors influence the likelihood of entering CR, the length of CR, and the curability of AML. In an embodiment of the invention, the methylation-based prognostic methods provided herein may be used to predict the probability of a subject's likelihood of complete remission following induction therapy wherein said likelihood of complete remission is correlated with changes in the methylation state of said subject. CR is defined after examination of both blood and bone marrow. The blood neutrophil count must be >1500/μl and the platelet count >100,000/μl. Hemoglobin concentration or hematocrit are not considered in determining CR. Circulating blasts should be absent. While rare blasts may be detected in the blood during marrow regeneration, they should disappear on successive studies. Bone marrow cellularity should be >20% with trilineage maturation. The bone marrow should contain <5% blasts, and Auer rods should be absent. For patients in CR, reverse transcriptase PCR to detect AML-associated molecular abnormalities and FISH to detect AML-associated cytogenetic aberrations are currently used to detect residual disease. Methods to detect minimal residual disease may become a reliable discriminator between patients in CR who do or do not require additional and/or alternative therapies. Prognostic factors are influenced by the treatment used.

Other prognostic factors include the following: age at diagnosis, chromosome findings at diagnosis, history of an antecedent hematologic disorder, history of a previous malignany, a high presenting leukocyte count, and other factors described in the FAB classification diagnosis of Table 1 (*e.g.*, leukemic cell characteristics such as ultrastructural features, immunophenotype, expression of the MDR1 gene, etc.). In addition to pretreatment variables, several treatment factors correlate with

prognosis in AML, including the quickness with which the blast cells disappear from the blood after the institution of therapy. In addition, patients who achieve CR after one induction cycle have longer CR durations than those requiring multiple cycles.

Treatment Options for AML

Although treatment of acute myeloid leukemia (AML) has improved dramatically over the past 30 years, the majority of patients with this disease will die within two years of diagnosis. Researchers have learned that the best way to cure patients with AML is to administer large doses of chemotherapeutic agents in a short period of time. The concept is to kill leukemia cells within 6 months before resistance to the drugs occurs. Therapy is divided into two phases: remission induction and post-remission consolidation/maintenance. Induction chemotherapy is administered to produce a complete remission (CR) in the bone marrow. Once CR is obtained, further therapy must be used to prolong survival and achieve cure. The initial induction treatment and subsequent consolidation therapy are often chosen based upon the prognostic factors described above. In an embodiment of the invention, the initial induction treatment may be chosen based soley upon the methylation-based prognostic methods provided herein or in combination with existing prognostic factors or markers. The influence of intensifying therapy with traditional chemotherapy agents such as cytarabine and anthracyclines in younger and/or lower risk patients appears to increase the cure rate of AML. In older and/or higher risk patients, the benefit of intensive therapy has been more difficult to document and therefore pursuit of novel therapies as consolidation for these patients is being actively pursued.

Remission Induction Therapy: During remission induction therapy, patients are given large doses of chemotherapy over a period of 5-7 days. These chemotherapy drugs kill leukemia cells and normal bone marrow cells. The major side effects of these drugs are related to toxicities of rapidly growing cells in the body, *i.e.*, normal bone marrow, skin and the gastrointestinal tract. Each drug also has specific side effects for other organs.

Figure 9 is a flow chart outlining the therapeutic options available to a newly diagnosed AML patient. For all forms of AML, except APL, standard therapy includes a 7-day continuous infusion of cytarabine, and a 3-day course of an anthracycline. The anthracyclines include daunorubicin (Cerubidine), doxorubicin (Adriamycin, Rubex), epirubicin (Ellence, Pharmorubicin), and idarubicin (Idamycin). Following induction, patients typically require 2-3 weeks for bone marrow blood cell production to recover. During this time, patients often require blood and platelet transfusions to maintain red blood cell and platelet levels. In order to reduce the risk of infection, antibiotics and blood cell growth factors that stimulate the bone marrow to produce normal white blood cells are often given during this

period of time. Neupogen® and Leukine® are white blood cell growth factors currently approved by the Food and Drug Administration to facilitate white blood cell production. After 2-3 weeks, blood counts will begin to recover and often return to normal. A bone marrow examination is repeated to see if a remission has been achieved. For patients in remission, the consolidation therapy will begin. If patients have not achieved a remission, another induction course of treatment will be given immediately. However, for patients with an HLA-compatible marrow donor, consideration should be given to having an immediate allogeneic stem cell transplant without receiving a second course of induction therapy. This will depend on chances of achieving a remission with a second cycle of chemotherapy. However, even if a remission is achieved with a second cycle of chemotherapy, remission duration is often very short despite consolidation.

For patients with acute promyelocytic leukemia (M3), all-trans-retinoic acid, Vesanoid®, may be included in the remission induction regimen. Patients with acute promyelocytic leukemia typically receive Vesanoid® at some time during their treatment course. There are ongoing clinical trials to determine the optimal time to administer this drug.

Strategies to Improve Remission Induction

New Drug Development: All new drugs for the treatment of patients with AML are tested first in patients with relapsed or refractory disease. When they are found to be effective, they are then evaluated in remission induction regimens.

Mylotarg®: Mylotarg® is a targeted chemotherapy, comprised of a monoclonal antibody attached to calicheamicin, an antibiotic that kills cancer cells. Monoclonal antibodies are proteins that can be produced in a laboratory and are able to identify specific antigens (small carbohydrates and/or proteins) on the surface of certain cells and bind to them. This binding stimulates the immune system to attack and kill the cells to which the monoclonal antibody is bound. Mylotarg® is targeted against the CD 33 antigen, a protein found on the surface of cancerous blood cells. Calicheamicin is an antibiotic substance that is toxic to cancer cells. Once the monoclonal antibody binds to the cancer cells, calicheamicin is absorbed into the cells and kills them. A significant benefit of this approach is that Mylotarg® mainly targets cancer cells, thereby sparing healthy cells from destruction. This is in contrast to chemotherapy or radiation, which do not differentiate between cancer cells or healthy cells in the body, a characteristic that leads to potentially intolerable side effects.

The European Organization for Research and Treatment of Cancer (EORTC) is currently conducting a clinical trial evaluating Mylotarg® plus intensive chemotherapy consisting of mitoxantrone, cytarabine and etoposide (MICE) as induction therapy for AML patients over the age of 60. Of the 34

patients in this trial so far, nearly 50% achieved an anti-cancer response to Mylotarg® alone. Approximately two months following Mylotarg® plus chemotherapy, over 40% of patients in the trial were in a complete remission (disappearance of cancer). At four and six months following therapy, the estimated survival rates are 65% and 57%, respectively. All patients had low blood cell levels from treatment, with other side effects being consistent with standard intensive chemotherapy regimens. Other clinical trials are ongoing to evaluate Mylotarg® either alone or in combination with other therapies.

Multiple Drug Resistance Inhibitors: Patients with AML may fail to achieve a remission or relapse because of chemotherapy drug resistance genes that can be present at the time of diagnosis or are induced by treatment. Several drugs are being tested to determine if they will overcome or prevent the development of multiple drug resistance in AML as part of remission induction strategies.

Post-Remission Therapy for Acute Myeloid Leukemia

If a complete remission is achieved and no further therapy given, over 90% of patients will have a recurrence of disease in weeks to months. Therefore, patients who achieve complete remission almost always undergo some form of consolidation therapy, including sequential courses of high dose cytarabine, high-dose combination therapy with allogeneic stem cell transplant (SCT), or novel therapies, based on their predicted risk of relapse (*i.e.*, risk-stratified therapy), their perceptions of the outcomes associated with each treatment, the availability of an HLA-matched sibling stem cell donor, their physician's bias concerning the appropriateness of each treatment option, and the geographic availability of each treatment. In an embodiment of the invention, the consolidation therapy may be chosen based soley upon the methylation-based prognostic methods provided herein or in combination with existing factors or markers provided above.

Post-remission therapy treatments are given as close together as possible. The more intensive the chemotherapy and the closer together the courses of therapy are given, the less chance the leukemia has of returning (*i.e.*, lower doses of drugs do not work as well as higher doses of drugs). In two randomized studies, high-dose cytarabine with an anthracycline produced CR rates similar to those achieved with standard 7 and 3 regimens. However, the CR duration was longer after high-dose cytarabine than after standard-dose cytarabine.

Risks and Benefits of an Allogeneic Stem Cell Transplant: If an allogeneic stem cell transplant is performed as consolidation, patients may proceed directly to the transplant following remission induction, as there does not appear to be an advantage to receiving chemotherapy in addition to that related to the transplant itself. In essence, the transplant is the consolidation treatment. Additional chemotherapy not

related to the transplant procedure for consolidation before the allogeneic transplant may increase toxicity without preventing relapses.

Patients with a suitable stem cell donor who should consider an allogeneic transplant as consolidation immediately after remission induction include patients with normal cytogenetics or adverse cytogenetic abnormalities, patients who require more than one induction cycle to achieve a remission, and patients who refuse to undergo the 3-4 cycles of consolidation and maintenance required for adequate control of disease with conventional chemotherapy alone. In an embodiment of the invention, patients with a suitable stem cell donor who should consider an allogeneic transplant as consolidation immediately after remission induction may further include patients with a poor prognosis based soley upon the methylation-based prognostic methods provided herein or in combination with existing factors or markers provided above.

Some patients with a suitable stem cell donor may consider delaying allogeneic transplant until first relapse. Patients over the age of 50-60, depending on other risk factors and general condition, patients with acute promyelocytic leukemia, and patients with "good" cytogenetic abnormalities (t8-22 and inverted 16) who can tolerate all prescribed consolidation therapy may not need to expose themselves to the immediate risk of an allogeneic stem cell transplant. In an embodiment of the invention, patients with a good prognosis based on the methylation-based methods provided herein, may not choose to undergo allogeneic transplant or may consider delaying allogeneic transplant until first relapse in order to not expose themselves to the immediate risk of an allogeneic stem cell transplant.

For patients who choose to have a stem cell transplant only if they relapse, it is important that it be performed at the very first sign of relapse. This requires bone marrow examinations every 4-6 weeks for the first 2 years after diagnosis. This strategy offers the best chance to catch the leukemia early when treatment will be more effective.

Consolidation Chemotherapy: Consolidation chemotherapy typically consists of 3 to 4 cycles of cytarabine given in high doses over 5 days in conjunction with additional chemotherapy drugs such as etoposide, daunomycin or idarubicin. Remission duration has been correlated with the dose of cytarabine and the number of cycles administered. In general, the more intensive the consolidation, the higher the cure rate.

The administration of consolidation chemotherapy interferes with the production of blood cells by the bone marrow, resulting in low white cell counts in the blood. There is usually a delay of one to two weeks after the administration of chemotherapy before the bone marrow resumes function, leaving patients with low blood counts for days or weeks. During this time, patients are often hospitalized and

given antibiotics and observed for infections. Neupogen® and Leukine® are growth factors that hasten the recovery of white blood cells after the administration of chemotherapy.

Consolidation chemotherapy is typically associated with 14-21 days of myelosuppression similar to induction for each of 3-4 courses. For patients who are unwilling or unable to undergo the complex and intensive chemotherapy required for consolidation therapy, either an autologous or allogeneic transplant may be considered, since these treatments condense the therapy and produce results that are equivalent or superior to the best chemotherapy regimens.

Strategies to Improve Post-Remission Therapy

Allogeneic SCT in first CR should be strongly considered by patients with high-risk karyotypes. Patients with normal karyotypes who have other poor risk factors (antecedent hematologic disorder, failure to attain remission with a single induction course, hyperleukocytosis, PTD or the MLL gene, and FLT3 abnormalities) are also potential candidates. If a suitable HLA donor does not exist, autologous SCT or novel therapeutic approaches are considered. In each of the above cases, a patient's methylation state as determined by the methods provided herein offers the patient and doctor additional information to consider while deciding whether to pursue allogeneic SCT or any other AML treatment available.

Possible Future Treatments

While significant progress has been made in the treatment of leukemia, many patients still succumb to leukemia and the complications of treatment and better treatment strategies are still needed. Future progress in the treatment of leukemia will result from continued participation in appropriate clinical studies. Currently, there are several areas of active exploration aimed at improving the treatment of leukemia.

Monoclonal Antibodies: Another approach is to deliver additional treatment directed specifically to cancer cells and avoid harming the normal cells. Monoclonal antibodies are proteins that can be produced in a laboratory that can locate cancer cells and kill them directly or stimulate the immune system to kill them. Some monoclonal antibodies have to be linked to a radioactive isotope or a toxin in order to kill cells and the antibodies essentially serve as a delivery system. Monoclonal antibodies such as Mylotarg® can be administered alone or with chemotherapy and are being evaluated to determine whether they can improve cure rates.

Mylotarg® is the first antibody-targeted chemotherapy and represents a breakthrough technology in the treatment of AML. It is currently approved by the FDA for the treatment of elderly patients with recurrent AML and is in clinical trials to evaluate its efficacy alone and in combination with other therapies in different stages of AML. Mylotarg® is comprised of a monoclonal antibody attached to

calicheamicin, an antibiotic that kills cancer cells. Mylotarg® is targeted against the CD 33 antigen, a protein found on the surface of cancerous blood cells. Calicheamicin is an antibiotic substance that is toxic to cancer cells. Once the monoclonal antibody binds to the cancer cells, calicheamicin is absorbed into the cells and kills them.

Researchers from Saint Louis University Health Sciences recently conducted a small trial to evaluate the effectiveness of Mylotarg® as consolidation therapy for patients with AML in first remission (disappearance of cancer). In this trial, five patients received Mylotarg® within one to four months of being in complete remission following standard induction and consolidation therapy. Four patients remained in complete remission for 10 to 15 months. Two of these patients later received an allogeneic stem cell transplant and are free of cancer at nine months after the transplant. All patients had severely low levels of white blood cells following treatment with Mylotarg®; however, there were no treatment-related deaths. Future clinical trials will be evaluating the effectiveness of incorporating Mylotarg® into consolidation therapy for AML.

Supportive Care: Supportive care refers to treatments designed to prevent and control the side effects of cancer and its treatment. Side effects not only cause patients discomfort, but also may prevent the optimal delivery of therapy at its planned dose and schedule. In order to achieve optimal outcomes from treatment and improve quality of life, it is imperative that side effects resulting from cancer and its treatment are appropriately managed.

Stem Cell Transplant: High-dose chemotherapy and autologous or allogeneic stem cell transplantation is currently a superior consolidation treatment option for many patients.

New Consolidation Chemotherapy Regimens: Development of new multi-drug chemotherapy treatment regimens that incorporate new or additional anti-cancer therapies for use as treatment is an active area of clinical research. New anti-cancer therapies that are being evaluated in combination with consolidation chemotherapy include the following:

Multiple Drug Resistance Inhibitors: Patients with AML fail to achieve a remission or relapse because of chemotherapy drug resistance that can be present at the time of diagnosis or are induced by treatment. Several drugs are being tested to determine if they will overcome or prevent the development of multiple drug resistance in AML as part of remission induction strategies.

Biological Modifier Therapy: Biologic response modifiers are naturally occurring or synthesized substances that direct, facilitate or enhance the body's normal immune defenses. Biologic response modifiers include interferons, interleukins and monoclonal antibodies. In an attempt to improve survival rates, these and other agents are being tested alone or in combination with chemotherapy in clinical

studies. Interleukin-2 is currently being evaluated as a maintenance agent after consolidation therapy. Newer biologic agents are in the developmental phase.

Treatment for Minimal Residual Disease: Following post-remission treatment, patients typically achieve a complete remission (complete disappearance of the cancer). Unfortunately, many patients in remission still experience a relapse of leukemia. This is because not all the leukemia cells were destroyed. Doctors refer to this as a state of "minimal residual disease." Many doctors believe that applying additional treatments when only a few leukemia cells remain represents the best opportunity to prevent the leukemia from returning. Immunotherapy to activate the body's anti-cancer defense system or other agents including monoclonal antibodies, biologic response modifiers and chemotherapy drugs can be administered over several weeks to months in an attempt to eliminate any leukemia cells remaining in the body.

Relapsed Acute Myeloid Leukemia

If a remission is not achieved or a recurrence occurs, there are essentially two choices of therapy. Since subsequent treatment with chemotherapy is rarely curative, a palliative approach can be adopted where biologic agents, such as Mylotarg®, or chemotherapy drugs are administered in non-toxic doses to keep the disease under control for as long as possible. In this situation, the emphasis is on the quality of life and supportive care measures.

The alternative approach is to receive more intensive treatment in an attempt to produce a complete remission. There are two main intensive strategies available. For younger patients, a bone marrow or blood stem cell transplant offers a possibility for control or cure of the leukemia. The other approach is to participate in clinical trials evaluating new treatments.

The most important factors predicting response at relapse are the length of the previous CR, whether initial CR was achieved with one or two courses of chemotherapy, and the type of post-remission therapy. When predicting response at relapse, a patient's methylation state as determined by the methods provided herein offers the patient and doctor additional information to consider while deciding which post-remission therapy to select.

Breast Cancer

Breast cancer is typically described as the uncontrolled growth of malignant breast tissue. Breast cancers arise most commonly in the lining of the milk ducts of the breast (ductal carcinoma), or in the lobules where breast milk is produced (lobular carcinoma). Other forms of breast cancer include Inflammatory Breast Cancer and Recurrent Breast Cancer. Inflammatory breast cancer is a rare, but very

serious, aggressive type of breast cancer. The breast may look red and feel warm with ridges, welts, or hives on the breast; or the skin may look wrinkled. It is sometimes misdiagnosed as a simple infection. Recurrent disease means that the cancer has come back after it has been treated. It may come back in the breast, in the soft tissues of the chest (the chest wall), or in another part of the body.

In an effort to detect breast cancer as early as possible, regular physical exams and screening mammograms often are prescribed and conducted. A diagnostic mammogram often is performed to evaluate a breast complaint or abnormality detected by physical exam or routine screening mammography. If an abnormality seen with diagnostic mammography is suspicious, additional breast imaging (with exams such as ultrasound) or a biopsy may be ordered. A biopsy followed by pathological (microscopic) analysis is a definitive way to determine whether a subject has breast cancer. Excised breast cancer samples often are subjected to the following analyses: diagnosis of the breast tumor and confirmation of its malignancy; maximum tumor thickness; assessment of completeness of excision of invasive and in situ components and microscopic measurements of the shortest extent of clearance; level of invasion; presence and extent of regression; presence and extent of ulceration; histological type and special variants; pre-existing lesion; mitotic rate; vascular invasion; neurotropism; cell type; tumor lymphocyte infiltration; and growth phase.

The stage of a breast cancer can be classified as a range of stages from Stage 0 to Stage IV based on its size and the extent to which it has spread. The following table summarizes the stages:

TABLE 2

Stage	Tumor Size	Lymph Node Involvement	Metastasis (Spread)
I	Less than 2 cm	No	No
II	Between 2-5 cm	No or in same side of breast	No
III	More than 5 cm	Yes, on same side of breast	No
IV	Not applicable	Not applicable	Yes

Stage 0 cancer is a contained cancer that has not spread beyond the breast ductal system. Fifteen to twenty percent of breast cancers detected by clinical examinations or testing are in Stage 0 (the earliest form of breast cancer). Two types of Stage 0 cancer are lobular carcinoma in situ (LCIS) and ductal carcinoma in situ (DCIS). LCIS indicates high risk for breast cancer. Many physicians do not classify LCIS as a malignancy and often encounter LCIS by chance on breast biopsy while investigating another area of concern. While the microscopic features of LCIS are abnormal and are similar to malignancy, LCIS does not behave as a cancer (and therefore is not treated as a cancer). LCIS is merely a marker for a

significantly increased risk of cancer anywhere in the breast. However, bilateral simple mastectomy may be occasionally performed if LCIS patients have a strong family history of breast cancer. In DCIS the cancer cells are confined to milk ducts in the breast and have not spread into the fatty breast tissue or to any other part of the body (such as the lymph nodes). DCIS may be detected on mammogram as tiny specks of calcium (known as microcalcifications) 80% of the time. Less commonly DCIS can present itself as a mass with calcifications (15% of the time); and even less likely as a mass without calcifications (<5% of the time). A breast biopsy is used to confirm DCIS. A standard DCIS treatment is breast-conserving therapy (BCT), which is lumpectomy followed by radiation treatment or mastectomy. To date, DCIS patients have chosen equally among lumpectomy and mastectomy as their treatment option, though specific cases may sometimes favor lumpectomy over mastectomy or vice versa.

In Stage I, the primary (original) cancer is 2 cm or less in diameter and has not spread to the lymph nodes. In Stage IIA, the primary tumor is between 2 and 5 cm in diameter and has not spread to the lymph nodes. In Stage IIB, the primary tumor is between 2 and 5 cm in diameter and has spread to the axillary (underarm) lymph nodes; or the primary tumor is over 5 cm and has not spread to the lymph nodes. In Stage IIIA, the primary breast cancer of any kind that has spread to the axillary (underarm) lymph nodes and to axillary tissues. In Stage IIIB, the primary breast cancer is any size, has attached itself to the chest wall, and has spread to the pectoral (chest) lymph nodes. In Stage IV, the primary cancer has spread out of the breast to other parts of the body (such as bone, lung, liver, brain). The treatment of Stage IV breast cancer focuses on extending survival time and relieving symptoms.

Based in part upon selection criteria set forth above, individuals having breast cancer can be selected for genetic studies. Also, individuals having no history of cancer or breast cancer often are selected for genetic studies. Other selection criteria can include: a tissue or fluid sample is derived from an individual characterized as Caucasian; the sample was derived from an individual of German paternal and maternal descent; the database included relevant phenotype information for the individual; case samples were derived from individuals diagnosed with breast cancer; control samples were derived from individuals free of cancer and no family history of breast cancer; and sufficient genomic DNA was extracted from each blood sample for all allelotyping and genotyping reactions performed during the study. Phenotype information included pre- or post-menopausal, familial predisposition, country or origin of mother and father, diagnosis with breast cancer (date of primary diagnosis, age of individual as of primary diagnosis, grade or stage of development, occurrence of metastases, e.g., lymph node metastases, organ metastases), condition of body tissue (skin tissue, breast tissue, ovary tissue,

peritoneum tissue and myometrium), method of treatment (surgery, chemotherapy, hormone therapy, radiation therapy).

Lung Cancer

Lung cancer is the rapid proliferation of abnormal cells in one or both of the lungs. While normal lung tissue cells reproduce and develop into healthy lung tissue, these abnormal cells proliferate rapidly and rarely form normal lung tissue. Instead, the abnormal cells proliferate, form tumors, and disrupt the lung, thereby decreasing lung function and eventually lead to death.

As used herein, the term "lung cancer" refers to a condition characterized by anomalous rapid proliferation of abnormal cells in one or both lungs of a subject. The abnormal cells often are referred to as "neoplastic cells," which are transformed cells that can form a solid tumor. The term "tumor" refers to an abnormal mass or population of cells (i.e. two or more cells) that result from excessive or abnormal cell division, whether malignant or benign, and pre-cancerous and cancerous cells. Malignant tumors are distinguished from benign growths or tumors in that, in addition to uncontrolled cellular proliferation, they can invade surrounding tissues and can metastasize. In lung cancer, neoplastic cells may be identified in one or both lungs only and not in another tissue or organ, in one or both lungs and one or more adjacent tissues or organs (e.g. lymph node), or in a lung and one or more non-adjacent tissues or organs to which the lung cancer cells have metastasized. Lung cancer includes squamous cell carcinoma (SCC), adenocarcinoma, small-cell lung cancer, and non-small cell lung cancer.

The World Health Organization classifies lung cancer into four major histological types: (1) squamous cell carcinoma (SCC), (2) adenocarcinoma, (3) large cell carcinoma, and (4) small cell lung carcinoma (SCLC). (see e.g. "The World Health Organization histological typing of lung tumours," Am J Clin Pathol 1982; 77:123-136; see also World Wide Web URL lungcancer.org). However, there is a great deal of tumor heterogeneity even within the various subtypes, and it is not uncommon for lung cancer to have features of more than one morphologic subtype. The term non-small cell lung carcinoma (NSCLC) includes squamous, adenocarcinoma and large cell carcinomas.

Lung cancer can be categorized into the following stages:

Stage IA: Tumor of any size found in the lung only. Tumor less than 3 cm without evidence of lymph node or metastatic spread.

Stage IB: Tumor of any size found in the lung only. Tumor greater than 3 cm plus atelectasis without evidence of lymph node or metastatic spread. Tumor greater than 3 cm, involves main bronchus, invades the visceral pleura, or associated with atelectasis or pneumonitis that does not involve entire lung; no evidence of lymph node or distant metastases.

Stage IIA: Tumor has spread to lymph nodes associated with the lung. Tumor less than 3 cm; ipsilateral peribronchial and/or hilar lymph node disease; no distant metastases.

Stage IIB: Tumor has spread to lymph nodes associated with the lung. Tumor greater than 3 cm, involves main bronchus, invades visceral pleura, or is associated with atelectasis or pneumonitis that does not involve the whole lung; ipsilateral peribronchial and/or hilar lymph node disease; no distant metastases.

Stage IIIA: Tumor has spread to lymph nodes in the tracheal area, including chest wall and diaphragm. Tumor less than 3 cm; metastases in ipsilateral hilar and mediastinal lymph nodes; no distant metastases. In advanced stages of Stage IIIA, tumor greater than 3 cm, involves main bronchus, invades visceral pleura, with atelectesis or pneumonitis that does not involve the entire lung; metastases in ipsilateral hilar and mediastinal lymph nodes; no distant metastases. In further advanced stages of Stage IIIA, tumor of any size that invades the chest wall, diaphragm, mediastinal pleura, parietal pericardium or superior sulcus tumors; or tumor in the main bronchus less than 2 cm distal to the carina but not involving the carina; or atelectasis or pneumonitis of entire lung; no lymph node or distant metastases.

Stage IIIB: Tumor has spread to lymph nodes on opposite lung or in the neck. Any size tumor; metastases in contralateral mediastinal or hilar lymph nodes; any scalene or supraclavicular lymph node(s); no distant metastases. In advanced stages of Stage IIIB, tumor of any size that invades any of the following: liver, mediastinum, heart, great vessels, trachea, esophagus, vertebral body, carina; or malignant pleural effusion; any lymph nodes (0-3); no distant metastases.

Stage IV: Tumor has spread beyond the chest, most often to the brain or bones. Any size M1 tumor; any nodal involvement: evidence of distant metastasis.

Early detection of lung cancer is critical to improving chances of survival. Physicians use a number of different tests to detect and diagnose lung cancer, including imaging scans that provide more accurate and sensitive results than conventional X-rays. Information from these tests enables the physician to determine the type and stage of the cancer and the best way to treat the disease. Tests include physical examination (e.g., detecting signs such as swollen lymph nodes in the neck or collarbone area); chest examination (e.g., examining the chest and listening to the lungs for abnormal breathing sounds or patterns); chest X-ray (e.g., identifying abnormal growths); CT scans and MRI's; PET scans

(finding cancerous tumors because of their ability to take up radioactive sugar); sputum cytology (e.g., examining coughed-up phlegm from the lungs to check for abnormal or cancerous cells); bronchoscopy (e.g., viewing of the lungs through a hollow, flexible tube (bronchoscope) that is passed through the nose and throat into the main airway of the lungs); and biopsy (e.g., removing lung tissue for examination under a microscope).

Genetics plays a role in the development of lung cancer. For example, some subjects may be more susceptible to developing lung cancer despite common risk factors such as smoking. Others may be susceptible to developing aggressive forms of lung cancer more likely to metastasize or invade surrounding tissues, thus making the disease more difficult to treat.

Prostate Cancer

Prostate cancer is the rapid proliferation of abnormal cells in the prostate gland. While normal prostate cells reproduce and develop into healthy prostate tissue, these abnormal cells proliferate rapidly and rarely form normal prostate tissue. Instead, the abnormal cells proliferate, form tumors, disrupt the prostate, and spread to surrounding tissues.

As used herein, the term "prostate cancer" refers to a condition characterized by anomalous rapid proliferation of abnormal cells in the prostate gland of a subject. In prostate cancer, neoplastic cells may be identified in the prostate only and not in another tissue or organ, in the prostate and one or more adjacent tissues or organs (e.g. spine, lungs, liver or brain), or in a lung and one or more non-adjacent tissues or organs to which the prostate cancer cells have metastasized. Prostate cancer cells often invade spine cells (e.g., vertebral column) and/or metastasize to the lungs, liver, and/or brain and spread cancer in these tissues and organs.

The prostate is about the size of a walnut and can be divided into two parts referred to as the right or left lobes. It lies just below the urinary bladder and surrounds the upper part of the urethra. The urethra is the tube that carries urine from the bladder and semen from the sex glands out through the penis. As one of a man's sex glands, the prostate is affected by male sex hormones (most notably testosterone). These hormones stimulate the activity of the prostate and the replacement of prostate cells as they wear out.

The prostate gland surrounds the neck of the bladder and urethra, and most prostate cancers initially occur in the peripheral zone of the prostate gland, away from the urethra. Tumors within this zone may not produce any symptoms and, as a result, most men with early-stage prostate cancer will not present clinical symptoms of the disease until significant progression has occurred. Tumor progression

into the transition zone of the prostate may lead to urethral obstruction, thus producing the first symptoms of the disease. However, these clinical symptoms are indistinguishable from the common non-malignant condition of benign prostatic hyperplasia (BPH).

Early detection of the disease has proven to be critical for survival among prostate cancer patients. For example, there is 100% five-year survival rates for prostate cancer patients diagnosed at the local and regional stage; wherease, the five-year survival rate for prostate cancer patients in which the cancer has metastasized is only 34%. Early detection and diagnosis of prostate cancer currently relies on digital rectal examinations (DRE), prostate specific antigen (PSA) measurements, transrectal ultrasonography (TRUS), and transrectal needle biopsy (TRNB). At present, serum PSA measurement in combination with DRE are the most common tools used to detect and diagnose prostate cancer. Both have major limitations which have fueled intensive research into finding better diagnostic markers for prostate cancer.

The most common method of staging prostate cancer is by using a system called the TNM system that stands for Tumor, Node, Metastases. Tables 3A, 3B and 3C below describe the characteristics of each stage and the available treatment options:

TABLE 3A: size of the primary tumor

Stage	Description	Treatment Options
TX	Primary tumor cannot be assessed.	Prostatectomy or radiation therapy may be chosen for Stage T1. In addition, hormonal therapy may be used before, during, or after prostatectomy or radiation. In other cases, watchful waiting may be an option.
T0	No evidence of primary tumor.	
T1	Tumor not clinically apparent.	
T1a	Tumor incidentally found in <= 5% of prostate sample.	
T1b	Tumor incidentally found in > 5% of prostate sample.	
T1c	Tumor identified at needle biopsy performed to investigate PSA elevation.	
T2	Tumor palpable and confined to prostate.	Treatment options for this stage often include prostatectomy and radiation therapy. In addition, hormonal therapy may be used before, during, or after prostatectomy or radiation. In other cases, watchful waiting may be an option.
T2a	Tumor involves one prostate lobe.	
T2b	Tumor involves both prostate lobes.	
T3	Tumor palpable and extends beyond prostate capsule.	Prostatectomy, radiation therapy, or both are common choices during this stage. In addition, hormonal therapy may be used before, during, or after
T3a	Tumor extends beyond prostate capsule, either on one side (unilaterally) or both sides (bilaterally).	

T3b	Tumor invades seminal vesicles.	prostatectomy or radiation. In other cases, watchful waiting may be an option.
T4	Tumor is fixed or invades adjacent anatomy other than seminal vesicles: bladder neck, external sphincter, rectum, levator muscles, and/or pelvic wall.	The treatment options available during Stage T4 are generally the same as those in Stage T3. However, prostatectomy is used less frequently.

TABLE 3B: extent of lymph node involvement

Stage	Description	Treatment Options
NX	Regional lymph nodes cannot be assessed.	Hormonal therapy is generally used. Prostatectomy or radiation may be used with hormonal therapy. Chemotherapy may be used later if hormonal therapy is no longer working. In other cases, watchful waiting may be an option.
N0	No regional lymph node metastasis.	
N1	Metastasis in regional lymph node or nodes.	

TABLE 3C: presence or absence of metastases

Stage	Description	Treatment Options
MX	Presence of distant metastasis cannot be assessed.	Hormonal therapy is generally used. Chemotherapy may be used later if hormonal therapy is no longer working. In some cases, watchful waiting may be an option.
M0	No distant metastasis.	
M1	Distant metastasis.	
M1a	Metastasis to nonregional lymph nodes.	
M1b	Metastasis to bone.	
M1c	Metastasis to other distant sites.	

In addition, the aggressiveness of prostate cancer may be measured using the Gleason scale (2-10), e.g., 2 = normal looking tumor, 10 = very abnormal looking tumor. Gleason grading system involves assigning numbers (called a Gleason grade) to cancerous prostate tissue, ranging from 1 through 5, based on how much the arrangement of the cancer cells mimics the way normal prostate cells form glands. Two grades are assigned to the most common patterns of cells that appear; these two grades (they can be the same or different) are then added together to determine the Gleason score (a number from 1 to 10).

A high Gleason score indicates that the prostate cancer is aggressive and likely to metastasize to surrounding organs or tissues. Prostate cancer most commonly spreads to the surrounding bones, including the pelvis, hips, pubic bone and spine. In 90% of prostate cancer metastasis, the cancer spreads to the spine, and often involves vertebral column. In 50% of prostate cancer metastasis, the cancer spreads to the either one or both of the lungs, while in 25% of prostate cancer metastasis, the cancer

spreads to the liver. In rare cases, prostate cancer may spread to the brain, with a poor prognosis (average survival 7.6 months).

There is no available marker that can predict the emergence of the typically fatal metastatic stage of prostate cancer. Diagnosis of metastatic stage is presently achieved by open surgical or laparoscopic pelvic lymphadenectomy, whole body radionuclide scans, skeletal radiography, and/or bone lesion biopsy analysis. Clearly, identification of susceptibility genes and other less invasive diagnostic methods offer the promise of easing the difficulty those procedures place on a patient, as well as improving diagnostic accuracy and opening therapeutic options. A similar problem is the lack of effective prognostic markers for determining which cancers are indolent and which ones are or will be aggressive. PSA, for example, fails to discriminate accurately between indolent and aggressive cancers. Until there are prostate cancer markers capable of predicting susceptibility to development of the disease, reliably identifying early-stage disease, and predicting susceptibility to metastasis, the management of prostate cancer will continue to be extremely difficult.

Inclusion or exclusion of samples for a prostate cancer pool to be used in a genetic study may be based upon the following criteria: relevant phenotype information for the individual (e.g., case samples derived from individuals diagnosed with prostate cancer); or type of prostate cancer diagnosed. Control samples may be selected based on relevant phenotype information for the individual (e.g., derived from individuals free of any cancer); and no family history of cancer. Additional phenotype information collected for both cases and controls may include age of the individual, gender, date of primary diagnosis, age of individual as of primary diagnosis, age of individual when sample collected, or method of treatment, height, weight, disease status, such as heart disease, hypertension, vascular disease, CNS disease, gastrointestinal disease, urogenital disease, asthma, other cancers, diabetes, and also smoking status. In an embodiment, the same phenotypic information is collected for the parents of cases and controls, making additional phenotypic analysis possible.

Based in part upon selection criteria set forth above, individuals suffering from prostate cancer can be selected for genetic studies. Also, individuals having no history of cancer, particularly prostate cancer, often are selected for genetic studies as controls.

Methods for Treating Prostate Cancer

Despite the prevalence of prostate cancer among men in North America and Europe, there is still no effective or specific treatment for metastatic prostate cancer. Surgical prostatectomy, radiation therapy, hormone ablation therapy, and chemotherapy continue to be the main treatment modalities. Surgery is often effective for early stage or non-aggressive prostate cancer. Radiation can be used for

early stage prostate cancer, and in advanced prostate cancer. Hormonal therapy may be used to remove androgens (LHRH agonists, anti-androgens); however, all prostate cancer becomes resistant to hormonal therapy eventually. Chemotherapy may be effective in advanced cases non-responsive to hormonal therapy. Chemotherapy agents used to treat prostate cancer include mitoxantrane plus corticosteroids; and estramustane plus taxanes.

Thus, provided are methods for identifying a predisposition to prostate cancer in an individual as described herein and, if a genetic predisposition is identified, treating that individual to delay or reduce or prevent the development of prostate cancer. Treatment of prostate cancer includes prostatectomy, radiation therapy, chemotherapy, cryotherapy and hormonal therapy.

Prostatectomy is the surgical removal of the prostate. A radical prostatectomy can be performed to remove the cancer from the prostate and from nearby areas where the cancer has spread. This type of surgery may help prevent further spread of the cancer. Prostatectomy may be used alone or in combination with hormonal therapy for the treatment of prostate cancer. It is most often used during early stages (Stages T1 and T2), when prostate cancer is located only within the prostate.

Radiation therapy uses high-energy rays to kill prostate cancer cells, shrink tumors, or prevent cancer cells from dividing and spreading. It is nearly impossible to direct these rays only at the cancer cells. As a result, they may damage both cancer cells and healthy cells nearby. Radiation doses are usually small and spread out over time. This allows the healthy cells to recover and survive, while the cancer cells eventually die. Radiation therapy may be used when prostate cancer has not spread beyond the prostate (Stages T1-T2). Like prostatectomy, radiation therapy works best when the cancer is located in a small area, and it can help prevent the cancer from spreading further. In early stages of prostate cancer, radiation therapy may cure the disease.

Chemotherapy is the use of powerful and toxic drugs to attack cancer cells. The drugs circulate throughout the body in the bloodstream and may kill any rapidly growing cells, including healthy ones. Chemotherapy is generally reserved for patients with advanced stage prostate cancer (Stage M+) that no longer responds to hormonal therapy.

Cryotherapy sometimes is referred to as cryosurgery, and it is a procedure where the tumor is frozen, allowed to thaw, and then frozen again. It may be used to treat early stages of prostate cancer in which the tumor has not spread outside the prostate.

The primary strategy of hormonal therapy is to decrease the production of testosterone by the testes or block the actions that testosterone has on the prostate cells. Hormonal therapy cannot cure prostate cancer. Instead, it slows the cancer's growth and reduces the size of the tumor(s). Drugs that

prevent the production or block the action of testosterone and other male hormones, called androgens. Two classes of drugs most commonly used as hormonal therapy in prostate cancer include: LHRH analog(s) (luteinizing hormone-releasing hormone analogs) or medical castration — class of drugs which prevent testosterone production by the testes; and Nonsteroidal antiandrogens (also called antiandrogens) — class of drugs which block the action of testosterone at the prostate.

Identifying Nucleic Acid Target Gene Regions

Selecting nucleic acid target gene regions of interest that harbor potential methylated sites may be based on a variety of characteristics known or available to those skilled in the art regarding the target gene of interest. Selection criteria may include for example the gene's physiological role or function in a biological pathway related to the disease/phenotype of interest, existence of mutations effecting disease/phenotype or sequence polymorphisms conferring predisposition to disease/phenotype of interest. Selection may also be based on known expression status or sequence motifs binding specific proteins relevant to methylation of gene regions/chromosomal regions. One skilled in the art would recognize that a considerable amount of information may be obtained through publication of data and experiments that may provide key indications that the methylation state of a particular gene may be of importance for future prognostic or diagnostic purposes that are the subject of the present invention.

Any type of disease condition that can be correlated with changes in the methylation state of a sample organism, tissue or cell can be analyzed with the methods of the present invention, some of these disease conditions include for example, cancer, cardiovascular disease (CVD), central nervous system disease (CNS), metabolic disease, inflammation, aging, morbidity, osteoarthritis, infection and drug response. Of particular interest are hematologic cancers, and include for example, acute myeloid leukemia and chronic myeloid leukemia.

Any nucleic acid, nucleic acid target gene region or gene may be have a potentially significant characteristic methylation state for diagnostic purposes. Consequently, any nucleic acid of interest may be analyzed using the method described herein, some examples of particular genes of interest include, ACSL6, ATP10A, BCL6, BCR, CA3, CCND1, CCND2, CD38, CDKN1C, CHGA, COL5A1, EGFR, ESR1, FLI1, FLJ32447, FLT3, FLT4, FRAT1, GABRB3, GAS7, GNAS, GPC3, HEAB, HIST1H4I, HOXA1, HOXA10, HOXA2, HOXA6, HOXA7, HOXA9, HOXC13, IL10RA, IRF4, KIT, LCK, LEP, LMO2, LYL1, MLLT6, MYH11, MYOD1, NFKB2, OLIG2, PAX5, PAX7, PAX8, PEG3, PHOX2B, PLOD1, PON1, PSIP1, PTPRN2, REL, RET, RUNX1T1, SBDS, SET, SLC22A3, SLC38A4, SNRPN, TAL1, TCL1A, TLX1, TLX3, TMPRSS2, TSPYL5, WDR66, WT1, ZIM2, ZNF198 and ZNF331. Each

gene may have particular regions of interest selected by a variety of methods including for example the presence of CpG islands. In a related embodiment, the gene of interest may comprise one or more PRC2 binding sites, wherein the target gene is selected from one or more of the following targets: CA3, CD38, EGFR, ESR1, FLI1, FLJ32447, FLT3, FRAT1, GAS7, GNAS, GPC3, HIST1H4I, HOXA1, HOXA10, HOXA2, HOXA6, HOXA7, HOXA9, HOXC13, IL10RA, IRF4, MYOD1, OLIG2, PAX5, PAX7, PAX8, PHOX2B, PTPRN2, SLC22A3, TAL1, TLX1, TLX3 and WT1.

Isolated Nucleic Acids

Featured herein are isolated nucleic acid target gene regions, which include the nucleic acid having the nucleotide sequence for the targets provided in Table 10, nucleic acid variants, and substantially identical nucleic acids of the foregoing. In Table 10, the amplicon sequence is provided, and Table 11 provides the location of the CpG units that were analyzed. Throughout the document and in the Figures and Tables, the target gene regions may be referenced according to their amplicon ID. The amplicon ID follows the general schema: databaseID_GeneName_AmpliconID. Also throughout the document and in the Figures and Tables, CpG sites are referenced according to their CpG ID. The CpG ID's refer to the specific CpG location within the particular genomic region. For example, each CpG ID follows the general schema: databaseID_GeneName_ AmpliconID_CPG_CPGposition in the amplicon. "GeneName" is the refseq gene name of the analysed promoter region, or in the case of intragenic regions, the nearest gene is identified. "AmpliconID" is the particular amplicon analyzed within the gene or region, especially relevant if multiple amplicons were analyzed for this gene. "CPG" is a constant text string. "CPG position in the amplicon" indicates which CpG Sites are enclosed in the measured CpG Unit. The numbers given refer to the CpG sites as counted from the 5' end of the analyzed amplicon sequence. Also, the amplification primers are provided in Table 10, wherein the left and right primers for each amplicon can be determined according to the numbers provided. For example, for ABL1, the left primer corresponds to the first 24 nucleotides of the amplicon sequence provided, and the right primer corresponds to the last 26 nucleotides of the amplicon sequence provided. However, single sequence amplification is occuring, therefore, the right primer sequence is complementary to the amplicon sequence provided and the left primer sequence is the actual amplicon sequence (and binds to the extended sequence generated from the right primer).

As used herein, the term "nucleic acid" includes DNA molecules (e.g., a complementary DNA (cDNA) and genomic DNA (gDNA)) and RNA molecules (e.g., mRNA, rRNA, and tRNA) and analogs of DNA or RNA, for example, by use of nucleotide analogs. The nucleic acid molecule can be single-

stranded and it is often double-stranded. The term "isolated or purified nucleic acid" refers to nucleic acids that are separated from other nucleic acids present in the natural source of the nucleic acid. For example, with regard to genomic DNA, the term "isolated" includes nucleic acids which are separated from the chromosome with which the genomic DNA is naturally associated. An "isolated" nucleic acid is often free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and/or 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of 5' and/or 3' nucleotide sequences which flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

Also included herein are nucleic acid fragments. These fragments typically are a nucleotide sequence identical to a nucleotide sequence in Table 10, a nucleotide sequence substantially identical to a nucleotide sequence in Table 10, a sequence (genomic or cDNA) corresponding to the targets genes disclosed in Table 9, or a nucleotide sequence that is complementary to the foregoing. The nucleic acid fragment may be identical, substantially identical or homologous to a nucleotide sequence corresponding to the genomic sequence of any target gene or target gene region of the invention, and may encode a domain or part of a domain or motif of a target gene polypeptide. Sometimes, the fragment will comprises the polymorphic variation described herein as being associated with cancer. The nucleic acid fragment sometimes is 50, 100, or 200 or fewer base pairs in length, and is sometimes about 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3100, 3200, 3300, 3400, 3500, 3600, 3800, 4000, 5000, 6000, 7000, 8000, 9000, 10000, 15000, 20000, 30000, 40000, 50000, 60000, 70000, 80000, 90000, 100000, 110000, 120000, 130000, 140000, 150000 or 160000 base pairs in length. A nucleic acid fragment complementary to a nucleotide sequence identical or substantially identical to the nucleotide sequence of Table 10 and hybridizes to such a nucleotide sequence under stringent conditions often is referred to as a "probe." Nucleic acid fragments often include one or more polymorphic sites, or sometimes have an end that is adjacent to a polymorphic site as described hereafter.

An example of a nucleic acid fragment is an oligonucleotide. As used herein, the term "oligonucleotide" refers to a nucleic acid comprising about 8 to about 50 covalently linked nucleotides, often comprising from about 8 to about 35 nucleotides, and more often from about 10 to about 25

nucleotides. The backbone and nucleotides within an oligonucleotide may be the same as those of naturally occurring nucleic acids, or analogs or derivatives of naturally occurring nucleic acids, provided that oligonucleotides having such analogs or derivatives retain the ability to hybridize specifically to a nucleic acid comprising a targeted polymorphism. Oligonucleotides described herein may be used as hybridization probes or as components of therapeutic assays, for example, as described herein.

Oligonucleotides are typically synthesized using standard methods and equipment, such as the ABI 3900 High Throughput DNA Synthesizer and the EXPEDITE™ 8909 Nucleic Acid Synthesizer, both of which are available from Applied Biosystems (Foster City, CA). Analogs and derivatives are exemplified in U.S. Pat. Nos. 4,469,863; 5,536,821; 5,541,306; 5,637,683; 5,637,684; 5,700,922; 5,717,083; 5,719,262; 5,739,308; 5,773,601; 5,886,165; 5,929,226; 5,977,296; 6,140,482; WO 00/56746; WO 01/14398, and related publications. Methods for synthesizing oligonucleotides comprising such analogs or derivatives are disclosed, for example, in the patent publications cited above and in U.S. Pat. Nos. 5,614,622; 5,739,314; 5,955,599; 5,962,674; 6,117,992; in WO 00/75372; and in related publications.

Oligonucleotides also may be linked to a second moiety. The second moiety may be an additional nucleotide sequence such as a tail sequence (*e.g.*, a polyadenosine tail), an adapter sequence (e.g., phage M13 universal tail sequence), and others. Alternatively, the second moiety may be a non-nucleotide moiety such as a moiety which facilitates linkage to a solid support or a label to facilitate detection of the oligonucleotide. Such labels include, without limitation, a radioactive label, a fluorescent label, a mass label, a chemiluminescent label, a paramagnetic label, and the like. The second moiety may be attached to any position of the oligonucleotide, provided the oligonucleotide can hybridize to the nucleic acid comprising the polymorphism. As used herein, "polymorphism" may refer to a CpG site that undergoes a methylation change.

Uses for Nucleic Acid Sequences

Nucleic acid coding sequences described herein may be used for therapeutic purposes. Also, included herein are oligonucleotide sequences such as antisense RNA, small-interfering RNA (siRNA), probes that form triple helical complexes that block the binding of transcription factors (*e.g.*, polycomb group protiens) and DNA molecules and ribozymes that function to inhibit translation of a polypeptide. Antisense techniques and RNA interference techniques are known in the art and are described herein.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to

complementary target RNA, followed by a endonucleolytic cleavage. Ribozymes may be engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of RNA sequences corresponding to or complementary to the nucleotide sequences set forth in Table 10. Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between fifteen (15) and twenty (20) ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for predicted structural features such as secondary structure that may render the oligonucleotide sequence unsuitable. The suitability of candidate targets may also be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

Antisense RNA and DNA molecules, siRNA and ribozymes may be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides well known in the art such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors which incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

PNA nucleic acids can be used in prognostic, diagnostic, and therapeutic applications. As used herein, the terms "peptide nucleic acid" or "PNA" refers to a nucleic acid mimic such as a DNA mimic, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of a PNA can allow for specific hybridization to DNA and RNA under conditions of low ionic strength. Synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described, for example, in Hyrup et al., (1996) supra and Perry-O'Keefe et al., Proc. Natl. Acad. Sci. 93: 14670-675 (1996). For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, for example, inducing transcription or translation arrest or inhibiting replication. PNA nucleic acid molecules can also be used in the analysis of single base pair mutations in a gene, (e.g., by PNA-directed PCR clamping); as "artificial restriction enzymes" when used in combination with other enzymes.

DNA encoding a polypeptide also may have a number of uses for the diagnosis of diseases, including cancer, resulting from aberrant expression of a target gene described herein. For example, the nucleic acid sequence may be used in hybridization assays of biopsies or autopsies to diagnose

abnormalities of expression or function (e.g., Southern or Northern blot analysis, in situ hybridization assays).

In addition, the expression of a polypeptide during embryonic development or during the pathophysiology of cancer may also be determined using nucleic acid encoding the polypeptide. Repressing the expression of a target polypeptide can be the cause of various disease states, such as cancer. In situ hybridizations using polynucleotide probes may be employed to predict problems related to cancer. Further, administration of human active polypeptide, recombinantly produced as described herein, may be used to treat disease states related to hypermethylated target genes.

Expression Vectors, Host Cells, and Genetically Engineered Cells

Provided herein are nucleic acid vectors, often expression vectors, which contain a nucleic acid target gene or nucleic acid target gene region. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked and can include a plasmid, cosmid, or viral vector. The vector can be capable of autonomous replication or it can integrate into a host DNA. Viral vectors may include replication defective retroviruses, adenoviruses and adeno-associated viruses for example.

A vector can include a target nucleic acid in a form suitable for expression of the nucleic acid in a host cell. The recombinant expression vector typically includes one or more regulatory sequences operatively linked to the nucleic acid sequence to be expressed. The term "regulatory sequence" includes promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence, as well as tissue-specific regulatory and/or inducible sequences. The design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, and the like. Expression vectors can be introduced into host cells to produce target polypeptides, including fusion polypeptides, encoded by target nucleic acids.

Recombinant expression vectors can be designed for expression of target polypeptides in prokaryotic or eukaryotic cells. For example, target polypeptides can be expressed in E. coli, insect cells (e.g., using baculovirus expression vectors), yeast cells, or mammalian cells. Suitable host cells are discussed further in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of polypeptides in prokaryotes is most often carried out in E. coli with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polypeptides. Fusion vectors add a number of amino acids to a polypeptide encoded therein, usually to the amino terminus of the recombinant polypeptide. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant polypeptide; 2) to increase the solubility of the recombinant polypeptide; and 3) to aid in the purification of the recombinant polypeptide by acting as a ligand in affinity purification. Often, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant polypeptide to enable separation of the recombinant polypeptide from the fusion moiety subsequent to purification of the fusion polypeptide. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith & Johnson, Gene 67: 31-40 (1988)), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding polypeptide, or polypeptide A, respectively, to the target recombinant polypeptide.

Purified fusion polypeptides can be used in screening assays and to generate antibodies specific for target polypeptides. In a therapeutic embodiment, fusion polypeptide expressed in a retroviral expression vector is used to infect bone marrow cells that are subsequently transplanted into irradiated recipients. The pathology of the subject recipient is then examined after sufficient time has passed (e.g., six (6) weeks).

Expressing the polypeptide in host bacteria with an impaired capacity to proteolytically cleave the recombinant polypeptide is often used to maximize recombinant polypeptide expression (Gottesman, S., Gene Expression Technology: Methods in Enzymology, Academic Press, San Diego, California 185: 119-128 (1990)). Another strategy is to alter the nucleotide sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in E. coli (Wada et al., Nucleic Acids Res. 20: 2111-2118 (1992)). Such alteration of nucleotide sequences can be carried out by standard DNA synthesis techniques.

When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. Recombinant mammalian expression vectors are often capable of directing expression of the nucleic acid in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Non-limiting examples of suitable tissue-specific promoters include an albumin promoter (liver-specific; Pinkert et al., Genes Dev. 1: 268-277 (1987)), lymphoid-specific promoters (Calame & Eaton, Adv. Immunol. 43: 235-275 (1988)), promoters

of T cell receptors (Winoto & Baltimore, EMBO J. 8: 729-733 (1989)) promoters of immunoglobulins (Banerji et al., Cell 33: 729-740 (1983); Queen & Baltimore, Cell 33: 741-748 (1983)), neuron-specific promoters (e.g., the neurofilament promoter; Byrne & Ruddle, Proc. Natl. Acad. Sci. USA 86: 5473-5477 (1989)), pancreas-specific promoters (Edlund et al., Science 230: 912-916 (1985)), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are sometimes utilized, for example, the murine hox promoters (Kessel & Gruss, Science 249: 374-379 (1990)) and the α-fetopolypeptide promoter (Campes & Tilghman, Genes Dev. 3: 537-546 (1989)).

A target nucleic acid may also be cloned into an expression vector in an antisense orientation. Regulatory sequences (e.g., viral promoters and/or enhancers) operatively linked to a target nucleic acid cloned in the antisense orientation can be chosen for directing constitutive, tissue specific or cell type specific expression of antisense RNA in a variety of cell types. Antisense expression vectors can be in the form of a recombinant plasmid, phagemid or attenuated virus. For a discussion of the regulation of gene expression using antisense genes see Weintraub et al., Antisense RNA as a molecular tool for genetic analysis, Reviews - Trends in Genetics, Vol. 1(1) (1986).

Also provided herein are host cells that include a target nucleic acid within a recombinant expression vector or target nucleic acid sequence fragments which allow it to homologously recombine into a specific site of the host cell genome. The terms "host cell" and "recombinant host cell" are used interchangeably herein. Such terms refer not only to the particular subject cell but rather also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, a target polypeptide can be expressed in bacterial cells such as E. coli, 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.

Vectors can be introduced into host cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, transduction/infection, DEAE-dextran-mediated transfection, lipofection, or electroporation.

A host cell provided herein can be used to produce (*i.e.*, express) a target polypeptide. Accordingly, further provided are methods for producing a target polypeptide using the host cells

described herein. In one embodiment, the method includes culturing host cells into which a recombinant expression vector encoding a target polypeptide has been introduced in a suitable medium such that a target polypeptide is produced. In another embodiment, the method further includes isolating a target polypeptide from the medium or the host cell.

Also provided are cells or purified preparations of cells which include a target transgene, or which otherwise misexpress target polypeptide. Cell preparations can consist of human or non-human cells, *e.g.*, rodent cells, e.g., mouse or rat cells, rabbit cells, or pig cells. In certain embodiments, the cell or cells include a target transgene (*e.g.,* a heterologous form of a target such as a human gene expressed in non-human cells). The target transgene can be misexpressed, *e.g.*, overexpressed or underexpressed. In other embodiments, the cell or cells include a gene which misexpress an endogenous target polypeptide (*e.g.*, expression of a gene is disrupted because of methylation event). Such cells can serve as a model for studying disorders which are related to mutated or mis-expressed target genes or for use in drug screening. Also provided are human cells (*e.g.*, cancer cells) transformed with a target nucleic acid.

Also provided are cells or a purified preparation thereof (*e.g.*, human cells) in which an endogenous target nucleic acid is under the control of a regulatory sequence that does not normally control the expression of the endogenous target gene. The expression characteristics of an endogenous gene within a cell (*e.g.*, a cell line or microorganism) can be modified by inserting a heterologous DNA regulatory element into the genome of the cell such that the inserted regulatory element is operably linked to the endogenous target gene. For example, an endogenous target gene (*e.g.*, a gene which is "transcriptionally silent," not normally expressed, or normally only expressed during development) may be activated by inserting a regulatory element which is capable of promoting the expression of a normally expressed gene product in that cell. Techniques such as targeted homologous recombinations, can be used to insert the heterologous DNA as described in, e.g., Chappel, US 5,272,071; WO 91/06667, published on May 16, 1991.

Target Polypeptides

Featured herein are isolated target polypeptides, and substantially identical polypeptides thereof. Such polypeptides sometimes are proteins or peptides. A target polypeptide is a polypeptide encoded by a target nucleic acid, where one nucleic acid can encode one or more different polypeptides. An "isolated" or "purified" polypeptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. In one embodiment, the

language "substantially free" means preparation of a target polypeptide or target polypeptide variant having less than about 30%, 20%, 10% and sometimes 5% (by dry weight), of non-target polypeptide (also referred to herein as a "contaminating protein"), or of chemical precursors or non-target chemicals. When the target polypeptide or a biologically active portion thereof is recombinantly produced, it is also often substantially free of culture medium, specifically, where culture medium represents less than about 20%, sometimes less than about 10%, and often less than about 5% of the volume of the polypeptide preparation. Isolated or purified target polypeptide preparations are sometimes 0.01 milligrams or more or 0.1 milligrams or more, and often 1.0 milligrams or more and 10 milligrams or more in dry weight.

In another aspect, featured herein are target polypeptides and biologically active or antigenic fragments thereof that are useful as reagents or targets in assays applicable to prevention, treatment or diagnosis of cancer.

Further included herein are target polypeptide fragments. The polypeptide fragment may be a domain or part of a domain of a target polypeptide. The polypeptide fragment is often 50 or fewer, 100 or fewer, or 200 or fewer amino acids in length, and is sometimes 300, 400, 500, 600, 700, or 900 or fewer amino acids in length.

Target polypeptides described herein can be used as immunogens to produce anti-target antibodies in a subject, to purify target ligands or binding partners, and in screening assays to identify molecules which inhibit or enhance the interaction of target with a target substrate. In a preferred embodiment, target polypeptides described herein are used to screen for competitive inhibitors of polycomb group proteins. Full-length target polypeptides and polynucleotides encoding the same may be specifically substituted for a target polypeptide fragment or polynucleotide encoding the same in any embodiment described herein.

Substantially identical polypeptides may depart from the amino acid sequences encoded by the nucleic acid targets set forth in Table 9. For example, conservative amino acid modifications may be introduced at one or more positions in the amino acid sequences. A "conservative amino acid substitution" is one in which the amino acid is replaced by another amino acid having a similar structure and/or chemical function. Families of amino acid residues having similar structures and functions are well known. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan,

histidine). Also, essential and non-essential amino acids may be replaced. A "non-essential" amino acid is one that can be altered without abolishing or substantially altering the biological function of a target polypeptide, whereas altering an "essential" amino acid abolishes or substantially alters the biological function of a target polypeptide. Amino acids that are conserved among target polypeptides are typically essential amino acids.

Also, target polypeptides and polypeptide variants may exist as chimeric or fusion polypeptides. As used herein, a target "chimeric polypeptide" or "fusion polypeptide" includes a target polypeptide linked to a non-target polypeptide. A "non-target polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a polypeptide which is not substantially identical to the target polypeptide, which includes, for example, a polypeptide that is different from the target polypeptide and derived from the same or a different organism. The target polypeptide in the fusion polypeptide can correspond to an entire or nearly entire target polypeptide or a fragment thereof. The non-target polypeptide can be fused to the N-terminus or C-terminus of the target polypeptide.

Fusion polypeptides can include a moiety having high affinity for a ligand. For example, the fusion polypeptide can be a GST-target fusion polypeptide in which the target sequences are fused to the C-terminus of the GST sequences, or a polyhistidine-target fusion polypeptide in which the target polypeptide is fused at the N- or C-terminus to a string of histidine residues. Such fusion polypeptides can facilitate purification of recombinant target. Expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide), and a target nucleic acid can be cloned into an expression vector such that the fusion moiety is linked in-frame to the target polypeptide. Further, the fusion polypeptide can be a target polypeptide containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression, secretion, cellular internalization, and cellular localization of a target polypeptide can be increased through use of a heterologous signal sequence. Fusion polypeptides can also include all or a part of a serum polypeptide (e.g., an IgG constant region or human serum albumin).

Target polypeptides or fragments thereof can be incorporated into pharmaceutical compositions and administered to a subject in vivo. Administration of these target polypeptides can be used to affect the bioavailability of a target substrate and may effectively increase or decrease target biological activity in a cell or effectively supplement dysfunctional or hyperactive target polypeptide. Target fusion polypeptides may be useful therapeutically for the treatment of disorders caused by, for example, (i) aberrant modification or mutation of a gene encoding a target polypeptide; (ii) mis-regulation of the target gene (*e.g.*, hypermethylated or hypomethylated); and (iii) aberrant post-translational modification of a

target polypeptide. Also, target polypeptides can be used as immunogens to produce anti-target antibodies in a subject, to purify target ligands or binding partners, and in screening assays to identify molecules which inhibit or enhance the interaction of target with a target substrate.

In addition, polypeptides can be chemically synthesized using techniques known in the art (See, e.g., Creighton, 1983 Proteins. New York, N.Y.: W. H. Freeman and Company; and Hunkapiller et al., (1984) Nature July 12 -18;310(5973):105-11). For example, a relative short polypeptide fragment can be synthesized by use of a peptide synthesizer. Furthermore, if desired, non-classical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the fragment sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoroamino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

Also included are polypeptide fragments which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, and the like. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, NaBH4; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; and the like.

Additional post-translational modifications include, for example, N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of prokaryotic host cell expression. The polypeptide fragments may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic, mass or affinity label to allow for detection and isolation of the polypeptide.

Also provided are chemically modified polypeptide derivatives that may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity. See U.S. Pat. No: 4,179,337. The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers,

carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the molecular weight is between about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog).

The polyethylene glycol molecules (or other chemical moieties) should be attached to the polypeptide with consideration of effects on functional or antigenic domains of the polypeptide. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al. (1992) Exp Hematol. September;20(8):1028-35, reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues, glutamic acid residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. A polymer sometimes is attached at an amino group, such as attachment at the N-terminus or lysine group.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, and the like), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus may be accomplished by reductive alkylation, which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the

appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

Substantially Identical Nucleic Acids and Polypeptides

Nucleotide sequences and polypeptide sequences that are substantially identical to a target nucleotide sequence and the target polypeptide sequences encoded by those nucleotide sequences are included herein. The term "substantially identical" as used herein refers to two or more nucleic acids or polypeptides sharing one or more identical nucleotide sequences or polypeptide sequences, respectively. Included are nucleotide sequences or polypeptide sequences that are 55% or more, 60% or more, 65% or more, 70% or more, 75% or more, 80% or more, 85% or more, 90% or more, 95% or more (each often within a 1%, 2%, 3% or 4% variability) or more identical to the nucleotide sequences in Table 10 or the encoded target polypeptide amino acid sequences. One test for determining whether two nucleic acids are substantially identical is to determine the percent of identical nucleotide sequences or polypeptide sequences shared between the nucleic acids or polypeptides.

Calculations of sequence identity are often performed as described below. Sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). The length of a reference sequence aligned for comparison purposes is sometimes 30% or more, 40% or more, 50% or more, often 60% or more, and more often 70% or more, 80% or more, 90% or more, 90% or more, or 100% of the length of the reference sequence. The nucleotides or amino acids at corresponding nucleotide or polypeptide positions, respectively, are then compared among the two sequences. When a position in the first sequence is occupied by the same nucleotide or amino acid as the corresponding position in the second sequence, the nucleotides or amino acids are deemed to be identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, introduced for optimal alignment of the two sequences.

Comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. Percent identity between two amino acid or nucleotide sequences can be determined using the algorithm of Meyers & Miller, CABIOS 4: 11-17 (1989), which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4. Also, percent identity between two amino acid sequences can be determined using the Needleman & Wunsch, J. Mol. Biol. 48: 444-453 (1970) algorithm which

has been incorporated into the GAP program in the GCG software package (available at the World Wide Web URL gcg.com), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. Percent identity between two nucleotide sequences can be determined using the GAP program in the GCG software package (available at World Wide Web URL gcg.com), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A set of parameters often used is a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

Another manner for determining if two nucleic acids are substantially identical is to assess whether a polynucleotide homologous to one nucleic acid will hybridize to the other nucleic acid under stringent conditions. As use herein, the term "stringent conditions" refers to conditions for hybridization and washing. Stringent conditions are known to those skilled in the art and can be found in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. , 6.3.1-6.3.6 (1989). Aqueous and non-aqueous methods are described in that reference and either can be used. An example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50°C. Another example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45□C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 55°C. A further example of stringent hybridization conditions is hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 60°C. Often, stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C. More often, stringency conditions are 0.5M sodium phosphate, 7% SDS at 65□C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C.

An example of a substantially identical nucleotide sequence to a target nucleotide sequence is one that has a different nucleotide sequence but still encodes the same polypeptide sequence encoded by the target nucleotide sequence. Another example is a nucleotide sequence that encodes a polypeptide having a polypeptide sequence that is more than 70% or more identical to, sometimes 75% or more, 80% or more, or 85% or more identical to, and often 90% or more and 95% or more identical to a polypeptide sequence encoded by a target nucleotide sequence.

Target nucleotide sequences and target amino acid sequences can be used as "query sequences" to perform a search against public databases to identify other family members or related sequences, for example. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul et al., J. Mol. Biol. 215: 403-10 (1990). BLAST nucleotide searches can be performed with the

NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to nucleotide sequences from SEQ ID NO: 1. BLAST polypeptide searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to polypeptides encoded by a target nucleotide sequence. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., Nucleic Acids Res. 25(17): 3389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used (see the World Wide Web URL ncbi.nlm.nih.gov).

Substantially identical nucleotide and polypeptide sequences include those that are naturally occurring, such as allelic variants (same locus), splice variants, homologs (different locus), and orthologs (different organism) or can be non-naturally occurring. Non-naturally occurring variants can be generated by mutagenesis techniques, including those applied to polynucleotides, cells, or organisms. The variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product). Orthologs, homologs, allelic variants, and splice variants can be identified using methods known in the art. These variants normally comprise a nucleotide sequence encoding a polypeptide that is 50% or more, about 55% or more, often about 70-75% or more, more often about 80-85% or more, and typically about 90-95% or more identical to the amino acid sequences of target polypeptides or a fragment thereof. Such nucleic acid molecules readily can be identified as being able to hybridize under stringent conditions to a target nucleotide sequence or a fragment thereof. Nucleic acid molecules corresponding to orthologs, homologs, and allelic variants of a target nucleotide sequence.

Also, substantially identical nucleotide sequences may include codons that are altered with respect to the naturally occurring sequence for enhancing expression of a target polypeptide in a particular expression system. For example, the nucleic acid can be one in which one or more codons are altered, and often 10% or more or 20% or more of the codons are altered for optimized expression in bacteria (e.g., E. coli.), yeast (e.g., S. cervesiae), human (e.g., 293 cells), insect, or rodent (e.g., hamster) cells.

Samples

The methods described herein can be applied to samples that contain nucleic acids, preferably a nucleic acid target gene region of interest, from any of a variety of sources, for any of a variety of purposes. Typically the methods used herein are used to determine information regarding a subject, or to

determine a relationship between nucleic acid methylation and disease. The samples used in the methods described herein will be selected according to the purpose of the method to be applied. For example, samples can contain nucleic acid from a plurality of different organisms when a phenotype of the organisms is to be correlated with the presence or absence of a methylated nucleic acid molecule or nucleotide locus. In another example, samples can contain nucleic acid from one individual, where the sample is examined to determine the disease state or tendency toward disease of the individual. One skilled in the art can use the methods described herein to determine the desired sample to be examined.

A sample may be from any subject, including for example, animal, plant, bacterium, fungus, virus or parasite. Animal may include for example mammals, birds, reptiles, amphibians or fish. Preferably subject mammals are humans. A sample from a subject can be in any form that provides a desired nucleic acid to be analyzed, including a solid material such as a tissue, cells, a cell pellet, a cell extract, feces, or a biopsy, or a biological fluid such as urine, whole blood, serum, plasma, interstitial fluid, peritoneal fluid, lymph fluids, ascites, sweat, saliva, follicular fluid, breast milk, non-milk breast secretions, cerebral spinal fluid, seminal fluid, lung sputum, amniotic fluid, exudate from a region of infection or inflammation, a mouth wash containing buccal cells, synovial fluid, or any other fluid sample produced by the subject. In addition, the sample can be collected tissues, including bone marrow, epithelium, stomach, prostate, kidney, bladder, breast, colon, lung, pancreas, endometrium, neuron, and muscle. Samples can include tissues, organs, and pathological samples such as a formalin-fixed sample embedded in paraffin.

As one of skill in the art will recognize, some samples may be used directly in the methods provided herein. For example, samples can be examined using the methods described herein without any purification or manipulation steps to increase the purity of desired cells or nucleic acid molecules.

If desired, a sample may be prepared using known techniques, such as that described by Maniatis, *et al. (Molecular Cloning: A Laboratory Manual,* Cold Spring Harbor, N.Y., pp. 280-281 (1982)). For example, samples examined using the methods described herein can be treated in one or more purification steps in order to increase the purity of the desired cells or nucleic acid in the sample. If desired, solid materials may be mixed with a fluid.

Methods for isolating nucleic acid in a sample from essentially any organism or tissue or organ in the body, as well as from cultured cells are well known. For example, the sample can be treated to homogenize an organ, tissue or cell sample, and the cells may be lysed using known lysis buffers, sonication, electroporation and combinations thereof. Further purification can be performed as needed, as will be appreciated by those skilled in the art. In addition, sample preparation may include a variety of reagents, which can be included in subsequent steps. These include reagents such as salts, buffers, neutral

proteins *(e.g.,* albumin), detergents, and such reagents, which can be used to facilitate optimal hybridization or enzymatic reactions, and/or reduce non-specific or background interactions. Also, reagents that otherwise improve the efficiency of the assay, such as, for example, protease inhibitors, nuclease inhibitors and anti-microbial agents, can be used, depending on the sample preparation methods and purity of the nucleic acid target gene molecule.

Nucleic Acid Target Gene Molecule

The methods provided herein are used to determine methylation states, including whether a nucleic acid target gene molecule contains a methylated or unmethylated nucleotide and determination of methylation ratios (methylated versus unmethylated) for one or more methylation sites or groups of methylation sites. Thus, nucleic acid target gene molecules used in the methods provided herein include any nucleic acid molecule. One or more methods provided herein may be practiced to provide information regarding methylated nucleotides in the nucleic acid target gene molecule.

The methods provided herein permit any nucleic acid-containing sample or specimen, in purified or non-purified form, to be used. Thus, the process may employ for example, DNA or RNA, including messenger RNA, wherein DNA or RNA can be single stranded or double stranded.

The specific nucleic acid sequence to be examined, (*i.e.,* the nucleic acid target gene molecule), may be a fraction of a larger molecule or may be present initially as a discrete molecule, so that the specific nucleic acid target gene molecule constitutes the entire nucleic acid component of a sample, It is not necessary that the nucleic acid target gene molecule to be examined be present initially in a pure form; it may be a minor fraction of a complex mixture, such as contained in whole organism DNA. The nucleic acid target gene molecule for which methylation status is to be determined may be an isolated molecule or part of a mixture of nucleic acid molecules.

The nucleic acid target gene molecule to be analyzed may include one or more protein-encoding regions of genomic DNA or a portion thereof. The nucleic acid target gene molecule can contain one or more gene promoter regions, one or more CpG islands, one or more sequences related to chromatin structure, or other regions of cellular nucleic acid. The nucleic acid target gene molecule can be methylated or unmethylated at individual nucleotides, such as cytosines; at small groups of nucleotides, such as cytosine-rich sequences, or at one or more CpG islands.

The length of the nucleic acid target gene molecule that may be used in the current methods may vary according to the sequence of the nucleic acid target gene molecule, the particular methods used for methylation identification, and the particular methylation state identification desired, but will typically be

limited to a length at which fragmentation and detection methods disclosed herein can be used to identify the methylation state of one or more nucleotide loci of the nucleic acid target gene molecule.

In one embodiment, the nucleic acid target gene molecule is of a length in which the methylation state of two or more nucleotide loci can be identified. For example, a nucleic acid target gene molecule may be at least about 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 225, 250, 275, 300, 350, 400, 450, 500, 550, 600, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2500 or 3000 bases in length. Typically, a nucleic acid target gene molecule will be no longer than about 10,000, 5000, 4000, 3000, 2500, 2000, 1500, 1000, 900, 800, 700, 600, 500, 450, 400, 350, 280, 260, 240, 220, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110 or 100 bases in length.

A nucleic acid target gene molecule examined using the methods disclosed herein may contain one or more methylated nucleotides, but is not required to contain any methylated nucleotides. The methods disclosed herein may be used to identify whether or not a nucleic acid target gene molecule contains methylated or unmethylated nucleotides, to identify the nucleotide locus of a methylated or unmethylated nucleotide in the nucleic acid target gene molecule and to determine the ratio of methylated versus unmethylated nucleotides at one or more methylation sites.

A nucleotide that has been identified as methylated in genomic DNA is cytosine. Methylated cytosines can be present in any of a variety of regions of genomic DNA. The methods provided herein may be used to determine the methylation state of a cytosine in any of a variety of genomic DNA regions. For example, methylcytosine is commonly found in cytosine-guanine dinucleotides termed "CpG" dinucleotides. In one embodiment, the methylation state of a cytosine nucleotide in one or more CpG dinucleotides in the nucleic acid target gene molecule is identified. Such dinucleotides are enriched in some regions of the genome, where these enriched regions are termed CpG islands. CpG islands may be found near promoter regions for some genes, including promoter regions for tumor suppressor genes, oncogenes, developmental regulatory genes, and housekeeping genes. Thus, the methods disclosed herein can be used to identify whether a cytosine in a CpG dinucleotide in a nucleic acid target gene molecule is methylated where the CpG nucleotide is located in a gene promoter region, such as a tumor suppressor gene, oncogene, developmental regulatory gene, or housekeeping gene promoter region. The methods disclosed herein also may be used to identify whether a one or more cytosines in a CpG island in a nucleic acid target gene molecule are methylated.

The methods provided herein may be used to identify the methylation of a plurality of nucleotide loci. Accordingly, methylation of one or more, up to all, nucleotide loci of a large nucleic acid target gene region may be identified using the methods provided herein. For example, the methylation state of a

plurality of nucleotide loci, up to all nucleotide loci of an entire CpG island may be identified using the methods provided herein.

Nucleic acid molecules can contain nucleotides with modifications, such as methylation, that do not change the nucleotide sequence of the nucleic acid molecule. Amplification of a nucleic acid molecule containing such a modified nucleotide can result in an amplified product complementary to the unmodified nucleotide, resulting in the amplified product not containing the information regarding the nucleotide modification. For example, the amplified product of a nucleic acid molecule containing a methylated cytosine will result in an amplified product containing either an unmodified guanine (for the complementary strand) or an unmodified cytosine at the location of the methylated cytosine. Reagents are known that can modify the nucleotide sequence of a nucleic acid target gene molecule according to the presence or absence of modifications in one or more nucleotides, where the modification itself does not change the nucleotide sequence. For example, bisulfite may be used in a process to convert unmethylated cytosine into uracil, thus resulting in a modification of the nucleotide sequence of a nucleic acid target gene molecule according to the presence of unmethylated cytosines in the nucleic acid target gene molecule.

In performing the methods disclosed herein, the nucleic acid target gene molecule is treated with a reagent that can modify the nucleic acid target gene molecule as a function of its methylation state. The treated nucleic acid target gene molecule can have a resulting sequence that reflects the methylation state of the untreated nucleic acid target gene molecule. In one embodiment, the reagent can be used to modify an unmethylated selected nucleotide to produce a different nucleotide. For example, the reagent may be used to modify unmethylated cytosine to produce uracil.

Reagents for Sequence Modification

A method for determining the methylation state of a nucleic acid molecule or nucleotide locus includes contacting a nucleic acid target gene molecule-containing sample with a reagent that can modify the nucleic acid target gene molecule nucleotide sequence as a function of its methylation state. A variety of reagents for modifying the nucleotide sequence of nucleic acid molecules are known in the art and can be used in conjunction with the methods provided herein. For example, a nucleic acid target gene molecule can be contacted with a reagent that modifies unmethylated bases but not methylated bases, such as unmethylated cytosines but not methylated cytosines, in such a manner that the nucleotide sequence of the nucleic acid target gene molecule is modified at the location of an unmethylated base but not at the location of the methylated base, such as at the location of an unmethylated cytosine but not at

the location of a methylated cytosine. An exemplary reagent that modifies unmethylated bases but not methylated bases is sodium bisulfite, which modifies unmethylated cytosines but not methylated cytosines.

Methods for modifying a nucleic acid target gene molecule in a manner that reflects the methylation pattern of the nucleic acid target gene molecule are known in the art, as exemplified in U.S. Pat. No. 5,786,146 and U.S. patent publications 20030180779 and 20030082600.

In one embodiment, the reagent can be used to modify unmethylated cytosine to uracil. An exemplary reagent used for modifying unmethylated cytosine to uracil is sodium bisulfite. Sodium bisulfite ($NaHSO_3$) reacts with the 5,6-double bond of cytosine to form a sulfonated cytosine reaction intermediate which is susceptible to deamination, giving rise to a sulfonated uracil. The sulfonate group of the sulfonated uracil can be removed under alkaline conditions, resulting in the formation of uracil. Uracil is recognized as a thymine by DNA polymerase enzymes such as Taq polymerase, and, therefore, upon amplification of the nucleic acid target gene molecule using methods such as PCR, the resultant amplified nucleic acid target gene molecule contains thymine at positions where unmethylated cytosine occurs in the starting template nucleic acid target gene molecule, and the complementary strand contains adenine at positions complementary to positions where unmethylated cytosine occurs in the starting nucleic acid target gene molecule. Further, amplification methods such as PCR can yield an amplified nucleic acid target gene molecule containing cytosine where the starting nucleic acid target gene molecule contains 5-methylcytosine, and the complementary strand maintains guanine at positions complementary to positions where methylated cytosine occurs in the starting nucleic acid target gene molecule. Thus, in amplification methods such as PCR, cytosine in the amplified product can mark the location of 5-methylcytosine, and thymine in the amplified product can mark the location of unmethylated cytosine. Similarly, in the amplified product strands complementary to the treated nucleic acid target gene molecule, guanine can mark the location of 5-methylcytosine and adenine can mark the location of unmethylated cytosine.

Exemplary methods for bisulfite treatment of target DNA can include contacting denatured DNA with a bisulfite solution that also may contain urea and hydroquinone, and incubating the mix for 30 seconds at 95°C and 15 minutes at 55°C, for 20 cycles. In one alternative method, the bisulfite treatment may be performed in agarose, and precipitation steps may be replaced with dialysis steps (U.S. Pat. No. 6,214,556 and Olek *et al.*, *Nucl. Acids Res.* 24:5064-66 (1996)). Variations of bisulfite treatment of a nucleic acid target gene molecule are known in the art as exemplified in U.S. Pats. Nos. 5,786,146 and

6,214,556, U.S. patent publication 20030082600, Tost *et al., Nucl. Acids Res.* 37:e50 (2003), Olek *et al., Nucl. Acids Res.* 24:5064-66 (1996), and Grunau *et al., Nucl. Acids Res.* 29:e65 (2001).

In the methods provided herein, a methylation-specific reagent-treated nucleic acid target gene molecule can have a different nucleotide sequence compared to the nucleotide sequence of the nucleic acid target gene molecule prior to treatment. Since the methylation-specific reagent modifies the nucleotide sequence of a nucleic acid target gene molecule as a function of the methylation state of the nucleic acid target gene molecule, the treated nucleic acid target gene molecule will have a nucleotide sequence related to the nucleotide sequence of the untreated nucleic acid target gene molecule, which reflects the methylation state of the untreated nucleic acid target gene molecule.

Amplification of Treated Nucleic Acid Target Gene Molecule

The methods provided herein also may include a step of amplifying the treated nucleic acid target gene molecule using one or more primers. In one embodiment, at least one primer is a methylation specific primer. In another embodiment, the primer contains one or more nucleotides complementary to the nucleotide treated using the methylation-specific reagent. For example, bisulfite is cytosine specific; when bisulfite is used, a primer used in a method of identifying methylated nucleotides can contain one or more guanine nucleotides. The amplification methods can serve to selectively amplify nucleic acid target gene molecules complementary to the primers while not amplifying one or more other nucleic acid molecules in a nucleic acid sample.

Methylation-specific primers, which are also referred to herein as methylation state specific primers, are designed to distinguish between nucleotide sequences of treated nucleic acid target gene molecules based on the methylation state of one or more nucleotides in the untreated nucleic acid target gene molecule. For example, methylation specific primers may be designed to hybridize to a nucleotide sequence of a reagent-treated nucleic acid target gene molecule arising from a nucleic acid target gene molecule that contained methylated nucleotides in preference to hybridizing to a nucleotide sequence of a reagent-treated nucleic acid target gene molecule arising from a nucleic acid target gene molecule that contained unmethylated nucleotides. Correspondingly, methylation specific primers may be designed to hybridize to a nucleotide sequence of a reagent-treated nucleic acid target gene molecule arising from a nucleic acid target gene molecule that contained unmethylated nucleotides in preference to hybridizing to a nucleotide sequence of a reagent-treated nucleic acid target gene molecule arising from a nucleic acid target gene molecule that contained methylated nucleotides.

The primers used for amplification of the treated nucleic acid target gene molecule in the sample can hybridize to the treated nucleic acid target gene molecule under conditions in which a nucleotide synthesis reaction, such as PCR, can occur. Typically, two or more nucleotide synthesis reaction cycles are performed to produce sufficient quantities of nucleic acid target gene molecule for subsequent steps including fragmentation and detection. In methods of selectively amplifying a nucleic acid target gene molecule using a methylation specific primer, at least one primer used in the amplification method will be methylation specific. Preferably the primers used in the amplification method are not methylation specific.

Primers used in the methods disclosed herein are of sufficient length and appropriate sequence to permit specific primer extension using a nucleic acid target gene molecule template. The primers are typically designed to be complementary to each strand of the nucleic acid target gene molecule to be amplified. The primer can be an oligodeoxyribonucleotide, an oligoribonucleotide, or an oligonucleotide containing both deoxyribonucleotides and ribonucleotides, in some embodiments, a primer can contain one or more nucleotide analogs. The length of primer can vary, depending on any of a variety of factors, including temperature, buffer, desired selectivity and nucleotide composition. The primer can contain at least about 5, 8, 10, 15, 20, 25, 30, 40, 50, 60, 70 or 80 nucleotides, and typically contains no more than about 120, 110, 100, 90, 70, 60, 50, 40, 30, 20 or 10 nucleotides.

The oligonucleotide primers used herein can be prepared using any suitable method, such as conventional phosphotriester and phosphodiester methods or automated embodiments thereof. In one such automated embodiment, diethylphosphoramidites are used as starting materials and can be synthesized as described by Beaucage, *et al., Tetrahedron Letters* 22:1859-1862 (1981). Methods for synthesizing oligonucleotides on a solid support are known in the art, as exemplified in U.S. Pat. No.: 4,458,066.

A primer used in accordance with the disclosed amplification and nucleic acid synthesis methods can specifically hybridize to a nucleic acid target gene molecule.

In methods provided herein, the nucleotide sequence of a nucleic acid target gene molecule can be modified as a function of the methylation state of the nucleic acid target gene molecule. Accordingly, the primer binding region of a methylation-specific reagent-treated nucleic acid target gene molecule that corresponds to a methylation state of a region of an untreated nucleic acid target gene molecule can be a primer binding region whose nucleotide sequence reflects the methylation state of that region in the untreated nucleic acid target gene molecule. For example, a region of an untreated nucleic acid target gene molecule that contains a methylcytosine at the 4th nucleotide and an unmethylated cytosine at the 7th nucleotide can be treated with bisulfite, which will convert the cytosine at the 7^{th} nucleotide to uracil

without changing the methylcytosine at the 4th nucleotide; thus, a primer binding region of the treated nucleic acid target gene molecule that corresponds to that region of the untreated nucleic acid target gene molecule will contain a cytosine at the 4th nucleotide and a uracil (or thymine) at the 7th nucleotide, and a primer complementary to such a primer binding region will contain an adenine at the locus complementary to the 4th nucleotide and a guanine at the locus complementary to the 7th nucleotide.

The methylation specific primers may be used in methods to specifically amplify nucleic acid target gene molecules according to the methylation state of the nucleic acid target gene molecule, and to thereby selectively increase the amount of nucleic acid target gene in a sample. Methylation state specific amplification methods include one or more nucleic acid synthesis steps, using one or more methylation specific primers.

In accordance with the methods disclosed herein, a nucleic acid target gene sequence can serve as a template for one or more steps of nucleic acid synthesis. The nucleic acid synthesis step or steps can include primer extension, DNA replication, polymerase chain reaction (PCR), reverse transcription, reverse transcription polymerase chain reaction (RT-PCR), rolling circle amplification, whole genome amplification, strand displacement amplification (SDA), and transcription based reactions.

In one embodiment an amplification step can be performed that can amplify one or more nucleic acids without distinguishing between methylated and unmethylated nucleic acid molecules or loci. Such an amplification step can be performed, for example, when the amount of nucleic acid in a sample is very low and detection of methylated nucleic acid target gene molecules can be improved by a preliminary amplification step that does not distinguish methylated nucleic acid target gene molecules from unmethylated nucleic acid target gene molecules or other nucleic acids in the sample. Typically, such an amplification step is performed subsequent to treating the nucleic acid sample with a reagent that modifies the nucleotide sequence of nucleic acid molecules as a function of the methylation state of the nucleic acid molecules. Although this method does not distinguish according to methylation state, the primers used in such an amplification step nevertheless may be used to increase the amount of nucleic acid molecules of a particular nucleic acid target gene region to be examined relative to the total amount of nucleic acid in a sample. For example, primers can be designed to hybridize to a pre-determined region of a nucleic acid target gene molecule in order to increase the relative amount of that nucleic acid target gene molecule in the sample, but without amplifying the nucleic acid target gene molecule according to the methylation state of the nucleic acid target gene molecule. One skilled in the art may determine the primer used in such a preamplification, or amplification, step according to various known factors and

including the desired selectivity of the amplification step and any known nucleotide sequence information.

In the methods of nucleic acid synthesis using a double-stranded nucleic acid molecule, the strands are first separated before any nucleic acid synthetic steps. Following strand separation, one or more primers can be hybridized to one or more treated single-stranded nucleic acid molecules to be amplified, and nucleotide synthesis can be performed to add nucleotides to each primer to form a strand complementary to the strand of the nucleic acid target gene molecule. In one embodiment, nucleic acid synthesis can be performed to selectively amplify one of two strands of a treated nucleic acid target gene molecule. In another embodiment, the step of synthesizing a strand complementary to each strand of a double-stranded treated nucleic acid target gene molecule is performed in the presence of two or more primers, such that at least one primer can hybridize to each strand and prime additional nucleotide synthesis.

In the methods of nucleic acid synthesis using a single-stranded nucleic acid molecule, a primer can be hybridized to the single-stranded nucleic acid molecule to be amplified, and nucleotide synthesis may be performed to add nucleotides to the primer to form a strand complementary to the single-stranded nucleic acid molecule. In one embodiment, the step of synthesizing a strand complementary to a single-stranded nucleic acid molecule is performed in the presence of two or more primers, such that one primer can hybridize to the nucleotide sequence of the strand of the nucleic acid target gene molecule, and one primer can hybridize to the synthesized complementary strand and prime additional nucleotide synthesis. For example, after synthesis of the complementary strand, PCR amplification of the nucleic acid molecule can be immediately performed without further manipulation of the sample.

In another embodiment, the step of synthesizing a strand complementary to a single-stranded nucleic acid molecule is performed separately from additional nucleotide synthetic reactions. For example, the complementary strand can be synthesized to form a double-stranded nucleic acid molecule, and the sample may be subjected to one or more intermediate steps prior to amplifying the double-stranded nucleic acid molecule. Intermediate steps may include any of a variety of methods of manipulating a nucleic acid sample, including increasing the purity of the nucleic acid molecule, removing excess primers, changing the reaction conditions *(e.g.,* the buffer conditions, enzyme or reactants present in the sample), and other parameters. In one example, the sample may be subjected to one or more purification steps of the nucleic acid molecule. For example, the primer used to create the strand complementary to the nucleic acid molecule can contain a moiety at its 5' end that permits identification or isolation of the primer or of a nucleic acid into which the primer is incorporated. Such a

moiety may be, for example, a bindable moiety such as biotin, polyhistidine, magnetic bead, or other suitable substrate, whereby contacting the sample with the binding partner of the bindable moiety may result in selective binding of nucleic acid molecule into which the primer has been incorporated. Such selective binding may be used to separate the nucleic acid molecule from sample impurities, thereby increasing the purity of the nucleic acid molecule. After performing one or more intermediate steps, such as purity enhancing steps, the nucleic acid molecule may be amplified according to the methods provided herein and as known in the art.

After formation of the strand complementary to the single-stranded nucleic acid target gene molecules, subsequent nucleic acid target gene molecule amplification steps may be performed in which the complementary strands are separated, primers are hybridized to the strands, and the primers have added thereto nucleotides to form a new complementary strand. Strand separation may be effected either as a separate step or simultaneously with the synthesis of the primer extension products. This strand separation may be accomplished using various suitable denaturing conditions, including physical, chemical, or enzymatic means, the word "denaturing" includes all such means. One physical method of separating nucleic acid strands involves heating the nucleic acid target gene molecule until it is denatured. Typical heat denaturation may involve temperatures ranging from about 8O°C to 105°C, for times ranging from about 1 to 10 minutes. Strand separation also may be accomplished by chemical means, including high salt conditions or strongly basic conditions. Strand separation also may be induced by an enzyme from the class of enzymes known as helicases or by the enzyme RecA, which has helicase activity, and in the presence of riboATP, is known to denature DNA. The reaction conditions suitable for strand separation of nucleic acids with helicases are described by Kuhn Hoffmann-Berling, *CSH-Quan tita rive Biology, 43:63* (1978) and techniques for using RecA are reviewed in C. Radding, *Ann. Rev. Genetics* 16:405-437 (1982).

After each amplification step, the amplified product will be double stranded, with each strand complementary to the other. The complementary strands of may be separated, and both separated strands may be used as a template for the synthesis of additional nucleic acid strands. This synthesis may be performed under conditions allowing hybridization of primers to templates to occur. Generally synthesis occurs in a buffered aqueous solution, typically at about a pH of 7-9, such as about pH 8. Typically, a molar excess of two oligonucleotide primers can be added to the buffer containing the separated template strands. In some embodiments, the amount of target nucleic acid is not known (for example, when the methods disclosed herein are used for diagnostic applications), so that the amount of primer relative to the amount of complementary strand cannot be determined with certainty.

In an exemplary method, deoxyribonucleoside triphosphates dATP, dCTP, dGTP, and dTTP can be added to the synthesis mixture, either separately or together with the primers, and the resulting solution can be heated to about 90°C-1OO°C from about 1 to 10 minutes, typically from 1 to 4 minutes. After this heating period, the solution can be allowed to cool to about room temperature. To the cooled mixture can be added an appropriate enzyme for effecting the primer extension reaction (called herein "enzyme for polymerization"), and the reaction can be allowed to occur under conditions known in the art. This synthesis (or amplification) reaction can occur at room temperature up to a temperature above which the enzyme for polymerization no longer functions. For example, the enzyme for polymerization also may be used at temperatures greater than room temperature if the enzyme is heat stable. In one embodiment, the method of amplifying is by PCR, as described herein and as is commonly used by those of skill in the art. Alternative methods of amplification have been described and also may be employed. A variety of suitable enzymes for this purpose are known in the art and include, for example, *E. coli* DNA polymerase I, Klenow fragment of *E. coli* DNA polymerase I, T4 DNA polymerase, other available DNA polymerases, polymerase muteins, reverse transcriptase, and other enzymes, including thermostable enzymes *(i.e.*, those enzymes which perform primer extension at elevated temperatures, typically temperatures that cause denaturation of the nucleic acid to be amplified).

Manipulation of Both Strands of a Nucleic Acid Target Gene Molecule

Methods of manipulating a nucleic acid target gene molecule subsequent to methylation-based sequence modification treatment, such as amplification and fragmentation, may be performed using only one strand of the treated nucleic acid target gene molecule, or using both strands of the treated nucleic acid target gene molecule. For example, primers used for amplification steps may be complementary to only one strand of the treated nucleic acid target gene molecule, or may be complementary to both strands of the treated nucleic acid. Accordingly, amplification steps may be performed to create at least two different amplified double-stranded products, where both strands of the treated nucleic acid target gene molecule is amplified into separate double-stranded products.

Alternatively, amplification may be performed such that only one of the two strands of the treated nucleic acid target gene molecule is amplified. For example, when amplification is performed using at least one primer that is selective for the sequence of one of the two strands, the strand hybridized to the primer may be selectively amplified.

After one or more steps of amplification, the amplified products may be subjected to one or more manipulation steps prior to additional amplification steps or prior to cleavage steps. For example,

amplified products can be subjected to one or more purification steps prior to additional amplification or prior to cleavage.

Methods for purifying nucleic acid molecules are known in the art and include precipitation, dialysis or other solvent exchange, gel electrophoresis, enzymatic degradation of impurities (*e.g.,* protease treatment, or RNase treatment for a DNA nucleic acid target gene molecule sample), liquid chromatography including ion exchange chromatography and affinity chromatography, and other methods of specifically binding nucleic acid target gene molecules to separate them from impurities (*e.g.,* hybridization, biotin binding). Purification steps also may include separating complementary strands of amplification products. One skilled in the art will know to select which, if any, purification steps to use according to desired level of purity and/or desired sample composition for subsequent amplification, modification or cleavage steps.

Methods for determining methylation in a nucleic acid target gene may include methods in which a single sample is treated in one or more steps, and then the single sample may be divided into two or more aliquots for parallel treatment in subsequent steps.

Amplified products may be split into two or more aliquots after amplification. For example, amplified products may be split into two or more aliquots after amplification but prior to cleaving the amplified products, amplified products may split into two or more aliquots after amplification and subjected to further steps such as one or more amplified product purification steps.

When amplified products are split into two or more aliquots prior to cleavage, different cleavage methods may be applied to each of the two or more aliquots. For example, a first nucleic acid target gene molecule aliquot may be base specifically fragmented with RNase A, while a second nucleic acid target gene molecule aliquot may be base specifically fragmented with Rnase T1. In another example, amplified nucleic acid target gene molecule may be split into four aliquots and each aliquot may be treated with a different base-specific reagent to produce four different sets of base specifically cleaved nucleic acid target gene molecule fragments. Separation into two or more aliquots permits different cleavage reactions to be performed on the same amplification product. Use of different cleavage reactions on the same amplification product is further described in the cleavage methods provided herein.

A sample may be divided into two or more aliquots in specifically amplifying different strands of a nucleic acid target gene molecule in different aliquots. For example, a treated nucleic acid target gene molecule can have non-complementary strands that can be separately treated with different primers such as different methylation state specific primers in separately amplifying the different strands in different aliquots. In another embodiment, complementary strands of an amplified nucleic acid target gene

molecule can be separately amplified in different aliquots, according to the primers used in each aliquot. For example, a sample of amplified nucleic acid target gene molecules can be separated into two or more aliquots, where the forward strand is transcribed in a first set of aliquots and the reverse strand is transcribed in a second set of aliquots. As will be appreciated by one skilled in the art, a sample can be divided into any of a plurality of aliquots in which any combination of the parallel reactions described herein may be performed.

Fragmentation in Conjunction with Nucleotide Synthesis

Selective nucleotide synthesis also may be performed in conjunction with fragmentation. A nucleic acid target gene amplified through a plurality of nucleic acid synthesis cycles will utilize primers hybridizing to two separate regions of the nucleic acid target gene molecule. Fragmentation of a nucleic acid target gene molecule in the center region in between the two primer hybridization sites will prevent amplification of the nucleic acid target gene molecule. Hence selective fragmentation of the center region of nucleic acid molecules may result in selective amplification of a nucleic acid target gene molecule even if the primers used in the nucleic acid synthesis reactions are not selective.

In one example, the sample may be treated with fragmentation conditions prior to being treated with nucleic acid synthesis conditions, and prior to being treated with a reagent that modifies the nucleic acid target gene molecule sequence as a function of the methylation state of the nucleic acid target gene. In such an example, the fragmentation conditions may be selective for methylated or unmethylated nucleotides. For example, a sample can have added thereto a methylation sensitive endonuclease, such as HPAII, which cleaves at an unmethylated recognition site but not at a methylated recognition site. This results in a sample containing intact nucleic acid target gene molecules that are methylated at the recognition site and cleaved nucleic acid target gene molecules that are unmethylated at the recognition site. The sample then may be treated with nucleic acid synthesis conditions using primers designed so that only uncleaved nucleic acid target gene molecules are amplified. As a result of the cleavage, amplification will be selective for nucleic acid target gene molecules that are methylated at the recognition site.

In another example, the sample may be treated with fragmentation conditions prior to treatment with nucleic acid synthesis conditions, but subsequent to treatment with a reagent that modifies the nucleic acid target gene molecule sequence as a function of the methylation state of the nucleic acid target gene. For example, a sample can have added thereto an endonuclease that cleaves at a recognition site that includes a C nucleotide at a particular locus, but not a recognition site that contains a T or U nucleotide at

that particular locus. Or vice versa, a sample can have added thereto an endonuclease that cleaves at a recognition site that includes a T or U nucleotide at a particular locus, but not a recognition site that contains a C nucleotide at that particular locus. The sample can first be treated with a reagent that modifies the nucleic acid target gene molecule sequence as a function of the methylation state of the nucleic acid target gene molecule, and then treated with such an endonuclease. The resulting sample will contain intact nucleic acid target gene molecules that have the desired methylation state at the recognition site and cleaved nucleic acid target gene molecules that have the undesired methylation state at the recognition site. The sample then can be treated with nucleic acid synthesis conditions using primers designed so that only uncleaved nucleic acid target gene molecules are amplified. As a result of the cleavage, amplification will be selective for nucleic acid target gene molecules that are methylated at the recognition site.

Transcription

Transcription of template DNA such as a nucleic acid target gene molecule, or an amplified product thereof, may be performed for one strand of the template DNA or for both strands of the template DNA. In one embodiment, the nucleic acid molecule to be transcribed contains a moiety to which an enzyme capable of performing transcription can bind; such a moiety may be, for example, a transcriptional promotor sequence.

Transcription reactions may be performed using any of a variety of methods known in the art, using any of a variety of enzymes known in the art. For example, mutant T7 RNA polymerase (T7 R&DNA polymerase; Epicentre, Madison, WI) with the ability to incorporate both dNTPs and rNTPs may be used in the transcription reactions. The transcription reactions may be run under standard reaction conditions known in the art, for example, 40 mM Tris-Ac (pH 7.51, 10 mM NaCl, 6 mM MgCl, 2 mM spermidine, 10 mM dithiothreitol, 1 mM of each rNTP, 5 mM of dNTP (when used), 40 nM DNA template, and 5 U/uL T7 R&DNA polymerase, incubating at 37°C for 2 hours. After transcription, shrimp alkaline phosphatase (SAP) may be added to the cleavage reaction to reduce the quantity of cyclic monophosphate side products. Use of T7 R&DNA polymerase is known in the art, as exemplified by U.S. Pat. Nos.: 5,849,546 and 6,107,037, and Sousa *et al.,* EMBO J. 14:4609-4621 (1995), Padilla *et al., Nucl. Acid Res.* 27:1561-1563 (1999), Huang *et al.,* Biochemistry 36:8231-8242 (1997), and Stanssens *et al., Genome Res.,* 14:126-133 (2004).

In addition to transcription with the four regular ribonucleotide substrates (rCTP, rATP, rGTP and rUTP), reactions may be performed replacing one or more ribonucleoside triphosphates with

nucleoside analogs, such as those provided herein and known in the art, or with corresponding deoxyribonucleoside triphosphates *(e.g.*, replacing rCTP with dCTP, or replacing rUTP with either dUTP or dTTP). In one embodiment, one or more rNTPs are replaced with a nucleoside or nucleoside analog that, upon incorporation into the transcribed nucleic acid, is not cleavable under the fragmentation conditions applied to the transcribed nucleic acid.

In one embodiment, transcription is performed subsequent to one or more nucleic acid synthesis reactions, including one or more nucleic acid synthesis reactions using methylation specific primers. For example, transcription of an amplified product can be performed subsequent to amplification of a nucleic acid target gene molecule, including methylation specific amplification of the nucleic acid target gene molecule. In another embodiment, the treated nucleic acid target gene molecule is transcribed without any preceding nucleic acid synthesis steps.

Fragmentation of Nucleic Acid Molecules

The methods provided herein also include steps of fragmentation and/or cleavage of nucleic acid target gene molecules or amplified products. Any method for cleaving a nucleic acid molecule into fragments with a suitable fragment size distribution may be used to generate the nucleic acid fragments. Fragmentation of nucleic acid molecules is known in the art and may be achieved in many ways. For example, nucleic acid molecules composed of DNA, RNA, analogs of DNA and RNA or combinations thereof, can be fragmented physically, chemically, or enzymatically. In one embodiment, enzymatic cleavage at one or more specific cleavage sites can be used to produce the nucleic acid molecule fragments utilized herein. Typically, cleavage is effected after amplification such that once a sufficient quantity of amplified products is generated using the methods provided herein, the amplified products can be cleaved into two or more fragments.

In embodiments where restriction enzymes are used, depending on the number and type of restriction enzymes used and the particular reaction conditions selected, the average length of fragments generated may be controlled within a specified range. In particular embodiments, fragments of nucleic acid molecules prepared for use herein may range in size from the group of ranges including about 1-50 bases, about 2-40 bases, about 3-35 bases, and about 5-30 bases. Yet other size ranges contemplated for use herein include between about 50 to about 150 bases, from about 25 to about 75 bases, or from about 12-30 bases. In one particular embodiment, fragments of about 3 to about 35 bases are used. Generally, fragment size range will be selected so that the mass of the fragments can be accurately determined using

the mass measurement methods described herein and known in the art; also in some embodiments, size range is selected in order to facilitate the desired desorption efficiencies in MALDI-TOF MS.

Base-specific fragmentation using nucleases is a preferred fragmentation method. Nucleic acid target gene molecules may be fragmented using nucleases that selectively cleave at a particular base *(e.g.,* A, C, T or G for DNA and A, C, U or G for RNA) or base type *(i.e.,* pyrimidine or purine). In one embodiment, RNases that specifically cleave 3 RNA nucleotides *(e.g.,* U, G and A), 2 RNA nucleotides *(e.g.,* C and U) or 1 RNA nucleotide *(e.g.,* A), may be used to base specifically cleave transcripts of a nucleic acid target gene molecule. For example, RNase T1 cleaves ssRNA (single-stranded RNA) at G ribonucleotides, RNase U2 digests ssRNA at A ribonucleotides, RNase CL3 and cusativin cleave ssRNA at C ribonucleotides, PhyM cleaves ssRNA at U and A ribonucleotides, and RNAse A cleaves ssRNA at pyrimidine ribonucleotides (C and U). The use of mono-specific Rnases such as RNase T, (G specific) and RNase U, (A specific) is known in the art (Donis-Keller *et al., Nucl. Acids Res.* 4:2527-2537 (1977); Gupta and Randerath, *Nucl. Acids Res.* 4:1957-1978 (1977); Kuchino and Nishimura, *Methods Enzymol.* 180:154-1 63 (1989); and Hahner *et al., Nucl. Acids Res.* 25(10):1957-1964 (1997)). Another enzyme, chicken liver ribonuclease (RNase CL3) has been reported to cleave preferentially at cytidine, but the enzyme's proclivity for this base has been reported to be affected by the reaction conditions (Boguski *et al.,* J. *Biol. Chem.* 255:2160-2163 (1980)). Reports also claim cytidine specificity for another ribonuclease, cusativin, isolated from dry seeds of *Cucumis sativus L* (Rojo *et al.,* Planta 194:328-338 (1994)). Alternatively, the identification of pyrimidine residues by use *of* RNase PhyM (A and U specific) (Donis-Keller, *H. Nucleic Acids Res.* 8:3133-3142 (1980)) and RNase A (C and U specific) (Simoncsits *et al., Nature* 269:833-836 (1977); Gupta and Randerath, *Nucl. Acids Res.* 4:1957-I978 (1977)) has been demonstrated. Examples of such cleavage patterns are given in Stanssens *et al.,* WO 00/66771.

Base specific cleavage reaction conditions using an RNase are known in the art, and can include, for example 4 mM Tris-Ac (pH 8.01, 4 mM KAc, 1 mM spermidine, 0.5 mM dithiothreitol and 1.5 mM MgCl.

In one embodiment, amplified product can be transcribed into a single stranded RNA molecule and then cleaved base specifically by an endoribonuclease. Treatment of the target nucleic acid, for example using bisulfite which converts unmethylated cytosine to uracil without modifying methylated cytosine, can be used to generate differences in base specific cleavage patterns that can be analyzed by mass analysis methods, such as mass spectrometry, and can be used for identification of methylated sites. In one embodiment, transcription of a nucleic acid target gene molecule can yield an RNA molecule that can be cleaved using specific RNA endonucleases. For example, base specific cleavage of the RNA

molecule can be performed using two different endoribonucleases, such as RNAse T1 and RNAse A. RNAse T1 specifically cleaves G nucleotides, and RNAse A specifically cleaves pyrimidine ribonucleotides *(i.e.,* cytosine and uracil residues). In one embodiment, when an enzyme that cleaves more than one nucleotide, such as RNAse A, is used for cleavage, non-cleavable nucleosides, such as dNTP's may be incorporated during transcription of the nucleic acid target gene molecule or amplified product. For example, dCTPs may be incorporated during transcription of the amplified product, and the resultant transcribed nucleic acid can be subject to cleavage by RNAse A at U ribonucleotides, but resistant to cleavage by RNAse A at C deoxyribonucleotides. In another example, dTTPs can be incorporated during transcription of the nucleic acid target gene molecule, and the resultant transcribed nucleic acid can be subject to cleavage by RNAse A at C ribonucleotides, but resistant to cleavage by RNAse A at T deoxyribonucleotides. By selective use of non-cleavable nucleosides such as dNTPs, and by performing base specific cleavage using RNases such as RNAse A and RNAse T1, base cleavage specific to three different nucleotide bases can be performed on the different transcripts of the same target nucleic acid sequence. For example, the transcript of a particular nucleic acid target gene molecule can be subjected to G-specific cleavage using RNAse T1; the transcript can be subjected to C-specific cleavage using dTTP in the transcription reaction, followed by digestion with RNAse A; and the transcript can be subjected to T-specific cleavage using dCTP in the transcription reaction, followed by digestion with RNAse A. These types of base specific cleavage patterns are exemplified below showing the theoretical cleavage products of a given nucleotide sequence TAACGCAT converted through bisulfite treatment to the sequence TAAACGTAT if methylated at the cytosine and to TAAATGTAT if not methylated.

	Non-methylated TAAATGTAT		Methylated TAAACGTAT
RNAse A C specific cleavage	TAAATGTAT	Introduction of cleavage nucleotide	TAAAC GTAT
RNAse A T specific cleavage	T AAAT GT AT	Removal of cleavage nucleotide	T AAACGT AT
RNAse T1 G specific cleavage	TAAATG TAT	Mass Shift	TAAACG TAT

In another embodiment, the use of dNTPs, different RNAses, and both orientations of the nucleic acid target gene molecule can allow for six different cleavage schemes. For example, a double stranded

nucleic acid target gene molecule can yield two different single stranded transcription products, which can be referred to as a transcript product of the forward strand of the nucleic acid target gene molecule and a transcript product of the reverse strand of the nucleic acid target gene molecule. Each of the two different transcription products can be subjected to three separate base specific cleavage reactions, such as G-specific cleavage, C-specific cleavage and T-specific cleavage, as described herein, to result in six different base specific cleavage reactions. The six possible cleavage schemes are listed below.

	Forward Primer	Reverse primer
RNAse T1	G specific cleavage	G specific cleavage
RNAse A: dCTP	T specific cleavage	T specific cleavage
RNAse A: dCTP	C specific cleavage	C specific cleavage

Use of four different base specific cleavage reactions can yield information on all four nucleotide bases of one strand of the nucleic acid target gene molecule. That is, by taking into account that cleavage of the forward strand can be mimicked by cleaving the complementary base on the reverse strand, base specific cleavage can be achieved for each of the four nucleotides of the forward strand by reference to cleavage of the reverse strand. For example, the three base-specific cleavage reactions can be performed on the transcript of the nucleic acid target gene molecule forward strand, to yield G-, C- and T-specific cleavage of the nucleic acid target gene molecule forward strand; and a fourth base specific cleavage reaction can be a T-specific cleavage reaction of the transcript of the nucleic acid target gene molecule reverse strand, the results of which will be equivalent to A-specific cleavage of the transcript of the nucleic acid target gene molecule forward strand. One skilled in the art will appreciate that base specific cleavage to yield information on all four nucleotide bases of one nucleic acid target gene molecule strand can be accomplished using a variety of different combinations of possible base specific cleavage reactions, including cleavage reactions listed above for RNases T1 and A, and additional cleavage reactions for forward or reverse strands and/or using non-hydrolyzable nucleotides can be performed with other base specific RNases known in the art or disclosed herein.

In one example, RNAse U2 can be used to base specifically cleave nucleic acid target gene molecule transcripts. RNAse U2 can base specifically cleave RNA at A nucleotides. Thus, by use of

RNAses T1, U2 and A, and by use of the appropriate dNTPs (in conjunction with use of RNase A), all four base positions of a nucleic acid target gene molecule can be examined by base specifically cleaving transcript of only one strand of the nucleic acid target gene molecule. In some embodiments, non-cleavable nucleoside triphosphates are not required when base specific cleavage is performed using RNAses that base specifically cleave only one of the four ribonucleotides. For example, use of RNAse T1, RNase CL3, cusativin, or RNAse U2 for base specific cleavage does not require the presence of non-cleavable nucleotides in the nucleic acid target gene molecule transcript. Use of RNAses such as RNAse T1 and RNAse U2 can yield information on all four nucleotide bases of a nucleic acid target gene molecule. For example, transcripts of both the forward and reverse strands of a nucleic acid target gene molecule or amplified product can be synthesized, and each transcript can be subjected to base specific cleavage using RNAse T1 and RNAse U2. The resulting cleavage pattern of the four cleavage reactions will yield information on all four nucleotide bases of one strand of the nucleic acid target gene molecule. In such an embodiment, two transcription reactions can be performed: a first transcription of the forward nucleic acid target gene molecule strand and a second of the reverse nucleic acid target gene molecule strand.

Also contemplated for use in the methods are a variety of different base specific cleavage methods. A variety of different base specific cleavage methods are known in the art and are described herein, including enzymatic base specific cleavage of RNA, enzymatic base specific cleavage of modified DNA, and chemical base specific cleavage of DNA. For example enzymatic base specific cleavage, such as cleavage using uracil-deglycosylase (UDG) or methylcytosine deglycosylase (MCDG), are known in the art and described herein, and can be performed in conjunction with the enzymatic RNAse-mediated base specific cleavage reactions described herein.

Methods for using restriction endonucleases to fragment nucleic acid molecules are widely known in the art. In one exemplary protocol a reaction mixture of 20-50 ul is prepared containing; DNA 1-3ug; restriction enzyme buffer 1X; and a restriction endonuclease 2 units for lug of DNA. Suitable buffers also are known in the art and include suitable ionic strength, cofactors, and optionally, pH buffers to provide optimal conditions for enzymatic activity. Specific enzymes may require specific buffers that are generally available from commercial suppliers of the enzyme. An exemplary buffer is potassium glutamate buffer (KGB). Hannish, J. and M. McClelland, "Activity of DNA modification and restriction enzymes in KGB, a potassium glutamate buffer," *Gene Anal. Tech* 5:105 (1988); McClelland, M. *et al.*, "A single buffer for all restriction endonucleases," *Nucl. Acids Res.* 16:364 (1988). The reaction mixture is incubated at 37°C for 1 hour or for any time period needed to produce fragments of a desired size or

range of sizes. The reaction may be stopped by heating the mixture at 65°C or 8O°C as needed. Alternatively, the reaction may be stopped by chelating divalent cations such as Mg^{2+} with for example, EDTA.

DNAses also may be used to generate nucleic acid molecule fragments. Anderson, S., "Shotgun DNA sequencing using cloned Dnase I-generated fragments," *Nucl. Acids Res.* 9:3015-3027 (1981). DNase I (Deoxyribonuclease I) is an endonuclease that non-specifically digests double- and single-stranded DNA into poly- and mono-nucleotides.

Catalytic DNA and RNA are known in the art and can be used to cleave nucleic acid molecules to produce nucleic acid molecule fragments. Santoro, S. W. and Joyce, G. F. "A general purpose RNA-cleaving DNA enzyme," *Proc. Natl. Acad. Sci. USA* 94:4262-4266 (1997). DNA as a single-stranded molecule can fold into three-dimensional structures similar to RNA, and the 2'-hydroxy group is dispensable for catalytic action. As ribozymes, DNAzymes also can be made, by selection, to depend on a cofactor. This has been demonstrated for a histidine-dependent DNAzyme for RNA hydrolysis. U.S. Patent Nos. 6,326,174 and 6,194,180 disclose deoxyribonucleic acid enzymes, catalytic and enzymatic DNA molecules, capable of cleaving nucleic acid sequences or molecules, particularly RNA.

Fragmentation of nucleic acid molecules may be achieved using physical or mechanical forces including mechanical shear forces and sonication. Physical fragmentation of nucleic acid molecules may be accomplished, for example, using hydrodynamic forces. Typically nucleic acid molecules in solution are sheared by repeatedly drawing the solution containing the nucleic acid molecules into and out of a syringe equipped with a needle. Thorstenson, Y.R. *et al.,* "An Automated Hydrodynamic Process for Controlled, Unbiased DNA Shearing," Genome Research 8:848-855 (1998); Davison, P. F. *Proc. Natl. Acad. Sci.* USA 45:1560-1568 (1959); Davison, P. F. Nature 185:918-920 (1960); Schriefer, L. A. *et al.,* "Low pressure DNA shearing: a method for random DNA sequence analysis," *Nucl. Acids Res.* 18:7455-7456 (1990). Shearing of DNA, for example with a hypodermic needle, typically generates a majority of fragments ranging from 1-2 kb, although a minority of fragments can be as small as 300 bp.

The hydrodynamic point-sink shearing method developed by Oefner *et al.,* is one method of shearing nucleic acid molecules that utilizes hydrodynamic forces. Oefner, P. J. *et al.,* "Efficient random subcloning of DNA sheared in a recirculating point-sink flow system," *Nucl. Acids Res.* 24(20):3879-3886 (1996).

Nucleic acid molecule fragments also may be obtained by agitating large nucleic acid molecules in solution, for example by mixing, blending, stirring, or vortexing the solution. Hershey, A. D. and

Burgi, E. *J. Mol. Biol,* 2:143-152 (1960); Rosenberg, H. S. and Bendich, A. *J. Am. Chem. Soc.* 82:3198-3201 (1960).

One suitable method of physically fragmenting nucleic acid molecules is based on sonicating the nucleic acid molecule. Deininger, P. L. "Approaches to rapid DNA sequence analysis," *Anal. Biochem.* 129:216-223 (1983).

Fragmentation of nucleic acid molecules also may be achieved using a nebulizer. Bodenteich, A., Chissoe, *S.,* Wang, Y.-F. and Roe, B. A. (1994) In Adams, M. D., Fields, C. and Venter, J. C. (eds.) Automated DNA Sequencing and Analysis. Academic Press, San Diego, CA. Nebulizers are known in the art and commercially available.

Another method for fragmenting nucleic acid molecule employs repeatedly freezing and thawing a buffered solution of nucleic acid molecules. The sample of nucleic acid molecules may be frozen and thawed as necessary to produce fragments of a desired size or range of sizes.

Nucleic acid molecule fragmentation also may be achieved by irradiating the nucleic acid molecules. Typically, radiation such as gamma or x-ray radiation will be sufficient to fragment the nucleic acid molecules.

Chemical fragmentation may be used to fragment nucleic acid molecules either with base specificity or without base specificity. Nucleic acid molecules may be fragmented by chemical reactions including for example, hydrolysis reactions including base and acid hydrolysis. An exemplary acid/base hydrolysis protocol for producing nucleic acid molecule fragments are known (see, *e.g.,* Sargent *et al., Meth. Enz.* 152:432 (1988)).

Mass Spectrometry

When analyses are performed using mass spectrometry, such as MALDI, nanoliter volumes of sample can be loaded on chips. Use of such volumes can permit quantitative or semi-quantitative mass spectrometric results. For example, the area under the peaks in the resulting mass spectra are proportional to the relative concentrations of the components of the sample. Methods for preparing and using such chips are known in the art, as exemplified in U.S. Patent No. 6,024,925, U.S. Publication 20010008615, and PCT Application No. PCT/US97/20195 (WO 98/20020); methods for preparing and using such chips also are provided in co-pending U.S. Application Serial Nos. 08/786,988, 09/364,774, and 09/297,575. Chips and kits for performing these analyses are commercially available from SEQUENOM under the trademark MassARRAY'". MassARRAY'" systems contain a miniaturized array such as a SpectroCHlP@ useful for MALDI-TOF (Matrix-Assisted Laser Desorption Ionization-Time of Flight) mass spectrometry

to deliver results rapidly. It accurately distinguishes single base changes in the size of DNA fragments relating to genetic variants without tags.

In one embodiment, the mass of all nucleic acid molecule fragments formed in the step of fragmentation is measured. The measured mass of a nucleic acid target gene molecule fragment or fragment of an amplification product also can be referred to as a "sample" measured mass, in contrast to a "reference" mass which arises from a reference nucleic acid fragment.

In another embodiment, the length of nucleic acid molecule fragments whose mass is measured using mass spectroscopy is no more than 75 nucleotides in length, no more than 60 nucleotides in length, no more than 50 nucleotides in length, no more than 40 nucleotides in length, no more than 35 nucleotides in length, no more than 30 nucleotides in length, no more than 27 nucleotides in length, no more than 25 nucleotides in length, no more than 23 nucleotides in length, no more than 22 nucleotides in length, no more than 21 nucleotides in length, no more than 20 nucleotides in length, no more than 19 nucleotides in length, or no more than 18 nucleotides in length. In another embodiment, the length of the nucleic acid molecule fragments whose mass is measured using mass spectroscopy is no less than 3 nucleotides in length, no less than 4 nucleotides in length, no less than 5 nucleotides in length, no less than 6 nucleotides in length, no less than 7 nucleotides in length, no less than 8 nucleotides in length, no less than 9 nucleotides in length, no less than 10 nucleotides in length, no less than 12 nucleotides in length, no less than 15 nucleotides in length, no less than 18 nucleotides in length, no less than 20 nucleotides in length, no less than 25 nucleotides in length, no less than 30 nucleotides in length, or no less than 35 nucleotides in length.

In one embodiment, the nucleic acid molecule fragment whose mass is measured is RNA. In another embodiment the nucleic acid target gene molecule fragment who's mass is measured is DNA. In yet another embodiment, the nucleic acid target gene molecule fragment whose mass is measured contains one modified or atypical nucleotide *(i.e.*, a nucleotide other than deoxy-C, T, G or A in DNA, or other than C, U, G or A in RNA). For example, a nucleic acid molecule product of a transcription reaction may contain a combination of ribonucleotides and deoxyribonucleotides. In another example, a nucleic acid molecule can contain typically occurring nucleotides and mass modified nucleotides, or can contain typically occurring nucleotides and non-naturally occurring nucleotides.

Prior to mass spectrometric analysis, nucleic acid molecules can be treated to improve resolution. Such processes are referred to as conditioning of the molecules. Molecules can be "conditioned," for example to decrease the laser energy required for volatilization and/or to minimize fragmentation. A variety of methods for nucleic acid molecule conditioning are known in the art. An example of

conditioning is modification of the phosphodiester backbone of the nucleic acid molecule *(e.g.,* by cation exchange), which can be useful for eliminating peak broadening due to a heterogeneity in the cations bound per nucleotide unit. In another example, contacting a nucleic acid molecule with an alkylating agent such as alkyloidide, iodoacetamide, P-iodoethanol, or 2,3- epoxy-1-propanol, can transform a monothio phosphodiester bonds of a nucleic acid molecule into a phosphotriester bond. Likewise, phosphodiester bonds can be transformed to uncharged derivatives employing, for example, trialkylsilyl chlorides. Further conditioning can include incorporating nucleotides that reduce sensitivity for depurination (fragmentation during MS) *e.g.,* a purine analog such as N7- or N9-deazapurine nucleotides, or RNA building blocks or using oligonucleotide triesters or incorporating phosphorothioate functions which are alkylated, or employing oligonucleotide mimetics such as PNA.

For some applications, simultaneous detection of more than one nucleic acid molecule fragment may be performed. In other applications, parallel processing can be performed using, for example, oligonucleotide or oligonucleotide mimetic arrays on various solid supports. "Multiplexing" can be achieved by several different methodologies. For example, fragments from several different nucleic acid molecules can be simultaneously subjected to mass measurement methods. Typically, in multiplexing mass measurements, the nucleic acid molecule fragments should be distinguishable enough so that simultaneous detection of the multiplexed nucleic acid molecule fragments is possible. Nucleic acid molecule fragments may be made distinguishable by ensuring that the masses of the fragments are distinguishable by the mass measurement method to be used. This may be achieved either by the sequence itself (composition or length) or by the introduction of mass-modifying functionalities into one or more nucleic acid molecules.

In one embodiment, the nucleic acid molecule to be mass-measured contains attached thereto one or more mass-modifying moieties. Mass-modifying moieties are known in the art and may be attached to the 3‘ end or 5’ end of a nucleic acid molecule fragment, may be attached to a nucleobase or to a sugar moiety of a nucleotide, or may be attached to or substitute for the phosphodiester linkage between nucleotides. A simple mass-modification may be achieved by substituting H for halogens like F, Cl, Br and/or I, or pseudohalogens such as SCN, NCS, or by using different alkyl, aryl or aralkyl moieties such as methyl, ethyl, propyl, isopropyl, t-butyl, hexyl, phenyl, substituted phenyl, benzyl, or functional groups such as N_3, CH_2F, CHF_2, CF_3, $Si(CH_3)_3$, $Si(CH_3)_2$, (C_2H_5), $Si(CH_3)(C_2H_5)_2$, $Si(C_2H_5)_3$. Yet another mass-modification can be obtained by attaching homo- or heteropeptides through the nucleic acid molecule *(e.g.,* detector (D)) or nucleoside triphosphates. One example useful in generating mass-modified species with a mass increment of 57 is the attachment of oligoglycines, *e.g.*, mass-modifications of 74, 131, 188,

245 are achieved. Simple oligoamides also can be used, *e.g.,* mass- modifications of 74, 88, 102, 116 . . ., are obtainable.

Mass-modifications also may include oligo/polyethylene glycol derivatives. The oligo/polyethylene glycols also can be monoalkylated by a lower alkyl such as methyl, ethyl, propyl, isopropyl, t-butyl and other suitable substituents. Other chemistries also can be used in the mass-modified compounds (see, *e.g.*, those described in Oligonucleotides and Analogues, A Practical Approach, F. Eckstein, editor, IRL Press, Oxford, 1991).

Mass modifying moieties can be attached, for instance, to either the 5'-end of the oligonucleotide, to the nucleobase (or bases), to the phosphate backbone, to the 2'-position of the nucleoside (nucleosides), and/or to the terminal 3'-position. Examples of mass modifying moieties include, for example, a halogen, an azido, or of the type, XR, wherein X is a linking group and R is a mass-modifying functionality. A mass-modifying functionality can, for example, be used to introduce defined mass increments into the oligonucleotide molecule, as described herein. Modifications introduced at the phosphodiester bond such as with alpha-thio nucleoside triphosphates, have the advantage that these modifications do not interfere with accurate Watson-Crick base-pairing and additionally allow for the one-step post-synthetic site-specific modification of the complete nucleic acid molecule *e.g.*, via alkylation reactions (*see, e.g.,* Nakamaye *et al., Nucl. Acids Res.* 23:9947-9959(1988)). Exemplary mass-modifying functionalities are boron-modified nucleic acids, which can be efficiently incorporated into nucleic acids by polymerases (see, *e.g.*, Porter *et al., Biochemistry 34:* 11963-11969 (1995); Hasan *et al., Nucl. Acids Res.* 24:2150-2157 (1996); Li *et al. Nucl. Acids Res.* 23:4495-4501 (1995)).

Furthermore, the mass-modifying functionality may be added so as to affect chain termination, such as by attaching it to the 3'-position of the sugar ring in the nucleoside triphosphate. For those skilled in the art, it is clear that many combinations can be used in the methods provided herein. In the same way, those skilled in the art will recognize that chain-elongating nucleoside triphosphates also can be mass-modified in a similar fashion with numerous variations and combinations in functionality and attachment positions.

Different mass-modified nucleotides may be used to simultaneously detect a variety of different nucleic acid fragments simultaneously. In one embodiment, mass modifications can be incorporated during the amplification process. In another embodiment, multiplexing of different nucleic acid target gene molecules may be performed by mass modifying one or more nucleic acid target gene molecules, where each different nucleic acid target gene molecule can be differently mass modified, if desired.

Additional mass measurement methods known in the art may be used in the methods of mass measurement, including electrophoretic methods such as gel electrophoresis and capillary electrophoresis, and chromatographic methods including size exclusion chromatography and reverse phase chromatography.

Using methods of mass analysis such as those described herein, information relating to mass of the nucleic acid target gene molecule fragments can be obtained. Additional information of a mass peak that can be obtained from mass measurements include signal to noise ratio of a peak, the peak area (represented, for example, by area under the peak or by peak width at half-height), peak height, peak width, peak area relative to one or more additional mass peaks, peak height relative to one or more additional mass peaks, and peak width relative to one or more additional mass peaks. Such mass peak characteristics may be used in the present methylation identification methods, for example, in a method of identifying the methylation state of a nucleotide locus of a nucleic acid target gene molecule by comparing at least one mass peak characteristic of an amplification fragment with one or more mass peak characteristics of one or more reference nucleic acids.

Methylation State Identification

Fragment measurements may be used to identify the methylation state of a nucleic acid target gene molecule or to identify the methylation state of a particular nucleotide locus of a nucleic acid target gene molecule. Fragment measurements may be used to identify whether or not a nucleic acid target gene molecule contains one or more methylated or unmethylated nucleotides, such as methylcytosine or cytosine, respectively; to determine the number of methylated or unmethylated nucleotides such as methylcytosine or cytosine, respectively, present in a nucleic acid target gene molecule, to identify whether or not a nucleotide locus, such as a cytosine locus, is methylated or unmethylated in a nucleic acid target gene molecule, to identify the nucleotide locus of a methylated or unmethylated nucleotide, such as methylcytosine or cytosine, respectively, in a nucleic acid target gene molecule; to determine the ratio of methylated nucleic acid target gene molecule relative to unmethylated nucleic acid target gene molecule in a sample, to determine the ratio of methylated nucleotide at a particular nucleotide locus on a nucleic acid target gene molecule relative to unmethylated nucleotide at that locus, and to provide redundant information to further confirm any of the determinations provided herein.

Additional Methylation Analysis Methods

Various methylation assay procedures are known in the art, and can be used in conjunction with the present invention. These assays allow for determination of the methylation state of one or a plurality of CpG islands within a DNA sequence. Such assays involve, among other techniques, DNA sequencing of bisulfite-treated DNA, PCR (for sequence-specific amplification), Southern blot analysis, use of methylation-sensitive restriction enzymes, etc.

For example, genomic sequencing has been simplified for analysis of DNA methylation patterns and 5-methylcytosine distribution by using bisulfite treatment (Frommer et al., Proc. Natl. Acad. Sci. USA 89:1827-1831, 1992). Additionally, restriction enzyme digestion of PCR products amplified from bisulfite-converted DNA is used, e.g., the method described by Sadri & Hornsby (Nucl. Acids Res. 24:5058-5059, 1996), or COBRA (Combined Bisulfite Restriction Analysis) (Xiong & Laird, Nucleic Acids Res. 25:2532-2534, 1997).

COBRA analysis is a quantitative methylation assay useful for determining DNA methylation levels at specific gene loci in small amounts of genomic DNA (Xiong & Laird, Nucleic Acids Res. 25:2532-2534, 1997). Briefly, restriction enzyme digestion is used to reveal methylation-dependent sequence differences in PCR products of sodium bisulfite-treated DNA. Methylation-dependent sequence differences are first introduced into the genomic DNA by standard bisulfite treatment according to the procedure described by Frommer et al. (Proc. Natl. Acad. Sci. USA 89:1827-1831, 1992). PCR amplification of the bisulfite converted DNA is then performed using primers specific for the interested CpG islands, followed by restriction endonuclease digestion, gel electrophoresis, and detection using specific, labeled hybridization probes. Methylation levels in the original DNA sample are represented by the relative amounts of digested and undigested PCR product in a linearly quantitative fashion across a wide spectrum of DNA methylation levels. In addition, this technique can be reliably applied to DNA obtained from microdissected paraffin-embedded tissue samples. Typical reagents (e.g., as might be found in a typical COBRA-based kit) for COBRA analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); restriction enzyme and appropriate buffer; gene-hybridization oligo; control hybridization oligo; kinase labeling kit for oligo probe; and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery reagents or kits (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

Preferably, assays such as "MethyLight.TM." (a fluorescence-based real-time PCR technique) (Eads et al., Cancer Res. 59:2302-2306, 1999), Ms-SNuPE (Methylation-sensitive Single Nucleotide Primer Extension) reactions (Gonzalgo & Jones, Nucleic Acids Res. 25:2529-2531, 1997), methylation-

specific PCR ("MSP"; Herman et al., Proc. Natl. Acad. Sci. USA 93:9821-9826, 1996; U.S. Pat. No. 5,786,146), and methylated CpG island amplification ("MCA"; Toyota et al., Cancer Res. 59:2307-12, 1999) are used alone or in combination with other of these methods.

The MethyLight.TM. assay is a high-throughput quantitative methylation assay that utilizes fluorescence-based real-time PCR (TaqMan.RTM.) technology that requires no further manipulations after the PCR step (Eads et al., Cancer Res. 59:2302-2306, 1999). Briefly, the MethyLight.TM. process begins with a mixed sample of genomic DNA that is converted, in a sodium bisulfite reaction, to a mixed pool of methylation-dependent sequence differences according to standard procedures (the bisulfite process converts unmethylated cytosine residues to uracil). Fluorescence-based PCR is then performed either in an "unbiased" (with primers that do not overlap known CpG methylation sites) PCR reaction, or in a "biased" (with PCR primers that overlap known CpG dinucleotides) reaction. Sequence discrimination can occur either at the level of the amplification process or at the level of the fluorescence detection process, or both.

The MethyLight.TM. assay may be used as a quantitative test for methylation patterns in the genomic DNA sample, wherein sequence discrimination occurs at the level of probe hybridization. In this quantitative version, the PCR reaction provides for unbiased amplification in the presence of a fluorescent probe that overlaps a particular putative methylation site. An unbiased control for the amount of input DNA is provided by a reaction in which neither the primers, nor the probe overlie any CpG dinucleotides. Alternatively, a qualitative test for genomic methylation is achieved by probing of the biased PCR pool with either control oligonucleotides that do not "cover" known methylation sites (a fluorescence-based version of the "MSP" technique), or with oligonucleotides covering potential methylation sites.

The MethyLight.TM. process can by used with a "TaqMan.RTM." probe in the amplification process. For example, double-stranded genomic DNA is treated with sodium bisulfite and subjected to one of two sets of PCR reactions using TaqMan.RTM. probes; e.g., with either biased primers and TaqMan.RTM. probe, or unbiased primers and TaqMan.RTM. probe. The TaqMan.RTM. probe is dual-labeled with fluorescent "reporter" and "quencher" molecules, and is designed to be specific for a relatively high GC content region so that it melts out at about 10.degree. C. higher temperature in the PCR cycle than the forward or reverse primers. This allows the TaqMan.RTM. probe to remain fully hybridized during the PCR annealing/extension step. As the Taq polymerase enzymatically synthesizes a new strand during PCR, it will eventually reach the annealed TaqMan.RTM. probe. The Taq polymerase 5' to 3' endonuclease activity will then displace the TaqMan.RTM. probe by digesting it to release the

fluorescent reporter molecule for quantitative detection of its now unquenched signal using a real-time fluorescent detection system.

Typical reagents (e.g., as might be found in a typical MethyLight.TM.-based kit) for MethyLight.TM. analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); TaqMan.RTM. probes; optimized PCR buffers and deoxynucleotides; and Taq polymerase.

Ms-SNuPE. The Ms-SNuPE technique is a quantitative method for assessing methylation differences at specific CpG sites based on bisulfite treatment of DNA, followed by single-nucleotide primer extension (Gonzalgo & Jones, Nucleic Acids Res. 25:2529-2531, 1997).

Briefly, genomic DNA is reacted with sodium bisulfite to convert unmethylated cytosine to uracil while leaving 5-methylcytosine unchanged. Amplification of the desired target sequence is then performed using PCR primers specific for bisulfite-converted DNA, and the resulting product is isolated and used as a template for methylation analysis at the CpG site(s) of interest.

Small amounts of DNA can be analyzed (e.g., microdissected pathology sections), and it avoids utilization of restriction enzymes for determining the methylation status at CpG sites.

Typical reagents (e.g., as might be found in a typical Ms-SNuPE-based kit) for Ms-SNuPE analysis may include, but are not limited to: PCR primers for specific gene (or methylation-altered DNA sequence or CpG island); optimized PCR buffers and deoxynucleotides; gel extraction kit; positive control primers; Ms-SNuPE primers for specific gene; reaction buffer (for the Ms-SNuPE reaction); and radioactive nucleotides. Additionally, bisulfite conversion reagents may include: DNA denaturation buffer; sulfonation buffer; DNA recovery regents or kit (e.g., precipitation, ultrafiltration, affinity column); desulfonation buffer; and DNA recovery components.

MSP (methylation-specific PCR) allows for assessing the methylation status of virtually any group of CpG sites within a CpG island, independent of the use of methylation-sensitive restriction enzymes (Herman et al. Proc. Nat. Acad. Sci. USA 93:9821-9826, 1996; U.S. Pat. No. 5,786,146). Briefly, DNA is modified by sodium bisulfite converting all unmethylated, but not methylated cytosines to uracil, and subsequently amplified with primers specific for methylated versus umnethylated DNA. MSP requires only small quantities of DNA, is sensitive to 0.1% methylated alleles of a given CpG island locus, and can be performed on DNA extracted from paraffin-embedded samples. Typical reagents (e.g., as might be found in a typical MSP-based kit) for MSP analysis may include, but are not limited to: methylated and unmethylated PCR primers for specific gene (or methylation-altered DNA sequence or CpG island), optimized PCR buffers and deoxynucleotides, and specific probes.

The MCA technique is a method that can be used to screen for altered methylation patterns in genomic DNA, and to isolate specific sequences associated with these changes (Toyota et al., Cancer Res. 59:2307-12, 1999). Briefly, restriction enzymes with different sensitivities to cytosine methylation in their recognition sites are used to digest genomic DNAs from primary tumors, cell lines, and normal tissues prior to arbitrarily primed PCR amplification. Fragments that show differential methylation are cloned and sequenced after resolving the PCR products on high-resolution polyacrylamide gels. The cloned fragments are then used as probes for Southern analysis to confirm differential methylation of these regions. Typical reagents (e.g., as might be found in a typical MCA-based kit) for MCA analysis may include, but are not limited to: PCR primers for arbitrary priming Genomic DNA; PCR buffers and nucleotides, restriction enzymes and appropriate buffers; gene-hybridization oligos or probes; control hybridization oligos or probes.

Another method for analyzing methylation sites is a primer extension assay, including an optimized PCR amplification reaction that produces amplified targets for subsequent primer extension genotyping analysis using mass spectrometry. The assay can also be done in multiplex. This method (particularly as it relates to genotyping single nucleotide polymorphisms) is described in detail in PCT publication WO05012578A1 and US publication US20050079521A1. For methylation analysis, the assay can be adopted to detect bisulfite introduced methylation dependent C to T sequence changes. These methods are particularly useful for performing multiplexed amplification reactions and multiplexed primer extension reactions (*e.g.*, multiplexed homogeneous primer mass extension (hME) assays) in a single well to further increase the throughput and reduce the cost per reaction for primer extension reactions.

Four additional methods for DNA methylation analysis include restriction landmark genomic scanning (RLGS, Costello et al., 2000), methylation-sensitive-representational difference analysis (MS-RDA), methylation-specific AP-PCR (MS-AP-PCR) and methyl-CpG binding domain column/segregation of partly melted molecules (MBD/SPM).

Additional methylation analysis methods that may be used in conjunction with the present invention are described in the following papers: Laird, P.W. *Nature Reviews Cancer* 3, 253-266 (2003); Biotechniques; Uhlmann, K. et al. *Electrophoresis* 23:4072-4079 (2002) - PyroMeth; Colella et al. *Biotechniques*. 2003 Jul;35(1):146-50; Dupont JM, Tost J, Jammes H, and Gut IG. *Anal Biochem*, Oct 2004; 333(1): 119-27; Tooke N and Pettersson M. *IVDT*. Nov 2004; 41; and the following published patents and patent applications: WO03080863A1, WO03057909A2, US2005/0153347,

US20050009059A1, US20050069879A1, US20050064428A1, US20050064406A1, WO02086163C1, US20050019762A1, US6884586, WO04013284A2, US20050153316A1 and WO05040399A2.

Disease-Related Discovery

In one embodiment, presence or absence of one or more methylated or unmethylated nucleotides may be identified as indicative of a particular disease outcome associated with methylated or unmethylated DNA. In another embodiment, presence or absence of one or more methylated or unmethylated nucleotides may be identified as indicative of a normal, healthy or disease free state. In another embodiment, an abnormal ratio of methylated nucleic acid target gene molecules relative to unmethylated nucleic acid target gene molecules in a sample may be indicative of a particular disease outcome associated with methylated or unmethylated DNA. For example, a relatively high number or a relatively low number of methylated nucleic acid target gene molecules compared to the relative amount in a normal individual may be indicative of the presence of a disease state associated with methylated or unmethylated DNA. For example, a relatively high number or a relatively low number of methylated nucleotide loci compared to the relative amount in a normal individual can be indicative of the presence or absence of a disease state (e.g., cancer) associated with methylated or unmethylated DNA.

Disease-Related Analysis

Increased or decreased levels of methylation have been associated with a variety of diseases. Methylation or lack of methylation at defined positions can be associated with a disease or a disease outcome. The methods disclosed herein can be used in methods of determining the propensity of a subject to disease and determining a treatment regimen for a subject having a disease.

Diseases associated with a modification of the methylation of one or more nucleotides include, for example: leukemia (Aoki E. *et al.,* "Methylation status of the pl51NK4B gene in hematopoietic progenitors and peripheral blood cells in myelodysplastic syndromes", *Leukemia* 14(4):586-593 (2000); Nosaka, K. *et al.,* "Increasing methylation of the CDKN2A gene is associated with the progression of adult T-cell leukemia", *Cancer Res.* 60(4):1043-1048 (2000); Asimakopoulos FA *et al.*, "ABL 1 methylation is a distinct molecular event associated with clonal evolution of chronic myeloid leukemia" *Blood* 94(7):2452-2460 (1999); Fajkusova L. *et al.,* "Detailed Mapping of Methylcytosine Positions at the CpG Island Surrounding the Pa Promoter at the bcr-abl Locus in CML Patients and in Two Cell Lines, K562 and BV173" *Blood Cells Mol. Dis.* 26(3):193-204 (2000); Litz C. E. *et al.,* "Methylation status of

the major breakpoint cluster region in Philadelphia chromosome negative leukemias" *Leukemia* 6(1):35-41 (1992))

The methylation state of a variety of nucleotide loci and/or nucleic acid regions are known to be correlated with a disease, disease outcome, and success of treatment of a disease, and also may be used to distinguish disease types that are difficult to distinguish according to the symptoms, histologic samples or blood or serum samples. For example, CpG island methylator indicator phenotype (CIMP) is present in some types of ovarian carcinomas, but not in other types (Strathdee, *et al., Am. J. Pathol.* 158:1121- 1127 (2001)). In another example, methylation may be used to distinguish between a carcinoid tumor and a pancreatic endocrine tumor, which may have different expected outcomes and disease treatment regimens (Chan *et al., Oncogene* 22:924-934 (2003)). In another example, *H. pylori* dependent gastric mucosa associated lymphoid tissue (MALT) lymphomas are characterized as having several methylated nucleic acid regions, while those nucleic acid regions in *H. pylori* independent MALT lymphomas are not methylated Kaneko *et al., Gut* 52:641-646 (2003)). Similar relationships with disease, disease outcome and disease treatment have been correlated with hypomethylation or unmethylated nucleic acid regions or unmethylated nucleotide loci.

Methods related to the disease state of a subject may be performed by collecting a sample from a subject, treating the sample with a reagent that modifies a nucleic acid target gene molecule sequence as a function of the methylation state of the nucleic acid target gene molecule, subjecting the sample to methylation specific amplification, then detecting one or more fragments that are associated with a disease outcome (measured as survivability). In another embodiment, the fragments are detected by measuring the mass of the nucleic acid target gene molecule or nucleic acid target gene molecule fragments. Detection of a nucleic acid target gene molecule or nucleic acid target gene molecule fragment can identify the methylation state of a nucleic acid target gene molecule or the methylation state of one or more nucleotide loci of a nucleic acid target gene molecule. Identification of the methylation state of a nucleic acid target gene molecule or the methylation state of one or more nucleotide loci of a nucleic acid target gene molecule can indicate the propensity of the subject toward one or more diseases, the disease state of a subject, likelihood of survival or an appropriate or inappropriate course of disease treatment or management for a subject.

Applications of Prognostic and Diagnostic Results to Pharmacogenomic Methods

Pharmacogenomics is a discipline that involves tailoring a treatment for a subject according to the subject's genetic profile (*e.g.*, genotype, methylation state or characteristic methylation state). For

example, based upon the outcome of a prognostic test described herein, a clinician or physician may target pertinent information and preventative or therapeutic treatments to a subject who would benefit by the information or treatment and avoid directing such information and treatments to a subject who would not be benefited (*e.g.*, the treatment has no therapeutic effect, the subject experiences adverse side effects, and/or the treatment poses unnecessary risks given the prognosis).

The following is an example of a pharmacogenomic embodiment. A particular treatment regimen can exert a differential effect depending upon the subject's characteristic methylation state. Where a candidate therapeutic response is correlated with a given methylation state, a therapeutic typically would not be administered to a subject determined to have a methylation state that correlates with a poor response, and conversely may be administered to a subject determined to have a methylation state that correlates with a positive response. In another example, where a candidate therapeutic is significantly toxic (*e.g.*, a chemotherapeutic agent) when administered to subjects, a subject with a good prognosis may be willing to endure the adverse effects and risks associated with the toxic therapeutic more so than a patient with a poor prognosis that is unlikely to survive regardless of the therapeutic administered.

The methods described herein are applicable to pharmacogenomic methods for preventing, alleviating or treating cancer. For example, a nucleic acid sample from an individual may be subjected to a prognostic test described herein. Where a methylation state or characteristic methylation state that is predictive of cancer outcome is identified in a subject, information for preventing or treating cancer and/or one or more cancer treatment regimens then may be prescribed to that subject.

In certain embodiments, a treatment or preventative regimen is specifically prescribed and/or administered to individuals who will most benefit from it based upon their likelihood of survival assessed by the methods described herein. Thus, provided are methods for determining a prognosis for cancer patients and then prescribing a therapeutic or preventative regimen to individuals according to their prognosis.

Pharmacogenomics methods also may be used to analyze and predict a response to a cncer treatment or a drug. For example, if pharmacogenomics analysis indicates a likelihood that an individual will respond positively to a cancer treatment with a particular drug or combination of drugs, the drug(s) may be administered to the individual. Conversely, if the analysis indicates that an individual is likely to respond negatively to treatment with a particular drug or combination of drugs, an alternative course of treatment may be prescribed. A negative response may be defined as either the absence of an efficacious response or the presence of toxic side effects. The response to a therapeutic treatment can be predicted in a background study in which the methylation state of subjects in any of the following populations is

determined: a population that responds favorably to a treatment regimen, a population that does not respond significantly to a treatment regimen, and a population that responds adversely to a treatment regiment (*e.g.*, exhibits one or more side effects). These populations are provided as examples and other populations and subpopulations may be analyzed.

The tests described herein also are applicable to clinical drug trials. A subject's diagnosis or prognosis may be determined using the methods described herein. Thereafter, subjects with a poor prognosis or diagnosis of an aggressive form of cancer may choose to participate in clinical trials that may increase their probability of survival but have unknown or high-risk side effects; whereas subjects with a good prognosis or diagnosis of an less aggressive form of cancer may choose to undergo treatments that have higher success rates but expose the subject to adverse side effects. Alternatively, subjects with a good prognosis or diagnosis of an less aggressive form of cancer might choose to enroll in a clinical trial for a treatment which decreases a risk of relapse or a clinical trial with known or low-risk side effects.

Also provided herein is a method of partnering between a diagnostic/prognostic testing provider and a provider of a consumable product, which comprises: (a) the diagnostic/prognostic testing provider determines a subject's prognosis; (b) the diagnostic/prognostic testing provider forwards information to the subject about a particular product which may be obtained and consumed or applied by the subject given their prognosis; and (c) the provider of a consumable product forwards to the diagnostic test provider a fee every time the diagnostic/prognostic test provider forwards information to the subject as set forth in step (b) above.

Results from prognostic tests may be combined with other test results to diagnose cancer. For example, prognostic results may be gathered, a patient sample may be ordered based on a determined predisposition to cancer, the patient sample is analyzed, and the results of the analysis may be utilized to diagnose cancer. Also cancer diagnostic methods can be developed from studies used to generate prognostic/diagnostic methods in which populations are stratified into subpopulations having different progressions of cancer. In another embodiment, prognostic results may be gathered; a patient's risk factors for developing cancer analyzed (*e.g.,* age, race, family history); and a patient sample may be ordered based on a determined predisposition to cancer. In an alternative embodiment, the results from predisposition analyses described herein may be combined with other test results indicative of cancer, which were previously, concurrently, or subsequently gathered with respect to the predisposition testing. In these embodiments, the combination of the prognostic test results with other test results can be

probative of cancer, and the combination can be utilized as a cancer diagnostic. The results of any test indicative of cancer known in the art may be combined with the methods described herein.

Examples of such tests are provided herein. For breast cancer, they include mammography (e.g., a more frequent and/or earlier mammography regimen may be prescribed); breast biopsy and optionally a biopsy from another tissue; breast ultrasound and optionally an ultrasound analysis of another tissue; breast magnetic resonance imaging (MRI) and optionally an MRI analysis of another tissue; electrical impedance (T-scan) analysis of breast and optionally of another tissue; ductal lavage; nuclear medicine analysis (e.g., scintimammography); BRCA1 and/or BRCA2 sequence analysis results; and thermal imaging of the breast and optionally of another tissue. Testing may be performed on tissue other than breast to diagnose the occurrence of metastasis (e.g., testing of the lymph node).

Risk of cancer sometimes is expressed as a probability, such as an odds ratio, percentage, or risk factor. The risk is based upon the methylation status of a target nucleic acid as described herein, and also may be based in part upon phenotypic traits of the individual being tested. Methods for calculating predispositions based upon patient data are well known (see, e.g., Agresti, Categorical Data Analysis, 2nd Ed. 2002. Wiley). Allelotyping and genotyping analyses may be carried out in populations other than those exemplified herein to enhance the predictive power of the prognostic method. These further analyses are executed in view of the exemplified procedures described herein, and may be based upon the same polymorphic variations (*e.g.*, methylation sites) or additional polymorphic variations. Risk determinations for cancer are useful in a variety of applications. In one embodiment, cancer risk determinations are used by clinicians to direct appropriate detection, preventative and treatment procedures to subjects who most require these.

Therapeutic Embodiments

The results provided herein are easily integrated into a biological model involving the PRC2 complex in cancer development. PRC2, and its subcomponent EZH2, bind to a set of developmental regulator genes. The polycomb complex recruits DNA methyltransferases and mediates, likely through DNA methylation, repression of these developmental regulators. In embryonic stem cells this mechanism is needed to maintain pluripotency (Boyer, L.A. et al. Polycomb complexes repress developmental regulators in murine embryonic stem cells. *Nature* 441, 349-53 (2006)). It has also been suggested that the same mechanism is involved in *de-novo* methylation of cancer cells. In this model the methylation changes are installed following a pre-programmed chromatin pattern used for repression in stem cells (Schlesinger, Y. et al. Polycomb-mediated methylation on Lys27 of histone H3 pre-marks genes for de

novo methylation in cancer. *Nat Genet* **39**, 232-6 (2007) and (Ohm, J.E. et al. A stem cell-like chromatin pattern may predispose tumor suppressor genes to DNA hypermethylation and heritable silencing. *Nat Genet* **39**, 237-42 (2007)). Studies in this area so far have investigated mainly colon cancer samples or colon cancer cell lines (Widschwendter, M. et al. Epigenetic stem cell signature in cancer. *Nat Genet* **39**, 157-8 (2007)). The present invention provides in part quantitative high resolution methylation data for at least seven different tumor types (excluding leukemias and prostate cancer). For every tumor type a different, but not exclusive, set of genes was identified that showed higher methylation levels compared to normal samples. Interestingly six out of these seven sets of hypermethylated genes were enriched for PRC2 target genes. Individual genes were associated with a variety of different tumor types. A relationship was found between the number of PRC2 marks and the number of associated tumor types. These findings suggest that PRC2 target methylation is a common event in cancer, and is not limited to individual tumor types. Without being limited by the mechanism, in one possible scenario, cancer develops from a silent stem cell, which had remained after embryonic development and now escapes growth regulation. In another more causal scenario, *de-novo* methylation originates from residual chromatin marks and represses key developmental regulators; thereby leading to deregulation of cell cycle control. Although the data neither supports, nor contradicts either scenario, it provides strong evidence that DNA methylation of PRC2 target genes is unlikely to be a consequence of flawed DNA methylation maintenance. The results provided herein indicate that PRC2 target repression through DNA methylation is a frequently activated mechanism in cancer cells.

Screening Assays

Featured herein are methods for identifying a candidate therapeutic for treating cancer. The methods comprise contacting a test molecule with a target molecule in a system. A "target molecule" as used herein refers to a target nucleic acid of the invention, a substantially identical nucleic acid thereof, or a fragment thereof, and an encoded polypeptide of the foregoing. The method also comprises determining the presence or absence of an interaction between the test molecule and the target molecule, where the presence of an interaction between the test molecule and the nucleic acid or polypeptide identifies the test molecule as a candidate cancer therapeutic. The interaction between the test molecule and the target molecule may be quantified.

Test molecules and candidate therapeutics include, but are not limited to, compounds, antisense nucleic acids, siRNA molecules, ribozymes, polypeptides or proteins encoded by a target nucleic acids, or a substantially identical sequence or fragment thereof, and immunotherapeutics (*e.g.*, antibodies and HLA-

presented polypeptide fragments). A test molecule or candidate therapeutic may act as a modulator of target molecule concentration or target molecule function in a system. A "modulator" may agonize (*i.e.*, up-regulates) or antagonize (*i.e.*, down-regulates) a target molecule concentration partially or completely in a system by affecting such cellular functions as DNA replication and/or DNA processing (*e.g.*, DNA methylation or DNA repair), RNA transcription and/or RNA processing (*e.g.*, removal of intronic sequences and/or translocation of spliced mRNA from the nucleus), polypeptide production (*e.g.*, translation of the polypeptide from mRNA), and/or polypeptide post-translational modification (*e.g.*, glycosylation, phosphorylation, and proteolysis of pro-polypeptides). A modulator may also agonize or antagonize a biological function of a target molecule partially or completely, where the function may include adopting a certain structural conformation, interacting with one or more binding partners, ligand binding, catalysis (*e.g.*, phosphorylation, dephosphorylation, hydrolysis, methylation, and isomerization), and an effect upon a cellular event (*e.g.*, affecting progression of cancer). In one embodiment of the invention, a test molecule disrupts the binding of a PRC2 complex to a target nucleic acid.

As used herein, the term "system" refers to a cell free in vitro environment and a cell-based environment such as a collection of cells, a tissue, an organ, or an organism. A system is "contacted" with a test molecule in a variety of manners, including adding molecules in solution and allowing them to interact with one another by diffusion, cell injection, and any administration routes in an animal. As used herein, the term "interaction" refers to an effect of a test molecule on test molecule, where the effect sometimes is binding between the test molecule and the target molecule, and sometimes is an observable change in cells, tissue, or organism.

There are many standard methods for detecting the presence or absence of an interaction between a test molecule and a target molecule. For example, titrametric, acidimetric, radiometric, NMR, monolayer, polarographic, spectrophotometric, fluorescent, and ESR assays probative of a target molecule interaction may be utilized.

Target activity and/or target interactions can be detected and quantified using assays known in the art. For example, an immunoprecipitation assay or a kinase activity assay that employs a kinase-inactivated MEK can be utilized. Kinase inactivated MEKs are known in the art, such as a MEK that includes the mutation K97M. In these assays, mammalian cells (*e.g.*, COS or NIH-3T3) are transiently transfected with constructs expressing target polypeptides, and in addition, the cells are co-transfected with oncogenic RAS or SRC or both. Oncogenic RAS or SRC activates target kinase activity. The target is immunoprecipitated from cell extracts using a monoclonal antibody (*e.g.*, 9E10) or a polyclonal antibody (*e.g.*, from rabbit) specific for a unique peptide from the target. target is then resuspended in

assay buffer containing GST-Mek1 or GST-Mek2 and/or GST-ERK2. In addition, [γ 32P] ATP can be added to detect and/or quantify phosphorylation activity. Samples are incubated for 5-30 minutes at 30°C, and then the reaction is terminated by addition of EDTA. The samples are centrifuged and the supernatant fractions are collected. Phosphorylation activity is detected using one of two methods: (i) activity of GST-ERK2 kinase can be measured using MBP (myelin basic protein, a substrate for ERK) as substrate, or (ii) following incubation of immunoprecipitated target in reaction buffer containing GST-ERK and [γ 32P] ATP, transfer of labeled ATP to kinase-dead ERK can be quantified by a phosphor-imager or densitometer following PAGE separation of polypeptide products (phosphorylated and non-phosphorylated forms). These types of assays are described in Weber et al., Oncogene 19: 169-176 (2000); Mason et al., EMBO J. 18: 2137-2148 (1999); Marais et al., J. Biol. Chem. 272: 4378-4383 (1997); Marais et al., EMBO J. 14: 3136-3145 (1995).

Modulation of oncogenic transforming activity by a target of the invention, or derivatives thereof, can be measured according to various known procedures, *e.g.*, Eva and Aaronson, Nature, 316:273-275, 1985; Hart et al., J.Biol.Chem., 269:62-65, 1994. A compound can be added at any time during the method (e.g., pretreatment of cells; after addition of a target, and the like) to determine its effect on the oncogenic transforming activity of a target of the invention. Various cell lines also can be used.

In general, an interaction can be determined by labeling the test molecule and/or the target molecule, where the label is covalently or non-covalently attached to the test molecule or target molecule. The label is sometimes a radioactive molecule such as 125I, 131I, 35S or 3H, which can be detected by direct counting of radioemission or by scintillation counting. Also, enzymatic labels such as horseradish peroxidase, alkaline phosphatase, or luciferase may be utilized where the enzymatic label can be detected by determining conversion of an appropriate substrate to product. Also, presence or absence of an interaction can be determined without labeling. For example, a microphysiometer (e.g., Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indication of an interaction between a test molecule and a target molecule (McConnell, H. M. et al., Science 257: 1906-1912 (1992)).

In cell-based systems, cells typically include a target nucleic acid or polypeptide or variants thereof and are often of mammalian origin, although the cell can be of any origin. Whole cells, cell homogenates, and cell fractions (e.g., cell membrane fractions) can be subjected to analysis. Where interactions between a test molecule with a target polypeptide or variant thereof are monitored, soluble and/or membrane bound forms of the polypeptide or variant may be utilized. Where membrane-bound

forms of the polypeptide are used, it may be desirable to utilize a solubilizing agent. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)n, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate.

An interaction between two molecules also can be detected by monitoring fluorescence energy transfer (FET) (see, for example, Lakowicz et al., U.S. Patent No. 5,631,169; Stavrianopoulos et al. U.S. Patent No. 4,868,103). A fluorophore label on a first, "donor" molecule is selected such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, "acceptor" molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the "donor" polypeptide molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the "acceptor" molecule label may be differentiated from that of the "donor". Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, the spatial relationship between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the "acceptor" molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (e.g., using a fluorimeter).

In another embodiment, determining the presence or absence of an interaction between a test molecule and a target molecule can be effected by using real-time Biomolecular Interaction Analysis (BIA) (see, e.g., Sjolander & Urbaniczk, Anal. Chem. 63: 2338-2345 (1991) and Szabo et al., Curr. Opin. Struct. Biol. 5: 699-705 (1995)). "Surface plasmon resonance" or "BIA" detects biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

In another embodiment, the target molecule or test molecules are anchored to a solid phase. The target molecule/test molecule complexes anchored to the solid phase can be detected at the end of the reaction. The target molecule is often anchored to a solid surface, and the test molecule, which is not anchored, can be labeled, either directly or indirectly, with detectable labels discussed herein.

It may be desirable to immobilize a target molecule, an anti-target antibody, or test molecules to facilitate separation of complexed from uncomplexed forms of target molecules and test molecules, as

well as to accommodate automation of the assay. Binding of a test molecule to a target molecule can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion polypeptide can be provided which adds a domain that allows a target molecule to be bound to a matrix. For example, glutathione-S-transferase/target fusion polypeptides or glutathione-S-transferase/target fusion polypeptides can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivitized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed target polypeptide or target polypeptide, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of target binding or activity determined using standard techniques.

Other techniques for immobilizing a target molecule on matrices include using biotin and streptavidin. For example, biotinylated target polypeptide or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical).

In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the immobilized component (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody).

In one embodiment, this assay is performed utilizing antibodies reactive with target polypeptide or test molecules but which do not interfere with binding of the target polypeptide to its test molecule. Such antibodies can be derivitized to the wells of the plate, and unbound target or target polypeptide trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using

antibodies reactive with the target polypeptide or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the target polypeptide or test molecule.

Alternatively, cell free assays can be conducted in a liquid phase. In such an assay, the reaction products are separated from unreacted components, by any of a number of standard techniques, including but not limited to: differential centrifugation (see, for example, Rivas, G., and Minton, A. P., Trends Biochem Sci Aug;18(8): 284-7 (1993)); chromatography (gel filtration chromatography, ion-exchange chromatography); electrophoresis (see, e.g., Ausubel et al., eds. Current Protocols in Molecular Biology , J. Wiley: New York (1999)); and immunoprecipitation (see, for example, Ausubel, F. et al., eds. Current Protocols in Molecular Biology , J. Wiley: New York (1999)). Such resins and chromatographic techniques are known to one skilled in the art (see, e.g., Heegaard, J Mol. Recognit. Winter; 11(1-6): 141-8 (1998); Hage & Tweed, J. Chromatogr. B Biomed. Sci. Appl. Oct 10; 699 (1-2): 499-525 (1997)). Further, fluorescence energy transfer may also be conveniently utilized, as described herein, to detect binding without further purification of the complex from solution.

In another embodiment, modulators of target expression are identified. For example, a cell or cell free mixture is contacted with a candidate compound and the expression of target mRNA or polypeptide evaluated relative to the level of expression of target mRNA or polypeptide in the absence of the candidate compound. When expression of target mRNA or polypeptide is greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of target mRNA or polypeptide expression. Alternatively, when expression of target mRNA or polypeptide is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of target mRNA or polypeptide expression. The level of target mRNA or polypeptide expression can be determined by methods described herein for detecting target mRNA or polypeptide.

In another embodiment, binding partners that interact with a target molecule are detected. The target molecules can interact with one or more cellular or extracellular macromolecules, such as polypeptides, in vivo, and these molecules that interact with target molecules are referred to herein as "binding partners." Molecules that disrupt such interactions can be useful in regulating the activity of the target gene product. Such molecules can include, but are not limited to molecules such as antibodies, peptides, and small molecules. Target genes/products for use in this embodiment often are the target genes herein identified. In an alternative embodiment, provided is a method for determining the ability of the test compound to modulate the activity of a target polypeptide through modulation of the activity of a downstream effector of a target target molecule. For example, the activity of the effector molecule on an

appropriate target can be determined, or the binding of the effector to an appropriate target can be determined, as previously described.

To identify compounds that interfere with the interaction between the target gene product and its cellular or extracellular binding partner(s), e.g., a substrate, a reaction mixture containing the target gene product and the binding partner is prepared, under conditions and for a time sufficient, to allow the two products to form complex. In order to test an inhibitory agent, the reaction mixture is provided in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the target gene and its cellular or extracellular binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the target gene product and the cellular or extracellular binding partner is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the target gene product and the interactive binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal target gene product can also be compared to complex formation within reaction mixtures containing the test compound and mutant target gene product. This comparison can be important in those cases where it is desirable to identify compounds that disrupt interactions of mutant but not normal target gene products.

These assays can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the target gene product or the binding partner onto a solid phase, and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the target gene products and the binding partners, *e.g.*, by competition, can be identified by conducting the reaction in the presence of the test substance. Alternatively, test compounds that disrupt preformed complexes, e.g., compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the target gene product or the interactive cellular or extracellular binding partner, is anchored onto a solid surface (*e.g.*, a microtiter plate), while the non-anchored species is labeled, either directly or indirectly. The anchored species can be immobilized by

non-covalent or covalent attachments. Alternatively, an immobilized antibody specific for the species to be anchored can be used to anchor the species to the solid surface.

In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds that inhibit complex formation or that disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds that inhibit complex or that disrupt preformed complexes can be identified.

In an alternate embodiment, a homogeneous assay can be used. For example, a preformed complex of the target gene product and the interactive cellular or extracellular binding partner product is prepared in that either the target gene products or their binding partners are labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 that utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt target gene product-binding partner interaction can be identified.

Also, binding partners of target molecules can be identified in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos et al., Cell 72:223-232 (1993); Madura et al., J. Biol. Chem. 268: 12046-12054 (1993); Bartel et al., Biotechniques 14: 920-924 (1993); Iwabuchi et al., Oncogene 8: 1693-1696 (1993); and Brent WO94/10300), to identify other polypeptides, which bind to or interact with a target of the invention.

A two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA

constructs. In one construct, the gene that codes for a target polypeptide is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified polypeptide ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. (Alternatively the target polypeptide can be the fused to the activator domain.) If the "bait" and the "prey" polypeptides are able to interact, in vivo, forming a target-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the polypeptide which interacts with the target polypeptide.

Candidate therapeutics for treating cancer are identified from a group of test molecules that interact with a target nucleic acid or polypeptide. Test molecules are normally ranked according to the degree with which they interact or modulate (e.g., agonize or antagonize) DNA replication and/or processing, RNA transcription and/or processing, polypeptide production and/or processing, and/or function of target molecules, for example, and then top ranking modulators are selected. In a preferred embodiment, the candidate therapeutic (*i.e.*, test molecule) acts as a target antagonist. Also, pharmacogenomic information described herein can determine the rank of a modulator. Candidate therapeutics typically are formulated for administration to a subject.

Therapeutic Treatments

Formulations or pharmaceutical compositions typically include in combination with a pharmaceutically acceptable carrier, a compound, an antisense nucleic acid, a ribozyme, an antibody, a binding partner that interacts with a target polypeptide, a target nucleic acid, or a fragment thereof. The formulated molecule may be one that is identified by a screening method described above. As used herein, the term "pharmaceutically acceptable carrier" includes solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration.

Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerin, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Oral compositions generally include an inert diluent or an edible carrier. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules, e.g., gelatin capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, sodium chloride sometimes are included in the

composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation often utilized are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art. Molecules can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, active molecules are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. Materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

It is advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete

units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Molecules which exhibit high therapeutic indices often are utilized. While molecules that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such molecules often lies within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any molecules used in the methods described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (*i.e.*, the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

As defined herein, a therapeutically effective amount of protein or polypeptide (*i.e.*, an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, sometimes about 0.01 to 25 mg/kg body weight, often about 0.1 to 20 mg/kg body weight, and more often about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight. The protein or polypeptide can be administered one time per week for between about 1 to 10 weeks, sometimes between 2 to 8 weeks, often between about 3 to 7 weeks, and more often for about 4, 5, or 6 weeks. The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment, or sometimes can include a series of treatments.

For antibodies, a dosage of 0.1 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg) is often utilized. If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is often appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (e.g., into the brain). A method for lipidation of antibodies is described by Cruikshank et al., J. Acquired Immune Deficiency Syndromes and Human Retrovirology 14:193 (1997).

Antibody conjugates can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a polypeptide such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors. Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

For compounds, exemplary doses include milligram or microgram amounts of the compound per kilogram of subject or sample weight, for example, about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram. It is understood that appropriate doses of a small molecule depend upon the potency of the small molecule with respect to the expression or activity to be modulated. When one or more of these small molecules is to be administered to an animal (e.g., a human) in order to modulate expression or activity of a polypeptide or nucleic acid described herein, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

Pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Pharmaceutical compositions of active ingredients can be administered by any of the paths described herein for therapeutic and prophylactic methods for treating cancer. With regard to both prophylactic and therapeutic methods of treatment, such treatments may be specifically tailored or modified, based on knowledge obtained from pharmacogenomic analyses described herein. As used herein, the term "treatment" is defined as the application or administration of a therapeutic agent to a patient, or application or administration of a therapeutic agent to an isolated tissue or cell line from a patient, who has a disease, a symptom of disease or a predisposition toward a disease, with the purpose to cure, heal, alleviate, relieve, alter, remedy, ameliorate, improve or affect the disease, the symptoms of disease or the predisposition toward disease. A therapeutic agent includes, but is not limited to, small molecules, peptides, antibodies, ribozymes and antisense oligonucleotides.

Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of cancer, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of target aberrance and the associated cancer, for example, a target molecule, target agonist, or target antagonist, or a target/PRC2 blocking agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein, or the proper prophylactic can be administered based on a diagnostic and/or prognostic result of the invention.

As discussed, successful treatment of target disorders can be brought about by techniques that serve to inhibit the expression, activity or binding of a target gene or target gene products. For example, compounds (e.g., an agent identified using an assays described above) that exhibit negative modulatory activity can be used to prevent and/or treat cancer. Such molecules can include, but are not limited to peptides, phosphopeptides, small organic or inorganic molecules, or antibodies (including, for example, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab')2 and FAb expression library fragments, scFV molecules, and epitope-binding fragments thereof).

It is possible that the use of antisense, ribozyme, and/or triple helix molecules to reduce or inhibit gene expression of hypomethylated target genes, such that the concentration of normal target gene product present can be lower than is necessary for a normal phenotype. Another method by which nucleic acid molecules may be utilized in treating or preventing a disease characterized by target expression is through the use of aptamer molecules specific for target polypeptide. Aptamers are nucleic acid molecules having a tertiary structure which permits them to specifically bind to polypeptide ligands (see, e.g., Osborne, et al., Curr. Opin. Chem. Biol.1(1): 5-9 (1997); and Patel, D. J., Curr. Opin. Chem. Biol. Jun;1(1): 32-46 (1997)). Since nucleic acid molecules may in many cases be more conveniently introduced into target cells than therapeutic polypeptide molecules may be, aptamers offer a method by

which target polypeptide activity may be specifically decreased without the introduction of drugs or other molecules which may have pluripotent effects.

Antibodies can be generated that are both specific for target gene product and that reduce target gene product activity. Such antibodies may, therefore, by administered in instances whereby negative modulatory techniques are appropriate for the treatment of cancer. Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD50 (the dose lethal to 50% of the population) and the ED50 (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD50/ED50. Compounds that exhibit large therapeutic indices often are utilized. While compounds that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

Data obtained from cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds often lies within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in a method described herein, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC50 (*i.e.*, the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

In another aspect, provided are methods for identifying a predisposition to cancer in an individual as described herein and, if a genetic predisposition is identified, treating that individual to delay or reduce or prevent the development of cancer. Such a procedure can be used to treat cancer. Optionally, treating an individual for cancer may include inhibiting cellular proliferation, inhibiting metastasis, inhibiting invasion, or preventing tumor formation or growth as defined herein. Suitable treatments to prevent or reduce or delay cancer focus on inhibiting additional cellular proliferation, inhibiting metastasis, inhibiting invasion, and preventing further tumor formation or growth. Treatment usually includes surgery followed by radiation therapy. In the case of breast cancer, surgery may be a lumpectomy or a mastectomy (e.g., total, simple or radical). Even if the doctor removes all of the cancer that can be seen at the time of surgery, the patient may be given radiation therapy, chemotherapy, or hormone therapy after

surgery to try to kill any cancer cells that may be left. Radiation therapy is the use of x-rays or other types of radiation to kill cancer cells and shrink tumors. Radiation therapy may use external radiation (using a machine outside the body) or internal radiation. Chemotherapy is the use of drugs to kill cancer cells. Chemotherapy may be taken by mouth, or it may be put into the body by inserting a needle into a vein or muscle. In the case of breast cancer, hormone therapy often focuses on estrogen and progesterone, which are hormones that affect the way some cancers grow. Any preventative/therapeutic treatment known in the art may be prescribed and/or administered, including, for example, surgery, chemotherapy and/or radiation treatment, and any of the treatments may be used in combination with one another to treat or prevent breast cancer (e.g., surgery followed by radiation therapy).

Combinations and Kits

In another embodiment, there are provided prognostic or diagnostic systems, typically in combination or kit form, containing a reagent that modifies one or more nucleotides of the nucleic acid target gene molecule as a function of the methylation state of the nucleic acid target gene molecule, such as bisulfite; one or more methylation specific primers for specifically hybridizing to a reagent-treated nucleic acid target gene molecule, such as one or more methylation specific PCR primers; and one or more compounds for fragmenting amplified nucleic acid target gene molecule, such as RNases, including RNase A or RNase T1. A kit also may include the appropriate buffers and solutions for performing the methylation identification methods described herein. For example, a kit can include a glass vial used to contain milligram quantities of a primer or enzyme. A kit also may include substrates, supports or containers for performing the methylation identification methods, including vials or tubes, or a mass spectrometry substrate such as a Sequenom SpectroCHIP substrate.

EXAMPLES

The following Examples describe a novel technique that uses base-specific cleavage of amplification products and Matrix-Assisted Laser Desorption/Ionization Time-Of-Flight Mass Spectrometry (MALDI-TOF MS) to perform large scale quantitative DNA methylation analysis across a set of candidate genes (n=147). This method led to the identification of clinically relevant AML subclasses, while highlighting methylated genes of potential pathogenic relevance. Also described is a methylation-based outcome predictor derived from AML-associated promoter methylation patterns that provide a basis for improved outcome prediction in AML.

Example 1

Bisulfite Treatment of a Nucleic Acid Target Gene Region

Bisulfite treatment of genomic DNA was performed with a commercial kit from Zymo Research Corporation (Orange, CA) that combines bisulfite conversion and DNA clean up. The kit follows a protocol from Paulin, R. *et al.* in *Nucleic Acids Res.* 26:5009-5010, 1998. Briefly, in this protocol 2 μg of genomic DNA is digested with a restriction endonuclease (EcoR1), then denatured by the addition of 3 M sodium hydroxide and incubated for 15 min at 37°C. A 6.24 M urea/2 M sodium metabisulfite (4 M bisulfite) solution is prepared and added with 10mM hydroquinone to the denatured DNA. The corresponding final concentrations are 5.36 M, 3.44 M and 0.5 mM respectively. The reaction is performed in a 0.5 ml tube overlaid with mineral oil. This reaction mix is repeatedly heated between 55°C for 15 min and 95°C for 30 s in a PCR machine (MJ Tetrad) for 20 cycles. DNA purification was done using the commercially available GENECLEAN kit from Q-biogene.

All bisulfite-based methylation analysis methods suffer from a considerable amount of measurement variability introduced by the chemical treatment of genomic DNA (*e.g.*, bisulfite treatment leading to DNA degradation) (Ehrich, M., Zoll, S., Sur, S. & van den Boom, D. *Nucleic Acids Res* (2007)). To determine if the variability is applicable to the model system used in this study, duplicate measurements of four control DNAs was performed in 96 amplicons and sufficient data stability was observed (R squared = 0.96, Figure 6A). The effect of primer design on the quantitative measurements was also analyzed by designing two different but overlapping amplification regions for the ERBB2 gene. The quantitative values from both reactions were almost identical and showed a high correlation (R-Squared 0.96).

Example 2

PCR and *in vitro* Transcription of a Nucleic Acid Target Gene Region

The IGF2/H19 gene region (Human Genome Chromosome 11:1,983,678-1,984,097) serves as an exemplary gene to demonstrate the effectiveness and feasibility of the methylation analysis methods disclosed herein. The IGF2/H19 region provides an ideal test case because of its hemi-methylated status. In a hemi-methylated region, the paternal allele is usually silenced by methylation, which results in an ideal 50/50 ratio. The presence of an expected 50/50 ratio validates the approach. As the following

Examples demonstrate, this is in fact the case, and the methods used to analyze IGF2/H19 were applied to the AML target genes disclosed herein.

IGF2/H19 was PCR-amplified from bisulfite treated human genomic DNA using primers that incorporate the T7 [5'-CAG TAA TAC GAC TCA CTA TAG GGA GA] promoter sequence. Two sets of primers were designed to incorporate the T7 promoter sequence either to the forward (5'-CAG TAA TAC GAC TCA CTA TAG GGA GAA GGC TGT TAG TTT TTA TTT TAT TTT TAA T-3'; 5'-AGG AAG AGA GAA CCA CTA TCT CCC CTC AAA AAA-3') or to the reverse (5'-AGG AAG AGA GGT TAG TTT TTA TTT TAT TTT TAA T–3'; 5'-CAG TAA TAC GAC TCA CTA TAG GGA GAA GGC TAA CCA CTA TCT CCC CTC AAA AAA-3') strand. Alternatively the derived PCR product was cloned into a pGEM-T vector system (Promega, Madison, WI) and re-amplified from the cloned DNA. The PCR reactions were carried out in a total volume of 5 µl using 1 pmol of each primer, 40 µM dNTP, 0.1U Hot Star Taq DNA polymerase (Qiagen, Valencia, CA), 1.5 mM $MgCl_2$ and buffer supplied with the enzyme (final concentration 1x). The reaction mix was pre-activated for 15 min at 95 °C. The reactions were amplified in 45 cycles of 95 °C for 20 s, 62 °C for 30 s and 72 °C for 30 s followed by 72 °C for 3 min. Unincorporated dNTPs were dephosphorylated by adding 1.7ul H2O and 0.3 U Shrimp Alkaline Phosphatase. The reaction was incubated at 37°C for 20 min and SAP was then heat-inactivated for 10 minutes at 85°C.

Typically, two microliters of the PCR reaction were directly used as template in a 4 µl transcription reaction. Twenty units of T7 R&DNA polymerase (Epicentre, Madison, WI) were used to incorporate either dCTP or dTTP in the transcripts. Ribonucleotides were used at 1 mM and the dNTP substrate at 2.5 mM; other components in the reaction were as recommended by the supplier. Following the *in vitro* transcription, RNase A (SEQUENOM, San Diego) was added to cleave the *in vitro* transcript. The mixture was then further diluted with H_2O to a final volume of 27 µl. Conditioning of the phosphate backbone prior to MALDI-TOF MS was achieved by the addition of 6 mg CLEAN Resin (SEQUENOM Inc., San Diego, CA).

Example 3

Mass Spectral Measurements of Transcribed Nucleic Acid Target Gene Region

Conditioning of the phosphate backbone was achieved by the addition of 6mg CLEAN Resin (Sequenom Inc., San Diego, CA) to the transcription sample. A 15 nl aliquot of the cleavage reaction was robotically dispensed onto a silicon chip preloaded with matrix (SpectroCHIP; Sequenom Inc., San

Diego, CAI. Mass spectra were collected using a MassARRAY mass spectrometer (Bruker-SEQUENOM). Spectra were analyzed using proprietary peak picking and spectra interpretation tools (Little, et al. *Nat Med* 3:1413-6 (1997)).

Example 4

Identification of Methylation Sites in IGF2/H19

The difference in the mass spectra results from a C-specific cleavage reaction of the forward transcript may be seen in Figure 1. The mass spectrum derived from the methylated template shows signals corresponding to the expected methylation sites. In this spectra each mass signal represents at least two CpG sites (cleavage at the beginning of the fragment and at the end) and two cleavage products therefore represent each methylated CpG site. The non-methylated template creates a mass spectrum that is devoid of any sequence/methylation associated signals. Figure 1 displays mass signals generated by cytosine specific cleavage of the forward transcript of the IGF2/H19 region (upper spectral analysis is the methylated template; lower spectral analysis is the non-methylated template). Methylation of the target sequence results in the generation of rCTP-containing transcripts; every methylated CpG is represented in the transcript by a cleavage site. Each of the cleavage products is labeled with a number, which indicates the CpG position in the template. These numbers can be cross-referenced with the cleavage products listed in Tables 4 and 5. The non-methylated target sequence does not contain cytosine and therefore does not contain cleavage sites. Mass signals are labeled with letters and the corresponding explanations are listed in Figure 1(B). A full list of expected cleavage products illustrates the predicted difference between methylated and non-methylated template. Predicted mass signals 12 and 13 are not found in the experimental spectrum, because the corresponding CpGs 23 and 24 are not methylated which results in concatenation of fragment 5167 and 12616 in a much larger fragment that can not be detected.

The below tables show the cleavage products of mass signals generated by cytosine specific cleavage of the forward transcript of IGF2/H19 in both the methylated (Table 4) and non-methylated (Table 5) transcript sequences.

TABLE 4

Molecular Mass in Da	CpG island position	Cleavage product type	Cleavage product composition and origin
653.41	OOMR	MAIN	5OH-AC-3p @447
669.41	OOMR	MAIN	5OH-GC-3p @227; 5OH-GC-3p @169; 5OH-GC-3p @116; 5OH-GC-3p @63

932.60	OOMR	MAIN	5OH-TTC-3p @431
1236.8	OOMR	MAIN	5OH-TTTC-3p @434
1277.81	OOMR	ANCH	5OH-GTTC-3p @59
1535.07	1	LAST	5OH-TAAAT-3OH @450
1648.03	2	MAIN	5OH-GAGTC-3p @65
1993.24	3	MAIN	5OH-GGTGAC-3p @171
2215.41	4	ANCH	5OH-GTTTATC-3p @35
2306.45	5	MAIN	5OH-GGAAATC-3p @162
3260.05	6	ANCH	5OH-GGTAATATGC-3p @83
3301.07	7	MAIN	5OH-GAATGGGATC-3p @118
3623.03	8	ANCH	5PPP-GGGAGAAGGC-3p @0
3893.46	9	ANCH	5OH-GAGTATAAGTTC-3p @177
3941.46	10	ANCH	5OH-GGGGTGTTTAGC-3p @128
4197.66	11	ANCH	5OH-GTAAGTATAGTTC-3p @70
4574.86	12*	ANCH	5OH-GTGAGGTTTGAGTC-3p @294
5167.26	13*	ANCH	5OH-GAGTTTTTAGGGATTC-3p @343
5512.47	14	ANCH	5OH-GTTTGTTAGTAGAGTGC-3p @42
5832.66	15	ANCH	5OH-GTTTATTAGGGGGTTTGC-3p @229
6211.9	16	MAIN	5OH-GGTTAATTGGATGGGAATC-3p @189
6234.88	17	MAIN	5OH-GGTTTGGGGGGTTGGTATC-3p @208
7106.46	18	MAIN	5OH-GGTTGTGGGGATTTTGTTTTGC-3p @140
7494.71	19	MAIN	5OH-GGTTTTTAGATAGGAAAGTGGTC-3p @93
8192.12	20	MAIN	5OH-TGGGTTTGGGAGAGTTTGTGAGGTC-3p @10
9870.16	OOMR	MAIN	5OH-GTTGGTAGGTAGGGAGTAGTAGGTATGGTC-3p @398
11366.1	OOMR	MAIN	5OH-GTGATGGTGGTAGGAAGGGGTTTTTTGTGTTATTC-3p @308
12616.9	OOMR	MAIN	5OH-GTAGTTGGTTTTTAGTTATGTGTAAAGTATGTGTAGGGC-3p @359
14763.4	OOMR	MAIN	5OH-GGTATTTTTTTTTGTTTTTTAGTATTTTATTTTTATTTTTTAGGAAC-3p @247

TABLE 5

Molecular Mass in Da	CpG island position	Cleavage product type	Cleavage product composition and origin
324.208	OOMR	MAIN	5OH-C-3p @449; 5OH-C-3p @430
524.192	OOMR	ACYC	5PPP-G-3OH @0
653.417	OOMR	MAIN	5OH-AC-3p @447
869.401	OOMR	ACYC	5PPP-GG-3OH @0
932.601	OOMR	MAIN	5OH-TTC-3p @431
1214.61	OOMR	ACYC	5PPP-GGG-3OH @0
1236.8	OOMR	MAIN	5OH-TTTC-3p @434
1889.03	A	DBLC	5PPP-GGGAGAAGGC-3p @0
2547.45	B	ACYC	5PPP-GGGAGAA-3OH @0

2889.83	C	MAIN	5OH-TATAGTGTC-3p @438 derived from PCR primer tag
2892.66	C	ACYC	5PPP-GGGAGAAG-3OH @0
3237.87	D	ACYC	5PPP-GGGAGAAGG-3OH @0
3623.03	E	MAIN	5PPP-GGGAGAAGGC-3p @0 derived from PCR primer tag
135810	OOMR	MAIN	5OH-TGGGTTTGGGAGAGTTTGTGAGGTTGTTTATTGTTTGTTAGT AGAGTGTGTTTGTGAGTTGTAAGTATAGTTTGGTAATATGTGGTT TTTAGATAGGAAAGTGGTTGTGAATGGGATTGGGGTGTTTAGTGG TTGTGGGGATTTTGTTTTGTGGAAATTGTGGTGATGAGTATAAGTT TGGTTAATTGGATGGGAATTGGTTTGGGGGGTTGGTATTGTGTTTA TTAGGGGGTTTGTGGTATTTTTTTTTGTTTTTTAGTATTTTATTTTTA TTTTTTAGGAATGTGAGGTTTGAGTTGTGATGGTGGTAGGAAGGGG TTTTTTGTGTTATTTGAGTTTTTAGGGATTTGTAGTTGGTTTTTAGTT ATGTGTAAAGTATGTGTAGGGTGTTGGTAGGTAGGGAGTAGTAGGT ATGGTAGC-3p @10

Cleavage product characterization legend:

MAIN = regular cleavage product

OOMR = out of mass range (molecular mass either too low or too high to be detected within the automated data acquisition)

DBLC = double charged molecular ion species (at half mass of parent molecular ion)

ACYC = Abortive cycling (incomplete transcription products generated during the first 10 nt of transcription)

All masses below 1300 Da cannot be detected reliably in the chosen mass window. The mass signal labeled A is a doubly charged molecular ion E. Mass signals labeled B and D represent so called abortive cycling products. Abortive cycling is the premature" termination during the transcribtioon process while the polymerase has still formed the initiation complex and has not yet reached the more stable elongation complex. During that phase the transcribtin might occasionally be terminated without generating a full lenght transcribt. Mass signals labeled C and E are expected main signals generated by cleavage of the transcription product.

The reactions described above provide ideal mass signal patterns that are well suited to identify methylation in mixtures that contain methylated DNA in a fraction as low as 5%, without selective PCR amplification. Figure 2 is an overlay of mass signal patterns generated by cytosine specific cleavage of the forward transcript of the IGF2/H19 region. In the depicted case, the template used for PCR amplification consisted of a mixture of methylated and non-methylated DNA. Mass spectra reveal increasing signal intensity of cleavage products with increasing amount of methylated template DNA. Methylation specific mass signals can be detected in mixtures containing as little as 5% methylated DNA.

Example 5

Statistical Methods

Base-specific cleavage reactions also can be used in determination of methylation ratios. For example, methylation induced C/T changes on the forward strand are represented as G/A changes on the complementary strand. These changes lead to a mass shift of 16Da (G/A mass shift) or multiples thereof, when multiple CpGs are enclosed in one cleavage product. In reactions where methylation results in a mass shift of nucleic acid target gene molecule fragments, one fragment represents the methylated template and a second fragment represents the non-methylated template. The intensities of the measured masses of these fragments can be compared to determine the ratio of methylated vs. non-methylated nucleic acid target gene molecules. Also, the base composition of the measured fragments differs only by one or a few nucleotides, which assures equal desorption and ionization behavior during MALDI-TOF measurement. Methods for intensity estimation of mass measurements such as "area-under the peak" and "signal to noise" can yield similar results. Depending on the sequence of the nucleic acid target gene molecule, multiple signal pairs can be used in determining the ratio between signal intensities. This information can be used to assess the degree of methylation for each CpG site independently, or, if all CpG sites are methylated approximately to the same degree, to average the methylation content over the complete target region. A direct correlation between signal intensity ratios and the ratio of the deployed DNAs can be determined for ranges of 10%-90% of methylated template. If the ratio between methylated and non-methylated template is below 10% or exceeds 90%, the signals that represent the lower amount of template can still be detected, but the quantitation can be subject to higher error.

All statistical analyses were performed using the R statistical environment[32]. Distances from gene start sites were calculated using the 'RMySQL' package and the SQL database version of the UCSC genome browser (genome-mysql.cse.ucsc.edu). Two dimensional clustering has been performed using the 'heatmap.2' function in the 'gregmisc' package. Classical multidimensional scaling has been performed using the 'cmdscale' function and visualization was done through the 'scatterplot3d' function is the same named package. Tests for statistical significance (t-test, Wilcox Test and Fisher's exact test) were performed using the standard function in R build into the 'stats' package.

For sequence motif detection, a permutation based method was used. N sequences from the pool of all analyzed sequences were randomly sampled, where N is equal to the number of sequences in the low or high methylation group, respectively. It was then determined how often every possible 6mer

(n=4096) is present in the sampled subset. One thousand permutations were performed for each analysis. A sequence motif was identified as being overrepresented if it occurred more often in the analyzed group of sequences than in any of the 1000 random draws.

Graphical representation of the gene tissue relationships was performed using the 'dot' algorithm implemented in Graphviz.

Example 6

Methylation Ratio Analysis

Determination of methylation ratios is enabled by a different base-specific cleavage reaction. Methylation induced C/T changes on the forward strand are represented as G/A changes on the reverse strand. Since cleavage schemes were restricted to C- and T-specific cleavage, methylation events led to a mass shift of 16Da (G/A mass shift) or a multitude thereof when multiple CpGs are enclosed in one cleavage product. The signal pair shown in Figure 3 demonstrates this. Figure 3 is an overlay of mass spectra generated by uracil specific cleavage of the reverse transcript of the IGF2/H19 region. Cleavage products derived from the methylated template contain rGTP at every position where the Cytosine of the forward strand was methylated. In contrast, the bisulfite conversion of non-methylated Cytosine to Uracile results in incorporation of rATP on the reverse strand. This 16Da difference between rGTP and rATP, or a multitude thereof when several CpGs are embedded in one cleavage product, can be detected unambiguously. The calculation of the area under the curve of mass signals specific for methylated and non-methylated template can be used to determine the ratio between methylated and non-methylated DNA used for amplification.

The cleavage product derived from the non-methylated template (C**G**CAACCACT) was detected at 3132 Da while its equivalent derived from the methylated template (C**A**CAACCACT) can be found at 3148 Da.

Reactions where one signal represents the methylated template and a second signal represents the non-methylated template can be used to determine the ratio of methylated vs. non-methylated template by comparing their signal intensities. The nucleotide composition of the measured fragments differs only by a single nucleotide, which ensures equivalent desorption and ionization behavior during MALDI-TOF measurement. Depending on the reference sequence of the target region, multiple signal pairs are available for determining the ratio between signal intensities. This information can be used to assess the

degree of methylation for each CpG site independently or, if all CpG sites are methylated approximately to the same degree, to average the methylation content over the complete target region.

A direct correlation can be seen between signal intensity ratios and the ratio of the deployed DNAs. The span of linearity of this correlation ranged from 10 % – 90 % of methylated template. The average standard deviation of the investigated concentrations was approximately 3%, with higher standard deviations towards both ends of the scale. If the ratio between methylated and non-methylated template is below 10% or exceeds 90%, the signals that are representing the lower amount of template can still be detected, but the intensity of signal does not correlate exactly to the actual ratio anymore.

Example 7

Methylation Pattern Analysis of IGF2/H19

The capability of base specific cleavage to determine the methylation status of each and every CpG within a given target region was determined. As outlined above, the C-specific forward reaction incorporates a cleavage nucleotide for each methylated CpG within the amplicon. The resulting cleavage products represent the existence of two cleavage nucleotides (exception: first and last fragment) or in this case two methylated Cs. Given the current limitations of MALDI-TOF instrumentation, a practical mass window ranges from around 1000 Da to 10000 Da. In this mass window, cleavage products with a length around 4 to 30 nucleotides can be detected. When the distance between two methylated cytosines becomes smaller or larger than this range, the resulting mass of the cleavage product might be too high or too low to be detected under standard conditions. The analysis of a single reaction still allows determining the methylation status of approximately 75% (depending on the reference sequence) of all CpG sites within the amplified nucleic acid molecule. To obtain information about all CpG sites, a set of four reactions were performed: C- and T-specific cleavage of the forward and reverse transcription product. This combination enables base-specific cleavage after each nucleotide (C-specific cleavage on the reverse strand equals G-specific cleavage on the forward strand; T-specific cleavage on the reverse strand equals A-specific cleavage on the forward strand). The combined information from these four cleavage reactions allows compilation of the exact methylation pattern. For the IGF2/H19 region described here, two reactions were sufficient to obtain the methylation status for each CpG site. However using four reactions provides the advantage of information redundancy. In this system 92% of all CpG sites were represented by more than one signal. This means that each methylation event is independently confirmed by more than one observation in one or more reactions. This redundancy is an important

aspect in potential diagnostic use. Figure 4 is a mass spectra representing all four base-specific cleavage reactions of the IGF/H19 amplicon. Numbers correspond to the CpG positions within this target region. Arrows point at the mass signals that indicate the presence of a methylated cytosine at the marked position. All methylated CpG's in the selected region were identified by one or more mass signals. Approximately 75% were identified by more than two mass signals.

The methylation pattern of the IGF2/H19 imprinted region in adult blood samples confirmed the segregation into methylated and non-methylated template strands reported by Vu *et al.* (*Genomics* 64(2):p.29331-40, 1999). Out of the 24 clones analyzed, 13 (54%) could be identified as methylated and 11 (46%) as non-methylated. No sequence changes were observed. Vu *et al. (supra)* showed by dideoxy sequencing of bisulfite treated DNA that 25 out of the 26 CpG sites within the amplicon are methylated. The only non-methylated CpG was found at position 470. The results indicated a slightly different methylation pattern in the studied sample DNA, where all CpG sites were methylated. The data also confirmed methylation of the CpNpG site at position 347. Due to the variability in individual methylation patterns, which have been observed by other groups, minor differences are anticipated.

The results demonstrate the capability of the method to discriminate methylated and non-methylated DNA nucleic acid target gene regions simultaneously and to reconstruct the exact methylation pattern. In order to support this contention, bisulfite treated genomic DNA was analyzed directly. The produced mass signal spectra showed signal patterns that are representative for the methylated template as well as those that are characteristic for the non-methylated template. The signal intensities for methylation-specific signals and non-methylation-specific signals were compared and the 50/50 ratio expected for hemi-methylated DNA, as in control blood samples, was confirmed. Figure 5 is a mass Spectra generated by uracil specific cleavage of the reverse transcript of the IGF2/H19 region. Genomic DNA was used for amplification. Dotted lines mark the position of mass signals representing non-methylated CpG's. Signals with 16 Da shift (or a multitude thereof) represent methylation events. The area-under-the-curve ratio of methylated versus non-methylated template approximates to 1, as one expects for hemi-methylated nucleic acid target gene regions. This indicates an unbiased amplification of methylated and non-methylated template for the analyzed region and validates our semi-quantitative capabilities.

Example 8

Analysis of Methylation in Cancer Samples

More than 400 genes were included in a high resolution scan to investigate DNA methylation changes in cancer samples. The genes were selected to include a majority of cancer consensus genes as described by Futreal and colleagues and a subset of known imprinted genes (Futreal, P.A. et al. *Nat Rev Cancer* 4, 177-83 (2004)). This set of genes contained more than 70 genes with associated PRC2 binding sites. All genes were analyzed in 59 cell lines derived from 9 different tumor types and control DNA from 6 normal tissues. The cancer cell lines are compiled by the National Cancer Institute (NCI) as the NCI-60 panel.

DNA methylation status was determined by gene specific amplification of bisulfite treated DNA followed by *in vitro* transcription and MALDI TOF analysis (Ehrich, M. et al. *Proc Natl Acad Sci U S A* 102, 15785-90 (2005)). The amplification regions were primarily designed to cover CpG Islands (CGI) overlapping with the 5'UTR of the target genes. When no CGI was annotated in close proximity, the sequence directly surrounding the 5'UTR was used for primer design. If no CpG dinucleotides were found in this region, the upstream flanking CGI was used.

The initial methylation data was filtered to exclude poor quality measurements. Poor quality was defined as amplicons with data available for less than 75% of all samples. These regions were excluded from further analysis. The filtered dataset contained 531 amplification regions, representing 430 genes. For excluded amplicons, PCR was identified as the leading cause of reaction failure.

All autosomal chromosomes and the X-chromosome are represented in the current gene set. The median amplicon length was 413 bp (range = 171 bp to 683 bp) and the median CpG content per amplicon was 33 CpG / amplicon (range = 6 CpG to 81 CpG per amplicon). For each sample a total of 11723 CpG sites were analyzed in 7216 CpG Units. See Table 11. A CpG Unit is defined as an analytical Unit which encompasses one or multiple subsequent CpG sites.

DNA methylation was analyzed in 59 cell lines comprised in the NCI-60 panel and used 6 commercially available DNA's from adult tissues to represent 'healthy' control samples.

The resulting data provides a comprehensive panel of cancer-related DNA methylation changes and can be integrated with previous datasets on mutational, transcriptional and proteomic profiles to obtain additional information about neoplastic transformations.

Clinical Colon Cancer Tissue

Tissue colorectal cancer and normal colon tissue samples were obtained from the Royal Melbourne Hospital (RMH) Tissue Bank; as part of the Ludwig Colon Cancer Initiative biomarker project. Samples were obtained with informed consent under the approved protocol from patients having a resection for histologically confirmed colorectal cancer and the normal matched tissue was obtained from the same resection specimen at a site adjacent to the tumor.

Tissue samples were snap frozen in liquid nitrogen within 30 minutes of collection and stored in a minus 80 degrees Celsius freezer. Matched tissue sample pairs were cut into $2mm^3$ cube sections weighing approximately 10-15mg. After manual dissection, DNA was extracted from the tissue sections using a QIAGEN DNeasy® Blood and Tissue Kit. Briefly, samples were first lysed using a Proteinase K digestion for 3 hours at 56 degrees Celsius followed by selective binding of DNA to a membrane; final steps involving a spin-column procedure allowed for the washing and subsequent elution of DNA with precipitated DNA resuspended in a buffer solution. DNA was quantified using a biophotometer, with A_{260}/A_{280} ratio in the range 1.7- 2.0. DNA samples were normalized to a concentration of 50µg/ml.

Methods

Amplification of bisulfite treated DNA was performed as described in Examples 1 and 2 using the primers described in Table 10. Some of the regions have more than 1 set of primers because more than one amplicon in that region was amplified. The PCR primers locations are provided in Table 10. To derive the primer nucleotide sequence (in a 5'-3' direction) from Table 10, the following steps can be performed:

For the left primer:

1) convert the genomic sequence to bisulfite modified genomic sequence (changing every C to T).

2) Take x (x refers to the number given in the table under Left primer length)nucleotides from the 5' end (left end) of the bisulfite modified genomic sequence.

3) (for hMC) attach 10mer tag to 5' end.

For the right primer

1) convert the genomic sequence into its reverse complement sequence (rcGS), including directional change so that the right (3') end of the genomic sequence becomes the left (5' end) of the rcGS.

2) convert the rcGS into bisulfite treated sequence (changing every C to T)

3) Take x (x refers to the number given in the table under Right primer length) nucleotides from the 5' end of the bisulfite modified rcGS.

4) (for hMC) attach T& tag to the 5' end.

Methylation data distribution for cell lines

The analyzed target regions were primarily designed within annotated CpG islands, which are frequently unmethylated in normal tissue. The data presented herein is in agreement with previous findings for normal tissue samples and confirms that CGIs with a CpG density >10% are generally unmethylated (<15% methylation)[17]. (Figure 6B). In the normal tissue samples, 76% of all amplicons showed mean methylation values below 15% methylation; only 5% of amplicons showed methylation levels above 85% methylation, and the remaining 19% of amplicons showed methylation levels between 15% and 85%.

In the cancer cell lines, a shift towards medium (between 20 and 80%) but not high (>80%) methylation levels was observed. Here, only 49% of all amplicons show methylation levels below 15% methylation, 2% show methylation levels above 85%, but 49% showed methylation between 15 and 85%. Differences in the distribution of CGI methylation between normal samples and cancer cell lines were further assessed by grouping the analyzed genomic regions into 10 bins based on methylation value deciles. All bins containing genes with methylation values between 20 and 80 % showed a 2 – 4 fold increase in the number of amplicons allocated to this bin in cancer samples. The groups below 20% and above 80% contained fewer amplicons in cancer samples compared to normal samples (Figure 6C).

These findings prompt the question whether it is more likely for a non-methylated gene to become hypermethylated or for a methylated gene to become hypomethylated in cancer. Methylation differences were analyzed for each amplicon between the group of normal and the group of cancer samples; this resulted in a distribution that is skewed towards higher methylation differences in cancer cell lines. Thus hypermethylation of CGIs is the most frequent event in the analyzed cancer samples (Figure 6D). However, analyzing the methylation differences for the group of amplicons that are methylated at low (< 20%) or high (>80%) levels in normal samples, it is just as likely to observe hypermethylation of low-methylated amplicons as it is to find hypomethylation of highly methylated amplicons (p value = 1, fishers exact test).

Given that amplicon-specific methylation changes might differ significantly between tumor types, each type of tumor cell line was analyzed individually. The results differ slightly for each tumor type, but in general the analysis confirms previous findings on an individual level. (See Tables 6 and 7).

Recent studies have shown a decrease of epigenetic marking in a 1kb window around the transcription start site. In active fly promoters, histone occupancy is decreased, while in Drosophila

melganogaster and in normal human tissue samples, DNA methylation is reduced within this core region (Eckhardt, F. et al. *Nat Genet* 38, 1378-85 (2006)) and (Mito, Y., Henikoff, J.G. & Henikoff, S. *Nat Genet* 37, 1090-7 (2005)). To further investigate this relationship, the distance from the 5'-UTR for each measured CpG in the dataset (>700,000 datapoints) was mapped. CpG methylation in normal samples showed the expected core window of unmethylated CpG sites within 1kb around the 5'-UTR (Figure 6E). In cancer cell lines, methylation averages are generally elevated, but the same symmetrical methylation decrease is observed. Thus these results confirm previous findings and expand their applicability to cancer cell lines.

Sequence motif confirmation and new motif detection

A set of CG-rich sequence motifs has been reported to be enriched in non methylated CGIs (Das, R. et al. *Proc Natl Acad Sci U S A* 103, 10713-6 (2006)). The amplicons of the invention were divided into sequences with low (<20%, n = 300) and high (>80%, n = 16) average methylation. The non methylated amplicons comprised significantly more of said sequence motifs ($p < 0.001$, Wilcox Test, mean in the low methylation set = 22, mean in the high methylation set = 8).

Next the amplicons were split into two groups based on the observed differences in DNA methylation between normal and cancer cell line samples. The group with high average methylation differences (ΔM >20%; p-value< 0.001, two sided t-test) comprised 89 sequences and the group with low differences comprised 121 sequences (ΔM <5%; p-value>0.05, two sided t-test). During amplicon design, target sequences were preferably selected to be located in CG rich regions; therefore, there is not an even distribution of sequence motifs. As a result, a permutation method was used to compare the distribution of 6mer oligonucleotides and to identify sequence motifs which are overrepresented in one of the two sets. Five sequence motifs were overrepresented in the set of non-differentially methylated sequences (ATACCG, ATACTA, ATAGAT, TATACT, TCATGG). A smaller set of four motifs were enriched in the differentially methylated genes (GACCTG, GCCAAG, GTCCCA, TTGAAG). The two sequence motif sets were annotated. Based on the annotations, binding sites for Sp1, a zinc finger transcription factor, were found to be enriched in the set of non-differentially methylated sequences (p value = 0.001, fishers exact test).

Confirmation of cell line results in colon cancer samples

To verify validity of the cell line-based results in clinical samples, the colon cancer cell line model was run in clinical samples. A set of 50 genes was selected that showed significant differential methylation (ΔM> 20%, p value <0.001, two sided t-test) in the colon cancer cell lines. To assess the specificity of our finding, 14 genes were selected that did not show any cell line methylation differences.

The methylation status of these genes was investigated in 48 matched sample pairs of colon cancer tissue and adjacent normal colon tissue. The majority of patients were male (M=30, F=18); the median age at diagnosis was 65 years (range 46 to 83). Fourteen patients had experienced local or distant caner recurrence and all stages I to IV were evenly represented. The analysis of methylation differences between the normal and cancer tissue samples confirmed the previous cell line findings for the majority of genes. In the set of differentially methylated genes, 42 out of 50 (84%) genes were found to be significantly differentially methylated in the clinical tissue samples. Additionally, all 14 genes that did not show a methylation difference were still not differentially methylated in the clinical samples.

Next, the methylation patters were used to characterize relationships among the colon cancer samples, and to explore potential associations with their clinical features. None of the clinical features (*e.g.*, age, stage, recurrence, location) showed a strong correlation to the resulting colon cancer methylation groups. The degree of similarity between methylation patterns derived from cell line samples and their tissue counterparts was explored using hierarchical clustering. As expected, the normal tissues grouped with the normal colon tissue samples and the colon cancer cell lines grouped with the colon cancer tissue samples. However, the segregation of normal and colon cancer tissue samples was not complete. A subset (n = 10) of colon cancer samples was found in the group of normal tissue samples.

In general, methylation differences between normal and cancer were larger in the cell line model compared to the clinical tissue samples. This effect might be caused by heterogeneity of the clinical specimens, which also include, for example, connective tissue or white blood cells. An additional explanation might be amplification of the methylation difference during cell culturing.

Finally, the findings were compared to results from a recent methylation study of colon cancer tumors that analyzed DNA methylation with a different technology (Weisenberger, D.J. et al. *Nat Genet* 38, 787-93 (2006)). A total of 38 genes were shared by both datasets. The results of both studies are in good agreement (92% concordance). Nine genes were found to be hypermethylated in colon cancer in both datasets, and 26 genes showed no colon cancer specific methylation in both datasets. Two genes were identified as hypermethylated only in the previous study, and one gene was found to be hypermethylated only in the present study. All together, the findings indicate that results obtained from the cell line model are to a high degree reproducible and applicable to clinical tissue samples.

Assigning classes to significantly differentially methylated genes

Genes were identified that were differentially methylated between each type of cancer cell line and normal tissues. The individual groups were examined to determine which genes overlap in multiple cancer types and which are found in specific tumor types only. Because several genetic loci were tested

in many separate runs (one for each cell line), the results will contain false positives that arise from multiple testing in high dimensional datasets. Although, not completely accounting for the issue in its entirety, a minimum difference of 20% as an additional selection criterion was implemented to filter out false positives.

A total of 71 genes were statistically significantly hypermethylated in at least one tumor type. A large fraction of these genes (n= 30, 42%) were found only in one tumor type, and nearly 10 percent were found in more than 5 tumor types (found in 5: TSPYL, PAX8, LEP, *PHOX2B*, TMPRSS2, found in 6: MYOD1, found in 8: PAX5). Table 6 and Table 7 provide gene targets that hypermethylated or hypomethylated in cancer cell lines, respectively. In Tables 6 and 7, a "1" indicates an association with a p-value less than 0.05.

TABLE 6: HYPERMETHYLATED TARGET GENE REGIONS

	Normal	Blood	Prostate	Breast	Ovarian	CNS	Skin	Renal	Lung	Colon
CCND1	0	1	0	0	0	0	0	0	0	0
LCK	0	0	0	0	0	1	0	0	0	0
MLLT6	0	0	0	0	0	1	0	0	0	0
SET	0	0	0	0	0	1	0	0	0	0
ZNF198	0	0	0	0	0	1	0	0	0	0
RUNX1T1	0	0	0	0	0	0	0	0	0	1
EGFR	0	0	0	0	0	0	0	0	0	1
ACSL6	0	0	0	0	0	0	0	0	0	1
FLT3	0	0	0	0	0	0	0	0	0	1
FLT4	0	0	0	0	0	0	0	0	0	1
TAL1	0	0	0	0	0	0	0	0	0	1
CD38	0	0	0	0	0	0	0	0	0	1
COL5A1	0	0	0	0	0	0	0	0	0	1
LMO2	0	0	0	0	0	0	0	0	0	1
MYH11	0	0	0	0	0	0	0	0	0	1
ZNF331	0	0	0	0	0	0	0	0	0	1
SNRPN	0	0	0	0	0	0	0	0	0	1
ATP10A	0	0	0	0	0	0	0	0	0	1
GABRB3	0	0	0	0	0	0	0	0	0	1
ESR1	0	0	0	0	0	0	0	0	0	1
BCL6	0	0	0	0	1	0	0	0	0	0
IL10RA	0	0	1	0	0	0	0	0	0	0
NFKB2	0	0	1	0	0	0	0	0	0	0
HOXA1	0	0	1	0	0	0	0	0	0	0
GAS7	0	0	0	0	0	0	0	1	0	0
HEAB	0	0	0	0	0	0	1	0	0	0
KIT	0	0	0	0	0	0	1	0	0	0
PSIP1	0	0	0	0	0	0	1	0	0	0
REL	0	0	0	0	0	0	1	0	0	0
TLX1	0	0	0	0	0	0	1	0	0	0
WDR66	0	0	0	0	0	1	1	0	0	0

SLC22A3	0	0	0	0	1	0	1	0	0	0
SLC38A4	0	0	0	0	1	0	0	1	0	0
OLIG2	0	0	0	0	0	0	0	1	0	1
TCL1A	0	0	0	0	0	0	0	1	0	1
CHGA	0	0	0	0	0	0	1	0	0	1
HOXC13	0	0	0	0	0	0	1	0	0	1
RET	0	0	0	0	0	0	1	0	0	1
PEG3	0	0	0	0	0	0	1	0	0	1
HIST1H4I	0	0	1	0	0	0	0	1	0	0
PLOD1	0	0	0	0	0	1	0	1	0	0
CCND2	0	0	0	0	0	1	0	1	0	0
FRAT1	0	0	0	0	0	1	1	0	0	0
PTPRN2	0	0	0	1	0	0	0	1	0	1
ZIM2	0	0	0	1	0	0	0	0	0	1
IRF4	0	0	0	0	1	0	0	0	0	1
HOXA2	0	0	0	0	1	1	0	0	0	1
FLI1	0	0	0	0	0	1	0	0	1	1
GPC3	0	0	0	1	0	0	0	0	1	1
CDKN1C	0	0	1	0	0	0	1	0	0	1
SBDS	0	0	0	1	0	1	0	1	0	0
HOXA7	0	0	0	1	0	1	0	1	0	0
HOXA10	0	0	0	1	0	1	0	1	0	0
GNAS	0	1	0	1	0	1	0	0	0	1
LYL1	0	0	0	1	1	0	1	0	0	0
HOXA6	0	0	0	1	0	1	0	1	0	0
BCR	0	0	0	0	0	1	1	1	0	0
TLX3	0	0	0	0	0	1	0	1	0	1
HOXA9	0	0	0	0	1	1	1	0	0	0
CA3	0	0	0	0	1	0	0	1	0	1
FLJ32447	0	0	0	0	1	0	0	1	0	1
PAX7	0	0	0	0	1	0	0	1	0	1
WT1	0	0	0	0	1	0	0	1	0	1
PON1	0	0	0	0	0	0	1	1	1	1
TSPYL5	0	1	0	1	0	0	1	1	0	1

PAX8	0	0	1	1	0	1	0	0	1	1
LEP	0	0	0	1	1	1	0	1	0	1
PHOX2B	0	0	0	0	1	1	0	1	1	1
TMPRSS2	0	0	0	0	1	1	1	1	1	0
MYOD1	0	1	0	1	0	1	0	1	1	1
PAX5	0	0	1	1	1	1	1	1	1	1

Seven genes were hypomethylated (found in 1 tumor type: TCL1A, SLC22A2, TRPM5, IGF2, PEG3; found in 2 KCNQ1, DLK1). As indicated in previous analysis, CNS neoplasm's (n=4) and Melanoma (n=3) had the highest number of hypomethylated genes. Interestingly almost all of the hypomethylated genes are known to be imprinted, which points to a loss of imprinting in these cases (See Table 7).

TABLE 7: HYPOMETHYLATED TARGET GENE REGIONS

	Blood	Breast	Lung	Normal	Prostate	Renal	Colon	Ovarian	Skin	CNS
TCL1A	0	0	0	0	0	0	0	0	0	1
SLC22A2	0	0	0	0	0	0	0	0	0	1
TRPM5	0	0	0	0	0	0	0	0	0	1
KCNQ1	0	0	0	0	0	0	1	1	0	0
IGF2	0	0	0	0	0	0	0	0	1	0
PEG3	0	0	0	0	0	0	0	0	1	0
DLK1	0	0	0	0	0	0	0	0	1	1

PRC2 target identification for colon cancer and all others

A comprehensive analysis by Lee et al. recently mapped the SUZ12 (suppressor of zeste 12) subunit of the Polycomb Repressive Complex 2 (PRC2) in embryonic stem cells and found its binding sites to be preferentially located at a distinct set of developmental genes (Lee, T.I. et al. *Cell* 125, 301-13 (2006)). A second study found that another polycomb group protein, EZH2 (Enhancer of Zeste Homolog2), interacted with PRC2 to recruit DNA methyltransferases and control CpG methylation (Vire, E. et al. *Nature* 439, 871-4 (2006)). Taken together, it is believed that PRC2 target genes are silenced by DNA methylation in cells that maintain pluripotency, and this silencing might facilitate abnormal clonal expansion. A retrospective analysis of DNA methylation data provided further evidence that PRC2 target genes are silenced in human colon cancer (Widschwendter, M. et al. *Nat Genet* 39, 157-8 (2007)).

In addition to SUZ12, PRC2 contains two more core subunits: EED (embryonic ectoderm development) and EZH2. PRC2 has been shown to mediate histone H3K27 methylation. Chromatin immunoprecipitation studies have mapped EED and H3K27 binding in ES cells and found high concordance with SUZ12 (Wang, H. et al. *BMC Genomics* 7, 166 (2006)).

The SUZ12, EED and H3K27 marks were used to determine PRC2 marks in the data set of 531 genomic regions. The target genes are provided in Table 9, the genomic amplicon sequences are provided in Tabel 10, and the CpG site locations are provided in Table 11. PRC2 binding information was found for 440 amplicons, including 79 amplicons with one or more PRC2 marks. The fraction of amplicons that contain one or more PRC2 binding sites was calculated for both the set of genes that did not show significant methylation differences and the set of genes that did show significant methylation differences in cancer cell lines versus normal tissue. The findings show a significant ($p < 0.001$, fisher's exact test) enrichment for PRC2 targets in the set of significantly hypermethylated genes in six out of the nine tumor types. Only the Melanoma specific gene set is not enriched for PRC2 targets, which may be explained by the high level of differentiation of melanomas. All other tumor types are 2 to 6 fold enriched for PRC2 targets (Table 8).

TABLE 8

Tissue	Fraction PRC target in non-significant genes	Fraction PRC target in significant genes	P-value, Fisher's exact test	odds ratio
Blood	0.15	0.33	0.237	3
Breast	0.12	0.67	<0.0001	15
CNS	0.12	0.52	<0.0001	8
Colon	0.12	0.56	<0.0001	9

Lung	0.13	0.73	<0.0001	18
Ovarian	0.15	0.70	<0.0001	13
Prostate	0.18	0.71	0.003	12
Renal	0.12	0.50	<0.0001	7
Skin	0.17	0.44	0.003	4
Normal	0.19	NA	NA	NA

A graphical representation of gene - tumor associations reveals that highly connected genes tend to be PRC2 targets. In contrast, the majority of genes without PRC2-marks are found in only one or two tumor types. These findings strongly suggest a common involvement of PRC2 targets in neoplastic development.

TABLE 9 – TARGET GENE REGIONS

Target Gene Region	Chr	Start	End	Length	CpG-Sites
201_ABL1	chr9	132577525	132577958	433	34
202_ABL2	chr1	177465262	177465849	587	68
203_AF15Q14	chr15	38673556	38673925	369	24
204_AF1Q	chr1	149298304	149298628	324	19
205_AF3p21	chr3	48697853	48698277	424	41
206_AF5q31	chr5	132327102	132327594	492	49
207_AKT2_01	chr19	45482785	45483311	526	57
208_AKT2_02	chr19	45482787	45483311	524	57
209_ALK	chr2	29997217	29997654	437	29
210_ALO17	chr17	75849710	75850074	364	19
211_APC	chr5	112224722	112225026	304	26
212_ARHGEF12	chr11	119712481	119712891	410	49
213_ARHH_01	chr4	39734501	39735101	600	81
214_ARHH_02	chr4	39734502	39735102	600	81
215_ARNT	chr1	149115560	149115763	203	15
216_ASPSCR1	chr17	77529129	77529451	322	32
217_ATF1	chr12	49443878	49444208	330	30
218_ATIC	chr2	215884932	215885516	584	51
226_BCL6	chr3	188944627	188944968	341	18
227_BCL7A	chr12	120840600	120841134	534	40
228_BCL9	chr1	145181137	145181448	311	31
229_BCR_01	chr22	21853331	21853838	507	69
230_BCR_02	chr22	21853333	21853838	505	69
231_BHD	chr17	17080723	17081162	439	27
235_BMPR1A_02	chr10	88506944	88507236	292	22
236_BRAF	chr7	140270275	140270618	343	16
237_BRCA1	chr17	38531626	38532076	450	25
238_BRCA2	chr13	31787393	31787925	532	48
240_BTG1	chr12	91062777	91063262	485	48
241_CBFA2T1_01	chr8	93184596	93185070	474	54
242_CBFA2T1_02	chr8	93184184	93184618	434	55
244_CBFB	chr16	65619930	65620344	414	22
245_CBL	chr7	107171268	107171726	458	34
246_CCND1_01	chr11	69160261	69160818	557	54

247_CCND1_02	chr11	69160263	69160817	554	54
249_CDK4	chr12	56435611	56436146	535	59
262_CTNNB1	chr3	41215651	41216173	522	58
263_CYLD	chr16	49333974	49334203	229	19
264_D10S170_01	chr10	61335497	61335783	286	14
304_FGFR1OP_01	chr6	167331449	167331820	371	39
267_DDIT3	chr16	31098230	31098474	244	13
270_EGFR	chr7	55053588	55053949	361	20
271_EIF4A2	chr3	187984488	187984899	411	37
272_ELKS	chr12	970533	971067	534	66
274_EP300	chr22	39817467	39817757	290	22
275_EPS15_01	chr1	51757105	51757518	413	47
277_ERBB2_01	chr17	35110079	35110362	283	23
278_ERBB2_02	chr17	35110081	35110361	280	23
279_ERCC2	chr19	50565436	50565898	462	41
280_ERCC3	chr2	127767790	127768382	592	51
281_ERCC4	chr16	13921687	13921995	308	20
282_ERCC5	chr13	102296508	102296807	299	19
285_ETV4_01	chr17	38978023	38978479	456	36
286_ETV4_02	chr17	38978021	38978479	458	36
288_EVI1	chr3	170346825	170347202	377	31
289_EWSR1	chr22	27994181	27994700	519	58
291_EXT2	chr11	44073738	44074158	420	54
292_FACL6	chr5	131374976	131375381	405	46
293_FANCA	chr16	88410663	88411053	390	46
294_FANCC_01	chr9	97119241	97119819	578	61
295_FANCC_02	chr9	97119240	97119819	579	61
296_FANCD2	chr3	10042822	10043297	475	41
297_FANCE	chr6	35527814	35528258	444	42
298_FANCF_01	chr11	22603534	22603929	395	34
299_FANCF_02	chr11	22603322	22603606	284	19
302_FEV	chr2	219557998	219558487	489	55
305_FGFR1OP_02	chr6	167331449	167331821	372	39
306_FGFR2	chr10	123347301	123347592	291	33
308_FH	chr1	239748987	239749478	491	47
309_FIP1L1	chr4	53938235	53938640	405	30
310_FLI1_01	chr11	128067717	128068237	520	31
311_FLI1_02	chr11	128070143	128070375	232	19

312_FLT3	chr13	27572720	27573293	573	45
313_FLT4	chr5	180009095	180009474	379	53
316_FOXO1A_02	chr13	40139039	40139631	592	56
317_FOXO1A_03	chr13	40136475	40136743	268	20
319_FOXO3A_02	chr6	108988061	108988515	454	38
321_FUS	chr16	31098697	31099112	415	39
324_GMPS	chr3	157071533	157072104	571	60
325_GNAS_01	chr20	56897562	56898110	548	56
326_GNAS_02	chr20	56898967	56899284	317	33
327_GOLGA5	chr14	92330376	92330722	346	28
328_GPC3	chrX	132947001	132947234	233	21
329_GPHN_01	chr14	66045075	66045469	394	32
330_GPHN_02	chr14	66044621	66045096	475	52
331_GPHN_03	chr14	66044061	66044371	310	23
332_GRAF	chr5	142130593	142130977	384	37
335_HIP1	chr7	75205858	75206444	586	55
336_HIST1H4I	chr6	27215048	27215399	351	32
337_HLF	chr17	50697142	50697471	329	45
338_HMGA_01	chr12	64505847	64506048	201	17
266_DDB2	chr11	47193104	47193534	430	24
364_LCK	chr1	32513746	32514155	409	40
367_LCX_02	chr10	69990108	69990465	357	32
369_LHFP_02	chr13	39074776	39075192	416	35
373_LYL_01	chr19	13074283	13074715	432	30
375_MADH4	chr18	46810401	46810721	320	33
381_MECT1	chr19	18655112	18655621	509	63
382_MEN1_01	chr11	64334283	64334680	397	27
385_MHC2TA_01	chr16	10880484	10880911	427	28
390_MLL_02	chr11	117811321	117811673	352	22
392_MLLT10	chr10	21862747	21863293	546	60
393_MLLT2	chr4	88147105	88147579	474	54
394_MLLT3	chr9	20610652	20611134	482	37
395_MLLT4	chr6	167971238	167971475	237	18
396_MLLT6_01	chr17	34113070	34113580	510	32
398_MLLT6_03	chr17	34114090	34114402	312	15
399_MLLT7	chrX	70232993	70233375	382	25
401_MSF	chr17	72789206	72789610	404	33
402_MSH2	chr2	47483700	47484020	320	34

403_MSH6_01	chr2	47863130	47863577	447	37
405_MSN	chrX	64804313	64804586	273	18
406_MUTYH	chr1	45578118	45578622	504	57
408_MYCL1	chr1	40140552	40140860	308	25
409_MYCN_01	chr2	15999936	16000536	600	74
410_MYCN_02	chr2	15998311	15998682	371	23
413_MYST4_01	chr10	76256270	76256743	473	43
414_MYST4_02	chr10	76255917	76256358	441	23
417_NCOA2_01	chr8	71478600	71479056	456	28
418_NCOA2_02	chr8	71479039	71479412	373	26
420_NF1	chr17	26445739	26446339	600	45
424_NPM1	chr5	170747765	170748284	519	43
425_NR4A3	chr9	101624591	101625034	443	26
429_NTRK_02	chr1	155095323	155095679	356	24
430_NTRK3	chr15	86600898	86601498	600	59
431_NUMA1	chr11	71469069	71469354	285	27
432_NUP214	chr9	132990566	132991025	459	42
433_NUP98_01	chr11	3774899	3775243	344	28
434_NUP98_02	chr11	3775642	3775908	266	20
436_OLIG2	chr21	33317392	33317712	320	22
438_PAX6_01	chr9	37027794	37028366	572	45
440_PAX6_03	chr9	37024512	37024773	261	21
443_PAX8_01	chr2	113751340	113751782	442	39
444_PAX8_02	chr2	113751758	113752141	383	31
445_PAX8_03	chr2	113751013	113751358	345	21
447_PCM1	chr8	17824948	17825351	403	33
448_PDE4DIP	chr1	143751199	143751586	387	32
449_PDGFB	chr22	37970352	37970936	584	63
450_PDGFRA	chr4	54789115	54789455	340	23
455_PIM1_01	chr6	37246325	37246801	476	47
456_PIM1_02	chr6	37246775	37247064	289	18
458_PMS1_01	chr2	190356952	190357548	596	66
459_PMS1_02	chr2	190357523	190357814	291	25
460_PMS2	chr7	6014874	6015442	568	43
461_PMX1	chr1	168900324	168900826	502	36
464_PPARG	chr3	12304698	12305108	410	53
465_PRCC_01	chr1	155004541	155004781	240	13
467_PRKAR1A	chr17	64019428	64019890	462	41

468_PRO1073	chr11	65021396	65021824	428	42
470_PTCH_01	chr9	97308581	97308982	401	39
471_PTCH_02	chr9	97308959	97309439	480	24
472_PTCH_03	chr9	97309851	97310140	289	12
474_PTEN_02	chr10	89613072	89613626	554	65
475_PTPN11	chr12	111341140	111341705	565	60
477_RAD51L1	chr14	67211132	67211662	530	64
480_RARA	chr17	35751090	35751589	499	47
482_RECQL4	chr8	145713246	145713583	337	23
489_SDHB	chr1	17252913	17253355	442	33
490_SDHC_01	chr1	159550943	159551171	228	15
491_SDHC_02	chr1	159550688	159550946	258	16
492_SDHD	chr11	111462512	111462918	406	30
498_SMO	chr7	128616273	128616798	525	47
499_SS18	chr18	21924328	21924906	578	51
501_SSH3BP1	chr10	27189110	27189610	500	40
505_STK11_01	chr19	1157536	1157912	376	27
506_STK11_02	chr19	1157893	1158270	377	24
507_STL_01	chr1	112963027	112963505	478	30
508_STL_02	chr1	112963759	112964145	386	33
509_SUFU	chr10	104253634	104254215	581	58
510_TAF15	chr1	28842061	28842518	457	39
511_TAL1	chr1	47463678	47464167	489	66
513_TCF1	chr12	119900742	119901144	402	21
514_TCF12_01	chr15	54998178	54998751	573	69
515_TCF12_02	chr15	54997492	54997723	231	20
516_TCF3_01	chr19	1597499	1597737	238	14
518_TCL1A_01	chr14	95249899	95250387	488	33
519_TCL1A_02	chr14	95250513	95250722	209	9
520_TEC	chr4	47966387	47966780	393	42
521_TFE3	chrX	48787429	48787872	443	40
566_AL080059_1_01	chr8	98359116	98359534	418	57
567_AL080059_2_01	chr8	98358787	98359140	353	35
568_AL137718_01	chr13	59635924	59636310	386	29
569_ANXA2_01	chr15	58477484	58477917	433	32
570_APOD_01	chr3	196827214	196827678	464	36
571_ATP5A1_1_01	chr18	41938228	41938674	446	33
573_ATP6V0E_01	chr5	172343262	172343800	538	45

574_Beta-NAP_01	chr15	81175787	81176040	253	19
576_BIRC5_01	chr17	73721633	73722084	451	42
577_C2_1_01	chr6	31977367	31977872	505	57
579_CA3_01	chr8	86537987	86538472	485	33
580_CA4_01	chr17	55582147	55582640	493	50
581_CCNA2_01	chr4	122964129	122964654	525	50
582_CCNB1_01	chr5	68498405	68499005	600	44
583_CCNC_01	chr6	100122997	100123403	406	34
584_CCND1_1_01	chr11	69160261	69160817	556	54
585_CCND1_2_01	chr11	69162041	69162617	576	56
586_CCND1_3_01	chr11	69164429	69164933	504	34
587_CCNH_1_01	chr5	86743924	86744401	477	28
588_CCNH_2_01	chr5	86744377	86744807	430	35
590_CD34_01	chr1	206150852	206151248	396	33
591_CD38_01	chr4	15389339	15389561	222	22
592_CD44_01	chr11	35117193	35117609	416	34
593_CD59_01	chr11	33713926	33714365	439	36
594_CDC34_01	chr19	482976	483323	347	31
595_CHGA_01	chr14	92458933	92459492	559	53
597_CKS2_2_01	chr9	91115463	91115793	330	28
598_CKS2_3_01	chr9	91115773	91116340	567	62
599_COL5A1_01	chr9	136673725	136674245	520	68
600_COL5A3_01	chr19	9981936	9982276	340	36
601_COL6A2_01	chr21	46356772	46357061	289	24
602_COX6B1_1_01	chr19	40825966	40826291	325	31
603_COX6B1_2_01	chr19	40825956	40826257	301	28
604_COX7A2L_01	chr2	42441636	42441989	353	27
605_CR2_01	chr1	205694281	205694660	379	34
608_DBI_1_01	chr2	119840575	119840964	389	31
610_DC13_1_01	chr16	79597712	79598092	380	41
611_DC13_2_01	chr16	79598348	79598723	375	32
612_DSTN_01	chr20	17498585	17499165	580	68
614_ECT2_2_01	chr3	173951176	173951692	516	33
623_FLT1_3_01	chr13	27966522	27966938	416	35
624_FOXK2_01	chr17	78070361	78070585	224	29
625_G3PD_01	chr12	6513830	6514401	571	57
626_GDI2_01	chr10	5895432	5896023	591	66
627_GLI_01	chr12	56139875	56140298	423	29

628_GNAZ_01	chr22	21742354	21742845	491	86
629_GNB2L1_01	chr5	180602827	180603383	556	37
630_HAL_01	chr12	94913485	94913865	380	24
631_hB23_1_01	chr5	170747765	170748284	519	43
632_hB23_2_01	chr5	170747765	170748284	519	43
633_HDAC3_01	chr5	140996361	140996781	420	36
636_HSPA8_1_01	chr11	122438457	122438798	341	25
637_HSPA8_2_01	chr11	122438090	122438482	392	36
638_ICAM1_01	chr19	10241875	10242277	402	35
639_IFITM1_01	chr11	300575	300909	334	19
641_IL10RA_01	chr11	117361721	117362144	423	29
644_KCNMB1_01	chr5	169748654	169748935	281	8
646_KIAA0683_01	chr16	1483654	1483960	306	30
649_KSRP_1_01	chr19	6376068	6376343	275	13
650_KSRP_2_01	chr19	6376069	6376343	274	13
651_LDH-A_01	chr11	18372332	18372825	493	41
652_LEP_01	chr7	127668076	127668670	594	59
653_LIAS_01	chr4	39136456	39136817	361	22
654_LLPL_01	chr16	66836600	66836896	296	28
655_LRP2_01	chr2	169926720	169927082	362	34
657_MKI67_01	chr10	129813761	129814000	239	14
658_mpp5_01	chr10	57790897	57791267	370	30
659_MRPL3_01	chr3	132704180	132704683	503	39
660_MYBL2_1_01	chr20	41729003	41729471	468	57
661_MYBL2_2_01	chr20	41729004	41729471	467	57
662_NDUFA6_01	chr22	40816187	40816786	599	49
663_NEDD5_1_01	chr2	241903199	241903499	300	38
664_NEDD5_2_01	chr2	241903907	241904446	539	65
665_Nm23_01	chr17	46585758	46586275	517	40
666_NMU_01	chr4	56196612	56197197	585	49
667_N-MYC_1_01	chr14	20563331	20563858	527	38
668_N-MYC_2_01	chr14	20562467	20562884	417	29
669_Notch4_01	chr6	32271333	32271746	413	41
670_NPD017_01	chrX	102727169	102727608	439	24
671_OXCT_01	chr5	41906021	41906603	582	50
672_PAK-3_01	chrX	110225987	110226378	391	30
673_PECAM1_01	chr17	59817588	59817941	353	14
674_PIK3CG_01	chr7	106295442	106295890	448	36

675_PLOD_01	chr1	11917237	11917716	479	40
676_PRDM1_01	chr6	106640781	106641136	355	32
677_PSMB6_01	chr17	4646233	4646687	454	23
678_PSME2_01	chr14	23686078	23686449	371	19
680_PTPRN2_2_01	chr7	158073675	158074048	373	34
681_RAD51_1_01	chr15	38774114	38774530	416	33
682_RAD51_2_01	chr15	38774749	38775137	388	37
683_rhoC_01	chr1	113051149	113051563	414	41
001_SEPT6_001	chrX	118710422	118710923	501	51
002_ATM_001	chr11	107598808	107599243	435	38
003_BCL11A_001	chr2	60634369	60634750	381	32
004_BCL11B_001	chr14	98808281	98808691	410	25
007_BCL5_001	chr3	188937964	188938293	329	19
009_BUB1B_001	chr15	38240272	38240679	407	31
010_CARS_001	chr11	3035200	3035521	321	31
011_CBFA2T3_001	chr16	87534056	87534546	490	36
012_CCND2_001	chr12	4253140	4253668	528	30
013_CCND2_002	chr12	4253833	4254352	519	35
014_CCND3_001	chr6	42016614	42017089	475	34
015_CDH1_001	chr16	67328704	67329209	505	50
017_CDK6_001	chr7	92300956	92301485	529	42
018_CHEK2_001	chr22	27467870	27468262	392	27
020_CLTC_001	chr17	55051668	55052177	509	45
021_CLTCL1_001	chr22	17659116	17659652	536	56
022_CMKOR1_001	chr2	237141716	237142026	310	21
023_COL1A1_001	chr17	45633408	45633912	504	36
024_COPEB_001	chr10	3816825	3817186	361	39
025_COX6C_001	chr8	100974721	100974933	212	19
026_CREBBP_001	chr16	3870965	3871413	448	46
027_DDX10_001	chr11	108040712	108041221	509	38
028_DDX6_001	chr11	118166720	118167251	531	60
030_ELL_001	chr19	18494063	18494512	449	32
031_ERG_001	chr21	38955346	38955681	335	20
032_ETV1_001	chr7	13995856	13996164	308	19
034_FBXW7_001	chr4	153675457	153675857	400	27
035_FGFR3_001	chr4	1765563	1766100	537	52
037_FSTL3_001	chr19	626625	626920	295	18
038_FVT1_001	chr18	59184906	59185126	220	21

039_GAS7_001	chr17	10042696	10043211	515	61
040_GOPC_001	chr6	118030207	118030715	508	40
041_HCMOGT-1_001	chr17	19999746	20000273	527	56
042_HEAB_001	chr11	57181484	57181963	479	38
043_HLXB9_001	chr7	156496339	156496819	480	41
045_HMGA2_001	chr12	64504118	64504535	417	32
047_HOXC13_001	chr12	52619125	52619630	505	52
049_HOXD13_001	chr2	176665504	176665745	241	22
050_HRAS_001	chr11	526559	527157	598	61
051_HRAS_002	chr11	524576	524948	372	28
052_HRPT2_001	chr1	191357448	191357799	351	45
053_HSPCA_001	chr14	101675929	101676415	486	36
054_HSPCB_001	chr6	44322980	44323329	349	25
055_IRF4_001	chr6	336391	336863	472	48
056_JAK2_001	chr9	4974748	4975284	536	56
058_KIT_001	chr4	55218601	55219070	469	54
059_KTN1_001	chr14	55116307	55116841	534	71
060_LAF4_001	chr2	100086961	100087361	400	37
061_LASP1_001	chr17	34279611	34280158	547	58
062_LMO2_001	chr11	33847058	33847485	427	37
063_LMO2_002	chr11	33847812	33848240	428	42
064_LPP_001	chr3	189354495	189354939	444	49
065_LYL1_001	chr19	13074402	13074932	530	44
067_MAFB_001	chr20	38750860	38751343	483	59
068_MAP2K4_001	chr17	11864591	11865051	460	49
069_MAP2K4_002	chr17	11865434	11865718	284	22
070_MDS1_001	chr3	170862884	170863415	531	54
071_MET_001	chr7	116099294	116099611	317	40
072_MKL1_001	chr22	39362391	39363197	806	76
073_MLF1_001	chr3	159771428	159771821	393	32
074_MLH1_001	chr3	37009285	37009728	443	39
076_MSI2_001	chr17	52688381	52688824	443	48
077_MTCP1_001	chrX	153952418	153952966	548	70
078_MUC1_001	chr1	153429956	153430351	395	23
079_MYH11_001	chr16	15858290	15858793	503	44
080_MYH9_001	chr22	35113893	35114426	533	43
081_NBS1_001	chr8	91065688	91066174	486	54
082_NCOA4_001	chr10	51242282	51242680	398	35

083_NF2_001	chr22	28329371	28329908	537	63
085_NFKB2_002	chr10	104144801	104145274	473	23
086_NFKB2_003	chr10	104145185	104145668	483	30
087_NFKB2_004	chr10	104144093	104144445	352	29
088_NFKB2_005	chr10	104144383	104144828	445	33
089_NIN_001	chr14	50368041	50368421	380	15
090_NONO_001	chrX	70420123	70420434	311	24
091_NOTCH1_001	chr9	138560542	138560790	248	23
092_NTRK1_001	chr1	155097132	155097659	527	46
093_PAFAH1B2_001	chr11	116519863	116520360	497	43
094_PAX3_001	chr2	222871383	222871886	503	38
095_PAX5_001	chr9	37024038	37024514	476	36
096_PAX7_001	chr1	18829422	18829659	237	15
097_PAX7_002	chr1	18830507	18830936	429	38
098_PBX1_001	chr1	162812066	162812615	549	51
100_PER1_001	chr17	7996232	7996656	424	31
101_PHOX2B_001	chr4	41444001	41444391	390	30
103_PICALM_002	chr11	85457381	85457760	379	29
104_PIK3CA_001	chr3	180349337	180349623	286	30
105_PLAG1_001	chr8	57286077	57286414	337	26
106_PML_001	chr15	72077492	72077906	414	27
107_PRDM16_001	chr1	2975298	2975662	364	29
108_PSIP2_001	chr9	15500616	15501143	527	64
109_RANBP17_001	chr5	170221621	170222169	548	61
110_RAP1GDS1_001	chr4	99401375	99401820	445	56
111_RB1_001	chr13	47775605	47776155	550	70
112_RBM15_001	chr1	110682735	110683276	541	35
113_REL_001	chr2	60961862	60962359	497	56
114_RET_001	chr10	42891820	42892158	338	20
115_RPN1_001	chr3	129851885	129852431	546	52
116_RUNX1_001	chr21	35184917	35185243	326	24
117_SBDS_001	chr7	66097520	66098025	505	46
118_SET_001	chr9	130490719	130490890	171	8
119_SFPQ_001	chr1	35430695	35431047	352	35
120_SFRS3_001	chr6	36669855	36670055	200	22
121_SIL_001	chr1	47552254	47552599	345	33
122_SS18L1_001	chr20	60151349	60151613	264	37
123_SS18L1_002	chr20	60152674	60153181	507	55

124_SUZ12_001	chr17	27287847	27288203	356	43
125_SYK_001	chr9	92603461	92603893	432	37
126_TCEA1_001	chr8	55097189	55097737	548	59
127_TFEB_001	chr6	41810490	41811016	526	54
128_TFG_001	chr3	101910877	101911384	507	56
129_TFPT_001	chr19	59310656	59311052	396	31
130_TFRC_001	chr3	197293205	197293682	477	47
131_THRAP3_001	chr1	36462320	36462698	378	39
133_TLX1_001	chr10	102881084	102881395	311	22
134_TLX3_001	chr5	170669340	170669753	413	38
135_TMPRSS2_001	chr21	41802132	41802569	437	30
136_TNFRSF6_001	chr17	71448337	71448803	466	42
137_TOP1_001	chr20	39090892	39091362	470	57
138_TP53_001	chr17	7532164	7532609	445	36
139_TPM3_001	chr1	152422158	152422410	252	19
140_TPM4_001	chr19	16048692	16049124	432	42
141_TPR_001	chr1	184610787	184611141	354	35
142_TRIM33_001	chr1	114855575	114855910	335	24
143_TRIP11_001	chr14	91576058	91576347	289	29
144_TSC1_001	chr9	134809948	134810385	437	39
145_TSC2_001	chr16	2037916	2038277	361	43
146_TSHR_001	chr14	80490972	80491378	406	27
148_WHSC1L1_001	chr8	38359472	38360010	538	54
149_WT1_001	chr11	32413036	32413392	356	47
150_WT1_002	chr11	32412703	32413062	359	28
152_ZNF198_001	chr13	19429932	19430275	343	24
153_ZNF278_001	chr22	30072715	30073093	378	30
154_ZNF331_001	chr19	58715785	58716233	448	24
155_ZNF384_001	chr12	6668855	6669283	428	27
156_ZNF9_001	chr3	130385378	130385695	317	41
003_IGF2R_003	chr6	160431853	160432481	628	45
005_SLC22A2_001	chr6	160599289	160599657	368	22
006_SLC22A3_001	chr6	160688805	160689077	272	20
009_SGCE_001	chr7	94123033	94123358	325	22
011_PON1_001	chr7	94791654	94792056	402	20
013_PON2_001	chr7	94901962	94902368	406	41
018_MESTIT1_001	chr7	129918328	129918858	530	34
019_COPG2_001	chr7	130004373	130004597	224	14

023_SYTB_001	chr11	1803689	1803982	293	18
025_LSP1_002	chr11	1859610	1859939	329	19
026_TNNT3_001	chr11	1904057	1904357	300	20
027_TNNT3_002	chr11	1905454	1905833	379	22
028_TNNT3_003	chr11	1906788	1906996	208	10
030_MRPL23_001	chr11	1925380	1925658	278	25
031_MRPL23_002	chr11	1930709	1931081	372	17
032_MRPL23_003	chr11	1934031	1934272	241	17
034_MRPL23_005	chr11	1939642	1939882	240	12
035_MRPL23_006	chr11	1942563	1942961	398	27
036_MRPL23_007	chr11	1947611	1947817	206	13
040_H19_004	chr11	1983261	1983752	491	38
042_IGF2_001	chr11	2110661	2111061	400	24
044_IGF2_003	chr11	2121965	2122388	423	38
047_ASCL2_001	chr11	2247867	2248329	462	59
051_BC050616_001	chr11	2377913	2378292	379	33
052_TRPM5_001	chr11	2391916	2392414	498	32
053_TRPM5_002	chr11	2398577	2399002	425	30
054_KCNQ1_001	chr11	2421953	2422332	379	25
055_KCNQ1_002	chr11	2423321	2423593	272	13
056_KCNQ1_003	chr11	2510596	2510967	371	19
057_KCNQ1_004	chr11	2511955	2512234	279	16
058_KCNQ1_005	chr11	2550439	2550859	420	24
059_KCNQ1_006	chr11	2552907	2553207	300	22
060_KCNQ1_007	chr11	2559808	2560120	312	18
061_KCNQ1_008	chr11	2677736	2678041	305	27
063_KCNQ1_010	chr11	2774363	2774757	394	22
068_CDKN1C_001	chr11	2861490	2861724	234	15
070_SLC22A18_001	chr11	2880014	2880448	434	28
071_SLC22A18_002	chr11	2886839	2887277	438	39
074_NAP1L4_001	chr11	2922455	2922829	374	20
076_CARS_001	chr11	3034784	3035181	397	31
077_OSBPL5_001	chr11	3071292	3071628	336	21
080_OSBPL5_004	chr11	3142680	3143112	432	59
084_OSBPL5_008	chr11	3210650	3211020	370	17
085_ZNF195_001	chr11	3391545	3391986	441	21
086_ZNF195_002	chr11	3401174	3401406	232	20
088_DLK1_002	chr14	100245239	100245459	220	12

091_DLK1_005	chr14	100271281	100271557	276	15
092_MEG3_001	chr14	100360100	100360493	393	25
093_MEG3_002	chr14	100362061	100362394	333	19
094_MEG3_003	chr14	100362585	100362810	225	13
095_MEG3_004	chr14	100363911	100364143	232	16
097_MEG3_001	chr14	100419237	100419637	400	28
101_NDN_004	chr15	22057019	22057428	409	23
102_NDN_005	chr15	22223252	22223670	418	29
105_SNRPN_003	chr15	22569356	22569698	342	28
107_SNRPN_005	chr15	22674608	22674881	273	23
109_UBE3A_001	chr15	23234955	23235465	510	73
110_UBE3A_002	chr15	23392822	23393324	502	29
111_ATP10A_001	chr15	23509898	23510365	467	29
112_ATP10A_002	chr15	23532141	23532509	368	20
113_ATP10A_003	chr15	23658607	23659121	514	43
114_ATP10A_004	chr15	23785703	23786045	342	23
115_ATP10A_005	chr15	23878503	23878788	285	16
116_GABRB3_001	chr15	24425349	24425703	354	26
117_GABRB3_002	chr15	24466474	24466763	289	18
118_GABRB3_003	chr15	24568107	24568366	259	13
119_ZIM2_001	chr19	61968659	61968953	294	13
120_ZIM2_002	chr19	61998579	61998953	374	30
121_ZIM2_003	chr19	62041908	62042346	438	27
123_ZIM2_005	chr19	62043954	62044200	246	9
124_ZIM2_006	chr19	62067585	62067965	380	30
125_USP29_001	chr19	62302435	62302863	428	31
127_USP29_003	chr19	62322196	62322469	273	27
128_ZIM3_001	chr19	62375472	62375840	368	24
129_ZNF264_001	chr19	62394699	62395208	509	49
131_AURKC_002	chr19	62443713	62443972	259	24
132_ZNF272_001	chr19	62483493	62483962	469	44
133_RAI17_001	chr10	80591728	80592105	377	12
134_FRAT1_001	chr10	99070069	99070493	424	23
135_ZNF215_001	chr11	6904285	6904809	524	43
136_WT1_001	chr11	32411966	32412340	374	19
137_SDHD_001	chr11	111462512	111462918	406	30
138_SLC38A4_001	chr12	45511305	45511701	396	29
139_HTR2A_001	chr13	46367732	46368191	459	9

140_CR601144_001	chr14	20528074	20528492	418	23
141_DI03_001	chr14	101095604	101096110	506	49
144_IMPACT_001	chr18	20260282	20260730	448	41
145_TCEB3C_001	chr18	42809465	42809852	387	28
146_NNAT_001	chr20	35581984	35582269	285	24
147_GNAS_001	chr20	56848822	56849135	313	30
148_TPD52L2_001	chr20	61966654	61966989	335	22
149_F2R_001	chr5	76047137	76047535	398	28
150_U2AF1RS1_001	chr5	112255229	112255506	277	6
HOXA1_AB01	chr7	27101762	27102043	281	18
HOXA1_SQ05	chr7	27109677	27110061	384	24
HOXA3_AB01	chr7	27116719	27117005	286	26
HOXA3_SQ01	chr7	27116526	27117002	476	45
HOXA4_AB01	chr7	27136693	27136896	203	17
HOXA4_SQ02	chr7	27136272	27136715	443	55
HOXA5_AB01	chr7	27149932	27150276	344	30
HOXA5_SQ03	chr7	27149843	27150375	532	39
HOXA6_AB01	chr7	27153596	27153836	240	18
HOXA7_AB01	chr7	27162508	27162921	413	31
HOXA7_SQ03	chr7	27162898	27163116	218	23
HOXA9_AB01	chr7	27171578	27171938	360	26
HOXA9_SQ03	chr7	27171098	27171594	496	48
HOXA10_AB01	chr7	27180431	27180694	263	23
HOXA10_SQ02	chr7	27180440	27180963	523	40
HOXA11_SQ01	chr7	27191540	27192000	460	28
HOXA13_SQ01	chr7	27205189	27205499	310	20
HOXA13_SQ03	chr7	27205751	27206281	530	72
005_ERalpha_02	chr6	152170751	152171138	387	34
ESR1_01_01	chr6	152170469	152170794	325	27
MYOD_01_02	chr11	17697769	17698203	434	47
002_E-cad_02	chr16	67329401	67329750	349	24
RASSF1	chr3	50352936	50353401	465	52
p53_03	chr17	7532346	7532539	193	20
007_RAR-beta_01	chr3	25444793	25445114	321	15
LINE-1	chr1	60878073	60879493	1420	41
ALU-M1	chr1	151803096	151804508	1412	23
ALU-cons	chr1	159390719	159391402	683	26
SATalpha	chr1	121151051	121151958	907	22

GSTP1-300+100_01	chr11	67107561	67107961	400	47
14_RUNX3_01_01	chr1	25130851	25131313	462	36
15_RUNX3_02_01	chr1	25129323	25129742	419	37

TABLE 10 – TARGET GENE SEQUENCES & PRIMERS

Target Gene Region	Left Primer	Right Primer	Genomic Amplicon Sequence
201_ABL1	24	26	GGCCTCCCAAAGTGCTGGGATTACCGGCGTGAGCCACCGCGCCCGGCCCGCTAGTTCTAATATTTATGCTTTTTGG AGGGTGAAGGGCTTGAAAGGCATCAAAAACCTTGGTTTCTAGGAGCGAGCCAAATTTTCTCCCTTAGAGACTGAAG GAGGTTATCCGACTCCGCTTCCAGGAAAATCCAATCCGCAATTTTTCCCTCGCTTTGGCTCTTCCAGGTCTCACTA CTCGCGCCGGGGAGACGCGGTCCGGCCTACGCTAGGCCGGCAAGAATCTACCAGGTCCCAGGAGGGCGGGGCCGAG CCCCAGAAGTCGGGGCCCGGGCCAGGAGTCTTGGTGCAGGCGGACTCGGGCGCGTGCCATGGGACCACAACTCCCG GCACGCACCGCGGACTGCGCCGAACACGGTTGGCTGGGAGATCCAACCCTACT
202_ABL2	25	27	CCCTGGCCCTGAGTGGCTGGGCCACCGGCGGCTCCGCACCCGGCCTCCTCACGGCAGCCGCCGCGCTGCCTCCAGG CGACTCACAGATTCTGCTTTTCCCTCCTCCTGTCGCGGCTCCGCGCCCCCAACGCCGCCGCCGCCGCCGCCGCCAC CGCCGCCGCCATCTTTAAACCACCGAGCGCTGGGAAAGCGTGGGACAGAGCGTCTCCCGCCCCCCGCCCCCCGCCC CCCGCCCGCCAGTCACCTCCGCCGCGGGGAAGGAGGGCTTCCCGGCTGCCGCCCCGCCCTGCCGCGCCGCGCCCCC CGTCCCCGCCCCCGCCTCCTCGCAGGGTGGGTCCCCCAGTGCCCACCTCATTTGCCGGCCACCGCTGCTTGAGGTC TTTCGTCCTCCGCGTCCTGTCGCCGCACCTCGGCGTCCCCCCCCTCAATCCGCCTCAGCCGACCCCCTCCCGCGTT CGGCTCCACACGCTACCGCCTTTGGGGTTGGTCGGTCTCCGGCCTTCCCCATCCCACCTCCACCTGTCAAATGAGT GAGTCGAGGGCTCAGTGCCACCGCGTGCGCAGCTCAGGTGCAGGCACAGGTGGGG
203_AF15Q14	24	23	CCACTGGGGAGGGGCAGAGGAAATTCGGTCGAAAAAGAGATAAAGCTGAAGGAAATAAAATTGGCACGGAGTCTGG GAAAGTAGTTTCCCTAAAGGAGTCTTAGAAATAGGGTTGGTCTGGAACCTAAGGGGCGGAGCCGACGCGTAGAGCC GCTTTGCGCGTGCGCATCACCTAGGCGGTTAGATTTGAATACTTCACTGAGGCGAGCCGGGCGTTGTGAGCGGACT GCTAGAGGCGGCTGTCTGTTTCCGCTCTAAGGAAACTCAGAGCGTGTGGACCCCAAACAAGTCTGCGCAAAATTTG TCGAGGAGGTTTGCCGCGGCAGGTAAAGAGAATGACTCTTTCGTTCTGGGCTTCAGGGAAGGCTT
204_AF1Q	25	25	GACTGGGACCTCTCTGGGAATCTTTCGGACCCTCTCCCTCCCACCTCCCCCAACATTCCAGTTCCTTCTTTTCCTT CTACTCTTCAGCGGCCTCAGCCTGCGCACCCCAGGAGCGTGGATGACTACGGCCACCCCGGGCGCGCACCCCTTTC CCACCACCCCAGCATCTCTGCAGCCCAGGACACCCGCCTCCCCCACACCCCGCATCCGGTGTGTCTCCGCCTGGCC CGGCCGGCGCGGCAGGCGGGCCAGGGGACCAACTGCACGGCCTCACCTGCTCTTCTCCACCATCCAGACGTTCAGC TACAGCTGGTGGGGGTGAGG
205_AF3p21	25	25	TGGTCTGTCAAGGGCCTGGTCTTTTGTGGGTGATGCTGACACTTGGGGTCTCAGTCCCCGTGGGTCCGGGGGTCTC AGGGTCAGGTTCTCAAACTCCCTGTCTGATAGAGGTCCTGGCCTCGGGTCCCGGAGAGGGTGGGGTCCCTGGGTCG GTTCCGCGGGGCTGTGAAGGGGTCCTGCCCCAGGGGCGCGGAGGCCGGGCGGGAAGGGGCGCACTCACCTGCAGGC GGCGCAGGTAGGCTGGCGGCACGTAGCCCGTCTCACCACTGCGCGCCCGCGCGGCCAGCCACCAGTGCGCGCTGCT TCGCTCTAGCACCAGGAAGGTCTCGCCCGCGGCGAACGCCAGCGCGTTGGGCTCCGCCGAGCGGAACGCGTACAGC GCGCGGTACATGAGGCCGGGCAGGGCAGGTGCAGGGAAGGTGGC
206_AF5q31	22	25	GGGCTGGGACAGCTGACTGAGGCGGCGGGGGCGGGTTAACGAAGACCTGGCACCAGGATCCCCGCCCCGTCCGCTG GCGGCGGCGACGGCAGCTGGACTCCTGCAGCCAGGGCTGTGACTGACGCAGCGGCCGTGCCACCATGTGACCAAGA CCGGGCGGGTGCGGGGCGTCACGTGATGCCTCTGCGCCCCTCCCCGCTGGGGGAGTAGGGGGCGGGGGTCTGTGGG CCGGCTGGGCCGGGAGGCGACGCCCGGGGTGGTGACGTTCCCGGCTGTGGGGTCTGATGACCCGGGCCAGGCAAAG GACCCGCCCGAGCGGTATAGGCCTGAGCCTCTGGGCACTGCGGCCGCGTCCGGCAGGGCTGCCACGGCAGTACAGG GCCTGCACATCCGGGAGCTCACGCCCTCCTGCGCGTAGCCCGCTAGTGAGGTTCCGAAGGGCGGGGCCGGGCCGAA

			CCGGATATGCCGGTTCTGGGGCTCAGGTGACAAACC
207_AKT2_01	26	26	CCCACTCAGCTCCTGAAGGAGGGGCTCGAGGGCCGCGGTCCCCCCGCCGGGCACGGGTGGTACAGCCCATCGCGGC
			ACCGCGGGGGGCCCGGACGCGACCATCGTGGGGGGGGCGTTCGGGGACACGCGCTGGCGCACTCACCTGTCACCGG
			CAGCCGCCCAGCCTCTCCGGCGGGGCTCTACCCCCGCCCATCGCCACGCTGCGCTGGTTCCCTTTCCTTGTGTTTC
			CCGGCAGCGGCAACGGCGCCGGCAGCGGCGGCGACGCCTCCTCCGAGGCAGGCCCAACGGCTAGCAC
			GGCGCGGCCCCCCCCGCCCCCTCCCCCCAGCCCCCGCTTACCGCCCCCCTCCCACCCTCTGGACGGAAATACCGCCC
			TCTCGCGCCACAAACAGGAAGTGACGTACAAAGAGCCAGAGACGAACTCTGAGAGAGCGAGAGCGCAAGAGCAGGG
			CAGAGAAGGAGGCGGGCTCACAGCAGGGCGCCTGCGCACATTAGACAACTTTGGGCCTGTGTGGGTTAGA
208_AKT2_02	24	26	CACTCAGCTCCTGAAGGAGGGGCTCGAGGGCCGCGGTCCCCCCGCCGGGCACGGGTGGTACAGCCCATCGCGGCAC
			CGCGGGGGGCCCGGACGCGACCATCGTGGGGGGGGCGTTCGGGGACACGCGCTGGCGCACTCACCTGTCACCGGCA
			GCCGCCCAGCCTCTCCGGCGGGGCTCTACCCCCGCCCATCGCCACGCTGCGCTGGTTCCCTTTCCTTGTGTTTCCC
			GGCAGCGGCAACGGCGCCGGCAGCGGCGGCGACGCCTCCTCCGAGGCAGGCCCAACGGCTAGCACGG
			CGCGGCCCCCCCCGCCCCCTCCCCCCAGCCCCCGCTTACCGCCCCCCTCCCACCCTCTGGACGGAAATACCGCCCTC
			TCGCGCCACAAACAGGAAGTGACGTACAAAGAGCCAGAGACGAACTCTGAGAGAGCGAGAGCGCAAGAGCAGGGCA
			GAGAAGGAGGCGGGCTCACAGCAGGGCGCCTGCGCACATTAGACAACTTTGGGCCTGTGTGGGTTAGA
209_ALK	25	26	TGAAACAGACCTGGAAGCTCAGGGGCGAGTCCAGAGACACTCAAGCACACTGGGCTCACTGGCTGGGACCTTGAGC
			CTCCCGCTCTCCGCCGCGAGTGCCGCCCCCCGTCTGTAGCTCGCTGCGCTCGGTACAGAGGAACTACTATGGTTG
			AAGGGAGGTGGCAGTTGGGTACCGTCCTCTCCTGCCCCCCCGCAGTCGGAGCTGGGGTCTGTCCCCTCTCGGGGCAG
			CCTCCAATCTCTGCAACTTTTAAGGCTGAGAACGGCGGCTCCCAGCTGCTGCACGCTGTCCTGGCCGCCTTTTGCG
			TTCCTTTTGGCTCCTCCAAGCTCTTCTGCCCGGTCTGGGCGGGAACCGAGGGCGGAGGCTGCCGTCTTGCGCACCC
			TCAAGCTATCTCTCCGCTGCGGGAAGGCTTCGGACTGTCTCGCCTGCTGAACTTCTGG
210_ALO17	30	25	GGAAAAGTGAAGTTGCAAAAACAGACTCCTAACTTTTACGAGGGAGGCATCGCCCCGTCTGAACCGCACCGCGCAG
			CGTCCTTCCGACTTGGCGAAGTCGCCCGAGCGCGGGGCTCAAGGCCAGGGTGGGCACCCCTCCCGGATGGCTGCCT
			GCAAGCCGGCGGGCCGGGCCCTGGGGGAGTCCAGGGCGGGAGGGGAAGGAGCTGTGCAAACATGGTGGTGGCCCTT
			CCCTGCCCCCCACCTTGTTGACTTTGGTTGTGGTTGGGGGATGGGCTTTGATTTGGGTGGCAGTGTCTGTGCTTGGG
			AAAAAATGTCAGAGAAAAAGACAGGAAGCGGATTGAATGCAACAGTGTTGGGTGCCTGGGG
211_APC	26	24	GGAATGAGAAGCTTTCATGATTCTCTCGCGAGAAGGGAAGTCTTCATGCCACGTCAGAGACTAGAGATCCTGGCGC
			CGAGCGACAGGTGCCGGAACAAACAGGCGATGAGAAATCGCGGACGCGGAACCATTTCTTGGGCAGGACTTCCGGC
			GGAAAAGCGGGCTGTCTCTCGGAAACTCAGAGCCGGGTTCCTCCCGGGTTTCTCCCTGCGGCTCCTG
			GGTTGTTGAGACTCTTGTGAAGATGGCTTGCGCTGCCCGCGCGGTCCCCCGGCCGACCAGGACAGGTGGGTTCTGAGG
212_ARHGEF12	25	27	GGCCTCAAAGGGATGGGGAGCAGTCCGCGGCGCTGAGAGACCCGGGTCCCTGTCACCTCGGGCCGCGGGACCTCTC
			CGCCGGCGCCAGCGGCTCGTCCCAGCACCGGGAGCCTGGTGAGGGCGGCGAGCACAGAAGGAGCCCCCGGGCCCGGG
			ACATGGAATCGCGCGAGCCCGGCGCGGGACGGCCGGAGACGCGGCCAACGCTGCGGCCACGAGCAGCCGGCAGCCC
			CAGATAGAGAGCCGGGAGGGAGGGCCCCGGCCCTTGCCGCGGCGGGGAGTTCGAGGCCCCGAGACTCCGGAGGAGG
			AGCCGACACCCGTCCGTGAGCTGATCCCGCCCCAGCCCCCGGCGGGAGTCCCCGGGTCCCCTTCCCACTGCGCGCGGA
			TTTCCCTCTCTGAGGAAGTTTATCCTTGTG
213_ARHH_01	25	24	CCCCTGATAAGAAAAGTGGGGACCACGGCCCGCTCTCGGGCGAGACTTGGGGGGTGGCGACCGGAAGCAGCCGAA
			CCGGCCGGGCAGGGCTTGCTCTCCAACGGGAGAGCGGGAGCGGGAGAGGTGGGAGCGCCCGCGGGCTCAAGTCCCC
			CGGGCCGCCGCGCCGAGGCGGAGCTCGGGGACGAAGCAGAGGTCGTGGCGGACAGCCGGCGGGCTTGGGGGGGGGC

			GGTGGGCGGCGATCCACCTGGGCGACGTGGCAGCCATTGCCGGCGCCTCGAGACCCCTCCCCACCCGGCCGCCCAC
			CCGCCCTCTCGCGGCGGGCTTCTGCGCGGCTGCTCTTCCCCGGCCGGACGGAGAGCGGCAGTGTCTCCCGCCGGG
			CGCGCTCGCCGTGTCTCCCCCGCGGCCGCAGCTGCTTGCTAGCCTTGCGCGGCGCGGGAGAGCGCAGTGGCGCCGG
			CGGGAAAGGGCTGCGGACCTGCGGCGCCGCGTTGTGCGTTCGACGACGCGGCACCGGCTTCGACGCCCTCTGCCCG
			CTCCAGAAGCAGGTAAAGGCGGCGGTGGGAGGCAGGGAGGCGGTCCAAGGTGAGGGCCCTGGAGGT
214_ARHH_02	24	25	CCCTGATAAGAAAAGTGGGGACCACGGCCCCGCTCTCGGGCGAGACTTGGGGGGTGGGCGACCGGAAGCAGCCGAAC
			CGGCCGGGCAGGGCTTGCTCTCCAACGGGAGAGCGGGAGAGGTGGGAGCGCCCGCGGGCTCAAGTCCCCC
			GGGCCGCCGCGCCGAGGCGGAGCTCGGGGACGAAGCAGAGGTCGTGGCGGACAGCCGGCGGGCTTGGGGGGGCG
			GTGGGCGGCGATCCACCTGGGCGACGTGGCAGCCATTGCCGGCGCCTCGAGACCCCTCCCCACCCGGCCGCCCACC
			CGCCCTCTCGCGGCGGGCTTCTGCGCGGCTGCTCTTCCCCGGCCGGACGGAGAGCGGCAGTGTCTCCCGCCGGGC
			GCGCTCGCCGTGTCTCCCCCGCGGCCGCAGCTGCTTGCTAGCCTTGCGCGGCGCGGGAGAGCGCAGTGGCGCCGGC
			GGGAAAGGGCTGCGGACCTGCGGCGCCGCGTTGTGCGTTCGACGACGCGGCACCGGCTTCGACGCCCTCTGCCCGC
			TCCAGAAGCAGGTAAAGGCGGCGGTGGGAGGCAGGGAGGCGGGTCCAAGGTGAGGGCCCTGGAGGTT
215_ARNT	30	25	TCCCCTCAGCCCTGGGTCTCCTTAGTTGTCAGCCCCTTCGGCCCCTCCCCTTTAGAGGCGCCCCAGTCCTCCGTCT
			CCTCACCGGGGTTGGCAGTAGTCGCCGCCATGGCCGCAGATGCCACCGCCGCGCCACCCCCCCCCCAGTGGG
			AGGAGCCGCCGCCACCGGAGCGGGAGGGGAAAAGAAAGGCCACTCCC
216_ASPSCR1	25	27	GAGCCTTCCCAGGGGTGAGGTAGAACGGCGCCGCGTGTCACCCGCATCGAGTACTCGGCGCCCGGCCGAGCCCAGC
			TCGCGAGGGCGCCGGGAAGAGGGAGGAGTGGAGCCCTAGACCCGCGTTCCCATTCCCGGGGCGTCCCCCGGAGCGGG
			AGCCCGGGTTGCGCGGTGGCAGATGTCCCGGCCGTGGGGCCTGGAAGCGATTTTTGCCGAGTCACTCACTGCACTT
			TTACTTGGGCACCTTGTGACCGCGAATCAATTAAATGTAAAAGTATTGGCTGGGCGCGGTGGCTCACGCCTGTAAA
			TCCCAGCACTGTGGGATG
217_ATF1	26	30	GGTGGGGTACAGCTCCTAAGGAGAAACGGAACCGCAGGCACCGTCCCTCTCCCGCTGCAGCCTGAGGAACGCGTTC
			CGAGGAACCCCTAGCCACAAGTCAGGACCGCGTACAAGATGGCGGCGCGTCACGTGGGCAGCGCGGTGACGCAGGA
			CGGCGGCCCGCGCGGAGGCAGCGCCATAGCCTACCCCAAACGCACACTAGTGCTCAGTTTTGCCCCCCTCCCCTCC
			CCCGCCCCCGCCCCCGCCCCCAGGCTTGTGTAGATCATGCCGCCAGTAGCGGCCCTGACTGCCGAGGAAACGGTAG
			CTTAGGACAGTTGGCTGTTAAGTGAC
218_ATIC	27	25	TTGCATCTGAAACTGAGCAGAGCAGGGCGCCGGGCAGGGCCGGCGGCCACGTGATAAGCCCGGAAACAGCTCCGC
			CCCCTCGCTTCCTGAGCCGCCACATCCCGGCAGCCCTCCTACCTGCGCACGTGGTGCCGCCGCTGCTGCCTCCCGC
			TCGCCCTGAACCCAGTGCCTGCAGCCATGGCTCCCGGCCAGCTCGGTGAGGCCCTAGCGGAGCGGCGCGGTCTGCG
			TCCTCGCCTGCGGCCCCCCCACGCTCCCGCCTTGGCGGCGGCGGGACCCGGCACTGCAGGGGCGGCGCTGCGG
			GATTGAAAGCCAGCGTCCCCGCTCCCCGGCCGGGCCGCAGCCTGCGTGGGGCCCGCCTTAGAGCAGCTCGCGGGTG
			TAAGACCTGGGGAGGCCCGGACCAGGCCTGCGAACGCAGGGTCCAGGTGCTGGCCTTGCGATTCGAGAATCTCCTC
			CCCCAGACCCTCCCAAGGCCTTGCAGAACACAGTGCAATGTGCTGCGAATCATGAGAAAAAATGTCTTCTCTTTCA
			GCCTTATTTAGTGTCTCTGACAAAACCGGCCTTGTGGAATTTGCAAGAAACC
226_BCL6	28	30	GGAAAGGGAGGCAACAGCCATTGGGAGCCAACACAGAGTCACGCAGCGCCCAAAATACAAACACCGCAGCGGCCAG
			AAATCCCGCCACCTTTCTCGTTCTCCCAGGCTGTCCTGTCGAGGTTCCCTGAGTCCCCCCGCACACTGAAAGGCAT
			CGCAGGTGCAGTGCGCACCCCTTTCCCACCCCACCCCAAGAAGCCCTGTCCCGCCATCAGTCTCTCTCCTCGGGATG
			AGCAGGGAGAGCGCGCGGAGGTTCCCGACTCCCTCGACTACAACCAAGAAAGAATAATTTTCAAAGTGTTCAACAT
			CCCCGCCCCCCAAGCTCCCCCAAAACACAGGGGCAGGGA

227_BCL7A	27	25	CTTCTCCACCCCATCTTGCCAAGGTTGCGGAAAGTAAAAATTGGCAGTATTGGCCGCTGCAGCTTCTTAGGGACG
			GGACCATGTGAAAAGGTGGGATCGTGCGAGCGGAGGAAGGACAGAAAAGCGAGGAAAGTCTATGCCGCCAGCGACC
			GGCAGGAGGCACGTCGGGCACGCTCGTCACCGTTTCCTGGCACGTGACCACCGCCCTGTCCCTTGTCGCTTTAGGGCC
			TGTCGCTTCCGGCGGTGGCGGTTGCCATGGGGACGGAGCTTGGGTGGCAACCAGAACTAGGGAGCTGGTGGAGAAG
			GTGGCGGCCGCTGGAAGGAGGCCCGGGAGGTGGCTGAGGGGTCCAGGCGGCGGACGACTCTGGCCTTTTGAAGAC
			CGGGGTGGGTGCTCTCTGTAAGTCCGGGGCGGAGGCCACGCGGCCCTGGCGAGGGGGCCCCCGACCTGGCGGGGTC
			TGGTGCCCCTTGGGGGGCGCTCACCCGACCTGGCCCTTGTGGGGCCTGGGGCGGCCCCAGGGAGACCTGAGTTGGA
			GG
228_BCL9	26	26	GGCCAACCTATTGGGACTGCCTCTTGCGGGCCGGGGGCGCAGCGGGTGGGCCGCCCGGTGGGCAGTTTACCCGCCC
			GCGCCAGGGCCTTCCTTCGCTCCTGCCGTGGGCGGAGAGAAACTGCGCCCGGGCTTGGTGGCCACGGCCCCCGCCT
			GCGCGGCGCGCGGGGCCGGCGGACGCCAGATGAATGAGGTCGCGGGCCCGGTAGCCAGGCCTGGCCCCCTGGCCTGT
			GGAGGGGAAACGTGGTGAGATCAGCGCCACCTGCAGGCCTCCGCTGAAGAGTTGGACGGCCTGGTGCACCAAGGAT
			GTAGGTT
229_BCR_01	29	25	TGCTGGCCAAGGAAAAGAAGAGCTATGACCGGCAGCGATGGGGCTTCCGGCGCGCGGCAGGCCCCCGACGGCGC
			CTCCGAGCCCCGAGCGTCCGCGTCGCGCCCGCAGCCAGCGCCCGCCGACGGAGCCGACCCGCGCCGCCGAGGAG
			CCCGAGGCCCGGCCCGACGCGAGGGTTCTCCGGGTAAGGCCAGGCCCGGGACCGCCCGCAGGCCCGGGGCAGCCG
			CGTCGGGGGAACGGGACGACCGGGGACACCCCCCGCCAGCGTGGCGGCGCTCAGGTCCAACTTCGAGCGGATCCGCAA
			GGGCCATGGCCAGCCCCGGGGCGGACGCCGAGAAGCCCTTCTACGTGAACGTCGAGTTTCACCACGAGCGCGGCCTG
			GTGAAGGTCAACGACAAAGAGGTGTCGGACCGCATCAGCTCCCTGGGCAGCCAGGCCATGCAGATGGAGCGCAAAA
			AGTCCCAGCACGGCGCGGGCTCGAGCGTGGGGGATGCATCCAGGCCCCCTT
230_BCR_02	27	25	CTGGCCAAGGAAAAGAAGAGCTATGACCGGCAGCGATGGGGCTTCCGGCGCGCGGCAGGCCCCCGACGGCGCCT
			CCGAGCCCCGAGCGTCCGCGTCGCGCCCGCAGCCAGCGCCCGCCGACGGAGCCGACCCGCGCCGCCGAGGAGCC
			CGAGGCCCGGCCCGACGGCGAGGGTTCTCCGGGTAAGGCCAGGCCCGGGACCGCCCGCAGGCCCGGGGCAGCCGCG
			TCGGGGGGAACGGGACGACCGGGGACACCCCCCGCCAGCGTGGCGGCGCTCAGGTCCAACTTCGAGCGGATCCGCAAGG
			GCCATGGCCAGCCCCGGGGCGGACGCCGAGAAGCCCTTCTACGTGAACGTCGAGTTTCACCACGAGCGCGGCCTGGT
			GAAGGTCAACGACAAAGAGGTGTCGGACCGCATCAGCTCCCTGGGCAGCCAGGCCATGCAGATGGAGCGCAAAAAG
			TCCCAGCACGGCGCGGGCTCGAGCGTGGGGGATGCATCCAGGCCCCCTT
231_BHD	25	25	TGGGAGAAGGGAAGGCAAACAGTCCCGTTTCATGGCAACATCAAATGAGATCACAGTCCTCATCCCCATAGACTTG
			GTTAATGGGCGTGCCCCCCAACCTATCTTCAAATCTCAGGGTCTCGGCGACGCCCTGGACTCTGGCCCTAAACCCTC
			CCCCATTACTCGTCCACCTGGGACCAACGAAAACTCGGACATGCCCCTCCGCCAACCCCTCAGACCCCCGCCTACC
			TGCTCCCCAAATCGAGGCCCGCGGGACACCTGGACTCGGCAGCCGGGGTCCCGCTCTGGGTCCCAGCCCCGCCCCT
			GACTGCGCTGGGTAGGTGGTCGCTGCGGGACCCGGACCGGCGGAATCACACCCAGAGCCCCCAAGCCCACGGCAGG
			GATGTCACCCCGGGGTGGCGAGGCTCTCAAGCCCGGGTTCAGGCTCTCAGGGGAGCTGGC
235_BMPR1A_02	27	26	GCTTCTGGAATCCTTAAATGGGAAAGGCGCTCACCTCCCCCGCCCCGGAGCGGCGAGGCTGATATTTGTGATTTGGC
			TCCGGACGCTGTGGGGAGGAACAGGGGAGAACAAAATGAGTTTCGGGCGGGGGTCGAGTGAGAGGAGCAGCCGGCC
			CGCCCCCGAGTCCCCGCGGGAAGGGGCCCTGGCCCCCGAGCTCCCGGAGCTGCTTCACCTGTTGTCCTGCGCGGCC
			TCCGCTCCGTGGCCTGGTGATTCCGTACTTCAGTTTTGGAAAACTTTCTGCTGGATTGCCTGGA
236_BRAF	29	25	TGCTGGGTAAAACAGGTGAAGAGAAATCCCCAAATAGAAAAGTGAAAAGGGCAGCGGACTGAGAAGGGGGGCAGT
			CCGGGAGAGGAGAGAGGAAATGATGAGCCCCATCATCCCCACGACCATGTAAGAATTACACGCGACAGTAACTCGG

			GCTGTTGTCTCAGCCCCAGCAACTAACCTATATCCTCCACGTCGAGGCCGCCGCCGCCCCCACCCCACAGAGATGC
			AGAGCTGGATACTTCAGCCAATCGTGACCTTCTCGGACCAACCCTGAGTTTCGCCCCCTATTGATAGCCTCCCGCT
			CAACCACCGCTGCCCCCAATCCCCCACATCTGGGGTGGGGG
237_BRCA1	29	26	CTGGGGCAAGTAGTCTTGTAAGGTCAGTGGCCTGCGGGGACGCAGTGAGCGCCGAATTTGCCTGGGGCAGGGGAAA
			TGCGCTCTGGCCCATGTCTGCGCACTCGTAGTTCCACCCCTCAGCCCCAGTGTTGTTATTTTCGGGTTCAGCTT
			GCTTTGCCCCCGTCTCCGTCGACGCAATCGCCACCAGTCAATGGGGTGGTCGTTTGAGGGACAAGTGGTAAGAGC
			CAATCTTCTTGGCGAAAACGCGGAGAAACGGGACTAGTTACTGTCTTTGTCCGCCATGTTAGATTCACCCCACAGA
			GATAGCGGCAGAGCTGGCAGCGGACGGTCTTTGCATTGCCGCCTCCCCAGGGGGCGGGAAGCTGGTAAGGAAGCAG
			CCTGGGTTAGCTAGGGGTGGGGTCACGTCACACTAAGAGGGTTTGGAGAAGTTCAAGGGAGGAATCCTGC
238_BRCA2	27	26	GCCCCTCCAAGCAGGGTGGCCTGGGACTCTTAAGGGTCAGCGAGAAGAGAACACACACTCCAGCTCCCGCTTTATT
			CGGTCAGATACTGACGGTTGGGATGCCTGACAAGGAATTTCCTTTCGCCACACTGAGAAATACCCGCAGCGGCCCA
			CCCAGGCCTGACTTCCGGGTGGTGCTGTGCTGTCGCGTCACGGCGTCACGTGGCCAGCGCGGGCTTGTGGC
			GCGAGCTTCTGAAACTAGGCGGCAGAGGCGGAGCCGCTGTGGCACTGCTGCGCCTCTGCTGCGCCTCGGGTGTCTT
			TTGCGGCGGTGGGTCGCCGCCGGGAGAAGCGTGAGGGGACAGATTTGTGACCGGCGCGGTTTTGTCAGCTTACTC
			CGGCCAAAAAAGAACTGCACCTCTGGAGCGGGTTAGTGGTGGTGGTTGGGACGAGCGCGTCTTCCGCAG
			TCCCAGTCCAGCGTGGCGGGGAGCGCCTCACGCCCCGGGTCGCTGCCGCGGCTTCTTGCCCTTTGTCTCTGCCA
240_BTG1	25	24	CTCTGGGCAGGGCTGTTAATTGTGCCGGTGACAAATCCGATGATTAATGGGCAGGGGCAGGAGGCGCGGGGAGACG
			GCACGTCCGTTCTGAGCTGGCTCCGGGGCAGCGGCGCAGCTTCCCACCCCGGGGCTGGGCCGCCGACCACGCAACG
			GTTGGAGGGGGCTGAGGAAAGGGGACGTCGAACCCACCCCAGCCCCACGGCTCCTTGTCCCCAAATCCGCCGACG
			GTCCTCGGACCGCAGCTCCCGCCTCGGTGGGCTTAAGTTTCTTTGTTGTGCGTGTTGTCTTCTCCTCTCCGTTTTG
			CCAGCTGGGGGGAAGGGGGCGCCCTCCGTCCAGCCCCTAAAGCCTCGCGGGGAACCGCTGTTAGCGGCCACCCAGC
			GCAACCACACCGGTCCCGCGGCGGGCCCAAGCGCGACCGGCCCCGGGGCGCTGCCGAGGTTCCCGCAGCCCCGAC
			GGCCGGACTCTGACCCAGGGATGTGGGGC
241_CBFA2T1_01	29	26	TTCTGTTGTTGCTGCTGTGGCAGACAAATGTGATGTGGGGCGCAGGGAATTGCCACTGTCACAGGCGGCGTCTGCG
			TCTCCCTCGCCCGCCCTCGCTCACTCTCGAGGAAGGCGACGCATTTATCTGCAGGGCGGCCGGGCGTCCGCCGGGG
			AGCAGGAGCGCCGCGCTGTGCGCCGAGAGCGCCCGCATCAGGCCGGCTCCGGCGCACGCTCGCGCCAGGGGCGC
			CGCGGCCGGTCGGGAGGGAGGCGGCTGCGCGGCCGCTACCAGGTGCAGGGGGGAGGACCCGCGGCGGGCGTGGGG
			GAGGTGGAGGTGGGAGACATCTGTGTTGTGCGGGGGTCACGGAGGTCAAGTATATGTTAACAATGGGCAGGCCCGG
			CACGCTAGGGCGCGCGGGCTGGCGGGCGGCCTCCCTCCCGGCCTCGCCCTCTCCCATGCAGGCTGGACGTGGGGTT
			GGCTCCCTAATGATGCCT
242_CBFA2T1_02	29	26	GGAACAGTAATTAATACAGTCAGGGGCCCGACCCCGCCCGCCCGGCCAAGCCCTACCGCGGACACTTAC
			ACTGCACAGGGCCGGAGAGTCCCACCATCCGCCACAGGCTCCGAGCTGCAAATAAAACTTCCCGTCGTCTCGGCCG
			GCCCGCGGGGCGACGGGGCGAGGACGCGGCGCGGCTTCCCTCGCGAGGCCAGAGTGTCCGCGGCCACTCGCCCACG
			CGCGCTCGCCACGAGACCGCGGAGTCGCGCCGCGGAGCGACTACGGCCGCCCGGCGCTGCGCAGAGAGGCTGCCG
			TGCAAAAAGCCCCGGGGTCGGGGACGCCAGCCAAACGCAACCTCCACGCAGAGCCCAAGACTTGCGGAGCTCTGCTC
			CCCTCCTCCCGCCTCCCTCCCTCCGCTTTTCTGTTGTTGCTGCTGTGGCA
244_CBFB	30	25	AAGGAAACTGAGGTTTAGTGGTCCAATTCTTATCTAAGGCCCCAGCCAGGTAGTGTAGCTGAGTGGGATCCCA
			TCTAAGACCCATCTGACTCCAAAAGCCACGACCTTTCCACCATGACTCGGTTGGATTCTTTGGTCCGTTTCCACCT
			CAGTCTTCAACGTGCAGAGCCTACACCCCTGCCGGTCGGTTTAGGGACGAAAAGTCCCCAAGGACTTAGGTTTCCT

			CGCGTTCAAGTGACAATCTGGGGTTACTCCGCGCACCTGGGGAACCCAGAAGTTCCAGATGACCGAGGAAGGGCGG TAGAAAAGGCCTGCGCTGGCTACTCCCGTCTGCTAAAGGCCAGGCGGATCCCCCCAACGACACAGCTCCACGCCGAGTG GCCGCGGGCGAGCAGGGGGAAAAGGGCCCTGATG
245_CBL	25	25	CCCTGAGCAACCTCCCACTGGAGGGCGCCTTCCGGAGCGCGCGTGTTTACACTTTGCTACACCAGGCGGAGGAAA CAAGCGCTCGCTGACCCCGGGGATTCCAAACCGTTACTCCGCCCCGCCGGGTGGGGCCAGCGCAACGGCCGAGCC TGCGCAGCCAGCCGGCTCCGGGGGCCCCGCGCACTACAAGTCCCAGAAGGCAGCTCTCCGCGGGCGGGCAGTCGC CTTATCTGCTTCTGGCTCATTTTTACCACTGCTCTCCCCTTCCCCGGTCCCCCTGGTGTCCTTCCACAGTTAAAG GCTACTTTCTCTTGAAGCACATGAGGAGAAGCCTTAGCAACCTCAATACCGAAGTTCTTCGCGCGCTCGCTCTTTC TGCCTCCGCCCGAACTATGCCTGAGTCCCTCACAGGAGTTGGATAGTAGAGGCGAGAGAAGGAAGTCTTTGCAGGC CA
246_CCND1_01	30	26	GGAAGGCTGCAGCTGCTATTTGGTGCTTTACCACCGCTGAGAAGGTGGAATGGTCACGGCCCGGTTCTGTCACTTT CTTCAGCCGGACAGTCGCCTTATTACGGATTCCAGTAGGGCCGAGCACACTCCTTCCTGCCCGTCTTTACAGATGA ACATGCTATCGCTCCAGCAGTACAACCCGCCTTATTACGTAAAAAAGCAGCCCCTATCTACCCGCAGGGAAGGAGT ATGTTCGGCACCACAGCTGGACTGGTGCTCGAGTTAAGCGTCCTGGGAGGTCCGCATGCGCTCCGGAACCGTAATG CGCGCTTTTTCTAAGCCTTACGGTAAACGCGGACGCAGGGCAACCACGTGGCGGTGGAACCGAGGCCCGGCGGGAA TGCGCGGAATGCGCGGCGCGGCCTCGCGCGGTTCCCGAGCCACGGCCCAGGGTCCGGCGGCGCGCTCTCGCCTC CTCCCCTCACCTCTCCCAGCCGCACCCCGGCCCTGGCCCTGCCGCCCAGAACTCGCTGGGCAAGTCGTGCCCCGCG TGAACACACAGAAGGGGCTTGGGGA
247_CCND1_02	30	25	AAGGCTGCAGCTGCTATTTGGTGCTTTACCACCGCTGAGAAGGTGGAATGGTCACGGCCCGGTTCTGTCACTTTCT TCAGCCGGACAGTCGCCTTATTACGGATTCCAGTAGGGCCGAGCACACTCCTTCCTGCCCGTCTTTACAGATGAAC ATGCTATCGCTCCAGCAGTACAACCCGCCTTATTACGTAAAAAAGCAGCCCCTATCTACCCGCAGGGAAGGAGTAT GTTCGGCACCACAGCTGGACTGGTGCTCGAGTTAAGCGTCCTGGGAGGTCCGCATGCGCTCCGGAACCGTAATGCG CGCTTTTTCTAAGCCTTACGGTAAACGCGGACGCAGGGCAACCACGTGGCGGTGGAACCGAGGCCCGGCGGGAATG CGCGGAATGCGCGGCGCGGCCTCGCGCGGTTCCCGAGCCACGGCCCAGGGTCCGGCGGCGCGCTCTCGCCTCCT CCCCTCACCTCTCCCAGCCGCACCCCGGCCCTGGCCCTGCCGCCCAGAACTCGCTGGGCAAGTCGTGCCCCGCGTG AACACACAGAAGGGGCTTGGGG
249_CDK4	26	22	GAGCTGAAGCTGCTGGTGCTGACAGGCGGGGGGGCGGCCCCGGGCCGAGCCGCAACCCCGGGGGGGCCGGGGAGGCG GCTGCGGCTGGGCGCCCTTCGCTGGCTGCTCCACCCGGGACGGCGACGGAGGAGGAGTACTACGGGTCGGA GCCGCGGGCCCGGGGCCTGGCCGGCGACAAGGAGCCGCGGGCCGGACCCCTGCCGCCGCCCGCCGCTGCCG CCCCCGGGCGCGCTGGACGCCCTGTCGCTCAGCAGTAGCCTGGACAGCGGACTCCGAACCCCTCAGTGCCGGATCT GCTTCCAGGGCCCGGAGCAGGTCAGGCCTGGGCACCTGGCCGGGCGCGGAGGGTGGAGGCGCGCACCTGGGGTGTC AGCGGAGACCGCGAGCAGGCGCGGCGCCTAAGGAGGCTGGGCGGGCCCCAGGACACGGAGTGGGAATGGGGTGAGG CCGAGGGGCTGGCAGGGGACTCCTGGAGCGCTTGTTGTCGTCGGAGGGTCAAGGGTCCCCAGGAAGGGGTGGGGCT TTC
262_CTNNB1	25	25	GGCTTGGGACAGGGGAGGATACCAGGGCCACCTTCCCCAACCCAGGCCGCGGGGGCCCGGCCTCCCCGATGCAGAC CACAGCGCCCTCACGGGCTGCCCTCAGGCCGCGCAGCGGGCAGCCGCCAGCCGTCACCCCGGGGAGCGTCCGTGGG GTGCCCAGGCACCCCACCCCGGCCCGGGGCGCTCAGACGGCAGCAGACTGCTGGGCGGCGCGGGGACTACTTTCCA CCGCCCCCTCGCGCCCCGCCCCTTGTCCTCGCGCGGCGGAACGCTCCGCGCTGCGCCGGTGGCGGCAGGATACAGC GGCTTCTGCGCGACTTATAAGAGCTCCTTGTGCGGCGCCATTTTAAGCCTCTCGGTCTGTGGCAGCAGCGTTGGCC

			CGGCCCCGGGAGCGGAGAGCGAGGGAGGCGGAGACGGAGGAAGGTCTGAGGAGCAGCTTCAGTCCCCGCCGAGCC
			GCCACCGCAGGTCGAGGACGGTCGGACTCCCGCGGCGGGAGGAGCCTGTTCCCCTGAGGTGCTTGG
263_CYLD	25	25	CAGATTGGGAGACTGAGGCACAGGCCGCTGGCGGGCCCCGACGGCCACGGTTGGCCTCAGGAGCCCGGGGCTGTGA
			TTCCTACCGACCGCGCCGCGGGGCGTACGTACCGATCGATTTTGCGGGTGTTGGTGGCTCCCGTCCAGGAATGGCA
			GTCGGGGTTCTGGCCTTGTTAATGGCGTGTTCTGCTTTTTCTTTCAGTTTCCCCCTTTCTAGGGTGAGGATGGTTC
			T
264_D10S170_01	24	26	GACTGGGGTTCCCCAGATTCTGGACGCACCCCTCAAACATGCTAGGGCTGAAAAAAGTCCTACCCGCCCCCAGC
			CACGCCGCCAGCCTCCAGCCCAGCCCCGGAGGGGCCTCCTCTCCAGAGGCTAAAAGGGACCATGAATGGTTGCCAC
			AGTAGCCTTCCCCCCGCACCGCGCAAGGGTCCTCAGACCCCCGAGGAGGACAGACCCGCGTGGCCCCGAAGGGATAC
			CTCCCTCTCCTCCCGGAAGCCAGCAGGTCCCCGCAGGGAGTGTGCTCTCAGAGGGTCC
304_FGFR1OP_01	29	27	GGACACACCTCTGAAAGGAAAATACAACTCGGCACCGCAGTTGACTCGGCCAAAGGAAAAAACTTAAGCTGAAAG
			CTGAGGCCTGCCCGAAGGAGCCTTTCCTGTGGCGCCTGAGCCGAGGGCTTCAGGGAGAGGGCCGCGCATCGCAGCG
			CAGCCGCCCGTCTTCCCGTGGCTTCCCTACGGCCGCGGCTCCCGCTGCTCCTTTCCGCCGGCCACGCGGGTCGCAC
			GACCTTCCCCCTCCCGCCCACCCTGAGGCGCTGAAGCCCTCGACGCCGGCCTCGGGAAAGGCGCGGCCACCGCCCGT
			TTCGGATTCCCGTTTCCTTCCTCCGGCGCGTCCTTCACCGTGGCCAAATCAGCCTCTCAACTGCTG
267_DDIT3	25	25	CTCTCTGGTCCCAAGGATGGCCTGGGCTGTTCCGCCCCGTGGCTCCCCAGGGGCCAAAGCCATGAGGATCCGGGTGA
			GAGCCCAGTGCTGGACGAGCCCGGGGCCCAGGGGTCCCGGCCGAAATCCCTGCTGTCTTTCAGGTCAAACGTCATA
			ATCCCCGAACCCCAGAAAGGCCGAAAGGCAAGGCAACCCTGAAAGACGACGAAGTCAACCTCAGGGCGCAGGAGAG
			GGAGGGCCAGTGTGCT
270_EGFR	27	24	GGTGCTTGACAAGATCTGAAGGACCCTCGGACTTTAGAGCACCACCTCGGACGCCTGGCACCCCTGCCGCGCGGGC
			ACGGCGACCTCCTCAGCTGCCAGGCCAGCCTCTGATCCCCGAGAGGGTCCCGTAGTGCTGCAGGGAGGTGGGGAC
			CCGAATAAAGGAGCAGTTTCCCCGTCGGTGCCATTATCCGACGCTGGCTCTAAGGCTCGGCCAGTCTGTCTAAAGC
			TGGTACAAGTTTGCTTTGTAAAACAAAGAAGGGAAAGGGGAAGGGGACCCTGGCACAGATTTGGCTCGACCTGG
			ACATAGGCTGGGCCTGCAAGTCCGCGGGGACCGGGTCCAGAGGGGCAGTGCTGGGAA
271_EIF4A2	25	25	GGGTCCTAGGCTTTACTTGGGGAAGGGTTGGAGGCAGCGGTCTCCACTCGGCCACGGCGCGGAGGCGACGGGACAG
			GACCGGTGCCGGTGAACCGTTGGCATCGCCCTCGCCAGGCCGCTCCGCCCGCGTCAATCACCCGGCTTGCGCATTG
			TTGGGGGCGGAGTTCGGCGCTCCGAGCTCTCGCGAGACGCTCCGCAGTTGAAACGGGATCGCCATGCGCTCGGCC
			TGGGGGGCTGCCTTTCCGGGCATCCGCAGGCCCCCAACCTTTAGGGAAGGCGCACACAGTGTGGATATTCGCCCTGAGG
			CTGCTGCTTTAGCTTGTGCAGGGGAGGCTAACGTGCTGAGACGGGTTGCAAAGGGCTATGCGCTTAAGGTGCAGTT
			GAGGTGGCCTGGAAGGGGTGTCTGACTGCAG
272_ELKS	23	21	AGGCTGAGGGAAAGGGAGGCAGCCGAGCCGGGAGCCCGGGAGGCGCGCTGCGCCCCGCGGCGGGGCTGGGGGCGG
			GGCTAGGTGTCTCGCGCAGGGGGCGGGGCGCGGTGACGTCGCGGGCGCCTGGGCCGTGCTGTGGCGGCGGCGGCGG
			CGGTAGTGGCGGCGGCGGCGGTGCCTGGGCGGCAGCAGCAGTAGCGGCAGCCCTGAGGACGGTGAGACGGCCG
			CGGCGGCGGCGACAGCGCGGAAGTCGCGCGGGACCCAGAGCTTCCCCCCCTGTCGCTAGTGCTGAGGCTTTCGCCTT
			TCCTACCCAGCTTCTTGCTCACGGCCCGGGCTGGGCAGGGCAACGCGCCCCCGGGGAGGGGCGGAGCTGTA
			GGTGAGGCTTCGCGACCCCCCTCCCCCTCCTCGGCAGCCCGGGGGGTGGGGAGGGGCGGGCCCCCACCCAGACCACCG
			GCGCCCACCCGCGGGCTCCACCCAGCCGGGCTCCGGGATCGGGCGGGAGCCGAGGCGGTAGATGTGGGGATCCTGG
			GG
274_EP300	26	27	CCCCTTTAAAGGGAGCCACAGGGTGACGCCGGGGGAGTTTGCGGAAGCGCTAACCGCGTTGGGGCCTAGGGCGGAT

			CCCGTGATTGGGACAGGCCCCGCCCCCGGCTCCACTTCCCCCATTGTGTGAGCGGCTCGGGCCTAGGCCCCGCCCC
			CCTCCGGAGGCCCGGCCACTCCCCTTTTCCACCCCCCCTTGGCTCATTTCCGGCCGCCGCTACCGCTAGCCTG
			TAAGGAGGATTCGGCAGAGGGAAGAAACAACAGCCGCCATCTTGTTTGTGTGCTAGGCTGGG
275_EPS15_01	26	26	GGAAACTTCCTGGGTAGGTGAAAGCTGCCCCCGCGGGAGCCGGCCCGGCACCGGCAGAGCGCGGCCGGGTCACAGTC
			CACTCGGCAGCGGCGCGGAGGGCGGCGAGGGCCGCGCGGGGCGGGGCAGGAGGCGCCCGACGACCCTGGGCGAGGT
			CGCGGCGGCCGCGAGGGGGGCTCCGGCTCCGGAGGGCGCCCTCCCGCAGTCGCACCCGCTTTCCCTCACACACCG
			GCCGCCCGGCCCACAAGCCAAGAAGCTGCCTGCTTGGCCCACAAGCCAAGAAGTCGGCGAAGCTGAGGGCGGTGGG
			GGAGGGGGCACCGGCCGGCCAAGCCCGGCGACGGGCGTGTGGCGTTACCTGTGTCAGAGAGAGCTGGGCCGCCGC
			AGCCATGGTGTTTCCATCATGCAAGGGAGGGGA
277_ERBB2_01	25	26	GAGCACCCAAGGTGGGTCTGGTGTGGGAGGGGACGGAGCAGCGGCGGGACCCTGCCCTGTGGATGCCCCGCCGAG
			GTCCCGCGGCCGGCGGGGCCAGAGGGGCCCGGACGAGCTCTCCTATCCCGAAGTTGTGGACAGTCGAGACGCTCAG
			GGCAGCCGGGCCCTGGGGCCCTCGGGCGGGAGGGGGCAGTTACACGGCAGCGGCTCGAGATGGCCCATCCAAGAGA
			CTGGCGCTTTCCAGGCTCCGAGGGGCTCCGGGAACTTGTCAAAGAAGTTCTCTGA
278_ERBB2_02	24	25	GCACCCAAGGTGGGTCTGGTGTGGGAGGGGACGGAGCAGCGGCGGGACCCTGCCCTGTGGATGCCCCGCCGAGGT
			CCCGCGGCCGGCGGGGCCAGAGGGGCCCGGACGAGCTCTCCTATCCCGAAGTTGTGGACAGTCGAGACGCTCAGGG
			CAGCCGGGCCCTGGGGCCCTCGGGCGGGAGGGGGCAGTTACACGGCAGCGGCTCGAGATGGCCCATCCAAGAGACT
			GGCGCTTTCCAGGCTCCGAGGGGCTCCGGGAACTTGTCAAAGAAGTTCTCTG
279_ERCC2	26	26	GGTAACCCTCAGGTCCTCAGGAGCCTCGGGGCCCCCTCAGTGTCTCCTCGCTATCACTGCTGCTCCCTGCGGCTGC
			CCCCGTCCCACACCCTTCACCCTCCCCTCGCCCCCTTGGGGACCCAGGCGCGCCCACCGATGACCCCATCTTCAAGA
			CCCCCCGCGCCCGCTAGCGAGCGCGACCCCCAGCCCCCTTCTCACTTCATGGCGCCGGCCGGGACTGTGCAGCGGG
			TCGACCCGCCTCCCTCATGAATATTCAGCGAGAGGCCGGGTCGTGGACATCCTCGAGGGCTCGCTCCACCTATATT
			ACGAGACCATTGGCTAACCTGCCCGTCAATCCGCTAGGGCAGAGCCAATCGGGATACTGCGCGTGCGCACGGAAAA
			GCGAGGGCGGCTGACTCTCGGGTGAGGCGGTGCGGGAGGCGTCACTGAGGATCGTCGAGGGCCAATCAAAAAGAAA
			ACATGG
280_ERCC3	27	30	CCCAGCAGGAGCCTTCAGGGTTCCCTCCGCACCGCTTGGCAGCATTTCACCTGCGCCGCCGCAAACTCCTAGCTAA
			GAGCCACCTGCATCCCGCAGGCGTTGCGCCCCCTCACCCGTCTCCCCCTAGGCCGAGTTCGCTGGGCTGCGCCCAGGT
			CCAGCATCTCTCCCGCCCAAAGGCCTGTCCCAACGGGGTGCGCGCGGGAGGGCCAGCAGGGTCGGCCGGCGCAGAG
			GCCCGGAGCAGCTCCGAGGCAGAGCGGGGGGCAGGGCCGGCAAGGGCAGTCGTGGCTGAGCGTGCCCGCGCAACGT
			CTCACCGCGCGGTCCGCTCGGTCTCTTTGCCCATGGCAGCTACAGCAGCAGAGAGAAGATGACCCCGCTCCCACAGG
			CCCGCCGCGGCATCCGCTCTGGGGGGACTTCCGGCTCAATCCGGAAGCTCCCTGTTGTCCACACAGGATGTCCCGC
			CTCTAGGCGCCGTGATGTGGGTGGCTGGAAGAGCGGAGAGCCAGCGACCGCCGATCTGTTAGCTCGTGCGACCCAG
			CGGCGGGGGTCCTCCACTGTTCATTTCTCTACAACTGAAGGAAAATACTGTGTTGAGC
281_ERCC4	26	26	AGCCTGCCTGGTGCTGGTGCTCAACACGCAGCCGGCCGAGGAGGTGCGGCCGCGCTGGCGCGGGAGTGAGGGGACT
			CCGAGAGTGTTGAGGGCCTCCTGAGCGGATGCGAGGCCTCTGACAGGGATGGAGGGGCTCTGAGGGGGATTCAGGC
			CCCTGACACTACGCGATGACACAGAGAAGGATGGCAGGGGTCCCCAGGGGGATGCAGGTCCCTCACACTGCGGGAA
			CACAGACGTATGTAAGGGGTCGCTAGGAGGATACCGGTCGCTCACACCGTGCGGGGACACTGATAAGAATTGGAGG
			GGCC
282_ERCC5	25	30	TGTAGGAGCAGGGAGGGCTTCCTCCCGGGGTCCTAGGCGGCGGTGCAGTCCGTCGTAGAAGAATTAGAGTAGAAGT
			TGTCGGGGTCCGCTCTTAGGACGCAGCCGCCTCATGGGGGTCCAGGGGCTCTGGAAGCTGCTGGAGTGCTCCGGGC

			GGCAGGTCAGCCCCGAAGCGCTGGAAGGGAAGATCCTGGCTGTTGGTATCCTTAACGCCGCGTTGGGACTTGGGGT
			GCAGGGATTCGGGGCTGGATTCCTCGCGGGGCTCTGCCTTGGGCACAGTGGCATCTGCAGGATGATGGTCT
285_ETV4_01	24	25	GAATGACCAAAAATCCCTTGGAGGGCGAGTTTTTTTGGGGAAACAGGCGGGGGTTCCAGAATCGGCCGTGTGTGTG
			TGTGTGTGTGTGTGTGTGTGTGTGTGGCGGAGGAGGGTCGCGGTTTGTCTCTCTTGCTCTTTACCTTCAGAG
			TCGAGGGGCGGCAGGGAGCCCCGGTCCATGAGCTTCCCCAGCGGGCCGATCAGCGCTTCGCGCAAGCTCCCATTTC
			CGGGCGATTTCTGCGAGAAGCGGGGAGAATGCCCGCGAGTCACCCTGAGGCGCTTAGTCTGGGGGACGAGGTTGGG
			GTCCTCGGGTGACTCAGGGGCGGGGCAGCCCAGGACTCCGCTGGGACTGCGGGGAGGGGGGCTGTGGTGAGAGTAG
			GGGCTGGGTGCGGGGCGGGCGGCGTGGAGGCCGGCGCGGCTCACGCTGCTGAAGGTGTAGGGCACTTGCTGG
286_ETV4_02	26	25	AAGAATGACCAAAATCCCTTGGAGGGCGAGTTTTTTGGGGAAACAGGCGGGGGTTCCAGAATCGGCCGTGTGTGTG
			TGTGTGTGTGTGTGTGTGTGTGTGTGGCGGAGGAGGGTCGCGGTTTGTCTCTCTTGCTCTTTACCTTCAG
			AGTCGAGGGGCGGCAGGGAGCCCCGGTCCATGAGCTTCCCCAGCGGGCCGATCAGCGCTTCGCGCAAGCTCCCATT
			TCCGGGCGATTTCTGCGAGAAGCGGGGAGAATGCCCGCGAGTCACCCTGAGGCGCTTAGTCTGGGGGACGAGGTTG
			GGGTCCTCGGGTGACTCAGGGGCGGGGCAGCCCAGGACTCCGCTGGGACTGCGGGGAGGGGGGCTGTGGTGAGAGT
			AGGGGCTGGGTGCGGGGCGGGGCGGGCGTGGAGGCCGGCGCGGCTCACGCTGCTGAAGGTGTAGGGCACTTGCT
			GG
288_EVI1	27	26	AGTGCCAGGAATTCAGATTTGGCAACCGCACCTGTGCGTCCCCGAAACCGACGGACACAGAGACACGGAGGGAG
			GGGAAGGAGGAGAAGAGCGCAAGGAAAAGAGGCCGACAAGCCGGCAGAGAAACCCACCGAAGGCCGGACGACCCAC
			CCCGGAGACGTGTCCAGACCGCACCGTTTCGCAGGAGGAACAAGGAAATCGCCCGGCTTAGCAACGTAGATAAGCA
			GCAGGGCTCCGCGAGACTGCGGGCGAGGAGGAAAGAAGGCTGGGGGCGGGGGCGCCCGTAGAAACGGTGCCCCGG
			CAGGAAACTGTCCGAAGTGACAAACTTTCACATCGCCCCAGACTTTTTTTCCTTTTAAAGTGAGGAGTTCTCTT
289_EWSR1	26	24	TGGTTCATCCCTCCTCCTGACCCCACCCCGTGGCCTGGCCCGATGGTCGCGCCCCGGGGTTGCGAGATTTGCGCCTGCG
			CAGTGCGGCGCCTAGAGGGAAAGCGAGAGGGAGACGGACGTTGAGAGAACGAGGAGGAAGGAAAATGGCGTC
			CACGGGTGAGTATGGTGGAACTGCGGTCGCGCCGGCGGTAGCCGGAACGCCCAAACTGGGGGTCGTTCGTCTCTGG
			GCTTGGCTGGGAAGACTGAGTGGAGTTGCCGAGAGGGGGTTGAGGCACCCGCCGCGGCCCGACGAGCTCGGGGATC
			CGCATTCCTCTCCCCTCCCCCAACCGGGCGGGCCGGTTCTGGAATCTTCCGGCGCCCGTGGCGCGCGGGGGCTTG
			CTGCGGCGGGGGCGCGCGGGGCCCGCCTTGGCCTCCATTGTGTGGCGGTCCTCGCGCCCTGAGCTCCGGGCCTCCC
			GCCACGTGGGCGGGGCCTGCGGCCTTCGAGGCCCTGCGTGAAGGGGAGGATTTGGCCAGGCCT
291_EXT2	24	21	GGACTCCTCCTGTCCAGCAGGAGGCGCGGCCCGGCAGCTCCCGCATGCGCAGTGCGCTCGGTGTCAGACGGCCCGG
			ATCCCGGTTACCGGCCCCTCGCTCGCTGCTCGCCAGCCCAGACTCGGCCCTGGCAGTGGCGGCTGGCGATTCGGAC
			CGATCCGACCTGGGCGGAGGTGGCCCGCGCCCCGCGGCATGAGCCGGTGACCAAGCTCGGGGCCGAGCGGGAGGCA
			GCCGTGGCCGAGGTAAGCGCGGCTCTCCAGGGCGGCGGCCGGGCGGCGCTGAAGCGAGGGCTCGGGCCTCCGGGG
			GCCGCTGCTGGGTCGGGACAAGGGCCGAGGGAGCGCGGCCGCGCGGAGGCTCCGTGGAGGCCCGTGGGCTGCGAGA
			GGCCACCCCCCAGCCCCGCCGGGGCTGTGACAATGACTGCC
292_FACL6	25	29	AGCTCAGCAGCAGGGGATGGGGGCTCGGCGGCCGCGGAGATGTAACACCTCCACCTCGGGCGAAGACCTCATAGCC
			TGCGGGAGATGGGAGTCCGGGACGCGGACAGGACGGGCACTTACCTACGAATAGCCAGAGGGAGCCCCCCCGACACG
			AGGAAGAAGGTCAGCATGGCGGTCAGCGGGGCCCGGCCCGGCCCTCCCCGACCCGCAGCCCCGCAGC
			CCCGCAGCCCCAGCAGCCCCAGCAGTAGCCGCGCCGCCGCTGCCGGGTATTTTTAGCCCCCGCCCTCCGGC
			CCCGCAGCTCCCGCCTCCCCGCGCCGCTGCGGAGACGGCTCAAGGGGGAGGGCGCGGCGCGCACTCGCAACCGAGC
			CTTACTCCCCTGCCCTGCAGCCTGGC

293_FANCA	22	30	GCCATGTTGGTCCTGGGGAGGCGCCTGCGCGCGGTGAGGTAGTTTTTGCGTTTGGCTTTGCCGCCGCGGTGTAGT CCGCGGGGGCGTCTCGCGCGGGCAGACTGCCGCCCCTCAAGCGTGGTTCCTGCCGGGAATGACTGGGGTTGGTCCT GAAGAGACCACCTGGCCAACCAAGCCGAGGCAGGCTCAGAGCGCCGCGGGAGCGCAAAGCCGCGCGCGCCTCTGA GCTCCGGGCAGCCGCTGTTCCTCCCGGCGGCCGAACGGTCCGCGCGCAGGGCGGTGTTTCGGCAGCCGGAGACCGC GCGGTAGCCGCGCCTGTATTCCCAGCGCTTTGGGAGGCCGAGGCTGGAGGGTCGCTTGAGCCCAGGAATTCCAGAC TAGCCTGGGC
294_FANCC_01	27	25	CTCCTTTGAAGAAGACATAGCTGCCTGCGCTCAATGAACAAAAGAACCAAAACGCCAACACCCGGCTCCCGCCTC TCCGGGGGCTCCCTTCCGCGCGACCCCAGCGCCGGCTCCCGCCCCCGCTTCCCCCGCCCTGGCCCCGCCCCGCGGG CTGGCACCGCCCCGCCACCTTCCGCCTCCCGCCTCCCGCCTCAGCCTTAGCCACAGCCCTGCGCCGGCGCGG GAACCCCTCTCGCCCACCGCAAGGCGCGCCTGGCCCACCCGCTCTCGCGAGCCTTCCCTCTTGCCCCTCGCCTCCT CCTCCCGCTCTCGCCGCTGACGTGTCGGCCAGACCCCCGAGGGAAGCCTCCGCCCTCGCTGCGTTCTGCGGCCTGC CGCTTACCGGGTGGTCCTCGCGGAGCTGCTTCAGCAGTTTGGGCAGTGGCGGAAAGGAAGCCACCGCCCGGGATC TGTGGCTTGAAAATTTGGCTTTGCCTCGTATTGGCTTTTTTGAGTTTTTTTGGAATTTTCCCGCGGTCGCCCGGCAG TGGAGCCGCGCGCGCACACGTGTCAGCAGTGCATTCTGGGGCCT
295_FANCC_02	28	25	TCTCCTTTGAAGAAGACATAGCTGCCTGCGCTCAATGAACAAAAAGAACCAAACGCCAACACCCGGCTCCCGCCT CTCCGGGGGCTCCCTTCCGCGCGACCCCAGCGCCGGCTCCCGCCCCCGCTTTCCCCGCCCTGGCCCCGCCCCGCGG GCTGGCACCGCCCCGCCACCTTCCGCCTCCCGCCTCCCGCCTCAGCCTTAGCCACAGCCCTGCGCCGGCG GGAACCCCTCTCGCCCCACCGCAAGGCGCGCCTGGCCCCACCCGCTCTCGCGAGCCTTCCCTCTTGCCCCTCGCCTCC TCCTCCCGCTCTCGCCGCTGACGTGTCGGCCAGACCCCCGAGGGAAGCCTCCGCCCTCGCTGCGTTCTGCGGCCTG CCGCTTACCGGGTGGTCCTCGCGGGAGCTGCTTCAGCAGTTTGGGCGGAAAGGAAGCCACCGCCCGGGAT CTGTGGCTTGAAAATTTGGCTTTGCCTCGTATTGGCTTTTTTGAGTTTTTTTGGAATTTTCCCGCGGTCGCCCGGCA GTGGAGCCGCGCGCGCACACGTGTCAGCAGTGCATTCTGGGGCCT
296_FANCD2	30	26	GGACCACCCAGAGGCAGATGTTGGAGTCAAGCAACAGTTCTGGCCCTGCCATCTTCACTGAAAGCTGGCTCCCAGC CGGTGATGGGCGAGCTTCTCTTCACCGGGGCGCAGTTGCTTCTCTCTGACGTCGCCTCTGGGCCTTCTCTCGCCCC TATGCCCGGCTAGCACACAGAACTCTGCTGCAGCGGTGAGCCCAGCTTATTGCCTTCAGCTGGGCTGCCCGGCCTTCC ACTTCCGGCGCGGAAGTTGGCGTCACGTCATGGCGCGCCTCGGTGGCGTCAGAGCGGCGTCGGGCCTGGCGGGAAA GTCGAAAACTACGGGCGGCGACGGCTTCTCGGTGAGTAAGTGGAGCAATGGTCGTAGTCTCTCGAGGCCCCGCTCC CCTGCGGCCTAATCTCTAAGTCCGGGCCGCGGTCGGCGTTCTCCTCTGGGGCTCCGCGCCCCGAACCTTGGCTTCC TCATCTGCCCTGAGATGGG
297_FANCE	28	26	CCACTACTTTGGGGAGTGATGAAGAAAGGGAGAGGGTTGGGGTCGTCAGCGGCGGATCCACCCCTCCATCAACCCC CGCCCCCGCCCCGCTCCAGGCTCCCTGGCCCGACACCGCCCACACAAACTAACCACTTGTTTTGTCCACGCCCCCTCC CATGGGCACGCCCCAGGCCTTGGCCCCGCCCACCTACTCCGGCTGGACTTGTGCCCGGCCCTGCCCCTTGCGACCG GCCCTCGCGCCCGGCCTCACGTTCAGGCTCCGCCCCCGGCCGCGCCTCCCTCCTTCCCTTCCCGACAGCGCGGGAAC GGCTGCGGCTTCGGGCGGCCGGGTTTCTCCGGTCTCCCAACGCCGAGGAGAGCTTGTAACAGGCGCTGGAGCTGGC CCGCCACCGCCGCGTCAGGGACGGCGCTGGAGTCCTCCGTTCCCCTCAGCCTCTGAGGC
298_FANCF_01	25	25	AGGCTCTCTTGGAGTGTCTCCTCATCGGCGTCCCGGACGCCCGGGCCGGGAAAGAGTTGCTGCACCAGGTGGTAAC GAGCTGCATCCCCGAGGGCCCGGTTCTCCAGCAGGCGCAGAGAGAGCAGGACGTCACAGTGACCGAGGGCCTGGAA GTTCGCTAATCCCGGAACTGGACCCCGCCCAAAGCCGCCCTCTTGCCTCCACTGGTTGTGCAGCCGCCGCTCCAGA GCCGTGCGAATGGGGCCATGCCGACCAAAGCGCCGATGGATGTGGCGCAGGTAGCGCGCCCCACTGCAAGGCCCGGC

			GCACGGTGGCGGGGTCCCAGGTGCTGACGTAGGTAGTGCTTGAGACCGCCAGAAGCTCGGAAAAGCGATCCAGGTG
			CTGCAGAAGGGATTC
299_FANCF_02	26	25	CCTTCAGGAAGTTGTTCTGAGGCAAGCGCTCCCACAGGCTGCTGAGAAACCTGGCGGGACGCTCCGCTTCGGCCTT
			CCCCACCTCCTGCAGACGCTCCAGCAGCAGCTCTCCGCCTGGGTCTTCATCAGAGAGTCCTCCTGGAGATTTGGGTTC
			TCTCTATAGCCATTGAAGCGCAGCATGTGCACCGCAGACCGCCGGCGGGCAAGGCGGGCCAGGCTCTCTTGGAGTG
			TCTCCTCATCGGCGTCCCGGACGCCCGGGCCGGGAAAGAGTTGCTGCACCAGGTGG
302_FEV	26	27	ACATGTTGATCAGCAGGGGCTGGGAGGCGCCGCTCTGTCTCATCGCCGCCGGGACTGGGCGGTGGGAGATGGGGG
			GGACGGGGAAGGGGGGCGAGGCAGGCTTTGCGCTCGGTGGCACCGATCCCCGCCCGAAGCGACCGCGGGTGACAAG
			GAGGAGAAGACGGCGCCGGGTCCGGCAGGGCCTGGCGGGAGGGGGCAGCCCGGGCGTGGCGGGGGTTGCGGGGGGG
			TCCTGGAGAAAACGCTTCCAGCTAAGGGGCCGCTTGGAACCCTCCGGCCCCCGCGCCGGGCCGCAATTTCCG
			TTTTAATTAAAGCGCTGCCGCCTCGGCCCCCAGGACCCCGCCCCCGCCCCTCTTATCGTCCCATCGCAATAAAGTC
			TCCAACGCGCCGCGCCACAGCCAAGCGCACCCGGCAGCCCCCCGCGCCCCGCAGCCGGGGAGACGCGCGGGGGATG
			GGCCCGGGCCATGTGCCCTGATGGGAGCCTAGA
305_FGFR1OP_02	29	28	GGACACACCTCTGAAAGGAAAATACAACTCGGCACCGCAGTTGACTCGGCCAAAGGAAAAAACTTAAGCTGAAAG
			CTGAGGCCTGCCCGAAGGAGCCTTTCCTGTGGCGCCTGAGCCGAGGGAGAGGGCCGCGCATCGCAGCG
			CAGCCGCCCGTCTTCCCGTGGCTTCCCTACGGCCGCGCTCCCGCTGCTCCTTTCCGCCGGCCACGCGGGTCGCAC
			GACCTTCCCCTCCCGCCCACCCTGAGGCGCTGAAGCCCTCGACGCCGGCCTCGGGAAAGGCGCGGCCACCGCCCGT
			TTCGGATTCCCGTTTCCTTCCTCCGGGCGCGTCCTTCACCGTGGCCAAATCAGCCTCTCAACTGCTGG
306_FGFR2	30	24	CCCATCACCTATGCAGCCACAGAGGGAGGACACGGAGCGTCCTCCACAATGCTAGTCCTTCCGCGCCCCCCGCCCG
			GAGGACGGTGCACCCGGCGTCCCGGCTCCCGTGGCGCCCACGTCCCCGGCTGGCGAAGCTCCCCGAGGCGTCTTG
			CGCGGCGATTACCTTGAATGGCAACGCTCCTCCGCGACCTGTGTTGTCCCCGCGCCCCGCGTGGGTCGGGATGGAG
			AAAGCGACGAGCCCGGGGTTGCGGGGAGCAACTCCAAACGCAGAAGAGTGGTCCTTGGGTCTT
308_FH	28	25	GGGCCTGAAAGCAGTGCAGTGCCCCTTGGCGAAACAAACCACACAGTTCAGAAACCACTAGATGCACAGGCGGCCAGT
			GTCCGGCCAGCAAGGCCCAGCTATGGGGCAGGACGGTGCGGGAGCTGCCCCTCTCCCAGCACCCTCCGCCCACGCC
			GGCACTGTCCTTGAGGGCAGCGCCCCGGGGCTGGGGGCCTGCGCGCCAGCAGCGAAGTTACCTCAAAACGCCC
			CGGCCTCGGCCCGCCACGGACGGCTCCGAGGAGGCGCGGGAGCGGGCCCAGTAGGACCCTCTCTGACAGCCCCCG
			TCCCTCCCCCAAGCGCTCTCCCGGGCTGCGGCTCCATCCCTGCGCCGGAAGAGGCGTCCCGAGGCCGGGAGGCCCGC
			CACGCCGGCACGGGCGCTAAGCCCAGAGTCTGGCGCGGCCCGGACGCCCGGGGAATCTCTCCCGCCAAGTCGCGGG
			CGCCCAGGCCGGCAGGCAGGAGGGCTGAAGGTCAC
309_FIP1L1	30	21	CAGGTAATGATTCTGTATCAAGGCTGATTAAAGAATAAAAGAAGGCCTTTCTGAAGATTAAAAAACAAATAAAAAG
			TTGAGAAGAAAAGAGCACGAAGAGTAGAAGGGAACAATGGTGTACTCGCCAGCAATGGCAATACGGGTTATTAAAAA
			GAAGGGTGGGGGCGGGGAACCCTGGCCGACTCAGGACGCCACGGGAGGAAGCCACGCAAAATAGCAAACCGGGATC
			CTAGAGGGGCGGGCCCACCTCAGCGCGCAGGCGCAACCAGGCCCAGGTGGCCGCCGCGGAAGCGAAGCCACCTAT
			ACGCGCCGCGCCGCTTGGGTCTCCTGCGCATGCGCAGACGGACCTGCGCTGGAGGCTTCATCTTTGCCGCCGCTGC
			CGTCGCCTTCCTGGGATTGGAGTCT
310_FLI1_01	30	26	GGGCTCAATTGCTCCTGAAGAAATAAAGAATTAATAAGTCACCTTTTTTCGCCTCTGTGGACACCCTTTTGAAATT
			TTTTCTTCCAATTGACTTGGATCTCCTCTGGATTTTTTTTCCCTCTTTCCCCCGTCGGACTCTTAAATAAAAGTGA
			GCAAGTCCAAAGCGTGGTCCGGAGAGCGTGGACAAGGTAACCTGTTTTGGATGTCCGGGAGAAGGGAGTCCGGCCG
			AAAGGGCCCAGCCCCTCGAGGCTGCTCCAACTGGGGCGCGGCGGCCCAGGAGGGAGGCGGGGAGGTCTCCGGGT

			TGGGCCGGGGAACGCCGGCCTCCAGGCTGGGTAGGGAGGACGGTCCAGAGCGCGGGCCTCCGGGTCTCACCCGGG
			AAAAGTCTGGGTCTGCTCTGCGCTGTTGCGTGCTGCGCTCCTGGGACCTGCTGACTGTCCTAGAGGGAACGTCCCG
			CGGTAGTGTCAGTTCCCTGGGGACCAGGAAGGGCGACTCTTGCCTGGGAGTCAGTGCTTGGGCC
311_FLI1_02	26	27	TCCAGGACCAGGGCTCCTGGAGCTGTCGCCTCCGAAAGGGTCCTGCGTCCTTCGGAGCCGCCTCCGTTGCAGGGGC
			CGGCTGTGAGCCCGCGCCCCGCGCCCGGCCATTCCCACCCCAGCCGCCGCCGCCAAGCCTGGGTCTAGGTTG
			CAAAGTGCAACCCAGGCGGAAAGGTGAGGGTTGGGTTCGCGTCTCACTTCAGAAAAGTTGACTGCTGTCTCTGAA
			AGGG
			GCTGCAGGTGGCTCTCTTAAGGATGCGCGTCACCGACCGCAAATTCCCTCGGACTGGTGCAAAGTGGAAGGGGGGA
			GGAACCCTCTCCCCAGAGGCAGGGACCGAGGCGGGAGAGCGGAGAGGTTGGGCAGAGCCGAGCAGCCGGTGCCTGGCG
			CAGCGCTGCAGCCGAGCCCACGTGCCCGCCGCGGTCCGCAGCCTGTGCTCGGCGGCCCCCCGGGCTCCCCGACTGC
312_FLT3	25	28	GGCGGGGAAGATTGGGCGCGGTCCCCGCCGGAGAAGTTGCACTGGCTCCGCGGCTCTGCCGCCTTGCTGCCCCTGTG
			AGTCCCCGAACTCTGTCGTTTGGATCCGGGGCGTGGGGACTGCAGGGAGCCCACAAACCACCCTCCTAGTGCGCTGG
			GATCTTTGAGGCCCTGAGAAAGGCGCTGAATCCGCTCGGCACGCTGGCAACTCCCGCCAGCGCACAGGCGAGCATT
			CCATTAAGAACCATTCCATTCTTAATTGTGGACTGATTTCCTTTGTCTCTGCCTCCCATCTCCCTAGGATGCTCAGGA
			CCCAGTCAGCGGCGGGATCAAGAAAAACAGGCAGGGTTTCA
			TCCAGGAGTCCCAGGCAGAGCCACAGTCGCAGGCACAGCGCGGCGCCCCGCTGCATCTCCGGCCGCTCGCGTGGG
			TCCGACCCGAGCGGCCGCGGCTCGGGCTGAAAGTGTCCGCGCGGGCGCCGGCTGGCCTGGGCGGGGCGGGGCGG
313_FLT4	27	24	GGCGGGGGCCGGAGGCGGGCCCGGGATTCAGGCCGCTCCCCGCGCCCCCCTCCCCCCGTCCCTCCCAGCCCGCCGC
			GGGGCGTCCGGTGCACCCGAGCAGTGCGCGCTCCGCACCACAGGGTCCGGGCCCCCTCCTGGGCGGCTCCGGGCGC
			GGGGACGCGGGTAACGCAGACGGTCTCGCGATGCGCTCCGGAGGTGATGGAGCCTGGTGGGCAAAGGGGAGCAAA
			CCTTCTCAGTGTTTTGATTGCTAGGAAGCAAACCAGCGTGGAGGCGCCGGCGACACTTTGTTTACTACGGAGCAGC
			AGAGCCGAGTACTCGGGAAGCCCGGGTGGGAGGAGGCGCTCGCTGCTCCCTGACCTCCGCTGCGGGCCGAGCCCGG
			CGGGCTGGCAGGGCAGGGGGCCGAGGGCCGGGGGTGGGCGGGCGGAGGCGGCCGCGCGAGGAATTCTACTC
316_FOXO1A_02	30	25	AATCGCTCCCCTCCTGGCTCCACCCACGATGTCTTTGCTGAACGACGTGGGGAATCGGTGGGTTTTGTTTGGTTTA
			ATGTTTTCTTTCGCTGCGATCTGTCAAGTCCTCCGGCCCCCCTCGCGAGCGGCACACGCCCCCCACCCCCGGCGCCG
			CGGCTCCTGCAGTCGAGTCCGCCGCCGAGGGACCCTTCTCCGTGCCCACCGGTCCGCACACCCCCGGGCTCAGCCTGTG
			CCATTCGGTCTAGCCAGAGGCGCGTCACCCAGCCGGCAGCCCCCAGCCGGATTCACTGTATTCTTGACCTTTTTTA
			AAATGCTAGAAATGAGGAACAGGGGCTCCGGCGCGGGGAGGAGATTATCTGGCCTCCCCTG
			TGAGAAACTGTCAGCTTGGGGAGGCCGCGCCACACGACTGGACCCCGCCCCCGGGAAGCCTCCCCGGAGCCGAGGGCC
317_FOXO1A_03	25	28	CCCGGGCCTTCTCCTCGGAGTCGGGAAGTGCCTGCCCCCCACGCTAAGTCTCCTGGCCACGCTCTGAAAGGCAAA
			AATGGCAAAAATCCTCCTTCAAGGCACCGCTCCCTCGACGCGCACCGCCACTCCCGACTCCCTCAAAACATTGGTCG
			CAAAGCCCCCCCCGCCTGGTCCTCCATGCTCAAGAATAGGG
			GGGGGAAACTGTCAAGATGGCAGCAGCGGGAGCAAGGAGGTGATGAACGTGCTGGTCCGGGTTTTCTAGCAGCCCG
			GGAGACTTGGCGCTTCCCGACCTGTTGGAAGATTTATGTTCCGACTCGCTCCCCTCCCCGGATCCCGACTGGGAAG
319_FOXO3A_02	26	26	GGGGCGGAGGGGACGACGTCCGCGAGAATGCAAACCACACAAAACCCCGAAGTGGCCGTCCCCGCCGGGCTCGAAC
			CTCTGCGAACACCCGCTGGGCTGCTGCTCCCCCCTTCTTTCTGTCTTTCCTTTATTTTTTGGAAGTGACAAGGGCCC
			ATCTGCGCCCCAGACCCCCCGTTCGCCCCTCTGGCCCGCGGGCGAAGAGGGGAGAGGGAGCTGCCCGCGCAGTCCCCGG
			GCTCGGGCCATTCGACCGGGTGGGGGGGTGACGGGGGGTCGCGGAGGCGGCCAGGCTAGGAAAGGGGAGAAGAGC
321_FUS	23	22	ACTGTGCCTTCATGGGGGTGGAGATAGATCGTGGGCTAGTCCTGCCGAGGAGAGAGGGGTTCTTCCTCAAAAAATA

			TGATTATGTATAGTATTCGCATGATTCTAGTTAACTTGTTTCCCTTCTGCCTGCTCGGACCCTCTACCTAC
			GAAGGGGGCGGAGTGCGTTCCTGCCTCCCCCTGCTCTTCCGCGTTTGGTGCGCGCCTGCGCGGTGCGTAGGCGGCG
			GAGCGTACTTAAGCTTCGACGCAGGAGGCGGGCTGCTCAGTCCTCCAGGCGTCGGTACTCAGCGGTGTTGGAACT
			TCGTTGCTTGCTTGCCTGTGCGCGCGTGCGCGGACATGGCCTCAAACGGTAGGTAAGGGCGCGAGGCGACGGCGGC
			GGCGCACCCGGCCGAGGCCTCCCAGCTGGGCTTTT
324_GMPS	23	27	GGGGCCTGTGGCATGTTTTATCTCGGGAGCGGCGATGCTTTGTTGATCTTGTCTGCGTGTCGAGGTCCGGGCGTCG
			GGGAGGGCATCAGCTCCCCCGCGGCCGCGTCGCTGGCCCCCCGCCCTCCCCCGCGCCGCTGTGGGGCGCAGAGCCCGCG
			AGCGCGGCGCGAGGGTGGGGGTAGGGCGGCGAGCGGGCTTGTGTGTCTGCGTGTCGGGGTGGGGGCTTCCTCGGCT
			CCCACCCCGTCCCCTCTGGGAGGCTGGGGGCCCCGTTGTGGCGATCCCCGGGGCCCCGCCGAAGGGCAGGGCAGGGTCGGG
			GCCTCCTGTGCGGCGTTGGAGCTGGGCCGGCCTCTGGTCTTCCCGCCACCCCGTTTCCCGCCTGCCCTCGGCGAGG
			CCCGCTCCATTCCCCCCCGCCAGCCTTGGGCTCCGCGGCGGTTAGGCCGGTTCTGGACGAACCCCTCGGAGCTGCAC
			TGTCTTCCCCCCTCCCCCCAACGCCCCCTGCAGGCCCGCGTGAGGGCTGGTGGCCCCCAGGGTCGCGCACTCCGTTCTCC
			CTCCCCGCTTCCTTCTTCAGAGAGGAAAGGGTGTGTCC
325_GNAS_01	21	25	GGTCCTCTGAAGAGGCTGGGGCGTCATCGGGGGCCGGTTAGAAGCTCTGCTCCCCGGCGGGGACACTCAGTCGCGTC
			GGCACCGCGGAGCGGGCTGCGTCAGGTGGCTGGCCGGCGCGCTCCCCCTGCTCTCTGGCTCCGGGCTGCGGCGCGC
			GGCGGCTGGAGCGAGCCCCCTGTCCCGGCGCGGGCGGCGGCGGCCGGCAGGCGCTGCCTTGCGTGTGAGTGC
			ACCTCACTCACATGTAAGTCGGGGAGCGCCCGGGGCCTCCCGCGGAAGTGCGAGTCGCCCGGCGCAGGCAAGAGCCG
			CCGGGTCCGGGACAAGGCAGGGGCGCCCGGGCGCCGCTGCCTTGCCCCGGGGCGCCTCCCGGGCACCCCCCCAATTCT
			CTCTCTTTTCTCTTCTCCATTGGCGTGCCCAAGAGCCAAACCAAGGAGCGCCTGAGGGTAAACAGACTCCTGCCAT
			CCGCGCCTTTGCACTTTTCTTTTTGAGTTGACATTTCTTGGTGCTTTTTGGTTTCTCGCTGTTGTTGGGTGCTTTT
			TGGTTTGTTCTTGTCC
326_GNAS_02	26	25	GGGTGCTCAACTTCCTGCTGCAGAAGCGCACGGAGCAGGGCCGCGGCTGCGGCTTCGTGTTCGGGGCGACCTGCTG
			CTTCCGAGTGTTCCTGGGCTGCGCCTTCTTCTCCTACTTGGGCGGCCGCGCCAAGCGCAGAGGCCGCGGGCGCTCC
			GGGGCCAGAGGCGCCTTCGGCTCGGCCATGGCGCCCGGCGCCGGGGGCGCGAGGAGCGGCTCATCTAGTCAGACC
			CCCCACCCCGCCACCGCCACCAGACACCACCATCGCTGTGTAGTGTGGGTTTTTATTCGTGTTCGTGTGTGTGT
			GGACACATTTTCC
327_GOLGA5	25	25	GAAAGCCACTCTGTTGTGGGGTCCTCGCTTCCCTTCCACGTCTCCCGGAAGCGGTAGCAGGGCCCCCGGCGGGTCGG
			GGAGGAGGTTTACTCAGCTTGGGCCCCCCTCCGGGCCAGCCGCCGAGGGGGCGCGGCCCAGGACGGCGGCTAGGCCG
			TAGTGCAGCCTCTCCGGAGTCCTCAGGTGAGGCGGAGGCGAGGGCCCACTGGACGAGACGGGGGTGTTAACGGTCC
			TAGGAGCGGGGGCGCAGTCCCTTCAGTGGAGACCCTGGTCTCTCCGTTTCTTCTTTCGGGTCGCGCTCATCTTCGCCC
			TGTTAGGGGCTGAGGAGGGTAACTGGAGAGACTCCTTGGGCT
328_GPC3	25	25	GGGCTGCAGTCTCTGGAAGAAGGAGCGGACTTGGTGACAGGTGGCGTCCGGCGGCGGCGGGGGCTGCGCCTGT
			CCCGGGAAGTCCAAGCTGAGCAGCATCGCCACCACCAAGCACGCGGTGCGCACGGTCCCGGCCATCCTGCTTCGCA
			GGGAGCTAGGAGAGCGCGGGAGAGTGGCAGCCGGAGCGAGAGCAGTCCCAGGACTCGGCAAGCCTGGCAGTGGCCC
			TGAGG
329_GPHN_01	25	25	GAGGTCTGGGACCTATGAGGCTGCTGTCCCTGCATTGCCTTAGGCTTTTCGCCTGTGGTGGCCCTTCTCTGCGGCC
			TCGGGAGGAGGGAAGGCTGAAGAAGGGAACCGCGGGGGTGCATTTTACAACCGCTGAGAACCGCCGGAGATTGGGG
			GTGTTCCCGCGGTCCCCTCCCCCAGGAGCCCGGGTCGACCCCGTGGGATGTTAGGCCCCAGCGCCTTC
			GGAAGCAAAGTCCTGGGCCCCCGGGACCGAGGGGCCGGTGCGGAGGGCGCTGCGGGGCTCCGCGCTGTCGGTGCA

			GGCGGCGGGATCCCGGCTCCGCAGTCTGAAGCATGCCGCTCTCGGCTGGCCTGGGCGCATCCTCCGCTAGTGCTCT TCAGAGAGAGGGGG
330_GPHN_02	30	24	TCCTCTCAGTCCTGCCATCTAGCTGCCTTGGGTCTCGCGCTCCGCAGAGCGTTCCGACACTCTCCGGCCTCGTTCT GCCGCCTCCGCGCGCTCTCCCCGTGCGGCCACCGCGCCCCCCCAAGCTTGCCTCCTTCTTGCCGGACTTGGGGCCGC GCGCCCTGACTCCTTCCCCTCCCGCGGACCCGCGCACTCCCGGCGCGCCTCTCCCCCACGCAGGCCACCGTGCAC TCTGTGGCCTCCCCCCTCCTTCCCCGCTCTCCTCGCGCTTCTCTGGCTCCCTAGCTGTCGCGCTCTCCTCGGCGAGC GCGCTCCCGGCCCGCGCGCTCCGGGCTCCGGTTTCTCCCGGCTCCTGTCAGTGCGGTGACTGCGCTGGGAAACATG GCGACCGAGGGAATGATCCTTACTAACCACGACCATCAAATCCGTGTCGGAGTCCTTACAGGTAACCGGGGGAGGA GGTCTGGGACCTATGAGGC
331_GPHN_03	25	23	AGGGAGAGCCCACTGAGGAAGCCAGCGGCTAGCACGAGGCAGGACATACCTCCCTCTTCGCCCACGGCGGCCT CTCTGTCATAGTAGCCACCGTTCTGCCACTCATGCAGCTTTCTAAGACACCTCTCGGTTCCCCAGCGCTTTCAGTG GGGCGGCCGGCCATTCCCGAGGGTTGCAAGAGGAGGCCCGGGGTGCTGAGCCAGCCTCGCTGCCCCCGCGTAGAAA GCCGGCCCGCCGGCGAGAGCCAGCCTAAGGCGCGGACAACCAACGAGGTGTCAGGCTCGGCAGGGGATTGCTTCTG TCTGGG
332_GRAF	30	25	GCTGGACAAGACCAACAAATTCATCAAGGAGCTCATCAAGGACGGGAAGTCACTCATAAGCGCGCTCAAGAGTGAG TGTCCCGAGCCCCTCGGGGACGCGGCTCCGGGGCGGAGGAACTGGGAGGTGGCGCTTAGCCCGGGTTGCCCGCGC GTCTGCCGGGTTTCTGCTCCCGGTACACTGGGGGACGGGTGTCGACGCCTCCGAGGCAGGAAGGATACGTAAAGCG GGCGAACCAGCAACCATCAGATGAAGAGAGACCCGTCGCTCCGCCTTTTGCGTTCAGGGATGGTCGGGAGGTGA CCCAGCGCGGGTGGTGCTCTGGGGCAGCGCGGGTGGGCGTGCGCGGCACGCAGGTGTCCCAGCAGTGGGG CCAG
335_HIP1	25	25	CCCAGGCCAGCTGGGGTACCCTGGGGTCCCCGACCTTCCTGGGATCGCCCAGATCTGCACGTCAATGCCCCCGCTC ACTACACCCTCGCCCCGTCTTCAACTGGGGCCTGCAAGACTCCTACTCCCTTCAAAGCCCCCTCCCGGACACCGCGT CCCTCAGGGTGCCCCCAGGGATGCCCCCGGGGTCCCCCGTCCTCACCTGAGTCCGCTCGAAGCTCTCGCGCTCCGCCG CCTCCAGCCCCAGCGCCGACCCCGCGCCGGCTCAGCACCTTGGGCAGTGGGTTGGGCACCTGCTTCATGGAGCTGGC CATCCGATCCATGTCGCCGCGAGGAGCCGAGTCAGGGGCCCTCGGCTGCCCCCGGGATCCCCCACGGCGCCGCCCGCC CCGCCCTACCCGCGGGGATCCGGCGCTAACGGGACGGCTCCCGCCTGCCATTGGCTGTGAGTTCTGCCAGTCTTCC AGAGACCCCGCCCCTCGCCGAACGGCTTCCCCCGCCCCCGCCCCTTCAGGAGCCCCTCCGCTGGCTCGGCCCCC GACTAGCCTCTCGGGGCCTCGAGGCGCGTGGTGACTGGTCTGGAGTCCTGTCAG
336_HIST1H4I	27	27	TTCTCTGACCACTTGATAATGTCAGGACGCGGCAAAGGAGGTAAGGGCCTGGGGAAAGGGGGTGCCAAGCGCCACC GCAAGGTGCTGCGCGACAACATCCAGGGTATCACCAAGCCAGCCATTCGGCGCCTTGCTCGCCGCGGCGGCGTGAA GCGCATTTCTGGCCTCATCTATGAGGAGACCCGCGGAGTGTTGAAGGTGTTCCTGGAGAACGTGATCCGGGACGCC GTGACCTACACGGAGCACGCCAAGCGCAAGACGGTCACCGCCATGGACGTGGTCTACGCGCTCAAGCGCCAGGGCC GCACCCTCTATGGCTTCGGCGGCTAAATGGCATTTTGAAGCCCAGTC
337_HLF	29	22	GGCCCAGGGAATCTGGCACCTGCTCCCCTGCAACCAGCCAGTGCTGCAAGGTCCCCGAAAATCGGCGCGAGCGGCG ACGCTAAACACGCGGCGGCGGGCGAGCGGCCAGGCGGGCGGTGCCGCGCGTGGCCCCGCCCCCGCACGCCTATG GGCGCGAGGTGCGGGCCCTGACGTCACTCTTGTCAGGGCCGCGGCACATGGGCGGCCGGATGCGCTGAGCCCGGCG CTGCGGGGCCGCGGAGCGCTGGGGAGCAGCGGCCGCCGGCGCGGGGAGGGGGGTGGGGTGGGACGGCGCACCGCCT CCGGTGCTGGCACTAGGGGCTGGGG
338_HMGA_01	25	27	GATCTGGGCTGAAGGGGCTAGAGTCTTGGGGGCCGGAGGCTCTTTCTCCCGCCTCCCGGGGCTGCTCGCGGGTCGG

			GGGCTGGCGCGCCGCAGCCGCCCCCTTGGCGCCCTCCTCCAAGCTCTCGGTGGCCCAAGACTCGCGCCCTCCCGAC
			AAAGAACGCATGGAGACCCGGCTGCCTGGTCCTTTTTGGGCTCTTTAAA
266_DDB2	24	26	TGAACAAGCCCTGGGCATGTTTGGCGGGAAGTTGGCTTAGCTCGGCTACCTGTGGCCCCCGCAGTTTTGTAGTCCCC
			GCCTTGTTTCTCCCCCAGAGGCCTCTCAATCCTCCCTCCATGATCTTCGCATAGAGCACAGTACCCCTTCACACGGA
			GGACGCGATGGCTCCCCAAGAAACGCCCCAGAAACCCAGAAGACCTCCGAGATTGTATTACGCCCCCAGGAACAAGAGG
			AGCAGGAGTCCCCCTGGAGCTGGAGCCCGAGGCCAAGAAGCTCTGTGCGAAGGGCTCCGGTACTGCCTGTGCCTGCT
			GCTTGAATATATTTCCGCCTTTTAGGGTGCTCGCGCAGGAGGCTGCAGCGGGGGATGGGTGCTCCGAGGCTCCCGAGG
			CCCGCGCAGGTCACGGGTGCCTCCGGCTGTGCATTCTACCTGCAGGTCCT
364_LCK	30	25	CCCTGCACAGCTGGTTCTTCAAGAACCTGAGCCGCAAGGACGCGGAGCGGCAGCTCCTGGCGCCCGGGAACACTCA
			CGGCTCCTTCCTCATCCGGGAGAGCGAGAGCACCGCGGGTGAGCGGGCGGCGGTCTCGACCGGGCGCGGGGGTGCC
			CCGGGGTGTGCCCGAGGGGGGGCGCAGGGTGAGCCCGAGGGTGGAGACACGGGGTGAGTCGGAGGGGGACGCGGGAT
			GAGCCCGAGGTGGGGGCGCGGGATGACCCGGAGTTGGGGGTGCTGGGTGAGCCCAAGGTGGGGGCGCGGTGGCGGG
			CCAGACTCACTGCGTTCTTTCGTCGCTTTGTCCATCCATTCATTCAGGATCGTTTTCACTGTCGGTCCGGGA
			CTTCGACCAGAACCAGGGAGAGGTGGTGA
367_LCX_02	25	24	GGTCTGTCCTGGGGAGACACTGCTGCTCCGGGGGGCTGACCTGGCGGGGAGTGGCCGCGCAGTCTGCTCCGGCGCC
			GCTTTGTGCGCAGCCGCTGGCCCCCTCTACTCCCGGGTCTGCCCCCCCGGGACACCCCTCTGCCTCGCCCAAGTCA
			TGCAGCCCTACCTGCCTCTCCACTGTGGACCTTTGGGAACCGACTCCTCACCTCGGGGGCTCGGGCCTTGACTGTG
			CTGGGAGCCGGTAGGCGTCCTCCGCGACCCGCCCCTCGCGCCCGCCGGGGCCCCGGGCTCCCAAAGTTGTG
			GGGACCGGCGCGAGTTGGAAAGTTTGCCCGAGGGCTGGTGCAGGCTTGGAGCT
369_LHFP_02	26	25	AAAGGGGGCAAGAGGCATTTTCCAGCCGGCTCTGGACGAAGGGAGGGATAAGGATGGGAAGGCAGCACCCCCCGG
			AGGCAGACGCCAAGAGCGGACGCGGCTGGCAGGCAGAGCCGACGGATCCGCCGAGCTCAGGAAGTCCGGAGCCCGG
			GAGCAGCCCAACTCCGGCTCCGGGGCAGAGAGGGAGCCCGGGAGAAAGCAGCGGAGCCCCACGCCCACGGGGCAGCC
			GAGTGATTTACTTACATGGCTGGCGGGCGGCGGCCACCTTCCCTCCCGCGTCCCGGGCGCACACACAACTTGCTGT
			CTTTCTCGGGCGGGAACATCCACGGGAAACCGGACCGTCCTGCCCTTCTTTGCCTCTGTCCCTAACAGCCGCAGAA
			CCCCGGGGCCCGACCTGGAAGAGCAGGGGTTGGCAG
373_LYL_01	25	25	AGGAATGCAGGCTGGGTCCCAGGCCCGGGATCCTCCACCTTTAGGCCCGCTCCCCCTCTTACCCCAGCACTGTTCTT
			GCAGCCTGGTGAGTGCCCTGGCTCTGTCCCGTCAGGGCTGGCAGTCTGGGCCAGGGTGTGGTTTCCAGCGTCAGGC
			CAGGCTCTGCTGTCTCGCGAGGGTCCGGCCTCAATGCTCCAGGCCCCGGCGTTGGGCCGCGCCTCCTCGTGGGCCT
			CGGAAGGCCAGGATAGCCGAGGTCTCCGCGTAGGTCCCCCCCCAGGGAAAGTGAGCGGCTCCCGGGCCGGCCCGCCT
			TCTCCCCGCCCCCGGCGGCCCGGTTTCCTCCCTCTCACCCCTGGCGGCGCAGCGGCCGGAGGATGCTGGCCCAGTG
			CAGATAAGGGCCAGGCTGCCTGGCCGCGCCTGATAAGGAGCCTGGCTGACCC
375_MADH4	28	23	GGCCCAGGCCCAGGTCCAGATTCAGAGCCGCCCGGCTGGCGCTGCCCTGTAGGCGCCTGCGCAGAGCGACCCT
			CCCCGTCACTCGGAGCGGGAGGCGGGGCAGCCGGGAGAAAGGAAAGGAAGCTGCGGGGGAAAAGGGCCAAACCCTGAAA
			TTACCCGGATGTGGTCCCCCGCGCGCATGCTCAGTGGCTTCTCGACAAGTTGGCAGCAACAACACGGCCCTGGTC
			GTCGTCGCCGCTGCGGTAACGGAGCGGTTTGGGTGGCGGAGCCTGCGTTCGCGCCTTCCCGCTCTCCTCGGGAGGC
			CCTTCCTGCTCTCCCC
381_MECT1	25	25	GGGGTGCCTGGCCCCCACCCTTGTGAATTGGGAGGATCTGGGTCAGGCCGTCTCCCTCTTGGGGGCTCCAGTGCCCC
			AGCCGATCCGCGGTCCTTGTCCAACAGCCCAGAGGCCGCTGTCCAGCGGGCCAGGAGGCGGATCACTGCGTCGGCG
			TTGAAATTTCCACTCGCGCTCCACCGCCCTTCCCGCGGGCCCCGAGCGCGCGCCTGGGCGCGCGCATGCGCCTTCG

			CCCCCGCGCCGCGCGCCGCTCCTGTGCGCCTGCGCCGCGCTCACGACCGCCGGCGCGCCTGCGCACTGCTCGCCGC
			CCGTGGGCCCAGCCGGCGCTTGCCGCGGTGGCACGGGCGAGTGGGGGGGGCGAGGAGGTGGAGGAGGAGGAGGAG
			GAGGAGGTGGCGGCGAGAAGATGGCGACTTCGAACAATCCGCGGAAATTCAGCGAGAAGATCGCGCTGCACAATCA
			GAAGCAGGCGGAGGAGACGGCGGCCTTCGAGGAGGTCATGAAGGACCTGAGCC
382_MEN1_01	30	25	CTGCTTCCCCACCCTCTTCAGCCTCTGCTCACCGGCTTCCCCTCTTTGTCGGTGAGACCCCTCAGCCGAGACTGC
			AGAGCCTTTTTGTCCCCCACAATTCCGGGACGCCCGGTACCCGATGGGGTGCGCCCCAAGCACCCCAATGAGGAGC
			CCCAATGGCCGCCCCGCCCCCTCTCTACGACTGTGCCCCCGGGGCTGTAAAGTCTGTCCAGAAAGCGCACCCAGGT
			CAAGCCCCCAAACCCCAAGGAGAGTCCTGGCCTCGGTCCCCCTCGCCCACCTCCGCGCTTACATCCCACACTAGGC
			ACCGCGGCGCACGCCGCCCGGAGCCTGCTGGGACATGAAGTCCCGCCCCTAGGGTCGCACTACCCGCCGGGAAGTG
			GAGTCTGGGCCCACCCC
385_MHC2TA_01	25	25	ACACAGCAAGTCTGGGAGGATGGGGGGATGGAATATGCAAAATGTAGGGCCGGGAAACACCTCGTTTCCAGCATCC
			CCGCAACGACTCTGCGCGGGAACCAGGAGCCGGGAACCCGGAGCTTGGCTTGCTGTGCCCAGAGCTCCGGGGCCGT
			GGGCGGGTGGCAGGAAAGCCTGGCGGCAGCTTCTGCAGAGAAGCCGGAGCGCAGACTGGGAGCGCGGAGCAGACAC
			ACTCCCCCGGCCACCCTTGGCCGACTCCGCGCCCGGGATCCTGCAGAGGTGCGCGCCCTTCTTGTACGCCAGAC
			TTTGGACCAGGGCCGCCGTTCCCTGAGCTTCACTTTCCCTGTTGGGTCATATTCCATCTCTAACTCTGGAATCTTG
			GGTATTGGGCTCTCCAGGCGGGGGGCCCTGCTCAGGGAGGCAGTAGG
390_MLL_02	30	25	GGGCCCCTTCCACCCAGTGTATCATAATGCCCAACGCTCTCCTCCTCCCCTCTCTTAATCAGAAACGTGCTCGCG
			AGCCCCCCTCCCTCTGCGTGCATACATTAGGGTCTGCTTTGCATGCAGCGGCAGGCAGAGACCGGAGGAAGAAGGG
			GCGGGGGCGCTTTTGCCCGCCTCTTCCCTCCAGGCCCCGTTAGCCACCCAGCTTCAGCTTCGTTGTAACACCGCGT
			CGTTAGCGGAGCACGCCGTGGCCTCAGTGCCCGGGCTGGAGAAACACAACCCAACTCCCTGCAGAAGGGCACGAAA
			GCCAGACGAGTGCACAGTAGAGCGAGGAGGTGGCAGGAGACCTGCCAC
392_MLLT10	29	25	GGGCCAGTCTTGGAGGAAAAGGCCAGCAGGTAGGTTCCCAGGGCACGGAGATGATGCCCCCGGGACTCCCCTCTG
			GCGATTCTGAGAAAACCCCTTCCCAGCCCTGGGCGTCCACCTCCCCCGCCACCTCCCAGGCCTCTTCCCGACGCTC
			ACACGCGGCCCGCGCCACCAGCGCTGCAGAGGGCGGCCCTAACGTCCCGCCCCCGCGTGCGCGCCCCCGCGCCCG
			TTCATTCCGGCCTCCGCGCCGCCGGCTCCCCCTCGCGCCCACCCCCAGCACACCTCGGCGGCGGCGAGCGGCGCG
			GGGGAGGGGGACGGGGCCCCGGAGGTAGGCCGGGGGCAGCCAACAGGCCGCGGCACGCCAGGGCTAGCCCT
			CGCCCAGGCCTCCTCCCTCACGCCGGCCGCAGGACGGGCGCGCACGCCAAGTGACGCTCCGAGGAGGAAGCGCAGC
			CCCCTTCCCCTCCCCTCGCTGCCCCTGGCCCAGCGGGAGCCCCCCCCTCCCCCCAGTGCGCCTGTGCGGAGGCCCTCT
			TGATTATGTGTGCC
393_MLLT2	25	25	GCAACTTTCTTGACAGGGGGTATCCCGGCGGACTCGGACAACTTCAAGTGAGCCCAGAGGCAATTTCTTTTCCTTT
			CTAACTGTGGCCCGCGTTGTGCTGTTGGCAGGCGTTGGGCGCCGGCGGTCTTCGAGCGTGGGGGCCCGCTGG
			CTTTCCCTTCTCAGAAACTGCGCCGGGGGCGCTCGCTTGCCCCGGATTCGGACGCGGCGCTCCCCGGGCTCGTCTG
			AAGTGCAGATCGCCGCAGAGGCCCCAGTGCCCGGATGTCCATCAGGATTAGCGCGAGCCAATACGGGCCGAGCCCG
			GGGCTGCGCCGAGGACGCCCGGGGCTCGAGAGCAGGTAGTCCCGTAACATCGGGGCGCCGCGCCGGACGCGTCCC
			CGCCCGGCTCCCGCCAAATGGTGAGCGCGGCGCTGGCAGCAGGGCCCGCGGGGTGAAGGCGCTCATGGACGGAAGAC
			CCCTGGCTCTATAAGCTG
394_MLLT3	24	25	CTCTTTTTGGCCTAGGAAAGCTTTCGTGCAAGTGGAAGACGACTTTCTCCACAAAGTGCTGTATGTTACTGTGCTC
			CGGACCGCGTACGAACACCATCCAGTCGTGGTGAAGCCCTCCACGGTGGGTTTTTTCCTCACCTGGGCGCGGTGC
			CCCAGCTCCAGCTTCACCTGCACGGCACACTGCGGGCAGGGGGAGGAGACAGCCGTGAATAACAGGAAGGCGAG

			GTTTCGGCAGTGAACGTTGCGCCTGACATTTTTTTCCTCCTTCTTGAAACGCACATAAAAGGAAACGGCGGTGCCC
			TCTGCATCCACGTTTCACGCGCGTGGGCGCGCACACTCCACACCCCCAAATATACCCGCCCCGGCCCGGCTTG
			GCCCCAGGCGCCCCGGGCCCCGCATCTACATCGGACAGGATTGTAACGGAATGTTATCCCCAGTCGGGAAGGGGGT
			CGGGGAAAAGAGGGAGAACACACTCA
395_MLLT4	24	24	CAGGCTGCCAGCTGGGAGGGGAAAGTCAGTATATCACAAAGTTCGGGAGGTGCGGGCTGCCTGATGGCACAGGCCCGG
			AGTCGGACGCGCCTCCGAGGAAAGGCGCGCCTTCTCCACCTTCGGGGCCGCGAGGAAGGGCCCTCTGCGGCGGCCTCT
			GCCCGGAGGGAGGCGCCGGCCCCAGGCTGGCTCCCTGAGAGGAGGAAATCACGCTCGCTCCTGGCCTGGTAAC
			AATGGGGGT
			AGGGTGACCTGAGACAAAGGCTTCCCGGCCCCTGTCTCCAAGTCGTCCATCCCTGGGGCGTAGGCACGTTTTAGTG
			AGCCCTGTCCGGCGAAACCCGAAACTGCGGCCACCTTGGCAGCGGTGGGCCCCAAAAGGAAATATTCAAATATTCT
396_MLLT6_01	25	25	GAAACTCGTGCATGATTTAGGACTGACATTTTTACGTTTAATTTTCTTGCAGTTTTATTCTTGCTAGTAAAGGTAA
			TTCGTTAGAAACCCTTAAGTGCAGTTTCTCCTCTGTGTCTTGTTTAACTTTTCGTGTTAGCGAAATTCACAAATTT
			GACCAAGGAACCGGAGCGCGGCCGTCCTCGCCGGGATTCCGGTCATCGCAATAATCTGGCTCTCGGCCCCTACTCC
			CAGGCACGGAGGTCGAAGAGACGGGCTTCCCCCTACACCGCCCTGTGTAGATGTAGCCTCTTCGTCCCGGCAGCCCT
			CCGAGATTCCCTGTGTCCACCGGAGCGAGGAGAGGTGTGGGGCTGCAGCCCAGA
			CACAGGTTGGGAAGAAGACTTTGGGCCGACGCCCCTCACTTCTCCCCCAGACCCAATTGCAGGGACTTTAGTCCTC
			TGGAGTGCTGCGTGTGAGTTACCTTGTGTGTCTGTTGCGTGCCTAGAGGTCAAGTGTAACTGGTGTTCGTGAGCA
398_MLLT6_03	26	25	CCTCGTGGTTTGCGGGTCTCTAACTCTCGTGGGTCTCTAAGCGCACCCGCGGGGCTGGAGCGGAGGTTCGTGTCTCT
			GGGAGGGTCAGTGGTGTGACTGAAGCTGGGAGTTAGCTCGTGTCTGTGGGTGCCTCGGTGTGTGTCTCTGGGGCTC
			TGAGTCCCC
			TGGCAGGAATGTGCCTCCTGGCCCTCGATGCTTCCCCCCTGAGGGGAGGCATCGTGAGGGACTGTGGCAGGCTTCA
			CTGAACGCTGAGCCGGGGAGGTCCAACTCCACGTATGGATCCGGGGAATGAGAATTCAGCCACACAGAGGCTGCCGCG
399_MLLT7	25	25	ATCATAGACCTAGATCCCGACTTCGAACCCCAGAGCCGTCCCCGCTCCTGCACCTGGCCCCTTCCCCGACCAGAGA
			TCGCTAACCAGCCGTCCGAGCCGCCCGAGGTGGAGCCAGATCTGGGGGAAAAGGTACACACGGAGGGGCGCTCAGA
			GCCGATCCTGTTGCCCTCTCGGCTCCCAGAGCCGGCCGGGGGCCCCCAGCCCGGAATCCTGGGGGCTGTAACAGGT
			CC
			GGCACCATGAAGAAGTCTTACTCAGGTGGGCTTCGCGCCCGGGGTGGGGAGGGGTCGGTGTCCCGGGACCAGCGCT
			GCTCACCTGAGTGCCTGCGGCCGGGAGTGGCGAGGCGCCCCCGGAGCTGAGCGAGTCCCCGCGGCGGGCACACTGC
401_MSF	30	25	AGGTCGAGTTCCTCCCCAGGACAGGGCCGCTGTCGGGCCGCTTTCGACCTGAGCCGACCGTCCCCTGCGCTGTCTCC
			AGCCCTTGCTCGAGTGTCGGAGGGGCTGCCCTGGGGGACGCTCCCTCTTCCTCGCCCCTTGCACCCTCGCAGGAAT
			CGCTGACTTTCCAGGTCGGCCGGGTGCTTTGGGTCCCTGTGCGTCTGTGTGGGTGAATGGGGTCGGGGCTAGGTGG
			AGGGGTGTCCTTGGGTTCAGCCTC
			CAGCCCTGGAAGCTGATTGGGTGTGGTCGCCGTGGCCGGACGCCGCTCGGGGGACGTGGGAGGGGAGGCGGGAAAC
402_MSH2	25	23	AGCTTAGTGGGTGTGGGGTCGCGCATTTTCTTCAACCAGGAGGTGAGGAGGTTTCGACATGGCGGTGCAGCCGAAG
			GAGACGCTGCAGTTGGAGAGCGCGGCCGAGGTCGGCTTCGTGCGCTTCTTTCAGGGCATGCCGGAGAAGCCGACCA
			CCACAGTGCGCCTTTTCGACCGGGGCGACTTCTATACGGCGCACGGCGAGGACGCGCTGCTGGCCGCCCGGGAGGT
			GTTCAAGACCCAGGGG
403_MSH6_01	27	26	AAATGCTGGGATCAGTGCCTGGCAAAGGAAAACTTTGTACAGCTGCAGGCTTTCACCATACACAACAGCATCGCTA
			ACGAATGCTATTACAATATTCATTTAGCGTTTACCAAGTGCCTACTCTATACAAATCTTGAGAATACAACGTGAAG

			GTGAACTGCTGACTAAAGTTTGGTCCCTTTCGCTCCGTCTCCTTGCGAAAATGCTCTAACGGCAGGAGGTCACGCG
			AGCGCTGGACGCGTTTCTCCCCGCGAGCCCCTTTCCGAGGCCTTTCGGGTCCCCCCGGTTATCCCCGCCCGGGCGG
			TGCGCGCCCCCGCTGTTCCCGCTTCCGCTCCAGAGAGGCAGGGCTTTCCGAGCCTGCTAGCCCCGCGGCCGCAACT
			AACCCCGGGTCGGAGTGTTCCGGCCCGGCCAGCCCCCGCGGCGTGAGGGAAGGGGAGCTCAGCAGTTC
405_MSN	26	25	CTAGTGAGGGACCCAATCTGAGTCCCCGGCCAGCCGAATCCAAGCCGTGTGTACTGCGTGCTCAGCACTGCCCGAC
			AGTCCTAGCTAAACTTCGCCAACTCCGCTGCCTTGCCGCCACCATGCCCAAAACGGTGAGTGCCGGAGGTGGGCG
			CTGTCGACCCCAATGGCTCTGGCTGAGCCTCATAGCCCTTTGCTGATGGCTGAGGGCTTGGCCAGCCACCGGCCCG
			CCTGGGACGCCGCGCCCTCCGCCATAGCCAAGGGTAGGGAGGGAAGGCC
			TCTGGAAAGCCCAAACCCAGCCACCCCACTACCCGCTACCCGCGGCCCACGCTGATGAAGACAGCAGAACACGGAG
			GCCCCGCGTTCCCGCCGCGAGAGCAGGAGAAGATTACCTCCCGCGAGCTCTAGCGCGCCCGGCTTTCCGGCGC
406_MUTYH	30	21	ACTCCAGGGGGCGTGGCTCGGGTCCACCCGGGCTGCGAGCCGGCAGCACAGGCCAATAGGCAATTAGCGCGCCA
			GGCTGCCTTCCCCGCGCCGGGACCCGGGACGTCTGAACGGAAGTTCGACCCATCGGCGACCCGACGGCGAGACCCCG
			CCCCATCCCCGACTGCCTGAACCGCGCCAGGAGACGGACCGCAAGTCCAGCGTACCCACACAGACGACTCAGGCGGGA
			GACGAGCGGTGTCATGGCCGCCGACAGTGACGATGGCGCAGTTTCAGCTCCCGCAGCTTCCGACGGTGAGCGGCTT
			CCCAGAGGTAGCCTTCAAAGCCTCTGCGCTCTGGGAGAGGGGAAGGCC
			GAGCTGGGGAATTAGGGCTACTCCCCGCCCCACCCTGCGCGCCTACTTTCCCCGGCGCACCCCGCTGGGTTCAGGT
			GCGCCCGAGCCGCCGCGAGGGGTAGGGGGAGGGAAACGCGCCACCTGGCGGCCCTCAGCCCTGAACTTGGGCTGGT
408_MYCL1	25	30	CCCGGCGTCCGTCTGGTCACCCGTCGGCCCGTTTCTTGAGCTCAGTGGCCCAAGCCTGGATGGCATCGAAGCGAAG
			ATTCCGGGATTTAGAGCCCGAAACGTAACCTTCCTGAGCTTCAGTTTCATCTGTAAAATGAAGGGATGGTAATGCT
			TACC
			GGGACTGGGTGGCCTCACCCCCAACCCGGTCATCCTCCAGGACTGCATGTGGAGCGGCTTCTCCGCCCGCGAGAAG
			CTGGAGCGCCGCCGTGAGCGAGAAGCTGCAGCACGGCCGCGGCCGCCAACCGCCGGTTCCACCGCCCAGTCCCCGG
			GAGCCGGCGCCGCCAGCCCTGCGGGTCGCGGGCACGGCGGGGCTGCGGGAGCCGGCCGCGCCGGGGCCGCCCTGCC
409_MYCN_01	26	25	CGCCGAGCTCGCCCACCCGGCCGCCGAGTGCGTGGATCCCGCCGTGGTCTTCCCCTTTCCCGTGAACAAGCGCGAG
			CCAGCGCCCGTGCCCGCAGCCCCGGCCAGTGCCCCGGCGGCGGCCCTGCGGTCGCCTCGGGGGCGGGTATTGCCG
			CCCCAGCCGGGGCCCCGGGGGTCGCCCCTCCGCGCCCAGGCGGCCGCCAGACCAGCGGCGGCGACCACAAGGCCCT
			CAGTACCTCCGGAGAGGACACCCTGAGCGATTCAGGTAAAGACCGAACTCGGGTCCGGCTGCCTCCCTGGGGCACT
			GGACCCCGGGTCGCGTCCCCTTTGTTAGTGCTCGTATGTCTTGGCCTGGGGAGCATTTTTGGAGGCAGT
			GGGAGGTAAGGAGCAGGGCTTGCAAACCGCCCGGCGCCCAGGGAAGCGACGAGCGCCGGGGCAAGGCAAGCCCTGG
			ACGGGATTGCGACGTGCGCACCGGGCGCCCTAATATGCCCGGGGGACTGTTTTCTGCTTCCGAAACAAAACCATCTC
410_MYCN_02	27	25	TGGGTTTTCCCAGAAAAGCCAGTTCCAGCCCCGAAGGCATCCTGGCTAGAGGAGACCCGCCCTAATCCTTTGCAG
			CCCTTACCGGGGGGGAGTAATGGCTTCTGCGAAAAGAAATTCCCTCGGCTCTAGAAGATCTGTCTGTTTGAGCTG
			TCGGAGAGCCGGTGCGTCCCCACCCCAGGCTGGGGTTCTTCTCCAAAGGGTGCCCCTGGAGGAAGAA
			GGGTGGCCTTAAGTGTCTTTGGTCTCCTCCAATGGAGCAGCGGCGGGGCGGACCGCGACTCGGGTTTAATGAGAC
			TCCATTGGGCTGTAATCAGTGTCATGTCGGATTCATGTCAACGACAACAACAGGGGGACACAAAATGGCGGCGGCT
413_MYST4_01	26	23	TAGCTCCTACCCCTGGCGGCGGCAGCGGTGGCGGAGGCGACGGCACCTCCTCCAGGCGGCAGCCGCAGTTTCT
			CAGGCAGCGGCAGCGCCCCCGGCAGGCGCGGTGGCGGTGGCGCGCAGCCAGGTCTGTCACCCACCCCGCGCTTCC
			CAGGGGGAGGAGACTGGGCGGGAGGGGGGAACACAGACGGGGGGGGATTCAGGGGCTTGCGACGCCCCTCCCACAGGC
			CTCTGCGCGAGGGTCACCGCGGGGCCGCTCGGGGTCAGGCTGCCCCCTGAGCGTGACGGTAGGGGGCGGGGGAAAGG

			GGAGGAGGGACAGGCCC
414_MYST4_02	24	26	GGAGAGGGAAAAGGCCTCCTGATTGGCGTCGTCTGCAGCCAATAAGGCTACGCTCCTCTGCTGCGAGTAGACCCAA
			TCCTTTCCTAGAGGTGGAGGGGCGGGTAGGTGGAAGTAGAGGTGGCGCGGTATCTAGGAGAGAGAAAAGGGCTG
			GACCAATAGGTGCCCGGAAGAGGCGGACCCAGCGGTCTGTTGATTGGTATTGGCAGTGGACCCTCCCCCGGGGTGG
			TGCCGGAGGGGGGGATGATGGGTCGAGGGGTGTGTTTATGTGGAAGCGAGATGACCGGCAGGAACCTGCCCCAATG
			GGCTGCAGAGTGGTTAGTGAGTGGGTGACAGACCCGTAGGCCAACGGGTGGCCTTAAGTGTCTTTGGTCTCCC
			TCCAATGGAGCAGCGGCGGGGCGGACCGCCGACTCGGGTTTAATGAGACTCCCATTGGGCTG
417_NCOA2_01	30	25	TGGTTGTTTATTTCAATGGAGATCCTCCCCCCAACTCCCTCCTCCTCCTCCTCCTCCTCCGCGTCTCC
			GCACTTGCGGAGAGACAGACGCGAGCTCGCGAGCAGGGGAGGGGGCTCGGGAGCCAGGCCGTCCCTCCTCTG
			CCTCCCCGGCAGTGGCCGCCGCCAAGTCCTGTCACCGGGAAAAGGACGGGGCGGAAACTTGCCTCTCGCGCCCCCG
			AGGAAGGGGCAAAGGTGGACGCAGGGTTGTCCGGGGAGCAGCCCCTGGCCGCGGGTCCGCAGCATCTCCGTCGGC
			AGAGTCCTCTGAGAAGGCGGCCCGGGGAGAGGTGAAGAAGAGGTAAGGGGACAGGGGACAAAATGGGTGACTGTGGT
			AGAGGGAGGGTGACCTAGAGGTGACTGGAACTGAAGAGAGAGGTCAACAGAGGACTGCATGGGAGGGCAAAGGGCAA
418_NCOA2_02	25	24	GGGAGGGCAAAGGGCAATGCCAAAAAGAAAACTAGCGACTGGGACGGGCCTGGGCCGCTGAGTTAGAGGCAGTGGG
			GCCTGGGGGCTGCAGACGGCAGGGACGGTGCCCCAGGACGAAGATCGGGGAGAGCCGAGTTCCAGGGTCGCCAGCA
			GAGGACCCTCGCGCCCGTCCGGCCGGACCCTTCGGCCAGCACCCTGCACCCCCTCGGGCGCACCTCACCCTACCCA
			ACTCCCGGTCCTGCCGCTGCTCCCCGGAGGCGCCCCGCATCCGTCAAGTCCCCTACGGCTCCAACAGGGAGAGGCT
			TCTCCCATTGCAGTCCTAGCTCCAGAGGGGATGGAGAGGCGCGACTGTGGGAGCTGGAAGGGGCACCAC
420_NF1	23	24	TGGGAGAAAGGCTAGCCCCAGGGCGCCCTAACTTCCAACTCCGGGAGCAATCCAAACCCGGAGGCCGGCGGGGAG
			GGGACAGCTGTAGGGGGCGGTGGGGATGGGAGTGGATGCTCCCGGGTCAGCTCTGGCACTCGCCAGCTGAGCCCAG
			CGCCAGTCTAGGTGAGCCCCACGGCGGTGAGGGACGCTCGCCAGACGGCCCAGAGGAGTTAGATGACGTCACCTCC
			AGGAGGACTCGCTTTTTCATTAATGAAACCGGCCGGCGCGGGCGCATGCGCGGCAGGCCGCCTTCCCTCTCGCTTC
			CCCCTCCCCTTTCCCAGCCGCGCTCTCAATCTCTAGCTCGCTCGCGCTCCCTCTCCCGGGCCGTGGAAAGGATCC
			CACTTCCGGTGGGGTGTCATGGCCGGCGTCTCGGACTGTGATGGCTGTGGGGAGACGGCGCTAGTGGGGAGAGCGAC
			CAAGAGGCCCCCTCCCCCTCCCCGGTCCCCTTCCCCCTATCCCCCCTCCCCCCAGCCTCCTTGCCAACGCCCCCTTTC
			CCTCTCCCCCTCCCGCTCGGCGCTGACCCCCCCATCCCCCACCCCGTGGGAACACTGGGAGCCTGCACT
424_NPM1	22	25	CTGGACCTGGAGGGATTGGAGCCGCGGGGGGAGCCGGTGGCGTGAAGGGGGAGGACGAGCGGCCTGAAGCGTCT
			GGGGCGTGAGCGGTCCGAGGCCCGGGGCCTGAGGTAAAGTGGAACCGGCCGCCTGGAAGTTCGGCCTTTGCCGGGG
			ATACGTGGCGGAGCTCCAGGCGTGGTTTATTTTCTAACGGCGGTGGTTCATAGGCTTCTGATGCCAGGCCCCGGGT
			TGGTGGTCCTGGAGGCTGGGTTCACCGGGAAGCATGGGCCTGCTTGTTGGAGCGGGTAGATGCACAGCCTGGCGTT
			ATTCTGGCCTCAGAGCCTGGAGCTGCCGGACGTAGACTTACCTCGCGTGCTTCGGCCAGTTACTGGGGGTGGGGAG
			GCGCGGCGCGGCGTGAGGAGGCCGCAACCGCTGGGAGCACGTGGTTGCCACGTGGTTGGGGGAGGGAGGGGGTGT
			GGGCGCTACATCCGGGACTCACCGGCGTGTTGCCACTCGTGAGCCAGGGATGCTGTGGCTCTG
425_NR4A3	24	26	AACTTTGAGTGTGGGGTTCCCTCCCCTGACCTTGCCGCCCGGCTCCGGCTTTGCTAGCCCAGCGGCCCGTAGGTTC
			TGATCTGAAACTTTTCCCCCTGTAGTGGGCCCCGCGGGGATCTCTGGAGCTCGTGGGATTCCTCCCCCCCACTCGAAGA
			GGCGAAAAGCCTCTAACAAAGAGGAGGACCGGGATTTGTGCTATAGCGGCTCCAGCGATGTAATTCAGGGTATTTC
			GGCTCTAGTTGTCATGGTAATGATGCTCTCGGCGGCGGCGGCGGCAGCGGCAGGCGGAGTTGCAGC
			TCCGGTGATGAACGGCAGTAATTTTCCTGCCTTTAAGTAGGATTGAAAATAGGAGCTCTGGTGGGTCCAAGTAAA
			TGTTGCTAATGGTGGCACCGAGCTGGTTCTCTGGAAGGAAGCTTAGGAGGGAAGGGCCTAGGC

429_NTRK_02	29	CCAGAGGGAGAAAATGACACAGGGTTCTGAGCAAAAGGCAGGCCGAGAGGCCAGCCAACCCTGAGGGCGGAGCAGC
	25	AGGCTGGGGACCGCTCCCAAGGAGGGCAGCGGGGGTCCCGGGGCGCGTGGGACTCCGCAGGGAGAGTCTCCCTGGA
		TCCCTCCGGGCGCGCGGCCCCCCAGCGCCAGCTGACAGTGCTGGCTGCGGTCCTTCCCAGGGCCGGCACGCAGGGG
		CCGCGCCCAGCTCCCGCCCTCCCCGCCCCCGCCTAAACAGATTGGTTCGCAGGGACCTTTCCGTTCTCTCCACCC
		CTCCCGCCAAGTCAAAATATTTAGCCTGACAACTGAGGGGAGGACAGGTCTG
430_NTRK3	30	GAGAAGGAAGATGCAGTAGGAGCTGCAGCAGCCGCCGCGAATGGCTCGCCGCGCGGCTGCAGAAATGTACAAGTGC
	24	TCCGAGCCTTACGAAACGCACGGGTTATCGGAGCGTCTTCCTCGGCTCCCTCCCTCCCTTCCTCCCTCCTCC
		CCTCCCTCGTCGCGGCCTCCTCCCCCCCGCCCCCGGGCTGGGAGCGGCAGGAGAGCGGAATCTCCCCCTCCC
		TCCCCTCCCCACACCCGTCTCTCTCCCCGCCTGTCCTCTCCCTCCTCCCCACCCACCCACCCACTCGCCGGC
		TCGCGGCTGTAGCCGGCACCGCCACCCGCAGCCTCGCGGCAGCCCGCCCGCTCCACGCCTCGCAGCGCGGCGCCCG
		CTAGCCGCAGCCCGGGGGAAACCGAGACCGAAGGGAAAAAGTTGCATTTGAGATTGCGAGGGTCGGGGCTGGGGAG
		GGAGAGTTGGCGAGCTGGCTGCACGACACGGAAAGGCGCTCTCCTTTCCACTTTTTGGCCCTCGCGCTACCCGGTT
		TTGCTGCAATCCGGACCGCGGTAGGAAGTGAAATGAACGTGGCGGAGGTGATTGGGGAGTGCTCCCAA
431_NUMA1	30	GGCCTCTCCAGCACCCCTTTTAGGCCTGAGCACCCGCAGGGGTGCCCAGGCCGCACGCCAAACGCGGGCCCGCGCC
	26	GGTTACCTGGCTGCGCGCTCCCGCTCTGCCTCGCGATTCTCCGGAATCGTACCTCTTCGTGGGCTCGCGCCAGCGC
		TGTGAGCGCACAATTAGTTTAAACTATGGCCCCCGCCCCCTCGCGCTGCCCTCTAGATTGGCCTCTGTCGGCGGGCC
		CGCTTAAGGACCCGGGAAAGGAAGTTTGAGGGCCACTGGGAAAGAGAAGGGGTATC
432_NUP214	30	TGGGCCACCCCAAGAAGAGAGACTTAACACTAGGTAAGCCCGCGCTGGCTGCGAAGGCGGGAGCGGCACCAGGACCA
	25	TCCAGGGCGCAGGCGCAGGGACCTCACGGCCACGCCACTACTCAGCCCGAGCTGGCCAATGGGGAGCGGCGGCCGG
		AAGAACGCGCGGCTTCGCTAGGTTCCGCGGCTTCCTCTGACCAAGCTTGACGTCACCAAAGCGCGCCGGAAATGCG
		AGGTCAACTGCGCGCCGCTGGCGCTGAGGGGAGGAAGTTTGCTGTCGAGCGGCCTGGGTTCCGTGGGCAAGGCCGT
		GGGAGGCAGCGTTGGCTGCTTCGACACACTGAGGGCGGCGCGATGGGAGACGAGATGGATGCCATGATTCCCGAGC
		GGGAGATGAAGGTCAGAGACTAACCGGGGCCTCCCTCCCTCTTTAGTCCTGGCGTTGCCTTGGAGCCCAGCTGAA
		AGG
433_NUP98_01	30	TGGGGTCCTTACACCACTGAATGAATGAGTACAACCAGACAGACACCCACTCGCGTGGGCAGCAACTGGAGACCTC
	25	CAGGCCTAGACCCCACTGATGTCCATTCTCTCCCAGGGCCTCCCAAAGCCGGGCCTCCCGGGCTCCGGGCCCCCGGG
		TCCTCAGCACCGCCCCCTCTCTCAGGCCAGAAGGTGCGCGCAGCGGCGCTAGACTTCGAAGCGGAGAGGCCCTGAGA
		CGCCCCGCGCCGTCCGCCCCGCCCGGAAGGGGGGAGAAACCTGCCGGTCTCGGCCGCTGCAGCTCGGGCTCCCGACTT
		ACCGCGGTTCGGTGGGGAAGGGGAAGTGTCAGGAGTCCCC
434_NUP98_02	27	CTTGTGAATGGCTAGATTGGGAAGCACCGGCGGGGTGTCGGGAAGGGTGGTGACGCAACATAGAGACTCCGCCCCC
	25	TTCCTTGGAGCGCCGCGACTCGGGCTGAGGGAGCTCGGGCCAATCAGAGGGACGGCCCCCAGAATGGCATGGTAACT
		ATTCGACCCTTTCCTTGCCCCGGTCCGCCGGCGCTGCTGGGAAGGCTTCCTAGTCTCTCTGCCCGCACTTCCCGCC
		CAGACCACGTGCGGAGCCTGAGGGCCCTCTTGGAAGGT
436_OLIG2	25	ATTCCCCAGGAAGGGGCCCCCAGCTGCGCGCGCTGGTGGAACCGCAGTGCCTGGGACCCGCCCAGGTCGCCCACCC
	25	CGGGCGCCGGGCGCAGGACCCGGACAAGTCCTGGGGACGCCTCCAGGACGCACCAGGGCAAGCTTGGGCACCGGGA
		TCTAATTTCTAGTTATTCCTGGGACGGGGTGGGGAGGCATAGGAGACACACCGAGAGGTACTCAGCATCCGATTGG
		CACCAGGGCCAAGGGAGCCCAGGGGCGACACAGACCTCCCCGACCTCCCCAAGCTACTCCGGCGACGGGAGGATGTT
		GAGGGAAGCCTGCCAG
438_PAX6_01	26	25 CCAGGCAGGAGGCAAAGAAGAGGCCCCGCCCTAAAGCCGAGGGCCCAGTTCTTCGAAAGCCTGTGGCCGGAGCTGG

			ACTCACAGGATTCGGGGTCCGTACAGCGCGCACGTGGTACCGCATCTTCGGCAGGCGGCGCCCTAATGCCCAGCC
			CCGCCCTGCTTCGTTGCCGGGCCTGAACTGTGTCAGCATTGAGGGTGGACGCCGAGTCGCGGCGAGTTGGTCCCT
			TGCGGTATAAACTTGGGGCTTCCCTAGGGGCGGTGCCCGGGATGGATGGGGGCGCCTCTCCACCTGCAACTCCCCCA
			GCGCAGAGCGCAAAAAGTGCACATCGCGGGCCAGCCGTCGCCTCGGGTTTCAGGCGGCGCCCGGGGCAAAAAGGA
			GCTGAGGATTGGTTTGGTCAAAACACCCATTTCAGTTGGCAGTGGGGTCCTCTGCGCCTACAGGGCTTCGAGCTC
			CGGGTGCGGGCTCACTGGGGCACCATGTGCCAGCGACTCGCCACCCGGAAATACTTGGGTTGCGCTAGAATACGCA
			ATGGGTCTGTGTTCGGGTAACCTGGTGCTCATGGTGGGTT
440_PAX6_03	24	25	GGGAGGGAAGGAAGGCTTCAGCCTGCGCCGGGCGCTAGCCAGCGCACCTACGGGAAGGGGCAGACCGAAGCGGAGC
			CCGGGAGCCCGGGTCTTCCAGCCGCACCTTCTATTAAGACATGCGCTTGGGGGTCGCGGCCCTCTGCGCTGTGCGC
			GGGGCCTGTGACATCTCCATGTGCAAACCCCGCTGCTTAGACGAGCGCAGGCCGGGTTTTTTGTTTTTGAAGAAATT
			AACTGCTCGGCCAAGCAGGTGCTTTTGAAAGGG
443_PAX8_01	25	24	GCCATGGCCCTGGGACTGGAGACTGCGCCGCAGAGCCCGGGCCCCCGCAGTGCGCTTGGCTAAATAGAGATCTCAG
			CCTCGCTGCGCGCCCGATCCGACCCTCCTTATTATAACAAATGTCCCGTTTGCAGAGCGGGACATCATATTCGCGG
			AGAATTCATTCTGAAATATTGATTTCCTCTCACTTCGCCGGCCCAAATCGATAGCGATGCGCCCTGGCCCCATAAA
			TCGCCTTCTCTGCGGCCGGCCGGGCTCCCATCCATCACTGCGGGCCGCGCTGCGCCTCCACCGCTGTCCGCACTCGC
			TGCGCGCCGGGACGGCTGCGCCCACCAGCCCTGACCCTGGAGCTCCTTCCCAGCAAAGACCCTGCCCAGCCCTGGC
			CGGGAAGGGGGAAAACAGGCATCGCGGCCTGGGAGCTCGAGTGTGTTTGAAGGCCCTGCTTC
444_PAX8_02	24	26	GAGTGTGTTTGAAGGCCCTGCTTCCGGGCGCAGGTGGGGAGGGGGGTTTTGACTCCGCGAGCGGCTTAGTCCTCACC
			AGCCGGACGCCCCGCGCGCGGCGCCCGGCCTGCCCGGTGCTGGGCCAGGAGGAGTCGGAGAGCACCTGAGTGCGCT
			GCCGGCTCCCGGGCCCGGGACCACCGGCTCCATTGCCGTTGGCTTGAGAGATGCGGGGAGCTCACAGTCCAGCCAG
			GGGAGTCACTGGGAAGGACTGCGCGCACCCGAGGAAGAGGACTTAGAGGTCGGGGACGGGGAAACGGCAAGTCCAG
			CACCGGTGCAGCCCAGGGACAGAGCACGAAGAATGTCCACACTAATGCGCCATGCAAGGCTGGGAATGGAGCTCAA
			AGG
445_PAX8_03	30	25	AAAGATTAAGGGACTAAAACCTGATCCTGACCTTAGATAGTGGCCTAGGAGCGCTCGTGGTTCCAGGACGCGGACC
			GTAAAGAGGTGCCAGGGAGCTCTGCTCGGTCCCAGGGCTCCCCCAACCCCGCCGCGCCGGGGAATGGCTGCGAGGTC
			TCTCCCCTGAGGACCTTGAAGGGACCCCCGCGCCTTCTGGGGGCAGCCGGACGATTCTGGCCCAGGTCTCTGAGGGG
			AATGGGGGCCGGGAGGGAGCATTCGTCTGCAGCTCTAGAGAGAACCCGAGTGAGAAATCTTCCGGCGCCCCAGGGG
			GTTCCCGCTCCCCCTCCTAGTTGGGCCATGGCCCTGGGACTG
447_PCM1	29	25	TTTGACAGGAGAGGCTGCTTCTTGTAGAGGTAATGCCTGCGCGTCCCCAGCCCTTGGCAACCTAGGGCGGCGCGCC
			CCAGAGGCGGGAGAGTAACGGCTCCGGGACACTCGGCCCTGTTGGGTCTGGCCACGGGCCCACGCCTCCTCTGTAG
			GTTCCCGGGTCTTCCTGCCCCGGGCTTCCCGTGCCCTAGGCGGTCAGTCCGCCCGCTCCCTCAGGACTGATCGCCG
			GGATCCCCCGGGTGAGCACCTCGCGACGCGTTGGTGATTGCAGGACTCCCTTCTTGCCTCCTCGCCCCTCCTGCTGG
			CCCTGTCGGGGAGGCTGTTCTGCGTCCCGGTGGCTCCGGCTATACCCCTTGCGGCGGAGGAAGCGGAGCGGGGAC
			TCTGGTTTGGGTGCTAGGGGCAC
448_PDE4DIP	27	30	GTTCTCAGTAGGAGGCTGGACTCAGAGCGGCGCGCCCGGGGCTGTTTCGTGAGCTGGAGCCAGCGGCTGCCCG
			GGCGGCGGTGCGCGCACTCTCCAGGCTGAGACACGACTGGCTGGCACGAGTTGCTCGGCACCAGCTGAGCTGTCAA
			CCGCGAGCGGAGGCGGGGCTCCCGACAACCAGTGTGCTGGGGCAGAATCGGCCCAGGTTACACGCCCCCTGAACCA
			CCCTCGCGTCTCCCCGACCCCTCTCTCGCTGGCTCAGATGAATGATGACGGCAGAGGGCAGAGGAGCTTAGAGGACG
			CGGTACCAAGCCCCGTCCCTCGCCCATCCCAACGAAGGTCTTAGAATACAATCAACCAACTACAGGAAGAAATTTGT

			AGAGGAG
449_PDGFB	25	25	CATTTTCTGGAAAGGCCCCCCAAAATCGGAAAGCGCGGAGCTGGGCACCTCAAGGCCCAAGTCTCCCCCAAAAAACT
			TTTTCCAAAGTTGGCTTTGCAACGGCAGCTCGAGCACACCCGGGCAGGGAGAGGTGCAAACTCCCGCCCGGCCGGGT
			AGGGGGGCGGGAGCGTGTGCGCCCTGGCGCGGGCCCGGGCGCGGGCACGGCTGCTCCGCGCGCGGCGTGCCC
			GCTGCGCGCTCGGCTGGGCCCGGCCGACAGGTGGACGCGGCGCGAGTCCGTCGGTCCGTCTGCCCGCCCGCTCGCC
			GCTCTGGGCGTCCTCTGCGGGCTGCGGGCTGCGAGCTGCGAGCTGCGGCTGCTCCGGTTTTCTCTTTGC
			AGCGAGGCTGGAGGGTGGGCTTTTTTTTTTTTTTTTCCTTTTTGCGCGCGTATGTATGTGTGCGCGCAAAGTAT
			CTCTATCTAGGGAATGAAAAATGGGCGCTGGCGGCCGGAGGGGAGCCCTAGGGAGGCAGCGGGGGAGGCTGCGGGT
			GCGCAGGGAGGCAGGCAGGCCGCTCCCGGCTGCAGGAGGAGAAGTTGCCACC
450_PDGFRA	27	28	TGGGAAGCCCCACTCTGCCCAGGTCTGGTTCCTGGAGCATCAGCGCCCCCTTTCCCTCGCCGGCAGGATCGTTTCC
			TCCCGACACTGGCCTCTCGCCTTGGGCGCAGGGTTTGGGGCTCAGCTGTCAATTCCAAGGAATTCGTAGGGTTCGA
			CCCACGCGGCGGGAGGGAGACGGAGGGAGAATCAAAAGGCATCCTCCCCCCACGACGCGGAGGCGGTGGTACGATTCC
			TCAAACGCCCCAAGCTTGAGCTTTTTTTTGTATGCGAGATAGAAGCCAGGGCAACCTCGCCCAGATAACCCCGAAAAC
			AAAGGCACGACCAGATAAGTGACTTCAAGGGAGTAA
455_PIM1_01	26	25	TGGGATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCGCGCCCTGCAACGACCTGCACGCCACCAAG
			CTGGCGCCCGGTGAGAGCACCCCCCGCCTCCGGCCCGGGGATGCGGGGCGGCGGGGATCTCCTGGGTGGGGAGC
			TGGCGGCTCGCGGGCCGGCACTGAGTCCCCGTGCTTCCCCCTTTCCTCTAGGCAAGGAGAAGGAGGCCCCTGGAGTCGC
			AGTACCAGGTGGGCGCCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGACAACTT
			GCCGGTGAGTGGGCGCCCCGCGGTGGGGAGGGCGCCGCGGGCGGGGGCGCACGGGCGTGCTTTAGCCCGGACGAG
			GGAACCTGACGGAGACCCTGGGCTTCCAGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGA
			GCTGGTGAGTGCCCTGCAGG
456_PIM1_02	25	25	GGGAGAGCTGGTGAGTGCCCTGCAGGAGCGACCCCCAGGATGAGTGGGTGGGGTGAGGGGCGCCCCCGACTCCCGC
			CCTAACGCGGCCCCCCTCGCCCCTGCAGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGA
			GCTCGGGTTTCTCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTGGAGAG
			GCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGAGCCCTGCAAGAGGAG
458_PMS1_01	28	25	TCTGGGCCAGAGAAAACTCAGCAAAAGCCGCCGCTGCTACCACCTCAGCGCCTCCCCCAACCCGCCCCTTCCTCT
			CGCGGCCGCACGTCACGTCAGGACCCTGGCAAGACAACGAGGATTTGCGTAGGGGGCGAGCCTCTGAGGCCACTTG
			GCTCTTACGGCCACGCAGGGCGCCGCAGATGCAGCCGGAGCCCGCTTTTCCCTCTCAGGACGACCCCTAGGCCGCC
			AGCAGTTCCCTACCGACGAAGGCGACTGTACAGCGTCCACCGCGTTCGTGCCCACTTACCCGCCGCCCCACTCCGG
			GCCGCCGGCTCGCAGCAGGACCAGCCCGGCTGCTACGGCCGCGGATACACGCCCTCAGGCCCGGCGCTGCGCAGCT
			TGCGGAAGCTTTCCCGGACAGACTCGCTGCCAGCGGATTGGCTGCGAGCAGCGCCAATCTCACGTTGCCCCCGGGC
			GAGGCGGGACTCAGTGCCGCGCTCTCTGCACCCGCTCTGCCGCGCGCGTGCTGGGTGCGGGTGCGGGTGCGG
			GGTTGGGCCTGCGCATCGGGTGAGACGCTGGCTGCTTGCGGCTAGTGGATGGTAATTGCCTGCC
459_PMS1_02	26	27	GGCTAGTGGATGGTAATTGCCTGCCTCGCGCTAGCAGGAAGGTAGTGTGGTGTGACTAACGGGTATTTATTATATC
			CTCGATGGCTCGAGGGCCCCCGTCCCCCTCTACTCGTCCTGGTCCGGGCGCGAACGCTATAGGGCAGCTAAGGGCGCT
			CCCCGCGGGGCGGGAAGCGAAGCCGGGCTTGCGGGCGCGCACACGTGGAACGCGTTTTCTGAGCAGGTCTGGGCTC
			CGGGGTGTTCTGGCTTGGTCTTTGTTGCGTCCCATTCCCCAGACCCTTCTGGGTGGAGGACTT
460_PMS2	24	25	GTGGGCAAGGCCTGTCTGGGACAGGCCGAACCCAACTCCTCACAGGGCCGAATCCTTTGCCCGCAGCCCAGGACCC
			CGAAGGAGCTTGCCTCGGCCTCAAGGCGCACCCCAAGGGGCACGAGATCGCTGCAACACTGAGGTCGCCACTCCGGG

			GCCTCCAGGGGGCTGCCTCGCCACGCGCCTCGGCCATGTTCCCCCCATTTCCAGGGAGGTTGGAATGCCGTGGGTC
			TCAAAGAGGGCGCGCGAGAGGGGACACCGGAAGACTGCGAGCCCCGCTCACCTCGAGCTCTCAGCTCGCTCCATGG
			ATGCAACACCCGATCCGCCTCGGGGACTGGGAAAGTTCCCTCCACAGGCGCTCCCGCCTCCCTGAACTC
			CCATTGGCTGCTTTCGACGTTGTGCTCCACCCTTTCCGGGCGGGCGGCAAAAATACTTCCCGTCTCTCCTTTTCG
			CCTATTGGCTCTGTCAAAGGTCGACTTCGTGACGTCAAAGAGCCTGGGCCAATCAGAGCACACCGGACTGCGTTTT
			CCCGAACGCCCCGCAGCAGGGTCAGAAGGGAGGTGGC
461_PMX1	25	25	CCTGGGACCAGGAGAGGTGATGGCAGACTTCAAAGGAAGGGCCAGTCACAGGGGAAACCAGATGAGAAAAGCGGGT
			CTCGGCCGAGGGCATAGCCAAGGAGAGGACGCTGGAGAGAGGCTCCAAGGTCCGGGACACTCCGAGGCCCTGCGGTC
			TCAGGCAGGGACTCTGTCCGCGGCGGACTCTCTTTACTTCGGCTAGGCACCGGCTCGGTTCATCCCGCACGCGGGG
			CGGCGGGGCTGGGCTGGGAAAAGGTCTTAGCGGGGTGCAAACTCAGAGAGCCAGCGCTGTTTGGGAAAGCAGCAGG
			TTAAAGATGCTGAGTCGGGTTGGAAGGGCTTCTCTCGGGCAGCGTATGACGGCTTGAGGGAGGGCACCAGGCACAG
			GGAGCAGGACTTGGCGCTGCTCAGGCTGCACTCTCCACGCGGGCACCGTAAGGCCGGGCGCGACCGGGAGGCCCCG
			AGAGAACGCCCGGCCCCAGACGCTGGAGCTGCTCTCTGCCCCCTGC
464_PPARG	23	25	GGGGCTGAGGCAGGGTCATGGTCCGGCAGGACCCGGACTGACGGGTCGCGGGCGGGCGGCTCACGGGTGACCGGGT
			GAAGGGGTCTTGGGCTGAGGGCACCCGGGCTGAGGGTCGCGTCTACCGGAGCGCGCACTAGGGGCGGAGGGCGCGG
			GCACAGAGAGCCGCGGCCGGTGCCGACTCGAGTGGACGCGAGCCGGTGCGTCCCGGCTTCCAGGACAGCCCCCTC
			GGGAGAGCGCCGGGTGGGCGCGGAGCCGGGGACACGGGGACCTCCGCGTCCCCGGCGGAGGTGCGCAAGCGTCGGG
			AGCCGCTCCGGGGGGAACTTTGGAGCAGGGTGTCTGGACCCGGGGAAGCGAAGATCCGCGTGCGTCCGTCCTGAGGC
			CGCGCGGCACCCCTGCTGAGGAGGAGGTCC
465_PRCC_01	26	25	GGCCTCAATCTGCCCCCTCCAATTGGCGGTGCCGGTCCCCCGCTGGGGCTTCCCAAGCCAAAGAAGAGGAAAGAGC
			CCGTGAAGATCGCGGCGCCGGAGTTGCATAAGGGAGATGTGAGTATCCGGGGAAGGCACCCCCCAAACTGTCCATCG
			GGTTTGAGTCGGCTGTAGGAGGGACATGTGGAGATTTCAGAACTCCTTCCTACAAACGCATCCGTGGATTCAAGGC
			CACTGGAATCCT
467_PRKAR1A	23	26	GGCAGGGCTCAGGTTTCCTGGACCGGATGACTGACCTGAGCCCGGGGCCCGGGCGGCGCTGGCCGGGCACAGGATG
			CGCGGCCCGGAGAGCGCATCCCGGCCATCCCGCCCGCGCTCGGCCCCCGCAGCGCAGCTGCTGCAGATCCGCGGGGGC
			CGCCACCTCCTCCGGGGGCTGGCAGCGACAGGACTCTCCCCGCCCCCGGGCCCCTCCCTTGCAGGGGCTGCG
			GGGAGGAGTCGCCCACCTGTCATCTGAGACGCCCCACGTGGGTCGGCCAGGGAGGGGGTGGAAAGGAGGGAGAAAA
			GGCAGAGGCGTCAAGGGAGGCCGGAGGGAGAGTGGGGTGGACAGAGGAGCGGAGGGACGAGAGGGAAGCGCACGAT
			AGCTGCGCGGAGAGAGAGCGAAGAGGCAGGCGGAGGAACAAAGGCGACCCAAGACACCCAGAGAGGGACAGGTAAGG
			AGGGGC
468_PRO1073	28	25	TGAAAATGGAAGTTGGGCAGCAGCTCCACGAAAGAAAGACCAGCCCCCCAAGTGCAGTGACAGCGCAGAGTAGCGAC
			CGAGAAGTTCCCAGGCCAGCTGCCACCCCGCCCCCCATGCCATTCCCCCAGAACAGGCACAGGCGTTAGGGCGGGGCG
			CGCGTGCGCAGTCACGCGCTGCGCCAACCGCCACAGCTCCGGGAAGGCGGCCAGGACCGGCTAGAGCCGGTTAGAA
			CCAGTGGCGCCCGCCCACGAGCCAGCGCCTCACAAAGGGAGGGCGGCTCACGGCCCTCGCGTATCCCTGCGCGGCG
			CTCGCGAGCCGCCCCTCCCCCGGCGTTTGTCCCTGACGCAGCCCCCACCGGTTGCGCAGTCCCTCCCCGCCCCCGCT
			CTCCCCCTCCGCAGCCTGCAGCCCGAGACTTCTGTAAAGGACTGGGGCC
470_PTCH_01	27	25	TGAGGAGGCCCACAACCAAGAACTTGCCGCAGTTTTTTTGAATGTAACAACCCAGTTTAAATAAGAGTCTCTGAAA
			CTTCGCTCTCAGCCACAGCGGCGCTTTCCGGCCAGTAGCCTTCCCCTGGGGACGAAGCAGAAGGGAGGAGTGAGCG
			CCGGGGAGTCGCGGCCCGCGCCCACGCCCGCTTGCGCGCACCCGCCCGGTGAGCCCCCCAACAGCCGTGGGGGCG

			CGGGTGGCCGCGGCACACGGACTCGCCCTCGAGACTGCAGCCCCGGCGGATCTGAGCGTCATGGGGGGCTCGGTCA
			TAAAGCCGGGCCGCAGCGTGGGAGCTGCACCTCGGGGACATCAGGGCGCCCCCACCCGCGGGATCCCTGAGCGACT
			TGGGGCACTGGGGCTGCAATA
471_PTCH_02	27	24	CTTGGGGCACTGGGGCTGCAATACAGAAGAGGAAGCCGAGGTAGAGAGGAGAGAAACCACTCGACACAGACAATAT
			TCACCCCAGAGCTGAGAAGGGAGGGGCTGCGTAATCCCAGCGATGGAGCCCAAGGTTCAGGAGCCAGCAAACCAGT
			CCTGCTCTGTCCATCACCCTCGGGGACGGGCGCTAGGGGCGAGCGCTCTTTGGAACAACATATTGCGGGTTCCCCC
			AACTGGACCCCCCGCCGAGAATGGTAGTAAGTGGGGATCCACGTGGTGAGCGCGGCCGCGGAGTTCACTCCCGACG
			CATTTCCATAGCGTGGGGAGAGGCTGTGTGAGCTGAATTAGGAAGTGGGGCAGCCAGCTGCAACTTACGACAATAT
			TTGTGATCGGAAGAGGGCAGCCACATGGATCTTTCCCTCCTCCCTTCCTTCTGGTTAAACGTAAAAAACAGCC
			GAGTGCAAAGGGAAGGGCTCAGGC
472_PTCH_03	29	25	CAGGAGTTTAGGCTGCAAATAGGGGCAGGGGCGCAGGAGGAAGAAGTTCAGGGCAGGGGGCACGGGGCAGGACAGT
			GCCGCGGCCGCCCTTGAGGTGGTCCGCCGTGGACGGCTTTCCAGTGCTCCGGAAAAGGCACACCAGGGAGGGCGTG
			TGTATACACACACACACGCACACACACACCTCCACCCCCTGCGGACCTCAGACAGCCCTTTCCTCCCAGGAC
			CAGAGGGAGGGTTTGAATTTTCAATCCCCATTTGTCTGCTGCTTTTCCTGGAGAGGTGTG
474_PTEN_02	29	24	GCTACACTGGGCATGCTCAGTAGAGCCTGCGGCTTGGGGACTCTGCGCTCGCACCCAGAGCTACCGCTCTGCCCCC
			TCCTACCGCCCCCCTGCCCTGCCCTCCCCTCGCCCGGCGCGGTCCCGTCCGCCTCTCGCTCGCCTCCCGCCT
			CCCCTCGGTCTTCCGAGGCGCCCGGGCTCCCGGCGCGGCGGAGGGGCGGGCAGGCCGGCGGGCGGTGATGTG
			GCGGGACTCTTTATGCGCTGCGGCAGGATACGCGCTCGGCGCTGGGACGCGACTGCGCTCAGTTCTCTCCTCTCGG
			AAGCTGCAGCCATGATGGAAGTTTGAGAGTTGAGCCGCTGTGAGGCGAGGCCGGGCTCAGGCGAGGGAGATGAGAG
			ACGGCGGCGGCCGCGGCCCGGAGCCCCTCTCAGCGCCTGTGAGCAGCCGCGGGGGCAGCGCCCTCGGGGAGCCGGC
			CGGCCTGCGGCGGCGGCAGCGGCGGCGTTTCTCGCCTCCTCTTCGTCTTTTCTAACCGTGCAGCCTCTTCCTCGGC
			TTCTCCTGAAAGGGAAGGTGGA
475_PTPN11	22	23	GGGATCCCCAGGCCTGGAGGGGGGGTCTGTGCGCGGCCGGCTGGCTCTGCCCCGCGTCCCGGTCCCGAGCGGGCCTCC
			CTCGGGCCAGCCCGATGTGACCGAGCCCAGCGGAGCCTGAGCAAGGAGCGGGTCCGTCGCGGAGCCGGAGGGCGGG
			AGGAACATGACATCGCGGAGGTGAGGAGCCCCGAGGGGCCCGGCGCGGGCCTCGGCCCGGCCACCGCCGCGTTCGG
			TTAGCCCCGTCCGGAAGGGGGCGCCCCGGCCGGGCTTCGGGCTCCCGCCCCGGGTCGGGGTTGGGGGCCGGTTCCC
			TCCTCGTCCCCCTCGCCCTCCAGGGGCCGGGGGCCGGCCCCCACCGCGCCCCCCACCCCTCGGGTCCCCCATTCATTTCC
			TGCCTCCCCCGAGTTCCGGCTGCGGCAGCCCCCGGGGATGCCCGTCAGGCCCGGGGCAGGTAGAGCCGCCGAGGGAAC
			CACGGGTGCCAGCGGCCAGGCTCAGCGCCGCATTCCTGACCCATTGCCTCATGAGAATTGCCTCATGGTGATTCCG
			AAATAACCCTGCTCACTTGGGGAGGCTCCTTGG
477_RAD51L1	25	26	CTTCTCCAGCCAGTGATTGCTGGAGCGCCGGCGCGAAAGCCTGACGAGAAGTCGGGAGACTGCGCGGCCTAGGCGA
			CTCCTGAGGGAGCGGTGCCGCCGGGGCGATCGGCAGTCGCGGAACCCGAGAAGTGCCGGGTCCGGGTTGGGGAA
			AGGCCGCAGCGAAAGGGGCCTAGGGGACCTGCGGGACTGGCAGCGCGGCCGCTTCCTCCCGGGCCCCCGCCGGCCG
			GCGAGGGGCGGGCGCTGCAGTGCACGCCGGGGGATGTAGTTGGCTCGGACGAGAGCGTCTCGTCCCCGGGGTCGCG
			CGTTGCTCCGGGTGCCAGGTTCAGCCCGCGCGGCGACAGCGGGCTTCGGCCCGATTTGATGTATGTTTGCGTCTAG
			ACGTCGTCCTCACTGTCATCGCGCTTTGCTTTGCCACCCTGACCCGAATTCCTCGTTTCGCGTCTTGACTGTTAGC
			TTTCGGCCCTGGAAAGATAGCCGGGCCAGGGGCTCTGCCTGCCGTCGGGAGGTGGAGCACTTTCTTGGAAGGC
480_RARA	25	25	AGGAGGGCCCCCTCTGCCTGTGTTTGTGCCAACAGCACCCGCGCTGCCGCGTCGGGTTCCGGCGGCCGGAGTCACA
			CATGATGTCACAGACAATGACACAAGCCGGTGTCTCATTCCGACACAGCGTCCGAGCTGCACAATGTCACACCCGG

			GTGCCAAACACTTGGCCCCGCGCGACCCGGCCCTACGCCTCCTGCCGCCGCTCTCCGCGTCTCCGGGGGAGGTGGC
			CCGGTTCGGCCGGGCAGGGGGCTGGCGGGCGAGCCCCCGCGGGCGGGCTGGCGAGCGGGTGATGTCACGGGCAGCGG
			TGGGTGGGTCACTCGGAGGTGAGGCGCCGCCAGGCGAGTTCAGCGAGAGTTCAGCCGCATTGCATTAGGCAAATGA
			GGCCCGGCCTGGGTGGGGGTGTGTTAAGGGGAGGACACCGGGACCACCCCCCTCTTCCCCGCCCCACCACCTCC
			TCCACCACGGCTTCGCTCGGCCAGGGACTGACCAAACCTTGGG
482_RECQL4	26	25	GGGTGCCTTTCAGATTGGCCTTGAGCCGCTGCCCGTAGTCCGGCACCGAGCCCTGGCGGCTCCGCCCTGGCGTAGA
			CTGTGGACTCTTGGTCGCAGCCCGATTCAGATGGGGCCCCCAGCAGCGGGGCTCTGGCGCCTGCAGGAGACAACAG
			GGGCACAGGCCAGAAAAGGCTGTTGTGGCGGCAGAAGCGCTCCCAGCCACCCCTCCCGCACCTGGAGCGAGGCCCG
			GCCCTTCTTCACTTTGCCCAGTCCCCCTCCCCAAGTTCTGTGCCCCACGGCGGCCTGGCCGCGACTCCGTGGCTCCC
			GCCACTCCGCCAAACAGGGAAGTGGGAGGAGGC
			CCTCCATCTCCCCTGAGGCCTTGCCCTATGCTTCCTCAGTCTCTCCGCAGCCCCATCAGCTCCAGGCAGTCTCTGTG
			GCTTTCCTGACTTTTCCCTCTCTGAGGCTCCAGGACTCACCTGCAGGCAGGCTCCGCCAAGGGTTGTGGCCGGCAA
489_SDHB	30	25	CCGGCGCCTCAAGGAGAGGCGACCACCGCCGCCATCTTGGCTCCTGACGTCAGCCCCACCCCTTAACCCCGAGGT
			CGCTCTCCGCCGGTGTCCCGTCGAACATCGCGGCGCCCAGCCTACATCCACTGAGGACCCACTAGCCGCGTACGAG
			CAACCAAGTGGGAGGCGGCTTCCCGGTTTCCCGGGTGGGCGGAGGGAAGGCGGGCAAGCACAGCGAGCGTGCGCAA
			TAGCGCAGTAGCGGCGCATGCCCATTTGGCTTCCCCCGTGACCTTCTCAGAAAGGGGAGGAG
			AGGACCCATGGGTGTGGAGGCCAAGCGCTCGGGGATCCTAGAGACCCCTTTTCCCGTCCCCCCCAGCCGCTCCCGGT
490_SDHC_01	25	27	GCGCTCCGTAGGGCTTCGGGGTCACTGACTTCGTATCGAGGGGCCCTCGGCTCTCGCCCCTTCTGTTTTCCCCACC
			TCCTCTAGTACTTCTAACGCAAATTGCTCTCGGGCCTGCACCCAGAGCCGAGCTCTGAGAAAATAACTTCAAGGTC
			GGAGAAGCTCCAGAGCCTTTTAAAGAGACTCTCGTCACATGACACCCCCAACCCCCGACCCCCAGCCGGCGCGCCTC
491_SDHC_02	30	25	CGCCCTCGGGTGGCGGGGCCGCCTGGCGTCACTTCCGTCCAGACCGGAACCCAAGATGGCTGCGCTGTTGCTGAGG
			TGACTTCAGTGGGACTGGGAGTTGGTGCCTGCGGCCCTCCGGAGATCTGAACTGGCCCCCTCACGTTTTGCTGATAA
			CTGTTTATCCTGTGCCTGGGCAGGGAAAGG
			GTGCCCAGGACCACCACCAAGGAAGGTGAAACTTCCTTTCCCTTCACCCTCCCCGTCCCCGCACCTGTGCAGTAAACTG
492_SDHD	30	25	CGCCTTCTGCTCGCGGCGGCCACCAGGCGCTGCAACTCCGCTTCATCGGCTTCGCCCAGCTCCGCCATTGTTCGC
			CTCAGGCTCGCCACCTTCCGACAGCTGTGTTTGCGCATGCCGACGGGTGTGCACCGCCTCTCGACTTCCGGTTCA
			CCCAGCATTTCCTCTTCCCTGTTTTCTTTCGTCGTCGGGTGGGAATTGTCGCCTAAGTGGTTCCGGGTTGGTGG
			ATGACCTTGAGCCCTCAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCTAGGAGGCCGA
			GGTGAGGGGTCTTCCCACCCTGAGGT
			GGGCTGCTGCTGCTGCTGCTGGGGGACCCGGGCCGGGGGCGGCCTCGAGCGGGAACGCGACCGGGCCTGGGC
498_SMO	24	25	CTCGGAGCGCGGGCGGGAGCGCGAGGAGGAGCGCGGCGGTGACTGGCCCTCCGCCGCTGAGCCACTGCGGCCG
			GGCTGCCCCCTGCGAGCCGCTGCGCTACAACGTGTGCCTGGGCTCGGTGCTGCCCTACGGGGCCACCTCCACACTG
			CTGGCCGGAGACTCGGACTCCCAGGAGGAAGCGCACGGCAAGCTCGTGCTCTGGTCGGGTAAGTGCGGCGGAGCCG
			GGTCTGGGGGGCGGGAGGTGCCGCGGTAAGATGGGGGCACCCTTGGAAAGAACAGGCTCAGGCCTGAGTTTTGGAG
			AGGGCGGGGACAGCACCCGGGAGAGTTGGAGGGACAGATCCCGAAACTTTGGGGGCAGGTTACGTGCAGGATGGGA
			CCCTCGGTCATGGGAAAAGGAGGGCAAGGAAGTTGACGAAGCGGGTCACAAAGGGCCTGAGCTGGTGGG
			TCCCAAACACTGCTGATTCCCAGCAGGCCCGCCTCCGCCTCGGCCCGGTCGACTCCGGGCCCGGCCCTTCCCCCCG
499_SS18	29	25	CGTCTGTCTCTCCCAGAGGCGGTAAGGGCCTGGCATCCGCAACCCCGCGCGGTTTCACCTTCTGAATCGCAGCGGG
			AGTGATCTCCCCCTTGCCTCGCTGCCTCGGGGCCGCGAAAGCCACAGACATGTTGCCGCCGTCACCACTATCGGCA

			AGTCCCGAGCGCTCCGGGTGAACGGCAAACTGGGGGAGAGACGCCGGCCTCTCGGGCTGAACCACCTCGGGAATGC GGGGAGGGGGGATGCTCCGGGGCCAAGCGGACGGGCGCGGGGCAGGCCTGAAGGAGGCACTCTGGCCAGGGATGT CTCGCTTCTGCGCACTCTGGGGGACCCCTAGCCCTGGCCGAACTTTCTTGACCGTCCCTGCATCCCCCGAGCTCTC CTTATGGGCACCCCCCTGGCCCTTTGCGCTAATGGTAGAGTCGCGCCCTAGTCCTCCCTCCGCTTCAGCGATTCAGG AAATGGTCCCGCCGCCGCGGGAGAAGGAGGCTGGGGCAGCCCCT
501_SSH3BP1	27	26	AATAAATAAAAGACACACACCCTCTGGGGGCTGAAACTGACATAATCGCCCCCACCCCACCCTCCGCCGACACACAAC ACACACCCCGCTGGTCCTCTCCCTTCTGCGGCTTCAGCCTCGTCCCTGCCCTCTCCTCTCCCCTCTCCCGTCCTGG ACCTCCTCTCCCGGCGCAGAGAGGCGGCGCGGCAGCTCGGGGGTATTCCGGGACTCCAGCCCTGCGGACTGGA GGCTACCTGGGGGGCGCGACCCCGGTGGCCGGGCCCTGGGGGAAGCGGACGAGGGGGGCGCCGGGCTGCGGC AGCGGCGGGCTCCCGGCTCCCTCGCCCATTTCTCTCTCCCCTTCTATCGGTTTCCACCACCACAGCCACTTCCTG TATCGCAGCCCCGACTCCCCTCAGCCCCGGCCACTCGCTCTGTCCCCGGTTGGGGCTGGGGCTTGCGGCTAGGGG CTCGGGTTGTGGTGGCAGCCGCTGAGGTCAGGGCAGTTCCCCACCC
505_STK11_01	27	25	GGAGGATGACCTAGCACTGAAAAGCCCCGGCCGGCCTCCCCAGGGTCCCCGAGGACGAAGTTGACCCTGACCGGGC CGTCTCCCAGTTCTGAGGCCCGGGTCCCCACTGGAACTCGCGTCTGAGCCGCCGTCCCGGACCCCCGGTGCCCGCCG GTCCGCAGACCCTGCACCGGGCTTGGACTCGCAGCCGGGACTGACGTGTAGAACAATCGTTTCTGTTGGAAGAAGG GTTTTTCCCTTCCTTTGGGGTTTTTTGTTGCCTTTTTTTTTTCTTTTTCTTTGTAAAATTTTGGAGAAGGGAAGT CGGAACACAAGGGAAGGACCGCTCACCCGCGGACTCAGGGCTGGCGGGCGGGACTCCAGGACCCTGGGTCCAGC
506_STK11_02	27	24	CCAGGACCCTGGGTCCAGCATGGAGGTGGTGGACCCGCAGCAGCTGGGCATGTTCACGGAGGGCGAGCTGATGTCG GTGGGTATGGACACGTTCATCCACCGCATCGACTCCACCGAGGTCATCTACCAGCCGCGCCGCAAGCGGGCCAAGC TCATCGGCAAGTACCTGATGGGGGACCTGCTGGGGGAAGGCTCTTACGGCAAGGTGAAGGAGGTGCTGGACTCGGA GACGCTGTGCAGGAGGGCCGTCAAGATCCTCAAGAAGAAGAAGTTGCGAAGGATCCCCAACGGGAGGCCAACGTG AAGAAGTAAGTATGGCTTGCTGGGGTCGGGGCCGGGCCAGTCACGGTGCTGATGGTTCTGTCTTCCTT
507_STL_01	27	25	TGCCCCAGGAGGTCTGGTCCTCTCACCCGCTGCCAAATTCTCACACAGCCTCAAAGGGATCCTCAGGGCGTAAAGC AGCCCCAGCCCCGCCACGAACCACACAAGAGGCCCCAGTCCCCGCCAGCCCGGCCCGCAGTCGCTCCCTCCAGCCTA GCGTCGGGTTTAGGCCAGGGACAGATGCAGGAGACGCTCCAACAGCTGCGGCTTCACCCACGCCGCCACGGTCCGC CATCTTGCCCGCTATCGCAGGCGCCAGGAGCTGGGAGGGGAGAAGGACAGGAAACCGGGAGTCGGGAATCCTGGGAT AGTGGCGGACCTGAAGTTGGCCTCTGTGAAGGCTGAGTCCTGGGGAACCGGGACCGAGAAGATTTCGAAGGTGGAG GAGCGTGTCTCAAGATTGGGGCTACCTGTTCTTTCGTGGGCAGGGAAGGGGCGGACAGCAGCGCCTATTCTGGAG GAACTGGACTGAGATGTGACCC
508_STL_02	30	25	ATTGGGAAAGATATTAGACTTCAAATCACCTAAGGCAAACCCTACTTCCTGGGGCGCGGGCGCGGGCGCTGGCGTT AGGAGACGTCACTCCCGCGCATAACTGACATGGGGCCCTCTTGGTCGGCGTTTCCGGGCGGGTCCTTCCGACGGCC GCCGCGGTGATTCCATCACTCGGCTTTCTTCCCGGCCTGCCTCGCGCCCGTAGCCGGGCTGGGCCAGAACAGCCCA AGATGGCCGACTTCGATGATCGTGTGTCGGATGAGGAGAAGGTAAGGGTCCGCCTCTCTCTTACCTCCTCCCCC CGACAGGGAACTGGGGCCCGGCCCGGCTGCGTTGGGAGCCTAGCAGTGTCCCCAGGAAAAAGAAGCTTCTTGGTCC ATGCTG
509_SUFU	30	30	AGACATTAGCCAATGGGTGCTTGGATAGGGTGCGCCGGCGCCCCGCCCCCCTTAGCGCCCCGCCGCCCCGAGGCAC CCTCTGGCAGACTCGGCGGCGGCAGCCTGGGCGGACAGTGCGCCCGTGCGCAGGCGCGGAGCTAGACCTCGCTG CAGCCCCCATCGCCTCGGGAGTCTCACCCACCGAGTCCGCCCGCTGGCCCGTCAGTGCTCTCCCCGTCGTTTGCC CTCTCCAGTTCCCCCAGTGCCTGCCCTACGCACCCCGATGGCGGAGCTGCGGCCTAGCGGCGCCCCCGGCCCCACC

			GCGCCCCCGGCCCCTGGCCCGACTGCCCCCCCGGCCTTCGCTTCGCTCTTTCCCCCGGGACTGCACGCCATCTACG GAGAGTGCCCGCCGCCTTTACCCTGACCAGCCGAACCCGCTCCAGGTTACCGCTATCGTCAAGTACTGGTATGCTCT GGGCCGCGGGGAGACGGACAGGCCGCGGGCTGGAAAGGGTTAAAGCGCCGAGGGCGAAGTAATTTGTGGGAGGTGGG AGGAGGGGTAGAGAATGGTTAAAGCACTCAGAAGGAGGGCTTCTTGCTG
510_TAF15	30	25	TTCCTCAACTGCCAGGGCCCAAGACTCACAGGCAGCAGCGTCTATCTCCCCATGATATGCAGAGACTGCCCCAGTG AAGCGTTCGTCTCAGCAGCCGGTCCGACTGCGCGGCCCTCCCCGACTACTTCCGGCACCGCTCCCCGCCTCCCAACC CGGAAACGCGCGGCTCTTCCGGCCGGCGGCGCCTCGCTTGCGCAGGCGCAGACTGCCCTCCGACACGTGGT GGCGATATTGAGCTGTGTGTAGGTACACCCTGCAGCTTGCGCTTTTAACTGCTTGTGGTTGAGTGGCAGCATGAGC GAGCTCTGCGTATTCCAACCCGGCGTTAAGAATCCTTCACTAGCTTTTCTTCCCGACGCTGCTTATTTATCTATCG GTAGCATGACGGGTAATTGACGCCCTCGGATGGCTTTGAGGTCGCCATTTTTGGTTGGTGCCTTTGTCTTGGTGTC A
511_TAL1	25	26	GCCCCTGGCCCCCTGGCCCCCTGACCTGCCGAGAGAGGCCAGCGGCTGGCTGAGGCTGTAGAGCAGCGCGCGGCCGGG GGCGGCGGGGGCAGCCAGCGCGGGAGGACTCAGCTGCACCATGCGGCCGTCGCCGGGCAGCTCCGCTGTAACCGAG GCGGGCGCGGGGGCCGGGCGGGCCCGGGAGGTCTGCACAGCTCGGTGGTGGGCACCCGATGGCGCGCTTCGGCCG TCGCCGCGTCGCGGCCCTTTAAGTCTCTCGCGGCGCCGCCCCCACCGGCAGGGCCGCCCCCCGGGCCTCCGCGCGC GCCCAGTTCGATGACTGGGGGCTCCGCTGCGGCCGCGCTCGTCTCCTTGGCGACGCCGTTCAGCAGGACCAGG TGCGGGGGGGGCCATGCTGGCCTCGGCCGCGTCCCGTCCCTCTAGCTGGGGGTCACTGCGAGCCGCCTCGCTCGGCG GCCCGCTCGGTCATCCTGTGGGCAGACAGACAGA
513_TCF1	25	25	CAGAACAGGCAGGGGCCCTGATTCACGGGCCGCTGGGGCCAGGGTTGGGGGTTGGGGGTGCCCACAGGGCTTGGCT AGTGGGGTTTTGGGGGGGGCAGTGGGTGCAAGGAGTTTGGTTTGTGTCTGCCGGCCGGCAGGCAAACGCAACCCACG CGGTGGGGGAGGCGGCTAGCGTGGTGGACCCGGGCCGCGTGGCCCTGTGGCAGCCGAGCCATGGTTTCTAAACTGA GCCAGCTGCAGACGGAGCTCCTGGCGGCCCTGCTCGAGTCAGGGCTGAGCAAAGAGGCACTGATCCAGGCACTGGG TGAGCCGGGGCCCTACCTCCTGGCTGGAGAAGGCCCCCTGGACAAGGGGGAGTCCTGCGGCGGCGGTCGAGGGGAG CTGGCTGAGCTGCCCAATGGGC
514_TCF12_01	25	26	CCTGAAGAGACCCACAAGTTCTATTCGGGGGGACCGACAGCCCGCCCCGGGAGGAAGGGGCGGCCAGGCCCGAAAG CCGCCTCCCCCCTCCCAGACCCGAGAGCTCGTGCGGGGCAAAGTGAACCGAGCCGCTGGGCGGTGCAAGGGGAAGCC CAAGCCCGTTCTCCCGGCCAAAGTGAACTTTAATCGGGGTGGTTGGATGCGGGCGGCAGGTAATTGCGG GCTAGCGAGCGGGAGTGGGGCGGCGGCGGGGCTGCGGGGCGCCCGCCGCGTCCCTGCCGGAGTGGGGG CGCCCCCGTCCCCCGCCTCAACTCCGCGCCCCCTTTGTACAGCGCGAAACCCGGGGTCCCCTCCAAGTTGGGGAGCG GAGTGGGGGCGGAGGCTCGAGTCGCGGGCGCTCAGGCCCGCTGGCGGCGCGCTCGGCCTGTGCGCCCCGTTCGGTG CCCGACTCGGGCCGGCGCCCAGGCTCCGGGGCGCGCGGGAGATCGGGCGGCTTCGGCCGCGGAGCCAGGCTCATTG TTCGGCAGGTCCGGGGCAGGGCAGCAAAAGTGGGAGGAGGC
515_TCF12_02	26	25	CACAAGGCTTTGTCTGGTTTGAGGTACGTTTTGCCCTTTCTCCCGCATTCGGCTCTGCATCGAATCTGACCGGCCG CGCCTACTCTCGGAACGGCCGAGGAGGATGGGTCTCCCGTCTCCACACGCGCGGTGTCTGCGCCGACTGCAGCCCT CCTGGACGGGAGCCTCTGGGCCCAGCTTAGGGTGGCGTCCAGCGTGACCTACTCGGGAATGGCAGCCTTCAGTGTC CTG
516_TCF3_01	25	25	AGCTGGGAGCAGAGCTGGGGACACCCGGGAACCTGAGACTGCGCTCCATCTAGGCCCGGCCCGTCCTGCTCCCGCCC CATCACAGACCAGAAGACTCTGAGGACTCGCGTGCCCTCAAGTGACGCTGCACACCCTGGACACCCACGCCCAGAGTG AGAAAACTCCAGACGATGACCCCGCTGTACCGCCAGGCAGAGTCCCTGCCGCTGAAAACTCGCTGTTCCCCCTGCC

			TTTGCTCTGG
518_TCL1A_01	28	24	GCTCAAAGTGGCTTCATCTGTGGGATCCTCCCTGCCCCATAGTGAGTGCTCCTTGAGTCCTCGCCCTTCCTAGGG
			CATCCCAAGCTCCCAGGGGCTGCCCCCTGCTGCCTCGCCATCCGCTCCAAAGCTGGCTGTACCTCGATGGTTAAGGG
			CAGCCAGGCGTGCTGCTTCTCGTCCAAATACACGAACTTCTCCCAGGCCCACAGGCGGTCCGGGTGGTCGGTGACT
			GCCTCCCCGAGTGTCGGGCACTCGGCCATGGCGTCCTCGGGCCGCCTAAGAAGCAAGAGCCAGAGCCTCTCAAGGC
			CGCTCGCTGGTCCCTGGGATGTGGGGCCGACCCTTTATATCCGGGCAGCATGCGGCCGCCACCAAGCGGCGGGGCG
			GGAGGACGGCCTTGGGGCGGGACCCCGGGTCGGGAGAACGACCTTGGGGCGGGCGTAAGGCAGGATGGGGCGGGG
			TTTGTGGGGGTCTTGGTGGCAAGTGAGGGTCC
519_TCL1A_02	25	25	CCCTCTGCTGCTGCTGGAGAGGCACCGGGGTGACCTTGGCCCTTTCTTCTTCTGGAAGACCCCCCCGCTTCCCTCG
			GCTGCCGGACCGGGACTCTGGGCCTCTGCTGGGAACTCACAGTCGACACCAGGATGCCCAGAGCCAGGACCCACTC
			CTCATCTTATGGGATCAGAAGAGACCCGCGCGGGCCTGAGTTAGGCCTGGGCTTTCC
520_TEC	21	22	GGAGGGGAGAAAATCCTTCCCCGTTCCTCGAGGGGCGTGTGGAAGCCGCCTCTTGCCGCGCTCATCCCCCTCCCCA
			CCCGTCCTCGCCCCGGAGTATCGCACTCCCGGGGCCGCCCCAGCCCCGCCGGCGCCCTTACCTGGCTGAAGCGCG
			GCTGCTGGGCGGACCTGGGGAGACTGCGAGGTGCAGTCTGCGCCGCGGAGTCCGGAGCCTAGCGCCCCAGAGTCCA
			GAGCAAAGCGCCCCGCCCCCGCCCTCTGATCTCCCGTCCCGCCCCCAATCACCCCGCCCCCGCCCCGATTGCTGGCC
			CCGTGGACGCCCTACCCCGCCTCTGATCCTGCAGGCCCGCCCAGTCCTCGATCGCCCCGCCCCGGTCGCTTGGGCC
			CTGGGTGGCAGGT
521_TFE3	25	25	GGATTCCTTAGGTGCCCCCCCCAAGACGGGCGCCCCGACGTCCTCCAAGGCTAGGCCGAGGGCCTCCAATCCCAGTC
			CGGGGCCCCCGCTGCCCCCGAGATCAGGCCCCCTGGGAGCCCCAGTCGGCACTCCCAGCCCCAGGCGGCCCCGCACC
			TGAGCAGCTGAGCCGAGTCGGCCGGCCTGCGCTCCTCCAACAGCACGAACACGGCTCGAGGGCCCTCCGCGCTGGC
			CTCTACGCCATCCCGAGCTGGTTCGGCCGCATGAGACATGACGCCCCGGCCCCGGGCGAGCCCTGCCAGGCCGGTCG
			GGCCTCGGCCCGGTCCCCCCTAACAAAATAAGAGTCCCCCCCTCCCCCCCAGCTCGCCACTGCCGCCTCCTCCGCTAAG
			CCATGGAGCTAGCACTGCGCGGGCGGGCGGCGTCTGGGAGATGGGCTGTGAGTCATCC
566_AL080059_1_01	24	25	GAGACTCTGGTACTGTGAAGGGTCCGGGTCGCGCGGGGCGTCGTCCGGAGCAGGGCGGACTCGGGCTTTGGCGCGG
			CCTTTGCCCCCGGTTTTTGGCGCGGGAGGACTTTCGACCCCGACTTCGGCCGCTCATGGTGGCGGCGGAGGCAGCTT
			CAAAGACACGCTGTGACCCTGCGGCTCCTGACGCCAGCTCTCGGTCGGGACCGAGCGGGTCTCTCCACGGCAACCG
			CCGACGTCACGAACGTACAACTGTACCGTCGCGAGAGGACGTGATGCGCCCGGTGATTGGCGCCGCCGCTGCGGCT
			GCGCAGGAGACGACCCCCGCGGGCGCTCCCCACCCCCATCTCGCGCGGACTCGCTTTAGGTCTCGGCGAGTTTCTCT
			GATATGCGCTCGCGGGGGTGCTGCCATTTCATCTCTTC
567_AL080059_2_01	24	24	CTACAGGTTTCTGGGGCCTTCTTCCCGGCAGGGCCACGCCGGTTTCCAACGCGGGGGGCATTTTTCGGCCTTCCCA
			CGGTTCCCGCTGTTCCCACGAAGACAGTGTCTGCGGCCAGGCGCTCCGAGAGAGATGCGGCCTTCCCCGGGCCGGG
			CCTGGCCGCGGCCTGCCCGTGGTCCCCCCGCAGCTCGGGCCCGCAGCGCGAGGCCACAGTCCAGGGGGAGCCGGCAG
			GCGGCCTCCTCCCCGAGCCGGAGGAGCTGCGCGGACGCAGCGGCTTCCAGGCCACCCCCACCCCGCGCCAGCCTGCA
			CCTGTGCCGCCTGGGTGTCTTCCCCGAGACTCTGGTACTGTGAAGGGTC
568_AL137718_01	26	25	GGAAAGAAGGTGGCCACTCAGCAAGCCGCAAGCTGGAAGCTGAGGGATCGACAACAGGTTTTACTCCCGGGGTCCG
			CCACCCAAACAGTCAGCACAGCCTAGCCCAACCGCTGAAGTCGGGGCCGCAGCCAACACATCTGAAAACTCCCGCC
			ACCCGTGTTGGCCCGGACTGGCCAATCCCGCGCCGCCGGATCAATGACACGCTGAGGCACCGCCCCTTCCGGGCA
			CTGCGAAACATGATTGGCCTTGCGGCCTGTCTATGCAGCCGCTCAACCCTTCCGGCGGTCCAGGCCGCTCACCTTA
			AGGACGCAGAGTGGCGTCAGATTTGGAGAAGCGCCGGGGACCGTGGAGGAAGTCATCGGCCTGGATTTCTTTGGAT

			TTGCAG
569_ANXA2_01	25	30	GCTGGCCTGGGTGGGGCTTTTATACCCGCCACATCCTCCCTAGGCGAGGCGAGGCCCGCCCCCGCCCCGCCT
			CCCCCTTACACGGCCCCGCTCCCACCCCAAGTCAGGGGTGACTCACCCCGGCCCCGCGGCCCGCGACCCGCCC
			TGGAACGCTCCCGAGCCGCGCCACGCGGGAGCGGCCCCCAGCGCCCCTGGCCCTGCCCTCCGAGAAAGCCCGGCCGA
			GGCTGCCCCGAGGCCCACAGGGACCCCGTTTCTTCCTCCTTTCCTCATTTTACTTCTTAAGTGCCACGTCGAGCTC
			TCAGCCTCGGCTTGGGTTAATAAATTAACAAGACTTTAGTAGTAGACTCTGGGCTTGATTAAGTGTTTTTTTTTT
			TTTTTTTTTTTTTTTGGCGTTAATGCAATGGAGGAAAGAATTGTTCCAAGAAAC
570_APOD_01	27	25	AGCTAAGGGCCTGTCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCA
			GAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATCACCCCGTCAGGGCCTCAGAGAGCAGCGCCTCTTCCG
			ACGGCCCCCATCCAGTCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCAT
			CACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCTCCATCACCCCAGTCATCACCCCGTCACGGGCCTCA
			GAGAGCAGCGCCTCTTCCGACGGCCTCCATCACCCCGTCACGGGCCTCAGAGAGCAGCGCCTCTTCCG
			ACGGCCCCCATCCAGTCATCACCCCCTCATGGTCCCCCGGGATCTGACGTCACTCTCCTCGCTGAAGCCCTGGTGAC
			TGTCACAA
571_ATP5A1_1_01	30	25	GGCCAGGAGTCTCAGGTAAAACCACAACTCCCAGAAATCCCGGGCCCGGCGAGGGGCGGGTGCCAACGGCGTGTGG
			GCGGGGCCTAGGGAGTGAGCGGGGCGCATCTCCCGCTAGGAGTTCCTAGTAAAGTGGCGGGAGCCGCAGCTATGGA
			GCCGCAGGAGGAGAGAGAAACGCAGGTGATGGGGCGGGAATGGGGATCGTTGGCCTCCTGGAAAACGCGTTTTTGA
			CACCCCCGCGCCGACAGCGGGTCTCCTGTGCGCGCCACGTCTACTTTTCTCTCCCCTATTCCACACATCCGTCTTT
			TAGTGCCGCCGTCACTATCTGCAAGCCCCCCCGTGCTTAGACTCTCCTGAAGGCCTTTCCCTTCCTGCCCGGGCCTC
			CCCTTGTTTGGATCTGGCCCGGGAGAGGCGTTGAGCAGCCCGTGTCCACAGACTCTGGAGTGGGAC
573_ATP6V0E_01	30	25	TGCCTCCAAGGAGCTGCAGCCAGGAGACAGCCAGGCGAAGGCGGGGCTCTGCCTCTGGGCTCCCCGAGGGGCGGAG
			GCCGGCGCGCGGGTCACGTGGGGGCGCGGGAGGCGGGGCTTGCACACGCTGGTCACGCGGTCAGCTATTGACACTT
			CCTGGTGGGATCCGAGTGAGGCGACGGGGTAGGGGTTGGCGCTCAGGCGGCGACCATGGCGTATCACGGCCTCACT
			GTGCCTCTCATTGTGATGAGCGTGTTCTGGGGCTTCGTCGGCTTCTTGGTGCCTTGGTTCATCCCTAAGGGTCCTA
			ACCGGGGGTAAGTGCGTGAGGCCCGCCTTGGGAGGAACGGGCGGTGAGGAGCTAGCAGGCCGGGGCGGGAAAGGC
			ACGACCCCCACACGGGTCAGAGAACGTTGCATGGGCGCCCCCCCGCGCTGCAGAGTCAGGCCCCCGACCCGGCGGAA
			CTCCTTGTGTTCCTTTTCGCAGCAGCTTCAGTGTCCTCCGGCCTGAGCGAGTGGAGGGTGACCTTTGGTGGACCCC
			CCTTGG
574_Beta-NAP_01	25	24	TCCCTAGGAAATGCCCTCTTCAGGGCGTCTTCTGCCCTTTAAAGCGACTTGGCTCGTCTCCAGATCTAAAGGTGGG
			CGAGTCTGCTGGACGGACGCTGGGACCGTCTTGCAGGGGATGTGGAATAGCTGCCCCCACCCCGACCACCTGGCC
			TCGGCGGGACGGGCCTCTGGGGCTCCGCTCTCCCCAGACGCACGCGCGGATGCTCACCCACGCCGTGGAGGGAAAG
			CGGGAACTGGAAAGAAGGCTGTGCC
576_BIRC5_01	30	24	TGGTCTTGAACTCCAGGACTCAAGTGATGCTCCTGCCTAGGCCTCTCAAAGTGTTGGGATTACAGGCGTGAGCCAC
			TGCACCCGGCCTGCACGCGTTCTTTGAAAGCAGTCGAGGGGGCGCTAGGTGTGGGCAGGGACGAGCTGGCGCGGCG
			TCGCTGGGTGCACCGCGACCACGGGCAGAGCCACGCGGCGGGAGGACTACAACTCCCGGCACACCCCGCGCCGCCC
			CGCCTCTACTCCCAGAAGGCCGCGGGGGTGGACCGCCTAAGAGGGCGTGCGCTCCCGACATGCCCCCGCGGCGCGC
			CATTAACCGCCAGATTTGAATCGCGGGACCCGTTGGCAGAGGTGGCGGCGGCATGGGTGCCCCGACGTTGCCC
			CCTGCCTGGCAGCCCTTTCTCAAGGACCACCGCATCTCTACATTCAAGAACTGGCCCTTCTTGGAGGGCTG
577_C2_1_01	25	27	GAGGCCTGGGGCTCTGGACTCCAAGGTGGCCCCGGTTGCAGGCTCTTCTCACCCCGCCCCCTTTACCGGCTGCCTC

			ATTCCTCCGCCCCCCCCTTACACGTTTGCACGCGCTTTTCACGTCCTCCCCCCGCCGCCAGCACGCACCGTGCAC
			GCCCTGCCCCCCACGCTCAGAGCTCCGTGGCACGCCCCCCCCAGCCCCACGACCCTGAGTGCACGCTCCTCTCACCTG
			GCCCGGTTCCGCGCGCTGTTTTTTTTAATCCCTTATTTTCCCCACCCCCCCCCGGGGCCGGCAGCGACCCCCCACACA
			CGGGCAGGGCCTGGGCAGCGCGCAGGCGCGGGATGCACGGGACGCGCGCGCGCGGGGCCGGCTCCGCGTGGGC
			GTAAGGGGGGAGGGGCGGGGCGGCTCGTGCCGTGTGTTCCAGGCCCCCGCGCGGCGGCGGCGGCGTCGGCTA
			GGACTCGGGGAGGGAGGAAGAGGGGAGGGAATTAAAGGAGCAGGATCCCC
579_CA3_01	28	25	CCCAAGAATGCATGGAGGAAGGAGAGGAGGACGAGGTGAGGGCCGCCTGCATTTCTGCACGTCGGCGCCGGTTAGAA
			ACCCTGCAGTTTTGAGAGAAGAAGAGGAGATGGAGGGGCCAGGAGCCACGACTCCCGGGAGAGCGCAGGGAGGG
			GCGTGGGTGCCCCTTCGCCCACCTCCGCCCCCGTCACCTCGACAGCTGTCCCGCTCTTGGAATTCATTGGCTTCCT
			CTACCCGGCCTCCCAAACACCACCCCAATCTAGTTTAGCCCCCCGCCCCACCCTCGCTGACCTAATAAGGCCATGC
			AGTGTGCGGGGGAGCTACATAAAAGCGCGGGCTCGCGGCGACTCTGCACCACGCAGGGGAAGAGAAGCAGGAGCC
			GTCCAGCACGGAGGAAGGCGACCATGGCCAAGGAGTGGGGCTACGCCAGTCACAACGGTGAGTGCAGGCAGCCGCG
			ACCCGGCCAGGAAGGGATGCCAGTCCAGG
580_CA4_01	24	27	GGCTCAGAGGACTCTTTGCTGTCCCGCAAGATGCGGATGCTGCTGGCGCTCCTGGCCCTCTCCGCGGCGGCCAT
			CGGCCAGTGCAGGTGAGCTCCCGGGCTCCGGCCCCAGGTGCCCCTCGGCGGTCCCCTCCCAGCTCCCGC
			CCCTGCAGAGGATCCCCCCCGCGGCGACCGGTGAGCGTCGGTGGCGCTGGGGTCCCGGGTTGCGTGTGCGCCGGGG
			GCCGCGAGGGTGCGGGAGGACTGGGCAGCGCGCGAGCTTGTGTGTGCACACGCGTGTCAGCACCGGCTGGGGGAGC
			GTGTGCACGGGTGTGCGCGGTGAGGGTGTGTGCGCGTGGCCCGGCGAGACGAGTTGGGAGTCCCTGATAAGGATGC
			GTCTCAGGCCGGGCGCGGGTGCTCCAGCCTGAAATGCCAGCACGTTGGGAGGCAGAGGCGGGTGGATCACCTGAGC
			CCAGGAGTTCGAGACCAGCATGGCCAACATGGTGAAA
581_CCNA2_01	26	25	GGGTTGATATTCTCCTGGTCCTCTTGGAGCGCCGTCTGCTGCAATGCTAGCAGCGCCGAGCCCGCCTCGCGGGTCG
			CAGGCCCCGGCGCAGAGTTGCCCAACATCACTGCTCCCGGGAGTGGACGGCGGGATCAGCCTGCGGCGCCAAGCAG
			CGTGCACTCTGCCCAGCCGACCACTCTCGCACCGACCCGGCCAAAGAATAGTCGTAGCCGCCGGTCGCAGCCCAGGCC
			AGCCTACCAGCCCGCCCGCTCGCTCACCCAGCTCGAGACCACGCAGGGCCGAGGAGGTTGCGAAAGGCGCAGGCAG
			GCACTGCCCAGCGTGGCGAGCCAAAGACGCCCAGAGATGCAGCGAGACGCCGCCGGAGCGGCGGCTGTTCTTGCA
			GTTCAAGTATCCCGCGACTATTGAAATGGACCAATGAAAGCGCTCGCGGCCTTGACGTCATTCAAGGCGACAGGGT
			CGCAGGCGAGTGAAGGGTAAACCAAAGGAAACTGAGCAGGGGCGGGCAGGAGGAGAAACAAACTGGC
582_CCNB1_01	26	25	GGCCTTTCCTGAGCTGGCATTGGCAACGCACACTCTTGCCCGGCTAACCTTTCCAGGTGGGCGGCGCACTGGCTTC
			ACTGCTCTCCAGGTGGCCGCTGCAGCTGCCCGAGAGCGCAGGCGCAGAGGCAGACCACGTGAGAGCCTGGCCAGGC
			CTTCCGGCCTAGCCTCACTGTGGCCCCGCCCCTCTCGAACGCCTTCGCGCGATCGCCCTGGAAACGCATTCTCTGC
			GACCGGCAGCCGCCAATGGGAAGGAGTGAGTGCCACGAACAGGCCAATAAGGAGGGAGCAGTGCGGGGTTTAAAT
			CTGAGGCTAGGCTGGCTCTTCTCGGCGTGCTGCGGCGGAACGGCTGTTGGTTTCTGCTGGGTGTAGGTCCTTGGCT
			GGTCGGGCCTCCGGTGTTCTGCTTCTCCCCGCTGAGCTGCTGCCTGGTGAAGAGGAAGCCATGGCGCTCCGAGTCA
			CCAGGGTGAGCCGCTTCGGACTGCGAACTAACGCGGCCTTCTTAGCTGCTGCCTCTCCCTGCCTCGCGG
			GAGCCTCCCGAGCGGGAGAGGGCCGCAGGAGCGATTTGGGGAGGAAGGTGGGAGGGGACTCACCAAGA
583_CCNC_01	25	25	ACTGAGCTGGGATCCAGGCCCAGGGGAGTCACAGGCCCCGTCCTCACAGCTCCCCCAAAAACCGGCCCCAGGTGAG
			AAGACGGAAGATCGCTTACTAGTGGGAGCTCTGCCAAAAGTTCCCTGCCATGGAACACAGCTTGCCCTGATAAAAA
			AGCACCAGCCGGCGGAGCGGCCCGCGGAGCGACCATAGACCCAGCCCGTCCGGTAACCGCGCTCCTCGATCAAATC
			AGCTCGGCTCGACTCCGCTCCGCGGCGACGGCGAAAGGAAGAGGATGGCCCCCTAGTCTCCTTCACGCCGGCC

			GACAACACTCAACTGTGCAAACCCGTTCCTATCGACAAAAGTTCCGGCCCGCGGTAGCGGAGGGAGCCGGAGGGGA GGTGCTGACCCTTGGAGGTGCTGAGA
584_CCND1_1_01	30	25	GGAAGGCTGCAGCTGCTATTTGGTGCTTTACCACCGCTGAGAAGGTGGAATGGTCACGGCCCGGTTCTGTCACTTT CTTCAGCCGGACAGTCGCCTTATTACGGATTCCAGTAGGGCCGAGCACACTCCTTCCTGCCCGTCTTTACAGATGA ACATGCTATCGCTCCAGCAGTACAACCCGCCTTATTACGTAAAAAAGCAGCCCCTATCTACCCGCAGGGAAGGAGT ATGTTCGGCACCACAGCTGGACTGGTGCTCGAGTTAAGCGTCCTGGGAGGTCCGCATGCGCTCCGGAACCGTAATG CGCGCTTTTTCTAAGCCTTACGGTAAACGCGGACGCAGGGCAACCACGTGGCGGTGGAACCGAGGCCCGGCGGGAA TGCGCGGAATGCGCGGCGCGGCCTCGCGCGGTTCCCGAGCCACGGCCCAGGGTCCGGCGGCGCGCTCTCGCCTC CTCCCCTCACCTCTCCCAGCCGCACCCCGGCCCTGGCCCTGCCGCCCAGAACTCGCTGGGCAAGTCGTGCCCCGCG TGAACACACAGAAGGGGCTTGGGG
585_CCND1_2_01	25	25	ACCCCAAAAGCAAGCAGTGTGGGGGGAAGGGGAGCTCGAGCGCCTTCGGAGCCCAGGGGCCGGCTTTCGGAAGCGT TTTCCCGGGCGACTTAAGGGCTTAACAATGGAAAACTCGCGGAGCCTGAGCCAAGTCCTTTCAAGTCGCCGCCAGG TATGCGGCTGCAGGTGACCCCACCTGGGTGCGCCGCCGCCAGCCGCCCTGGTGGAAAAGCGGGTGCGGGAGGTC GCTGGCGAAAGGTCGGGACTGGTCCCTGCACACCGCCCCCCAACCCAAGCCCCGAGCCCCGCGGCGCGCAGCCGC GCTGAGTCCCGGGGTCTGCGTCGCGGCGCGCCGGTTCCTGAATGAACGCGCTCCCTTCCCCCGCCTGAATGAAGGT TCCCACAGCCAGGGACGGTGGCGAACACGCGCCTGCAGCGGAATTCGCTTTCTCCTGACCGACCATCCGCCCAGGC CGCGGTCACCGGGGCGGGGGCGAGGGGGCGAGGAAGCGTGAAGGTGATTTCAGTTAATTTTGGATTTTCTTTCAA ACAACGTGGTTACCCTCCCGACTGGGCCACTTGCCCTTTGTCTC
586_CCND1_3_01	25	21	GGGTTACCCCCTTGGGCATTTGCAACGACGCCCCTGTGCGCCGGAATGAAACTTGCACAGGGGTTGTGTGCCCGGT CCTCCCCGTCCTTGCATGCTAAATTAGTTCTTGCAATTTACACGTGTTAATGAAAATGAAAGAAGATGCAGTCGCT GAGATTCTTTGGCCGTCTGTCCGCCCGTGGGTGCCCTCGTGGCGTTCTTGGAAATGCGCCCATTCTGCCGGCTTGG ATATGGGGTGTCGCCGCGCCCCAGTCACCCCTTCTCGTGGTCTCCCCCAGGCTGCGTGTGGCCTGCCGGCCTTCCTA GTTGTCCCCTACTGCAGAGCCACCTCCACCTCACCCCCTAAATCCCCGGGGGACCCACTCGAGGCGGACGGGCCCC CTGCACCCCCTCTTCCCTGGCGGGGAGAAAGGCTGCAGCGGGGCGATTTGCATTTCTATGAAAACCGGACTACAGGG GCAACTCCGCCGCAGGGCAGGCGCGGCGCCTCAGGGATGGCTTTTGGG
587_CCNH_1_01	30	25	GGCTACTGGGAAAAACCTTCCCCCAACATCATCTCTTGACAAGTGAACGGCTCTTGCCACGCACTACCTTAGCACAC TACTTACTCTCTTCTTCACTACGTTACAAAGACTGGTTACTTGTCTGCCATTCGACGACGGGATGGCGTTGTTCG TCTTTGTACCCACGGAACCTGGCAAGGTGCTCGCTTATTTTGATAGAAAAACGCACACTCCCGCGCCGCAGAGGCAGAG AAACGACGGAGCGAGATTGTCCTGGGAGCCAGAAGAGCTCCCGCAGCTGCTCAGAATTTAGTGACCGGGCAACTGG GCAACCGTTGGGAAAACCTCACCTTCCCGTTGGCCACGGCTTTGCATCTGAATTTGCGGTTGGCGTCAGCCCGCAG TCTTGCCAGCTGCTCCTCGCTGGAGAAGGTCCAGTGCCGCTTCTGACTACTGTTGTGGTATCATTATGGAATCGTGA CCAGGTCCAGAGGGTCTGCAG
588_CCNH_2_01	25	28	TGACCAGGTCCAGAGGGTCTGCAGACGAGAACCCAAACGCATCAGCGTCCTGGCGTAAAACACCCGTACCCCCACC GAAGATCTCGCGGAAGCCTAGGGCGTCCGGCTAGCCGGCGCTGTCGTCACGATTACGCGGCCAGCCCG TACGCAGTTGCATTTCCGGAGCGGACTAGGAACAGACCGTATCCCGGGTTCGTTAGGGCGCCCACTGAGACGTAAG TGGGCGGAGCCTAGAGAACGCTCCTCTCGGTGAGTCTGGGACATAGCTCCGCCCCTTCCAGGCAAGATTTAAAGGA GAAGCGCCCGGCAAGAGTGTTCAAGGGGCATAAACTGAGGGTACGGAGTAGGCAGATGTAAATTCACAGGGGATAA TCAGAAATGAGGAAAGGATTTCGTAGGGTGCTCATTTTTAAATAGAGGCC
590_CD34_01	22	30	GGGTTGGGCAGGGGTCCCTTCCCTCCGTGAGACTCTGCTCTGCTGTTCAGCCTCCCAGAAAGCCTCCACCCTCCCC

			GCGGCGAAGCCAAGCGGCCGCGGCGCGGGCGGTACTCACGCAGCAAACTCAGCAAGCAAAGCGCGGTCCAGCCC
			CGCGGCATCCTGGGCCCTGCGCGCGCCCCCTGCGGACCAGCATCCTTCCCGCGCGGCTCCTAGAGAGACGCACCG
			AGTGGAAGACACTACTCGGCTTGGCCAGGACGCGCTCTTCCCGCCCCCTCCGCCCGGGAGAGGGGTGGGGGATTCT
			TGCTTTTTTCCTCTCTTCTCCCCTCCCTTTTTAGTCTTGGCAAGGCAGCGCCTCTCCTTGGCTGCTACTAACTTGA
			GCTCCCCCTGGTTGGTC
591_CD38_01	30	25	AAGTACACTGAAATTCATCCTGAGATGAGGTGGGTTGGCGACTAAGGCGCACCGGTGGGCACTGCGGGGACAGCAG
			GGCCCCGCGCGCAGGGAAGCCGCCCGGATCGCCCGGAACCGGGCATCTTCCGTGGCGGGTCAGCCGAGAGCCCGCC
			GGGTGGTGCTGAGTAGGGAGTCCCGGGCTCCGCGGCCGCTTTCAGGAGCAGCTGGCCTTGGC
592_CD44_01	25	26	GCCCCCCTTGCTTGGGTGTGTCCTTCGCTCGCTCCCTCCCTCCGTCTTAGGTCACTGTTTTCAACCTCGAATAAAA
			ACTGCAGCCAACTTCCGAGGCAGCCTCATTGCCCAGCGGACCCCAGCCTCTGCCAGGTTCGGTCCGCCATCCTCGT
			CCCGTCCTCCGCCGGCCCCCTGCCCCGCGCCCAGGGATCCTCCAGCTCCTTTCGCCCGCGCCCTCCGTTCGCTCCGG
			ACACCATGGACAAGTTTTGGTGGCACGCAGCCTGGGGACTCTGCCTCGTGCCGCTGAGCCTGGCGCAGATCGGTGA
			GTGCCCGCCGCAGCCTGGGCAGCAAGATGGGTGCGGGGTGCTCAGCGCGGACCCGGCGGCAGCCCCTCCGGCTGAG
			TCGGCCCTGGGGGACTGGAGTCAAGTGAGCTGTCTG
593_CD59_01	25	20	ACTCAGGAGGCTGTGGCAGGAGAATCGCTTGAACCCGGTACACGGAGGTTGCGGTGAACCCAGATCGCGCCACTGC
			ACTCCAGCCTGGGCAACAGCGAAACTCCATCTCAAAAAAAAAAAAAAGTCCGTTTCGCCCGACACCTGCTTTTTCAA
			AATTACACATTTAGACCGCGAGGGGAGAGAGGAACTGCCGTGACCACGGAGGGCTGGCCTTTCCCCCGGCGCAGTT
			TCTCTGGACCGCTAGAGCTTCCCTTGAGACGAAAGCGATGGCAGGGGCCCGGGTGCGAGGCTGCCCCCGAGGGAAT
			GGGGGGCGCGACGGGGGTAACGGGGCTGCTTCTGGGAGAGGGCGCGCTCCCCGTTTCTCCTTCCTCGTAGATAAAA
			TGAAGCCAGCGTTCGGCTAGGACACCGGGCCGCGGTGACGGGTTGGAAGGGCCAGGCCT
594_CDC34_01	25	25	GAGCTCAAGGGGCTGCAGGAAGAGCCGGTCGAGGGATTCCGCGTGACACTGGTGGACGAGGGCGATCTATACAACT
			GGGAGGTGGCCATCTTCGGGCCCCCCAACACCTACTACGAGGGCGGCTACTTCAAGGTGAGCGCGGCGACCCCCGC
			CCGGGTCCCGGAGCCCACGAGCGACCTCGGGCGCCGGGAACCAGCTCCCTGCCCCGCGGTCCTAGCGCTGTTGCTG
			GGCGGGCCCCGAAGCCTCCTGGCTTGGGCTCGTTTCCCTTCTATGGCCACGTTCCCCCACCCAGCTCTGCCCGGCC
			CCCTCCTCGGACCGTCTCGGGGACCTTCAGCCTCTGCTGCAGT
595_CHGA_01	25	23	TGGAAGAAGGCAAGGTCCAGAGATCCGAGTGACTTGCCCAGGGACACAAGGCAAATCGGTGGAAATCGTCGAGGGGT
			GGAGGATCAGCCACAGCCCCCCGCCTCCCCACGCCACCTCTTGGAAACCAGATACCCGCCTCGCGGCCAAGACCCAC
			CAGCTCCAAGCGGCGGAGGCCAGAGGTAGCGAGGGGTGAGGTTAGAGGTGGGGGCGAGCGGGGACTGGACACCTGG
			GGAGTGGGGAAAGGGGAAGGGGGCGGCACCGCTGACGTCATTTCCGGGGTCGGGGTATATAAGCGGGGCGCGAGGG
			CGCTGCTGCTGCCACCGCTCCTGCCACTGCAGTGCTCGAGCCCCGTGCAGGGGAGCTTGCGGGAGGATCGACCGAC
			AGACGGACGCACGCCGAGGCACTGCGCCCCCAGCCCCGCGCCGGTGCCACCGCAGCCCGACCCCGGCCGCCAGTCC
			AGCCGCCCCTCGCCCGGTGCCTAGGTGCCCGGCCCCACACCGCCAGCTGCTCGGCGCCCGGGTCCGCCATGCGCTC
			CGCCGCTGTCCTGGCTCTTCTGCTCTG
597_CKS2_2_01	25	26	GAGCCTGAGGGGATACAAGGGATCACGAGGAGCGCCATCACCGTGCAAGGTCGACAGCTTCCGCTCAAAGCCCTGT
			GGCCCACGCTTCCGGCCTCGACCGACTACGTCATCACCAACAACCCCGTGATACCTCACTCCACCTTCAGGTCCTCCG
			TCCCAACGGTTCCGTGTCCTGGAACTTTCCACGTTCCTGCGCACGCGCTCTGCGGCCCTTAACGTCCCGACTTCGC
			CCTCCTCTGGCCACGCCCCTGCCCGTTAAGGGCCCTGCCACCCCCGTGACGTACCTATCTTCCCTCGGGCAACCTC
			GCAACAGATCTCTGATTGGCTGACCC
598_CKS2_3_01	26	24	GATCTCTGATTGGCTGACCCAGGAAGCGGACTTTGCGAGGCGGCGGCGACGATAGGCTGGCAGCCGGCCGACTTCC

			GCAGAAGGTGATTGGTCGGCGCTGCTGTCCAATCGGCGGCGGGCTGTCGGATTCAAATCCGGATCGTTGGGACTGC
			GGTCGTTAGTCTCCGGCGAGTTGTTGCCTGGGCTGGACGTGGTTTTGTCTGCTGCGCCCGCTCTTCGCGCTCTCGT
			TTCATTTTCTGCAGCGGCGCCAGCAGGATGGCCCACAAGCAGATCTACTACTCGGACAAGTACTTCGACGAACACTA
			CGAGTACCGGTGGGCGCCTTTCTTAGACCCCGAGCCGGCTCCCTCAGCCGGGGCGGCCCCCGCGGGCGGGCGACCCAG
			GCATAGTAGGGTCGGGGGTGGGGGCCTGGGGGGCGGAGCCCGGGGCCGAGGGCGAGGGCCGGGGTTTGG
			GGTCGCGGCCACCTGGCGCCCCGCGCAGTCGGACATGGTTGGGTGCCTGGCCGCGCCGGGCCGGTTGGGCCTTTGT
			TCGGTGTGCGCGGAGGGTGAGGGAAGAGTGCCCAC
599_COL5A1_01	28	25	GAGGTCCCCATGACCTCCTAAAGTGGTGCGGTCCCTGCTGAGTGCGCTGCCCGGGCCGTGACCCGCGCCCCTGTGC
			GTCCCCGCGCGCCTCCGAGCGCCCCTGTGCGCCCCGGCCCCGCGCCCCGGCATGGACGTCCATACCCGCTGGAA
			AGCGCGCAGCCGCTCCGCCCGGGCGCCCCCGCTGCTGCCCCCGCTGCTGCTGCTGTGGGCGCCGCCTCCG
			AGCCGCGCAGGTAAGGGCGCCCCGGGGCGCGGGGCTGCGGGATGGGGCGCGCCAGCCCGGGCGCCGCTGTCATCC
			CCGGGCGCCTTCGCCCGCAGAACTTTCTTCTTCCTTGGCCTGTGGAATGCACGGGCCAAGACCACGAATGCCATTTGC
			TGGGGGCCCCCCCGAGATGACGACACGCAGACACAATGCCCGCGGGCGCGCCGCCCCTCCCCAGACGGGCGG
			GTCGGGTGGGGCTGTCGCGCGAGCCGAGGAAGGACCGAGGGCTGGATCAGCAGGAGGGGTTGTC
600_COL5A3_01	25	25	GTGGACCCTGGGTCCCATCTCTTCCCTCCCGGCTCACCGGCCTGCGTCCCCGGCAGAAGCTGCAGCGCGGCCAGGA
			GCAGGCAGAGACCGGCCCCGCGGCTGGCCCAGGTCCCGGCGGGCGGTTCCCCATCCCGGCGGGCCCACGGGCAAGGCGGG
			GAACCAGTCGGGGCGGCTGCGGGGCGCGGCGACTTCTCTCGGGCTCGGTGCAGTCACTCGCGGCGGCCGCTCCTCTCA
			GGGTCCGCGCGGGAAACTGCCCGAGACCCCGCCCTGGCCTCGCCCTGCGCTCCAGCGCCTGGCCAGGCGGGGCTTTTT
			GGAGGGGGAGCGCTGACAGCTGGACTGGGAAGTTGG
601_COL6A2_01	30	25	GTGGCCCCCAACCAGAACCTGAAGGAGCAGGGCCTGCGGGACATCGCCAGCACGCCGCACGAGCTCTACCGCAACG
			ACTACGCCACCATGCTGCCCGACTCCACCGAGATCGACCAGGACACCATCAACCGCATCATCAAGGTCATGGTGAG
			CCGCGGGCGGGAGCACCGTCCACGCGCCAGGGGTGGCCACGGTGGGCCGTCCACCCACTCCGGGCCTCACTTTACC
			CCTCTGTGAGTGCGGAGGCCGAAGGAGGAAGCTCCGGGCAGGGCCTGGGCCACTCAGGTGT
602_COX6B1_1_01	23	25	TGAGGGGGCACCTGGGCTCCCCTCACTCGGGATCCGTTACTCCTCACAGAGCCCGACTCTCAGGCTCTTCCGTGGT
			CCGGGGACTGGACAGACATGGCGTGCACAGCCTGGGACTCTTGGAGCGGCGCCTCGCAGACCCTGGGCCCCGCCCC
			TCTCGGCCCGGGCCCCATCCCCGCCGGCTCCGAAGGCGCCGCGGGCCAGAACTGCGTCCCCGTGGCGGGAGAG
			GCCACCTCGTGGTCGCGCCCAGGCCGCCGGAGCAACACCAGCTGGGACTGTTCTGTGGGGCCCGACGGCGATA
			CCTACTGGGGCAGTGGCCTGG
603_COX6B1_2_01	25	26	CTAGAGTTTTTGAGGGGGGCACCTGGGCTCCCCTCACTCGGGATCCGTTACTCCTCACAGAGCCCGACTCTCAGGCT
			CTTCCGTGGTCCGGGGACTGGACAGACATGGCGTGCACAGCCTGGGACTCTTGGAGCGGCGCCTCGCAGACCCTGG
			GCCCCGCCCCTCTCGGCCCGGGCCCCATCCCCGCCGGCTCCGAAGGCGCCGCGGGCCAGAACTGCGTCCCCGT
			GGCGGGAGAGGCCACCTCGTGGTCGCGCCCAGGCCGCCGGGAGCAACACCAGCTGGGACTGTTCTGTGGGG
604_COX7A2L_01	25	25	GGGCAGAAGCCTCCCCTGGCTCCAACGCCGCGACTGCCTGTCGCCGAGGCTAGGGCCGCCACTTCTCATGTCCGAG
			CTGGCCAGGCGCCACTCGTACCTGCGGGCTATAGGCCTCCGAAGCCCATGCTCCTGCCAACTTCTGCGTGAAGCCA
			CTAAACTTGTAGTACATGACGCCCAGAGTCCGGCTTCCCGCATCCGCTGCCAACGCGACCGCCCCAGAGAAGGACC
			CCGCCTCCCCGGCTGTGGTCCCGAGACTCAGCGCAAGGACCCGGTGCTGGGACTAGGGCTGCCCGAAGATCGCCTA
			ACTTAAAACCTGCACACTTAAGCCGCATTGGGGAACCAAAAGCCAGGGT
605_CR2_01	30	25	CTCTCCTGGCTCACAGCTGCTTGCTCCAGCCTTGCCCTCCCAGAGCTGCCGGACGCTCGCGGGTCTCGGAACG
			CATCCCGCCGCGGGGGCTTCGGCCGTGGCATGGGCGCCGCGGCCTGCTCGGGGTTTCTTGGCTCTCGTCGCACC

			GGGGGTCCTCGGTGAGCTGGGAGGGGGAGCACGGAGGTGGGGACGCGTCCCGGGCAGGGAAAGTTTCTGTGCCGCG
			ATGCAAAGCAGGGGGCCAAAAGCGAGACGGTGGGGGCAGTGCTCGACGCGTGTCCGCCTCCCGCTAGCTTGAGGG
			ACCACTGCAATAAACCGCCTGGTCCTGATTGTCCCCACTGGCCCCTCCGGGAGCTGGGACCTCCAGAATTGGAGG
608_DBI_1_01	25	25	TCTCCTCTAGACCCCAAGGGAGGAGCGGGTCCCGCCCGCCATTCCCAGGTCTCAGAGTTTACTTGTCCAGAGATGC
			AACTTCCGGCCTCTTCAGGCCGGGCAAGATTTAAGGAAAGAAAAGAAACATAAGGACCTCCGTTCTTCGGTCTCCG
			TCCCCTCCCCCTTCCCCCGCGTGCCGTCCCCACAACGGGCCAGGACTGAACCCAACTCTCGACCAACTCCCGGCAGC
			AAAACTAAGCACCCTACTTCCGTTGTCCCCACCTGTTCCCGGCGTCCCCTTCGGCTACTCCCGGCGTTTGCGCAAG
			CGGTCCCACGTGGGCTCGGGCGGGGCTAGCGCCGCGGCGGGGGCTGGGCACGCCCCTAGCGCATAGCTGGCTTCTG
			ATTGGCTTT
			GGGTCTTCCTGGTCCCCACCTCCTGGGGCCGACGGGCGGCAGGAAGGGGCTCGGCGGGACGCGCCATCAGGGACCT
610_DC13_1_01	26	25	GAGGAGGAACAACGGAACGCGTTCGGAACGGCCTGGACTCCCGAGACTCACCCGACTCGTGGCCACACCGGGAGAA
			CTGAAGCGGCAGTAGCCGGCGGAGACGCCCGACCCGAAGGCCGGCTGCTAGGGAGCAGACAGCTGAACCGCTTGCC
			AGACGCCGAAACCCAGTGACGCCCTCCACCGGCTCCACCGTGCTCCCGGCTCCTCGCCCCCGCCGCGCGGCCCC
			AAGGCGCATGCGCCGCCTGTCCTGGAGGGGCCCATTTCCGTCCGTCGTGGGGGGAGGCACAGTGAGTCCACTGGGG
			CTCTTGAGGAGTGAGACTGCAGGAGATGTGGGCCGGTAAGAGAGCCCCGGGCGGCACTGGATCGGGCCCCGGAGGG
611_DC13_2_01	27	25	TGTGGGGCCTTGAGGAAGCCAGATCCCAGGCCTCGGGGGTGGCTTTTTCGCAATTGTCGCACGTTGTGAGGCGCAG
			GATTGGCGCTGGGTCTCGGGCTCGGGCGAGGAACTACGGTTCGGGCCGAGGTGAGGGGGGCGGTGGCGCTGTGCCG
			GCTGTGACGTCACCTCGCCCGCGGTGGGGCGGGTGGAGCCTTTCGTAGGCTCGCGACTGCGTCAGGGGAGGGCCGT
			GTGGTCATGTGACCAGGGGCTCCGCTCTACGATCCTGGGGTTGCTTCCTTTCCCAGAGTTGGGGTTTTGCT
			CTTCAGCAGATGAGGGAAGCTCCCCTCCGAGACTCTGGATAGCCGCCGGGGGGCGCTTGCCTGGCCGGCTGGTTGC
612_DSTN_01	27	24	GTAGCAACGGCAGGCGGTGCGTGACGTGCGCAGCCGCGTTCCGTCCTGAGGCGCGCCCGCCCGGGGTAAGCTCGC
			GCCGCCGCGTCAGCTCAGCGCTGGGTCTCTCGGTCCCGCAGCCGTGAGGAGGACGGTCTGCATACTCGCTGCCCGC
			CGGCTCCCTCCCCCGCGTCCCTGCGACCGCCGCGGCGAAGATGGTGAGTAGGAGGGAGGCCGAGGCGTGGGCCGAG
			GCGGCCGGGAGCAGTGTGTCTCTGGGGCGCCGCGGAGTCGGGGCTAAGGGGGTGAGCCGTGCCTCAGCCCGGGGAG
			GGACCCGGTCCGGCTGCAGTGTCCGGGCTGCGGGTGAGGGGGGGTCTCTGGGCCTCCGTCTCCCGCCGTCCTGGCT
			GGGCCCCCCGCCCCCGGGTGGATCCCGCGGCTGTTGCGCAGCTCCCAGCTGGGGCGAGGCCGCCGCCCTGAGCGTG
			GCCTCTGCGGGTGTCTCCAGACCCGGCCTTGCAACAACTGGCTGGGGT
			CTGCCTATGGGAAAGAGGTTGACATCACGCGCCAATCGGCATGGCTCTTAGAGAGAGCAGCTTAGTTTTGAATCG
			GTTGTGGCGGCCGCCGGCGAGGAATGGCGGTATTTGTGAGAGGAGTCGGCGTTTGAAGAGGTGGAACTCCTAGGGC
614_ECT2_2_01	27	25	TTTTTTGAGAGTGGTAAGGACTCTGTGTGAGTGAGAGAGGTGCAAGTGGGCGAGCGGCTCCAGAGCCAAGGGCTCT
			TTTGCCTGCGGTCGACGTCCCCGCCCCTAGTGACCGCGAATTCCGGAGCGCCCCAGCTCAGGCTTCCCGGATCCGG
			GAACTCCCTCGCCGCACCCCACCCCAGCAGCCGGGCCCTGACGCGGAGTGGGAGACCGAAGCCCCCAGTATTGCT
			GGGCATCTTCGCCCTCACCTGTTGGCTCTTTTGGACAGAAGAGTGTGGGTGAAGGGAGGGAGTTGGGAAAGGGATT
			TTGGCAAGCCGCGCAGCCCTGTGGCTTTGGGGGCCGGCACTTGCAGCCTTTGGGGGCTTA
			GCCCCAGGTCCTCTGGGAATGGGCTCTGGGTGCCAGGCAGGTCCCGGTGCGTGCTCCTAGTGCCCAGGGCCTC
623_FLT1_3_01	25	29	GGCAGTGAGACCCCAACCCGACAGCTGGATAAGGGATCAGCGATCCTGTCGCAAACGGACAGCCCCAGCGCGGACC
			CGGTCTGAGCGCTGATGCTCGCGGGTCCAGGCCAGCCACTCCTCGAGGCGCTCCCTCGGAGAAAGGGCGCAGCGGC
			CCCAAGCGTGCCCGCTGCAACTAGTGTCCCAGGTTCTCGCCGTAGCCAGCTTCTCCGGGCTACAGCCTCGTCTCCC
			CGCGTGCACCCCGCCCTGGCCTCGGAGGCTCTGCCCTCCGGCCGCCCCATCGCAGCCCGCCTCAGGCCCCGGCCCC

			CAGCCGCGCCTCACCTGTGAGAAGCAGACAGCTGAG
624_FOXK2_01	26	22	CCAGTCCTGGAGCTGCTGGTTAAAAAACGAACGTGTCACCGGGTCCCCTGGGTCTGAGGCCACGCGGCACGCGGCCC
			CTCCGCGATATTCCCGCACCTCGCGGGGAAAAGGCCGCTCGGCGGCCGGGCCTGGGCTCGCGGGCCGCCGCCTATC
			CGCACCCCGGCGTCCACGCCGGGTTGGGGGCCGCTGCGTGCCTGGCGCCCGCTGTGACCTTGGGCCTGGTCC
625_G3PD_01	25	25	GGCCTCAAGACCTTGGGCTGGGACTGGCTGAGCCTGGCGGGAGGCGGGGTCCGAGTCACCGCCTGCCGCCGCGCCC
			CCGGTTTCTATAAATTGAGCCCGCAGCCTCCCGCTTCGCTCTCTGCTCCTCCTGTTCGACAGTCAGCCGCATCTTC
			TTTTGCGTCGCCAGGTGAAGACGGCGGAGAGAAACCCGGGAGGCTAGGGACGGCCTGAAGGCGGCAGGGGCGGGC
			GCAGGCCGGATGTGTTCGCCGCTGCGGGGTGGGCCCGGCGGCCTCCGCATTGCAGGGGCGGGCGGAGGACGTG
			ATGCGGCGCGGGCTGGGCATGGAGGCCTGGTGGGGGAGGGGAGGCGTGTGTCGGCCGGGGCCACTAGGC
			GCTCACTGTTCTCTCCCTCCGCGCAGCCGAGCCACATCGCTCAGACACCATGGGGAAGGTGAAGGTCGGAGTCAAC
			GGGTGAGTTCGCGGGTGGCTGGGGGGCCCTGGGCTGCGACCGCCCCCGAACCGCGTCTACGAGCCTTGCGGGCTCC
			GGGTCTTTGCAGTCGTATGGGGGCAGGGTAGCTGTTCCC
626_GDI2_01	22	25	AGGGGAGGGCTGTGACTGAGCCTCCGCAGCCGGGGCGGGGCCTGCAGGCGCCGGGAGGGCCGCCAATCAGGCGCTC
			CCGGCACTCTAATTGGTTACGTCCCCGTCGCTCGCTCGCACAACTTTTTTCCTTCCCCGCCTCTCGCGAGAGGAAAAGG
			GCGGGGCGTCGCCATTTTGGCTTCCGGTTCCCCTTGCGGCCTCTGCCACGGTGGTTCGGGAGGCGGCGCGCGGGCC
			GGGGTGGAGGTGCACGGAGCCGCGGGCGGGGACTGCTGGCCACCACCGTTCTGACTCCCGCCGTCGGGGCGGGAGC
			TCGCTCGGTCCAAGGTCCCAGAGCCGGATCGCCGCCCTTGGACTTTGAGCGGGCGCGTGCGGCGGCCACGTGGGCG
			AGGAGCGCGGCCGGGCTGCCTCTCGGGGGTGGCGGCCTTGGTTCCTCCCGCGGGGCTGGGCTTGCCGGGGCCCGG
			AGCCCGCCGGGAAGAGTTCGGAAATCACACGTGTCCTTTTTCCCGCTCTGTGCCCTCCTTGTTTAGTGCGTTGCCG
			GTGGGCGCTTTAGGAAATTGGTAGGAGGAAAAGCGGCTTCTTTTGAAAGGTAACCCTT
627_GLI_01	23	24	GGGGTCCTGGGGGTGCAATAAGCCCGGCACCCCCTTCTCTTGCTTCCAGCTACCCCGCCTCATCCTCCAGAACGGCA
			AGAGGGAGGGAAATAGAAGGGAGGTGAGGGGCGAGCGGGAAGAGCGGCGGCGCCAGCGGCTGGAGAGAGAAAAA
			GTTTTTGCAAAAGGGAAAAAAAAAAGTTTGCGCTTCTCGCGGGTGGTCCGGGCTTGCGGCCCGGCGGGCTGGGCCGG
			CGGGAGGGCTGGGGGCCAGGTTGGGGGGGTGGGGGTGGCATCGAGGCTGCGCTGCCGTGGCCCTCTCCGCCCCCCC
			TCCCCACCGCACACCCCCCCAGCCCAGACTCCAGCCCTGGACCGCGCATCCCGAGCCCAGCGCCCAGACACAGAGGTGA
			GAAGGGGGGGGCAGGCGGGGGACCACCTGGGAGCAGTGGGGGAG
628_GNAZ_01	26	27	CTGCCTGTGCCCAATGGACAGAGGGCCGGCGCTCGTGGCGGGGCGGAGGTGCCCGGCGCGTGGTGCCCGGCGGGCG
			CGCGGCACCCCCCCCGCCGCGCGGTTGGCCTGGCAACGGGCTGCGCTCGCGGCTCCGCCCCCCTGCCGGCGGCGCGCG
			GCGCGGGGCGGGCGGACCCGCGGACTGGCGGCGGCGGCGGGCGGCGGGCGGCGCGGGAGGGCGGGCGG
			AGGGAACCAGGCCGGCCGGAGTGTGTGCGCCGCCCGCGGTCCGGTCACGTCCCCGCGTGGGCGCCGCTGCCCGCGT
			CGTACGGAACGAGGGCGCCGCGGCCCCGTGCTCGCCGCCCCCGCCCCCGCCCTGCCCGGAGCAGCTCGGCAGA
			TGCTCTGTGCTGCGGCCCGGAGGTGAGTGAGCCGACCCGCGGCCGGCGCGCCGCTGAGCCTCAGGGGTCGGGG
			GCACGGCCGGGGCATCCACCTTGCCCCCACTTGGG
629_GNB2L1_01	26	22	GAGAACCAGGGGCAGAAAAAGTAGGCCGACACTTGAGCCACGAGGTCCTCTGGAGTCCACCTGCCTCCCCACGAGC
			CTTGGGCCGGGCGGCAGCTCAGAAACAGCCTCTGGATTTCAGCACCGACACTCAGATGGCATGTTGGGGTCATCAC
			CGCCCCGCCCCGGCCCCTAGGCCCCCGGCCACACTACGAAGGAGAAGGCAAAAGATATTTTAAAAGTTTCCAACTCT
			CCAACCCTCCTAGCAGCTGCGAGCTGATGTACACGTAGGTTCTCATCTGCAATGTGGTTCGCCCGGTTGAGGCCT
			AGGCTCGGGTCCGCACGCCCCCAATTCACAATGGGGCAGAGAAGTCTGTCAGTCCCCGCCAACTCGCGCGCCACCGG
			CCTGCCACACCACACGCGGAATTCCCTACACGACACGCGGAATCCCCCCAGCCCTGCAATCTCGGGTCCTGAAATCT

			ACCTTAGTCCGTACCTCGAGAGGCGGAGAGGATCATGTCCGGGAACTGCGGGGTAGTAGCGATCTGGGTTACCCAG
			CCGTTGTGGCCCTTGAGGGTGCCA
630_HAL_01	25	27	ATTTTCCCTGAGGTGGGGGTTCAATGCTGCAAAGACTAAGCCAGGCCAAACCGCACCCGTTCGCGGCCCTCTCCTG
			CAGCCACTCACCCACTTCCACGAACTCGTTGTTCTCTAGGGCCACCTCGAGCCGGTCCTCGTTGTCCAGCAGGCCC
			AGGCCCTTGCACCGGCGCACAAGGAAGTGCGCGTCATCCACGGAGGTGAAGCCACCATTGTCGGGCTTATTCTTGA
			TATAGCGCCTCACGGCCTCCCGGCCCAGCCAGCCCACAGTGAGCTGCGCGTCCTGGCAGGGCACTGCCAGCCATTC
			CCCACGTACGTGCACCGTGTATCTGGGCATGGCTCCGCTGCAGCCTGAGGTCCTCAGCTGGTCACAGGAGGGGAGA
631_hB23_1_01	22	25	CTGGACCTGGAGGGATTGGAGCCGCGGGGGGAGCCGGTGGCGTGAAGGGGGAGGAGACGAGCGGCCTGAAGCGTCT
			GGGGCGTGAGCGGTCCGAGGCCCGGGGCCTGAGGTAAAGTGGAACCGGCCGCCTGGAAGTTCGGCCTTTGCCGGGG
			ATACGTGGCGGAGCTCCAGGCGTGGTTTATTTTCTAACGGCGGTGGTTCATAGGCTTCTGATGCCAGGCCCCGGGT
			TGGTGGTCCTGGAGGCTGGGTTCACCGGGAAGCATGGGCCTGCTTGTTGGAGCGGGTAGATGCACAGCCTGGCGTT
			ATTCTGGCCTCAGAGCCTGGAGCTGCCGGACGTAGACTTACCTCGCGTGCTTCGGCCAGTTACTGGGGGTGGGGAG
			GCGCGGCGCGGCGTGAGGAGGCCGCAACCGCTGGGAGCACGTGGTTGCCACGTGGTTGGGGGAGGGAGGGGGTGT
			GGGCGCTACATCCGGGACTCACCGGCGTGTTGCCACTCGTGAGCCAGGGATGCTGTGGCTCTG
632_hB23_2_01	22	25	CTGGACCTGGAGGGATTGGAGCCGCGGGGGGAGCCGGTGGCGTGAAGGGGGAGGAGACGAGCGGCCTGAAGCGTCT
			GGGGCGTGAGCGGTCCGAGGCCCGGGGCCTGAGGTAAAGTGGAACCGGCCGCCTGGAAGTTCGGCCTTTGCCGGGG
			ATACGTGGCGGAGCTCCAGGCGTGGTTTATTTTCTAACGGCGGTGGTTCATAGGCTTCTGATGCCAGGCCCCGGGT
			TGGTGGTCCTGGAGGCTGGGTTCACCGGGAAGCATGGGCCTGCTTGTTGGAGCGGGTAGATGCACAGCCTGGCGTT
			ATTCTGGCCTCAGAGCCTGGAGCTGCCGGACGTAGACTTACCTCGCGTGCTTCGGCCAGTTACTGGGGGTGGGGAG
			GCGCGGCGCGGCGTGAGGAGGCCGCAACCGCTGGGAGCACGTGGTTGCCACGTGGTTGGGGGAGGGAGGGGGTGT
			GGGCGCTACATCCGGGACTCACCGGCGTGTTGCCACTCGTGAGCCAGGGATGCTGTGGCTCTG
633_HDAC3_01	26	25	CTTCATAGGGTGTCCAGCTCCTGGGGGTGGGGAGAAGAGAGTTCGTCAGCTCTCACCCCTGGAGTTGCCAACCCCGC
			CTCAAAACCTCCGTGTCCCAACTCCTCATGCATATCCCTGTTTCCTCACCGTAGTGGAAGTTGCCCACGTCGGGGGT
			CGTAGAAATAGGCCACGGTCTTGGCCATGGTGCCGGCGGGAGCAGGCCCCGCACCTCCGCCCGCCCGCCCGCGG
			CCGCCGCCAGCCCCTCCCCGGCCGTGCGTGCTGCGCAAGCACGTAGCCGGCCTCTGCGGAACTGGGCGTTGCGGCC
			CCGCCTCCATCCACACCCAGGCCACGCCCCCCAGGGGAGCTCCGCCCCCTCGCCCGGCTCAGCTCTCCCGGTATCTGG
			GGCTTTGAGCGTCCCGGTTGGGCAGGGAACTGGCCAGCAT
636_HSPA8_1_01	28	25	GGGCAAACTTGGAACTAACCAATGATAGCGGCGCTAGCCGGGATCTTGGCCGGCACAGAACTGGGGGCGGAATCGC
			GCGGGGCCTGAAGGGAGGGGTTTGGGCGCGGGAGCCGGGCAGGGAGAAGACGGAAGTGGAGCGAGGACAAAATGGCT
			GCGAAGGTTGTTGCTCCCCTCCCCCACCCACGTCCGAATCCTCCTTTCCATGCCCCACCTTCGTGTTCCAGACGGG
			CCTCTAAGTGCCCCGGGTTTCGCGAATCTGTATTTCATAGCGTGGCTTTGGACAAGGGCTGACCCCGAGGGGCTGG
			GGCGAAGGTTCCGGCTTCAGGGTGCCACTAGGGCTGC
637_HSPA8_2_01	25	25	ATCTTAGAACCTTCCAGAAGGGGCCCGCCCCTGCTGCCTGCCATTACGGCTTCCCCGGCCAATAGACGCCCGGCTG
			CCCTTACAAGACCCAATCACAAGCCCGGCTCCACTCCTCGGGCCTCGCCCCCTTCCGCACCCCACCCACGCGCTC
			CGCCTCACGATAACGCACTCACCGCAGCGTTCTGGAACTTTCAAGCTCGCCCCCGCTCTCCGGACGGCCCCGGGGA
			AAGGGAGGGTGGGGCGCAGCGAGTCCGCGCGCGGGAGTCCTCAGTTACCCCGGGCGGGGAGGGGAGCGTCCACCT
			CTACGCATGCGCCCCCCAGCTTCCGCGGGAGGGGGGCGGAAAAAGGAGGAGGAAGAGGGCGGCGAAACTTGGA
			ACTAACCAATGA
638_ICAM1_01	26	24	GCCTGGGGGCTGCTGCCTCAGTTTCCCAGCGACAGGCAGGGATTTCGAGCGTCCCCCTCCCCTCCCTCGTCAAGAT

			CCAAGCTAGCTGCCTCAGTTTCCCCGCGGAGCCTGGGACGCCAGCGGAGGGGCTCGGCGCGTAGGGATCACGCAGC
			TTCCTTCCTTTTTCTGGGAGCTGTAAAGACGCCTCCGCGGCCAAGGCCGAAAGGGGAAGCGAGGAGGCCGCCGGGG
			TGAGTGCCCTCGGGTGTAGAGAGAGGACGCCGATTTCCCCGGACGTGGTGAGACCGCGCTTCGTCACTCCCACGGT
			TAGCGGTCGCCGGGAGGTGCCTGGCTCTGCTCTGGCCGCTTCTCGAGAAATGCCCGTGTCAGCTAGGTGTGGACGT
			GACCTAGGGGGAGGGGCATCCC
639_IFITM1_01	30	21	GAGCTGTCTGGAGCAGCCAGTCCTGCAGATGTGGGCAGCTCAGGGCCCGTGGGAGGGAGGGGCTTTGTGCCCAGG
			GCAGCAGCTGAAGGAGCCCCGGGCCTCGCAGCCCCTCCTGGGTGACCAGGTGCTGCTTCGTGGCAGCTGCCCCCTC
			CCGTCCAGCGGGTATGGGCCCTGCTCCCCCGTGGTGGGGGCGGCGCAGGAGAGTGGAGCGACCCTCATCTAAGTTA
			CCTCTACCCGGGTCTGAGCCCCCGGACAGACACCCCCGCCCCGACCTGGTTACAGCGCCCTTCCCCGGTTCGGTCT
			CCGGTGTGCGCATGTGGGGTGCCCCATGGG
641_IL10RA_01	25	25	GGGACTTTGGGGGCAGGTCTGCATAAACTGCTTAGTTGTGGACCCCCCCTCCAACAATTAGGTAGGGGACTACTCAG
			TATTCATCCATCGGTGTCCTCAGACCCCCAGACGGGGAGGCCCTGGGGCAACGCCAAGACTCACACCGGCGTCCTG
			GCGCCTTTGCCCTCAAGGGCCTGCAACTACCTCCTCCCCATTCGGAGCGGCCGCGGCCACATCCTTAACGCCAAGC
			CGGCACGCCAGGCAAAAGCGGCTCGGACGCCCTCACCCCACCTTCCGCACTCAGGGCCGAGGCTGTGCCTGGCCAC
			CTGCTTCCCAGCACATGCACACACGCGCGCGCACACACCCACACACGTACCCACGGCCGGCCGGGCTACCCG
			GACCACTTTGATCCGAAGGCACTGGAGGCCCAGAGGGAAGGAA
644_KCNMB1_01	25	24	TGCTGAAGCTCTGTGGCCTCTTTTGGGGTGGGGCGGGGGTCCAGGCAGAAAGAAACTGTCTGCTGCTCAAGACCC
			ACAGGACGCCGGGAAGACTGTGAGTACCGGGCCTGAAAGCACTTGGGAAGTGATTTCTCTGAAGACCGGGCTGGAG
			GGAGACAGGGGAAAGCAGCCTGCCACGGGGCAGGGAGGGAGGCAGGCAGGAGGACTCCCTTCCTCTCGGGGCTGTC
			CTTCTGGATGGAGGGCCCGTGGTCTGGTGGCCAGTGGGGAGGGTGGCACAGTG
646_KIAA0683_01	22	29	GGTTGGGCTCCAGGTCTGGTTGGGTCGGGTCCAGGTCGGGTAGGAGTCCGGTCGGGGTCCGGGTACAGGTCGGGGT
			CCGGGCCTGGATCGGGGGGCGGGTCCGCGTGCGGCTCCTCTAGCCCCCGAACCCGTGTTCCCCGTAAGCTGTTGGTTT
			CTAAGGGGCGGAGGAATGGCGACTGGAGCCACCTCTCACCGCTCAGGGAGCCGGGAGGGCCGGCAGCTCCCGCGGG
			CCGAGTTTCCCGCCTTGGGTGCGAGGACGCGTGGGGCCGCGCTGTGCCCGGGGAACACTCACCAGCATCTCTAGCC
			TC
649_KSRP_1_01	26	28	CTGAGAAGGCAGGAGGCCCAATGAAACGCGAGTGCCAGATTCGCGGGGCGGCTTCAGAATTAGATTGACGGTTCTG
			AAGAGTCACGTGGACTGTAAGGCCGGGCCTAGTGGAAGACTCCTATGGACCGGCTGGGTGGGCGTTAGGTTTGATA
			GTCGTGGACACAAGCCAATGAATGCACGTGAGAGGTGGTGCTTGTAAAGATGGGCAGCCAATTAATCCAATTCCTG
			ACGAGTTCTGGGTGATGAGGTTGGCTTTGGACTTTAATTGCTTCCCT
650_KSRP_2_01	25	28	TGAGAAGGCAGGAGGCCCAATGAAACGCGAGTGCCAGATTCGCGGGGCGGCTTCAGAATTAGATTGACGGTTCTGA
			AGAGTCACGTGGACTGTAAGGCCGGGCCTAGTGGAAGACTCCTATGGACCGGCTGGGTGGGCGTTAGGTTTGATAG
			TCGTGGACACAAGCCAATGAATGCACGTGAGAGGTGGTGCTTGTAAAGATGGGCAGCCAATTAATCCAATTCCTGA
			CGAGTTCTGGGTGATGAGGTTGGCTTTGGACTTTAATTGCTTCCCT
651_LDH-A_01	28	25	TCTGGACACTGAGAAACAGGGATGAAGAAGAAACAGATCCAAGCCTTCCTGAGAGTAACCTCCCCAGGTTTCATGG
			ATGAGGAAACTGAAGGTCGTCCTGACTCAGGCTCATGGCTCCGACCCCGGCTTCTGTGGTTGGAGGGCAGCACCTT
			ACTTAGACTCCCAGCGCACGTGGAGCAGTCTGCCGGTCGGTTGTCTGGCTGCGCGCGCCACCCGGGCCTCTCCAGT
			GCCCCGCCTGGCTCGGCATCCACCCCCAGCCCGACTCACACGTGGGTTCCCCGCACGTCCGCCGGCCCCCCCCGCTG
			ACGTCAGCATAGCTGTTCCACTTAAGGCCCCTCCCGCGCCCAGCTCAGAGTGCTGCAGCCGCTGCCGCCGATTCCG
			GATCTCATTGCCACGCGCCCCCGACCGCCCGACGTGCATTCCCGGTACGGTAGGGCCCTGCGCGCACGGCGCCC

			AGAGGGATGGGCGGGTAGAGCCAACTGCCTCTGGTTC
652_LEP_01	23	30	CCTCTAACCCTGGGCTTCCCTGGCGTCCAGGGCCGTCGGGCCGAGTCCCGATTCGCTCCCACCCCGAAGCCGCGC
			CAGGACCAACGAGGGCGCAGCCGTATGCCCCAGCCCGCTCCGCGGAGCCCCTCACAGCCACCCCCGCCCCGACCGC
			GCCCCGCGCGGCTCGAAGCACCTTCCCAAGGGGCTGGTCCTTGCGCCATAGTCGCGCCGGAGCCTCTGGAGGGACA
			TCAAGGATTTCTCGCTCCTACCAGCCACCCCCAAATTTTTGGGAGGTACCCAAGGGTGCGCGCGTGGCTCCTGGCG
			CGCCGAGGCCCTCCCTCGAGGCCCCGCGAGGTGCACACTGCGGGCCCAGGGCTAGCAGCCGCCCGGCACGTCGCTA
			CCCTGAGGGGCGGGGCGGAGCTGGCGCTAGAAATGCGCCGGGGCCTGCGGGGCAGTTGCGCAAGTTGTGATCGGG
			CCGCTATAAGAGGGGCGGGCAGGCATGGAGCCCCGTAGGAATCGCAGCGCCAGCGGTTGCAAGGTAAGGCCCCGGC
			GCGCTCCTTCCTCCTTCTCTGCTGGTCTTTCTTGGCAGGCCACAGGGCCCCACACAACTCTG
653_LIAS_01	26	25	TGAAACACAAACACTGGGGGTGAGGCCGACGCAAGGCCCCGTTTTTCCACCAAACTACGCCGCACAGAGCTCCACTC
			CTACTGGAGACTGCCAGGCGGAAGTTCCAGACAAGATGTCGGAGGACGGGAGACCGACAGCGGGCCCCAGTGTGTC
			CCAGCCTGGAAGGAGCAGCCCCAAAGCGAGAATTACGAGGCCCAGCAGTCGAACTCCCACTCAGCCCAACCCTGGA
			AGTCCTATGCGGCGGTGCCATCCCGGCAAGACTGAGAGGGCGGGAATAGGCCCAAAAAGCCCACAACAGGATTCGCA
			TCTGGCGCCGCCAGGCTCATATGGCGCTTGCCGAGCTGGGGGACAAACAGGACAAGG
654_LLPL_01	25	25	TCCAGGAAGCAGGGGGTTGGGCAAGGGCGGGGCGGCGACCTCCGACTGGGAGGGGCGTATATGGCGGCGAGTCCCT
			ATTGGCCAGCCATTTGCGGGAGGCGGGCCCTGATTGGCCGGGGGGGATGCGGGGCGGCGGGGTTAAGCG
			CGTCGCCACCGCCCCCGCCTAGGCGAGAGCCCAGAGAGCTGAACCTGCATCCCGGACCTGCGGCGACCGTCGTACA
			CCATGGGCCTCCACCTCCGCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGTTCCTCTTGCTG
655_LRP2_01	22	25	GCTAGGGAGGGCAGGCTGCAAACGGCGGAGAACCTCGTTCTCCCGCAAAGTGCTTTCCAGGAGCATCGGACCAACG
			CCCGTGGGAACAAAGACAGGGTCTCCGTGGGGTGCGCTGTCACCGAAACTGGCGGGGCTGCTTCTTCTCAAGTTTGCT
			GCCGCTCAGTTCCTGGCGAGCGAAGAGGGGCGCTCCCGCTCCGGCTTCGCGAAGCAACCTGAGCGCCCCACCGGGA
			GCAGCTCCCGCGCCGCCGGCCCCTAGCCCCCTGCCCGGACGCTCTCCCCCTCCGGCCTCCCGCGGACCCGACCCT
			GCCACAGCCGGGGAAGTGGGGGCTCCACGAGAGGCTCTGGCTGGGCTCTTACCTTGGC
657_MKI67_01	28	27	TTTATTCTGTGACTAAGGTATTTTCCTCTTTCTCAGCTAAAACGTCCGCGCGCCGCCGGGGCTCACCTTCCAAA
			CAAGCAGGTGCTGAGGCTCAGGGGAAAGTGGGGACCGTCGACCCCCGCTCCTTTTGATAGTAACCAGGCGTCTCGTG
			GGCCACATTTTCTAAACAGTAAGTTGAGTATAATCCGTAGGGGAAGGCCAGGTATAATCCGTAGGGGAAGGCCAGA
			AGCAAATTTAC
658_mpp5_01	30	26	CACATAGGGGCCCACACAAGGTCCTCCCAGGCCCGGCCCCAGCTGCCACTTAGCCGCAAACACTTACTCTAGGGCTGC
			AGCTTCCGCCTCTGTCTCCGCTGCCTCCATCTTTCCAGGCGCCGAGTTCAGCTGCCTTCCCACAATCCCTAAGATT
			ACTTTGAAGTCACAGTCGACTTCGCGCCGGGGCAGGCGATTGGCTGCAGAGGTTAGTGGCGGGGCATCAAGGACCA
			TTGTGCGCTCTAATTGGCAGGCGCGGATTCGCTCGTTGGCGGGCCTCGCTGCTTGGCGCAAGCGCGGTTATGGCTA
			GGCGCGCACGGGCTCTGCGCCTGCGCTAGTCCTTACGCGGTGCCAGAGACTATAAGTGGGCTTG
659_MRPL3_01	30	27	CCCAGGGGAGGCCCAACTGCACCAGGCCATTCCACTGCTTCAGGACGCAACTGTGCAGGTAGGACACCCTCACACC
			TTCCTACCTGTTCCCCGGGCCCAGGGCAGCACCCAGGCCGTCCCCGAGTCGACCCAGCACCTGGGCGCCGACCTGC
			GTCAGCAGCCTCCCAACCCGGCATGGATTAGCCCGGGAAGACTCGACTCACGACTTCCGGGCGCCCTGCCGCTCTGC
			TTTCAGGGAGTCCCCACGCCACCGCCACGTGGACGCAGTAGCCGTGGGGAAGTTTTCGCAATGGCCGCCGGAACGG
			TCGCCGGCCGATGCTCTCTGCGACGGAAAGAAAGCCGCCGGACCCACTTCCGGTGCGTTTTACAATGAACTCCGGG
			CACTCGAGTCGCTCCCCGGAAACTATAGTTCTGCTTCCACCGTTGTCCTACTTTGGATGTGAGTTGGAGTAGGTAG
			GGGTGGGAAGGGACTGACTCGCCTCTCCAGGGGTAAAATAAAAGGGA

660_MYBL2_1_01	22	26	GCCCTGGAGGGTCTGGGCAGGTGCCGCCCCGCAGGCCCCGCCCCGCCCCCTGGCTCCGCCCCTCACTCAGG CCCCTCCCCCGGCGCCCCGCGCGCCAGGACTGGGCGGCGCCGACGCGCTTGGCGGGAGATAGAAAAGTGCTTCAACC CGCGCCGGCGGCGACTGCAGTTCCTGCGAGCGAGGAGCGCGGGACCTGCTGACACGCTGACGCCTTCGAGCGCGGC CCGGGGCCCGGAGCGGCCGGAGCAGCCCGGGTCCTGACCCCGGCCCCGGCTCCCGCTCCGGCTCTGCCGGCGGCCG GGCGAGCGCGGCGCGGTCCGGGCCGGGGGATGTCTCGGCGGACGCGCTGGTGAGACGAGCCGGGAGGGCTTGGGC CCCTCCCCCTCCCTTTAACTCACCCCTCCCCCACCCAGATACCCCCGACCCTCCCCAGGCTCCCACCAAGCTGGGG TGTGTGTGTGTG
661_MYBL2_2_01	21	26	CCCTGGAGGGTCTGGGCAGGTGCCGCCCCGCAGGCCCCGCCCCGCCCCCTGGCTCCGCCCCTCACTCAGGC CCCTCCCCCGGCGCCCCGCGCGCCAGGACTGGGCGGCGCCGACGCGCTTGGCGGGAGATAGAAAAGTGCTTCAACCC GCGCCGGCGGCGACTGCAGTTCCTGCGAGCGAGGAGCGCGGGACCTGCTGACACGCTGACGCCTTCGAGCGCGGCC CGGGGCCCGGAGCGGCCGGAGCAGCCCGGGTCCTGACCCCGGCCCCGGCTCCCGCTCCGGCTCTGCCGGCGGCGG GCGAGCGCGGCGCGGTCCGGGCCGGGGGGATGTCTCGGCGGACGCGCTGGTGAGACGAGCCGGGAGGGCTTGGGCC CCTCCCCCTCCCTTTAACTCACCCCTCCCCCACCCAGATACCCCCGACCCTCCCCAGGCTCCCACCAAGCTGGGGT GTGTGTGTGTG
662_NDUFA6_01	25	24	TTGGGTTCTGGGTACAACAGTGGCTCGGCCTGGGCCCTGGGCACATCACTTCACCTCTCGGTGCCTCCGCTGCCTC ACCCACAAAGTGAGTGTGTCACTGACAGTCATCGTCCTCCCGCCAATTGCGAAGGACACAAAGAGACCAAAGCTCCG ATAGCACGTACGAATGCTAGGCACGGCCGGTCTGACCACCGCGCCGCCAGGTCCGGCCCATGGTAGGCTCGGG TGACCCTCTTCCCCTGAAGCACCCCGCAGTCGCCTCTGCCCAAGTTGGTGACCTCAGCTGGGCCCATGAGAAACCCC GGCCGGGCCGGCTACGACCTTGAGCGGCGGCCTCCGGGTCCCCACGTAAGCCGCTACCTCTCACCAGTGTTCGGCA CCTCCCGATACCAGGCGCGGTAGAGCTCGCGCACACCCTCCGCTTGGCCTCGTTCATGTCCCGACTGAAAATGGGCTT CACGAAGGTGCTGGCGGTAGAAGTAGCTTGGCGGACGCCGCTCCCCCGCCATCTTGCCAAAGCATCCACTCCACAAC CCCACCCCTTTGCAAGCAGCGCGTGCGGACCGCGGGCGAATGTCTTTTCCCATTGGCTAAGGAGGAA
663_NEDD5_1_01	25	25	ACACCAGAAGGAGAAAAGCTAGGGGCCGCGCCAGCTCCGCCCTCCCCCGCGGGGCGGCGGGCCCCAGCCCGGGCACA GGAAGGCCACGTCCCCGGGGAGGGACGCCCCGACTCGATGGTCTGCGCAGGGCCCCGTCGGCCCCACGTGACGTGCGC GCAGCCAATCCCAGAGAGGCCCCCCGATCATCGAGACGGCGGCGGTGGTGGGCTAGACGAGTTTCGCGCGGCCGCT CGCCGTCCCCCCGCCCCAGTCGTACTCGGCGCCCCCAGCTCGGTGCTGCCGCCATCTTCTTGGAGGACAGGAGGA
664_NEDD5_2_01	27	28	TGAGCCAGGAAGCAGTTGGCAAAGGGCGGGGTGACGCGGTGACGCAATCCGCCTGCGCGCTGGGCGGGGCGGGGC GGGCTGGGGCGGGCTGTGAGCGGACCGCGAGCGCTGGGCGGGTCCGCGGCGCGGTCGGTCGGCGCCTGTTCTCGGG CTGTTTGGCGGGTGAGTGTCTCGCCGGTGTACCCCGCACAAGTTGTGGGCCGGCCCTCCCGAGGAGCTGCGGGGGA CGCGCCGCTCGTCCCATACTCTCGGGCGGTGGTCGGCTGGCTCTGGGGTGCCGGCGGGGCGGTGTGGGGGAGGGGC GGCCGAGCCCAGGCTCTTCGGCACTTATCGTGGGCTCCCCCGTCCCGGGCGGTCCTAGTGCCGGCGACAGTGGCTC CGACACGGGCAGGCCCGGGCGCGGGAGTGGGGATTCCGGTGACCCCTTGTTGACCCTGCGGGAATTCCTCTGCACT GTCGTCGGTGCTGGGCCTCGGGGCGTCGAGTGCGGTCGAGGTCGGAGGTTTGGTGCTTGGAGGGAGGATACAGGT TTAGGCC
665_Nm23_01	28	25	GGTGGAGAGAAGAAAGCAAGCAGCTAACCGGAAAGGTCTGAAAAAGCTAGCGCCGGAAGTTAAACTGCAGAAAGTT GTTCCCTAGAATGACTGCCTACTCCCAAGAGGAAGCGTGGGCGAGCGGTGTTCTGCAAAATGGGCTCTCCGGCAGC GGATCTGCGCAGAAGCGTTCCGTGCGTGCAAGTGCTGCGAACCACGTGGGTCCCGGGCGCGTTTCGGGTGCTGGCG GCTGCAGCCCGGAGTTCAAACCTAAGCAGCTGGAAGGGTAAGAGGTGTTCGGGATCCTGAGAGGAAAAAGAAAGGAG TGTAGTCGCGGGAGTGGGTTAGGTGAGGAGTTAGTGAAGAGATGAGTTCAGCTCTAAGAGGCGGCGAGGAGGATCG

			GATGGGAGGAGGGGCAGGGAGCGCCTGTGGACAAGTGCAGACCGGTCGGCGCACGTCCCACGCCACGTGGACTCGC
			CTTTGTCGGTGGCCGCCTTCTCGTCAGGCCGCGACGACAGGGCTGTGCCTTATTTGTGTC
666_NMU_01	30	25	TCTCTCCAATAATTGCAATCAAAGGGAAAACATTTTAATGTTCACTATTTTAGTACCCGTTTCCACGGGCCGGGGG
			GTCTGGAAATCCCGAGGATGAGGGAACCCTACCAGTCTCCATCTATCGCAGCCGGCCCGGCGCAGGGTCTCCGCTG
			GGCATCAACGAGCAGGGCCTGGGTATTTCGGCCCTGGCCGGGCCCCTTGCTCCTACGTCGCTAGTTGCCCTGGGGA
			GGCGACCTGTGCCTGGGAGGCGGGAAACCCCGCGGCACCAGAGAAGCCAAGTGAAGTCCCAGAAGCCAAGTAAAGG
			TGAGAGAAAGAGGGTGGAGGAGAGCGGTGAGTGGAGCCAGAGAGAGGCGCGCATGGCGTGGAAGCGGCCGGGTGCG
			GGGCCGTCTTACCTCGGCAGGCGCCCGCGCACCAGGCGAGCAGCAGCAGCAGGAGCGGGGACGCCGCGGC
			CACCTGTCCGGCGGGCGACCTGGGGCGGCAGCTCTCTGTTCGCAGCATCTCGGCGGCTGCGGGAGGCTCGGTGCTA
			GGGACGCTGCGCTGCGCCACGCGTAGCTGGTGCTCCACCTGGTGCCCTGGCTG
667_N-MYC_1_01	26	25	GGGGATCCCCTCAGCCCTGAGAGGGATCCCTCGGCTGCCCTCAGCACCGCCCCATCCACGACCTGGATCTGCAATTG
			CACTCTGGCTCCTTCCTTCGCCCCCCAGACTCAGTGGTGGGAACCGGTAGTGGGGAGACGAACCCGGGATACTGACA
			CCCCACGAGTTCGACTCCCCCCGCCCGAACACAGAGAACTAGATTAAGAAAGGAGGAGGTGGGCGGGACCGCCGCT
			GAGGAGGCGGGGGTCTCGCCGGCTGGCAGGGGCAGGTGTGCTGGCGCCGAAAGGGGGCACGGGGGAACGTCGAGGG
			CGCAGGAGTTCCGACTCCCTCGTGCCCAGAGTCCTGGTACCTCTCCTCTCTTTGCTGCGTCCCGACGCCTGCTCTC
			CGGCTGCTCCGGGAGAAGTTGGACAACAAGGCGGGGAGGTGGGGGCGGGGAATGCGGGGGGCGCCGCTATAAATAGAG
			GGCGATCGCGGGCAGGCGGGGGGTGGGGAGAGGATGGCCAACAGGGACTCTGGGGTCAATGCCTCAAGGGG
668_N-MYC_2_01	25	28	GGGGGAATAGGGGATCCCCCAAAATTTTTGACAGCTCTCCAGTAAGAGGAGGGTAGCAGAGCATGGCTGTTTCCCTC
			CACAATTTAAAAACAAACACAAAGATTGGTGCCGTCGCTTCTCTCCTCTACTCAGTCTCCGTGTAGGTCCCACGAG
			TGGAGAAAGGGAGAGGAGCGGTCCCACAATCTTCTCCCGTTCTCCCCCGACGGCCCGCGAAGGCAAGCGCCATC
			GGGAAGGGATGGGTAGGACAGAGGAGACCGGCCGGGCCCAGCACACCCGGAACCCGTCCCTACGAGTCCCTACGCAGC
			CCGTCCGCGTGGAGACTGACACCCTTGCGTGGCCGGTGCCAAGCGCCCCGGACCTTGCACACAACCTCGCGCGCAC
			CCCAAACACGCCCTGCAGCTCTTGGAGCCTCAGCCTT
669_Notch4_01	30	25	CCCAGGGCCACCCAATCACAGGGCCAGTCATCCGTTGAGACCCTGCCTCCGCGCCCGGCAGCCACTCCGTATCTTC
			CTCGCATTATCGCAGGGTTGGGCCGAGGCCCGCGCATGCCTGCAGAAAACCTACGGCCGCGAGGGGTCGGGCCTCC
			TCCTGCTCCCTACTCCCCGAGAGGCTCCGGCAATGAGAATAGGCCCCCGCCCCCCCGCGCAGCCAAGTCTACGGACCAA
			GTCCGAGCCTGCAGACAAGCTCCGCCCCCCACGAGGGCCTGCTCCGGCTGACACGTCCGGCAGCGCGGCAGAGCCC
			CGCCCCCCATGCGGGGGCACGCTTACTGACACCGTCCGTGCGCGCGGGAAGGGCCCAGCCTCGCGGCCCGGCGTGGC
			TTTGTGACGGGCCTCTGGTGGCCCAGCCCCCTTC
670_NPD017_01	29	26	GGTTCCTGGGCTCCTAATTCTTGGTCCAGCTTCTTCCAGGTCAGTGTGCGGGCCTTCCACGCTGCCAGCGGAACAC
			TGGAATGGCGGAAGGGGAACGGGTACGGCAGGGGGAAAGGCTGGGGGTGGGGTCGAGTCGAGGGAAGCTGG
			CCCGAGTGTGGACAGAGATGGCGGTGGGAAAACGGCTAGGGGTGGCTGAGGGGGAGCACGTAGGCAGTGGGCAGAG
			GGTGAGGAAGGCGAGCACACCCCCAAGTATCCATGCTCGCTTTCCAGGCACATCCTCTTCTCTGCCCTCCGTCCATTT
			TGGAGCCGGAGATGGTGGGCTGGGGCCGCCCCCAGTAGTGAGACAGTGGAAGTAAACCCCATCTGCCGTTCCCGTGC
			GTAGAGAAAAACGTTGACCGCGAGGCTGGGGAGGAGAGTTGCCTCTGAGGAAGAAGGGC
671_OXCT_01	27	25	GGATGCCAGATCCCAGGCTGGAGAGAGCGGGTAGGGGCAGAGAAGAAAACGCGGGCACCACTCAGGGTTTGGTCCA
			CGTTCTTCCTGCCCATGGCCTTCCTCTTCCCCCGCACTTTACCTTGTACCAGGTTGCCCCCAGATCCGCGGGCAGAG
			GCGCAGAGCCGAAGCCCGGAGGAGAGGAGTTTGAGAGCCGCCATCTTCGGGCGGTGAGGCAGGAGGAGGCTGCGGG
			TTGGAGCGCGCGTTTGAGCGTCGGTGCGCGACTGCGAAGGAAACCCGGGCGGGCTGGAGGCTCGACAGCGCGTCGA

			TGACGTCCTCCCGGCCTTTCGAGCCGCACGCCACCGGCGCGCTGCTGGCTGCTTTTAAAAGAAGTGAGGCTGG
			GCGGGGCCCCGGCGGGGAGAAGAGGCTCTGTGCAGCCGGGGCGGATCGCGGGGAAGTTCCTCTCAGCGCCTCAGGT
			GTCTGGGCGTGTGCAGCTGTGTTGGCGCACACTTGCCGCTACAGCCCTTCTGTCAGCCCTTTAGCTTCGATGGGGC
			GCTGGTGGCCGCCTCCCCCCTAGGTTGTGGATGAGTCTTGGCCTAGGGTTC
672_PAK-3_01	30	25	ACCATCTGATTGGCCTAGGTAAGGTGCAGAGCTCGGGTGACGTAATAGCAGAGAAGGGCTAGGGAGCGGTTGCCGA
			GCAGGGGCTCTACCGCGGCGGGCAGCTGTGCCAGCTAACCGTCTGGGATCTCGCACTGGGGCTGCAGCTTTTCC
			CCGCCTCGAGCCAGTGTGCGGGGGCGGGAGAAGAGCCAGGGGAGCGGGCTGGGCCCGGGGCTGCGGCTGCGGCCG
			CGGGGCTGCGGCTCCCCCAGCCCCGCCAGCTGGAGCGCTCGGAGGTAGAGGAAAGGTCTTGACGGGGTGGCTGGATC
			CGTGGCAGGTAAATCCCGCGACTAACTGCACCCGGGCTACCGCGGGGAGGGGGTGGCTGTTGGATGATGCTTTAA
			GGCTGCTGGGC
673_PECAM1_01	24	25	AGGCTGGAGGCAGGGAGGAATCCCCTCACAGTGCCATGAGAAGGGCCCCCAAACCCAGGCGAGACAGAGGGAGGGT
			CAAGAACGCCAAGGCAAATGTCACTTGTGCCTTGTTTTTCCCTAAAGAAACTAAACAAAGCGGCCGCGTTCGGTG
			GCCCCTCAGGAAGGCCGGTCATTTCCTGAGGAGATATCAGGCCAGCCCAGGCCCCATTGTTCCCGGTTTCCAGCCA
			TGGCTGCCATTACCTGACCAGCGCCACAGCCGGTCTCTCTGCAGGCGCCGGGAGAAGTGACCAGAGCAATTTCTGC
			TTTTCACAGGCGGGTTTCTCAACGGTGACTTGTGGGCAGTGCCTTCTG
674_PIK3CG_01	27	25	GGAGCAGATGAAGGCCCAGGTGTGGCTGCGAGCGCTGGAGACCAGCGTGGCGGCGGACTTCTACCACCGGCTGGGA
			CCGCATCACTTCCTCCTGCTCTATCAGAAGAAGGGGCAGTGGTACGAGATCTACGACAAGTACCAGGTGGTGCAGA
			CTCTGGACTGCCTGCGCTACTGGAAGGCCACGCACCGGAGCCCGGGCCAGATCCACCTGGTGCAGCGGCACCCGCC
			CTCCGAGGAGTCCCAAGCCTTCCAGCGGCAGCTCACGGCGCTGATTGGCTATGACGTCACTGACGTCAGCAACGTG
			CACGACGATGAGCTGGAGTTCACGCGCCGTGGCTTGGTGACCCCGCGCATGGCGGAGGTGGCCAGCCGCGACCCCA
			AGCTCTACGCCATGCACCCGTGGGTGACGTCCAAGCCCCTCCCGGAGTACCTGTGGAAGAAGATTGCC
675_PLOD_01	30	26	GGACTTGGGCATATCTGCAGAAAAACCCTTCCCCACTAGGCAGGCGCGGGGAGGGCGTGGAGGGGCGGGTGGTG
			CCGCCCCCGGGGCGGGCCCAGTGCGTGGCAGCGGGACCTGCGGCCCCCGTCGCGAAGTTTCCAGCCCTGCGAGCGCC
			GCCGGGTCGGCCGATCGTCCCCCATACCTCGGCCATGCGGCCCCTGCTGCTACTGGCCCTGCTGGGCTGGCTGCTG
			CTGGCCGAAGCGAAGGGCGACGCCAAGCCGGAGGGTGAGGGAGCGAAGGCCGGGGCGGGAGCGCGGATCCGGGCG
			GGAGGGCTGGTGTCGGGCTGCCTCCCTGGGAACGACCTGAATGGGAGGCCTGGGCTGGAGAGGGAGTCTGGGTTCC
			GGCTCCTTGTCCACTTAATCGCTGGTGACTTGAACAAATCACTTCCCCTCTTGGGGCTGCGGTTCCTGCTTCGGGA
			AGGAAAGGGTGACAGCTGAGTCC
676_PRDM1_01	25	29	CTAGCAATCTGGGGGAAAGCCCTGGGCTCGGCCAGGTGGTGTTGGCCACGTTGGCCACGCCCCCACTTCGCGCAGC
			CGAGTGGCTAAGGAAATCTTAAGCAGGGAGGGGAAGCCAGACGGTTAACACAGACAAAGTGCTGCCGTGACACTCG
			GCCCTCCAGTGTTGCGGAGAGGCAAGAGCAGCGACCGCGCACCTGTCCGCCCGGAGCTGGGACGCGGGCGCCCGG
			GCGGCCGGACGAAGCGAGGAGGGACCGCCGAGGTGCGCGTCTGTGCGGCTCAGCCTGGCGGGGGACGCGGGGAGAA
			TGTGGACTGGGTAGAGATGAACGAGACTTTTCTCAGATGTTGGATATTTGC
677_PSMB6_01	29	25	TTTGCTGACTTTCTTGTTTTGTTTGCTTGCCACGCTGCCATCAAGTGCTCACTGTCGCAAAAGAACCGTCCCC
			ATGCAGTACTGTACTTTTCTTTTCCCTTCTGCCGTCAACCTCGGAGTAGCTTCGCTCCCAGAAGGCCTCAAAGCGC
			GACCAAAGAGCGTGACAGAGCGCTTTACGACAGTTGCTTTGAGGCAGTACCGGAGGAGAAAGATGGCGGCTACCTT
			ACTAGCTGCTCGGGAGCCGGGCCAGCACCGGCTTGGGGGCCGGAGGCGTTCACTCCAGACTGGGAAAGCCGAGAA
			GTTTCCACTGGGGTGAGGAAGGAATCGGGGTTCATAGGACGTGCACAAGGCCTGACGCGATGGGAAGATAAAGCCT
			GAGTGGGGTTGAGAGATCTGGCAGGGGTGGAGAGGAGGTGGAATGTGTTGTGCTCCAGGAATGGGGAGAGGTAC

678_PSME2_01	26	26	CCTGGGGTGGAGAAGGACTAGCAGCTCTTAGAAGAGAGCGGGCAGGGGTTGGGTGAGGGTCTTCCCTCTGCCTTCA GGACAGACCGGAGATGGGGCGGGACTCGCTCGAGAGGGGTTAGGGCCGGCCAGAGTCGGTTCCCCTGCAGGGTGGG ACTTCCTCGGTGAGGCCCCGGAGCGTACCGGACTGGTCCAGCTAGAAAAAGAAAAGGTTTTGAGCTGAATAGGATAAC CCCGCGCCTGCGGCTATCCGGAAGGGGTGGAACCAGATTGGGGGAAGGCGGGGAAGAGCGCTTGACTGAGGGAAGA TGCTGGCGCGCTCTGAGGGAGGAGCCAGGAGCCATTTGCCTTCTCATTGGTTGGGACCTGGCCCTCC
680_PTPRN2_2_01	25	28	CCTACTCTGCTGGGGACCTGGGCAGGCGGCCTCTACCCGCGGGGCCCCGCGCGTCGAATTAACGCCTTCCAACC GTTTCTTTAATTTAAACGTAACGGGCCACTTGCGCATCGGGGCGCGCGGAGGTGGACCCAGTCGACCTCCCCTGCA GCGCGGGCGGCGCCCAGGCTCGGTCCCAGGAAAGCTCCCGGAGGGCCCAGGGCGTGGGCTGGGGCCAGGCGGGCTC TGGGGCAGAGCAGGGTGAGGCCTGTTGCGGGCCTGGTCTCCTCGCCGCCGTCCCGCCCGGGGTCCTGGGGGATGTC GCGTGTCCTCCTCAGGAGACAGTGCCACTTCCAAGAGGTCCTAAGACAAAGGGGGCCAGTAGGGGCCTC
681_RAD51_1_01	30	29	GAAGTGCCAAAAGCTGACATTCAGATACTGCCGAAACAAACCACACAAGAGCGCTAGGGCCCCCCGCTAATAGTCCAGC TGCGATGGTGAGAACTCGCGGACCCCGCCGGCGATGCATGCCGGGAGATGTAGTCCCGGGCCGACGCATTACCTCTT GGGAGTCGTGGTCTTCGATCTGGTAAACAGAAGACGGCAACTCGGTTAAGTCTTCCCCCACCGCCCCCTGAAATCC CTCGCCCCACCCGCGAGGGACTGGGGTAGGAGTAGGGGCGTTGCCGTGGTTAGCCTCGAACTCCTAGGCTCAGACG ATACTCTCGCCTCGGCCTCCCGAGCAGCTGGGACTACACGCGTGAGCCACCGCCCCCGGCATAAAGTTTGAATTAG TCCTTACGCAAAAAGGGAAGAGGGCAGTCTGTAAAC
682_RAD51_2_01	25	30	GGAACTGCAACTCATCTGGGTTGTGCGCAGAAGGCTGGGGCAAGCGAGTAGAGAAGTGGAGCGTAAGCCAGGGGCG TTGGGGGCCGTGCGGGTCGGGCGCGTGCCACGCCCGCGGGGTGAAGTCGGAGCGCGGGGCCTGCTGGAGAGAGGAG CGCTGCGGACCGAGGTGAGTGTGTGAGGCGCAGGCTGGGCCCTCCAGAGCCGCGGCTCGTCCTCGCCCACCTGCGT CCTGGCCGGTCCAGTGCTCAGCGGCAGTTGGGGCCTCCGCGCGCAGTGTGAAAACCCGGACGTGGCAGGGCGTGTCC GCGCCCGACCGACCCTCAGCTGCTGGGGCGAAAACACAAGTGGACCTCAGTCTTTAGAACTAGGGGAGAAACATTA GAGCCTTT
683_rhoC_01	24	30	GAGGAAGGGAAAGTGCTCTCCTGGGGACGAGTTCCCAAGACGCCCCACCGCCCGCAGCCCCGGCCCAGGGTACCTT CCGCTCCGCCGCCTCCAGCTGCGCGGCCGGTGCCGGAGGCTCAGACTGACCCCAGGGCCCCGCCCGCCCTCCTCC AGCGCCGCGGCGGGGAGGGCGGGCCCGGCAGGGGGAGGGTCGGCCGGGGGCCCTTGGCTCGGCCCGCCCCGGC CCCGCGCAGGGCCGCAGCCACCGGCCCCCCTCCGCAGGCCGGGCGAGCGGGGGGAGCACGACCCGGGTGGACTCAG GGGGAGAGCCACGGGGAGATTCCTGGACTGCGGAGGAGCCGGGCGAGCGGGGGGAGCACGACCCGGGTGGACTCAG ACTCTGCCCAGCCTTCAATCCCCTAGGGGAGGAC
001_SEPT6_001	28	25	GGACTTCTTTGGGTCACAGACAGAACCCCGGCGCCGCCGCCCGCCCGGGAAGACACGAGCGCGCGCGTGCA CACATACGCGCACACCGATACACACACACAGACGCAGTCACATATGTAATGCATATAGAGAAACCCTATCCCAGCCAG TCACCTCCCCGCCCCCCTCGCCACTCACCGCCTTCTGCCCCAGGCTAACCCCAGCCCCGCGCCTCTTTGCCTGTGC GGTCCCGGGTCACAACGGGCAGCCGTGCGCAGGGGCGCGGCAAGGCCAGGGTGCCAGGGACCCGGAGGGCTCGGCG GCTCCTACGGCCATTCATTCGGCAACGCCCCCAGCCGTGGGGCCGCAGCTGCAGCGAGGGAGGCGGTGGCGCTCACT GCGGCTCTTGGGCAATGCAAGTTCAGCCGCCGGCCCGCAGGTTTTGCCTGCCCCCCCTGCCGCCCCCCCGCCGC GCGCCACCACCGTTTTCCGGGACAGGCTGAGGGACTGAGCTGCTG
002_ATM_001	21	30	GCTGGCCATTGGTGGACATGGCGCAGGCGCGTTTGCTCCGACGGGCCGAATGTTTTGGGGCAGTGTTTTGAGCGCG GAGACCGCGTGATACTGGATGCGCATGGGCATACCGTGCTCTGCGGCTGCTTGGCGTTGCTTCTTCCTCCAGAAGT GGGCGCTGGGCAGTCACGCAGGGTTTGAACCGGAAGCGGGAGTAGGTAGCTGCGTGGCTAACGGAGAAAGAAGCC GTGGCCGCGGGAGGAGGCGAGAGGAGTCGGGATCTGCGCTGCAGCCACCGCCGCGGTTGATACTACTTTGACCTTC

			CGAGTGCAGTGGTAGGGGCGCGGAGGCAACGCAGCGGCTTCTGCGCTGGGAAATTCAGTCGTGTGCGACCCAGTCT
			GTCCTCTCCCCAGACCGCCAATCTCATGCACCCCTCCAGAGTGGCCCTTGACTCC
003_BCL11A_001	26	25	GGGGCTGGACATGAAAAAGAGACCAGGACAAGCCAATGGCCAGTGCGGGGAGGGGGAGGTGCGGGGCGGGGGCTC
			CGCGGACGCCCAGACGCGGCCCCCGGGGGAGGGGCGGGCCGAGGGGAGGGGGCGCTGGGGCCGCGGCTCACCAGTG
			GCCGCAGCGAGCGCCGCGGCGTGGCCGGGAGAGAAGGGGTGGCAGGGGTGGGAGGAAAGGGTGGGG
			GGGAGCAAGACGTGCGCCCTGCTCCCCCCCACACACGCGGACTCTAAAATGAAAGATTATTCAAAAAAGAAAAAAA
			TAGAGCGAGAGTGCACCGGGAGGCTGCAGCCCCGGGCTGGGGAAGCGCGGGCGGAGGGAAGCCAGGTAGAGTTGCT
			C
			ATGGCTGGGGCTGCCTCTGTACAATGGGATAAAATTCAAGTTCAAGTGCGGACGTGACGTTTAATCTGCACTAGAG
			ACAAAAAGACCCAGAGAGTCGGAGCACTGGGGGCGACTAGCGGTGGCTTTTTAACATTGTACCCTGTAAGAGAACA
004_BCL11B_001	26	24	AGAAAGCACACACAGAGACACACTCGCGCGCGCGCACACTCACACACACACACAGTCGCCAGTTGCGCAC
			ACCCGCAGCCCAAGCCGGACACACGTGCAAACCGCGTTTTTGTGCGCTCATCTCCCCCGAGCCCCGGCTGCGCAAC
			AGCGGGAGGGGGTTGGGGGGGCCACTGGGCAGCTTATTTTAAAATAAAAGAAAAATCGTCCTTATATCTCCTCCA
			TCCTGGGAGCAGGACCCCCCTGAGAAGGGGG
			GGCTGGCACCAGAAAGCCCCATTTTCTCGCTCACACATAAGAGCACAAACACCAGCCCTGCGCGCCGGGGCAAGCC
			TAGGCAGACTTCGCTACCCCACCCCGACCACTCCGTACCTGTCTTCCAGGGACTGCCCGCCCCTGGGCGATCCCACC
007_BCL5_001	27	25	TCGAAGCCCCCCCGCAAGGCGCGACGGAGGCTTTGTGGTATGACCGTGGCGGCCCTTAATTTAGTTACATTCAAATA
			AAACTTTTGGTGCACCTCGGTAGCTAACATTGTGTGTATGCCTTTTTTTTTTTTTTTTTTTCCTGTTACGCC
			GTCAATGCAGCAGGCAATGAGGGGA
			AAGTTCTGGTGCTTTAAGTGTTCCTCGCTCGGCTCAGAGACTCGGCTTCGAGCCGCGACTCAAGACAGCACCTGGG
			GGTATTTGTTTTTGCCTAAGCCTGCTGCACTTCCACGGCCATTGAATCCCAAAAACTACAATTCCCATTATGCACCG
009_BUB1B_001	25	25	CGAGTTCGCGGACTAAACAGGCATAAACTACAAGCCCCAGAATGCCTTGGGCGAGACGCGAGAGCACGGAGGAGCG
			GAGGGGCGTGGCCACGTCGACCGCGCGGGACCGTTAAATTTGAAACTTGGCGGCTAGGGGTGTGGGCTTGAGGTGG
			CCGGTTTGTTTAGGGAGTCGTGTACGTGCCTTGGTCGCTTCTGTAGCTCCGAGGGCAGGTTGCGGAAGAAAGCCCAG
			GCGGTCTGTGGCCCAGAGGAAAGGCCT
			GGCTACAGACACTTCCTAGAATCTGATGCAACCGCCGCCCCGGAAGTCGCGCCCCACGCCGGGCCCGTCTTCCGGG
			ACACGCCCGGTCGCTAGGCAACTACCAGGGGCTCCGGATGTCGCCGGCCCGGACATGCTGGGAGCTGTAGTTCAA
010_CARS_001	30	24	CCCAATGGCGACCCGCGCTCCGGAGCATCGCGCGGCCAAGCGTTCAGTGGCCGTGCTGGGAGTAGTCAGCCCAGCC
			GCGGGGAGACAAGCACTAAAGACTGAGCGTCCTGTAATAGGTGTTTAAGTCATGATTGCGCTAAGCGCCGTGGGGA
			CCAGGCCCAGCCTGGAG
			GGCCCTGGAATGGGCCTGAAGTCAGCCGGCCTCAGCCCACAGGGTGAATGAGGGTGGGCACAGCCCGGCCGCGGC
			CCCAGCACACACGGGCGGACGCAGGGGCGGGGAGCGCCAGCCCCGCAGTGTGTTCGGAGCCCAGCGGCTCTGAGT
011_CBFA2T3_001	26	26	CGCCGCCACCAGCCTGGCCGCCTTCTGCTCCACGTAAGTGAAGTCAGCCGTCTAGGGCTGCGTTTCCAGCCATCTG
			TCCCTCCACAGAGGCTCACACCTCCCTCCCCGCTGTTCCCACAGCCTGGCTCGGGGCCTGCCCAACACAGATGGAC
			GCTTCCCAAAGGCTGTGCGCGCCATCGCTGCCACCCGGCTGTGCCGAGGCCCCGCGGCCGTCAGGACCCCCAGGGACC
			GCATGCCAGGCAGGGTCCAGGACCCCCCAGCGCGGACCACCTTTAGCCTGCGGGGCAGCGCCGGGGACCCGGGCAGG
			AGGGAGAGGAGGAGCAGGAGGGAGGCTCTGGACCCCCCC
012_CCND2_001	25	25	GGGAGAGGGAGGAGAGCTAACTGCCCAGCCAGCTTGCGTCACCGCTTCAGAGCGGAGAAGAGCGAGCAGGGAGAG
			CGAGACCAGTTTTAAGGGAGGACCGGTGCGAGTGAGGCAGCCCCGAGGCTCTGCTCGCCCACCACCCAATCCTCG

			CCTCCCTTCTGCTCCACCTTCTCTCTGCCCTCACCTCTCCCCCGAAAACCCCCTATTTAGCCAAAGGAAGGAGG
			TCAGGGGAACGCTCTCCCCTCCCCTTCCAAAAAACACAAAAACAGAAAAACCTTTTTCCAGGCCGGGGAAAGCAGGAG
			GGAGAGGGGCCGCCGGGCTGGCCATGGAGCTGCTGTGCCACGAGGTGGACCCGGTCCGCAGGGCCGTGCGGGACCG
			CAACCTGCTCCGAGACGACCGCGTCCTGCAGAACCTGCTCACCATCGAGGAGCGCTACCTTCCGCAGTGCTCCTAC
			TTCAAGTGCGTGCAGAAGGACATCCAACCCTACATGCGCAGAATGGTGGCCACCTGGATGCTGGAGGTAGGT
013_CCND2_002	25	25	CCAGATAAACTGGGGAGGCAGAGGGGGAGGAAAATCTGGGAGAAGCGAGGCTGTCCTGGGCGGGGGTAGGGGAGC
			ATCCCGCGCGCGTGTTCCTGCATGTGGCTGCCTCTTCTTCCCACCCCCCTCGCGACCTGTCTTTGCGAAGCCGCC
			GCGGCTGCTTGCGCTGCGGCCAGGAAGAGAGTCGGGGCCTGAAATCGGGACCCCGAGTAGAAAGGCAACCCCCCC
			AAAAGGCCAGAGCAAATTCGTCTTGGCCTCAGGTCCCCGCCTGTGGTCGCGACTCCGCGCTGGCACTTCACCGGGG
			AGGTGGAGGGAGGAGGGAGAAGGAGAGAAACGGGGAATTCGGGAGCCCCGGAAGTCCCATTGAAGAAACGCGTGTT
			TCAGGGGAACCCAAAAGAACCGCTTCTTGCCCCTCACTCCAAGTCTTTGCCCAGCGAGCCGTGTGCCCACGTATGC
			ACAGCTCTGGACCTGCCGTGGTTTCGCCATGTTGCTTTGCAAACTCCCTTTGGAAAGGCTGGG
014_CCND3_001	30	26	TGGTAGCCAGAGAGCTGGGACCTCACCCCCATCACCGCCACCACTGCACACACCCGAGGGGAAGGGAGGAGGCTCC
			TGCCGCTGCCTCCTGCACTTTTCATTTCCCTGTCGGCCGGAACAGGGCGCGCGCCACCCCCATCGCCTTCCCCGCC
			AGAACCCCGCGAAAGACACAGGAACCGGCTCCCGGGCGGGGCGGCCGAGCCCAGGGTTTTCCAGGCGCGCTCTCC
			GGAGAAGGCCGGGAGGCGGAGGGAAGCGGGAGACGCTGTGAGAAGCCGAAGGGGAGAGAGTGTCCTTGGTCCCGTT
			TGCTCGGCCCCGAAGAGAGGCACACAGTTAGGGTGCCAAGTGACTGGCAGTCACTGTCGGGAGGAGCCGATTAGGGCTC
			GGGAAAGCAAGGGAGGCAGCTGGCGTGGGTGCCCTAGTGAAAGGCCAGGCCCCCGGGAGTCTTAGCCTCGGAGCATC
			CTGCAGATTGCTGTGGGGA
015_CDH1_001	26	24	GGAACTGCAAAGCACCTGTGAGCTTGCGGAAGTCAGTTCAGACTCCAGCCCGCTCCAGCCCGGCCCGACCCGACCG
			CACCCGGCGCCTGCCCTCGCTCGGCGTCCCCGGCCAGCCATGGGCCCTTGGAGCCGCAGCCTCTCGGCGCTGCTGC
			TGCTGCTGCAGGTACCCCGGATCCCCCTGACTTGCGAGGGACGCATTCGGGCCGCCAAGCTCCGCGCCCCCAGCCCTGC
			GCCCCTTCCTCTCCCGTCGTCACCGCTTCCCTTCTTCCAAGAAAGTTCGGGTCCTGAGGAGCGGAGCGGCCTGGAA
			GCCTCGCGCGCTCCGGACCCCCCCAGTGATGGGAGTGGGGGGTGGGTGGTGAGGGGCGAGCGCGGCTTTCCTGCCCC
			CTCCAGCGCAGACCGAGGCGGGGGCGTCTGGCCGCGGAGTCCGCGGGGTGGGCTCGCGCGGGCGGTGGGGGCGTGA
			AGCGGGGTGTAGGGGGTGGGGTGTGGAGAAGGGGTGCCCTGGTGCAAGT
017_CDK6_001	30	25	GAGGATAAGAAGAAAGTGCAATCAGACAGCCCAGAAGCCTTCCTCGGGGTTCCTCCAGACTCCCCTCCTCCTTT
			TACGAAGCCTCCATCGCTACCCTCCGCGCGCTCCTGCCCTCTCCCCAAGCCGCTTAATCCTTCCTGGTTCCTCCGAG
			AAAAGCGAAGTTACTTTTCTTTCCCTGCAGGGCTGAAGCCGTCTTCGCGCGGAGAGGGTTGCAGGGGCCCCTCGGGG
			ATGAGCGAGCGGCGCGGGACGCAGTGGAACGGGAGGGGGCGTGCCGAGCAGCCCAGAGTGTGCCGGGAGCGCGGGG
			GAGGGGAGGCGCCGGGCACGTCAATGTCACGGCTTAATATTTATCCCTATATCATTGTGTTGCGCCGCTACCCTCC
			CCGCCTCCTGAGGCCCGGACGTGCAGGGAGACGGGGTCCAGGGGTGCCGGAGGGCGTTCAGGGGTCGCGCACAAGC
			TGGAGCGGAAGGACTGTGGGTCCATCCGTGTGGGGCCGCAGAATGTGGGTGGGGCTCCCCAGGACCCTGTAAC
018_CHEK2_001	27	25	GGACCAATGAGGAGCAGCAGATGTGGCCGTCAGGCGCCGCCTCAATGCCTCCTGGGAGTTGTAGTTTAGAAGGGAG
			AGCGGAACTTAGAACCCGGGTTCCCCTCGGGTGATCCCGCCCCCTCGACTCCCCCAGCCAATCAGCAACATTAGTCT
			GGTTAGACGCTCTCTTTGCTTTTCCCCACGAGTGACCACGGCTAGATAGGCCGCCGGCCAGATGTGGCGGGGGAGA
			GCCGGGGCTTTGCTCCCGGGTGTGGGGGTTTTGGCCGACAGGGGTTCCCAGAAGGAGACCGCTAAGCTGCGATGCTG
			CGTCGCAGGCGGGAAGCAATTATCCCCGCTGTTGGAACTGCGGCGGCCCATGGGGCCCCGGGCGGGAGGACAGGTT
			CTTCTGCCCCACA

020_CLTC_001	28	25	GAGCTCTCCATTTCTGGCAGCAATCAGCCGACCCTTCCCCATCAGTATCACGTGCACCTGGAAGTACGTGGGTGGG ACCTAAAGCGCCCACGGAAGTGACGTCGGTCGCCCCGAGTCGCATGATGTGGCAAAATGAAAAAAAAAAAGTGGGG GGAGAAAGAGAAGACTGGCGAAAGTGATGAGTCTAAAAAAAGTAGTCCCTCCGGTTCCTCTGTTTCCCCCCATGTGG CGTCAGGAAGCGAGGCACCGGGCGCACTGCGCGCCCCGAATTCCTGCGCCCGCCGCGCGGCTCCGTGGAGGGGT ACATAAGGCGGAGGGGGTGAGGCGACTGGGCGGAGTTCTGTCGCCGGGATCCTTCCGCTGGGCTCAGCCGTTTCCG GAGTCTGCGCTGCGCCCGGTTCCGCCATTGCGGCTCTCCTGGCCCCTGGAGCCTCCGCCCCCGACCCGAGCTCTTT CGTCTGCCTGCCAGTTTCCTGCGTCCCCGGAGAGGATCCTGCTGAGCCCAGCC
021_CLTCL1_001	25	26	CCTCACCTGGAAGTGCTCCTGAAAGCGAACAGGGAGGATCTGCGCCATGGCTGGTGCGGGACCTCGGCGGCGGCGG CGGCAGCGGCAGGAATGAACGCCGACCCCTCGCGCGGGCTGACCGGTGGCGACAGGCGCAGTGCCCCGAGC TCCCGGTCCTGGCCCCCGCCCTCCTCCCTGACCGCGCCCCGGCCCCGCACCCCCTTTCCCCGCCCCTTCCCCCGCCC CTGCCCCGCCCCCTGCCCCCGCCTCTGCCCCCGCCCCCTGCCCCCCGCCCCTCTGCCCCC GTCCCGCCTGCGCGGATCCCCTCCGCCCGCTCCGAGGGTCCGCGGAAAGTAGTCCCGCGCGCCCTCTGCCCTGACGC GGTGTGTGCCAGCTACCCGAGTGAAAGGTTTTCGGGGGATTTAATCCTGATGGGGTCTGCGGCGGCCCTTGCCCAGC GCCTTCCACATGTGGAGCGGGCCAGTGGTGCTAGTTCTGCCGCCAACTCTGGACGGTTGAGTTCAGGGCCACTTTT TACT
022_CMKOR1_001	30	25	GGTCCCCCACAGAAAGAAACAGGACAGAAAAAAGTCAGGACACGTATGCTGTGGAGAGGTCGAGGTCTCGCCTAGAT CTTGGGTGTGGGTAGACGCAGCCGCTGGCAGTTTTCCTTTCCAGCGTCTCTGGGGAGCCTGGAGATGTCCTTGGTG CCGATGTGACACGAAGAGTGATTGCGCCGCCCTGCAGAGGCGGTGGCGGGACGCTGCGCTCGGGCTGGGAAAGGCC GGCCCCAGGGCGACCCCCTCCGGAGGCCCCCGGAGAGCAGGTGTGCACCTCGCCTCCCGCTGGGCAGCCAGTTCAGG AGAAAA
023_COL1A1_001	30	26	CCTGATTGCTTCTACATCTTGGGCTTCAAATGCCCCGCTCGGCGCCCCCATCCCATCTTCGACGTGCTTTCCTCAC TCTGCACCCAGATCCCCCACTTCCCCCGGTTGCGCGCTCGGGATTCTCTCTTGCACCAACTCACGCCGCGCTCCACCC TCACCTCCCGCTCCCGGGGCGCGTTCAACCCCAACCTCGCCCCAGGGTGAGCTCCCTCCTGTCTCAGGGCGCCGAG GAAGAGCCCTCATCATCTCCCCTTCCATTCCCGAGTCTCCGGATCATCCACGTCTCGTTTTAAGCCGCGGCCCCCGG GACCAAGCGCAAGGCGCGATATAGAGTATCCTTGCACTCCCCAAAAGTTTGGGACTTACTGTCTTCGTCTTGGCCCT CGACTTGGCCTTCCCTCTTGGCCGTGCGTCAGGAGGGCGGTGGCCGCCTAAGAGGAGCCAGGAGCCGGAGGTCCACAAA GCTGAACATGTCTAGACCCTAGACATGTAGACTCTTTGTGGCTGGGGA
024_COPEB_001	28	25	TGGTCCCCATGACAAGCTCCAGCTGTGGCGTCTGGAGCGGGGACAGGCTCCGAACTCGTGCCAGGGGCTCGGCCGG GCTGTGCCGGGAGTTGGGGCTTCCCTGGGCGGACGCTGATCGCAGCCTGGAGGATCGATCGGCGGGGGCGCTGCGC CCGCTCCCCCCGGTGACAGCGCGGGGCCCAGGCCCAGCGGACCGCAGAGAGCACCGGGTCTGAACCCCAAACAGCCG ACCCGGCCCGCGCCCCGGCGCCCGCAGGGAACCGCGGCCGGCTGCGTTTACCTGTTGCCAGTACTCCTCCAGAGAC GGCAGCGCCGAGAAGTAGCCGGTCTCGTGCACGATCTGGAGCTCCTGGAAGATGCTG
025_COX6C_001	26	23	CCAAGGTCACAATGGCTGTGAAAAAGCGCAGCGGGTACCAGCCCCGGGCCAGCTCACTCCGAAGCCAGCTGGGTTC TCGAGGGTCCCCGCAGCCCACCCGGCTTCGGTGGGGCCGTCGCAACCCACCCCGGTCCGTGGTCCGCCCGCCGCCCT CCCTCAGGCCGCAGCGGAAGCGTGAGAGAGTAGATGCGGGAGAGGCCTGAAGCTGCACCA
026_CREBBP_001	28	25	GGCTGAGCCACAGCTTTTGTTCTGATGGCGACCAGGCGTAGAGGGCCGGGGCTCCGGGCCCCAGCGGGCTCCGGGA GCGGCGGCCTGGCCGCGGGCTGGGCTCTCGGGCGCGGATTCGACGCCCAGCCCGGGCCCGCCGTCCCGCTGGGGCCG GCGCTGCGTGTTCCCAGCTCCTCGCGTCCCCTTCCCCAGACCCTCCTAGGTGGCGTCGGTCGGGAACGGTCGGGGC GACCCCAGCCCAGGCCGCGCCACTAGCCTTCGCCGCCGGCCAGGGAAGTGGAATGGCCTCTGCAGGTTACAGACCG

			CCCTTGGGTCCTGCCGACGAGGTGGGCGGATGGGGAAACTGAGGCGGGGGGCGAGCAACTGCTCCAAAGTGGTCGA
			GGCAGGAAGTGGCAGGGCCGGGATTCGGGTCCCGCCCTACCTCGTGACACTAGGGAGTGAGGGGGCCT
027_DDX10_001	30	30	TAGCAAAGTTGAACCTGGAGCAAATGTGTTAATAGCCCTTAAAGGGTCAGTGTATGACGTCACCATAGTAACAACA
			ACAGTGCGCATGCGTTTTTTTTTTAAAGAGCCGGCGTGCTCCCGGCTCGGCTCAGCTCGCCCCCTTCCGTGGAGTGC
			TGCGCCCCCGTTTCCCCAGGCTGCCCCTCCCAGCAGGAGCCAATTCGCCAATCACAGCCCTCCTTTTCCTGACGTC
			ATTGGCGCGTGCCCCGGTTTCAAAAGCTCGGGGGCGGGCTTCTGAGTTCGCGCATGCGCCTCTGTGCGTTTGTCCC
			ATGCTGGTTCCGTGAGTCTGGCCTTAGGTGTCTCGTGTCTGGGGTTGATCCGAGCTGTCGCCGCCGCCGCCGCAAT
			GGGCAAAACGGCCAACTCTCCGGGTTCGGGAGCCCGACCCGGTGCGGAGCTTCAATCGCTGGAAGAAAAAA
			CACAGCCATAGGCAGAACAAAAAGAAGCAGTTGAGGAAGCAACTGAAGAAACC
028_DDX6_001	27	22	GGGGGCTCCCCACAGCCCCCAAAGCACCGCTGACCTCGACCCCACCACCTCACCCCAAGCCTCGCGACTCGGGCCC
			GTGTCCTACCAACGAGGCCACTCCCGCTCGGCACCCTCGGTCCTTTATTGTTGACTCGAAGCTCCCAAAATGGCGG
			ACGCTCCTTCCTCCTCGGAAACCTCCGCCCCGCCCCCACCCAGCCCTCTCGCTACGGCCTCCTCTCGCCCCCGCCCC
			CGCCCCGCTCCGAGGGGCGCGCAGGCCAGCCGCCCGAGCCGCCGGCTCCCCCGGCTGTCCAGCCCTACCTCCTCCG
			CTGCCCGCTCTCGTGGCGCCGCCGAAGTCGCCGCCTGGCTGAGCTAACTCGGCTCCTCTGCCCCCTCCCTCGCTCG
			CCCGTTCGCCCGCCCGCCTCCTCCCTCTTTCCCTGCCTCTCCGCATGGCGGCGACCGCGGCTCCTCCTCCACT
			CAAGATGGCGAAACCTCGGCCGCCGCGGCTATATTCGCCGCGGCGTCACTGCCTTCCTGGCCTGGTGGAGAGG
030_ELL_001	30	25	GCCCCATGAGGGCCCCACAAGGCCCACAGTCAACGCCCCAAGTTGTTGCATATTCATAAGGCACTTATGGCCCCGC
			CTCTTCAGGCCCTAGGGGTGGCCACTTCCGTGAACGAACTCCGCCTCAACACGCGCACCCCTCCAGGCCCCGCCTC
			CATAGTATTATACATAACCCTGACTCAGCCAGCCAGGCGCGTCAAAGCCCCGCCCCTACAGCCGCTGACGTGATGC
			ATTATTTATGAGATCTCTACAGTCTTCCGTCTTTGGCTTCTGTGGAAAGCCGCAGAGAGGGCGTGGAGGGGCGGAG
			CCGGCTCGAAACACGTGGGTGGGTAGGCCCCGCCGCGGCCGGGAGGGTGGGCGTGGCTATGTAAACGGAGCGCGC
			GCGTTGGACGCTGGGTTGGACACATAAGGCATCCCTTAGGCGGGGTGGATGGGACTTCCACCCAGGGAA
031_ERG_001	27	26	GGGTGCAGCCAGGAGGCTCAGCTTGTCCGCCTCCGGGGCTCGGGGCTAAGCCCCTTCCAGAAGTTTTCGTTTCTAC
			GCGAATTCCGACCGCAAAATCCAGCTTACCTGAGCGCCGCTCCTCTTCTCATGTCCCTCGGGGGCCGTCACGAC
			CGTCCCGGAGCGATCTCTAGGAACCTGTCCCGCAGCGATCTCTTGCACACTCTCCCCATTCCGACCAAGTGAAAAC
			TACCCATGTCCCTCCCTCTCCAAACTTTAACAGCCAAGAATTTCAGCAAACAGCCAGAAAGAAAGCTAAGTCTCCC
			CCCGCCCCCCCACCCCAAGGGAAGGGAGGGAA
032_ETV1_001	28	28	CAGGGGCCTCCAATCCAAACTGATGGATCGCTGCCTCCCATTGGCTCCGCGTCTCTTTCACAAGATCAGATTTCGG
			GCTGTCAATCAGGCGGCTTGCTGCCCCTTCCCGCGGGTCTCCCTCGCCCCTCTGCCCTAGGGGGTGCTCGGCCGGT
			AGGCGCTGGGTCCTCAGCCTGGAAGCGCCACGGAGAGACTCGATTTCCTCTGTAACCCGCTGCTTATTGTTAAGGC
			GCCTGGGGATACTGAAACCGTGTGTTTCGAGTCGCCAGTTCCCATTATTGGGGTGTTAGGTCCACTATTGGGCTGG
			TTTTC
034_FBXW7_001	30	26	TGGAGAACATCAGCAAAACTCCAGGAGGAAGCGCCGGCATCCTCCCCACTTTCTCCCCCTCAATTCCCTCTCCCGGG
			GCCACTCACACTTTTAGAAAAGAGCCGCGGCGCCGAGAAAGTGGGTTGGTTCCCTTCCTCCTTCGGACTGAAGCGG
			CAGCTGCGGAAGGCTCCGGCGCGGTACTGAGGAAGAAGCGGTGCTCGTGTCGCTAAACCAGGCGGCAACCCGGGTC
			TCTTCCGCGCTGCCAGGGGAGGGAGGCGGCGGCCCCGCTTACCTCCTCTTTCCTCTTCCTGGGTCTTTTCAGGC
			TGCGGCTTCTGCCCGTCCAGGGCCACTTCTCCCGGGACAGTCAGGTTTGGGAGACTCCGGATTTTGTTTTGTAAA
			GTTTCCTCTGGGTGGAGGCT
035_FGFR3_001	27	20	GGCAGGTAAGAAGGGACCCACTAGGCACGGGAGAGGCCGGCCCGTGCGGGCAGAGGCGTTGGGGACGGGAACCGGC

			CCCGGGTCGGAGGGGCCGCCGGGTGTGAGTGACGCCCCCGGGGTTAGAGCCCGGATTCCGCTGCCTCCTTGCCGGAG AGCGCGGCCAGAGCTAGCGCGGCGACTTGTGGTGCGCCCGGAGCCGCAGCTACCCTCCAAGTGCGAGGCCACCACG GGGAGCCAGGCTGGGGGTTGGCGTCCGCAGCCCCGATCCCCTGCGACTCCCTAGCCCTGGCCTGTCGGGAGGGCGC GGGGGGCCCCATTTCCACGATTCCCGCTGTTGTTATTCGGGTTCTGCGCAGACGGAAAGTTCCCATTGTTGGCGTC CCCCTCCCCCGGGCCCCAGTTTGTGGCCAGCTTCGGCCAAGGCGAGAGACCGGACTTCTAAGGGTGGGTGTGCGCG TCAGCGAAGCCCGGCCCCTGCCCGCCCGAAGAGGCAGCAGCCTCCAGCGTCCCCGCTGCCGACCCTGCCCCTGCCT GGGGG
037_FSTL3_001	25	29	GGGCTGATGTGGGGCAGAGCTGCCCAGGGGCCCAGGACAAAGGCCAGGCGTGCGCGCACACACACACACACACA CACACACACGCAGTGGCCTCCCTGGGGGCCGTGGCTGGGCGAGGCCTGCTGTTGTCCGAGATGCTGGAAGGAGCTG TGTCTCTGGGTCTGTCCCGGCCGCACCCCGTTCTGTCCCACACCCAACCACTCCCCACCCACAGGCCGGCTCCAGC GGCCAGGTGGACGGGTGCGCGGCCCGCGCTGTGAGCAGGGAACCATATCCAGCTGAGGTTTTGGGTG
038_FVT1_001	25	27	ATCCCAGGGATGTTGCATGGATTCACGAGCAGCCACACAGAACCCCTGGGGCCCCGGGAACCCTGCGGCCGGCGGGGT CCCCCGTCGCACGCTCTCCGGCCCTAGGAGGAGCCCGAGGCTGCGGAGGGCGGGTCCGCGAGGCCGGGTGCCGGGG CCGGGGGAAAAGCGCCGGGGTGGACGGCGGCAGGTGACCTTCCCCATTTGGCCATGCCTTCCTGGGGA
039_GAS7_001	23	25	GGGCTCAGGGGGAGGAGACCCAGGCGCCGCGGGCTCCGGAGACAACTTCCCGGGAACGCGGAACGCGGCTGCCGC CGCGAGGGCTGGCCGGGGCCGGGACCGGGCCCGCCCTGGCGCGCGGAAATGCGCAGCTCCCCCG GGAGGTGGGACCCGGAGCATCCCCCGCGCGGCAGGACTCCCGCGGCGGGCGGCCGTGGAGAGGAGCTGGCGGCCGGGTG GCCGGGCGGGGGTTAGCTCACTGGCGAGGGGGCGGGCCGGGGCCAGGGCGGCCACGCCCGCGGAGGGCTGC GCGCTCCCTCGCAGAGGGGCCTGTCACTGGGGAGAGGGGCTCCCACTCGCGCCCCCACCGCCGGGGACCGCGGGAA TGGAAACGCCCCCTCTGTTCTGTGCCTGCTTTGTAGGCCTGGCGGCCCGTGGCGTGCGGGCGGCTTCTTCGAGGTGT CTGCGAGGGATCGTTTGTGGTTGTCATTGTAGTGGTTGAACCTGGGGTTGAACTTGTCT
040_GOPC_001	22	26	CTGCTGGGACTGAGGGGACCCCCGCGCGCGGCACACTCCGTCACCTCCCTTCACCTCGCGCCGTTAACGCCAG CAGCACAGTCACAGAACCGCAGGAGTAACGAGGCTGAAGCTGAGGCGGCAACGGCGGCGACACACGGAAGACTCAG TCAGTCCCACCTCCCAGCCTGCCCCCGCTGCGCATGCGTAGCGAAGAGCTGGGCGGACGCAGCCACGAGGGACAAA ATAGGCGGGGACAGGATGCGATCTTGGCCTATGAAAGGCCTCAGCTTGGGAGCGGCCTGTCAGCGGCCATATTAAC AACTGGCAAACTACGGCTTGAATCCCTGAGAAACGGAGGCGCGTGGTTTCTGCACCCTGGTTGGCGGGAGCCGTTCCAA ATGAGAAAGGTGTCCACGTCGCAGAAAGGAAGGATTTCCGCCGGTTTGACTTAACAGTTGGCGGGAGCCGTTCCAA AATCCTCCCAGAAAGTTGCTGCGGTGGCATCTAGGGTCAGGGAGGGGAGAGC
041_HCMOGT-1_001	30	25	GGGCCTTCTGGCAGCCAAGAAGGAAATACAGATGAGGTGGGCGGACAGTATGCAGATGACGGGGGCGGGCCGCGCC TGGCGGGCGGTGTGCAGTTGAGGTGGTCCGGCAGGATGCAGATGAAGGGGGCGGGCCGCGAGGGCGGGCTTGATGC AGATGAGGGGGCGGGGCCCACGGGCGCGGGAGAGCAGCGGCTCCGCCGGCAGCTGCTGGGAACTGGAAGGCGCCCG GTCCTTTCTTTGACTGGAGCGGACCCGCCGGACGCAACCGCCTCGCCAGCCGGAGCCAGCGCGAGCTCGGCACGGT GGACACCCGGTCCGAGGCCGGCAAGCCGGCTGGTGCCCGAGTCGGCCAAGCATGGGCAACCACTCAGGACGGCCCG AGGATCCGGAACCAGGTCTGTGCGGCTGGCGGGGGTCGCGCCGCAGCCGCAACCCCACCCCCTCCAGGCGCCCT TCCCCCACCGCCTCCGGCTCGCGGCGCCGACTGGGGCGAGCGAAAGGCTAAGGTCCTGGGGTGTGATTCTT
042_HEAB_001	24	25	TGGGCTGCAGGGGAGCAGGAAATCTGGGGCGAGATTCCCGCCGCGGACGCGCACTGCCGAAGCCTGGTCCCTCGAC CTGTCCCCTGCCCAGCGCGGGGGCGCAACCGCCACGCCTCCTCACCCCTCCCTCCGGCTGCACGAATAATGACAACA GCCGCCCCTCCCACCTTTGGCGTCACGTTCAAAACAATCCTTTGACTACAACTCCCAGAAGGCCGAGCGGCTTAGC GAGTGCACCCCGCTCTCGGCTGCTCCGGCAAACTACACATCCCAAAGGGCAGCGCGACCGCGTGTCCTTTCACAG

			CGCAAGTGCGGAACTGCGTTTGTTTCCGGCGTGGGTCCGGGCAAGAACCGCTTGTAGTTTGGTTTAAATTCTGCAC
			GGGAGGACCTTCTGAGTTTACCTGTTGGGCTCCTGGCTGCGCAGGTGAGTTAAAAAAAGGGCAGGAACACAACTGT
			CACCTCCTTGGGGTCTGGGGACA
043_HLXB9_001	24	25	GAGGCTCAACCTGGGGCCTCTGCCCGCCCTCCCCTGGGTGCGGAGCCGGACGGCGGGCACTGGCAACCCCCGGGCC
			CCTGGAGAGCCCCCGCGGCGGCCCAAGACCCGCTCCCGAGACACGTGGGCCCCTCCGGACTTGGTTGGTCCCTGGAG
			CCAGCTGCGCGCGTCCTCTCCGGCCTCCTTGTCGGCGCTGGAGTGGGTCCACGTCTGCCTTGCGGAGCGCGGTGGT
			TCCACGCTCCTGAGCGCCCACGCTGCGCAGACCTGGCCGCTCTGCGAGGCGACGGCAGCGCACTGAAGACCGTGGT
			GTTTCCCAAGCCCTCCCTGCTCTCGGGCCTCCAGGGCGCAGCAGGGAGGGTTTTGTCCCCGTGGCCAAAGCTCTG
			CAGGTCGAACCTTATCTGCTATGGGAAGGCCCCCGCATTTTCAGGTGTGTGTGCGGGGGTGTGGGGGTGTAAACGCG
			CATGTGAGTGTGAGTTTGGCCTCC
045_HMGA2_001	26	28	CCAGGACAACTGCCCAGGGGTGACCTCGAGAGGCGGGTGGAGCTAGGCCCACGGCGAGCCAGCCCGGGATCCCCGG
			CCTGTCCCTTTAACCCCGCCGCCGGGCGGGAGCACGTGAGCGGGGCTCCGGGTGGCACCCGGGCGCCGCCGCCGCC
			GAGGCAGTTGTATTTCGAACGCTGCCTCTGGCTAGCAGCCAGGCGCCTTGGCTCGGCGGTCCGCCTGGCCTCCCTC
			CTCCTCATACTTTTCTTCCTGCGCAACCCCCTCCCCTTTATCCGCCCACGATTAGAGGTGGGCACTCCCCCCACCA
			CCACCCCCTCCCCCAAGCGCAAGCGCGTGCACGCACACACCACACACACTCACACTCACACACTCACACACACAC
			TCATCCCACTTGAATCTTGGGGCAGGAACTCAGAAAA
047_HOXC13_001	25	25	ATGGATGGTCTGGGCAGCAGCTGCCCGGCCAGCCACTGCCGCGACCTGCTTCCGCACCCCGTGCTGGGCCGCCCGC
			CGGCTCCCCCTGGGCGCCCCCTCAGGGCGCCGTCTATACGGACATCCCGGCCCCCGGAGGCGGCGCGCCAGTGTGCCCC
			GCCGCCCGCACCCCCCACCTCGTCCAGCGCCACCCTGGGCTACGGCTACCCCTTCGGGGGCAGCTACTACGGCTGC
			CGCCTGTCGCACAACGTGAACCTGCAGCAGAAGCCTTGCGCCTACCACCCGGGCGATAAATACCCGGAGCCGTCGG
			GCGCCCTGCCCGGTGACGACCTGTCCTCTAGGGCCAAGGAGTTCGCCTTCTACCCCAGCTTCGCCAGCTCCTACCA
			GGCGATGCCCGGCTACCTGGACGTGTCGGTGGTGCCCGGGATCAGCGGGCACCCGGAGCCGCGTCACGACGCCCTC
			ATCCCCGTCGAAGGCTACCAGCACTGGGCTCTCTCCAATGGCTGGGACA
049_HOXD13_001	25	25	GAGTGGGTGGGTCCAGCCAGGCCTGGGCCGGGAGCCAGGCTCCCCCGCGTTCCTACCCCCACGTGGCCGCGCGCAG
			CCAATGGCACGCCCCCGGCGGGGGCCCTCGGGGCGGGAGGCGGCCCCCCGACCGGCCCAGGCCCCCTCCCAACCTG
			AACTTCGTTTTTTATAAACGTCCCGCGATGAGCTAACCTGTTGGAGGGCAGGCGGGCCGGAGGCGGGAGGCTCACAG
			AGGGAGAGAGGGC
050_HRAS_001	30	25	AGGAGTTCAAGACCAGCCTGGCCAACATGATGAAACCCTGTCTCTACTAAAAACACAAAAAATTAGTCGGCTGCAG
			TGGCGCGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATCGCTGGAACCCGGGAGGCGGATGTTGC
			GGTGAGCCGAAATCGCGCCACTGCACTGGGCAACAGAGCGCTACTTCGTCTCAAAACAAAAAAGGCGTTTTACAGT
			CAGGCAAACCCTGCCTCTGCCCAGTCCAGCGCCCGCCTCGCCCTCCTGCGCCGGTCGCTGCTGACCCGGGGCTCCA
			CCCACGTGCGGTCCCGGGGTCCCGCCTGCCGTCCGTCCACCGCGCGGTCGCAGTCAGAGCTCGGCTCGGGGCGGA
			CACGCATGAACGCGAGTGAGAAGCGGCGACTGGACGGCGGGCAGCGTGTCCCGCGGCCGGGCACTCGGGTGC
			GCTCCGGCGTCCGGTGTGTTCCTGGTCCTCGGGGGCGCTTCCCCCCGGTGCTTCCTTTGCCGTCGCCTCACT
			TCCAACCGAAGGTCAGGACGGCAGGCCTCGGCCCCAGGGGCGACCCTTCCACCTGGGAAAGGTGGG
051_HRAS_002	27	25	TGACCCAGTGATGGGAAAAGGGACCCAGCCCTCAAAGGCAGGGCTGACAGCTGAGCGCTCTCAACCACGCACCCAA
			ATTAGAAGCTGCTGGGTCGGCAGAAAGGCTAAAGGGAGGCGCCCGAGGGCTGAGGTTACCGTCCTCCAGAACAGGT
			CTGGCCACGGCGGAGCGCGCCACGGCGTGCCCGGGCAGGCTAGTGCCAGCCTGCAGGCCCCGCGGCGCTGGTGCCT
			CCGACAAGTATTTGCTGAGCGCCTACTGCGTACTAGGCGCCGCCGAGGGGAGGGCAGACCCGGGCAGCGCCCCGCA

			CCCCCGGCGGGGAACCGGGGGCATCTTTCAGCCACAGAAAGCTGGAGAAGACAGAGGAGCTCCTGGGA
052_HRPT2_001	24	25	TGGGGATGGAAGTGCTGACCCACTGCTCAGGTACGCGCGCACCTGACGCCGCTTGGTGCGCCGCGGGTACTGG GTACGTGCTCCGCGCGCGCGCCCGGCAAAGTTCCCCGTACGTGCGCCGTACGTGGGCGCGGTGCCCCAGCGCTC AGCGTTTCAGCGAGTGAGTGGGCTCCGTGCCCAGCTGAAGTCTGGGAGGGGCACTTTTCCAGGCGGTCGCGGCTCC CCCTGGCGGCGGATGTGCCTCGCTGGAGGGGCGCAGTCAGGCGTTCTCCGCGGGCAGCCGGCGGCGGGGCCTTGCC TTACAGCGCGGGGTCCTCGGCGGCCTGGGTGGCTACTGCCCCTGCTG
053_HSPCA_001	26	26	GGGGGAAGAGGGAGCACCAGGAACAGCGCCTGCGCGGTGGGCGTGATCCGGGCACTTAGGGCAGGATGAACGCTGC TTTCCAAGATGGCGACGGAGGGAGGAAGGAGATGAACGAGATTAAGACCCAATTCACCACCCGGGAAGGTCT GTACAAGCTGCTGCCGCACTCGGAGTACAGCCGGCCCAACCGGGTGCCCTTCAACTCGCAGGGATCCAACCCTGTC CGCGTCTCCTTCGTAAACCTCAACGACCAGTCTGGCAACGGCGACCCGCCTCTGCTTCAATGTGGGCCGGGAGCTGT ACTTCTATATCTACAAGGGGGTCCGCAAGGTACCGACCCGGGCGTCACCGGAGCCAGCCAGCGGCGTAGGCAGAGG CCGGGAGCAGGGCGGTGACAGTGGGGCCAGGGTGACCGAGAGGGGTGGCCGTCGCTCTTACTTTGAGTGGGCCGG TAACTCCACTGGGGTACTCCTGAGGAGAGG
054_HSPCB_001	27	24	TCCTTTAGGGAGCCTTAGTCTAGATGTCGGGGTGGCTTGTGGATAACGCTCTGGATTTTTATAGGGTGAGGGTAGT GGTGGGTGAGGTTTTTTGAGTCCTCCTCGGTTTTCTCTAGTGTGTTTGGGGGGTGGGCTTTCTCTCGGCGCCTGC TGGCCGTAGCGAGGTGGGCTGTGGGGTTGGGGCAGTGGGCGGCTGGCAGCTGCACGTGGTGGCCGCGGCGCCGGG ACGCTGCCATTTTTGCCCCTCCACTTCCGGACGCGGCTACGGGGCGTCGGAGGGGGACCGCAGGGTGGCGGGGGTG CCCGCTCGGGTGACTCAGCACGGCCTTGTGGGACTGGCTTTGTCA
055_IRF4_001	25	27	TGATTGACTGGCCTCCTGAGGTCCTGGCGCAAAGGCGAGATTCGCATTTCGCACCTCGCCCTTCGCGGGAAACGGC CCCAGTGACAGTCCCCGAAGCGGCGCGCCCGGCTGGAGGGTGCGCTCTCCGGGCGCGGCGAGGGTCGCCA AGGGCGCGGGAACCCCACCCCGGCCGGCAGCCCCCAGCCTTCACGCCGGCCCTGAGGCTCGCCCGCCCGGCCGG CCCCGGCTCTCGGCTTGCAAAGTCCCTCTCCCCAGTCCACCCCCGGCCCCCACAGGCCTCGGCGCCCCCGCCGC CCCAGGCCCCGCCCCAGAGAGTTCTATAAAGTTCCTCTTTCCCACCTCGCACTCTCAGTTTCACCGCTCGATCTTG GGACCCACCGCTGCCCTCAGCTCCGAGTCCAGGGCGAGGTAAGGGCTGGAGTCGGGCAGGAGGAGGGTGTGAGGC TGATACCAGAGAGGAC
056_JAK2_001	28	26	CTGGGGAGCCAGCCAGGGTGAGTCACTCCCGGCCGCTTCCCTGGAGGGCGGCGGCCACACACACCCGCCCATCT AGTGAGGGCCGGGCCCAGCGCTGGCGCCTAGCTCCAGCCGGGCACCAGCGTTTCGCGAGGCGCCGCCGCCTTAACT TCCTTGCGCGCTCACGCCCAGGGGCCGTCCCAGGAATCTCCACGCGCTCGGCCGGCTTCCCGAGAGGCAGCTGCC CTGCGTGGCCCGCGCCTGCCGGTCCCGCGACCAGCACCGAGCGGCGCACGCGCACTGCAGGACGCGCGTCCGGCTC TCCCCCAGCCTCTATCCGGCCCGGTCTCCTGCCATTCGGGGAGACTGCAGGCCAACCGGAGAGGGTGAGTTCGAAGC TAGCAGGGCGGCGAAGCCAGTGTCGCCCGCGGCGTTGAGAAGACGGTGTGGCCCCGGAGAGGGTGGAGACAACTGT GACGGGCTTCCCGGCTGCCCGAAGTGGGAGTGGTGTGGGGCTGCAGGAAGGAGAGGAGAGGAAGGGGGG CAGC
058_KIT_001	24	22	CATCCCAGGGGTGGAAAGGTGGAGAGAGAAAGGGGCTCCGGAGTCAAGAGCGGGGAGAGAGGGCGCGCGCCCTC CTCCTCCCGGCGGGCACGGCCCCCCCGGCATTAACACGTCGAAAGAGCAGGGGCCAGACGCCGCCGGGAAGAAGCGA GACCCGGGCGGGCGCGAGGGAGGGGAGGCGAGGGGGCGTGGCCGGCGCGCAGAGGGAGGGCGCTGGGAGGAGGG GCTGCTGCTCGCCGCTCGCGGCTCTGGGGGCTCGGCTTTGCCGCGCTCGCTGCACTTGGGCGAGAGCTGGAACGTG GACCAGAGCTCGGATCCCATCGCAGCTACCGCGATGAGAGGCGCTCGCGGCGCCTGGGATTTTCTCTGCGTTCTGC TCCTACTGCTTCGCGTCCAGACAGGTGGGACACCGCGGCTGGCACCCCGACCGTGCGACTACTCGGCGAAGCCTGT

			GCCTGGGAGAGGTG
059_KTN1_001	26	23	GGATAGTCAGGGGGTAAATCTAGTGCCGTTTGCTGAAGTTAAAAGGCGTGGGAGCCAGGTGGTGCCCTGGAGGGA
			GGGCCGCGCGAGACGAGACCAACCTTCGGGACAGGGGAGAGCGGGGGCTACTGAACGCAGGGGATTCCGCTGAGCCT
			CCAGCCCCTGAGCGTCCACCTTCGGCCCAGCTGGGGGACGCGGTCTCGGGAAGAAAGCCCGGAATCCCGAGCCGGC
			CAGCCGCGAGCAGCGAGTACCGGAGCGCGTGGGCAGGCGCGCGGAGGCAGAGGCGGGCCGGCGGCTGTCCCTTTAA
			GGGGCCGGTCTCCCGGCGCCGCCGGCCCAGACGCCAGGACGTGCCGGGTCCGCCCCGCCCCCGCCCGAAGCCGCCC
			GTTTCCTGCCGAGCGGCGCGACGGCACCTGAGCGACTGCGGCGGCGGCGGCGGCGCCTCGGAGCGGG
			CGGCCCGGGCTGTAGTGCCGGCGCCGCGTCTTCCCGGTCTCCTTTCCCGGCCGCACAGGGTGAGGGAGAGCAG
			GC
060_LAF4_001	30	25	GGGTGGATCCCCCAGGCATTAGTGACACAGTCTTCAAATCGCTTCTTTTCCTCCCCACGGCTGCGCTCTGCCCCTGG
			CTACCTAGATCACCAGTCCCTGGGCTGGGGCGGCCGCGCGAGGGAGGGGAACAGGAGAGGGGGAAACAGACGGG
			CAGGCGGCCACGCATCCCACCCGGGGAGGCAGAAAAGGGCTGGCGAGGCAGGCGCCCCCGACCCACCCCCCA
			CGGCGGCCGGCCGCCCCGGAGCCCCCCGGCCCAGGTGAGGACGCGCGGGCCGCCGCGGCCGCCCCTCGCCGCTCCCGC
			CCGCCCGAAGCGGCCGGCACGGGGACTTACCACAGTGACTCGAGGTCCCATTCCTGGAGCAGGGCTAAGTCGAAGC
			TGTCCATGGTGGGAGGTGTC
061_LASP1_001	21	23	CTGGGGAAGGGCCCTGGGCACCGGGCGCAGTCAGCCTGAGAGCGCTGAGGCGCCAGCACCGCGGGCCCCGCCGTCC
			CCCCAGGAACCCGCCCCCCGCGCAGCCCCCACGTCGCCCGGAGAGCGCGCCTCGCTGCGCGTGCCCTTGCCCGCGCCC
			GAGGCGCGTGCCCGCCCCCAGTGCAGCCCCCTCCTCCCCGCTGTGTTTATTAGGGGAAGGAGGCGGAGGCGGAGGCC
			AGTTCCCCAGCTCCAGCCGCCGTCGCTGCTGCCTGTGTAGTTGCAGCCGCGCCGCCTCCCGCCAGCTCGCCTCGG
			GGAACAGGACGCGCGTGAGCTCAGGCGTCCCCCGCCCCAGCTTTTCTCGGAACCATGAACCCCAACTGCGCCCGGTG
			CGGCAAGATCGTGTATCCCCACGGAGAAGGTGAACTGTCTGGATAAGGTGAGCCCGGGACCGGGAGACGCGTCTTTG
			CAATCCCCCCGCAGTGCTCCGAATCCAGGGAGGAGAGAAGGGCCGGGTCTTTGCCGCCTTATCCCCGCGATCCCAGG
			AGAATGGAGGGAGGG
062_LMO2_001	26	26	AGACCAAATGGACAAAGAGAAAGGAGAGGGAAGAAGGGAGCAGAGTCAAGCCCAGAACGCTCTCCG
			GACTGCACCTGCGCGCCTCCAGGCTCTCCTCGTGCCTGCTCCCGTGCAAACTTTCTGGCCCGTGGTGGCTTTGGGG
			AGCGTCCCAGTAGCCTGGAGTGGCCCCGCAGAGGCGCCGGGCCGACCCCTGTCCCTGCCGCCCGCCCAGTCCCT
			CTCCCAGAGCCCCCGGAATCACCCGGGAGGAAGGAGGAGCCCAGCGCTCGGCACAGGGGGCCAAGGGCACGCCGCG
			AGCGCGCACCTGGAGCCCCCCTCGCGGGCCGCCCGGGTCCCCCCGACGCTCCGGGACGCGAGGCCGTGGACACCGGG
			GGTGGCAGGGGCAGGGGGGCCGCACTTACTCTGAAGGGTCCAGGCTC
063_LMO2_002	28	25	CTGCTGCTCAGGACTTAACCTTCCATCCCGGTCCCGCCGCCACCGCCCGGTCCCTCTCGCGCGCTGTCGCCGG
			CTCCGCGCCGCCCGCGGGATGGTGTGCGCCCGCCCGGCCGCCCTCGCACCTTCGGCCCGGGTCGCGG
			CGCGCTGCTCGCCGCCGAGGGCAGAGAGGGGGCGGCGCCTAGGGGCGGGAGGGCGTGCGTCTCTCTCCGGG
			CTTCCTCCTCTCTCGGGAAGGTCTATTTTCGCTCAGCTTCCCTCTGTCTCTGGTTTCATTTCCTTTTTCCTGATCA
			CGATTCAAATACAATAGAAGGAAATCACATTTAAAGAGACAGCTGCCCGGTCCCCCCACCTCCCCTTTTTCTTCC
			TTTTTTTTTTTTTTTTTTAAACGGGGCTCCTGGGGATTAGCAATACA
064_LPP_001	24	25	GCTGCAAGGTAAGGGCTGGCTGCACGGCCCGGGGCGCGGGCGTGGGGCGCTGGGCGCGGCGGCGCTCGAGGA
			GGCCAGTGTGGGGCGCGGGCCGGCCTGTCCGGGGCTGGGGACAATGGGAGGGGGAGTGCCCGGGCACCTCCTCC
			TCTGCCTCTGCCTCCGCCTCCAGCCGCCGCCGCCGCCGCCGCCACCACCACCGCGCTGCCCCGGCTGCC
			TCCTCCCTGAGGTATTGTTGCAAATCCTTCCTTCCCCTCACCCTCCACCCGCGGGCGCCTCGGGAACCCCCAGCCC

			TCCCCCGGCGCGAGCGCCTCCGGGGTGGCAAGAGCGCAGGGCGCGCGCCCTGCTCTGGCCTGGCCCGCTGTGCGGA
			AGTGCCGGCCGCGGCCCAATCACGGGGTGCACGCCATGGGGGAGGGGGACCCAGAGTTTTTCCA
065_LYL1_001	25	25	GTCTGGGCCAGGGTGTGGTTTCCAGCGTCAGGCCAGGCTCTGCTGTCTCGCGAGGGTCCGGCCTCAATGCTCCAGG
			CCCCGGCGTTGGGCCGCGCCTCCTCGTGGGCCTCGGAAGGCCAGGATAGCCGAGGTCTCCGCGTAGGTCCCCCCCA
			GGGAAAGTGAGCGGCTCCCGGGCCGGCCCGCCTTCTCCCCGCCCCCGGCGGCCCGGTTTCCTCCCTCTCACCCCTG
			GCGGCGCAGCGGCCGGAGGATGCTGGCCCCAGTGCAGATAAGGGCCAGGCTGCCTGGCCCGCGCCTGATAAGGAGCCT
			GGCTGACCCCGGAGGAAACCAGCGGCGGGGACCTAGCAGCGCGGGCCTCCCGGCCCCCGCCCCAGCCGGCGCTGG
			CAGGACTCGGTCCGCCACCCCTCAGGGCTTCGCCTTCCGCTCCCCCAGCCACTGTAGGGACCCCGGGCCCTCTGGGG
			ACCCGGGCCCCCAGGGCAGCCGGGGAGGGAGGTGCCTGGATGCACGCAGGGGGTAAACTGAGGCAGGGAAGCTGC
067_MAFB_001	22	22	GGGCTGGTGGGCAGCTCTGGCCCCATGCTCAGCTCCGCGGCCATCGCTGAAGCGAGGCGCAGCCGCCGCTGCCGCC
			CGGGAAACTTTGCGGCCGGCCGGAGCGCGCCGAGCCAAGCGCGGGGGGGAAGAGCGGAGAAGAGCTGGGGAGGCGG
			GGAGCGAGGGCGCAGCGGGCCGGGGCCGCCGGCCAAGCCTTTGTCTGGGGACGCGGCGGCGCCGGAGAGTCCCG
			AGGCTGCCTGCACCGCCCCCAGAGCTCTGGGCTGTGCCCGCGCAGGGACCGGGCCGGGTAGAGTCGGGCGGGGTGGA
			GAGGCAAGCGGAGCGCGCGGTGGGGCTGAGGGGAGGCGTGGGGCGAGTGCCCGTTGCTCGCTCTCTAGCTCTCTTG
			CTCTTACGCTCTCTCGCTCGCAGCCGCTCGGCGGTGCAGCTGTGCTGGATCCGGCGGCGCCGCAGCCTTT
			TTATCGCCTCCTGATGTCACTGGGGTG
068_MAP2K4_001	25	24	ACCTCCATGGGAATGATGAAAGCTGCGTACCTTCTTTCCGCACAAATGCAGGCCCACCTTTAATTCTGCAAACCAC
			TTTAGGCCCCCGCGGGCCCGCAGCCCTGGTCCAAGACAGCTGTCTGCTTCACAGGTCGCGCACCCAGAGCCGGGCGG
			TTCTGCAGCTCAGCATCTGGCCCGGGCTGCGCGTCGGGCTCTGGCGGGGGCGTGTCAGGAGGCGTGTCCGGGGCGT
			GTCGGAGGCGGGGCCAAGGCGGGGGTAAGCCTCGCCCCTCGGCCGTGCGAGAGGCCGAGCTTGCTGCATTGCAGCC
			GCCGCGGCGCCGCTCGGCTCTTCACTCCCAACACAATGGCGGCTCCGAGCCCGAGCGGCGGCGGCTCCGGGGGCG
			GCAGCGGCAGCGGCACACCCCCGGCCCCGTAGGGTCCCCGGCGCCAGGCCACCCGGCCGTCAGCAGCATGCAGGGTAA
			GGAA
069_MAP2K4_002	22	30	GGGCCTGCCCCCCTGGTCCCTGACGCCGCTCAGGTAGGCGGCGAAGACAGCGGCCCCGGCGCCCCTCGGCCCC
			GCCGCCGCAGTGGGCCCCGCTCAGGGCCATCTTGGCTGTCGCCGGGCACAGCTGGAGCCGGACCACCGAGCTGACC
			TCGGGCTACGGGGGCCTCTTGGAACCTGCGTTTTTCAAACTTTTGCAGGGTTTCTGTGCGCTGGAAGGGATGGGGGT
			GGGGGGCGGGTTGCCCAGGCCTGTGCCACCTGTAAGGTAGGTAGGCTGCATTGGCC
070_MDS1_001	26	25	CTCTCTGCCTCCTGCTCCTAGGCTGCCGCCGCTGGCTGTGTGCCCTCCACTCCCGGCTCTCCGAGCGCTCGCTGGG
			CCTCTTCTCTCCCCACGTCCGAGCGCTCGCTGGGCCTCTTTCCTCCCCACCTGCGCGTGGCTGTGCGGAGCCGGTA
			GCTCTGCTCTGCCCGTGCCCCCGCCCCCACACCCGCGATCACAGCCCCCACCTTGGTGTCCCCTACTCCCCGCCGCA
			GTCCTCCCGCCGCGCAGCGCCGCGCGGAGAGCATGGCCGAGCGCACAGCGCCCACTACCGCAGCCGCGGCTCGGC
			GCAGTCCACACCCGCCCCGCCCGCGCAACTTCCAGCGGCCGCCTCGCAACTTTTCCCAAGTCCACCACAGCCGCCCGCC
			GCCGCCGCCACTGTGGCTCCCTCTGAGCCGCCTACCCTACCCAAACCCCAGAAACACAAACCGAGGCTCGAAAAGGCT
			CCCTTCTCCTGCCGGCCCCCCATCCCCCGCGCCCCCCTCCTCCCACACCCGGGACTAGCTGGTTGGCCAGAGGCA
071_MET_001	28	22	CTTCTCCACCTAGAAAGTTTCACCTTGTCGTGGGCGGGGCAGAGGCGGGAGGAAACGCGACCCCCGCGGGGCCAGG
			CGCGGCGCGGACGGCAGGAAGGGCGGGGGCCGATTTCCCTCTGGGTGGTGCCAGTCCCCCACCTCAGCGGTCCTCGG
			AACCCGCGGACTAGGGGACGGACAGCACGCGAGGCAGACAGACACGTGCTGGGGCGGGCAGGCGAGCGCCTCAGTC
			TGGTCGCCTGGCGGTGCCTCCGGCCCCCAACGCGCCCGGGCCGCCGCGCGCGCCGATGCCCGGCTGAGTC
			ACTGGCCAGGGCCAG

072_MKL1_001	21	25	GTGGGGGAGGGGTCCCCAACCCGGACTCTCACTCACCGCCTCGCGCGGCTCCCGGCCGGGTTCCGCGGCTCGCCCC ACTCCGGCTCTAGCCGCCCGCGTCTCCTCTCGAGGCTCACTGTCCAGCCCGGGCGCACGGAGCTGAGAAGTCGCCG CCAGCGGAGGGCGTGTGGCCAGCGGCAACCAAGAGGGTGGGAAAGATGGGACCGTCGCTCTCGCCGCCGCGGCCAC CACAGACACTGCCGCCGCCGGCTCCTCTCAGCCACGGAAGCTGCGGGCCCGCCCACCACGCCCGCCTCCCGTCCTG AAGACTGTCCCGCTGGAGAAGTGACGGCGGCGCTAGCCAATCAGAGGCCTGATCGGGGTCGTGATCGGCGGACTAAA GGGCGGGCGGAGAAGGAAGCGGCATGAAGAAGGCGAAAACGGCGGCCTGACTTCCTGTGACTGACGGCACGGCGCA GCCAATGGGCAACGGGGAGATGACCTCATCTCTGAGGAAAGTCTGGAACTGGCTGAGCTGCGGCGAGGGGGTTGGC GACGAGCCGGGGGCGGAGCTCTGGGCCTTAAAGAGGCCGCAGCCCTGTGGTCACCCTGTGAAGGGAAGGGCGGTGG ACCCTGCCGGATCTTGCGAAGTTGCCAAGGGGTCAATGCCCAGGCGCGAGTAATTACTGCATTAATCCCAGACCCC ATCCCGATTCTTGTCGGGACTGAAGGGTCTCCGCCTGGGGCTCCGAAGTCGATCATTTCACATTCACGCTTCCCA AAACGAGACACAATAAATTCCGCTCTGGCCTGGAGCCTTGAATTCC
073_MLF1_001	27	30	GGGTGGTCTAATGTTTTGGTTCCTGCAGCCCAGAGAACAAGCTATCCCATCCCACAGGAGCCTTGGCGAAAAGCTC CCCGGCCGGCGCAAGGCCAGACTTCTCGCCTCCACTGTGTTGATTGCGGTTGCCAGGGCAGCGGCGCATTGCTCCC CGCCTCGTCCTGGTGACGTCACAGAGCAATGTCCAATGGGAAAGCAGCTCGGTGTCACGCACCTCCTATCCCGGCG GGCACCGCCTGCGCCGCGGCGAGTGAGGCGTCGTCCGTACTGGAGGCTAGCTCTTGTCGCGGCCGCGGCGAGTTAA CATCGTTTTTCCAATCTGTCCGCGGCTGCCGCCACCCAAGACACAGAGCCAGAATGTTCAGGATGCTGAACAGCAGTT TTGAGGATGACCC
074_MLH1_001	25	25	CTCTCTTCAGGAGTGAAGGAGGCCACGGGCAAGTCGCCCTGACGCAGACGCTCCACCAGGGCCGCGCTCGCCGT CCGCCACATACCGCTCGTAGTATTCGTGCTCAGCCTCGTAGTGGCGCCTGACGTCGCGTTCGCGGGTAGCTACGAT GAGGCGGCGACAGACCAGGCACAGGCCCCATCGCCCTCCGGAGGCTCCACCACCAAATAACGCTGGGTCCACTCG GGCCGGAAAACTAGAGCCTCGTCGACTTCCATCTTGCTTCTTTTGGGCGTCATCCACATTCTGCGGGAGGCCACAA GAGCAGGGCCAACGTTAGAAAGGCCGCAAGGGGAGAGGAGGCCTGAGAAGCGCCAAGCACCTCCTCCGCTCTGC GCCAGATCACCTCAGCAGAGGCACACAAGCCCGGTTCCGGCATCTCTGCTCCTATTGGCTGGA
076_MSI2_001	22	20	GGTGGCTGGAAACAGGGCACAGCGGAGGGCGGGCGGCTGGTGCCATTCCCGGATCTCGGCGGCAGGGGCCGGCAAA CTTGAATGGAGAGGGCGAACTAGAGAGGGTGGGGGGCGTCTTCTCCCAGGTCCGGGTGAGGAGCCGCAGCAAGCTC CCCGCGCCTCCCCCTCCCCCGATCCACCCGCCCCCCCGCAGCCCATGTGATCCAGGGAAGTCGGGGTGCGCTCCCCCT CGCCCTGCGCCCTGCCGGCCCGGAGGCGGGGTCCCCCTCCGCCCGCGGGTTCGCGCGCCACCCTTGTGGGTCCGGC CGTGGGGGGCCGAGTGTGCGCGCGCGGGCAGGCGGGGGGCCGCACGGGGGTGCGTGACGTCACCGGCATTGGTTACA CGACGTTCTAGAACTCCGCCCCACGTGCGCCGGGGAGGGGGGAGGAGGGAGGAGGGAGATGGG
077_MTCP1_001	25	23	GTTTTGGGACTGACTTTCAAAAGAGCGTCCCCCTGGCTCAAGAGGCCGGCGTTCGCGGAGATGTGCGTCTTAAAGGG CTGTCCCCCAAGCGTGTAGGCCGCGCACGGGTCTCCTTAGCGGGCGGGCAAAATGGGCGCCGGTACTCGGGAGGCG CCTGCCCAGGCGCCCGGGCGCCGCTCACAGAGTACGTCCGCCTGCGGCCCCAGAGCGCCGCCTCCCTGCCGCCCCC GCCGCCCGGCCTGACGCCCGGACCGCGGCCGGCCACCGCCCTCCGCCCCGACGGCCACGCCTGCCCCAAACCGCGC GGGCGTTTCCCAGGTGCTGCTGGGCGGGCCCCCGCCCCCGTGCCCCCAAGGCCCGCCCGCGCGCCAGCCGCGCCC CGCTGCCCCCCTCCTCGCCCCCCACAGCCCCGCCCCCCACAGCCCCGCCCGCTCCCTAAGCCCCCGCCCCCTAGGAACCC GCGCGCCGAAGGCCAGGCCTGGGCGGAGCGCACAGCGCTGGGCGCTGGGGAGGCTGCGCCGCAGCACCCGGTTGGT CAGGACCAAGTGGGCC
078_MUC1_001	24	25	GGGAGTGGGGGAAGAAATTTCCACTTAAGGGAGTAAACCTGGGCTCCGATGAACCCTAGGGTCCTTCCTTGCCACT CTCCACCACTGGCCAGGAGCTCCTCCCGCCCTCTAGTGGTCACCGGGAGCCTTGCGGGGCTGGGCCGCGCAAGCTG

			AGGGGCCGCTCGGACCGGGCGGAGAGGAGTAAGGGCAGCGCTGCCTAAGTGAGGCAGCGAGAGCCCGCGAGAGGGA AGCAGGGCCCGGGAGAGAAGGGTCACTGCCGTGGCCAGGGAGGGAGGAACGCACAGCATGGTGGACGGCTGGGAGC TTTAGGAGGGGGCACTCCGGGACGCGTGGTGGCGTCTGGAGGAAATGGAGCTAAGCGGGTGGGGTCCTGAGGT ATGTGGAAGGGGCAC
079_MYH11_001	25	25	CTACTTACAGATCTCCAACTGGGGGGACTAGTGGAGAGGAAACTGGATGGCGAGCTCGGATCTGACGCACCTCCCA GGCCCGGAGCGTCCAAATCTCCCTGCGCGTCCTCGGACGCCTCTCTTTATAGACCCGGAGCTGCCCGCGGCTGGGAA AGGGGAGGAGGCCGAAGGGGTGGAGTTGGGGAGGGTCCCTCGCGGCCCCCTCGCCGCGCCCCTGCAGGGCGCACC CCCGGCGGGAGCGCAAGGAGCTGGGGCGCTCGGGACAAGGGTGCACGGAACAGGTGCGCACCGCACAAGGGCGCAC GGAACAGGTGCGCACAGGGACGGGAGTCTCAGCCCCGGCCCCAGGCGGTCGCAGACGCTCCGGATCCCTAGAGAAA GGGGTCGAGCAGGCAGTGTCTGTGCGGGATGCTTGAGAACGTCTTCCCTGAGTCGGTTCCGGCCGCAAAGGCTTT AACCTCTTCCTCCCCGTGTCGGGGCTGTGGTGGATCTGACTTGACAT
080_MYH9_001	30	25	GGGAGCTGCAGCAGGTCAGCCTTGCTTAGCCTTCCGTGCCCTGCCCAGGAACCGCGGTGATCTGCGCGCCTCACCG CACCCAGCTCGGCTCCTCGCCGCCTTCCCGCCCCGCCCTCGGAGCCGCGGGACCATTCCCAGCCGGGAGCCGGCTC CGGGGCGGAGCCTGGGGCACAATCCCGCCCCCTTCCTGCTACACCCACTGCAGGCCGCGCCTGGCCTTGATGGGCA GACGTATTGGCCTGTGGAAAGGGGGTGGGCGGAGCCTCTGCGGCCAGATGGGTGGGGATTCAACATCCTCTTTCCG CCCCACCTCCACCCGCTCCACCTTCCCCCGCGCTTCCTAGGCGGGAGCCCCGCCCTCTAGGGCGGTCCAACGGAC AGCCAGGTTCTAGGACAAGGATTGACACAGGGGGAATCCAATCAGGAGGCGGCGACTCGGGGCGCGGAGAGCTCCG GGCCCGGGGTTTTGGTGCCTTGCCTGGGCCGGGGCGAGGCCCTGCGGGAGCCGACTGGGAAGGTCTGGAACTCTGAC A
081_NBS1_001	20	30	GGAGGACTGCCACCAGGGGGCGCCGCAATCACCCCACCGCCCGCGCTGAATTCCAGCTCACAGCCGCCGTGCTGCC CGGGAAGAATATGCGCTTGCCATACAGCGTACTCGCCGCTTCTGCGACCGCTTCCGCAGCGTCCCCGGGCAGGAAC GGACGCGACGCAGGAATCACCCGCAGGCCCTCCCCCGAGGCAGTCGCTACCGGGAAAATAGGCCCCGAGGCTTCCC TTCTGCCCTTACCTCCTGCCGGGCCCGCGGCAGCAGTTTCCACATCGGTCCGGCTCCTCAGGGCTGGGGCCG ACGTGCAACCGCGTAACCGGGGCTGCTAGACGAGCGCGGATACGGCGCCTGCGGTCGGCATGGGCTCCGGGACGTG CGCGCTCCCGGGAGCCACGCAGGCTGCCTTGGATGAGGCGGGAGTGCGACTTGGGCGCTTGCCCGCCACCTGGTGG TTGGAAAAGGAACAGCACAATCTGTATTGA
082_NCOA4_001	25	28	CTGGCTGGGAGCAGGGCAACAATGGGCGGAGTTTTCCGCTCCTCCCCGCCCTTGGCTTGAGCGCTCCAGCTCGCTA GTGGCCCGGGCGAACTGGAGTTGCCGTGTGACGCGTGGGCGGGACGAGGCCCGGGCTCGGGGACCTTTCGCACTCG GGTCAGGGGTAAAGCAGCCTGTCGCTTGCCGGGCAGCTGGTGAGTCGGTGACCTGGCCTGTGAGGTACGTCTGGCA GCCCAGGGGCCGTAGCGGGAGCCCTTGAGGCCGGTAGCCTTGCAGGGCTGGCGCCGGGCAGGAGCCGGGTCGCAGC GGCTGACTGCACAACTGCGTGCGAATCGGCGACCGGGGCGAGGGCAAGGGCTCCTGAGGCCGCTTGGAAAGGGCTT TTGGGAAGTCTAGAAAGC
083_NF2_001	25	25	ATTGGTGGAGTCACCCCAAAGGAGGCGGGACGGAGCGGGAAAGTCCTGCCTACCTTGGCCTTCCCAGCCAATCGCA GCATCTATGCGTCAGCCTCCGGTTCGGTTGCGCTGCGCGTAGTGGTCTGGGCGACCTGAGGGCGGGGCCGGGAGCA GGCCCCGGGCTGTGGGGAGGGTGCGCTTCCCGCGGGCGCGCGGAGTGAGGACGGTGACAGCCACGCGCGCGCGTAC GCGCCCGATGCAGCGCGGCCCCGTGACCCTAGTCGGCCGCTGAGAGGCGCGCGGAGTCTGGGCCGCTGCCGTCTAG GGGTCCCGTCCCGAGGCGTCCCCGGCATCTCCGGCCCGAATCCCGGAGTGCCGGGTCGCGCCTGCACCGAAGGTCC CGGCTCCTGTGCCCTCCCTGCAGCCGTCAGGGCCCGTCCCCCAACTCCCCTTCCGCTCAGGCAGGTCCTCGCGG CCCATGCTGGCCGCTGGGACCCGCGCAGCCCAGACCGTTCCCGGCCGGGCAGCCGGCCACCATGGTGGCCCTGA

			GGCCT
085_NFKB2_002	30	25	GAAACACACTTGTGGAGCTGTGATGGAGACACACTCTTGTATTAGGTGGGGGGGGGGGGGGGGAGCGTGCAGAGA TCTCCCTGTCGCCTGCGCGCCCAGAACCGGTGCGGTGTGGGACCAGCTGCTGTTGTGAGGTTTGGGAGAGAGAAA AAGAGCCCACTCCGAGGAGGAGACACTTTTCCCGCAGCCCCAGAATCGCGTTCTCGGGGCAGAACCCCGGGGCCTC CCACAGGAAAGAGCCCCCGCCTACAGGCTGTTCGAAGGGGAGGCCGTCCGACAGCAGGAATGTCCCCCCAAAAGCC CCCGGGGTTTATCAGCCGTGGCCTCCCTCCTGGCAGAAAATCCCAAGGTTGCTCCAGACCGGGGGAGGGGAGCGGG AGGCGGACTTGGCCCCAGACTGCCAGCCTCCTCCCGGCCGTGAAAGACCCTCCTGTTCCCTGCCCTGGAGGGAGGA GGGGGCTTAACCCCCAC
086_NFKB2_003	30	28	GGACTTGGCCCCCAGACTGCCAGCCTCCTCCCGGCCGTGAAAGACCCTCCTGTTCCCTGCCCTGGAGGGAGGAGGGG GCTTAACCCCCACCGGGGCTTCCCGGATTCTCCTAGACCTCTGCCCCGCTGAAAAGCAGCGGGAGCCCCGTAGACTGT CGAGGGCCTCCCGCCCCTCCCGTCGCGAGGGCGGGGCCAGTGGCGTCATTTCCAGGCCCGCCCCCTCGGCCCCGC CTCCCCTTGGTATTTTCGGGACTTTCCTAAGCTGCTCTAACTTTCCTGCCCCTTCCCCGGCCAAGCCCAACTCCGG ATCTCGCTCTCCACCGGATCTCACCCGCCACACCCGGACACAGGCGGCTGGAGGAGGTCGGACCCTCCCCCCAAATCTG GGCCCCCATCTCCCGCCCACCCCCATTTAGATCTGACCCCCTCCCCCCACGCCACTCCTCCCAACTTTAGGCGGCCG TCTAAAATTCTGGGAAGCAGAACCTGG
087_NFKB2_004	24	25	GCCCTGAGTGAGCCTGTCCCCTCTCAGGGGCGCGCCCGAGTCGCTCCGGGTTGGCTGCGCCAGTCCAGAGTTAAAC TTTCAGCCAATGAAAAAGGGCGCGAGGCGTGACGCACGGAAACGTCATGGGAATTCCCCCCTCCGGGGGCCGAGA AGGGGCTTTCCCGGCCCTGAGCCCTGCTGGCAGGCGAGGTGTCGCGACCGGTCCCAGGTGGGTCGGGCGCGGAGAG AAGCCGCAACCAGAGCCGCCGCCACGGTGAGTGGCTGGATTCAGACCCCTGGGTGGCCGGGACAAGAGAAAAGAGG GAGGAGGGCCTTTAGCGGACAGCGCCTGGGGCTGGAGAGCAGCAGCTG
088_NFKB2_005	26	27	CAAGAGAAAAGAGGGAGGAGGGCCTTTAGCGGACAGCGCCTGGGGCTGGAGAGCAGCAGCTGCACACAGCCGGAAA GGGCGCGCAGGCGACGACACTCGGATCCACGTCGACACACCGTTGTACAAAGATACGCGGACCCGTACGTACACCTGT ACCTGTGCTGGCGCACACACGGCAGCGTCCGTGCAGTCGCACTCGCACACACATGCACACGGAGACGTGCCCACCG GTGCACTGGTGCCTGCACCCACACCCTTCACGCACAAACTCAAGATACGCTCACCCGTGTCCGTACATCAAGACAG GCGCTGACACACACCCACACTGAGAAGCTCGGGATTCACCTATCTACACACATGCTCGCTTGCACACTCATGTTGA CGCCATGGACACACAACATGCAACCCAAGCACTACAGCCGAAACACACTTGTGGAGCTGTGATGGA
089_NIN_001	27	27	CATTGGAAAGGGTGTTCAGGAGGCAGAAGGGCTGTAGAAGTGACTCGGAACCCTGTAGAGCGAGCGCGACCCTCCT GCCGGGTCTACACTGGCTTCCGCACCTGCCCACCACGTCCTCACAGGCTCCCGCCCCTGTGCAGCCTTCTCCGGGT GAAGCTAACCCTCGGTCGCAAGCCACACAGGACGAAAACTCCTTGGAGTTGGTGGTTCCCAGCCCAACAGTTGCTC GATATTAATCGCCTCCTACCTACTACCCCAGAGTCTGCGTTCTCACTCCCCCATCCCTACACTTCTGATCTCATTG CAGTCAAATAGGATCCCAAGTCCAGGCCATGGTTCTTTTTGAGCTGCAGGGTTAAATGTGTTGCCCTTGAAGGATC
090_NONO_001	30	25	GGGAGCTAAACCTTGATTGGCAGTTTAGCTAACCAATCGAGAACGCCATTTTGTACCCCTTGGCAGGCACCGAGCT CCGTCGTCTCGTTTCCGGCGGTCGCGCTCTTTCTCGGGACGGGAGAGGCCGTGTAGCGTCGCCGTTACTCCGA GGAGATACCAGTCGGTAGAGGGTGAGTTTTGGGACGTCTTGGTTCTTGTTTGGGAGGGTAGTGGGATTTCTTGGAA CAATCAGCGAAGGAAGAGGCTAGGGCGAAGCTAGGTTTGGAGGGTGGATGGCGCTTCCGAGGCCCCTTGAGGCCTT GTCTCTG
091_NOTCH1_001	30	25	GTTTGAAAGTTTTCAGAGGCCAAAAGTTTGAGCCGGGGCTGCGGAAGGATCCGGCTCTGGCGGTTGCCGCGCTCGG CGACAACTGGCGACTGAAATTTGCATGTGAATAAGCGGAGGAGCCCGGGGCGGAATGGGGAGGGCGAGGCCGCGGA CAGCCGTGTGCACCGTGCGCTGGGCCGGGCGGGGAGCAGCTGAGGCCACGTTGGGGGACCCCCGGGCCCGGGGCAGG

			GCTCTGGGAGAGTGGCCTAG
092_NTRK1_001	25	26	GCCCCTAACAGGGGAGGGGGCAGAGGGGGGGCGTCAGAGAGTAGGAAGCGGTGGAGAAGAGGGCAAGGCGGGG
			CCGGGCCGGGGGCCGCTGGCTCCGCCCTTTCCTGGCGGCTGGGTCTTTAACACCGCCCAGCGCACATGTCGGGGGAG
			GCCTGGCAGCTGCAGCTGGGAGCGCACACAGACGGCTGCCCCGCCTGAGCGAGGCGGGCGCCGCCGCGATGCTGCGAG
			GCGGACGGCGCGGGCAGCTTGGCTGGCACAGCTGGGCTGCGGGGCCGGGCAGCCTGCTGGCTTGGCTGATACTGGC
			ATCTGCGGGCGCCGCACCCTGCCCCGATGCCTGCTGCCCCCCACGGCTCCTCGGGACTGCGATGCACCCGGGATGGG
			GCCCTGGATAGCCTCCACCACCTGCCCGGCGCAGAGAACCTGACTGAGCTGTGAGTGTCCGGCGGGCGGTGGGGGG
			GCGCGGGGACAGGCAGGCATTGCAGTGCCCCGAGGGCGCGGACTCGCTGCTTGTTTGCTGGTCAGGCAGGA
093_PAFAH1B2_001	26	30	CATGGGTGGAAGAGGAAGCCAAGTTGGCTGAGTGTGAAGGGAATGGCGTCAGTGTGACTTCACGCCACATCGTCCC
			GAATGCCAGCTCCACACACTGCGGTGGCACGAACGCAGGATTGAGAGATGCAGCTGGAGTAAAGAGAAGCCCATGT
			CCCTCAGACGCCACACACAAAATGGGGGTAACCGCGAGAACACAAGCAGGGTACCCAACGGGGTGTGGCGGGACACCTG
			GGCGCACGCCGCCAGCGCCCGGGAGAGCGAAGGCGGGGAGAGAGGAACCACGCTGAGGCGTGGCAGGATGGGGGCG
			GGACTTCCGGAAGCCATTTGGCTGAGTGGCAGGGAACCGGAAGTGGAGGAGCTGCTGCTGGTGCTGGGGCCGGAG
			GAGGGACGCGCCGGAGCGGGACCGAGCGAGCGACCGACGCGCCACCCGCCGACGCCTCAGCCGCTTG
			GGGCCCGCACGGACCCTCTACTTCAGTGAGTGCATCCAGGG
094_PAX3_001	26	25	GGGAATGGGCTTCCTGGAAGCACCAAAGGAGCCTGCGGAGCCTGGGGATGGGGTGAGGCAGCCGGTCCCAGGCCCT
			GGGATCCAGGCGGCGCGCTGAGGCCCTCCCTTACCTTCCAGCGGGAACCCGCTACGCGGGTAGTTCTGCCCCGGGC
			CCGGCCGCATCATCCTGGGCACAGCGCCGGCCAGCGTGGTCATCCTGGGGGCAGCTTCGCTCGGAAATTATATCCA
			GGTGAAGGCGAAACGGAAAGGCGAGTGCGGCGCGGATGACCCTCGGGAACTATCCGGAGCGTGGAGAGCCCCTCCC
			CAAAACGGCTGGAGAGAGAGGGAGGGACGCGGGGAGGGGGGCTGTCGGTTCCTAGTCCAGAGGCCGGAGCTGGAAC
			CCGGGAAAGGGGAGGACGGGGAGGCCCCGGAGTCCAGGATCCCGAGCCCAGGGCGGAAAAGTTTGGTACGAGTCTG
			GGCAAATGTTTCCAGCGACTGGGGTCCCTGAAAAGGGGGCTCAGAGAG
095_PAX5_001	25	25	CAGGACTTGATGGAATGGACAGGGAAAAGTTTCCACTTTTTGTGCCTTTTTTTTTTTTTTTTTTTTTTTTTT
			TTTTTTTTGGTGCCAGGGGCCGCTCACAGGTCGGAATAATTCAAGCCTTCCGCTCCCCCGCCGAGCTGGGGTAGC
			TGATCACTGAGCTGAAACTAAACGTTTTAGGTGGAAAAAAAAGCGTCCGAAGGCACCGTGAAATGATTAAGGAACTA
			AAGAGCTTCTCGCCATGTGAGATCATGTCCTGTTCTCGCCAACATCACAGATGTCCCCAGACACGCCGCGCCCCCC
			AGCGCGCCGCCCCCACACTGCCGGCCCGGAGCGAGGAAAGGGTAGGCGCTGCGCGGCCGGGCCTGCTCAGCGCGCCA
			GACGTGGCGGACCCGGCCCGGCCGGAGTAGAGCGGGGAAGCCGGGAGAGCAGCAGTGCTGCTGCCGCGCCGCCCCAG
			ACTTTTATAGGGGTTGGGGG
096_PAX7_001	27	27	GGGAGCCTCACTGGAGGAATTTCAGAGGGTGTAAGACGAGGGAGAAGATGAGAAATAGGGCGGACTCTGGCCCTCG
			GAGGCCAGAGAAAGGCGAGACTCCAGAGAGGCGCCGGACCCGAGGCAGACATTCCCATACAGCCGGGACTCCGAG
			AGCAGCCGTGGGCGACCTGGGGGCCGGGACTCGGCGGATCCGGCCCATTCATCAAAGGAAGGCACTGGGACAAAG
			TTGGCCCCC
097_PAX7_002	24	25	GTTTGACTGCAGCCAGGGGTGGGGGGTAGGGAGTGTGTGTGGAGGGGAGAAGAGGTTAAAAAAAAG
			AAGACGAAGAAGACGGAAAGAAAGAGATCGCAGCAGGGGTGAAGGGAGCGGACGGGAAGCGATTTTTGCCGACTTT
			GGATTCGTCCCCGGCGTGCGCAAGAATGGCGGCCCTTCCCGGCACGGTACCGAGAATGATGCGGCCGGCTCCGGGG
			CAGAACTACCCCCGCACGGGATTCCCTTTGGAAGGTAAGAACGCCCAGGCTGGCCTCGCCGCGACTCCGCCGCCCG
			GAACTCGGGGTCCTTGGAGAGGCTGCGGTCTCCAGGGGACGGTGGCGGCGCCGGCGATAGCAGAGGGATCCCGTTC
			TCTTCTGGGTCCCAGTCCGGGCGCGGAACCCAGGGAGTTTCTGGGACCC

098_PBX1_001	25	25	ATAATGATGATGCTGGGAGCTGGACCGTCGTAGATTGTCGCCTGAGTCTTGCTGTAAGACGCTGCACAATTAGATT AGAGGAGAGGGCTAGGGGTGGCCGCGAACCCCCCTCGCAAATCTGTTGACTTCACCGCAGGGCTGATGCGCGCAGCA TAGAGGACGCTTGGGAGCGCCCGGCCACTGCCCGGTCCGCCGGCGCGCCGTCGCACCCGGTCTTCTCTGCA CCCTGCGCCTTGCACCGGCCTCCCTCTCCCGTTCGGGCGTGCGGCCCCCCTCAGACTCTGCCCTTGAGTTCCCAGCG CAGGCCGCACGTCACCGGCCGCCAGCGCGCGGACCGCGAAGCCAAGTGTCCCCCAAGCGGGGCTTGCTGTGTTTTC ATCATTTCCCTTGCCTGGCCCGGGTTGCAGTGGTCAGCCGCAGCGGTCTGCTCCCGGCGGCGGCCCGAGGCTCCCC CGCCACCTCTTCTGTCCCGGCTGACTTAACTCTTCTCCCAAAGGGTGGTAAAGAGAGGGCCGCCGCCCCCCAGGGG GAAGACATCCTCTTGGG
100_PER1_001	21	25	GGTCCTTGGGGGCAGGGAGAGGGTGGGTAGCGGTAAGGACGACAGTGTGCCCTCTGCCTGGGCCGAAAGTAGCCCA TCAGATTGGAAGTGGCAGCGGTCCGGCTCAGGGACGGAGATCGGCCCCAGGATGGCCGCAGAGATGCCTACCTGGT CGCAGGAGTGTCCTCCGCACGCCTGCCCGCCGCTCCAGCCCGCAGCCGAGTGGAAGCTCCACCGGGCGGGCGG GGAGGCGGGTTGCATAAATGCCGGGCACTGCCCCCCTCATTGGCCTCTTGCCGACGGAGCCGCAGGCCCCCGCCCCGA TTGGCTGGGGATCTCTTCCCGGCGCCTGATTGGCTAGTGGTCTCCACTAAGGTCAGGGCTGTGTCACACACACGGG CGCACGTGGACCTGGGTGCTGGTGCTGGGCTGAAGAGCCCCAGA
101_PHOX2B_001	25	25	CATGGGGCCCTAGGTCCTTCTCACTCGAGGCTCCAGGACTTCGAATTTCACCAGCCGCCCCTCACCCCACACCTCC CCGGACCAGTGCGGCGGAGCGGGGTCGGTTTCCAGGCGCGCGTACCTGGACTCGCGCCTCTGTGAGGTCGATCTTC AGGGCCAGCTCCTCCCGAGTGTAGATGTCGGGGTAGTGAGTCTCCGCGAAGACCCTTTCCAGCTCTTTGAGCTGGG CACTGGTGAAAGTGGTGCGGATGCGCCGCTGCTTGCGCTTCTCGTTGAGGCCGCCGTGGTCCGTGAAGAGTTTGTA AGGAACTAGAGTATGACAGAGGAGACAGAAAGTGAGCAAATCAGCCGGCAGCTCGCCGGCCGTGGAGCTAGAATGT GAGGACTCCA
103_PICALM_002	25	25	GTGGCCTTGCATACTGTCTTGGATACGGCAGAGCCGGTGACACTGTGCTGGGCGGCAGTGATTCGGTCCGTCAGGC TCTGGCCGGACATCTCTGCAGCTCCTCCACCACCCCACCCGCTCAGCAGCCGGCGGGGACTGGGACCCCCCAAGAGC CGGAGGGTCCCCCACCCCCCCACCGCACCCCCCTACCCCCCACCGGCTCCTCTTCCCCGCCTGCCGGCCTGGGGCGCGGTTC GGGGCCGCGCGCTGCCACCAGTCCAGAGAGAACCGGCTCGTGTCACCCGCGGAGTCGGACAAGATGTCGGGCACTC CCTTGCCCCCGCCTCAGTTCAGCCCACCCCTTCCCGGGTCAGCTGGAGCCGGGCAGGGTAAGAGGAACAGGCAGC
104_PIK3CA_001	25	22	TTGCTTCTACTCCCAGTTTTGGGGACGGGGCGGCTGGAGGTTGAGGAAGTGCGCCCAGGGCCGCCCCGGCCGC GGTGGCTCTGTCTCCCGCGCCCTGCACGCCCACCCAGCCCGCGGGTGGAGGGGCTGCCCGCGAGGACTGCGGCTCAA GGGACGCGGGCGCGAAACCGCGAGCTTTTCTTGAGGGGCTGTCACGCCCGAGGACTCCGGCCCCGCCAGCCTGGCG GCCCTGCGTTTGCCTCTTACTGGGTTTAAATCGCCCGGCAGGGGTATGGAAGGAACAC
105_PLAG1_001	22	28	GGGGTCCTGAGCAGGGGCTGAGAGTAGCACACAAACTTTTCCTCCTCCTGCCGCCGCTGCTCCTCTGCCCCCTCG GCTAGTCCCATAATTTAAATAACCCTGATATATTTCTCCCGCTAAACGCCTCGCCGCCCCGGACCCCCGGAGAAC TCACCGCGGGGCTTTAACATCCTCCCTCCGGCCCGTCCGCCGCCTCTACACCGCCCGCGGAATTTCTAATAATTTT TTTCTCATATTTCGGGCTGGACGCGGCGGGCCTGGAAATTGTTTCCTTACGCCTCTTTCCAGCAGCCATTGTAGTG TATGCGCTGCCCCCTGCAGCCCAACTTGCAGCTG
106_PML_001	23	25	GCTGTGCTCAGGATGCCTGGAGGCGTCGGGCATGCAGTGCCCCATCTGCCAGGCGCCCCTGGCCCCTAGGTGCAGAC ACACCCGCCCTGGATAACGTCTTTTTCGAGAGTCTGCAGCGGCGCCTGTCGGTGTACCGGCAGATTGTGGATGCGC AGGCTGTGTGCACCCGCTGCAAAGAGTCGGCCGACTTCTGGTGCTTTGAGTGCGAGCAGCTCCTCTGCGCCAAGTG CTTCGAGGCACACCAGTGGTTCCTCAAGCACGAGGCCCGGCCCCTAGCAGAGCTGCGCAACCAGTCGGTGCGTGAG TTCCTGGACGGCACCCGCAAGACCAACAACATCTTCTGCTCCAACCCCAACCACCGCACACCCCTACGCTGACCAGGT

			GAGTAGGCCGGCACAGGGTGGGGTGGTGCATCCA
107_PRDM16_001	27	25	GGGGCCACCTGGGTCCTTTTAAAGTGTCCGGGTGCGGCCCCGGGCGGGAGCGCCGAACACGGAATGTTTTCTTA
			AAGGGCCAGTTCCGAGCTGCGCTGAAAAGGGGGGGGGGAGAGGGGGGAGATAAGTGAGACGAAGACCGAGAAG
			GCCGAGGAGAGCCCCCCCAATCCCGCGCCGAGGCGGCGGCGGCGGCGGCGCGACGATGAGGATGATGAATA
			CATTGCAAAGTTTTTTTGGCCCCGGCGAGGGGTGTCAGATTGAGTGCTCTGTGCGCATGTGCGAAGGTGTCCAAAC
			TGACAATGCTGGGGAGATGAAGATAGTGTGTGGCTGCTTCTGGACTCAAGGAGGAGGAGA
108_PSIP2_001	26	30	CATGGGAGAGAAAAAGGCAGGGATTCCGAGAAGCGAGCGGCCCCCTTCCGCCCACGCAAGGCCTCCCCCGCAACCT
			GCTGCCCAGCGGCTGCAGCCTCGGCCCCCTCGGCTCCCGGGCGGGCCGCGTCCACTTCCCCGCTACAGCCAGGAGC
			GACGCCACCGAGGGGGGGGCGGGGCGAGTCCCCGTCGCCCGCTCACCTGCCGGGGCCGCGGGCGCCGACGCTGCGG
			TTGCTGGCCGGTCGCCTCTACCCGCGTCCCACGCAAGCCACCCTGCGCCACCCAGCTGCCGCAGAGGCGTCTCAACGGC
			TCGGAATCGCAACCGCGCCGCCGCTGCCGCCGCGTAGCTGCGCTGCTCCCGCGCGGCTCCCGCTCGGCGCCCGCT
			AGCACTGGGGCGCGACCAACTGTTTACCGAGAGAGGGGGGATGTTGCAGCACCCGGCGAAGCTGTGTGGCTCCGAA
			GCGGATTTTCTGGAAACCCTACGTCCCCAAGTTCGCTTTCATGTAACAGGTGCATGCAGATGGAGAGGAAG
109_RANBP17_001	26	25	CTGCACTTCCAGGTCAGTGTGCTCTGCGCCGCGGGCCCCGCGCTCCCGCCACGCTGGGAACCCGGCGGGACGCGTCTG
			GAGACCGAGGGCCGAGGACAGCGGCGGAGGCCGCAGGGCCGTGGGCCGGTGTCCCCGGAGTCCCAGCCCCTGCCTC
			TGCCCCTAGCCGGGGACCGGGACACTGGTCTGGGCTGCACACCCCAGGCCCGGGCCGGAGCCCGAGAAAGGGGCGG
			CCGAGCCTGGGTTGGAGGCGGCGGGTGGAGGGGGCGGGGACAGGCCCAGGGCTCGTCCCGGGGAAGGTGCGGACG
			CCGGCAGCACGCTCGCTGACCGCGGCTTTAGTGTTGCCAGGGCAGGTGGGAGTCCCAGCTGGGCCGGCTTTGGCGC
			GCCTCGCGCGGCTGCCGAGCGGTGGAGCAGCCTTCCCGCCTTCCCGCCGCGTCGCCGGCGCGGCTCTATCGTCAGC
			CTCCCTCCACACAGTTGAGCCCCAGCCGGAGCGGGGGCTTGGGATCCACCGAAGGAGCGGCGGCAGCGGTTGGACT
			TTAATTGGCCAGAGGA
110_RAP1GDS1_001	25	25	GAGGGGTGGAAAAGGCACTGAGCATGCTCGGTGGGGAGGGCGGGGCGCTCGTGGGCTGCGAGTCGGGGCCGGAGCT
			CTTCAGGCCGGCTCCCGCGCCTCCGCCCGCTCGGAGCCGCGCCCGCCAGGCTGCGCCCGCCAGTCCC
			GCCCCGCCCCGCCCCGCCCCCCGCCGCTCGTCCCCGCCGCGGCCGCGCCGCCTGCAGCAGCACCAGCTGCT
			CCTCCCCGGCGCCCCCCCCGCGGTCCCTCCCTGGCTGCGGGAGAGACGGAGGTAGAGGAGGACACAGAGCCG
			CGCCGCCCCGCACCACAGACCTTCGCCTCGCCCCCGGTTCCTCACCCTCGGGAGCAACATGGGTAAGTCATCCT
			TCCTCCGCCGTCATCGCCTGACATTTTTTTCTTTCTCGGCGTGCTGCAGGGTGGGAAGCATTTCT
111_RB1_001	35	27	GGCCCACAGTCACCCACCAGACTCTTTGTATAGCCCCGTTAAGTGCACCCCGGCCTGGAGGGGGTGGTTCTGGGTA
			GAAGCACGTCCGGGCCGCGCCGGATGCCTCCTGGAAGGCGCCTGGACCCACGCCAGGTTTCCCAGTTTAATTCCTC
			ATGACTTAGCGTCCCAGCCCGCGCACCGACCAGCGCCCCCAGTTCCCCACAGACGCCGGCGGGCCCGGAGCCTCGC
			GGACGTGACGCCGCGGGCGGAAGTGACGTTTTCCCGCGGTTGGACGCGGCGCTCAGTTGCCGGGCGGGGAGGGCG
			CGTCCGGTTTTTTCTCAGGGACGTTGAAATTATTTTTGTAACGGGAGTCGGGAGAGGACGGGGCGTGCCCCGACGT
			GCGCGCGCGTCGTCCTCCCCGGCGCTCCTCCACAGCTCGCTGGCTCCCGCCGCGGAAAGGCGTCATGCCGCCCAAA
			ACCCCCCGAAAAACGGCCGCCACCGCCGCTGCCGCCGCGGAACCCCCGGCACCGCCGCCGCCCCCTCCCTG
			AGGAGGACCCCAGAGCAGG
112_RBM15_001	23	25	CTTCCTGAGGGACTGGAGGGCCCCGACACAGCCGGAAAGCCTGCCCCCGCCCCTTGGCCGGCACAGGTACGACGGCGGG
			GAGCTCAGAAGTTTCGAACTCCAAGGGCCGAAGCACAGCCAAACACCCCCACGGAACTTAACAAATGTTTGTGGGGA
			GAACGCCCGAAAACGCGGGGAGGCGGGGCTGGCGCCACAGTCACCCTCTCGCGACATCTAAGTGACGTCGCCACAGCAA
			GCACGTGTTCTAGTCTTTCACCTTCAGTCAGCCTCCTCCGTTATACAGGCCTACCCCTTTAAGCGAGTGATGGACA

			GTTATTTCAGCCTATCAACTTCCTTGCCGACATCCAATCAGATTTAAACTTCTTTAGCCGCCGGAGGAGTTGGAA
			AAAGGGGGTCGAAAGAGGGAGCTTACCGTCTCTCGCGATATCGCTGTGAGCCTGCCTCTCTGGAAAAAACGCCGAA
			ACTGATGGCCCGACCTCCCAAATAGTGGTTTAAAGGACGGGTTTATAAGCCAATGAAAGGGATAAGGAGGTGGTT
			GCTGCTGTC
113_REL_001	24	24	AGAACAACCTGGAGGAGGGGGATTTCTCAGGAGCCAGCGGCCTTCTCACGCTGCTAGCCGTCACCTCCCGGCTCCC
			GCCGTTCCCTGCGCTCCCCGAAGCCCACCCCAAGCTCCCGCTCCCTCGACCCCCCTCCCAAGCCAGCCGCCGCAGCAG
			CGCCGGGGGCGTATGCGTGGGGGCCGGCGGGGAGCGTGCGCGGGGACAGGCAGGGGCGGGGCGCTGGGGCGGTCG
			CGCGCGCGGCGGCCGCGAGGTCGCCCCGCCCACGCCTCCGGGTGAGGGTTGCTGCGTCGGCCTACGTCAGCCGCG
			GGAAATTCCCCTCCCGCCAGGCTGCTCGCCTCTCGGCTGGGCCAGCACTCGGCTCTCCCCGCTCCGCCCCCTGCCC
			CTGGCTCCCGTACGGTGGACGGCGACGCTGGGTGACCCGGGGTGCAAGAATTCAGGGGTTGGGAAGGTGTGAGCCG
			CAAACCCAGCGGAGGGCGGGAAGAAGGAGGAGGCCTCTAGG
114_RET_001	25	25	TCCAAGGGTTGGACCAGTGCTGGAGGGGGGGAATCACAAACTGCCCTTCCAGGACCCTACCCTCTCTACTACCCCAG
			GATGCTGAAAAAGGCTATTCTGCCTCTCTTCCCCTGCTCAGCTCTTCCCGCCTCCTGGCCCCAGCAGAG
			GCCGCGCTCCCACTGCGCCTCTCGCCTCTGAGAAATGGCGCAGCAAGCGCTCCGCGGAGAGCCTGGAGGCGGGGCG
			CCCTTCTCTGAGTCCGCGGGTCGCACCCCGAGCCAGTCGGCCAGACCTGCATCCCGCGTAGCATCCCTGCCCTCT
			CTGTGCAGCGGAAAGGGCAAAGGCAGGGACTGC
115_RPN1_001	26	25	GGGGCCCCTGGCCACCCAGGACTCCTCGCGGGCCCCGAGGCAATCCCACGGACCCCCTGTGCCCCGCCCGCCCC
			GGGTCTCCGCATTTCCTGAGGCCTAGAGGGGCGCGGGCGGAGTCGGGGGACCGCCAGGAAGGGAGGCGGGAAGGGT
			CCCGGGAGCGGCGGCGAGGGGTCGCCCACACTCACCTGCACGCCCAGGTGCGCCAGCCGGCCTCGAGCTCAGGCT
			CCAAAGCCAGCAGGAAAGAGGTAGCTCGGGACGTGGAGCCGCCGCCCAGGTGCGCCAGGACCACCTCGGCCGTCAC
			CTTAGCCAGGTGGCTGCTTAGGTCCACTGTGCGCTTCACGTCCTCATTGATCAGCGGCGGTGCCTCGGAGGAGGCG
			CTGCCCGGCGCCGGGGCCCCAAGTCCCAAGCAACAGGAGCAGAAACAAGCCGGCGGCTGGCGCCTCCATGACCGGGA
			AGAGCAGTGCGCCAGGGCGGGTAGGGCCCGGGCGCGGTAGCCCGCCCTCCCGCCACTGAGCAGCCGTTCATTGGGC
			AAGGGCTGGTGACA
116_RUNX1_001	30	25	ACTTTCTAACTCTGTCCCTGAGAAGAGTGCATCGCGCGCCCGCCCGCCCGCAGGGGCCGCAGCGCCTTTGCCTG
			CGGGTTCGGACGCGGCCCGCTCTAGAGGCAAGTTCTGGGCAAGGGAAACCTTTTCGCCTGGTCTCCCAATGCATTTC
			CCCGAGATCCCACCCAGGGCTCCTGGGGCCACCCCCACGTGCATCCCCCGGAACCCCCGAGATGCGGGAGGGAGCA
			CGAGGGTGTGGCGGCTCCAAAAGTAGGCTTTTGACTCCAGGGGAAATAGCAGACTCGGGTGATTTGCCCCTCGGAA
			AGGTCCAGGGAGGCTCCTCTGG
117_SBDS_001	27	30	AAATAAAGAAGAAACCCTTGGCTTAGGCGCCAAGCTCGGACAGCGACGTCTCATGCTCACAGCAGGAATGTTCCAT
			TTCCTCCCCGGCCAACACCCCAGCCTGGCCCATTCACTCGACTTGGGCAGAGACAGGCCGCCTCGGAGGTGACGGC
			TCAGGCCCAGGCCCAGGCCCGAGGGAGGGGGCTACTCACACGCCGCTCCGCCAGCCGACGACCTTGTTTTTGTAGC
			AGGCGATTTCGAAGCGCTTCCCGGCACGCTTCATCCGTACCACGGCCACATTGGTTAGGCGGATCTGGTTGGTGGG
			GGTGAAGATCGACATCGCGGCTGTTCAAAGACCCAGAAGCCGGCGAACCAGGGCTGACCCGCGCCGTCCAGCCTGA
			AGGCCACCAGCGCCTCGCGGTAACGACCGATCGGCGCGCGGCACTGACCCAACCACCAGTGCGCGGCGCCGCGACT
			CACTAGCTTCAGGCAGCCGTCACAGTGTGTCTGGCAGGCTTACTTACTG
118_SET_001	25	27	GAGAGGAAGGGTGACTTGCTCAAGGGTACAAGCTTGCTGGGCAGGGCTTGGACTAAAACCCAGGAATGGCCCTGCG
			CGCGGATTACACAGCCTGGGGCTTCGCACACGAGCCCGAGTTTGAGTCCGATCGGCAGTTCCCCATCTGGCATCCA
			GAATGGGGTGCCCCCTGCT

119_SFPQ_001	24	24	GCCTGAGGAGGTGTGGTAGGGACCCCGCTGCTTGGCGGGGTGGGTGGCGGCGCCCCGGGAGGGGCCGAGGTGACTG CAGGCGGCGGGGTCGGAGTCGGGCCTGGCCCGGACCCTGGCGGGGCCCCCGAGGTTGGTGGAGTGGCGGGCGGGGC CGAGCTGGAGGCTGGTGGTGCGCTGCCTACTCCGGGAGCGGGGCCGGGTCCCTGAGCAACGACGGGCTTGGAAGAG TCCTGCGGCGGTGGCGGCGGCTGCTGCTGCTGATGCGGCGGCGGCTGATGCGGTGGCGGCTGCT GCGGCGGTGGCTGCTGCGGTGGTGGCTGTTGCTGCTGTTGGTGTGGAG
120_SFRS3_001	25	25	GGAAGAGGAGTCTGTGGGTAACCTGGAGGTCGACAGACCGGGAGGAACGCTCGAGGGAGCACCAGGCCTGTTACAA CGAGCGCGCGCCGACGCACGTCTCCACCCACCCGGCGCAACCGCCAGAGCGCGCTCCCAGCAACCGCGGCTCTCGC TGCGTTTGTAGCCATACGTCACGGCCTCTTCTGCTTCTCATTGGGGGA
121_SIL_001	30	29	GCCTCTCAAGGGGAAACCAGGAGCACAAAGCTCCACTTACCGCAACTTCCGCGGAGCTGAGGTCTGTTTGCAGGGT AGGAGCGGGAGCCGGCTCCAAGGAGCGCCACCGCCGACTCCGGCCCCCGCCTCTGGGACGTTGGGGTCGCGGGAACT GAGGCGGCAAACACAAGCTCGCGAAACTGAAGGCCGCGCCACGCCTGCTGACTGGTCAGAAACCTCGCCAGTCAGG GAGCGGGGGTGGTGCTAGAGAGCCGCGCACGGTCGCCGTTACGTATTGGTGTGCCGACCAATCAGCGCCCCGCACT GGTTCCGCGCTCGACCAATCCCAAGTCTTCTTGGAGAACTG
122_SS18L1_001	23	25	GGGGCCAGGGGTGCTCAAGATGGCGTCGTCACGGCCCCCGTGCCCCGGGGCCCCCACGCGAGGCCGGGCCCCAAGCGA GGCGCTGAGTGGGGAGAACGAGCGCTCGCGGCTCACGCCAAACGCCGCCTCTGCAGGCACTCGTGGAGACCGGCAG CGGGGCCCGCGCTCAGCTACAGCCCTGACCGCCCGCGCTGCCCCCGCGCACGCCCGCGGCGCCCACAGCGCCG CGCCCGGCCCCGGCCCTCTCTGGGCTCCCCCAGCCCC
123_SS18L1_002	24	30	GCTGGGAACTGTCCTGGGCTATGCCGGGCGCACGGGGACCCCTCGGGGCCGGAGCCGCGCGGCGAGGGCTTGTCGCGC TCCGCAGCCAGCTTCGGTGGCGACGGCGGCGGTACTCGTTTTCTGCGCTCATTTTGGTTAGTGGTGAGGGGCCCG GGTCGGCCTCCGGGCGCACTTGCGACCGCGGGGACTGTGGCCGGGGCTGCCCCTCTTGCTCCTGGAGCGAGGCGCG AACGATGGAGGCACGGAAGGACGCGTCCCGATCCCCATTTGCGGGGCATCGTTACGCAGCCCGGCCCCGTAGGGAG CGCACCGCCCCCCTCCGTATCCTCGCGGCTACGCCGGGTTTCAGCGTGACACCCTCGCCAGCCGCCTCGCCTAACAA ACTTGACGGATTTGCTCCCACAACCTTTCTTCTAGCTCCGTAAGTTTCGGCCTTGTGGTTTTCAAGAGACAGCGTTTA TGTGGGTTTGGGACACCGTTATCCAAAGCCCTAAGTTTTGAAATTGAGACT
124_SUZ12_001	27	23	GGGGCAACAAACTAAGGATCTAGACTCGCTAAACCGCTCGCTGGGTCCTTCTCTCCCCACAATGCACCGGGGCCA GCAGGAAGGCCGCTCCGACCCCTAATTTTCCCGCGAATTCAGTTCAAAGAGGCGGCCGGCCCGCGATCGGCAGCG CGCACGGGCCAACCAAGCCGCGCCTCCGCGAGAAGCGCCTCCGCGTGACTGACGGGGAATCCGCGGGCCAACGGG CTGGGCGGCCCGGCGGTGCGCGCTCCCGCCGGCCAATCAGAGCGCCGGGCGGGGGAAGTGGGCGGAGCGAGGCCAG GGTAGGGTGAGCGGCCTCCGAAGCGGAGCGGGGCTCTGAGGAGACACTTTTT
125_SYK_001	25	25	TTGGAGCTTGTTGGTTTGGTGACCAAGATACACTCCAGGGAATATGCCATGCAGTGGAGTCTCTTCCCCGGCACTG CATAGCAAAAAGGAAAGGGCCGCTGGGTGTCTGTGGGTCCTGGGCAGTCACACAGAAGCCACCGCGCTGGCGGGGAGGA GGGGGACCGATGCGGTCCATGTCCCGGGCAGCCCCACCTTCTCTGCCTGCGAAGGGCCCTTGTCCGGCGGGAGGAG AGAGGCGCGCCCCACCCGGGCTCCTCTACACCTGCCGCCGCCTGGGCCGATTCCGCGGCCTCGCCCGGCGCTTCA GCCGATTCCCGCCCAGCTCCGGGCTCATGGGCGCGGTCAGCAGGGCGGCCAGGGCGGCGCGACACTGGGA GGAAGTGCGGGCCGCCTGCCCGGGCGCGTTAAGGAAGTTGCCCAAAATGAGG
126_TCEA1_001	29	25	GCACCATCTTGTCCATCTTCTTGGCAAAGCGGACCACTTCGTCCTCCATGGCTCCGGCAGGTCTTCTCCGCGCCCA CCCCGCTGGCAAGGGGAAGTGGGCGAAGCTGGAGCGGAAGACACAGCAGGAGCGACCCCCCGGCGCGCAGCAACCCC CACCACCGCAGGCCCGGCCTAGGCCCCCTTCCTTACGAACGAAGCCCGCGGCGGCGGCGGCGGCGGCTC CGGCTCCTCCTCCCCAGGCAGCGACAATCGAACACCGCGCGCGACGTGCAGGCGCTACCAACTGACTGCAGATCGC

			TGGTGAGGGGCGAGCCCATGTTCCCGCCAGGCGGGCGTCGGGCTAGTGGGCAGGCGTGGCTTCCGGCTAGAGGGTC
			GTGGAAGGCGCCCGGTTTTGCTGCGCGTTCACCTCCGGTCCCGCCCCCTCACGGGGCGGGTTTCGGCCCCCTATT
			GCATCGGGACATCCCGGAGTTTTAGAACTCGCGGAGGCCCAAGTATCTCGAAACGGGGGCAGATTCCGAGCATGGA
			ACTTTGGCAGGTTTTA
127_TFEB_001	25	23	GGGAGGGAGATGGTACTTCCACCCGCCCCCCCATCAGCCCAGCCCCCGGGGCGTGGCGCCGCTCTGGCCCTCCC
			ACTCCCCCCCGCTGGCCTGGCCAGACTCAGCCCCCCGCACACCTCCCCTACCTCCGACCCCCCTCTCAGGCATCGCCGG
			CCCCAGCCGTGTCCGGTGGAGGGGAGTGGGCGCGGGGCCCGCGCGTCCCTCAAACTTCTTGCGAGTTCACCATCA
			CGCCTCCCGCCCCCTTCGACTCCCAGCTCCGGGCCGGGAAGGCCCATGCCCGCCCCGGCCCCCTCCCGCCCGGTTACAT
			AAGGTCGCGGAGAAGCCGCCCCCGGCCCCGCCTGAAGGGAGGGGCCGAGGGGGCTCCCGGCTCGGCGGGCAGCGC
			CGCTCGGGCCACGCGCTGGGCGCCCGGGGGCGGACGGACTGCGGGTGGGTGGCGGCGCGCACGGTCCTGCTTCCCT
			CTCCTGCCGGCATCCCCCCACCCTCCCACCTGTCTCCGGGACCCACGGGATAGGGGCCAGGGAGCCTGGGT
128_TFG_001	27	22	TCATCCAGTGAGAAAGCAGGGACTCTTCGGCCTAGGCAGCCGGGACCCAGCCAGCCCTGCGCCTCGCCGTCGCG
			CATGCGTCCTGGGTATGTCCACGCGCAATAAGGAGGGGCGAAAGGACATTTTTTTTTTTCTTGCTCCCGCCTCTGT
			TCTTCCCCCACCTGCCACGTACAGAGCCCAAGTTCTCGCTAGGCTTGTTGGTCAGCGCGATTGGCCGGGGCCCGC
			GCGAGCCTGCGAGCGAGGTGCGGCGGTCGCGAAGGGCAACCGAGGGGGCCGTGACCACCGCCTCCCCGCGACGCCC
			CAGTCCAGTGGCCTCGCGTCCGCCCCATTCAGCGGAGACCTGCGGAGAGGCGGCGCCGGCCTCCGCAAGCCGGT
			ATGGCCACTGGAGACGGGGGTTGCGGGCGCTCTGTCCGAGGAGGCCGGGAGACTAGGAGGCGCTGGGAGGGCCTCG
			TTCGAACCGCGCGGCAGCTGGGGTCGGAGGCACTGTGGGAAGGGGGCTGGAG
129_TFPT_001	28	23	TGCTTAAAGGCCTTGCTTTCTTGTCTAACGCCGCAACCAGTCCTCTGAGTTGCCAACGTCTTTCTTCTTGTCTCGA
			CGCCCCGTCGTCCGGCCACAGCGATTCTCTGCTTAGCAGGATCGGTCCACAGCGGGACGTGAGTCCCTTTCCTCCT
			CGCGGCTTACCGCCTCTCTCCGCCTAGTGCCAGGTGCTAATAAAGTTGTTGTTTCAAATGCGGCCAGGAACATCGC
			GAGCGGGGACCAATCAGAGAGTAGCTTTGCCTCTATAACGGCGCGAGAGTGAGACGTCATCGGTGAGCGACTAACG
			CTAGAAACAGTGGTGCGCGGAGAGGAGGTGAGTGTGATGGAGACCACGGGGAGCGGGAGGCTGGGCTCCTGGGT
			CTGGGAGAAGAAGTGT
130_TFRC_001	26	30	GGCTCCCTATGGCTGCTGGACAGCACCGGAGCGGCCGCTCCAGCCAGCCCCGCAGGATGAAGGGAGGACACGAGGG
			TCGGTGTAGTTCTAGAAGCCCGCACTCACACTAGCGCGTCCTCCCGTCCCGAGCCGCCACCCGATATCCCGACGCTC
			TGAGGGGATGGCGGCCCCCTAACCGGCGGTTTATAGCCTGGCCCCGCCCCCCGGCCCCCAGGGGGGCTGTGCGTCACT
			TCCTGAGGCACGTACGCTCGCGAGGTGCTCTGACAGATCGCCCGGGGGCGGGATGCGCGCGCAGCGGGCGGGGC
			CCTATGCGGAGGGCGCTGCGGGCGAGGCGAAGGCCAAGGGAAAAGGCGCCAAGGCAGCAGGTGCCCCGAGGAGCCG
			CGCGATGGGCGCACTGGCCTCTGCCTCGGCGCCTTCCTCCACCCTGGTAGCCTGGCAGCCCTCCGCCTGACCTTGAC
			CAACCTCCAGTCCCTGCAGTG
131_THRAP3_001	24	25	TGGTTCCAAAAATGGTGGGGCAGTGGCGTCAGCAACGCCCCCGCCCCTTCCGTCCACCGCCCTCCTCCATCTCCAG
			GCCACCCAGGCGGGGGGAGGGGACGGCCCCGAGCAACCCACGTGACCGCCGACACAACCGAGCGCGTGACGCAAAGCG
			GCGGGCCCAACGCTCGCCTTGTCTTTTGGGAAACGTAGTTCTGATGGCAGCCAAGTCGGCCAGGAGAGGAGGGCGT
			AGGACTACATTTCCCAGGAGGCAGCGGGTCTACGCCGTCGCCGTCGTCGGAGAGCGGAGACGCTGGGCGCGCTGTG
			GGGCGGGGGCGAGGTTCGGGCTGGTTGTTCCGTTGCGAGCTGCAGCTGCGATCTCTGTGGTAGGCCCAGGTGAG
133_TLX1_001	27	24	GGGAAGCAGAAGCCAGAGAGGGGAAGAAATACGGCGCCCCCTCTCTCCCTCCCCCTTCTACTTTAGCCTTTC
			TGCGCACTTCGCTTCCAAGTCTCCGCGCAGCCAGGAGCCGCTGTTGCCTCCCAGCCCCTGCTAGCTGCCCCCCGAG
			CCGAGCGCAGCGAGCGCCGCCGCCCGGCCCCCCGGTGGGCCAGGGCCAGCATGGAGCACCTGGGTCCGCACCAC

			CTCCACCCGGGTCACGCAGAGCCCATTAGCTTCGGCATCGACCAGATCCTCAACAGCCCGGACCAGGGTGGCTGCA TGGGACC
134_TLX3_001	27	25	CTCAATTTCCCCTGGATGGAGAGCAGCCGCCGCTTCGTGAAAGACCGCTTCACAGGTGAGCAGACTGGCGACCAG GCTCCAGGCCTCCGCCCTCTCGGGGCCAGAGGCGCCGCGCCCTGTGCGCTCCACTCCCGGAAACCATTTCAGAGGC CCAAGCGCGGCGGAGGCCTCGGCCCCCAGGGCCCCGGGCAGCCGTGGTGGGGAGGGTAATCGGAGAGTTGCAGGAAA ATAAGCCCGTGCCCGGGGGAAGGGACAGGGGGCGAGGGGGGTCTCCCCGACCGGCTTGGTGTCTCTGGAAACGCGCGC GACCAGCGAAATAGCGGAGCTCTCCGTGTCCCACGGGGCGCCACGGGGTCCGCATGGGGCCTGAACGGTGGCGGAG CCGGGCTGGGCTTCAGGGGCCCTCCTGTGTCTC
135_TMPRSS2_001	24	25	GAGGGACCCATAAGGGACTCTGGGGCGCTTCCCGGGCCCGGCCACAGCGGCCAACCTGCCCCTCTCCGGTCCGCGG CGCAGCGCTGCCCGAGGGCTCGAGTTTGGGTTAAGGAAGGGGATTCTGGGGAGCGCTCCTGGAGTCCTGGGTGAGC CCCCGGAGCTGCTACCTCACGAGCTCCTGTAGGCGGCCCGGCCCCGTCTTGGCCTCCGGGGAACCCACTGTAGCCTC TGGGCAAGGACCCAGGGTAGGCCTTGGGGACTGCTGGCCCAAGCACGAGTGGCGGGGACACAGCGCCGGACGCCCA AGACCCTCCCCAGTCCGCCTAGGCTGGCATTTCTTGGCCCCCACCAGCGTCCGGTGGAAAGTGCTCCCCCGGATGG TCCCAGGTCTCTCGGCACCACCGGCCAGGGCGGGAGTGAGGAAGTGGTGGGACACAC
136_TNFRSF6_001	28	22	CTCAGACTATGGGGATTTTCTAGGCTTGGTTTGCCAAGGCCAAAGGGCTACAGAGTAACCCCGTCCCCACATGTAT TCAGCCGACTCCATGCCAGGCGTTTTACAGATCCCGAGACCACCCCTAAGCAAGACCCCTAGCCGGAGTCGCCCCT CCGTCCCGAGACTCCGCGCCCCTCAATGCGTCACCCTTCTGAGCGCCCGGCCTATCTGGCCCCGGAGCGCAGCCTG TAACGCTCTCAGCCCCGGAAGCCTCCTGTTACGCGCCGTGCCCCCGGAGGTGCGGCCGCTGGGACCAGCGCCGGCC CTGGCTCCATTCGGGTCGCCCAGCCCGGCCAGGACTGGCCTCCCGCTTCCAGCCGCTGCCGGCACCCTCAGCCGTC TGGCCTCCCCGCGGAAAGGCGGGCGCGAGGCATCCTGGGAGTCGCAGTCGGCGGTCGACTCACCCGCCCTCACAGAG GAGGTGGGGGA
137_TOP1_001	27	25	TGTTACACAACTGCTGGGGTCTGTTCTCGCCGCCCGCCCGGCAGTCAGGCAGCGTCGCCGCCGTGGTAGCAGCCTC AGCCGTTTCTGGAGTCTCGGGCCCACAGTCACCGCCGCTTACCTGCGCCTCCTCGAGCCTCCGGAGTCCCCGTCCG CCCGCACAGGCCGGTTCGCCGTCTGCGTCTCCCCCACGCCGCCTCGCCTGCCGCCGCGCTCGTCCCTCCGGGCCGA CATGAGTGGGGACCACCTCCCACAACGATTCCCAGGTACGGCCCGGCCTGACCCTGGCGGCCCCGGACCCCGGCCTG GCCGTCCCGCGACCCCCCGGCGCAGGCCCCGACCCCAGCCCCGGCCAGCTTTGACAGGCCGGAGCCCCCGGTG AGGGGCCGCCTGCCCGGAGTAGATCGGCTCGCTAGGCCGCGAGCGAGGCCGCGAAGTTACAGTTCGAGGCAGGGAT GGCTGCCCCTCTGTG
138_TP53_001	27	26	GGAGACAGGTCTGAAGCCTGGAGAATGAGATGCAGAAGAGGTGCAAGACCTGCTGCGCCCTCTGCAGGCGGCGGGGG GGGCGGTGCAGGTGCTTTAAGAATTACCGCGGGACTCGGTAGGGGGAGCGTAGGCGCTTCTCGCCAAGATAGAAGC GTTCAGACTACAACTCCCAGCAGCCACGAGGAGCCCTAGGGCTTGATGGGAACGGGAAACCTTCTAACCTTTCACG TCCCGGCTCCGCGGGTTCCGTGGGTCGCCCGCGAAATCTGATCCGGGATGCGGCGGCCCAATCGGAAGGTGGACCG AAATCCCGCGACAGCAAGAGGCCCGTAGCGACCCGCGGTGCTAAGGAACACAGTGCTTTCAAAAGAATTGGCGTCC GCTGTTCGCCTCTCCTCCCGGGAGTCTTCTGCCTACTCCCAGAAGAGGAGGGAAGCACAGGTGGG
139_TPM3_001	26	25	CCTGCTGCTGCAGAACCTGGATCTTGCGCTTCACCGCCTCGATGGTGGTGATCCCAGCCATGGTGCCCACCCAGCT ACTGCTCGCGCTCCGGTTCCTGCCTCCTCCGCTCGGCGTTGCAGCCTCCTCTCACCCTTACTTCCGCCTGCTACGC CCTGAAATACCGGAACTCACCAACCCGCCCCGGATGTGACGTCCCTCTGCCGCCCCTCCCACCGCCAGGCAGGCGG GAAGGCAGTCCACTGGAGGGAGAG
140_TPM4_001	22	25	TCCTTCCTGGGCCTGGGACAGGGGAGGGGGCGCCGCCTCCGGGTCGGGCGGGGCCGGCCAAGCGGGAAATGGGGGG

			ATGGGGCGGAGGGGGTGAGCGATCTCCGGGTGGAGAAGTGGAGCGGCGGGAGGGGGCGTATCGTGCAGGCTCCGAC
			TCCGGGGCTGGCGCCGGGTCCCGGGCCGAGGGGAACCCGCGACCGGACTTGTGGGGGAGAATGAGGATGAAAACG
			TGGAGCTTCCATTGTCTAGGGTTTGACCGGCCGACAGGGATTTCGACGGGGGACCGGGGATCTGGGGAGGGGGTCG
			CACTTTCTCGCCTCTTTCGCGGCTTCCCGGCTTCTGCTTGCTTCCCTGACCGTTCCCAGGGGCGCGGCCGGCGACGT
			GTCTGCTCCAGGCGGCGGGGGGATGGGGGGTGGAGGAAGTTCAGCCCCAAG
141_TPR_001	25	25	GTGGGGCCAGGGACCCCAGTGGCAGCGGCCGACGGGGTAGAAGCGGAGAAGAAAGGCGAAGACCAGCAGGACCCAG
			ACGCCTGGGCCGCCGCCTCTATCACCTCGCTCGGTGGCTCGCGCGCCGCCCGCCGGAGACTCCCGCGGCGGGA
			CCCTGGGAAATCGAGTCCACCCTCAGCGGCAGCGTTTCAGCAACAGCACCTCACCGCCCGCGACCGAAGTGCGCGC
			GCAGCCGTTGGAAGCTACGAACCCTGGGAACCCGAGCTCAGAGGCTATCCCTGATCCTCTTGCGCACCCAATTTTC
			CGGCTTCCAGCTCCACCCACTTCAGGCCTTGTAGGGCTCTGGGAAATGTA
			GTAGCCTTTGGCTGGGGTTGGTTATGAACTCCGACACAGCGGTGGTGCATACGGAAGGGTGGTAGCCGGGACGGTT
			CCGGTCCCTGCGAGCGTGTCCCGGGCGTCTCCGCGGAAGTTTCACCTGCCGCGCTCGATCGCCGGGACCTCCT
142_TRIM33_001	25	27	GGGTCTCTGCTGTGCGTAGACCAGCCGCGTTCCTTGGGTGGCCGTGGAGCACTAAAGCGGGGCTTATTGTTTGTT
			TGGTTTTGGTTTTTTTTTTTTTTTGTTTTTTGTTTTTGAACTGAGGATCTATCAGAAATAGGCTGAAAA
			GACCGAGTGAGGAAGAAACTCTTTAACAGCT
			TCTTTCTCAGCTCTAATGACTTTCCTCAGTTCCGTGGGTTACTCCTGCCAACTCGACGCCGGCCGCCATGACACTC
			GCTCGGAAAGCGGCAGCGGATCATAGAAAAGCGCCGCGGTGGCGTAGACAGGCCCCGCGAAGCCGCCGGACGTGTC
143_TRIP11_001	30	25	CTTGGCGCAAGGGAGGCTGGGATCGCGGAGGACCGAGCGCGGGCTGGATTAACCGCAGCCAGTGCCTAGCGCAAGG
			TTAGGTGCATGCAGGCGGCCAGCTTCGGCCGGGAAGGAATGGCCTGGATAACTGGGGCAT
			GGAAGGAAGAGGCTCTTCCACTCATAACTGACGATGTGGGTTGGACGAGAAAAAAAGTAAGGAGGGTTTTTATGGA
			GGGGGGCGGGGCCGGGCGGAAGGATCCGAAAGGAGGCTGCGAAGAGATCTTGTGACTCCGCGAAGGAGGCAAAAAG
144_TSC1_001	30	25	AAGGGCCGGCCGGCGGAGGAGGCCACGCGAGAGCCCGAGGGGGCGGGCGGTCACGTGACTGGCGGGCGGG
			GGGACGCGGCGGAGAGGCGTAAACAAGCTGGCGGCGCCTGGGTGTGGTTGGAGCGCCCTGCCCCTGCCCCCCGAGT
			CGTTTCTGCCCTTCGCTTGCGTGGCGCCCTCCGAGGGTCTCTCTGTGGGCGGCCTCAGAGCAGCGATCCTGTTTCC
			CAAGGAGCTGCTGGGGCCCGCGTGGGTGAAGGGCCTGCTTGGGAGCTTTGGAGTTGC
			AGAACTACAACTCCCAGCAAGCTCCCAAGGCGGCCCTCCGCGCAATGCCGCTACCGGAAGTGCGGGTCGCGCTTCC
			GGCGGCGTCCCGGGGCCAGGGGGGTGCGCCTTTCTCCGCGTCGGGGCGGCCCGGAGCGCGGTGGCGCGGCGGGG
145_TSC2_001	30	25	TAAGTGGCGGTCCCCACGGGGCAAGTGGCGGTCCCCACGGGGCAGCGGCCTAGAGAGGCGGACCCCGCAGTGTCCG
			GGTCCCGGGCCCTCACCCGCGCCCCACTGCAACCCGACTCCGGAGCTCCGAGCATCCCTTAGTTTTAAGTCATGGCG
			GGTGCGAACGGGTCTCTGCTGCAGGCGGCTCCGTGACAGCTCCTGCTTCACATGGGT
			GGGAACCTGGAATTATTTCTGCCATTCCCGATTCTTCCCAGCAGATGGCCCCAAAGTTCAGTTCCTGAATTGCCTC
			GCGGAGCCGCGGGCTGCAACGTGAGGCGGCCGCTGCCAGTCGACTCAACCACCGGAGTGGCCCCTGCAGTTGGATA
146_TSHR_001	28	25	GCAACGAGAATCCTCCAGGGGTGCAGGGCGACGGCTTCGGCCGCACCGCGGGCTAGCCAGGGCTGCGTGCCCGCCT
			CTGACCCTCAGCAGAGGTGTCTCTGGCCAGGAGGAGCTGAAGTTCTGCAGGACATTGGTCCGCCCGCGGACAGTCC
			ACTCCGCGGGGACTTTCTCTGGATAAGGAGTGCGTGCGAGTGGCTCCCAGGCAGACAGGGTGTCTAGAAGGCTACA
			CGCTAGGGAAGGTGGCTCCTTGGATT
			GGTAGGGTCTGCATTTGGAAAGCCGGGGGCGATGCAAGACCGCCTTGGCGTCGTCTCCCTCTCAGCCCCGGCTGAG
148_WHSC1L1_001	23	25	CTGTCGGATGGTCCCCCTCCCCCGGTTGCAAGCAGTAGGAGACCCGGCCGGCGCCGGCTCGCCGAGGGAGCGCC
			CTCGACCTCCCCCGGCAGGCGCCGGCCCCGCGCCCTCTTCCTGCTCTGCTGCGGCCCGGAGGCTTGTGGGTAACCG

			GGAGGACGACGTCAGCGCCCGCCGCATCCCCCGGGTGCCCCCCCAGCCGCGGGGGACCGCGACGGCTCCGTGACCGTC ACGTGCCGGAGGCCGCGGCTGCTCGCGGCCAGACCTTCGCATCGAGGGACGTGAGGGACATTTGTCCTAGAGGGCC CAAGATAAGAACGAGAGGAAGAACCGGGAGGCAACTCTCCGTCATCCTCTAGCCCCCCCGCATCCTAGGAAACGTAT GGAAAACAATGGAAGGTTAAGTGTGTCACAGTGATCTGGCCCTGCAGGAGTGTGCCGACCAGGTGATATTTCCTG GGGCCT
149_WT1_001	25	25	GGCTCCTGTTTGATGAAGGAGTGAGGCGGCGGCGCGGGGGTGGCGGCGGAGCCGGTGGCGGCGCGGGGCCGCCCA ACGACCCGTAAGCCGAAGCGCCCGGGGGCGCAAAGTCCAGCACCGGCGCCCACTGCGCCGCGCTCACAGGCAG GGCACAGCCGCCGCCGCCACCCAGGGAGGGGACGGCGGGCAGCAGCGCGTTCAGGTCCCGCACGTCGGAGCCCATT TGCTGCGGCTCAGACCCGGACGCCCCCGCGGCTCCTCCGGCCCTGGAGACGTTCAGCGCTGGCCTCGGCGGCGCCTA ACTTGGCCCAGATGCCGCCCCGGGTCCCGGACTCCCTGCTCTGGCTGCTG
150_WT1_002	25	25	TTGGGAAGCAGCTGGGTAAGAGCTGCGGTCAAAAGGGGTAGGAGAGGGGGGGTGTCCTAGAGCGGAGAGTCCCTGGC GCCACTGCCCCCGCGCGTAGGGGGCGCTCCCCGGCCTACTTACCCTGATTGCGAATAGCGGGCTGGCTCTCGAGGCA GCTGGGCAGGTAGGGCGCGTTAGGAAACATCCTGGCCTGGCCGGATGACGCCTGGCTGGGCGGAGGAGGACCGAAG GGCCCGTAGCGACAGGCTCCGGCTGTGCCAGTGAACTGGCCGGAAAAGTGGACAGTGAAGGCGCTCAGGCACTGCT CCTCGTGCGGCTCCGCGCCGCCCCAGCTCGGCTCCTGTTTGATGAAGGAGTGAGG
152_ZNF198_001	26	25	GGTGGGAGCCCAGCTCCAGGGGAGCCCCGCAGCTCCCTCCATCTTGGTTGATGGAGGCGGGGAGCTGCGTCTGGGTC TCTCCACCGTCGTGCCCGTCCCCTGTGGCCCCGCGGACGCAGACGCCAGCAGCCGGGGTTGTTCCCTTGGCCGAAT GGCAGAGTCCAGTTGGGGCTTCCCGAGGACAAGTTTCCCGGCCCCACGGGGTTTGGTTTTTAGGGGGTCCCAAGTT CCCACAGTCGTTCCGACAAAATGGAGGACGTCGTCTCCTCCTGCTGCAGCCATGGCGGGAGGTGGGGGACTATTCC CCACGGGGCGCGGCGAGGGTGGAAGGGCCTCCACTGCCC
153_ZNF278_001	23	25	GGGGGCTGCAGTCTCAGCCCCCCCCGGACCAATGCAAACGAAGCGCCGAGCCAGCAAACCAGCTCCCACTGCCCCTC CCCTGCCCGCTGAGAGTGGCGGCTAGCAGGGTGGGGGGGCAGGAACTGAGGGGTGCGGATCCGGGCCCCCCCAGCCT GCGAAGCGCACTCGCAGGTCGAGCGGGCGTCGTCCACCCCTTCGGAGCCCCGCTTTCATGCGTGAAATTCCCAGAAG TCGCCTGCGACCGCCTCCCTGCTTCAAACACCAGAGAGGGCCCGGGGTCCTGGCCGGAGACAGGCCGAACCTCCGG AGCTGCTTCTGCACCCGGTACATTGATCGATCTGATGGGCTGCGCGCCCGGAAGAGCTGGAGAGATGAAGCCAG
154_ZNF331_001	25	25	TTGCCTGCAGGGAAACACTGATGGCGCCCTTCCAGATACGTCGATTCCCGGTTATGAGCTACATTTCCCAGAAG CCCTCAAGGCAGGACGCCCTTAGGGTCGCGTAGAGTTGCATGCTGGGAAATCCTGACAGCCGCTTCCAACTCTGTG GATTTCCGGGTTATGGACTACATTTCCCAGAGGCCTCTGGGTCACGGCTCCATTTGCGCCGTGTAGAGTTGCATGC TGGGAAACACTGACGGGCGCCCTTCCAGCTGCGTCGAAGCTTCTCTGGTTTCGCATTACATTTCCCAGAGGGCCTT GGGGCACAGTCCAATGAGGAGCGAGCCGGGTGGCCGGCTGAGGGGCGTGCTTCATGCTCGCGGGATTTTTTAAAAAT GGTTTCTCCTGGATCTTATCCCAACTGCGCCTGAGACCTTGTTTCACCTCCTGATGTGCTGGGTGTGG
155_ZNF384_001	29	25	CCCCCCAACAGGCTCAGAGAAGAGCTCTGCGGAGAGAAGGCGGGAGCGCCGGAAACGAAAAGGGGGGAGGGAGGGA AATAGCAATGTAGGGGGGGCGCTAATGGAGAAAGAGGGGCGTGCAGAAGCCGAGTCACTTCCGGGAGTGGCTGGAA CACTTCCGGCGCCGCTAGCGCTGCGAGATATTCAGGGCAGAAGTTACGATAACTCGGGGCGGAAATAGCTTCTGCC CAGCGACTGGGAAGAGGGGATGTGACGCTATAGCGGAAGTGAAGGCGGGTTCCGCTAGGGGCAAAAGCTGAAACCG GAGGACTCCGGCCCTGAGCTTCCGGAAGGGACATCTGGGGAAGGTGGGGGGGTGGAAACGCCGACAGGTTCATGAAT TATCCATCAAGGTAGGAGAGGAGGTGTGGGTTCTTCAGATGCTGGGAC
156_ZNF9_001	28	25	AGAGGCTGTTTATTTTGAGGGTCCTTGCCTGCGCCACACGCGGGTCTGCACACGGCCCCCACATACGCCGCTGCGCA CGGCTCTCCTCCGCCTCGCCCACGCGGCCAATCAGCGCGCGGGGTTCGGCAGTCCAATCAGAGCCGCCCGCGGCAG

			GGCCGCCCACTAGAGCGCGGCGCGGGGCGGGTGTTTCTGCGCGCAGCGTCTTTTCCCGCCGTGCCCCGCGCGGC
			CTTTCACGCCGGGATCCGGGTCCCGGTGCTTCTCGGTTCATTCCCAGCTGGGTCCGGGCCCGGCCAGACTGGGTGG
			AAATCTGGCTGAC
003_IGF2R_003	24	25	GGTGCTCTGTGCCCTGGTGCTGAGCACATTGCCGAGAAGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGCTCATCGC
			CGAGAAGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGCGCATCGCCGAGAAGGAGCGGGTGCTCTGTGCCCTGGTGC
			TGAGCGCATCGCTGAGAAGGAGCGGGTGCTCTGTGCCCTGGTGCTGAGCGCATCGCTGAGAAGGAGCGGGTGCTCT
			GTGCCCTGGTGCGGCTGAGAAGGAGCGGGTGCTCCGTGCCCTGGTGCTGAGCACATCGCCGAGAAGGAGCAGGTGC
			TCCGTGCCCTGGTGCTGAGCACATCGCCGAGAAGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGCGCATCGCCGAGA
			AGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGCGCATCGCCGAGAAGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGC
			GCATCGCCGAGAAGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGCGCATCGCCGAGAAGGAGCAGGTGCTCTGTGCC
			CTGGTGCTGAGCGCATCGCCGAGAAGGAGCAGGTGCTCCGTGCCCTGGTGCTGAGTGCATCTCCACGACGGCAGCA
			CCTGATGGAGGGAAGCTGGG
005_SLC22A2_001	30	25	GGCCTTCCCTGCTTGCTTCCTTGAGAAAATCTCCACCATTTGCTTCTCCATCTGAGCCCTGAGCTCACTCTCTTAC
			CTCGGTGACGATGGACGAGCCAGGCGTCTCGTACACCCAGCCGTCCCGGCAGGGGCCCAGTGGCAGGCGGCTCCTG
			TTGGTGTCCAGGCTGGCCAGGGGGTCCACGCAGTCGAAGGTGCTCTGGTTCCAGTCCACCTCGTAGCGCCTACACT
			GTCTTGGGGAGGCTTCGCCCGCAGGTCCTGGGCCCGGCACCGTGTAGTTCAGTTCCTCTGCAGGACTCCAGCCGCA
			GCGCAGACTCAGCTCGGCCACTCCGGGGCTCCGGCAGCGGTGGTCAGGGGTGAAGCCCAGGAAG
006_SLC22A3_001	25	25	GGGCAGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCTGCCCCACATGGGCGCAGGAGGCCTCC
			GCACGCGCAAGGGCCAAGGGCTGGAGGGGGCTCTCCCGGGCACAGGCACCGGACCCGGGGCGCGCGCGCGTCCT
			TAGTCCCCGGGCTGCACTCCGGGCCGCTGAGAGATCGGGTCCCAGAAGTTCCGGGAGTGGTCGGGTGACCCTGGAA
			CTTTCTTCTTCTGGAGCCCGACCTGGGGCTGACTGCAGAGCAGG
009_SGCE_001	25	25	GCCAGGGGTCAAGCCTGGGGAGAGAGAAGCTGGGCCGGGGAAATGGGGTACAGGGTGTACTGAAGGAGGGGTACGG
			TGGGGTCCGGGACAGAAAGAGAGGCTGGTGCCCAAAGGGCGCGCTCAGGCGCCCGGAACCCGAGCGGGGGAGGGGG
			AGGCGGCGGCCTGTTGGCCCCGGGACCTCCACGTCGCGCGCAGGCCACTAACCTGTCAGCAAGAATGTGCCAGTGG
			TCGCGGGGCTCATCCTGCGTGTCCCCCGACCCTGTCCCGTCCAAGCACAGGGGTCTCCCCAGCTCCCCACCACCGGGG
			CAATTGCATTCTTGGCCTGGC
011_PON1_001	27	29	AGAAGACTGGTGGTTCCTGAAGAGTGCCAGTCCCATCCCCAAGAGGGTGAGCGCAATCAGCTTCGCCATGGTCGGG
			GATAGACAAAGGGATCGATGGGCGCAGACACCGACGGGCTAGGAGGCTCTGCCTGCCTGCAGCCGCAGCCCTGCTG
			GGGCAGCGCCGATTGGCCCGCCCCGCCCCTCCCCGCCGGGTCGGCAGCTAGCTGGGCCGACCAGGTGCACAGAAGG
			CGTGGCTTGCGGTCAGCCCCCACCGCAGGAGCTCAGCACTTTCAGCCAAAAGTCCCATTTTGCTCCTTCCAACTGT
			AAAGAGAGAAGACAGAGAATAGGTGCCTAGTCCAGTCGGGAGGGGAAATCAAACAAGCTGAAGTAAATTGCCATG
			GGAAAGGACAGTCAAGCTTTGG
013_PON2_001	26	24	GGTTCAACTAGCTGGGGAGGGACAGCATTCAAAAATTCTCCACCCCCGGCCGCAGGGCCAGGTCCCGCAGGAATC
			CCTCCCCCAGCCTGCGCCCTCCCCGCACCACGCGGCCACCCCGAGCCTGGGGACCGCCGAGGAGGGGCGCGCGGGA
			GTCCCACCTACCTGAGTGCCAGAAGCCTCTCGCCCAGGAGCGCCAGCGCGATCCCCAGCAAGCCCACAGCCACCAG
			CCGCCCCATGGCGCGGGAGCCGGGCGCGCTGCCTCGCTCCGGCCTGGCCAGCAGCTCCGTGGGCGGTGCCATCTTC
			CCGGCTCGATGGTGCCCGGCCGCGCTCCGCCCCCGTCCTCCGCCTAGGCCGAGTCCCTGCGTCGGGGCCGCGGAGGCT
			CCGCCCTGGGCCTGGCCCTGGTCTTT
018_MESTIT1_001	27	25	AAGGGGGCTTTGCTCTCCTAATTGTGCCCACTGTTCTGTGCAGCGCGGACCGGCGCATGCAGCGAGCGGGGCTGCG

			AGGGCGCTGCTGTGGCCAGGCGTCTGGCATGCTGACCACGTCGCGCTGCTGTAAAGGAAACCTGCCCCGCGCAGCG
			GCGGTGGCTGGAGCGGGAGAAACCGGACTTTGTGCAACTTTGGCCATAGTGGCCATCCCATGAATCTGTTTACTAG
			CTTGGTGGTGGGTCCAACAGAGCTTGTTGCTCCCTAGCCGCTTGCTCGTGCCCTTGGTGGTTACCGGTAGTTAAGC
			TTAGGGCGCATAGGGCCCTCGTGGCTCGCCACCTCTCACGGTTCAGTACCCACGCTTCGAACGAGGGATGGGAGCA
			GGCGCCACGGCCGGCACCCCAGAGCCCTGCTGCCCCTTAGTTCGAGCGGCCATCCTCCTGTGGGGCTTGTGGGCAG
			CCTGTGGGGTTTGTGGGCGGCCTGTGGGGTTTGTGGGTGGTCTAAGGAAAGAGTTGGGGCACTCAGGGGTCTGC
019_COPG2_001	25	30	GAGGACTGAGGGGTCTGTGTTCACCCGATGACCGTGGCCTTTTGATAATCCACTGCGGGGCCCTCCCGTTGCGGA
			AGGCGCTCTCCCCGGGCGCGGTTCTGGTGGGCATGTCTCTTCCAAGAGCGATGCGAGTGTCAGTGGTTCCCGAATCAC
			TTTGGAAATTGGCCTTTCACTCGCTGACTTCTTGGAAGCTACGACAAAGCACAGGCACACCCTGGTGAATGTGG
023_SYTB_001	30	25	TGATGTCTGCACACAGATGATGCCTGCATGCAGTGACACCTACACGCAGTGGGCCTGCCCGCAGTGATGCCTGTACG
			CAGTGGGGCCTGCACGCAGTGGGCCTGCCCACAGTGACGTCTGCACGCAGTGACGTCTGCCCACAGTGGGGCCTGC
			ACGCAGTGACGCCTACATGCAGTGATGCCTGTACGCAGTGACGTCTGCCCACAGTGGGGCCTGCACGCAGGGCGTT
			TGCTCACGGCAGGTGCGTGCATGGTGGAGGCGGTGCCGCGGGGCTTTGGTCCAGCCTGGTCAAGG
025_LSP1_002	25	25	CATGGCCAGGAAAGGGGGAGACAGGAGGGAGGAAGAGGGCGAGACAGCATGGTGGCCGGCGAGGGGCCGCG
			AGGAAACCTCATTCTGGGGCTCCCCAGGGCCCCTGGGCCCCATCCAGGCAGCTGCGAGGCCAGGCCGGGTGCTGCC
			ACATCAGCACACAGCTGCGGCCGCTTCCGTAATGGAGGCTGAGAGCCCCGCCGCCCCTTCCTCCCTCGGGGCTG
			GCTGATCTCCCATTCCCACGGAGGGGAGCAGGTATTTCCAGATGTGCATGCCGGAGAGTCGGCCGGGAGGACGCACT
			TTCCAGATGTGGGGATGTGTGTGCC
026_TNNT3_001	27	25	TGGGGTGCTCCCAGATGCTGAGAGCAGGGTTTGGGGACATGGGACTGGGGCGGTGGCCGCGCCTGGGCTAACTCTG
			ACCGTGTCTTGCTCGCTCCCCGCACGCACCCCACCCTCGGCCTCGAGTGGCGACGGGCTTTTCCATTAACCTCGGA
			CGCTTCTCCCATTGACCTCTGACCCGCGGTTTTGCCTCTTGTTCCGTGGCCCTCCTTGGCCCGTGAAGTTCATGAACC
			AGGTACGTGCATGACTTCGATGCCACATGGGCACGTGTGGCCATGTGGGGGGTGCAGGACCCAAGAAGGAAC
027_TNNT3_002	25	24	GCAGGGCAGGGTGGGGCAGGAGCAGAGGAGGCAGGGCCGCAGGACAGCTTTTGCCGCTTGGCTGTGTGCTCGCTCC
			CCGAAATTGCTCAGCCTCCCACCCGACCTCGCCCTCCTCCCTGGCCGGCCTTCCCACCCGGAGGGGCTCCCTCAGCC
			ACGCACTGCGTCCAGCAAAACCACTAAGTCAGGGAGGCCAGGGCGGGCAGCCCATTCATCGTCCTCACCGCGCTGT
			TCCTTCCGGGCCCTTGGCTGGAACGCTCAGGATGCCCCCACCGCTCACTCCCGGTGCACATGTGCCCCCAAGGCATCC
			GGAACGGGTGACCTCAGGCCCACCTGCAAAACCAAGAGCGCTGGCGGGCTCTCTGTGGTGTGCAGGGGGCTCCCA
028_TNNT3_003	25	25	GGCACACCCTGGAGAAGAGAGTGTCCGAGTGAGAGGGGTGGGCCCCTTGCCCGCCACAGGCCCCTTGCCCACTGCT
			CCCCCGCAGCCGCACTGGCTTTTCTCTTGCATGTGTGCTTGTGCCTTTGCCACCTGGAAGACACCGCAGAGGAGG
			ACGCGGAAGGTAAGGGCCCGTCCCTGCCGCCGGAGGTGCAGGACCCTGGCTCTAGC
030_MRPL23_001	25	25	CCAGGTTTAGGGCAACCCCAGGGGGCGGCGTGGCCGGGCTGGGGACAGAGGGTCCGAGCCAAACCCATGGAGGCC
			ACGGTGCCCCCGCGTGGGGAGTGGGAGGGTGGCCCGGGGTCAGGCCCGGGGCTGGTCCCGCAGCCAGGGCCGAGGG
			AGCTGTTTGGAGACGTTTCTGATCGTCACGGGGCGGGGCCACGTCGGCTGTTGGGTCCAGGCGGGGAGGCCCCGGG
			CGGCCCCCACCGCAGCGCGGGCGCGGCCTGAGGCAGAGGAGCTGGGAATC
031_MRPL23_002	25	25	CAACTGTGTCCTTGGGGATGTTTGTGCCGGAGACGCTGCGCTGGGGCCCAGGGAGCCCCCGTGAGGCCGGATCTCA
			GGGCCTCAGCGCAGAGGCAGGCTCCACATAAGGTCATGCTCCGTCACGGCCTTGGGGGTGTTAGTGGTGGCGCTGG
			GAGCACGTGAGCACTGGGGCACATGGGGCACGTCTCAGCGTCCGGCCGTTTTGTGATTTGAAGTTTGAATTCTCT
			GTGGGCAAAGGCAGCCATCACAGGCCTAGTGGGTTTCAACTCCAACGCACACCAGGGTGTCAGAGCATGGGAGGCC
			CCGGCCTCTGGAGAGCCTGTCCTTGGCTGGGTTTCAGCCTCGGAGGCAGAGTGTGAGGCCCCTGAGGG

032_MRPL23_003	25	25	TCTGGCTGGAGCCTTTGTTCTCCCCCTTAGGCCCATGGACAGACCTTCACGTTCCCAGATCTGTTTCCCGAGAAAG ACGAGAGCCCTGAAGGCAGCGCTGCCGACGACCTCTACAGCATGCTCGAGGAGAGGAGGCAGCAGAGGCAGAGCAG CGACCCGCGGCGGGGCGGCGTCCCCAGCTGGTTCGGGCTGTGACGGGGTGGCCAGCAGGGACGCGCCCCAGGTGGG CAGCTGTGGCAGA
034_MRPL23_005	30	25	AGGCTGCTGTAGCCTCACTGAGGAAGTGACTGTCCCAGGCTCTAGAGGTGCCTGAGGGCGGCCGAGGGATGGGGCC GGCTCCACAGACGTCCCTACCGTGGAGCTCCAGATGGTGTGCTCATGAAGGCGACATCTTCCTGGGCTGCTTCTCA CGAGGGGCGCAGGTGGGCTCCCGAGTGGCCTGGAAGCTGGGGAGAGGCGTGGATGCGGATGGCGTGTTGCTCTTGG GCTGGCCCCCAG
035_MRPL23_006	25	24	CATGCCTGCTGCCAGAGAGGGGGAGGGCCGAGCCCGGCCTCGCAGGTCTCATTTCCCGTCTCGCGTGCGTGGCG CGAGTGAGGGGTGCCCTGGGGGAAGGGTGGCCCCAAAGAGCTGGACCCCTGCAGTCCCCGCTGGGGCTCCCGCCTT GCCCTGCGGCCCTCGCCTCCCCGTCGGCAGGGACAGCGTGGGTCCCCCCATCGCCACATTGGAGACACAGCCTGTT GCGCCCCCCACTTTGTTAACTACGCTTGGTAGTCAGGGTGTCCCCAGTGGCGGGAACAGCAGCAGCGGTCTCCTCA GGGCCAGCGGAGGGCACGGCTTCTGCCAGCAGGACAGTATGGATGGCACACCCGCCGAACACTGCGGGCCGAGTGT TGGGGCTTGGAGACCCCA
036_MRPL23_007	25	30	GTCTGAGTGAGAGGGCCAGGGGCCTCAGCCGTCATGGAAACCCGAGCCTTGGCAGCAGCGGCACCCACTCCAAGTT CCGGGGAGCGGGGTGCACGCGGGAGAGCGGCAGGATGTGCTTCCCGAAGGCCCGAAGCCTGCAGGCTGCACTAGGA CGGCCCCTCCTGCCGGACCCCTCGCCCCAGCCTCCAGCTCCAGCCCTGCAGGG
040_H19_004	27	26	GTGTCACCTGGGTGGGACATGGGCATAGCACATCACCTGGGTGGGACACGGGTACGGCACGTCACCTGGATAGGGA CACGGGTACGGCACGTCACCCGGGTGGGACACGGGTACGGCACGTCACCCGGGTGGGACACGGGTACGGCACGTCA CCCGGGTGGGACACGGGTACGGCACGTCACCCGGGTGGGACACGGGTACGGCACGTCACCCGGGTGGGACACGGGT ACGGCACGTCACCCGGGTGGGACACGGGTACGGCACGTCACCCGGGTGGGACACGGGTACGGCACGTCACCTGGAT AGGGACACGGGTACGGCACATCATGCGGGTGGGACATGAGTACACAGCGTGTCATTAGATAGAGGGGCTTTCTCTTCT CTCTCCCCTGTGGCTGGGACCTACCCAGATATAAGTAATGGGATAGCCCACTTGGGCTTTGCCAGTTCCCTGAGGC TGCCATAAGGAAGCCCCAGAAACTGGGCTGATTGG
042_IGF2_001	25	24	ACTGGGTCAGGAGAAGCCCCAGGGGGACGTGGAACCGAGAGATTTTCGGGATGGAACCTGATGGAAACGTCCGTGG TCAGGAGGAGGCTGCAGGATGGTGGCGCCGGCTGCAGACTTGCGGCAGTTTTGCTCACTTCCGATTGCTGGCCAT CTCTGGGGGGGCGCCCCCGTGGGCGGGTCTTGGGTGGGTAGAGCAATCAGGGGACGGTGACGTTTGGCCTCCCTG AACGCCTCGAGCTCCTTGGCGAGCACGTGACCCCGGCGGGCACGCAGGAGGGCAGGCAGGCCCCTGCGCAGGCGCT GGGTGGACTGCTTCCAGGTGTCATATTGGAAGAACTTGCCCACGGGGTATCTGGGGAAGTTGTCCTGGGAGGGGAA GGGGCTGGTCAGCAGGTGCC
044_IGF2_003	25	23	GGGTGTAAGGAAGAAACCCAAGGGCCGCGAGGGAGCGACCAGGACGCTGCTTCCCGGGCGCTCCCGGGACTCCCAG ATACCTGCTCGGTCCCCGCGTGGGAGGTCCGCAGGCTCCCCCTCGCCCCCACTGCGCCTCCGCGCTGCGA GCCTAGGCGAAGCCGCGGCCGAGCCGCCACCGGGGGCAGGCTAGTCCCCGGCTTGGCTTGGGGGCCCGGAGCACCC CCGGTGGCCACCTCCGGCCTGCCCCGGAGCTTTGCGCGCCGCGTTCGGGCCTTCGCCAGCACACCAAACAAGGGTGAA ACCAGTTTTGTTTGGGTAACACTGAAGAGCAGAGGAAGTGGGGAGGAAAATGAGAAACACGGGGCCCGGGAGGAGG GGGGTGCAGGGCTGCACGCCGCTGGGGTGCCAGGGGTCTCTTT
047_ASCL2_001	27	26	TCTCCACCTTGCTCAGCTTCTTGCTGGCGCCGCCGTGCGGCACGTGCTGCCGCAGCGCCTGGAAGCCCAAGTTCAC CAGCTTCACGCGGTTGCGCTCGCGCTCATTGCGCCGCGCTACGGCCGCGTCGCCTCCGGTCTCTGCGGTGGCC GGTCGCCGCCGCCGGCTGCAGCGCAACAGTTCCGGGGACGCGGGTCTCCGCCCGGGCAGCGCAGCCGACACGGGACGG

			GGGGCGCAGGGGGCGCGGACCTGGGCAGTGTGCCGCCGTCCATCGCGCCTGCATCCACCCGCCCGCTCCAGGTCCC
			GGCGCGCCGCAGGAAGGTGCAGGCAGAGGAACCGGAGGCGACGGGGAAAACTGTGGCGCCCCCAAGGGGCTTCTGG
			CACGGCGCCGCCAGGCAACTCCCCAGGGCACGCGTCCTAGGTCGTCTGGAGCCCGGGGATAGGAGGCCTAGTGGTG
			GCAGGC
051_BC050616_001	26	26	CCAGCAAACCCCTAGGGGTGGGAAAGCGTCGGCCCAGCTAGCGGGTCCAGCAGGGCTGCCCCCTTCACCGTGGCCC
			AGCGGTCACGACCCCACGTCCTCATCGCGGGCTGGGACTGCCTCTGCGTCTGGCCTGAGCGGGACCGTGGGATCCT
			GGGGAGCCCCGCCTCGGTGCACTGACAGAGCCCAGAAGGAGTGACGGTTACCGCTTCCGGTCAGGACCGGAAGTGC
			CGGGAACGGCATTCGTCCTCCGTGCGAGATGACGCACTTCCTGCCTGAGGCGGCCGCTGTTCTCGCGGCTTCCGGC
			AGGTGGCGCTGAGACCACGGGAAGCCAGCCTGGCTGTCGGTTAGCCCTCGAGCATTCTGGGAATTGCAGGCCTGG
052_TRPM5_001	29	25	GGTGCAGGCAGGTGGTCTTGCTCCAGCAGCGGTTCCGGCGCACCAGCAGGGCGAAGGCGCGGGCCTCACTGTTGCT
			GTAGCACTCGGAGAAGAGGTCTGCCCCCGGAGGCCCTGGCCGCTAGGACGAGACGCCGATGCCCGGCCCGGCCCCC
			GACGCCCCTCCTCCATCCCCTGCCCAGACCTGGGCTCTGCAGCCGCACCCTGCGTTCAACACGCAGGGCCCAGCCA
			GGCCTTCTGCCCCCCTCCGGCCTGCTCCGGGCCCTTCCTGAACCTCCGTCCTTCTCCGGCTCTGTCCCTCCCCAGC
			AGGACAAAGGGAACCTCTGCCACGCTAAATGTCCCTCGTCCTGCGGCAGGGCCCAGTGTATGCCCGGGGTGTGAGG
			CTGTATCGTCCTCACCACGTGCACAGCGGTCCCACACTCAGGGTCTGGGGCCGCCTCCACCCCAGGCAGAGCCGTC
			TGTCCTCTCCTATGGAGGAGGCCCCCTGAGGGCACCTGGAGCC
053_TRPM5_002	26	25	AAGCTGCTTGCCCAGGCTTGGAAAGGGCTCGGGGCCTGGGCCCGTGTGGTACAGGAGGGGGTGAGGGCCCGCGCCA
			CAGTCTACGCTGGCCGTTCCCTATGCGGTACTGCCACCTGCCGGCCGTGTGCTGGCTCTGCCCGCTCCCTGCTCTT
			CCTCCAGCTCGAGTCCTGTCCTCCCAGAGCTCTGCCCGCTGCCCAAACCCTTCTGAGCCCCTGCCTCCAGGCCCCC
			AGCGGTCGTGGTGCTGGGAGCTGGACGTGCACCTGGGCCTCCTCCAGAATGCGGCGGTGCAGGACGCGGCCCAGCG
			AGGCCATGCCGACAGCAACCACACGGACCTTGGTGGACGTGCTGGCCAGCGAGTGGTCGCGCACGGCCTGCCCGAC
			ATGCCTGGCCAGGCCCACGCGGAGGGCACTGGTCAGGATCCAGGC
054_KCNQ1_001	28	25	GGGAGGTACCTGACAGTGGTGGTCCCATCTCACCCTCCCGGTCCAAGGGCCCTGGTGGGAAGCGACCCGAGCGTAT
			TCGCCGCCCGCAGCTCGCGCGCCTGGGCACCCGGGGGCGCTCACAGTGATCGCGGGGCCAGCACACCCTCACCCAG
			GACATCCCTTTCCTCCCCCCCAACCCCCAACTCCGGAGTGGCTCAGAGGGAGGGAAAGTAGATGCCGGCACCCTACCC
			CGCCCCCTCCTGCCCCCGCTGTGCCGTTCTCGGTCGTGGTATCGGCCAGGCCTTACCCCTTCCTCCCTGGCGCAGCT
			GGGGTCCTCCTCCGGGCCAGGCAGAGCAGGCGGCATCAGAAGTGGGGGCCAAGCAGGTGGGTGAGGGCAGGGCA
055_KCNQ1_002	25	25	AAGGTGCTTCCTGAGAGCTGGTGTGGGGGAGCTCTGTCCCAGCGCCACCTGCCCCGTCGGAGCTGCGACCCCGGAG
			CAGAGGAGGGGAAGGAAGTGGGGAAACGCAGAAACACAAACTCTGCACTCTCCCTTGAAGTTCAGAGGCGCTGCTGT
			GTCTGGGGGTGCGCATCTTCTCGCAGGCCCGGCGTGGGGAGGGAGCCGGCTGGGGAGGGGACCACCTGGAGCCCAG
			AATTTGGCTCCACACCTCCGGGAGGGTAGTCCAGGTGTGAATCC
056_KCNQ1_003	25	25	GAGGCTTCAGGCCTGGAGGAGTGAGGACGGCTGTTGGGTTCTTGATTCCAGCAGAGGGAGGCTGTGCAGGGTTGCA
			GGAAGGACGGTTGGGGGCGCTTCGGGGAGGTACGAGAAGCAAAGGTGTTTGCAGCCCTTGGGGCCAGGCGGCGGGA
			AGGCCTGTAGACGCCAGAGGGCGCTCGTGCTACATGCAACTCAGGAGCTGCTGGCACCCGCCAAGGAGTGCTGAGC
			GCGGGGAGCCCAAACCACAGCCTTGGGGAACCCAGGAGGGGCCGGGCGGGTGCAGGACCCGCATGAGGGATTCCGA
			GAGCACGATGTTTAAATGTTGGGGGAAAAAATGGATCAAAGCGATGTGTTCCCAGGGAGCCCCTGTT
057_KCNQ1_004	26	25	GACCCTGTAGGGAGTCTCTGGGCCTCCGTGACGGCCCTGGGCGGCCCTCTCTGTGGAACAAGGTCGGGTCCTGTCC
			TCAGCGCCCTGGCCTCCACTTGCTCAGGGCGCCCGCAGGCCCGCAGGTCCTCACCTGGTGTTTTTCACCTGGGACC
			CGCAGCTGCTCTGATGAGGAGCCTGCTCTGCGCACGGCCTGGGGCGGTTTCCCGCAGCACCATTTCTGCCGCTGCC

			GGGAAAAGACGCAGAGCAAAGGCACCTTTGCCCAGGTTGGGGAACCAGTGG
058_KCNQ1_005	25	25	AGGGCTGAGCCTCATTCTGGGGGTAACCCCCACCCGCCACTTACCGGAGTTGTGAGGAGTGGGCTATATTGAAGCC GGCCCTGTGCATGTGAACCGCGCTGGAGCGGCGTAGGACGCCCCAGTGATCGCTGGGACTCGCTGCCTTAGGCGTCT GCACAGGAGGCTCCCAGCCTGCGGTTCCTGGAGCCCGACACTGTGTGTTTCTGGCCTAGGAGCTGATAACCACCC TGTACATCGGCTTCCTGGGCCTCATCTTCTCCTCGTACTTTGTGTACCTGGCTGAGAAGGACGCGGTGAACGAGTC AGGCCGCGTGGAGTTCGGCAGCTACGCAGATGCGCTGTGGTGGGGGGTGGTAAGTCGGAAACTTCCAGGCATGGGG ACAGGGGCAGCTCAGGCTGAGGAGTGGGCAGGACATCTGG
059_KCNQ1_006	25	25	CTGCTGCCCTGCCTGCCTTCCCAGCCGCCCACTGGAGCTGTGGGCAGCGGACGCTACTCCCCAGCCCCCCAGCCCG CAGCAGAGCGGCACTCCCCACACCCACACCTGTGCAAACATCCGCCCGCTGGCCGGGAACACGGCCCCTTTGTGCCC GGCTTGGCATCAGTGCCCCCGGCCCCACACCGTCAGCTGCAGCCCGAGCCTCGGCCATCGCGCGCCCTGGCCTGGCCA TTGTTCCCGCCAGGCCCCGCGCCCCTGGTCGCCCTGGGCCCCCCACCGCCCAGGGCTGTGGGGCAAACAGCT
060_KCNQ1_007	25	25	CAGGGCACTAGTGGGGCAGGGGCCTGGGTGGCGCCAGGGCTCAGCAGAGGCCTGTCCCGCCCTGTGGCCTGGCGG CGGTGGCTGGCGTTCATCACTGTTCGTTAACGTGCTCATCGGTACAGCCTGGTTTCCCGCAATGTGGCCGCTTCTG CTACCTGAGCCCTCCGAGCCTCCTGCTGTGGCAGTTCTGGGCAGTCGCGTGAGCCGTGTGCACCTGCCTCTCTGTCC GCGTGTGCGCCTGTGCACCCCTGCCCGGGGGTGGCCATGGGGCTTCTCCCCACCCTCCTCCTCAGTGGCTGG TGGAAACC
061_KCNQ1_008	27	25	CCTGGCAGGATCTTGCTGAGGAGCTCCCTGGAGGTCCGTGCTGAGGCGACGCGGCGACCGTTCTGCCTGGAGACTG CGGCAGCGCTCCGACTGCCCCCGCCGCTGCCGACGTGGCGACCGCCCCCCACCTGCTGATTGGGCGGCAGCAGGGG AAGGCTTGCGGCGGGCTGCTGCACGGATTGGCTGGGTGCGGAAAGTGATGTGCCGTGTCCTGTCATTGGCCGAAAG AGTCTCGTTTTGATGCCACCCGGGCTCAGATTGGCCCAGCGGGTCCAGCGCCGCATGAGGCACTGGCTGGGTGTGA G
063_KCNQ1_010	25	25	ACACCCTCTCCATGGGGAAGGAAAACGTGCCCCCGAAGGGGCCTGTGTCCAGGTTCCTGCCCACTCAGCCCCTCGGG GCCGTGTCTCCCTGCGTCAGAGCTGGGCCTGAAGATAATGGGCCCACTGAGGTGCAGGCGGTGGACAGACCCAGGA AGACCTCGTGGGTTTCCCAGGAAGACAGAGACTGGGAGCCATTCTTCCCGGCGGCAGCGGCTCTCGGCCTGTCCTT GTCCCCACACAAGCCCCCACTGCTGCGCCGTCCCTCCTGCGCCACCTGACAGATGTGGCGGTGAGAAAACGATGGG GCAGGGAAACGTTCGCCATTCGGTGCCAATAAAGGCCGCCTTTATCCCGACCGTAAATGGTTTCTGTGTGGAGTGA GACTGTGCCTGTCC
068_CDKN1C_001	30	23	CTTAAAGCTTTACACCTTGGGACCAGTGTACCTTCTCGTGCAGAATACATTTAGATATAAAAAGACGTTATTAATA CATTGCACAGTTTTCAAAATTTAAAAACAAAACCGAACGCTGCTCTGCGGCAGCCGCCGCCGGTTGCTGCTACATG AACGGTCCCAGCCGAGGCCCAGCGCCCTTCCAACGTCCGCTGCCCCGGCAGGTTCCCTCGGGGCTCTTTGGGCTCT AAACTG
070_SLC22A18_001	26	26	GAGGGCTGGAACTCAGACCCAGAGGGGCGGTCCCTGTTGCAAGTCATCTCCCGAAAGGGCGGGGCCGGGGCTCATC CCGGAAGGACCGGTGTCTAGGTCACCCTGGAGCGCTCACACCCACCGGCACCCGTGCCCAAGCCCGCCCCTGCAAAG GCAGGTACTCGAGCACACTCCGGAGAGGGCGGCCTCTGAGCCCCGAACCCCGGCGCAGCGTCGCACCTC TGCCCAATGAGGTGCCCCTGACGTGCCTGCTGCGGCTGCCCTGCTCCCCCCAGCCTCCCTGCATCCCGGGATGGGG GAGGGCGCCAGGCGCAGCTCCCGGACCCTCAGGGGTCTCCCCGCCCTACCCCACCAGCCTGGGTTCGGTACCTCGG GGCTCAGATGTGCAGTCAGCTGTTAATGTGGCAAAATTTGGGGAAGTCCTCTGC
071_SLC22A18_002	26	22	TGAGAGGAGGGAGGCCTCCCAGCAGCCGCCCAGGCGCCCCGCCCTCCATCCCCATCCCGCACTCCAGCCTCCCTG GTCAGCCCCGCCTGGGCAGCCCCTGGACGGGGGGAAGGGGACACTGACCGCCTCCGTGAGGGTCCGACCCGCCCCT

			CGGCCCCCAGGTTCGCAGACCAGCGCGGGGCGCGGGCGCTCACGCTCTCCTTCCTGGCTGCCTTGGCGCTCTA
			CCTGCTCCTGGCGGCCGCCTCCAGCCCGGCCCTGCCCGGGGTCTACCTGCTCTTCGCCTCGCGCCTGCCCGGAGCG
			CTCATGCACACGCCTGCCAGGTAGGGCCGGGGGGACTGGAGTCCAGGTGGGGCCGGGTCGGGGGCAGCCTGCGGAGG
			ACCCGGGACACCTCCAGGGAGGTCTGCGTGCGCGCGGGGTCTGGCCCTAAGGGCTGGA
074_NAP1L4_001	25	25	TCAGACAGGATGAATGGTGGGGCCCCGCAATGGGGCTACTGAGAAAGCAGGACTTGACGCTCATACGCTCCACTGA
			AACGCAGGACTTCCCAGCCCAGTCCCTCAGTGGAGAAGACTGCCGAAGCCCGGCTCCGGCAGCAGGGTGGCGCCTG
			CGTCATGAGGACGGGCTCGCATCTTCAGCCCTGGTGGCAGGGAGCGGCGTTTCTTCCGCACAGGCCTTGCGCCTGC
			TAGGAAGTGGCACATCTTCCTGCTCAGGGCACCAAGGTGGTTCAGAAACGTTAAGGACGAGCCACAGCGAAAAGCC
			GCAGTCCTCACAGGCAAGAAGGGATAAATAAATATGAGGTGACCCGCAGCAGCTCTCACCTGGGCTGGTG
076_CARS_001	25	23	CAGGAGTCCCAGGGGTCCCAGTGGCCGTCCCTCGGAGCCGGGCACCCGTTGTCCTTCGGATCCTAGGACGTGCCAC
			CCCTCGAACCTCAGGACCCGCCGTCCCTCAGACCCCGGGCACTGACACCCCTCAGACCCCGAGCACCCCCGCCCCT
			CGGACCCAAGGACGTGCCGTCCCTCAGACCCCGCGCACTGACACCCCTCAGACCTCGGGCACTGCCGCCCCTCAGA
			CCACGGACACAGCTGCCCCTCAGAACCCATGCACCCGGGCCCCTCAGACATAAGGACTCGCTGCCCTTCGAGCCGA
			GCACCCAGCGCCCCAGTCAGGCCCCCAGCCGCCCTCAGCCTGGCCCGGCCGCGCTCACCCTGCTGCCCGGAGGA
			ATCTGCCATGGCTGGGA
077_OSBPL5_001	24	25	GCTGTGGTCAGCAGGGTCCCTGGGCGCTGACAGGCCTCACCTCTCGGACTCCAGCTCCGTCTGCTCCTCCAGCGGC
			ACCGTGTGCTGCCTCAGCCTCTGTCTGCGGACCTCCCCGCTCGGGGTCCAGAAAAGCGCACTGCTTCCGCTCCCTT
			CCTCCTTGATAAACACGTCCCTGTCCTGCCCCAGATGGCCAGCGGGGTCAGAGGCTGGCCTGGCGTTGACCGCCCG
			GCCGTGCCTGCCCTGAGGGACGGCCCCCTTACCCAGTGGCCACTGAGGCTCGCCAGGACTTCCTCTCCCGACGTGAT
			CTTTCCCGAGATCTGGTTGATGCTGGTGCTAC
080_OSBPL5_004	27	25	TCCTTTAAGCCCCACCAAGTGGGGAGCCGAGCTGGGCGCGCCGCTTCCCACTCGCGGGCCCCACCCGCCCCAACCC
			GCCAGGCGCCGACCCGTCCTGGCCCCGGGGCGCCCCCCAGGCTCCCGCGCTCCCCCAGCTCCCCCAGCGCGCGACCGGCC
			CCGCGGCGTGGTTCCCCCGCACTGGCTACTGCCAGGGTCCGCGGGGCTGCGGCGCGAGCTCCTGGATCCCTTCGGCC
			GGCCCCCCGCGGCCCTCGGTTCGCTCCGGCCCTGCCCGGCGGGGCCCTCCGGATCCTTCCCAGCCCGCCATCCCCC
			CGCCGCCCTGCCGCCCCCCCGGGCCGCCGCGCTCCTACCTCCTACCGTGCCGCGAGCTCGGTGCTCCGGGCCGGCCG
			GGCGCCGCGGGGGCTCCACTGGCGGCGCGGGCCTGGCTGCAGGAAATGCCAGC
084_OSBPL5_008	27	25	CTTCCAGTGCCCTGCCTTAAGGGAGATCGCAATTGACGTGCCAAGAGAAGGAAACAAGGTCATTTTTGGCCTCT
			GTTCCTCCCCGAGTCCAGGCCCTAGCAACTCTTTTCTCATCTTTGTCTTTAGAAAAATCTCCGAGGTAGAGAAGAG
			TGCAGAAACAGCACGGATTTGCTCCGGAGCGTTTCCCACTCTGCGCAGTCCGCCTGACCTCTCCTCTTGCGGACCA
			AGTGAGAGCAAGTTTCCCGCACGTGGCCTTTGACCTGTCACTACATCAGCAGGCATCCCCCCAGGGCACCGGCATCC
			TCCATCCCCAAAACGGAGGGGCCGCACACAGGTCGTCTGGCGTCTGTGCAATGCTGGTGTCTGATG
085_ZNF195_001	25	26	TGTGGGAGTGTGGGGCATCCTAGCTTTTCCTCGGCCCCCAGTTCTTTCACTTCCACTGGAGTCCCGCAGGGACAGC
			TCGGGGACCATGCAGGCCCGGGTGGGCGTGTGGGCTCACATAGCTCGGTGGTGAACAGCTGGCACGTCTCTGGGTT
			GCGGACGATAAGGGCCACGTAGACTTGAGGAGCCCGCTGGTGCTCCCGGTAGGCAGCCAGCCTCCGCAGGACCGCG
			ACCAGCGACACGATGGATTCTGGGCAATACAGCACGTCTACGGTGAAAGCTTCAGGTTACTGAAAGGGACCAGCGG
			ACAGTTCCAGGTCATGCTGACCTCAGCAGCAGGGCGAGGCCAGAGAGGCAGTCATATGAGACTAGTAGATGCC
			ATTTGACCATTTGGGCCATTAGATGGAAAGGCAATTGCTTGGGTGAAAAAGGAGAACCCTT
086_ZNF195_002	25	25	GGAGAGTTTGAGGCAGGCCCAGGAGCGAGCCCACGGTCTGCCGACGCGGAGCCAGGGACGGGCCCCAGGATCCGGA
			GCTTCAGGCGGGGCCGAGTCCGGGTTTGGGGCCCGGGAGTCGGGGCCGGTTAGGGCGAGGGTCCCCGGGATCGTCC

			GGTCAGGCCTTGGGCCAACGTAGGCACTCTCGCAGTTCCTCCGCCTTCAGGAAGGTCTTTTTGGCAGGGGCCTTAT GGGT
088_DLK1_002	27	25	AGCCACCTGGCTGAACTTGCTGGGAACCGACGTCAGGAGCAGGAGCTAGGCTGCAGTGGGCCTCACGGGGGCCTGG ACGGGGAGAGCGGCTCCGTGGGCCTCTGGGGCCTTCCCTCTCCACGCAATTGCGATCCCAGTGATGGGTGGGACAGA GATCCCCGTTGTCCCTGTCACCGCTCCCGCCTCCACTTGCCGGGCCTGAGGACAATTGAGGGGCTCTG
091_DLK1_005	30	25	AAAACAAGGCAACAGAACCAGGGCTCAGTGCCGACGCCCCTACCCTGGGGGTCTCGGCCACATGGTCCTCGTGAAA CCGTTACGAGTGCTGTACATGACCACCCACTGTGCAAAGAGCTACGATTGCTTTCGTTCGTTAATTCTCACACACC ACATCCGACTCGCACTCACATCCAGCTCAACATCGCTACCTTTAGATCTTTCCGATTGATTTGAGATTTAGCGGAG TGCAGCGGCTGTGTGTCAGTCAGAGAGAGCCCCCAGGTTGGCTGCTGGG
092_MEG3_001	27	23	GGCTGGCTTCTCACTGGGAGGCTCAACTTCCCGCAGGGGCGCCAGGCCCTGACACGGAGAGACTGGACATTAGGTGT CTGGAAGTTTCTCCCTTCTAGGGGCTCCAGGAGCATCCCCACCCTGAGGCCTGGGGCTCCCACCGGAACGTCAACTCAT GCCCTTGTGGGGCTGCAGGGCTGACGCGGGCTGGCACTGTGTCTACGACAGCCTCCCGGGCCCCCGGGTGCGTGGC TGCGGATGCTCTCTGGCGGCCACCACACAGTTCCCACGCGCGGCGGGTGAATGCGAGCCCCCTTGTCAATGCGTGCCCC TCGCCTCTGCCCCCCGAGAGGCTAGCAACCGGGCCTGCCGGCGTCTGATTGGCCGTGGGGGCCTGACGACAGGGGCT CCTGGTTGCTGAT
093_MEG3_002	29	25	CTAGAGCAATTTGTCATAGAATCTGGGGGGCTCATTTTTCCGGCCAATCACTTTAGAGAAATGAGCGCATTGCAG CAGAATGCGCTGACGTCAGAGACCACACCCCTTCTGCGCCTCCATATAAACCCCACCCAGCCAGCCCCTAGCGCAGAC GGCGGAGAGCAGAGAGGGAGCGCGCCTTGGCTCGCTGGCCTTGGCGGCGGCTCCTCAGGAGAGCTGGGGCGCCCAC GAGAGGATCCCCTCACCCGGTGAGTGGTTGGCCATCCTTGCCGCAAAGGATGTGCAAAAGGAAGACGGCATCCGCTT CTGGGATGGGCTCTGTCCTCCTGGACATG
094_MEG3_003	27	26	GGGAGGAATCAGATGGAACTCCTCTTGGATTCGGGTATACGGCAGTCACTGGGGGGCGAACCCCGGATTTCCTGTA TTAGAAGCCGCCTCTAGAATCGCGTTAATAGTGGGAGATATGGCGGCGATGCCTTCTGCGTGCCCCATGAATTAGGG GGGGGAAGCACCCGAATAGAAGGGTCTCCCGGGCATATTTGCCTCGCCAGCTGTTGGCCAGGTTTTTGGTGGA
095_MEG3_004	26	25	GACTGGGTCTTTCTGACTTTAGTGAACGTGTGTTTAATTGGATTGACGAAGGTGGGAGTCGGGATTTCTGCTTTTC CCTGTAGCAGGCGGAGCGGCGCTCCAGAGGGGCCTGGCGCAGGTCCGCTGGGTGGCCCACCTTCCTCTGGGGCTGG GGCCCGGTGGCTGGGGGCGCAGGAGGCGCCTGGTGCGGGCGGGAGGCGCTGCGCCGCAGCCACAGGTGGGCTCTGG CTGG
097_MEG3_001	24	25	GTGCCTCTCTAGGGCAATGCATGGCGGGGGCGGGCGGAAGCAGTTCTTCAGGCAGTAGGGAGAGTGGAAGGTGCAG CGGCCTTTGATCCAGTCGACTTCGGGGGCGTGGACTCGGAGCCAGCGGATGCCTAGGACCACAGAGAAGTTCGGTG AAGGTACGATGTCAAATTCGATGGACTCCTGGTGGTTCTGGTGGATACACACCAGGGGCTCCGTGTAGAGCCAGAC AGGCTCGTTGCCAATCAGCGAGCCGTCCACGGATTGGACCGGCTGTGGGTACGGCTTCTCGTAGAGCTCGACGTAG TGCTCTTGGGCGAACTTCTCATCCATGAAGTTGCCGTCAGCTCCCGAATCCACCAGGGCCTGGACCGCGACGCTGT GGTAGGGGTTCACTCTCACC
101_NDN_004	26	26	GCAGGGCTCATGGGGCTGCCCTTGTTCGCCGCCTTTTCTCCATCGCTCAGACCCTCACTTCCCCGCCAGTGCAGGT TTCTGCCCCCTCAATCCTTTTGGAGGTGTAGGTGGGATCCATGGAGGAGAAAACTCGGATCTGCAGGCTCCTCTCC ACCTGGCGCCCACACAGGTGATGGTGGGAGCAGCCTGAAGGGAAGTGCCGGTGCGGGGGTCGCAGCTGCGCAGTGA GGGGAACCGGAGGCTGCCGCGCAGGCTGGGCTTGGGGGCGGGAGCCAGGCCCACGTGGGGCGTGAGGGCCGCGGGT GGAGGGCGAGGCTGACAGGGAGTGAGGGAGGAAGGTGGAGGGCGGTGATCAGAAGGCGCGGCTGACAGGGGGAGAG GGCGGTGAGATCTACAGGAGAACTCAGGG

102_NDN_005	25	30	GCTGGGAGCAGCCTGAAGGGAAGTGCGGGTGCGGGGGTCGCAGCTGCGCAGTGAGGGGAACCGGAGGCTGCCACGC
			AGGCTGGGCTTGGGGGCGGGAGCCAGGCCCAGGTGGGGCGTGAGGGCCGCGGGTGCAGGGCAAGGCTGACAGGGAG
			TGAGGGAGGAAGGTGGAGGGCGGTGATCAGAGAGGGCGCGGCTGACAGGGGGAGAGGGCGGTGAGATCTACAGGAGAA
			CTCAGGGCGGATGTCTGAGGGGTCTGCGCTGGGCTTTCCGGTGGCTTCGCCCGGAACGCGCGCTTGTTCCTGAGGC
			GGTGCCTGCCTGTGTCGTCGTCCCTGTTTGTTCTTCAAACGTCAGGATTTCTCCGTGTTTCCCAGACCGTAACGTA
			CATTTAAAAAGCTTGCTTTCTGTCACATATGCCCTTTT
105_SNRPN_003	25	30	CTCACAGGGATGGTGGCAGGAAATGCGCCATTGTTCGGCGCAGCGAAACAGCCCGCAGTGCGCTGTAGGAAGGTCA
			CATGACAGAGGGGGAAGACGGTGGCCGGCAGCAGCCGATCCACTGCGCGCCTGCGCGGCTCCGGTGGCGTGAATGT
			CGCTGGTCTCCCGTCACCGTTTCCGTTTCCGGGCGAGTCTGTTCGGCTTATGGCGTCTGCTAGGAGTCTCCTATCC
			GGCGTTTGTGCCGCAGAAAACCTTTAACCTGCGTTTTACCCGTAAACATTTTCCTTTTTAGGCTTCCTATCATTGT
			TTTGGTTCTTGCTCCTGTATTAACTTTGTTTTTGGTTT
107_SNRPN_005	25	30	AAGGTCACCTGACAGTTGGGGAGAACGGCAGCCCGCAGGGGCCGATCTTCGGCGCGCCTGCACAGCGCAGGCGGAA
			TTGGGGCGCCTTTTCTCCTTCCGGTTTCCGTTCGCGCCCCGAGGGTCTGTTCCGCTTATGGCGCCCGCCGGG
			AGTCTCCCTTTCTTCGCAAGCGTTAACCTGCGTTTTACTCGTAAAAATTTGCTTTCTAGGCTTCGTATAATTGTTC
			TGGTCTTGCACTTTATGTGTGCATTAGCCTTGAGTTTGCTTGTTG
109_UBE3A_001	23	23	GGGCTGAGGGGCCCTCCTGCCAGGGGCTACAGGCCGCGAGCTATTCCGAGGAGGAGGCGCCGCCGCCC
			CGCAGCCGAGCGCGCCGGGTCGGCAGAGGTGAAGCGTAAGTAGGCGGCGGATGGCGGGCGCCCGCGCTGGCGGATG
			GCTACGCGGCGGAGGGGTGCGCGAGCGAGCGAAGCCTGGTGTGTCGGGTCCTGGCGAAGGGAAAAGGCCCCGTCGT
			CTCCTGTAGTCACCCCGAGCCCAGCGCCACCATCTTGGGAGACACACGGATCTCGCGGCCGCGGCGCAAGACGGGA
			GGACTGGCTGGGCGGGCCGAGTATCCCGGCAGGCAGCGCGCCGCCCGGCCGAGGGCTCCAGGCCGGGACG
			CGGGGACGTGGGGCGGGGCCAAGACGCGCGGGAGGGCGCCGCGCTCCGCCCCTCCTTCCTTCGCCGGCCCCGCCTC
			CCTCCCGCTTGCCGTCGCCGCCGGCGCACGGGCCATTGGGAAGAGGAGGTGGCC
110_UBE3A_002	25	25	TCTGGCTGTTCCCAGGAGGGCTGAGCGCAGCAGTCAGAAGCTGGCACGGAAGGGAGAAGGAGGCCGATGGGAACAG
			CACTGACAACAGCCCGTGACAGGGCCGGCCCTTCTGTCTGCACCAGCCCAGCACGCCGGGCTGCACAGCAGATTCT
			CCAACGCGTCTTCCAGACCTCAGCTTCCACACTGTGACGGTTAGCAAGGCTGACGGGCGTGGACGGCGAGGGGTCG
			GGAAGAGTGAGAACGTTTAGGATCATGCATGTCTAATTTTATTGAAGCAGGGGCCCCATCTAGCTGTGTGCGGCTGATT
			CCATATGTCAGGCAGGGCGGCGTGTAAACGGCCCTGAAGTTGCGCCGTCTGTCTGTGTGAACAGGAGCTGCTTCCT
			CCGCAGGACTCCAGCTGCTGTCCGTGGCCGGGCCATGCGATGGAAATGGAAACAGCAGAGTAAGGCGGTGCTGATG
			TGTGTGCCCGATTTCTCCTCGGGAGGAAAGCCCTCTTGGTGTTGAA
111_ATP10A_001	26	25	CAGGGGTGGGAGTACCTGAAGAGCAGGGCTGCAGGAGATCCATGACCACTGAGTCGGCCCCCTTGGTGTAGACGTT
			GATCTCATCGGTAAGCGGGTGCCGGATCACCACTGACATCCTCTTGCGGACGGAATCGAAACCCAGTGTGTGCAGG
			AGCTCGAAGGTGAGCCTGCCCAGGTGGGGCAGCTCCACTGACACTTGGTCGTGCAGCCGCTCCACAAGCACGCAGT
			TGTAGGCTCTGGCCGCATACACCAGTGCGGCCTCATCCGGGCTCTCCGCCTCGTACCGCAGCTCGCGCTCTGACTC
			CTGCTCCTGAGCAAGCTCCGAGGCCCAGTTGTCCGCCTGGCTGCTGTAGCCGTTGCTGGCGATGGCCGAGGTGGGC
			TGGCCCAGCCTCTCCTCCAGCCTGAGAAGCATGCCGTCGCTGGACGGGGTGGACGGGAAGCTGGAGCCCAACTTGT
			GGCTGGACTTG
112_ATP10A_002	30	25	GCCAAGAAGGCTCAGGTGCTGGGCCACATTCCCAAACAGCTACACCATGTGGCAAAGAGTATTAAATGCATACTTT
			ATAACTGAGAATGTGTAAACACCTGCCTATGTAGTTATCAAACAGAAGGATGCGCGCAGGCAGACACGATACTC
			ACATGCAGCCGCGAAACCTACTCAGGTCGTTGTTTGGCTTCTCGCATTCGATCACGCTGGTGAACGTCAAAGGATT

			GAATTCGGAGACCTAAAATAACAGCACGTAGACATTAGAGAAATCCGGGCTCAGGCTGCGCCGTTCTAAAAGGCAC
			TCGCTTTCTGTCTCGCATCCGCGGCAGGCACATTTCACGGGGGAAGAACTCTGCCTATGAATC
113_ATP10A_003	26	25	TTCTAGCCTTGGGATCATTCTGGCCCCGACACGGAGTGACAGGGGATCCCCACGCGTCCCCGCATCCAGGGCGCCC
			CTTTAGCTGCGGCGGAGGCACAGAGAGGCCTTGGCGGCGCTGTGGCTTCGGTCGGCACCGGGTCCCGCGCAGCCGG
			GCCCTCCACACCCTGAGTGGAGCTGCCTTCTAAGCACACCCAGCCCCTGCCAATCACTGTGCCCCAACACCAAGTTCCCGG
			GGCGCCCTGCCCTGCGCCACCGCGCGCTCGCTCGCCCGCCCGCCCCAACTCACCTGCTGAAGACCAGGCAGCCCAGG
			TGGTTGATCTTGTGGTCGGAGCGGTGGCGGCTGTAGTCCTCCCACAGGTCCCTGAAGGCCGTGATGGCCAGGATGA
			AGAGCACCGGCGCCAGTGCCAGGCCGGGCTGGAAGGCGTTCACCGCCGGCACGAAGTTGAGCAGCGCGATGAAGAC
			AAAGTACACGTTGGCCGGGCGGTGGAACTGCTCGAACAGGTTCTTGGGCAGGAAGGAC
114_ATP10A_004	24	25	GGGGGAGCCAAAGAGCAGGGAGGCCGAGGTGGGAACACTGGACGTGGAACCTGAGACTACCCCAAAGCCTGCGTTG
			TAGCCCGCTTAGGGGCTGCAGGCTGAGGGGGGCGCGGCAAGACTCCAAGTAGAAGCGGACCTTGAGAGGCAGCCAG
			GCCAGGCGGCAGCCGCGCCCGGAGGGTGCGGAATGAGGAGCGCAAGGTGGGCAGAGCGTGAAACCTTCACCGACTG
			CACCTCCGCCCTCGCTGCCCTACCGGAATCCCCAGGTGGGAATCCGCTCCCAGTCCGAGATCCTGGGCTCGGGGGT
			TCTGGCCGGCCCGAAGGACTGCTGCATCTGGTTTGGGT
115_ATP10A_005	25	25	CTGGGTGAAAACCAGGAATCCTAACCGCTAGACCATGTGGGAGATGACAAGTAACCGTTGAATTCTAAACCAATTG
			AATCATTTCCCGCCTGCCCTTGCTTTCCGCCTTCTGCCACGCCTCCCGACACAAATCCCTGTCTGCGCCTGCGCCTG
			CGCGGGCTTTCGGTGCTGACCGCTTGTTGATAGAGGTGTGCTCCTTCTCGAAAGGCGGAGGCAGGGCTGGGCGCTG
			TGGCTGCTGGCACTACCCAGTTCTTCAGCAGCGCTGTGCCTGGAGGCCCCCAGCCCC
116_GABRB3_001	26	25	TGCTCTTTACAGGAGAGGCTGAAGCTCGGGGAGGCGCAGGGGCGGAGTGTGGGGAGAAGCAGCTCCCGGGAGACGG
			AGGGCTTTGCGAAGCGGCGGCAATCAGGGGCGGGGCCTGGAAAGGAGGGCAGCGCGGAAGCTTGGCCCCGAGAGGG
			AGGAGGCGTGGTCTGTGGCTCGAGGGGCGTGGCCCGTAGCGGAAAAGGCGTGGCCCAGCTCAGGAGCCTGGCGGGC
			AAGCTCCTCCCCTGTGCGCGGCGCTGTGCGGCGTGGAGAACCTCGCCCTGGGAGGGTGGGCCTGATTAGATTAGCAC
			ACACCGGGAAGAGACAGGCTGTCTCCTGGCACTGGCTCTTGGCTGTGGCA
117_GABRB3_002	26	26	TGTGCAGGATGCTCCAGGTGGGCATGGAGGGGCGGGAGAGGTAAGGGTAGGCGGGAAGAGGGGCCCGGGACACAGT
			CTGCAGCAGCAGGGCAGGGCACGGCGCACTGGACAGACCCGGTCCAGGCACTGCAGCATGGGCTCCGGGAGGTGGC
			AGGTGCAGGTCTGACGACACAGCAGGGTCGTGGCTGGCTGCGGAGGGGCGCGGGAGGCTGGGCGCAGAGGTGGCCGCC
			AAGGCGCGGCTTCGGAGCACGGCCTGGGAAGGGAGGAAGAGGAAGAGGAGGAGCCCAGGC
118_GABRB3_003	26	21	AGTCCAGGAGGCAGCCTTGGAAAAACCGCAGAGACACCCCTGGAACGCACAGACCACTGTCTTCGTTCCCCTTTCC
			TGCAGCCAGAATCTCTTTCCAAACGACACAACAAAGGAAACCTTAAGTACCTCTTACCTAGAATATAGGAGCCACCCC
			CACATCTCGCCTCTCCCCGGTTCCCCAGCGCCTGTTGCTAAGGAGGCGAGACAGCGCTCGGGAAACCTCGGGACCAG
			GCGACAGAGCGCTGGAGGAGCTGGGAGCCCA
119_ZIM2_001	27	25	GAGCAAACCTGTGAGAGGGTGAGAGTCCGTCCGTGTAGGTGAGGGAGCTAGCAAGAGTGTGAGCGAGTGCGAATGT
			CCCTACAAGTGTGGGCGCGTGATGTGTTTGAAGGTGTGTTGTTCTGAGAGGGTGTGTGTTGGGGTCAACGAGGGTG
			CATGTGTGTGAGTGAGGAAGCCTGAGTGTGTGGTGTGTGCGCGAGCCAGCAAGCTGGAATGGCTCTCGCGTGCTTG
			TAGATCATGAGCGTGACTTGGTGGCTTTCTGTGATGGTATTGGGTGTGTATGGCTTTTTGCTGTCC
120_ZIM2_002	24	25	GCCCAGGCCCCCTGGCTGGCTACCCGCTCGCCGGCCGCTATCCTACCCCGGGCCCAGCGAACTTACCTCGCACGCC
			TCACGCCCTGGCCTGGCTGAACGTCTCCACGCCCTGACCAAAACCAGCAGCGCATGCGCCGTGGCTTGGCTTGCGCG
			TGCGCTCTGCGGTGGACGGGCTGAGGAACCACAGCCGCTCCTGGCCAAGTGCCCTGTGAGACACGAGGATAGGGTT
			GGTACGGCGAGGAGAAGGGCGGCGACGTAGGAGGGCGCTCCTGTGACCTTCCTCTTAAAACTAACGCCTTCTGTT

			GGTGGTGGGCGCCTGTAACCCCAGCTACTCGAGAGGCTGAGGCAGGAGAATTGCTTGAACCTGGGAGGCA
121_ZIM2_003	30	25	GGGGACTGAGCCAGTCCCACTGGCAAAACAGCCTGGCGACCAGCACACACAGCCCAAGGAGCGCGGCACTCCACAG
			CTTTCCATCACCGCAAGGCAGGCACAGCAACCGTGGCCCCGCCCCTCCCTGTGGACAACCCCACACCTATGC
			GGCAAACCGCAGCCGCCCCCGATCAAAGATGGCACCCAGGTGGGCGGGGCTTGAACAGACCGTCCCGCCCATGCCAC
			CTGCAGCCACTTCAGCCTTGCCCCCGCCGCATCTGCCGCCAACCAATCCGGGCAACGCCTGCGCGGCAAACCTCAGC
			TGCCCCCCATCAAAGATGGCGCCCAGGCGGGCGGCCTTGTCTCGCCCAACCAACTAGGACAGCGCCTGCGCAGCAA
			ATCTCAAGCACTTTCATTAAAGATGGCGCCCCAGGTGGGTGGGGCTTGAACAAACCACT
123_ZIM2_005	30	26	GGGGCTTCTGTGCTAGCCAATCAGCAGCCTCACCGCCCTCTCCGGGCCCCCTCACCACAGCCCTGTGACGTGCCAA
			TCAGGCTGCGGTTGCCACAGCAACAGTTTGGCGCGAAGGCTGGGGGCTGACGTCAGGGAGTGGCCGTGAGGGACCC
			CAAAGCCAGGTCTGGAAAAGGGGGGTGGGTTGGGTGGTGGGGGTGCAGCCCCCCAAAGAAATGGGGGTCGAAATGGA
			GGAAACCCCCACTGAGATG
124_ZIM2_006	26	25	GGTGGGGCAAGGCAGAGAAGAGACCACGTCTGGCGGATGAGTCCTGTGATTATCAGGTCACCTGGGTAACGCCCAA
			CCACGACGGGCTGGGTCTCAGCGCGAGGCCTGCAGCCCGGCGCCGACTGGAATCCCCAGCACTGCCGTCTGGAGGA
			CATCGGCGGTATCTCCCCCAAGAGACGGGAAGTCTGTGTGTCGAAGAGGCGCGGGACGCAAGCCCACCAACCTGGCC
			GACCCCAGGGAAAGGCCGAGCGTCCAGCCCGCGGGGGCCCAAGATGGTGCCAGAGTTCGAGGCCCTCTGTGCATGC
			ACCCCGCCCGCCTTCGAATCTAGCCTGTTCGCCGTTGTGGTTTGTCCTCCCGGTTCCTCTGAAGGAGTTGGTCAGT
125_USP29_001	30	23	AGTTCATCTGCTGAGAAAAATGCTTTGAGATAAACCTGGAGCCACAGCTCTCTGCACAGTCAGATCGCAGGAACGC
			GGCCTAGCTGCTTCAGCCACGTTCTCGCGGCGCCACCTGGTGGCCATGGACCGCCATCGCCGCTGGACGTCAGGGC
			CGCCAGGCCCAGCGAGATGTCACCTCCTCTGAGGAGCCTTCCAGGATCGCACCCGGCACGCGCTCCACGCCTCGTT
			GTCTGTTCTTCGGAGCACCGACCATGATCACAAATCAGCTCGCTCGCTGTGTTTCCTGCCGGGTCGCTACCGCCAT
			GATCCGCACGTAGTGGTCAAGGCTGAGGTTGTATGAATGTGGACGTTATAACCCTGGCTCCCTCTCCCTCCCTATG
			CTGGGCTCCCCCTCGATCCCCAGGCGGTGGGGTGCCCCTGGTTTTTCCT
127_USP29_003	26	25	GCCCTCAGAGGGAGAGATGGAAGCTGGCAGGACGCAGTTGCTACCGCGCGGACCCGGCCCCCGACCAGCCTTGGCC
			CCTCGCGCGCCGGGACAGGGCCACAAATGACTGCACCTGGGCTTCGCTGGCCCAGGCACCACGCGACTCTAAGCGC
			GCCCAAAGCGACCCTCTGCGCAAACTACCCCCGGGGACGACGTCACCCGTGAGGTCCCGCGGCGCCTCCTCCTCCTAAA
			GCTCGGCTGGGAAACCGTCCGCTTCCCCAAGACTTGGGGGCTTGT
128_ZIM3_001	26	26	CAAGGTAGGGTCCTGTATTTGGGGACCGCTGACGTTTGGGTCCCCCTCCCGCGGCTGTTAGCGCTGCGTGGCCCGA
			GACCTGCGGTCGGGCGGGGATTAAGGCTGCTTTCCGGAGGGCCCCGGCCGCGTGGTCGCCCTGCCAGAGCGGTTGA
			TGTCAGGCAGTGCTGGGAGGCGTTGCTCTCCGGTTCGCTTCTCTCCTGTTGTCCTAACTCTGCATCTCTCCCGGG
			TGAATCACAGAGCTGTAAACTAAAAATCAAATTCTAAGCTCCCAGCCAACTGAATGGACCCCCTCCTCTCAGCTAAG
			AGCATGGCAAACTTAACCGGAAACACTAGTTCGGCCGCGATAGGAAGGAGATGGGACATGCCTC
129_ZNF264_001	27	25	CTGGAGAGGTCTGTAGCCACTGAGGGCCCCGGTCGGGGCCGCTTTGCAGGTCCCTAGTCAGGACCGAGGCAGGGGAG
			TAGGATAGGAATCCCCGCCGCACCTTTGTACGAGCCTGACCCCTTCCGTGGGTTTGTTCCTGGGTCGCCGTCAAGC
			TGCGGTCTCTCCTCCCCCGCCCTTCAGCCCCGCGGTCTCCAGGGGCGGCGCCCTGGGTCTGGAACGCGGTTGCCAC
			CGAGGAGGCGGCGGCCCTGCGTCTGGAACGCCGTTGCCACCGAGGAGGCGGCGGCCCCGAGCGCGCCTGGAAGCCC
			CGGGCAACCGGCCAGGGTCGGGCACAGGTGGGGTCCGTCAGGCCGCCCCGGGGCTCCTCTGTCCCAGCTCTGCGGCC
			CAGGGGGTGACGTGATGGCGGCAGCGGTGCTGACGGACCGGGCCCAGGTGAGTGGACGGTGGCTTCGCGGTTGCCG
			CTTCCTTGCCAGCGCTGAGGCGGTTTCCGAAGTGGGTGGGAGCCCAGGTATCC
131_AURKC_002	25	27	TGGGGCCAATGATGGTCCAGGACAGGGGCGTTTCCTGTGGGTTGCGAAGCTTGGGGCGGGACTTCCGGCATTTGGA

			TGGGACGTAATTTGGGAGCGACGGTTCCGTCCACGCCGGCTCTAGGGAGGGGGCGGTGTTCCGTGGCCGCCTCCCT
			GGCGGCGCTGGGGAAATGAGCAGGTAGGAGGCCGACAGCGACCTCCGCGTCTCGGAGCGAACCGTGAGCCTCCCCG
			TAACGAGAGAGTTTGACTGTCAGCCAAGGTC
132_ZNF272_001	30	25	GGTAGATGTAAGGGAAAAACTGCATTACCCAGAAGGCACTGCCCCTTGCGTCGGCCGCGGACTCTGGGCCATTGAC
			GACCCAGGACAGGAGAGTTTTCTGCGGGCCAGGGCGGCGGAGGCGGGACTTCCGCTTCTTCGTGTGACGTCATCTC
			CGTGGGCCGGTTTGGCCCTGAAACAGTGTGGGGCCTAGAGCGCTGGGTGGGCGCGTTCTGCGGCCTGAGCAGGGAC
			GGGTAGTGAAGCGGTTACGCCCCTTCTTCGCGTCTTGGCGGGAGCCTGACGCCCCGCTTCTCCCCTAACGAGGTGT
			CCCACCGGCGCCCGCCGAGGCCTAGGCCTCCGCAGCCGCCCTCCGTCTCCTCAGCCCCGACGCTGCGCCTTGGGCC
			TTGTGCGCATTTTTTTCGGGGGAAAACTGAGGCTCGGAGTGCGAAAGTCAGCCGAGGTCGCCCCGCCCAGGACAGA
			GAAGGGCTGTGGT
133_RAI17_001	26	26	TGATATGGTGGCAGTGGGCAGTGGCCTCATGGTCAGTGCCGGCCTCTACTGTGGGTAGACCCGCTGACCTCCCAC
			TTTCATTGCAGCAGGATGGAGCTGGAGTGAGGTGGAGGGGCCGCAAGCTGCTGACCGGCGTGTGGAACACTGGTGG
			TTTGCAGATCACTGAGGTAGGTGTGCCACGGGGCTGGCGGGAGGTGGCTGGGTCGGACGCAGGTGAGTCCTCATGA
			GGGCAGGTGCTAGCCCTAGCACGCTGGACCTTTGACTCGGGCCTCAGCCCTGAGGGGCAGGAGCGGGCACAAGCCA
			CCTTTGCTGGGACCTCATCATGCCCCCCAATGGGCTGTCCCCTCTACCTGGCACCCAGGGACCTCTTGGCCTGGC
134_FRAT1_001	25	25	CAGACTGGAGGGCAAGGGGTTCCCTTGAGGGCTGCAGTTCTACTCAGGCTGGTGGAGAACTCTGGCTTTGGAAGC
			GAGAGTAAAAAAGCTAATGACGAGGAACCGAAAAATCGCGAGTGTTTCGCGGGTAACTGGGGTTGAGGGCCAAAATA
			TTTGGAATGAAGGACTTTGGCCCTATTTAAGGCAGATTTTACAGAGCGCACCTCAAACGTACAAGTCAGTAGGACT
			CCTTATTTGGCGTGACCCGACCTGGCCGCGGAGCCTGCATTTCCTCGCAGCCTCTCAGTGCCCTCCAGCCCCGCGA
			CCATGTGGCCACAATCCACGCTTCTCCGGATCGCGGTGCGCCGGAACCACGGAGGATGATGCCAGTTACTTGCTTT
			ACCTTTTCAGGGCTGGCTCCTGATCCACTTTGGGGGAGGAGAAC
135_ZNF215_001	27	22	GGGGCTCCTAGGGGGTTCCTTCCACAGCTGGTGCGCGTGCGCAAGAGTGCGTCGAGGTTGTTCCGCGGCAATTTAT
			GAAACTCGGAGCCGGCAGTGAGTTGAGGGTTCGGCGAGGTCAGGGATTCCTAGTTGCAGCGTGATTACCAACGCCA
			GCTCCCTTCACTGTCCAAGACAGCGATTCCGCGGCTCCTCTGAGAACTGGCGCTTGTGAGTGACTGAACGGGCCAC
			TGGAGAGGAGCGGTGCTCACGGGTATCGTTCTCGTCAGCGGCGGTGGGGACGCGGGGTCTTGGAATTGGGAATCA
			CGCTTGAGGGCGTCCATGCGGAACGTGCAGCTTACCTCAGCTTGCTTGCAGTTACCCAGTTTCCACGCTGCCCTCC
			AAGGTCTGTGCCGGAAAACCTGGAGGAGGGCGCGAGCTGACGGGAGGGATGGAAACGTGGGCTGCGGAAGTAAGAC
			AAGCGTTGAGAGCAGCGACACAGAGGGCGAGGGGGTGGGCGGCGGACGCGGTCAGGATCCAGCTC
136_WT1_001	30	25	GGTCTTGAAGAAATACTGTCCCAGCTGAGCCCCCGCGTTTACAAGATGAAGAGGCGCCCCAGATGCGCTGAAAGAAA
			GGCCAAAGCTCGTGCCTCCTTCCACTGCCTGCGGTAGAACCTGGTCCCGCATAGCTTGGACTCGGATAAGTCAAGT
			TCTCTTCCATCCCCAGAACCTGCGTGGCCGCGCCTGAGCGAAGCCCAGTGAAGATCCACTTCTGTATTACCATAC
			GCGGGAGCTATCCACGGACACGACGCTGTTCCAGAAAGCCATTTAGTTACTGGAGGTGCATGTGCTCATTCTAGTT
			CTCTACGATACTTAATGTGCACCTAAGTGTGTGCCAACACCGTATTATAAGGGCTGGAGGTGCTCCTGGA
137_SDHD_001	30	25	GTGCCCAGGACCACCAAGGAAGGTGAAACTTCCTTTCCCTCACCCTCCCCGTCCCCGCACCTGTGCAGTAAACTG
			CGCCTTCTGCTGCTCGGCGGCCACCAGGCGCTGCAACTCCGCTTCATCGGCTTCGCCCAGCTCCGCCATTGTTCGC
			CTCAGGCTCGCCACCTTCCGACAGCTGTGTTTGCGCATGCGCGACGGGTGTGCACCGCCTCTCGACTTCCGGTTCA
			CCCAGCATTTCCTCTTCCCTGTTTTCTTTCGTCGTCGGTGGGTGGGAATTGTCGCCTAAGTGGTTCCGGGTTGGTGG
			ATGACCTTGAGCCCTCAGGAACGAGATGGCGGTTCTCTGGAGGCTGAGTGCCGTTTGCGGTGCCCTAGGAGGCCGA
			GGTGAGGGGTCTTCCCACCCTGAGGT

138_SLC38A4_001	25	25	CCTCTCCTGGACTCAAGGGTGCTCCCGGCTTACGCTTCTCGGGGCTTCCCGGGTCCGGGTTCCCTCTCCCCGTCT CACTTTCTTCCTTCATTCGCTCTTCTCTCAATTTTTCCTCCATCAGCTCTAACCTGTAATCAATTCCCGCCTTCTG CCCCTCCTCCCTAGGCTTCTCTTAGCTCGGTTGCCGCGACCCCCACTATCCGTCCCCGTTCGCATTTCTGCACCGCC CTGCCCTTCACTCCAGCGCGCAGCAGGCCGGGCAATCCGACCGCGCGGTAAGCCGCCCTCGGAACCGCTGGCGCAG TTTTCAGACTCGCCCACCGCCCAGAGACCAGGGGCCCACATCCAGCTCTGCTCTCGCCTTCTCCCTTGAAAGAGAC TCCTTGGGGGCTCCCC
139_HTR2A_001	27	25	TTTTCTCTAGGGACACTGCCATGATGACGAGTATGTTTCCAGCAATAGTTAGAATAATCACTACGGCTGTCAGTAA AGCAGACCAGTTTTTTTCCTGGAGATGAAGTAAGGAGAGACACGACGGTGAGAGGCACCCTTCACAGGAAAGGTTG GTTCGATTTTCAGAGTCGACTGTCCAGTTAAATGCATCAGAAGTGTTAGCTTCTCCGGAGTTAAAGTCATTACTGT AGAGCCTGGTGTCATCATTTAATTGCATTAGGGAGTTCGTAGTTGAGCTCAAAGAAGTATTTTCTTCACAAAGAAT ATCCATGTCTAAGCCAGAACTTGTAGCAGATGAGGTGTAGAAGGACTAACAGGTTATAGTTCTGCTCACCATTCA CCTTGATGTACCCACACTCTGTAACACTGAGGCTGGTGTACATGCTGTTCTCCCGGGGCTGGATTTTTGTCTTCCA TTA
140_CR601144_001	26	25	GGGTGAGTGCCTACATTCCCTGCTGTCGGAGAGACTCTGGATCTGCAGAGACATCTCCGCGCAGAGGAGGAGCGCT CCTGGCAGCCCCCGCCCTAGCGATTGCCAGCAACTTTCCTTTCTGCCAGGAAATCAACCTACCTTTCTCTGCCTGC AGGCGCTCGCCGCCTTAGTACCCGGAGTGACCCAGGTAGATAACAAGTCCGGTTTCCTGCAGAAGAGGCCTCATCG CCAGCACCCTGGCATCCTAAAGCTGCCGCACGTGCGGCTGCCACAGGCACTGGCTAACGGTGCCCAGTTATTGCTA CTTGGTGAGTAACGGCGGGAAAGCGAGAAGAAACGGGACTGGACCTACATGCAAGTGATTCCGCTTTTCGTCTTTG GCCCATAGGGAGCGCTGGGCCCACTATGGAGAATCAGG
141_DI03_001	26	25	GGAGATGGAGAAGAGGGGCCACCTTCTCATGCCACCCCGCCGCCAATCCTCCAGGCACACTCGGGCGCTTGACCTG CTGAAGCCTGTAGCCTCAGGTCCAGTGAGGAGCTCACGGGACAGAGGGCCCTACCAGAGCCACGAAAACCGGAGGG GGGGACCTCCGCCCAAGGCAGGCGTCTCTGCGCGCCCGCTGGGGCCCTGGTCCTGCAGTTGGCTTCTCCCGACACG TTCCTTCGCTGCCGAAAGCGATTCGCCCGCGCTCTACCGAGCCCAGCCAGCTCCTACCTCGGCCCGGGCGGCGAGC GCTGTCTCCCGTCCCGAGAAGAAGTTTCGCGGCTGGTCCCGGGGCGGCAGGCGCACGGGACGCTGGCGGCGGCGGCG GCTTCCGACTTGGGCTCAGACCCCGCCGCTCCAGACAAGTCCCCGCGACTGCGACAGTGTCTCGGGCAGTTCAGCT CCCCAGACGGGAGACAGACCCTCGCGACCTGGTTCAGGCCTTGCCCTGGG
144_IMPACT_001	26	25	TGTGGACTGAGGTTTGAGTCCCTTCCCGGGACGCGGTGGTAAATGACTCCCTAAAGTCTCCTGGCCATTCCGATGG CGCCAAGGCCGCAATGGGCAAGCAAAGCCCCCCGCCCCGGCGCATTCCTAGGAGACAGAGCCGTGAGGGCCTCTG GCTGCAACTCGCGAGGGTCGGCTTTCCCTGGGTCTCCGCCCTACGGGAGACAGTGAAGGCGGGAGCAAGGCCCCAA CCGAGAACCCCACCCCCAAACCCGGGGGCCAGGAGCCCTTTACACCCTTCGGCCCGCCACCCGGAAGCAGATGCCGG CGGCGCGGCGTGGCAGGGTTGTGGTTCCGGGTCGGGCCGCGCCGCAGCCAGCTCTCGGCTCGCAGCCGCAGCGCCC CGCCCCCGCGCTCCGGACCTGGCAGGCGGCGGCTGCAGGGCAGGTCCAGGGGCCACATGGCTGAGGGG
145_TCEB3C_001	28	25	AGCCTCTCTGACTGGCTTTCCTGGACAGGAGGCGATTTCTGAGCCGAAGCCCCGCGGGACGATTTGTGCCCCTTGC TGTGGCTCCCCCACCGCTTCCCCCTGGGGTTGGCCCTGGCAGCCTTGACCCAGCAGAGGCCCGCCCTGAGCGGCGTG AGCGTGGCCTCTTCCGGGTTGCTCCCCCGGGCACAGCGGGCTCAGGGCCCTCGGGCATCGGGAGGGGAGCGGTGCGC GTTGGAGGGTCCCGATGGGGGCCGGAATCAGCTGGGGCCATTCTGGGGCGCTTTCTCTCGGCTCTGGGCTCGCGAC TGGGAGACCTCGGGTGAGGTCTCTGTTGCCCCGGAGGTGTTCTGCGTGCTGTCCGTCTGTGCTCAGGGCTGTGAGA TGGGCTC
146_NNAT_001	26	23	TGGGCCAGGCAGCTTGCTGGAAAGAGGTGCTTTCGGCTGGCTACCGGTGCGCGGGGACCACACTCACAAACCGCAT

			TCCGGTCTTCCCGCCCGAAAATCCGCGCTGTGCGAGGGACCCACAAGACTGGCGGTCTAAAAGGGACCCGCCTCAC TTGGAAACGGGGCTGCGGTAGCCACAACCCTCCGGTAGCGGTAGCGTAACCCCGTTCGGTGATCCAGCCGCACAGC GCAACGGGTACAAAGAACCCCACTGGCTAAGGCCGACCTACCAGGGCTTGGGGGAGG
147_GNAS_001	27	25	GGAGGCAGACCTTGAGCTGTCCCTCCCCGAGTGCCTAGAGTACGAGGAAGAGTTCGACTACGAGACCGAGAGCGAG ACCGAGTCCGAAATCGAGTCCGAGACCGACTTCGAGACCGAGCCTGAGACCGCCCCCACCACTGAGCCCGAGACCG AGCCTGAAGACGATCGCGGCCCGGTGGTGCCCAAGCACTCCACCTTCGGCCAGTCCCTCACCCAGCGTCTGCACGC TCTCAAGTTGCGAAGCCCCGACGCCTCCCCCAAGTCGCGCGCCGCCCAGCACTCAGGAGCCCCAGAGCCCCAGGGAA GGGGAGGAG
148_TPD52L2_001	27	28	CTGGAAAGGATCTCAAGGGGTCAGAGTTTGAGCCGCCGAGGCGCGCGAGCCCCAGCACTCCTAGGCAGCTGCATCC GCCCCGGAAGATCCCCTGGGGCCCTGCGCTGGCTTTCCACAGCGCCATGTTGGACGGTCCTCCCCACTTCCCACCTT CCCAGTCCTCCCCGCTACTCTGACCGTTCTACCTGTGATTCTCGCTGGTGGAGTCAACCTGGAATGGATTCCCGCCG AACCACGCCTCCCTTTCCTGGTTCGCCCGCAGTTTCGGCCTATCAGGTTGAGTCGGGTAAACCAGGACGGGCCAAG CGGCACTCTCATTGGATATCACTGGTGGGGG
149_F2R_001	30	25	TCTCATTTAGGGGCAACCCTGTCACTACATCATAAACTTTTAAATCCGTGATCCCCACGTTACAAAAGCAGAAGTC CCTTTTAGACTTTTAGCGAAAACTGAACTTTGCCGGTGTCCCACACGGAGGGAGGGAGGACGGGAGGCCACGCCAG GGCTGCGGGGCTGCAGGGCGTGGACGCATCCTGGCCGGGGCGTCCACTGTCGACGTCTCCACATCCCAGGAGGGTC GAGACGGCCGCGGGAAGCAGCCTGCGAGCCGTGCGGCCCCATTCCAAGGACCCCGCCAGTGTGAGTCACTGACAGC TTCGCGAATCAACGGTGCCCAGAGGAAAAAACTTCTCATTTGGACTTCTAGGCCCGGCAGTGGCCGGCGGCCAGGG CCCCCCAGTAGGGCAGGG
150_U2AF1RS1_001	28	30	GGCAAGATGGCTGCACTTGAGAAGATGACGTTTCCCAAGAAGATGACATTTCCAGAGAAACCAAGCCACACAAAAAGT ACAGGGCCGCCCTGAAGAAGGAGAAACGAAAGAAACGTCGGCAGGAACTTGCTCGACTGAGAGACTCAGGACTCTC ACAGGAGGAGGAAGAGGACACTTTTATTATTGAAGAACAACAACTAGAAGAAGAGAAGCTATTGGAAAGAGAGAGGAA AGATTACATGAGGAGTGGTTGCTGAGGGAGCAGAAGGCACAAGAAGAAT
HOXA1_AB01	29	30	GCTTGGACCACAACTTGAGTGGGAGTAGGACACCCCCAGGTTCCCGGAAGTCTGGTAGGTAGCCGGCTGGGGGTGG CGATGGTGGTGGTGGTGGTGGGGCGAACCGATCTGCACCCCCCCTGCCCACTAGGAAGCGGTCGTCGCCGC CGCAACTGTTGGCGCTGACCGCGCACGACTGGAAAGTTGTAATCCTATGGTCCGAGGGGTAGGCTCGGGCTGAGCA GGTCCCCGAGTCGCCACTGCTAAGTATGGGGTATTCCAGGAAGGAGTTCATTC
HOXA1_SQ05	29	30	CCCCCTCCCAGTGTCCAGCCCAGAGTCTGCGCCCCGGGCCCATTGTTAGCAGGCTATTCCACGGCAGCTTTGCATC TGGCTCCGGCGGGAAGCGGAAAACGGGAGGCGGCTCTCGAAGCTTCCCGACCTTCCTGCGCCATCAACTTCTCAGG AGTGGCTGGAGAAAGATGCATGTGCCAAGCGAGACAACACCCCAGGTCCATGTGTCCAAATCCCCGTAGCCAGGG CGGCGGCCAGCCAAAGAAATGCCGCCCCGAGCAGGCGCGTGCGGCTCCTGGCATTCTGGGTTTCATACCCGTAGGG CTCGGGTGCGGTGAGTATTTCCGATTTCCAGGAAGTCTGTTGGAAGTTACCAGCAGGGAAAGAGAAGATGCTTGCT CCTC
HOXA3_AB01	25	30	TTGGCTGCCTGGTAGGGGTAGCCACCGTAGATCGCCGAGCTGTCGTAGTAGGTCGCTTTTTGCATCGCGTTGTTTC ACGATCTTGATCGCACACACTCTGACAGGGGTTTGACACCCGTGAGGGCGCACATTGGCACGCCCCCGCGGTCACGTG ACACTCCGCCGCCAATGGCCGCCCCGCGCAGACCTGGTGGGGCGAGAAGCGCAGCGCGGTGAGGGCTCCGCGCAAA TCCATCTTACTCTCAATAGCTAAGTGACATGAAAGCCATAAAAGAAAAAGTGGTCAGC
HOXA3_SQ01	25	30	TCCCAGGCTTGGAGGCTGGCTAGGTGGGGCGCTCAGGGTGCGCAGGCACGCCTCACTCAGTTCGTGTGCCTTGGGG TGGCCCCCGGCGCTGGAGGGAGACTGGAGGGAGCAGGCGGGTCGGTGGTACTCGCCGTCGGCGCCCAAAGCGGCGG

			ACGCCGGGTACGGCTGCTGATTGGCATTATAAGCGAACCCGTTGGCTGCCTGGTAGGGGTAGCCACCGTAGATCGC
			CGAGCTGTCGTAGTAGGTCGCTTTTTGCATCGCGTTGTTTCACGATCTTGATCGCACACACTCTGACAGGGGTTTGAC
			ACCCGTGAGGGCGCACATTGGCACGCCCCCGCGGTCACGTGACACTCCGCCGCCCAATGGCCGCCCCGCGCAGACCT
			GGTGGGGCGAGAAGCGCAGCGCGGTGAGGGCTCCGCGCAAATCCATCTTACTCTCAATAGCTAAGTGACATGAAAG
			CCATAAAAGAAAAAGTGGTC
HOXA4_AB01	22	30	GAGGGAGCTGGGGCTGCTGCAGCGGCAGGTGCTGGGTCGGGGGCGCTGGGGGCTGCTGGTAGCCGGGGCCCCCGCC
			CGGGCCGCCGTCTGCGCCGCCCGAGCCGCTGTGCTGCGCGTACTCCTCGAAGGGAGGGAACTTGGGCTCGATGTAG
			TTGGAGTTTATCAAAAACGAGCTCATGGTCATTAATTTGTGAAGTGCAAAA
HOXA4_SQ02	25	22	TGGATCTTCTTCATCCAGGGGTACACCACGGGCTCCTTGCCCTTCAGGCCCAGCGGGCTCTTGTCGGCCAAGAGCA
			GCGGGCACGCCGGGGGCGCTGCCCCCTGCCGGACGCCTGGGGTGGCGGGGCCGCCTCGCAGCGCCGCGGGGCCGC
			TGGGGGCACGGCGCGAGGCTGCAGGGGCGGCGGCAGCTGGGGCTGCAGGACGTGGCTCGCATGCAGGCCGTGCGCT
			GGGCCCTTGGCTTGCGCCGGGGGCTGCTCGGGCTGGGGCGGCCGCCCGGGGCTGGCGCCGCGCTGGTAGCCATAGG
			GGTAGGCGGTGTCCGCGGCCCCATGCGCGGGGTACAGCGCGGCAGCAGGGTAGGCGGGCTCGCGGGCGGTCCGCGG
			CGCGTAGTAGGAGGCAGTGGGCTCTCGGCCGCCCGCCGTGAGGGAGCTGGGGCTGCTGCAG
HOXA5_AB01	28	30	CCTGCCTGATGACCTCTAGAGGTAAACTCGTGCACTAATAGGGGAGTTGGGTGGAGGCGAGGGGGGTGGCGCGCGC
			GCCCCGGGCGCGTGCCCGCCGCCAGTTGCCGCCGTTCAGCCGGACTCGAGCGCCACCCGCTGGAGGCAGGGCTCAT
			CGCCCAGCTTCCGACCGGGGGCTGCAAGGGCCGGGGTCGAATTGAGGTTACAGCCCATTATGGCAAAATTATTGCA
			TTTCCCTCGCAGTTCCATTAGGATGTGTACCAATTGTTAGGCCGTCAGCTGCCGATCGCGCCCGGCGAGGATGCAG
			AGGATTGGGGGGAGGTGGTGACTTGCATTTTATTTACAAC
HOXA5_SQ03	25	30	CTGGGACATGTACTTGGTTCCCTCCTACGTAGGCACCCAAATATGGGGTACGACTTCGAATCACGTGCTTTTGTTG
			TCCAGTCGTAAATCCTGCCTGATGACCTCTAGAGGTAAACTCGTGCACTAATAGGGGAGTTGGGTGGAGGCGAGGG
			GGGTGGCGCGCGCCCCCGGGCGCGTGCCCGCCGCCAGTTGCCGCCGTTCAGCCGGACTCGAGCGCCACCCGCTGG
			AGGCAGGGCTCATCGCCCAGCTTCCGACCGGGGGCTGCAAGGGCCGGGGTCGAATTGAGGTTACAGCCCATTATGG
			CAAAATTATTGCATTTCCCTCGCAGTTCCATTAGGATGTACCAATTGTTAGGCCGTCAGCTGCCGATCGCGCGCCC
			GGCGAGGATGCAGAGGATTGGGGGGAGGTGGTGACTTGCATTTTATTTACAACAACTTTATTTCCCCCGTTTTGCA
			GCCCCTCTTATTTTTGTGTCGAGGTTGGGGTCGGTACTGACCGTCCTGCCAGCAGCTCTGAATTTTGAAAATACAG
HOXA6_AB01	24	27	GGGGCCCCCTCTGCTTGCCACTGCCCGAGGGCGAGGCGCCACTGAGGTCCTTATCAGAATAGAAACACGAGGCCCCG
			TACTCGTAGGACGCCCCGGTTGCAGGCCAGGACCGAGTTGGACTGTTGGTAGAAACAAGGTGAGGTGTACGTCTTGT
			CCGGGAGACTCGACGCCCCCGTACGAGGCCGGGAAGGGCCTCAGCGCGTCATAGCCAGCCTGGTAGAGGGGCAGCTG
			GCCCAAGAAGGA
HOXA7_AB01	25	25	GGGGGCTGTTGACATTGTATAAGCCCGGAACGGTCGAGGCGAAGGCGCCGGCGCCCGCCCCGTAGCCGCTTCTCTG
			TGAGTTGGGAGCAAAGGAGCAAGAAGTCGGCTCGGCATTTTGGAACAGAGAAGCCCCCGCCGTATATTTGCTAAAA
			AGCGCGTTCACATAATACGAAGAACTCATAATTTTGACCTGTGATTTGTTGTCGGCAGCTTTCAGTGTCGGTTTT
			ACGAGGTAGAGTGATATATGATAACATTACACCCCCAGATTTACACCAAACCCCATTTTCTTTGGACGGAGCTCG
			CCGCAGCACGTGACCGCCCACATGACCGCCTCCGCCAATCTCAGCAGTCCTCACAGGTGGTCTCGCTCCGCAGGGC
			CCGCAGCCGCCTAGAATGGAAGGGCAAGAGGCT
HOXA7_SQ03	28	25	CTAGAATGGAAGGGCAAGAGGCTCAAATATGCGGCCAAAGAATCCGCCCGCGCCCGGCGGCCTGGCGCGTCCCGC
			GGAAAAAGACCTGGAGGCTCCGCGGGAGCGCCCAGCTGGCGGCCAACCTCCGCACTGGGGTCTGCGGACGCCAGGC
			GGCCCGGCCCCCACGCAGCACCCCCCCACCCCGCCCCCCCCGCCGACTCCTGCTAGTGAGCCCTGGACC

HOXA9_AB01	26	30	CCCAGGGCCCCAGTGGTGGCCATCACCGTGCCCAGCGCCTGGCCCGCCCGGCCCGACCCACGGAAATTATGAAACT GCAGATTTCATGTAACAACTTGGTGGCACCGGGGGGGAAGTACAGTCACCTAATAAGTTGCCGGCGCCCGCGCCCC CATTGGCCGTGCGCGTCACGTGCCCCGTCCAGCAGAACAATAACGCGTAAATCACTCCGCACGCTATTAATGGTCCG ATGTTTTGCAGTCATAAATTTTTATAGCAAAAGCCATATGTTTTTATGTAAAGGGATCGTGCCGCTCTACGATGGGG TTTGTTTTAATTGTGGCCAACGACGATTAAAAGATCAAATCTAGCCTTGTCTCTGT
HOXA9_SQ03	30	26	TTTTCTCTATCAACTGGAGGAGAACCACACAAGCATAGTCAGTCAGGGACAAAGTGTGAGTGTCAAGCGTGGGACAGT CACCCCTTCTGGCCGACAGCGGTTCAGGTTTAATGCCATAAGGCCGGCTGGAGGGCAAGCCCGCGAAGGAGAGCGC ACCGGGCGTGGGCTCCAGCCAGGAGCGCATGTACCTGCCGTCCGGCGCCGCCGCCACGGGCGCCTGGGGGTGC ACGTAGGGGTGGTGGTGATGGTGGTACACCGCAGCGGGTACAGCGTTGGCGCCCGCCGCGTGCACTGGGTTCC ACGAGGCGCCAAACACCGTCGCCTTGGACTGGAAGCTGCACGGGCTGAAGTCGGGGTGCTCGGCCAGCGTCGCCGC CTGCCGGGGAGGCTGGCCCAGGGTCCCCGGCGCATAGCGGCCAACGCTCAGCTCATCCGCGGCGTCGGCGCCCAGC AGGAACGAGTCCACGTAGTAGTTGCCCAGGGCCCCAGTGG
HOXA10_AB01	30	22	AGCCCTTTCTGGCTGACATTTCTTGTGCAAAACATGCTGAATACGATTAGCAATCCCCCCGCACCGCGGCGGGCGC CCGCAGCCAATCCCGAGCCAGAGTTTCCGCGCGACCACTCCCAGTTTGGTTTCGTAGGCGCGGGGCCGCTCTCCGA GGGCGCCCTCAGAGCCCCGCGATTGATATAAATATGTAATCTGTATTGATGGGCCAGGAGACGCACCCCGACACCTT GGCCCGAAGGCCGGGAGCTGTGGGGGCTGCCCCCAA
HOXA10_SQ02	30	25	TGGCTGACATTTCTTGTGCAAAACATGCTGAATACGATTAGCAATCCCCCCGCACCGCGGCGGGCGCCCGCAGCCA ATCCCGAGCCAGAGTTTCCGCGCGACCACTCCCAGTTTGGTTTCGTAGGCGCGGGGCCGCTCTCCGAGGGCGCCCT CAGAGCCCGCGATTGATATAAATATGTAATCTGTATTGATGGGCCAGGAGACGCACCCCGACACCTTGGCCCGAAG GCCGGGAGCTGTGGGGGCTGCCCCCAACGTGGCTGGTGGGGGCCTGGCCATTGGGCTCGCCCCGCCCCTACCCGGA CGTGAGCCCCCATACCGGGGTCCCTTAGAAGGGCCCTTGGGCCCCGCGCAGTTAACAAGTGGGGTGTTTATGGTGCG CGCCCAGTCTGCCTTGGGTGCTCACCATCCCTGTCGCAGAAGCTGCCACTAGTCCCCGGTGTACTCTAACCACTGA AGCGGCCGTGTCGGGGACTCACGCGCTTCCCATTCAGCTCTGGAACTGGCCCCTTGTCTGA
HOXA11_SQ01	30	24	CTTTCTTTGTAGCCACCTCAGGGGAAGCAACAGATCGTCACTCGGTGTTCTCACCGAAAGCACGTAATCGCCGGTG TAACTCATGTTGGCTGGGGGGCCTCCCGGCGCGCGCGGAGAGGCTGGGGTGCGCCCCCATGCAGCATGCTTGTGCT CAATTGCAGGGTCCTCGTTCTCGAGTGTGCAGAGGGCGGTGAGAGCTCAACTCTCGTCCCCACCTCCCACCCGCAG CTCCCCGGGTGGGTGAGGGATGCCCTGGGACTGGGGATAGCCAGGTGGGAGTCCGTCGCTGTGTGGCCTGTGGTCTC GGAGTCTGTTCTCCTGGAGTCTCGCATTTGCACCCCCCTTCTTCGCAGTCCCCCTCCCATAGACTTGCTCTGGGAAG CGCCTCTGCCTCCGACCCTAGCCGGAACCCCCTTCGGGGCCAGAGTTTGAAGCCGTGGATGTGCCTGGTGGCT TGTC
HOXA13_SQ01	26	25	AGGGCAGACCAGGAAGAGAACAGAAACGCACCCGGGATCGCCCGGGTGCGAGCGGAGAAGAAGCTGGAGCAGAGCC GGAAGACCAGGGCTGGGAATAGGTCGTCATTTACCGGGCAGAGTGGACTTCCAGAGGTGGGGAGGCTGCGCCTGCT CTTTGGGGCAGTACATTTGGCCGTTCCAGCCGTTGGGCAGCGCCCAGGGCTGGTAGCTTTCCATGGGAAGACCCAA GGGTTCGTGGCGCGACTCGCCGGGGCCCCCGAGGCCCGGCACCACTGGCATATCCAGGTAGCCAGGCATGGGCTGA TGGTGG
HOXA13_SQ03	22	28	GAGCAGGGGCTGCATTGCTTGGCGGCCTCTGCGCCCGCCGGGCCCGGGACCTCCCGAGGACGACGCGG CGGCGGCGGCGGCTGCAGCGGCAGCCGCGGCAGCAGCGGCGCGACGGGGGCGCCTCCCCCGGGGGCGCT GCTGTAGGCGGACGCGGCTCCTGGCGCCAAGGGCGCCGGTGCGCCATCAGGTTGCGGCACTGGTTGGCCGCGGCC GCCGCCGCAGCCGCGGCCGCCGCCACCGAGAAGTTGCCCCCTGCCGCCGCAGCCGCCGGTGGGGGAAGCCCCC

			CGCCCCCGGCCCCGGCAGCCGCCGCTGCAGCCGCTGCTGCAGCCGCCGCCCCTTCCATGTTCTTGTTGAG
			CTCGTCGGCCACCAGGCCGCCGCCGTTGTCGTAGAGAAACATGACGGTGGGCTCGATCCAGCGGGGGTGGAGGAGC
			ACGGAGGCTGTCATAGCCCGAGCCGCATGGAGAAGACCCCAGTGGCGCTGTTTTAAAAAGCCCCCAAGAAGTGA
005_ERalpha_02	30	26	CCTCCACACCAAAGCATCTGGGATGGCCCTACTGCATCAGATCCAAGGGAACGAGCTGGAGCCCCTGAACCGTCCG
			CAGCTCAAGATCCCCCTGGAGCGGCCCCTGGGCGAGGTGTACCTGGACAGCAAGCCCGCCGTGTACAACTACC
			CCGAGGGCGCCCGCCTACGAGTTCAACGCCGCGGCCGCCGCCAACGCGCAGGTCTACGGTCAGACCGGCCTCCCCTA
			CGGCCCCGGGTCTGAGGCTGCGGCGTTCGGCTCCAACGGCCTGGGGGGTTTCCCCCCACTCAACAGCGTGTCTCCG
			AGCCCGCTGATGCTACTGCACCCGCCGCCGCAGCTGTCGCCTTCCTGCAGCCCCACGGCCAGGCAGGTGCCCTACT
			ACCTGGA
			GGGAGACCAGTACTTAAAGTTGGAGGCCCGGGAGCCCAGGAGCTGGCGGAGGGCGTTCGTCCTGGGACTGCACTTG
ESR1_01_01	28	30	CTCCCGTCGGGTCGCCCGGCTTCACCGGACCCGCAGGCTCCCGGGGCAGGGCCGGGCCAGAGCTCGCGTGTCGGC
			GGGACATGCGCTGCGTCGCCTCTAACCTCGGGCTGTGCTCTTTTTCCAGGTGGCCCGCCGGTTTCTGAGCCTTCTG
			CCCTGCGGGGACACGGTCTGCACCCTGCCCGCGGCCACGGACCATGACCCTCCACACCAAAGCATCTGGG
			ATGGCCCTACTGCATCAGATC
			GGGGACAGTGGGTGGGCATTCAGACTGCCAGCACTTTGCTATCTACAGCCGGGGCTCCCGAGCGGCAGAAAGTTCC
MYOD_01_02	25	24	GGCCACTCTCTGCCGCTTGGGTTGGGCGAAGCCAGGACCGTGCCGCGCCACCGCCAGGATATGGAGCTACTGTCGC
			CACCGCTCCGCGACGTAGACCTGACGGCCCCCGACGGCTCTCTCTGCTCCTTTGCCACAACGGACGACTTCTATGA
			CGACCCGTGTTTCGACTCCCCGGACCTGCGCTTCTTCGAAGACCTGGACCCGCGCCTGATGCACGTGGGCGCGCTC
			CTGAAACCCGAAGAGCACTCGCACTTCCCCGCGGCGGTGCACCCGGCCCCGGGCGCACGTGAGGACGAGCATGTGC
			GCGCGCCCAGCGGGCACCACCAGGCGGGCCGCTGCCTACTGTGGGCCTGCAAGG
			GGGTACTGGAGAATAAAGACATCTCCAATAAAATGAGAAAGGAGACTGAAAGGGAACGGTGGGCTAGGTCTTGAGG
002_E-cad_02	30	24	GGGTGACTCGGCGGCCCCCTCCCGGGAGTTCCTGGGGGCTCGGCGGCCGTAGGTTTCGGGGTGGGGGAGGGTGACG
			TCGCTGCCCGCCCGTCCCGGGGCTGCGGGCTGGGGTCCTCCCCCAATCCCGACGCCGGGAGCGAGGGAGGGGCGGC
			GCTGTTGGTTTCGGTGAGCAGGAGGGAACCCTCCGAGTCACCCGGTTCCATCTACCTTTCCCCCACCCCAGGTCTC
			CTCTTGGCTCTGCCCAGGAGCCCGGAGCCCTGCCACCCTGGCTTTGA
			GCTGCCCCTTGGCTGCCCCTTCCGCTCTCGTAGGCGCGCGGGGCCACTACTCACGCGCGCACTGCAGGCCTTTGCG
			CACGACGCCCCCAGATGAAGTCGCCACACAGAGGTCGCACCACGTGTGCGTGGCGGGCCCCGCGGCTGGAAGCGGTGG
RASSF1	22	25	CCACGGCCAGGGACCAGCTGCCGTGTGGGGTTGCACGCGGTGCCCCCGCGCGATGCGCAGCGCGTTGGCACGCTCCA
			GCCGGGTGCGGCCCTTCCCAGCGCGCCCAGCGGGTGCCAGCTCCCGCAGCTCAATGAGCTCAGGCTCCCCCGACAT
			GGCCCGGTTGGGCCCGTGCTTCGCTGGCTTTGGGCGCTAGCAAGCGCGGGCCGGGGCCACAGGGCGGGCCCC
			GACTTCAGCGCCTCCCCCCAGGATCCAGACTGGGCGGCGGAAGGAGCTGAGGAGAGCCGCGCCAATGGAAACCTGGG
			TGCAGGGAC
p53_03	22	30	GAGCCCTAGGGCTTGATGGGAACGGGAAACCTTCTAACCTTTCACGTCCCGGCTCCGCGGGTTCCGTGGGTCGCCC
			GCGAAATCTGATCCGGGATGCGGCGGCCCAATCGGAAGGTGGACCGAAATCCCGCGACAGCAAGAGGCCCGTAGCG
			ACCCGCGGTGCTAAGGAACACAGTGCTTTCAAAAGAATTGG
			AGGAGGGTCTATTCTTTGCCAAAGGGGGGACCAGAATTCCCCCATGCGAGCTGTTTGAGGACTGGGATGCCGAGAA
007_RAR-beta_01	26	25	CGCGAGCGATCCGAGCAGGGTTTGTCTGGGCACCGTCGGGGTAGGATCCGGAACGCATTCGGAAGGCTTTTTGCAA
			GCATTTACTTGGAAGGAGAACTTGGGATCTTTCTGGGAACCCCCCCGCCCCGGCTGGATTGGCCGAGCAAGCCTGGA
			AAATGGTAAATGATCATTTGGATCAATTACAGGCTTTTAGCTGGCTTGTCTGTCATAATTCATGATTCGGGGCTGG

			GAAAAAGACCAACAGCC
GSTP1-300+100_01	23	27	CGGCGCGCCAGTTCGCTGCGCACACTTCGCTGCGGTCCTCTTCCTGCTGTCTGTTTACTCCCTAGGCCCCGCTGGG GACCTGGGAAAGAGGGAAAGGCTTCCCCGGCCAGCTGCCGCGGCGACTCCAGGGCGCCCCTCTGCGGC CGACGCCCGGGGTGCAGCGGCCGCCGGGGCTGGGGCCGGCGGGAGTCCGCGGGACCCTCCAGAAGAGCGGCCGGCG CCGTGACTCAGCACTGGGGCGGAGCGGGGCGGGACCACCCTTATAAGGCTCGGAGGCCGCGAGGCCTTCGCTGGAG TTTCGCCGCCGCAGTCTTCGCCACCAGTGAGTACGCGCGGCCCGCGTCCCCGGGGATGGGGCTCAGAGCTCCCAGC ATGGGGCCAACCCGCAGCAT
14_RUNX3_01_01	24	26	GGGAGAGCTGGCCCCTACCCACCTCGGGACCTCACAGCACGCCCTCAGGCCGTGTCGAAAGGAAGGACGGCAAAGG TCCCTTACTGAACCTTTTAAGAGAGGCCTGCGCCTGGCAGTTGTCGATTGCGGACCCAGGCCCGCGCGCCCTCGGAC GCGCTGGCACGAGCAGCAGAACTAGAGGAAAGCGAGTGATCCAGCCTGGGCGCTCCCACCTCCGGGAACGTCTCCG AGAAGGCGCAGCGCGTCGTGGCCAGGTAGGGCCCTGGCCGGGGGCGGGCAACACGTGCTGCCCTCGAGCAGGTTGC GGGACCATGACCCGCTGTTTCAGGTGGTGGTAAATTCCATTTGTCGAATGGTTTCGGTTTGCACCGTGCCCTTTGC TTGTTCCTCCGCCTGATTTCTCCCTCTCCGCTTACGATGGGTTCACAGACAAGTTTCCAGAGAATGAGGGACTCTT GTGGGC
15_RUNX3_02_01	30	24	CCCCAGAACAAATCCTCCAGAATCAAGTggcgggccgcggccgccgcgcgggTTAGTAccccccgggccccgcg gggcgggcTGGCGGAGCGACGCGTCGCACAGCCAATCGGCGGAGCCCCCATCGCGGGCACCTCGGTGGCGTTCGC GGGGAGGAACGGGGCCTGCCGGAGGCCGCCCAACGGGGAGGGCGGAAGGCGCCACCCCGCGGAGGAGGCCCCAGT GCCACAGCCCCAGGGCCCCCGAGAGCTCTGGGAGCCCGGGCAAATGCTAGAAATTTGCTTAGAACGTCCGGGTCCC ACGGAAGGCGCCCTTGCCGCCCTCTCTCGGGTCGTAGCTCCCTGACGCTGGGGCGCAACCCCTTCGCTCCTCCTCC CCGCTGGCCGCGGCCGGGCTTCCCCAGCTCTTGCTGCTT

TABLE 11 – CpG SITE LOCATIONS

Target Gene Region	CpG Unit Location
X201_ABL1	X201_ABL1_CpG_1.2, X201_ABL1_CpG_3.4.5.6, X201_ABL1_CpG_7, X201_ABL1_CpG_8, X201_ABL1_CpG_9, X201_ABL1_CpG_10, X201_ABL1_CpG_11, X201_ABL1_CpG_12.13.14, X201_ABL1_CpG_15.16.17, X201_ABL1_CpG_18, X201_ABL1_CpG_19, X201_ABL1_CpG_20.21, X201_ABL1_CpG_22.23, X201_ABL1_CpG_24, X201_ABL1_CpG_25.26.27, X201_ABL1_CpG_28, X201_ABL1_CpG_29, X201_ABL1_CpG_30.31, X201_ABL1_CpG_32.33, X201_ABL1_CpG_34
X202_ABL2	X202_ABL2_CpG_1.2.3, X202_ABL2_CpG_4, X202_ABL2_CpG_5, X202_ABL2_CpG_6.7.8, X202_ABL2_CpG_9, X202_ABL2_CpG_10.11.12.13, X202_ABL2_CpG_14.15.16.17.18.19.20, X202_ABL2_CpG_21.22.23, X202_ABL2_CpG_24, X202_ABL2_CpG_25, X202_ABL2_CpG_26, X202_ABL2_CpG_27.28.29.30.31.32, X202_ABL2_CpG_33.34.35, X202_ABL2_CpG_36.37.38.39.40.41.42.43.44.45.46, X202_ABL2_CpG_47, X202_ABL2_CpG_48, X202_ABL2_CpG_49.50.51.52.53, X202_ABL2_CpG_54.55, X202_ABL2_CpG_56, X202_ABL2_CpG_57, X202_ABL2_CpG_58.59.60, X202_ABL2_CpG_61, X202_ABL2_CpG_62.63.64, X202_ABL2_CpG_65, X202_ABL2_CpG_66.67.68
X203_AF15Q14	X203_AF15Q14_CpG_1.2, X203_AF15Q14_CpG_3, X203_AF15Q14_CpG_4, X203_AF15Q14_CpG_5, X203_AF15Q14_CpG_6.7, X203_AF15Q14_CpG_8.9.10.11, X203_AF15Q14_CpG_12, X203_AF15Q14_CpG_13, X203_AF15Q14_CpG_14.15, X203_AF15Q14_CpG_16, X203_AF15Q14_CpG_17.18, X203_AF15Q14_CpG_19, X203_AF15Q14_CpG_20, X203_AF15Q14_CpG_21, X203_AF15Q14_CpG_22.23, X203_AF15Q14_CpG_24
X204_AF1Q	X204_AF1Q_CpG_1, X204_AF1Q_CpG_2, X204_AF1Q_CpG_3, X204_AF1Q_CpG_4, X204_AF1Q_CpG_5, X204_AF1Q_CpG_6.7.8, X204_AF1Q_CpG_9, X204_AF1Q_CpG_10, X204_AF1Q_CpG_11.12.13.14.15.16, X204_AF1Q_CpG_17, X204_AF1Q_CpG_18, X204_AF1Q_CpG_19
X205_AF3p21	X205_AF3p21_CpG_1.2, X205_AF3p21_CpG_3.4, X205_AF3p21_CpG_5.6.7, X205_AF3p21_CpG_8.9, X205_AF3p21_CpG_10.11, X205_AF3p21_CpG_12, X205_AF3p21_CpG_13.14, X205_AF3p21_CpG_15, X205_AF3p21_CpG_16, X205_AF3p21_CpG_17, X205_AF3p21_CpG_18.19.20.21.22, X205_AF3p21_CpG_23.24.25, X205_AF3p21_CpG_26.27.28.29, X205_AF3p21_CpG_30, X205_AF3p21_CpG_31.32.33.34, X205_AF3p21_CpG_35, X205_AF3p21_CpG_36.37, X205_AF3p21_CpG_38.39.40, X205_AF3p21_CpG_41
X206_AF5q31	X206_AF5q31_CpG_1.2.3, X206_AF5q31_CpG_4, X206_AF5q31_CpG_5.6.7.8.9.10, X206_AF5q31_CpG_11, X206_AF5q31_CpG_12, X206_AF5q31_CpG_13.14, X206_AF5q31_CpG_15.16.17.18, X206_AF5q31_CpG_19, X206_AF5q31_CpG_20.21, X206_AF5q31_CpG_22.23.24, X206_AF5q31_CpG_25, X206_AF5q31_CpG_26.27, X206_AF5q31_CpG_28.29, X206_AF5q31_CpG_30, X206_AF5q31_CpG_31.32, X206_AF5q31_CpG_33, X206_AF5q31_CpG_34.35.36.37, X206_AF5q31_CpG_38, X206_AF5q31_CpG_39, X206_AF5q31_CpG_40.41.42, X206_AF5q31_CpG_43, X206_AF5q31_CpG_44, X206_AF5q31_CpG_45.46.47, X206_AF5q31_CpG_48, X206_AF5q31_CpG_49
X207_AKT2	X207_AKT2_01_CpG_1, X207_AKT2_01_CpG_2.3.4.5, X207_AKT2_01_CpG_6, X207_AKT2_01_CpG_7.8, X207_AKT2_01_CpG_9.10.11, X207_AKT2_01_CpG_12.13, X207_AKT2_01_CpG_14.15.16, X207_AKT2_01_CpG_17.18.19, X207_AKT2_01_CpG_20, X207_AKT2_01_CpG_21, X207_AKT2_01_CpG_22.23, X207_AKT2_01_CpG_24, X207_AKT2_01_CpG_25, X207_AKT2_01_CpG_26.27.28, X207_AKT2_01_CpG_29, X207_AKT2_01_CpG_30.31.32, X207_AKT2_01_CpG_33, X207_AKT2_01_CpG_34.35.36.37, X207_AKT2_01_CpG_38.39, X207_AKT2_01_CpG_40,

	X207_AKT2_01_CpG_41.42.43.44, X207_AKT2_01_CpG_45, X207_AKT2_01_CpG_46, X207_AKT2_01_CpG_47, X207_AKT2_01_CpG_48.49.50, X207_AKT2_01_CpG_51, X207_AKT2_01_CpG_52, X207_AKT2_01_CpG_53, X207_AKT2_01_CpG_54, X207_AKT2_01_CpG_55, X207_AKT2_01_CpG_56.57
X208_AKT2	X208_AKT2_02_CpG_1, X208_AKT2_02_CpG_2.3.4.5, X208_AKT2_02_CpG_6, X208_AKT2_02_CpG_7.8, X208_AKT2_02_CpG_9.10.11, X208_AKT2_02_CpG_12.13, X208_AKT2_02_CpG_14.15.16, X208_AKT2_02_CpG_17.18.19, X208_AKT2_02_CpG_20, X208_AKT2_02_CpG_21, X208_AKT2_02_CpG_22.23, X208_AKT2_02_CpG_24, X208_AKT2_02_CpG_25, X208_AKT2_02_CpG_26.27.28, X208_AKT2_02_CpG_29, X208_AKT2_02_CpG_30.31.32, X208_AKT2_02_CpG_33, X208_AKT2_02_CpG_34.35.36.37, X208_AKT2_02_CpG_38.39, X208_AKT2_02_CpG_40, X208_AKT2_02_CpG_41.42.43.44, X208_AKT2_02_CpG_45, X208_AKT2_02_CpG_46, X208_AKT2_02_CpG_47, X208_AKT2_02_CpG_48.49.50, X208_AKT2_02_CpG_51, X208_AKT2_02_CpG_52, X208_AKT2_02_CpG_53, X208_AKT2_02_CpG_54, X208_AKT2_02_CpG_55, X208_AKT2_02_CpG_56.57
X209_ALK	X209_ALK_CpG_1, X209_ALK_CpG_2.3.4.5, X209_ALK_CpG_6.7.8, X209_ALK_CpG_9.10.11, X209_ALK_CpG_12.13, X209_ALK_CpG_14, X209_ALK_CpG_15, X209_ALK_CpG_16.17, X209_ALK_CpG_18.19.20, X209_ALK_CpG_21.22, X209_ALK_CpG_23, X209_ALK_CpG_24, X209_ALK_CpG_25.26, X209_ALK_CpG_27.28, X209_ALK_CpG_29
X210_ALO17	X210_ALO17_CpG_1, X210_ALO17_CpG_2.3, X210_ALO17_CpG_4, X210_ALO17_CpG_5.6, X210_ALO17_CpG_7.8, X210_ALO17_CpG_9, X210_ALO17_CpG_10.11, X210_ALO17_CpG_12.13, X210_ALO17_CpG_14, X210_ALO17_CpG_15.16.17, X210_ALO17_CpG_18, X210_ALO17_CpG_19
X211_APC	X211_APC_CpG_1.2, X211_APC_CpG_3, X211_APC_CpG_4.5, X211_APC_CpG_6, X211_APC_CpG_7, X211_APC_CpG_8, X211_APC_CpG_9.10, X211_APC_CpG_11.12, X211_APC_CpG_13.14, X211_APC_CpG_15.16, X211_APC_CpG_17.18.19.20, X211_APC_CpG_21.22.23.24.25.26
X212_ARHGEF12	X212_ARHGEF12_CpG_1.2.3, X212_ARHGEF12_CpG_4, X212_ARHGEF12_CpG_5.6.7, X212_ARHGEF12_CpG_8.9.10, X212_ARHGEF12_CpG_11.12, X212_ARHGEF12_CpG_13, X212_ARHGEF12_CpG_14.15, X212_ARHGEF12_CpG_16.17, X212_ARHGEF12_CpG_18.19.20, X212_ARHGEF12_CpG_21.22.23, X212_ARHGEF12_CpG_24.25, X212_ARHGEF12_CpG_26.27, X212_ARHGEF12_CpG_28.29, X212_ARHGEF12_CpG_30, X212_ARHGEF12_CpG_31, X212_ARHGEF12_CpG_32, X212_ARHGEF12_CpG_33.34.35.36, X212_ARHGEF12_CpG_37, X212_ARHGEF12_CpG_38, X212_ARHGEF12_CpG_39, X212_ARHGEF12_CpG_40, X212_ARHGEF12_CpG_41.42, X212_ARHGEF12_CpG_43, X212_ARHGEF12_CpG_44.45, X212_ARHGEF12_CpG_46, X212_ARHGEF12_CpG_47.48.49
X213_ARHH	X213_ARHH_01_CpG_1.2.3.4, X213_ARHH_01_CpG_5, X213_ARHH_01_CpG_6, X213_ARHH_01_CpG_7, X213_ARHH_01_CpG_8.9, X213_ARHH_01_CpG_10, X213_ARHH_01_CpG_11, X213_ARHH_01_CpG_12, X213_ARHH_01_CpG_13.14.15, X213_ARHH_01_CpG_16.17.18.19.20, X213_ARHH_01_CpG_21, X213_ARHH_01_CpG_22, X213_ARHH_01_CpG_23, X213_ARHH_01_CpG_24.25, X213_ARHH_01_CpG_26.27.28.29.30, X213_ARHH_01_CpG_31, X213_ARHH_01_CpG_32, X213_ARHH_01_CpG_33.34.35, X213_ARHH_01_CpG_36.37, X213_ARHH_01_CpG_38.39.40.41.42.43.44.45, X213_ARHH_01_CpG_46, X213_ARHH_01_CpG_47, X213_ARHH_01_CpG_48.49.50.51.52.53.54.55.56, X213_ARHH_01_CpG_57.58.59.60, X213_ARHH_01_CpG_61, X213_ARHH_01_CpG_62.63.64, X213_ARHH_01_CpG_65, X213_ARHH_01_CpG_66.67.68.69.70.71, X213_ARHH_01_CpG_72, X213_ARHH_01_CpG_73.74, X213_ARHH_01_CpG_75.76, X213_ARHH_01_CpG_77.78, X213_ARHH_01_CpG_79.80, X213_ARHH_01_CpG_81
X214_ARHH	X214_ARHH_02_CpG_1.2.3.4, X214_ARHH_02_CpG_5, X214_ARHH_02_CpG_6, X214_ARHH_02_CpG_7, X214_ARHH_02_CpG_8.9, X214_ARHH_02_CpG_10, X214_ARHH_02_CpG_11, X214_ARHH_02_CpG_12,

	X214_ARHH_02_CpG_13.14.15, X214_ARHH_02_CpG_16.17.18.19.20, X214_ARHH_02_CpG_21, X214_ARHH_02_CpG_22, X214_ARHH_02_CpG_23, X214_ARHH_02_CpG_24.25, X214_ARHH_02_CpG_26.27.28.29.30, X214_ARHH_02_CpG_31, X214_ARHH_02_CpG_32, X214_ARHH_02_CpG_33.34.35, X214_ARHH_02_CpG_36.37, X214_ARHH_02_CpG_38.39.40.41.42.43.44.45, X214_ARHH_02_CpG_46, X214_ARHH_02_CpG_47, X214_ARHH_02_CpG_48.49.50.51.52.53.54.55.56, X214_ARHH_02_CpG_57.58.59.60, X214_ARHH_02_CpG_61, X214_ARHH_02_CpG_62.63.64, X214_ARHH_02_CpG_65, X214_ARHH_02_CpG_66.67.68.69.70.71, X214_ARHH_02_CpG_72, X214_ARHH_02_CpG_73.74, X214_ARHH_02_CpG_75.76, X214_ARHH_02_CpG_77.78, X214_ARHH_02_CpG_79.80, X214_ARHH_02_CpG_81
X215_ARNT	X215_ARNT_CpG_1, X215_ARNT_CpG_2, X215_ARNT_CpG_3, X215_ARNT_CpG_4, X215_ARNT_CpG_5.6, X215_ARNT_CpG_7, X215_ARNT_CpG_8.9.10.11, X215_ARNT_CpG_12.13, X215_ARNT_CpG_14, X215_ARNT_CpG_15
X216_ASPSCR1	X216_ASPSCR1_CpG_1.2.3.4, X216_ASPSCR1_CpG_5, X216_ASPSCR1_CpG_6, X216_ASPSCR1_CpG_7.8.9.10, X216_ASPSCR1_CpG_11.12, X216_ASPSCR1_CpG_13.14, X216_ASPSCR1_CpG_15.16, X216_ASPSCR1_CpG_17.18.19, X216_ASPSCR1_CpG_20, X216_ASPSCR1_CpG_21.22.23, X216_ASPSCR1_CpG_24.25, X216_ASPSCR1_CpG_26, X216_ASPSCR1_CpG_27, X216_ASPSCR1_CpG_28.29, X216_ASPSCR1_CpG_30.31, X216_ASPSCR1_CpG_32
X217_ATF1	X217_ATF1_CpG_1, X217_ATF1_CpG_2, X217_ATF1_CpG_3.4, X217_ATF1_CpG_5.6.7, X217_ATF1_CpG_8.9, X217_ATF1_CpG_10.11.12, X217_ATF1_CpG_13, X217_ATF1_CpG_14.15, X217_ATF1_CpG_16, X217_ATF1_CpG_17.18.19.20.21, X217_ATF1_CpG_22, X217_ATF1_CpG_23, X217_ATF1_CpG_24.25.26, X217_ATF1_CpG_27, X217_ATF1_CpG_28, X217_ATF1_CpG_29, X217_ATF1_CpG_30
X218_ATIC	X218_ATIC_CpG_1.2, X218_ATIC_CpG_3.4, X218_ATIC_CpG_5, X218_ATIC_CpG_6, X218_ATIC_CpG_7.8, X218_ATIC_CpG_9, X218_ATIC_CpG_10, X218_ATIC_CpG_11, X218_ATIC_CpG_12.13.14.15.16, X218_ATIC_CpG_17, X218_ATIC_CpG_18, X218_ATIC_CpG_19, X218_ATIC_CpG_20.21.22.23.24.25, X218_ATIC_CpG_26.27.28.29.30.31, X218_ATIC_CpG_32, X218_ATIC_CpG_33.34.35, X218_ATIC_CpG_36.37.38.39.40, X218_ATIC_CpG_41.42, X218_ATIC_CpG_43.44, X218_ATIC_CpG_45, X218_ATIC_CpG_46, X218_ATIC_CpG_47, X218_ATIC_CpG_48, X218_ATIC_CpG_49, X218_ATIC_CpG_50, X218_ATIC_CpG_51
X226_BCL6	X226_BCL6_CpG_1, X226_BCL6_CpG_2, X226_BCL6_CpG_3, X226_BCL6_CpG_4, X226_BCL6_CpG_5, X226_BCL6_CpG_6, X226_BCL6_CpG_7, X226_BCL6_CpG_8, X226_BCL6_CpG_9, X226_BCL6_CpG_10, X226_BCL6_CpG_11, X226_BCL6_CpG_12, X226_BCL6_CpG_13.14.15, X226_BCL6_CpG_16, X226_BCL6_CpG_17, X226_BCL6_CpG_18
X227_BCL7A	X227_BCL7A_CpG_1, X227_BCL7A_CpG_2, X227_BCL7A_CpG_3, X227_BCL7A_CpG_4.5, X227_BCL7A_CpG_6, X227_BCL7A_CpG_7, X227_BCL7A_CpG_8, X227_BCL7A_CpG_9, X227_BCL7A_CpG_10, X227_BCL7A_CpG_11.12, X227_BCL7A_CpG_13.14, X227_BCL7A_CpG_15, X227_BCL7A_CpG_16, X227_BCL7A_CpG_17.18, X227_BCL7A_CpG_19.20.21.22, X227_BCL7A_CpG_23, X227_BCL7A_CpG_24.25, X227_BCL7A_CpG_26, X227_BCL7A_CpG_27.28, X227_BCL7A_CpG_29, X227_BCL7A_CpG_30, X227_BCL7A_CpG_31.32, X227_BCL7A_CpG_33.34.35, X227_BCL7A_CpG_36, X227_BCL7A_CpG_37.38, X227_BCL7A_CpG_39, X227_BCL7A_CpG_40
X228_BCL9	X228_BCL9_CpG_1.2.3, X228_BCL9_CpG_4.5.6, X228_BCL9_CpG_7.8.9, X228_BCL9_CpG_10.11.12, X228_BCL9_CpG_13.14, X228_BCL9_CpG_15.16.17.18.19.20.21.22.23, X228_BCL9_CpG_24, X228_BCL9_CpG_25.26.27, X228_BCL9_CpG_28, X228_BCL9_CpG_29, X228_BCL9_CpG_30, X228_BCL9_CpG_31
X229_BCR	X229_BCR_01_CpG_1, X229_BCR_01_CpG_2, X229_BCR_01_CpG_3.4.5.6.7, X229_BCR_01_CpG_8,

	X229_BCR_01_CpG_9.10.11, X229_BCR_01_CpG_12, X229_BCR_01_CpG_13.14.15.16.17.18, X229_BCR_01_CpG_19.20.21, X229_BCR_01_CpG_22, X229_BCR_01_CpG_23, X229_BCR_01_CpG_24.25.26.27, X229_BCR_01_CpG_28, X229_BCR_01_CpG_29.30, X229_BCR_01_CpG_31.32, X229_BCR_01_CpG_33, X229_BCR_01_CpG_34, X229_BCR_01_CpG_35.36, X229_BCR_01_CpG_37, X229_BCR_01_CpG_38.39.40, X229_BCR_01_CpG_41, X229_BCR_01_CpG_42, X229_BCR_01_CpG_43, X229_BCR_01_CpG_44, X229_BCR_01_CpG_45.46.47, X229_BCR_01_CpG_48, X229_BCR_01_CpG_49, X229_BCR_01_CpG_50, X229_BCR_01_CpG_51.52, X229_BCR_01_CpG_53.54, X229_BCR_01_CpG_55, X229_BCR_01_CpG_56.57, X229_BCR_01_CpG_58, X229_BCR_01_CpG_59.60, X229_BCR_01_CpG_61, X229_BCR_01_CpG_62, X229_BCR_01_CpG_63, X229_BCR_01_CpG_64, X229_BCR_01_CpG_65.66.67.68, X229_BCR_01_CpG_69
X230_BCR	X230_BCR_02_CpG_1, X230_BCR_02_CpG_2, X230_BCR_02_CpG_3.4.5.6.7, X230_BCR_02_CpG_8, X230_BCR_02_CpG_9.10.11, X230_BCR_02_CpG_12, X230_BCR_02_CpG_13.14.15.16.17.18, X230_BCR_02_CpG_19.20.21, X230_BCR_02_CpG_22, X230_BCR_02_CpG_23, X230_BCR_02_CpG_24.25.26.27, X230_BCR_02_CpG_28, X230_BCR_02_CpG_29.30, X230_BCR_02_CpG_31.32, X230_BCR_02_CpG_33, X230_BCR_02_CpG_34, X230_BCR_02_CpG_35.36, X230_BCR_02_CpG_37, X230_BCR_02_CpG_38.39.40, X230_BCR_02_CpG_41, X230_BCR_02_CpG_42, X230_BCR_02_CpG_43, X230_BCR_02_CpG_44, X230_BCR_02_CpG_45.46.47, X230_BCR_02_CpG_48, X230_BCR_02_CpG_49, X230_BCR_02_CpG_50, X230_BCR_02_CpG_51.52, X230_BCR_02_CpG_53.54, X230_BCR_02_CpG_55, X230_BCR_02_CpG_56.57, X230_BCR_02_CpG_58, X230_BCR_02_CpG_59.60, X230_BCR_02_CpG_61, X230_BCR_02_CpG_62, X230_BCR_02_CpG_63, X230_BCR_02_CpG_64, X230_BCR_02_CpG_65.66.67.68, X230_BCR_02_CpG_69
X231_BHD	X231_BHD_CpG_1, X231_BHD_CpG_2, X231_BHD_CpG_3.4, X231_BHD_CpG_5, X231_BHD_CpG_6, X231_BHD_CpG_7, X231_BHD_CpG_8, X231_BHD_CpG_9, X231_BHD_CpG_10, X231_BHD_CpG_11, X231_BHD_CpG_12.13, X231_BHD_CpG_14, X231_BHD_CpG_15.16, X231_BHD_CpG_17, X231_BHD_CpG_18, X231_BHD_CpG_19.20, X231_BHD_CpG_21, X231_BHD_CpG_22.23, X231_BHD_CpG_24, X231_BHD_CpG_25.26, X231_BHD_CpG_27
X235_BMPR1A	X235_BMPR1A_02_CpG_1, X235_BMPR1A_02_CpG_2.3, X235_BMPR1A_02_CpG_4.5, X235_BMPR1A_02_CpG_6, X235_BMPR1A_02_CpG_7, X235_BMPR1A_02_CpG_8.9.10, X235_BMPR1A_02_CpG_11.12.13, X235_BMPR1A_02_CpG_14.15, X235_BMPR1A_02_CpG_16, X235_BMPR1A_02_CpG_17, X235_BMPR1A_02_CpG_18.19.20.21, X235_BMPR1A_02_CpG_22
X236_BRAF	X236_BRAF_CpG_1, X236_BRAF_CpG_2, X236_BRAF_CpG_3, X236_BRAF_CpG_4.5, X236_BRAF_CpG_6, X236_BRAF_CpG_7.8, X236_BRAF_CpG_9.10.11, X236_BRAF_CpG_12, X236_BRAF_CpG_13, X236_BRAF_CpG_14, X236_BRAF_CpG_15, X236_BRAF_CpG_16
X237_BRCA1	X237_BRCA1_CpG_1, X237_BRCA1_CpG_2, X237_BRCA1_CpG_3.4, X237_BRCA1_CpG_5, X237_BRCA1_CpG_6, X237_BRCA1_CpG_7, X237_BRCA1_CpG_8, X237_BRCA1_CpG_9.10.11, X237_BRCA1_CpG_12, X237_BRCA1_CpG_13, X237_BRCA1_CpG_14, X237_BRCA1_CpG_15, X237_BRCA1_CpG_16.17, X237_BRCA1_CpG_18, X237_BRCA1_CpG_19, X237_BRCA1_CpG_20, X237_BRCA1_CpG_21, X237_BRCA1_CpG_22, X237_BRCA1_CpG_23, X237_BRCA1_CpG_24, X237_BRCA1_CpG_25
X238_BRCA2	X238_BRCA2_CpG_1, X238_BRCA2_CpG_2, X238_BRCA2_CpG_3, X238_BRCA2_CpG_4, X238_BRCA2_CpG_5, X238_BRCA2_CpG_6, X238_BRCA2_CpG_7, X238_BRCA2_CpG_8.9.10.11.12, X238_BRCA2_CpG_13.14, X238_BRCA2_CpG_15, X238_BRCA2_CpG_16.17.18.19, X238_BRCA2_CpG_20, X238_BRCA2_CpG_21, X238_BRCA2_CpG_22, X238_BRCA2_CpG_23.24.25.26.27.28.29.30, X238_BRCA2_CpG_31, X238_BRCA2_CpG_32.33.34,

	X238_BRCA2_CpG_35, X238_BRCA2_CpG_36, X238_BRCA2_CpG_37, X238_BRCA2_CpG_38.39.40, X238_BRCA2_CpG_41.42, X238_BRCA2_CpG_43, X238_BRCA2_CpG_44.45.46.47.48
X240_BTG1	X240_BTG1_CpG_1, X240_BTG1_CpG_2, X240_BTG1_CpG_3.4, X240_BTG1_CpG_5, X240_BTG1_CpG_6.7, X240_BTG1_CpG_8, X240_BTG1_CpG_9.10, X240_BTG1_CpG_11.12.13, X240_BTG1_CpG_14, X240_BTG1_CpG_15, X240_BTG1_CpG_16.17, X240_BTG1_CpG_18, X240_BTG1_CpG_19.20, X240_BTG1_CpG_21.22, X240_BTG1_CpG_23, X240_BTG1_CpG_24.25, X240_BTG1_CpG_26.27, X240_BTG1_CpG_28.29, X240_BTG1_CpG_30.31, X240_BTG1_CpG_32, X240_BTG1_CpG_33, X240_BTG1_CpG_34, X240_BTG1_CpG_35.36.37.38, X240_BTG1_CpG_39.40, X240_BTG1_CpG_41.42.43.44, X240_BTG1_CpG_45, X240_BTG1_CpG_46, X240_BTG1_CpG_47.48
X241_CBFA2T1	X241_CBFA2T1_01_CpG_1, X241_CBFA2T1_01_CpG_2.3.4.5.6.7, X241_CBFA2T1_01_CpG_8, X241_CBFA2T1_01_CpG_9, X241_CBFA2T1_01_CpG_10, X241_CBFA2T1_01_CpG_11.12.13.14.15, X241_CBFA2T1_01_CpG_16.17.18.19.20.21, X241_CBFA2T1_01_CpG_22.23, X241_CBFA2T1_01_CpG_24.25.26, X241_CBFA2T1_01_CpG_27.28.29, X241_CBFA2T1_01_CpG_30.31.32.33.34, X241_CBFA2T1_01_CpG_35.36.37.38, X241_CBFA2T1_01_CpG_39.40.41.42, X241_CBFA2T1_01_CpG_43, X241_CBFA2T1_01_CpG_44, X241_CBFA2T1_01_CpG_45, X241_CBFA2T1_01_CpG_46, X241_CBFA2T1_01_CpG_47.48.49.50.51.52.53, X241_CBFA2T1_01_CpG_54
X242_CBFA2T1	X242_CBFA2T1_02_CpG_1, X242_CBFA2T1_02_CpG_2.3.4.5.6, X242_CBFA2T1_02_CpG_7.8, X242_CBFA2T1_02_CpG_9, X242_CBFA2T1_02_CpG_10, X242_CBFA2T1_02_CpG_11, X242_CBFA2T1_02_CpG_12.13.14.15.16.17.18, X242_CBFA2T1_02_CpG_19.20, X242_CBFA2T1_02_CpG_21.22.23.24.25.26, X242_CBFA2T1_02_CpG_27.28, X242_CBFA2T1_02_CpG_29, X242_CBFA2T1_02_CpG_30.31.32.33, X242_CBFA2T1_02_CpG_34, X242_CBFA2T1_02_CpG_35.36, X242_CBFA2T1_02_CpG_37.38.39.40, X242_CBFA2T1_02_CpG_41, X242_CBFA2T1_02_CpG_42.43.44.45.46, X242_CBFA2T1_02_CpG_47, X242_CBFA2T1_02_CpG_48.49, X242_CBFA2T1_02_CpG_50, X242_CBFA2T1_02_CpG_51, X242_CBFA2T1_02_CpG_52, X242_CBFA2T1_02_CpG_53, X242_CBFA2T1_02_CpG_54.55
X244_CBFB	X244_CBFB_CpG_1, X244_CBFB_CpG_2, X244_CBFB_CpG_3, X244_CBFB_CpG_4, X244_CBFB_CpG_5.6, X244_CBFB_CpG_7, X244_CBFB_CpG_8.9, X244_CBFB_CpG_10.11, X244_CBFB_CpG_12, X244_CBFB_CpG_13, X244_CBFB_CpG_14, X244_CBFB_CpG_15, X244_CBFB_CpG_16, X244_CBFB_CpG_17, X244_CBFB_CpG_18.19, X244_CBFB_CpG_20.21.22
X245_CBL.	X245_CBL._CpG_1.2, X245_CBL._CpG_3.4.5, X245_CBL._CpG_6, X245_CBL._CpG_7.8, X245_CBL._CpG_9, X245_CBL._CpG_10, X245_CBL._CpG_11.12.13, X245_CBL._CpG_14, X245_CBL._CpG_15.16, X245_CBL._CpG_17, X245_CBL._CpG_18.19.20.21, X245_CBL._CpG_22.23.24, X245_CBL._CpG_25, X245_CBL._CpG_26, X245_CBL._CpG_27, X245_CBL._CpG_28.29.30.31.32.33, X245_CBL._CpG_34
X246_CCND1	X246_CCND1_01_CpG_1, X246_CCND1_01_CpG_2.3, X246_CCND1_01_CpG_4, X246_CCND1_01_CpG_5, X246_CCND1_01_CpG_6, X246_CCND1_01_CpG_7, X246_CCND1_01_CpG_8, X246_CCND1_01_CpG_9, X246_CCND1_01_CpG_10, X246_CCND1_01_CpG_11, X246_CCND1_01_CpG_12, X246_CCND1_01_CpG_13, X246_CCND1_01_CpG_14, X246_CCND1_01_CpG_15, X246_CCND1_01_CpG_16, X246_CCND1_01_CpG_17.18, X246_CCND1_01_CpG_19, X246_CCND1_01_CpG_20.21, X246_CCND1_01_CpG_22, X246_CCND1_01_CpG_23.24, X246_CCND1_01_CpG_25, X246_CCND1_01_CpG_26.27, X246_CCND1_01_CpG_28, X246_CCND1_01_CpG_29.30, X246_CCND1_01_CpG_31.32, X246_CCND1_01_CpG_33.34.35.36.37.38.39.40, X246_CCND1_01_CpG_41,

	X246_CCND1_01_CpG_42.43.44.45.46.47, X246_CCND1_01_CpG_48, X246_CCND1_01_CpG_49.50, X246_CCND1_01_CpG_51, X246_CCND1_01_CpG_52.53.54
X247_CCND1	X247_CCND1_02_CpG_1, X247_CCND1_02_CpG_2.3, X247_CCND1_02_CpG_4, X247_CCND1_02_CpG_5, X247_CCND1_02_CpG_6, X247_CCND1_02_CpG_7, X247_CCND1_02_CpG_8, X247_CCND1_02_CpG_9, X247_CCND1_02_CpG_10, X247_CCND1_02_CpG_11, X247_CCND1_02_CpG_12, X247_CCND1_02_CpG_13, X247_CCND1_02_CpG_14, X247_CCND1_02_CpG_15, X247_CCND1_02_CpG_16, X247_CCND1_02_CpG_17.18, X247_CCND1_02_CpG_19, X247_CCND1_02_CpG_20.21, X247_CCND1_02_CpG_22, X247_CCND1_02_CpG_23.24, X247_CCND1_02_CpG_25, X247_CCND1_02_CpG_26.27, X247_CCND1_02_CpG_28, X247_CCND1_02_CpG_29.30, X247_CCND1_02_CpG_31.32, X247_CCND1_02_CpG_33.34.35.36.37.38.39.40, X247_CCND1_02_CpG_41, X247_CCND1_02_CpG_42.43.44.45.46.47, X247_CCND1_02_CpG_48, X247_CCND1_02_CpG_49.50, X247_CCND1_02_CpG_51, X247_CCND1_02_CpG_52.53.54
X249_CDK4	X249_CDK4_CpG_1.2.3.4, X249_CDK4_CpG_5, X249_CDK4_CpG_6.7, X249_CDK4_CpG_8.9.10.11, X249_CDK4_CpG_12, X249_CDK4_CpG_13.14, X249_CDK4_CpG_15.16, X249_CDK4_CpG_17, X249_CDK4_CpG_18.19, X249_CDK4_CpG_20.21.22.23.24, X249_CDK4_CpG_25.26.27, X249_CDK4_CpG_28.29.30.31.32.33.34.35.36.37, X249_CDK4_CpG_38.39, X249_CDK4_CpG_40, X249_CDK4_CpG_41, X249_CDK4_CpG_42, X249_CDK4_CpG_43, X249_CDK4_CpG_44.45.46, X249_CDK4_CpG_47.48, X249_CDK4_CpG_49, X249_CDK4_CpG_50.51, X249_CDK4_CpG_52.53.54, X249_CDK4_CpG_55, X249_CDK4_CpG_56, X249_CDK4_CpG_57, X249_CDK4_CpG_58.59
X262_CTNNB1	X262_CTNNB1_CpG_1.2.3.4, X262_CTNNB1_CpG_5, X262_CTNNB1_CpG_6, X262_CTNNB1_CpG_7.8, X262_CTNNB1_CpG_9, X262_CTNNB1_CpG_10, X262_CTNNB1_CpG_11, X262_CTNNB1_CpG_12, X262_CTNNB1_CpG_13.14, X262_CTNNB1_CpG_15.16.17, X262_CTNNB1_CpG_18, X262_CTNNB1_CpG_19.20.21, X262_CTNNB1_CpG_22.23.24.25.26.27.28.29, X262_CTNNB1_CpG_30.31.32.33.34.35, X262_CTNNB1_CpG_36.37.38, X262_CTNNB1_CpG_39.40, X262_CTNNB1_CpG_41, X262_CTNNB1_CpG_42.43.44, X262_CTNNB1_CpG_45, X262_CTNNB1_CpG_46, X262_CTNNB1_CpG_47, X262_CTNNB1_CpG_48, X262_CTNNB1_CpG_49.50, X262_CTNNB1_CpG_51, X262_CTNNB1_CpG_52, X262_CTNNB1_CpG_53, X262_CTNNB1_CpG_54.55, X262_CTNNB1_CpG_56.57.58
X263_CYLD	X263_CYLD_CpG_1.2.3, X263_CYLD_CpG_4, X263_CYLD_CpG_5, X263_CYLD_CpG_6, X263_CYLD_CpG_7, X263_CYLD_CpG_8.9.10.11.12, X263_CYLD_CpG_13, X263_CYLD_CpG_14, X263_CYLD_CpG_15, X263_CYLD_CpG_16.17, X263_CYLD_CpG_18, X263_CYLD_CpG_19
X264_D10S170	X264_D10S170_01_CpG_1, X264_D10S170_01_CpG_2, X264_D10S170_01_CpG_3.4, X264_D10S170_01_CpG_5, X264_D10S170_01_CpG_6, X264_D10S170_01_CpG_7.8, X264_D10S170_01_CpG_9, X264_D10S170_01_CpG_10.11.12, X264_D10S170_01_CpG_13, X264_D10S170_01_CpG_14
X304_FGFR1OP	X304_FGFR1OP_01_CpG_1, X304_FGFR1OP_01_CpG_2, X304_FGFR1OP_01_CpG_3, X304_FGFR1OP_01_CpG_4, X304_FGFR1OP_01_CpG_5, X304_FGFR1OP_01_CpG_6, X304_FGFR1OP_01_CpG_7.8, X304_FGFR1OP_01_CpG_9, X304_FGFR1OP_01_CpG_10, X304_FGFR1OP_01_CpG_11.12.13, X304_FGFR1OP_01_CpG_14.15.16.17.18.19, X304_FGFR1OP_01_CpG_20.21.22, X304_FGFR1OP_01_CpG_23, X304_FGFR1OP_01_CpG_24, X304_FGFR1OP_01_CpG_25, X304_FGFR1OP_01_CpG_26, X304_FGFR1OP_01_CpG_27.28.29, X304_FGFR1OP_01_CpG_30.31, X304_FGFR1OP_01_CpG_32.33.34, X304_FGFR1OP_01_CpG_35.36.37.38, X304_FGFR1OP_01_CpG_39
X267_DDIT3	X267_DDIT3_CpG_1.2, X267_DDIT3_CpG_3, X267_DDIT3_CpG_4, X267_DDIT3_CpG_5, X267_DDIT3_CpG_6.7,

	X267_DDIT3_CpG_8, X267_DDIT3_CpG_9, X267_DDIT3_CpG_10, X267_DDIT3_CpG_11, X267_DDIT3_CpG_12, X267_DDIT3_CpG_13
X270_EGFR	X270_EGFR_CpG_1, X270_EGFR_CpG_2, X270_EGFR_CpG_3, X270_EGFR_CpG_4.5.6, X270_EGFR_CpG_7.8, X270_EGFR_CpG_9, X270_EGFR_CpG_10, X270_EGFR_CpG_11, X270_EGFR_CpG_12.13, X270_EGFR_CpG_14, X270_EGFR_CpG_15, X270_EGFR_CpG_16, X270_EGFR_CpG_17, X270_EGFR_CpG_18.19, X270_EGFR_CpG_20
X271_EIF4A2	X271_EIF4A2_CpG_1, X271_EIF4A2_CpG_2, X271_EIF4A2_CpG_3.4.5, X271_EIF4A2_CpG_6, X271_EIF4A2_CpG_7, X271_EIF4A2_CpG_8.9, X271_EIF4A2_CpG_10, X271_EIF4A2_CpG_11.12, X271_EIF4A2_CpG_13.14.15.16, X271_EIF4A2_CpG_17.18, X271_EIF4A2_CpG_19, X271_EIF4A2_CpG_20.21.22, X271_EIF4A2_CpG_23.24, X271_EIF4A2_CpG_25.26, X271_EIF4A2_CpG_27, X271_EIF4A2_CpG_28, X271_EIF4A2_CpG_29.30.31, X271_EIF4A2_CpG_32, X271_EIF4A2_CpG_33, X271_EIF4A2_CpG_34, X271_EIF4A2_CpG_35, X271_EIF4A2_CpG_36, X271_EIF4A2_CpG_37
X272_ELKS	X272_ELKS_CpG_1, X272_ELKS_CpG_2, X272_ELKS_CpG_3, X272_ELKS_CpG_4.5.6.7.8.9.10, X272_ELKS_CpG_11.12, X272_ELKS_CpG_13.14.15, X272_ELKS_CpG_16.17.18.19.20.21.22.23.24.25, X272_ELKS_CpG_26.27.28.29.30, X272_ELKS_CpG_31, X272_ELKS_CpG_32, X272_ELKS_CpG_33.34.35.36.37.38, X272_ELKS_CpG_39.40, X272_ELKS_CpG_41.42.43, X272_ELKS_CpG_44, X272_ELKS_CpG_45, X272_ELKS_CpG_46.47, X272_ELKS_CpG_48.49.50, X272_ELKS_CpG_51, X272_ELKS_CpG_52.53, X272_ELKS_CpG_54, X272_ELKS_CpG_55, X272_ELKS_CpG_56, X272_ELKS_CpG_57.58, X272_ELKS_CpG_59.60, X272_ELKS_CpG_61.62, X272_ELKS_CpG_63.64, X272_ELKS_CpG_65, X272_ELKS_CpG_66
X274_EP300	X274_EP300_CpG_1.2, X274_EP300_CpG_3, X274_EP300_CpG_4, X274_EP300_CpG_5.6, X274_EP300_CpG_7, X274_EP300_CpG_8, X274_EP300_CpG_9.10, X274_EP300_CpG_11.12, X274_EP300_CpG_13.14, X274_EP300_CpG_15, X274_EP300_CpG_16.17.18.19, X274_EP300_CpG_20, X274_EP300_CpG_21, X274_EP300_CpG_22
X275_EPS15	X275_EPS15_01_CpG_1.2, X275_EPS15_01_CpG_3.4, X275_EPS15_01_CpG_5, X275_EPS15_01_CpG_6.7.8, X275_EPS15_01_CpG_9, X275_EPS15_01_CpG_10.11.12, X275_EPS15_01_CpG_13.14, X275_EPS15_01_CpG_15.16.17.18, X275_EPS15_01_CpG_19.20, X275_EPS15_01_CpG_21, X275_EPS15_01_CpG_22, X275_EPS15_01_CpG_23.24.25.26, X275_EPS15_01_CpG_27.28, X275_EPS15_01_CpG_29.30, X275_EPS15_01_CpG_31, X275_EPS15_01_CpG_32, X275_EPS15_01_CpG_33.34.35, X275_EPS15_01_CpG_36.37, X275_EPS15_01_CpG_38, X275_EPS15_01_CpG_39.40, X275_EPS15_01_CpG_41.42, X275_EPS15_01_CpG_43.44.45, X275_EPS15_01_CpG_46.47
X277_ERBB2	X277_ERBB2_01_CpG_1, X277_ERBB2_01_CpG_2.3, X277_ERBB2_01_CpG_4.5, X277_ERBB2_01_CpG_6.7.8.9, X277_ERBB2_01_CpG_10, X277_ERBB2_01_CpG_11, X277_ERBB2_01_CpG_12, X277_ERBB2_01_CpG_13, X277_ERBB2_01_CpG_14, X277_ERBB2_01_CpG_15.16.17, X277_ERBB2_01_CpG_18, X277_ERBB2_01_CpG_19.20, X277_ERBB2_01_CpG_21, X277_ERBB2_01_CpG_22, X277_ERBB2_01_CpG_23
X278_ERBB2	X278_ERBB2_02_CpG_1, X278_ERBB2_02_CpG_2.3, X278_ERBB2_02_CpG_4.5, X278_ERBB2_02_CpG_6.7.8.9, X278_ERBB2_02_CpG_10, X278_ERBB2_02_CpG_11, X278_ERBB2_02_CpG_12, X278_ERBB2_02_CpG_13, X278_ERBB2_02_CpG_14, X278_ERBB2_02_CpG_15.16.17, X278_ERBB2_02_CpG_18, X278_ERBB2_02_CpG_19.20, X278_ERBB2_02_CpG_21, X278_ERBB2_02_CpG_22, X278_ERBB2_02_CpG_23
X279_ERCC2	X279_ERCC2_CpG_1, X279_ERCC2_CpG_2, X279_ERCC2_CpG_3.4, X279_ERCC2_CpG_5, X279_ERCC2_CpG_6.7, X279_ERCC2_CpG_8, X279_ERCC2_CpG_9.10.11, X279_ERCC2_CpG_12, X279_ERCC2_CpG_13.14, X279_ERCC2_CpG_15.16.17, X279_ERCC2_CpG_18.19, X279_ERCC2_CpG_20, X279_ERCC2_CpG_21,

	X279_ERCC2_CpG_22.23, X279_ERCC2_CpG_24, X279_ERCC2_CpG_25, X279_ERCC2_CpG_26, X279_ERCC2_CpG_27, X279_ERCC2_CpG_28, X279_ERCC2_CpG_29, X279_ERCC2_CpG_30.31.32, X279_ERCC2_CpG_33, X279_ERCC2_CpG_34, X279_ERCC2_CpG_35, X279_ERCC2_CpG_36, X279_ERCC2_CpG_37.38, X279_ERCC2_CpG_39, X279_ERCC2_CpG_40.41
X280_ERCC3	X280_ERCC3_CpG_1, X280_ERCC3_CpG_2, X280_ERCC3_CpG_3.4.5, X280_ERCC3_CpG_6, X280_ERCC3_CpG_7.8, X280_ERCC3_CpG_9, X280_ERCC3_CpG_10, X280_ERCC3_CpG_11.12, X280_ERCC3_CpG_13, X280_ERCC3_CpG_14.15.16.17, X280_ERCC3_CpG_18.19.20, X280_ERCC3_CpG_21, X280_ERCC3_CpG_22, X280_ERCC3_CpG_23, X280_ERCC3_CpG_24, X280_ERCC3_CpG_25, X280_ERCC3_CpG_26.27.28, X280_ERCC3_CpG_29, X280_ERCC3_CpG_30.31.32.33, X280_ERCC3_CpG_34, X280_ERCC3_CpG_35.36.37, X280_ERCC3_CpG_38, X280_ERCC3_CpG_39, X280_ERCC3_CpG_40, X280_ERCC3_CpG_41, X280_ERCC3_CpG_42.43, X280_ERCC3_CpG_44, X280_ERCC3_CpG_45, X280_ERCC3_CpG_46.47, X280_ERCC3_CpG_48.49, X280_ERCC3_CpG_50.51
X281_ERCC4	X281_ERCC4_CpG_1, X281_ERCC4_CpG_2.3, X281_ERCC4_CpG_4.5.6.7.8, X281_ERCC4_CpG_9, X281_ERCC4_CpG_10, X281_ERCC4_CpG_11, X281_ERCC4_CpG_12.13, X281_ERCC4_CpG_14, X281_ERCC4_CpG_15, X281_ERCC4_CpG_16, X281_ERCC4_CpG_17.18, X281_ERCC4_CpG_19.20
X282_ERCC5	X282_ERCC5_CpG_1, X282_ERCC5_CpG_2.3, X282_ERCC5_CpG_4.5, X282_ERCC5_CpG_6.7, X282_ERCC5_CpG_8, X282_ERCC5_CpG_9, X282_ERCC5_CpG_10.11, X282_ERCC5_CpG_12, X282_ERCC5_CpG_13, X282_ERCC5_CpG_14.15.16, X282_ERCC5_CpG_17, X282_ERCC5_CpG_18.19
X285_ETV4	X285_ETV4_01_CpG_1, X285_ETV4_01_CpG_2, X285_ETV4_01_CpG_3.4.5, X285_ETV4_01_CpG_6.7, X285_ETV4_01_CpG_8, X285_ETV4_01_CpG_9, X285_ETV4_01_CpG_10, X285_ETV4_01_CpG_11.12, X285_ETV4_01_CpG_13.14.15, X285_ETV4_01_CpG_16.17, X285_ETV4_01_CpG_18, X285_ETV4_01_CpG_19, X285_ETV4_01_CpG_20.21, X285_ETV4_01_CpG_22, X285_ETV4_01_CpG_23, X285_ETV4_01_CpG_24, X285_ETV4_01_CpG_25, X285_ETV4_01_CpG_26, X285_ETV4_01_CpG_27, X285_ETV4_01_CpG_28.29.30.31, X285_ETV4_01_CpG_32.33.34.35, X285_ETV4_01_CpG_36
X286_ETV4	X286_ETV4_02_CpG_1, X286_ETV4_02_CpG_2, X286_ETV4_02_CpG_3.4.5, X286_ETV4_02_CpG_6.7, X286_ETV4_02_CpG_8, X286_ETV4_02_CpG_9, X286_ETV4_02_CpG_10, X286_ETV4_02_CpG_11.12, X286_ETV4_02_CpG_13.14.15, X286_ETV4_02_CpG_16.17, X286_ETV4_02_CpG_18, X286_ETV4_02_CpG_19, X286_ETV4_02_CpG_20.21, X286_ETV4_02_CpG_22, X286_ETV4_02_CpG_23, X286_ETV4_02_CpG_24, X286_ETV4_02_CpG_25, X286_ETV4_02_CpG_26, X286_ETV4_02_CpG_27, X286_ETV4_02_CpG_28.29.30.31, X286_ETV4_02_CpG_32.33.34.35, X286_ETV4_02_CpG_36
X288_EVI1	X288_EVI1_CpG_1, X288_EVI1_CpG_2.3, X288_EVI1_CpG_4, X288_EVI1_CpG_5, X288_EVI1_CpG_6, X288_EVI1_CpG_7, X288_EVI1_CpG_8, X288_EVI1_CpG_9, X288_EVI1_CpG_10, X288_EVI1_CpG_11, X288_EVI1_CpG_12, X288_EVI1_CpG_13, X288_EVI1_CpG_14, X288_EVI1_CpG_15, X288_EVI1_CpG_16.17, X288_EVI1_CpG_18.19, X288_EVI1_CpG_20, X288_EVI1_CpG_21.22, X288_EVI1_CpG_23.24, X288_EVI1_CpG_25.26.27, X288_EVI1_CpG_28.29, X288_EVI1_CpG_30, X288_EVI1_CpG_31
X289_EWSR1	X289_EWSR1_CpG_1.2, X289_EWSR1_CpG_3.4.5.6, X289_EWSR1_CpG_7.8, X289_EWSR1_CpG_9.10, X289_EWSR1_CpG_11, X289_EWSR1_CpG_12, X289_EWSR1_CpG_13, X289_EWSR1_CpG_14, X289_EWSR1_CpG_15, X289_EWSR1_CpG_16, X289_EWSR1_CpG_17.18.19.20.21, X289_EWSR1_CpG_22, X289_EWSR1_CpG_23, X289_EWSR1_CpG_24.25, X289_EWSR1_CpG_26, X289_EWSR1_CpG_27.28.29.30, X289_EWSR1_CpG_31,

	X289_EWSR1_CpG_32, X289_EWSR1_CpG_33, X289_EWSR1_CpG_34.35.36, X289_EWSR1_CpG_37.38.39.40.41.42.43.44.45.46.47.48, X289_EWSR1_CpG_49.50.51, X289_EWSR1_CpG_52.53, X289_EWSR1_CpG_54.55.56.57, X289_EWSR1_CpG_58
X291_EXT2	X291_EXT2_CpG_1.2.3, X291_EXT2_CpG_4, X291_EXT2_CpG_5, X291_EXT2_CpG_6.7, X291_EXT2_CpG_8.9, X291_EXT2_CpG_10, X291_EXT2_CpG_11.12.13.14, X291_EXT2_CpG_15, X291_EXT2_CpG_16.17, X291_EXT2_CpG_18, X291_EXT2_CpG_19, X291_EXT2_CpG_20, X291_EXT2_CpG_21, X291_EXT2_CpG_22.23.24.25, X291_EXT2_CpG_26, X291_EXT2_CpG_27.28, X291_EXT2_CpG_29, X291_EXT2_CpG_30.31, X291_EXT2_CpG_32.33, X291_EXT2_CpG_34.35.36.37.38, X291_EXT2_CpG_39, X291_EXT2_CpG_40.41.42.43, X291_EXT2_CpG_44, X291_EXT2_CpG_45.46.47.48.49, X291_EXT2_CpG_50, X291_EXT2_CpG_51.52, X291_EXT2_CpG_53.54
X292_FACL6	X292_FACL6_CpG_1.2.3.4, X292_FACL6_CpG_5.6, X292_FACL6_CpG_7, X292_FACL6_CpG_8, X292_FACL6_CpG_9.10, X292_FACL6_CpG_11, X292_FACL6_CpG_12, X292_FACL6_CpG_13, X292_FACL6_CpG_14, X292_FACL6_CpG_15, X292_FACL6_CpG_16.17.18.19.20.21, X292_FACL6_CpG_22, X292_FACL6_CpG_23, X292_FACL6_CpG_24, X292_FACL6_CpG_25.26.27.28.29.30.31, X292_FACL6_CpG_32.33.34, X292_FACL6_CpG_35.36.37.38.39, X292_FACL6_CpG_40, X292_FACL6_CpG_41.42.43.44, X292_FACL6_CpG_45, X292_FACL6_CpG_46
X293_FANCA	X293_FANCA_CpG_1.2.3.4, X293_FANCA_CpG_5.6.7.8, X293_FANCA_CpG_9.10.11.12.13.14, X293_FANCA_CpG_15, X293_FANCA_CpG_16.17, X293_FANCA_CpG_18, X293_FANCA_CpG_19.20.21, X293_FANCA_CpG_22, X293_FANCA_CpG_23.24.25.26, X293_FANCA_CpG_27, X293_FANCA_CpG_28.29.30.31, X293_FANCA_CpG_32.33.34.35, X293_FANCA_CpG_36.37, X293_FANCA_CpG_38, X293_FANCA_CpG_39.40.41, X293_FANCA_CpG_42.43, X293_FANCA_CpG_44, X293_FANCA_CpG_45, X293_FANCA_CpG_46
X294_FANCC	X294_FANCC_01_CpG_1, X294_FANCC_01_CpG_2, X294_FANCC_01_CpG_3.4.5.6.7.8, X294_FANCC_01_CpG_9.10.11.12.13.14.15.16, X294_FANCC_01_CpG_17.18, X294_FANCC_01_CpG_19.20.21.22, X294_FANCC_01_CpG_23.24.25, X294_FANCC_01_CpG_26, X294_FANCC_01_CpG_27, X294_FANCC_01_CpG_28.29, X294_FANCC_01_CpG_30.31.32, X294_FANCC_01_CpG_33.34.35.36, X294_FANCC_01_CpG_37.38, X294_FANCC_01_CpG_39, X294_FANCC_01_CpG_40.41.42.43.44, X294_FANCC_01_CpG_45.46.47, X294_FANCC_01_CpG_48, X294_FANCC_01_CpG_49.50, X294_FANCC_01_CpG_51, X294_FANCC_01_CpG_52.53.54.55, X294_FANCC_01_CpG_56.57.58.59.60, X294_FANCC_01_CpG_61
X295_FANCC	X295_FANCC_02_CpG_1, X295_FANCC_02_CpG_2, X295_FANCC_02_CpG_3.4.5.6.7.8, X295_FANCC_02_CpG_9.10.11.12.13.14.15.16, X295_FANCC_02_CpG_17.18, X295_FANCC_02_CpG_19.20.21.22, X295_FANCC_02_CpG_23.24.25, X295_FANCC_02_CpG_26, X295_FANCC_02_CpG_27, X295_FANCC_02_CpG_28.29, X295_FANCC_02_CpG_30.31.32, X295_FANCC_02_CpG_33.34.35.36, X295_FANCC_02_CpG_37.38, X295_FANCC_02_CpG_39, X295_FANCC_02_CpG_40.41.42.43.44, X295_FANCC_02_CpG_45.46.47, X295_FANCC_02_CpG_48, X295_FANCC_02_CpG_49.50, X295_FANCC_02_CpG_51, X295_FANCC_02_CpG_52.53.54.55, X295_FANCC_02_CpG_56.57.58.59.60, X295_FANCC_02_CpG_61
X296_FANCD2	X296_FANCD2_CpG_1, X296_FANCD2_CpG_2, X296_FANCD2_CpG_3.4, X296_FANCD2_CpG_5.6.7, X296_FANCD2_CpG_8, X296_FANCD2_CpG_9, X296_FANCD2_CpG_10, X296_FANCD2_CpG_11.12.13, X296_FANCD2_CpG_14, X296_FANCD2_CpG_15, X296_FANCD2_CpG_16.17.18.19, X296_FANCD2_CpG_20.21.22.23, X296_FANCD2_CpG_24, X296_FANCD2_CpG_25.26.27, X296_FANCD2_CpG_28.29, X296_FANCD2_CpG_30, X296_FANCD2_CpG_31, X296_FANCD2_CpG_32.33, X296_FANCD2_CpG_34.35.36.37.38.39.40.41
X297_FANCE	X297_FANCE_CpG_1, X297_FANCE_CpG_2.3, X297_FANCE_CpG_4.5.6, X297_FANCE_CpG_7, X297_FANCE_CpG_8,

	X297_FANCE_CpG_9, X297_FANCE_CpG_10, X297_FANCE_CpG_11, X297_FANCE_CpG_12, X297_FANCE_CpG_13.14, X297_FANCE_CpG_15.16.17.18, X297_FANCE_CpG_19, X297_FANCE_CpG_20.21.22.23.24, X297_FANCE_CpG_25.26, X297_FANCE_CpG_27.28.29.30.31.32, X297_FANCE_CpG_33.34, X297_FANCE_CpG_35, X297_FANCE_CpG_36, X297_FANCE_CpG_37.38.39, X297_FANCE_CpG_40.41, X297_FANCE_CpG_42
X298_FANCF	X298_FANCF_01_CpG_1.2.3, X298_FANCF_01_CpG_4.5.6, X298_FANCF_01_CpG_7, X298_FANCF_01_CpG_8, X298_FANCF_01_CpG_9, X298_FANCF_01_CpG_10, X298_FANCF_01_CpG_11, X298_FANCF_01_CpG_12, X298_FANCF_01_CpG_13, X298_FANCF_01_CpG_14, X298_FANCF_01_CpG_15, X298_FANCF_01_CpG_16, X298_FANCF_01_CpG_17.18, X298_FANCF_01_CpG_19.20, X298_FANCF_01_CpG_21, X298_FANCF_01_CpG_22.23, X298_FANCF_01_CpG_24, X298_FANCF_01_CpG_25.26, X298_FANCF_01_CpG_27.28, X298_FANCF_01_CpG_29.30, X298_FANCF_01_CpG_31, X298_FANCF_01_CpG_32, X298_FANCF_01_CpG_33, X298_FANCF_01_CpG_34
X299_FANCF	X299_FANCF_02_CpG_1, X299_FANCF_02_CpG_2, X299_FANCF_02_CpG_3.4.5, X299_FANCF_02_CpG_6, X299_FANCF_02_CpG_7, X299_FANCF_02_CpG_8, X299_FANCF_02_CpG_9, X299_FANCF_02_CpG_10.11.12, X299_FANCF_02_CpG_13, X299_FANCF_02_CpG_14.15.16, X299_FANCF_02_CpG_17.18.19
X302_FEV	X302_FEV_CpG_1.2, X302_FEV_CpG_3.4.5, X302_FEV_CpG_6, X302_FEV_CpG_7, X302_FEV_CpG_8, X302_FEV_CpG_9.10, X302_FEV_CpG_11, X302_FEV_CpG_12.13, X302_FEV_CpG_14, X302_FEV_CpG_15.16, X302_FEV_CpG_17.18.19.20, X302_FEV_CpG_21, X302_FEV_CpG_22.23.24.25, X302_FEV_CpG_26, X302_FEV_CpG_27, X302_FEV_CpG_28.29.30.31.32.33, X302_FEV_CpG_34, X302_FEV_CpG_35.36.37, X302_FEV_CpG_38.39, X302_FEV_CpG_40, X302_FEV_CpG_41, X302_FEV_CpG_42.43.44.45, X302_FEV_CpG_46, X302_FEV_CpG_47, X302_FEV_CpG_48.49.50, X302_FEV_CpG_51, X302_FEV_CpG_52.53.54, X302_FEV_CpG_55
X305_FGFR1OP	X305_FGFR1OP_02_CpG_1, X305_FGFR1OP_02_CpG_2, X305_FGFR1OP_02_CpG_3, X305_FGFR1OP_02_CpG_4, X305_FGFR1OP_02_CpG_5, X305_FGFR1OP_02_CpG_6, X305_FGFR1OP_02_CpG_7.8, X305_FGFR1OP_02_CpG_9, X305_FGFR1OP_02_CpG_10, X305_FGFR1OP_02_CpG_11.12.13, X305_FGFR1OP_02_CpG_14.15.16.17.18.19, X305_FGFR1OP_02_CpG_20.21.22, X305_FGFR1OP_02_CpG_23, X305_FGFR1OP_02_CpG_24, X305_FGFR1OP_02_CpG_25, X305_FGFR1OP_02_CpG_26, X305_FGFR1OP_02_CpG_27.28.29, X305_FGFR1OP_02_CpG_30.31, X305_FGFR1OP_02_CpG_32.33.34, X305_FGFR1OP_02_CpG_35.36.37.38, X305_FGFR1OP_02_CpG_39
X306_FGFR2	X306_FGFR2_CpG_1, X306_FGFR2_CpG_2, X306_FGFR2_CpG_3.4.5.6, X306_FGFR2_CpG_7, X306_FGFR2_CpG_8.9.10.11.12, X306_FGFR2_CpG_13.14.15, X306_FGFR2_CpG_16, X306_FGFR2_CpG_17.18.19.20, X306_FGFR2_CpG_21.22.23, X306_FGFR2_CpG_24.25.26.27.28, X306_FGFR2_CpG_29, X306_FGFR2_CpG_30, X306_FGFR2_CpG_31.32, X306_FGFR2_CpG_33
X308_FH	X308_FH_CpG_1, X308_FH_CpG_2, X308_FH_CpG_3, X308_FH_CpG_4.5, X308_FH_CpG_6, X308_FH_CpG_7.8, X308_FH_CpG_9.10.11.12, X308_FH_CpG_13, X308_FH_CpG_14.15.16.17, X308_FH_CpG_18, X308_FH_CpG_19.20, X308_FH_CpG_21.22, X308_FH_CpG_23, X308_FH_CpG_24, X308_FH_CpG_25.26.27, X308_FH_CpG_28.29, X308_FH_CpG_30.31, X308_FH_CpG_32, X308_FH_CpG_33, X308_FH_CpG_34.35, X308_FH_CpG_36.37, X308_FH_CpG_38.39.40, X308_FH_CpG_41.42, X308_FH_CpG_43, X308_FH_CpG_44.45.46, X308_FH_CpG_47
X309_FIP1L1	X309_FIP1L1_CpG_1, X309_FIP1L1_CpG_2, X309_FIP1L1_CpG_3, X309_FIP1L1_CpG_4, X309_FIP1L1_CpG_5, X309_FIP1L1_CpG_6, X309_FIP1L1_CpG_7, X309_FIP1L1_CpG_8, X309_FIP1L1_CpG_9, X309_FIP1L1_CpG_10, X309_FIP1L1_CpG_11.12, X309_FIP1L1_CpG_13, X309_FIP1L1_CpG_14.15.16, X309_FIP1L1_CpG_17, X309_FIP1L1_CpG_18.19.20.21.22.23, X309_FIP1L1_CpG_24, X309_FIP1L1_CpG_25, X309_FIP1L1_CpG_26,

	X309_FIP1L1_CpG_27.28.29.30
X310_FLI1	X310_FLI1_01_CpG_1, X310_FLI1_01_CpG_2.3, X310_FLI1_01_CpG_4.5, X310_FLI1_01_CpG_6, X310_FLI1_01_CpG_7, X310_FLI1_01_CpG_8.9, X310_FLI1_01_CpG_10, X310_FLI1_01_CpG_11.12.13.14, X310_FLI1_01_CpG_15, X310_FLI1_01_CpG_16.17, X310_FLI1_01_CpG_18.19, X310_FLI1_01_CpG_20, X310_FLI1_01_CpG_21.22.23, X310_FLI1_01_CpG_24, X310_FLI1_01_CpG_25.26.27, X310_FLI1_01_CpG_28.29.30, X310_FLI1_01_CpG_31
X311_FLI1	X311_FLI1_02_CpG_1.2, X311_FLI1_02_CpG_3.4, X311_FLI1_02_CpG_5.6, X311_FLI1_02_CpG_7, X311_FLI1_02_CpG_8.9.10.11.12.13, X311_FLI1_02_CpG_14.15.16, X311_FLI1_02_CpG_17, X311_FLI1_02_CpG_18.19
X312_FLT3	X312_FLT3_CpG_1.2, X312_FLT3_CpG_3, X312_FLT3_CpG_4, X312_FLT3_CpG_5, X312_FLT3_CpG_6, X312_FLT3_CpG_7, X312_FLT3_CpG_8, X312_FLT3_CpG_9, X312_FLT3_CpG_10.11, X312_FLT3_CpG_12, X312_FLT3_CpG_13, X312_FLT3_CpG_14.15.16.17.18, X312_FLT3_CpG_19.20.21.22, X312_FLT3_CpG_23.24, X312_FLT3_CpG_25.26.27.28, X312_FLT3_CpG_29.30.31, X312_FLT3_CpG_32, X312_FLT3_CpG_33, X312_FLT3_CpG_34.35, X312_FLT3_CpG_36, X312_FLT3_CpG_37, X312_FLT3_CpG_38.39, X312_FLT3_CpG_40, X312_FLT3_CpG_41, X312_FLT3_CpG_42, X312_FLT3_CpG_43, X312_FLT3_CpG_44.45
X313_FLT4	X313_FLT4_CpG_1, X313_FLT4_CpG_2.3.4.5, X313_FLT4_CpG_6.7.8.9.10, X313_FLT4_CpG_11, X313_FLT4_CpG_12.13.14.15, X313_FLT4_CpG_16.17.18.19.20.21.22.23.24.25, X313_FLT4_CpG_26.27, X313_FLT4_CpG_28.29.30.31, X313_FLT4_CpG_32.33.34.35.36, X313_FLT4_CpG_37, X313_FLT4_CpG_38.39.40, X313_FLT4_CpG_41.42.43.44.45, X313_FLT4_CpG_46.47, X313_FLT4_CpG_48, X313_FLT4_CpG_49.50.51, X313_FLT4_CpG_52.53
X316_FOXO1A	X316_FOXO1A_02_CpG_1, X316_FOXO1A_02_CpG_2.3.4, X316_FOXO1A_02_CpG_5, X316_FOXO1A_02_CpG_6, X316_FOXO1A_02_CpG_7, X316_FOXO1A_02_CpG_8, X316_FOXO1A_02_CpG_9.10, X316_FOXO1A_02_CpG_11.12.13, X316_FOXO1A_02_CpG_14.15, X316_FOXO1A_02_CpG_16, X316_FOXO1A_02_CpG_17.18.19.20.21, X316_FOXO1A_02_CpG_22.23.24, X316_FOXO1A_02_CpG_25, X316_FOXO1A_02_CpG_26, X316_FOXO1A_02_CpG_27, X316_FOXO1A_02_CpG_28, X316_FOXO1A_02_CpG_29, X316_FOXO1A_02_CpG_30.31, X316_FOXO1A_02_CpG_32.33.34, X316_FOXO1A_02_CpG_35, X316_FOXO1A_02_CpG_36, X316_FOXO1A_02_CpG_37.38.39.40, X316_FOXO1A_02_CpG_41, X316_FOXO1A_02_CpG_42.43.44, X316_FOXO1A_02_CpG_45, X316_FOXO1A_02_CpG_46.47, X316_FOXO1A_02_CpG_48, X316_FOXO1A_02_CpG_49, X316_FOXO1A_02_CpG_50.51, X316_FOXO1A_02_CpG_52, X316_FOXO1A_02_CpG_53, X316_FOXO1A_02_CpG_54.55.56
X317_FOXO1A	X317_FOXO1A_03_CpG_1.2, X317_FOXO1A_03_CpG_3, X317_FOXO1A_03_CpG_4.5, X317_FOXO1A_03_CpG_6, X317_FOXO1A_03_CpG_7, X317_FOXO1A_03_CpG_8.9, X317_FOXO1A_03_CpG_10, X317_FOXO1A_03_CpG_11, X317_FOXO1A_03_CpG_12, X317_FOXO1A_03_CpG_13.14, X317_FOXO1A_03_CpG_15.16, X317_FOXO1A_03_CpG_17, X317_FOXO1A_03_CpG_18, X317_FOXO1A_03_CpG_19, X317_FOXO1A_03_CpG_20
X319_FOXO3A	X319_FOXO3A_02_CpG_1, X319_FOXO3A_02_CpG_2.3, X319_FOXO3A_02_CpG_4, X319_FOXO3A_02_CpG_5.6, X319_FOXO3A_02_CpG_7, X319_FOXO3A_02_CpG_8.9, X319_FOXO3A_02_CpG_10, X319_FOXO3A_02_CpG_11, X319_FOXO3A_02_CpG_12, X319_FOXO3A_02_CpG_13.14.15, X319_FOXO3A_02_CpG_16, X319_FOXO3A_02_CpG_17.18.19.20, X319_FOXO3A_02_CpG_21, X319_FOXO3A_02_CpG_22, X319_FOXO3A_02_CpG_23, X319_FOXO3A_02_CpG_24.25.26.27.28, X319_FOXO3A_02_CpG_29.30, X319_FOXO3A_02_CpG_31.32, X319_FOXO3A_02_CpG_33, X319_FOXO3A_02_CpG_34, X319_FOXO3A_02_CpG_35.36.37, X319_FOXO3A_02_CpG_38

X321_FUS	X321_FUS_CpG_1, X321_FUS_CpG_2, X321_FUS_CpG_3, X321_FUS_CpG_4, X321_FUS_CpG_5, X321_FUS_CpG_6, X321_FUS_CpG_7.8.9.10.11.12.13.14, X321_FUS_CpG_15.16, X321_FUS_CpG_17, X321_FUS_CpG_18, X321_FUS_CpG_19, X321_FUS_CpG_20, X321_FUS_CpG_21.22, X321_FUS_CpG_23, X321_FUS_CpG_24.25.26.27.28.29, X321_FUS_CpG_30, X321_FUS_CpG_31.32, X321_FUS_CpG_33, X321_FUS_CpG_34.35.36.37, X321_FUS_CpG_38.39
X324_GMPS	X324_GMPS_CpG_1, X324_GMPS_CpG_2.3, X324_GMPS_CpG_4.5, X324_GMPS_CpG_6.7.8, X324_GMPS_CpG_9.10.11.12.13.14.15.16.17.18, X324_GMPS_CpG_19.20, X324_GMPS_CpG_21.22.23.24, X324_GMPS_CpG_25.26, X324_GMPS_CpG_27.28.29.30, X324_GMPS_CpG_31, X324_GMPS_CpG_32.33, X324_GMPS_CpG_34.35.36, X324_GMPS_CpG_37.38.39, X324_GMPS_CpG_40.41, X324_GMPS_CpG_42.43.44.45, X324_GMPS_CpG_46, X324_GMPS_CpG_47, X324_GMPS_CpG_48.49.50, X324_GMPS_CpG_51, X324_GMPS_CpG_52, X324_GMPS_CpG_53, X324_GMPS_CpG_54, X324_GMPS_CpG_55.56, X324_GMPS_CpG_57.58, X324_GMPS_CpG_59.60
X325_GNAS	X325_GNAS_01_CpG_1, X325_GNAS_01_CpG_2.3, X325_GNAS_01_CpG_4.5, X325_GNAS_01_CpG_6.7.8, X325_GNAS_01_CpG_9.10, X325_GNAS_01_CpG_11.12, X325_GNAS_01_CpG_13.14.15.16.17.18.19.20.21, X325_GNAS_01_CpG_22, X325_GNAS_01_CpG_23.24.25.26.27.28.29.30, X325_GNAS_01_CpG_31.32, X325_GNAS_01_CpG_33, X325_GNAS_01_CpG_34.35.36.37, X325_GNAS_01_CpG_38, X325_GNAS_01_CpG_39.40.41, X325_GNAS_01_CpG_42.43.44, X325_GNAS_01_CpG_45.46.47.48.49.50.51, X325_GNAS_01_CpG_52, X325_GNAS_01_CpG_53, X325_GNAS_01_CpG_54.55, X325_GNAS_01_CpG_56
X326_GNAS	X326_GNAS_02_CpG_1, X326_GNAS_02_CpG_2, X326_GNAS_02_CpG_3.4.5.6.7.8, X326_GNAS_02_CpG_9, X326_GNAS_02_CpG_10, X326_GNAS_02_CpG_11.12.13, X326_GNAS_02_CpG_14, X326_GNAS_02_CpG_15.16.17.18, X326_GNAS_02_CpG_19.20.21, X326_GNAS_02_CpG_22.23.24.25.26.27, X326_GNAS_02_CpG_28, X326_GNAS_02_CpG_29, X326_GNAS_02_CpG_30, X326_GNAS_02_CpG_31, X326_GNAS_02_CpG_32.33
X327_GOLGA5	X327_GOLGA5_CpG_1, X327_GOLGA5_CpG_2.3, X327_GOLGA5_CpG_4, X327_GOLGA5_CpG_5.6.7, X327_GOLGA5_CpG_8, X327_GOLGA5_CpG_9.10, X327_GOLGA5_CpG_11.12, X327_GOLGA5_CpG_13.14, X327_GOLGA5_CpG_15, X327_GOLGA5_CpG_16, X327_GOLGA5_CpG_17, X327_GOLGA5_CpG_18, X327_GOLGA5_CpG_19, X327_GOLGA5_CpG_20, X327_GOLGA5_CpG_21, X327_GOLGA5_CpG_22.23, X327_GOLGA5_CpG_24.25.26.27, X327_GOLGA5_CpG_28
X328_GPC3	X328_GPC3_CpG_1, X328_GPC3_CpG_2.3.4.5.6.7.8.9, X328_GPC3_CpG_10, X328_GPC3_CpG_11.12.13, X328_GPC3_CpG_14.15, X328_GPC3_CpG_16, X328_GPC3_CpG_17.18, X328_GPC3_CpG_19, X328_GPC3_CpG_20, X328_GPC3_CpG_21
X329_GPHN	X329_GPHN_01_CpG_1.2.3, X329_GPHN_01_CpG_4.5, X329_GPHN_01_CpG_6, X329_GPHN_01_CpG_7.8, X329_GPHN_01_CpG_9.10, X329_GPHN_01_CpG_11.12, X329_GPHN_01_CpG_13, X329_GPHN_01_CpG_14.15, X329_GPHN_01_CpG_16, X329_GPHN_01_CpG_17, X329_GPHN_01_CpG_18.19, X329_GPHN_01_CpG_20.21.22.23.24, X329_GPHN_01_CpG_25.26, X329_GPHN_01_CpG_27.28, X329_GPHN_01_CpG_29.30.31, X329_GPHN_01_CpG_32
X330_GPHN	X330_GPHN_02_CpG_1.2.3, X330_GPHN_02_CpG_4.5, X330_GPHN_02_CpG_6.7.8.9.10.11.12.13, X330_GPHN_02_CpG_14.15, X330_GPHN_02_CpG_16, X330_GPHN_02_CpG_17.18.19, X330_GPHN_02_CpG_20.21, X330_GPHN_02_CpG_22.23, X330_GPHN_02_CpG_24.25.26, X330_GPHN_02_CpG_27, X330_GPHN_02_CpG_28, X330_GPHN_02_CpG_29.30.31, X330_GPHN_02_CpG_32.33.34.35, X330_GPHN_02_CpG_36.37.38.39.40.41.42.43.44, X330_GPHN_02_CpG_45, X330_GPHN_02_CpG_46, X330_GPHN_02_CpG_47, X330_GPHN_02_CpG_48,

	X330_GPHN_02_CpG_49, X330_GPHN_02_CpG_50.51, X330_GPHN_02_CpG_52
X331_GPHN	X331_GPHN_03_CpG_1, X331_GPHN_03_CpG_2, X331_GPHN_03_CpG_3, X331_GPHN_03_CpG_4.5, X331_GPHN_03_CpG_6, X331_GPHN_03_CpG_7, X331_GPHN_03_CpG_8, X331_GPHN_03_CpG_9.10, X331_GPHN_03_CpG_11, X331_GPHN_03_CpG_12, X331_GPHN_03_CpG_13.14.15, X331_GPHN_03_CpG_16.17.18.19, X331_GPHN_03_CpG_20.21, X331_GPHN_03_CpG_22, X331_GPHN_03_CpG_23
X332_GRAF	X332_GRAF_CpG_1, X332_GRAF_CpG_2.3, X332_GRAF_CpG_4, X332_GRAF_CpG_5, X332_GRAF_CpG_6.7.8.9, X332_GRAF_CpG_10, X332_GRAF_CpG_11.12.13.14.15.16, X332_GRAF_CpG_17.18, X332_GRAF_CpG_19.20, X332_GRAF_CpG_21, X332_GRAF_CpG_22.23, X332_GRAF_CpG_24.25.26.27, X332_GRAF_CpG_28, X332_GRAF_CpG_29.30, X332_GRAF_CpG_31.32.33.34.35.36, X332_GRAF_CpG_37
X335_HIP1	X335_HIP1_CpG_1, X335_HIP1_CpG_2, X335_HIP1_CpG_3, X335_HIP1_CpG_4, X335_HIP1_CpG_5.6, X335_HIP1_CpG_7, X335_HIP1_CpG_8.9, X335_HIP1_CpG_10.11, X335_HIP1_CpG_12.13, X335_HIP1_CpG_14.15.16.17, X335_HIP1_CpG_18.19, X335_HIP1_CpG_20.21.22, X335_HIP1_CpG_23, X335_HIP1_CpG_24.25.26, X335_HIP1_CpG_27, X335_HIP1_CpG_28.29, X335_HIP1_CpG_30.31.32.33.34, X335_HIP1_CpG_35.36, X335_HIP1_CpG_37.38, X335_HIP1_CpG_39, X335_HIP1_CpG_40.41, X335_HIP1_CpG_42.43.44, X335_HIP1_CpG_45.46.47.48, X335_HIP1_CpG_49.50.51, X335_HIP1_CpG_52.53, X335_HIP1_CpG_54.55
X336_HIST1H4I	X336_HIST1H4I_CpG_1.2, X336_HIST1H4I_CpG_3, X336_HIST1H4I_CpG_4, X336_HIST1H4I_CpG_5.6, X336_HIST1H4I_CpG_7.8.9.10.11.12.13, X336_HIST1H4I_CpG_14, X336_HIST1H4I_CpG_15.16, X336_HIST1H4I_CpG_17, X336_HIST1H4I_CpG_18, X336_HIST1H4I_CpG_19.20, X336_HIST1H4I_CpG_21, X336_HIST1H4I_CpG_22, X336_HIST1H4I_CpG_23, X336_HIST1H4I_CpG_24, X336_HIST1H4I_CpG_25, X336_HIST1H4I_CpG_26, X336_HIST1H4I_CpG_27.28, X336_HIST1H4I_CpG_29, X336_HIST1H4I_CpG_30, X336_HIST1H4I_CpG_31.32
X337_HLF	X337_HLF_CpG_1, X337_HLF_CpG_2.3.4, X337_HLF_CpG_5.6, X337_HLF_CpG_7, X337_HLF_CpG_8.9.10.11.12, X337_HLF_CpG_13, X337_HLF_CpG_14.15.16.17.18.19.20, X337_HLF_CpG_21, X337_HLF_CpG_22.23, X337_HLF_CpG_24, X337_HLF_CpG_25, X337_HLF_CpG_26.27, X337_HLF_CpG_28.29, X337_HLF_CpG_30, X337_HLF_CpG_31.32.33.34.35, X337_HLF_CpG_36, X337_HLF_CpG_37.38.39.40.41, X337_HLF_CpG_42.43, X337_HLF_CpG_44.45
X338_HMGA	X338_HMGA_01_CpG_1, X338_HMGA_01_CpG_2.3.4.5.6.7.8.9, X338_HMGA_01_CpG_10.11, X338_HMGA_01_CpG_12, X338_HMGA_01_CpG_13.14.15, X338_HMGA_01_CpG_16, X338_HMGA_01_CpG_17
X266_DDB2	X266_DDB2_CpG_1, X266_DDB2_CpG_2, X266_DDB2_CpG_3, X266_DDB2_CpG_4, X266_DDB2_CpG_5, X266_DDB2_CpG_6, X266_DDB2_CpG_7.8, X266_DDB2_CpG_9, X266_DDB2_CpG_10, X266_DDB2_CpG_11, X266_DDB2_CpG_12, X266_DDB2_CpG_13, X266_DDB2_CpG_14, X266_DDB2_CpG_15, X266_DDB2_CpG_16.17, X266_DDB2_CpG_18, X266_DDB2_CpG_19, X266_DDB2_CpG_20, X266_DDB2_CpG_21.22, X266_DDB2_CpG_23.24
X364_LCK	X364_LCK_CpG_1, X364_LCK_CpG_2.3, X364_LCK_CpG_4, X364_LCK_CpG_5.6, X364_LCK_CpG_7, X364_LCK_CpG_8, X364_LCK_CpG_9, X364_LCK_CpG_10.11, X364_LCK_CpG_12.13.14.15, X364_LCK_CpG_16.17.18.19.20, X364_LCK_CpG_21, X364_LCK_CpG_22, X364_LCK_CpG_23, X364_LCK_CpG_24, X364_LCK_CpG_25.26, X364_LCK_CpG_27, X364_LCK_CpG_28.29, X364_LCK_CpG_30, X364_LCK_CpG_31.32.33, X364_LCK_CpG_34.35.36, X364_LCK_CpG_37, X364_LCK_CpG_38.39, X364_LCK_CpG_40
X367_LCX	X367_LCX_02_CpG_1, X367_LCX_02_CpG_2, X367_LCX_02_CpG_3.4, X367_LCX_02_CpG_5.6.7.8.9, X367_LCX_02_CpG_10, X367_LCX_02_CpG_11.12, X367_LCX_02_CpG_13, X367_LCX_02_CpG_14, X367_LCX_02_CpG_15.16, X367_LCX_02_CpG_17, X367_LCX_02_CpG_18.19.20,

	X367_LCX_02_CpG_21.22.23.24.25.26.27.28, X367_LCX_02_CpG_29.30.31, X367_LCX_02_CpG_32
X369_LHFP	X369_LHFP_02_CpG_1, X369_LHFP_02_CpG_2, X369_LHFP_02_CpG_3, X369_LHFP_02_CpG_4, X369_LHFP_02_CpG_5, X369_LHFP_02_CpG_6.7, X369_LHFP_02_CpG_8, X369_LHFP_02_CpG_9, X369_LHFP_02_CpG_10.11, X369_LHFP_02_CpG_12, X369_LHFP_02_CpG_13, X369_LHFP_02_CpG_14.15, X369_LHFP_02_CpG_16, X369_LHFP_02_CpG_17, X369_LHFP_02_CpG_18, X369_LHFP_02_CpG_19, X369_LHFP_02_CpG_20, X369_LHFP_02_CpG_21.22.23, X369_LHFP_02_CpG_24.25.26.27, X369_LHFP_02_CpG_28.29, X369_LHFP_02_CpG_30, X369_LHFP_02_CpG_31, X369_LHFP_02_CpG_32, X369_LHFP_02_CpG_33, X369_LHFP_02_CpG_34.35
X373_LYL	X373_LYL_01_CpG_1, X373_LYL_01_CpG_2, X373_LYL_01_CpG_3, X373_LYL_01_CpG_4, X373_LYL_01_CpG_5.6, X373_LYL_01_CpG_7, X373_LYL_01_CpG_8.9.10.11.12.13, X373_LYL_01_CpG_14, X373_LYL_01_CpG_15.16, X373_LYL_01_CpG_17.18.19.20.21.22.23.24, X373_LYL_01_CpG_25.26, X373_LYL_01_CpG_27.28, X373_LYL_01_CpG_29.30
X375_MADH4	X375_MADH4_CpG_1.2.3.4, X375_MADH4_CpG_5.6, X375_MADH4_CpG_7, X375_MADH4_CpG_8, X375_MADH4_CpG_9, X375_MADH4_CpG_10, X375_MADH4_CpG_11, X375_MADH4_CpG_12, X375_MADH4_CpG_13, X375_MADH4_CpG_14, X375_MADH4_CpG_15.16.17.18, X375_MADH4_CpG_19, X375_MADH4_CpG_20.21.22.23.24.25, X375_MADH4_CpG_26, X375_MADH4_CpG_27.28, X375_MADH4_CpG_29.30.31.32.33
X381_MECT1	X381_MECT1_CpG_1, X381_MECT1_CpG_2, X381_MECT1_CpG_3.4, X381_MECT1_CpG_5, X381_MECT1_CpG_6, X381_MECT1_CpG_7, X381_MECT1_CpG_8.9.10, X381_MECT1_CpG_11.12, X381_MECT1_CpG_13.14.15.16, X381_MECT1_CpG_17.18.19.20.21.22, X381_MECT1_CpG_23.24.25.26.27.28.29.30.31.32.33.34, X381_MECT1_CpG_35, X381_MECT1_CpG_36.37.38.39.40, X381_MECT1_CpG_41.42.43, X381_MECT1_CpG_44.45.46.47, X381_MECT1_CpG_48.49, X381_MECT1_CpG_50, X381_MECT1_CpG_51.52, X381_MECT1_CpG_53, X381_MECT1_CpG_54, X381_MECT1_CpG_55.56, X381_MECT1_CpG_57, X381_MECT1_CpG_58.59, X381_MECT1_CpG_60, X381_MECT1_CpG_61.62.63
X382_MEN1	X382_MEN1_01_CpG_1.2, X382_MEN1_01_CpG_3, X382_MEN1_01_CpG_4, X382_MEN1_01_CpG_5.6, X382_MEN1_01_CpG_7, X382_MEN1_01_CpG_8, X382_MEN1_01_CpG_9.10, X382_MEN1_01_CpG_11, X382_MEN1_01_CpG_12, X382_MEN1_01_CpG_13, X382_MEN1_01_CpG_14.15, X382_MEN1_01_CpG_16.17, X382_MEN1_01_CpG_18.19.20, X382_MEN1_01_CpG_21.22.23, X382_MEN1_01_CpG_24, X382_MEN1_01_CpG_25, X382_MEN1_01_CpG_26.27
X385_MHC2TA	X385_MHC2TA_01_CpG_1, X385_MHC2TA_01_CpG_2, X385_MHC2TA_01_CpG_3, X385_MHC2TA_01_CpG_4, X385_MHC2TA_01_CpG_5.6, X385_MHC2TA_01_CpG_7, X385_MHC2TA_01_CpG_8, X385_MHC2TA_01_CpG_9.10.11, X385_MHC2TA_01_CpG_12, X385_MHC2TA_01_CpG_13, X385_MHC2TA_01_CpG_14, X385_MHC2TA_01_CpG_15.16, X385_MHC2TA_01_CpG_17, X385_MHC2TA_01_CpG_18, X385_MHC2TA_01_CpG_19.20.21.22, X385_MHC2TA_01_CpG_23.24, X385_MHC2TA_01_CpG_25, X385_MHC2TA_01_CpG_26.27, X385_MHC2TA_01_CpG_28
X390_MLL	X390_MLL_02_CpG_1, X390_MLL_02_CpG_2.3.4, X390_MLL_02_CpG_5, X390_MLL_02_CpG_6, X390_MLL_02_CpG_7, X390_MLL_02_CpG_8.9.10, X390_MLL_02_CpG_11, X390_MLL_02_CpG_12, X390_MLL_02_CpG_13.14.15, X390_MLL_02_CpG_16, X390_MLL_02_CpG_17.18, X390_MLL_02_CpG_19, X390_MLL_02_CpG_20, X390_MLL_02_CpG_21, X390_MLL_02_CpG_22
X392_MLLT10	X392_MLLT10_CpG_1, X392_MLLT10_CpG_2, X392_MLLT10_CpG_3, X392_MLLT10_CpG_4, X392_MLLT10_CpG_5, X392_MLLT10_CpG_6, X392_MLLT10_CpG_7, X392_MLLT10_CpG_8.9.10.11, X392_MLLT10_CpG_12,

	X392_MLLT10_CpG_13, X392_MLLT10_CpG_14.15.16.17.18.19.20.21.22, X392_MLLT10_CpG_23.24.25.26.27.28.29.30, X392_MLLT10_CpG_31.32.33.34, X392_MLLT10_CpG_35.36.37, X392_MLLT10_CpG_38.39, X392_MLLT10_CpG_40, X392_MLLT10_CpG_41.42, X392_MLLT10_CpG_43.44, X392_MLLT10_CpG_45, X392_MLLT10_CpG_46, X392_MLLT10_CpG_47.48.49, X392_MLLT10_CpG_50.51.52, X392_MLLT10_CpG_53, X392_MLLT10_CpG_54.55, X392_MLLT10_CpG_56, X392_MLLT10_CpG_57, X392_MLLT10_CpG_58, X392_MLLT10_CpG_59.60
X393_MLLT2	X393_MLLT2_CpG_1.2, X393_MLLT2_CpG_3, X393_MLLT2_CpG_4.5, X393_MLLT2_CpG_6.7.8.9.10, X393_MLLT2_CpG_11.12, X393_MLLT2_CpG_13.14.15.16.17, X393_MLLT2_CpG_18, X393_MLLT2_CpG_19.20.21.22.23, X393_MLLT2_CpG_24.25, X393_MLLT2_CpG_26, X393_MLLT2_CpG_27.28, X393_MLLT2_CpG_29.30, X393_MLLT2_CpG_31.32.33, X393_MLLT2_CpG_34.35.36, X393_MLLT2_CpG_37, X393_MLLT2_CpG_38.39.40.41.42, X393_MLLT2_CpG_43.44.45.46.47, X393_MLLT2_CpG_48.49.50, X393_MLLT2_CpG_51.52, X393_MLLT2_CpG_53, X393_MLLT2_CpG_54
X394_MLLT3	X394_MLLT3_CpG_1, X394_MLLT3_CpG_2, X394_MLLT3_CpG_3, X394_MLLT3_CpG_4.5, X394_MLLT3_CpG_6, X394_MLLT3_CpG_7, X394_MLLT3_CpG_8, X394_MLLT3_CpG_9.10, X394_MLLT3_CpG_11, X394_MLLT3_CpG_12, X394_MLLT3_CpG_13, X394_MLLT3_CpG_14, X394_MLLT3_CpG_15, X394_MLLT3_CpG_16.17, X394_MLLT3_CpG_18, X394_MLLT3_CpG_19.20, X394_MLLT3_CpG_21, X394_MLLT3_CpG_22.23.24.25.26, X394_MLLT3_CpG_27.28.29.30, X394_MLLT3_CpG_31.32.33, X394_MLLT3_CpG_34, X394_MLLT3_CpG_35, X394_MLLT3_CpG_36, X394_MLLT3_CpG_37
X395_MLLT4	X395_MLLT4_CpG_1, X395_MLLT4_CpG_2, X395_MLLT4_CpG_3, X395_MLLT4_CpG_4, X395_MLLT4_CpG_5.6, X395_MLLT4_CpG_7.8, X395_MLLT4_CpG_9.10.11, X395_MLLT4_CpG_12.13.14, X395_MLLT4_CpG_15.16, X395_MLLT4_CpG_17.18
X396_MLLT6	X396_MLLT6_01_CpG_1, X396_MLLT6_01_CpG_2, X396_MLLT6_01_CpG_3, X396_MLLT6_01_CpG_4, X396_MLLT6_01_CpG_5.6, X396_MLLT6_01_CpG_7, X396_MLLT6_01_CpG_8, X396_MLLT6_01_CpG_9, X396_MLLT6_01_CpG_10, X396_MLLT6_01_CpG_11, X396_MLLT6_01_CpG_12, X396_MLLT6_01_CpG_13, X396_MLLT6_01_CpG_14, X396_MLLT6_01_CpG_15, X396_MLLT6_01_CpG_16.17.18.19.20, X396_MLLT6_01_CpG_21, X396_MLLT6_01_CpG_22, X396_MLLT6_01_CpG_23, X396_MLLT6_01_CpG_24, X396_MLLT6_01_CpG_25, X396_MLLT6_01_CpG_26, X396_MLLT6_01_CpG_27, X396_MLLT6_01_CpG_28.29, X396_MLLT6_01_CpG_30, X396_MLLT6_01_CpG_31, X396_MLLT6_01_CpG_32
X398_MLLT6	X398_MLLT6_03_CpG_1, X398_MLLT6_03_CpG_2, X398_MLLT6_03_CpG_3, X398_MLLT6_03_CpG_4, X398_MLLT6_03_CpG_5, X398_MLLT6_03_CpG_6.7, X398_MLLT6_03_CpG_8, X398_MLLT6_03_CpG_9, X398_MLLT6_03_CpG_10.11, X398_MLLT6_03_CpG_12, X398_MLLT6_03_CpG_13, X398_MLLT6_03_CpG_14.15
X399_MLLT7	X399_MLLT7_CpG_1, X399_MLLT7_CpG_2, X399_MLLT7_CpG_3, X399_MLLT7_CpG_4, X399_MLLT7_CpG_5, X399_MLLT7_CpG_6, X399_MLLT7_CpG_7.8, X399_MLLT7_CpG_9, X399_MLLT7_CpG_10, X399_MLLT7_CpG_11.12, X399_MLLT7_CpG_13, X399_MLLT7_CpG_14, X399_MLLT7_CpG_15.16, X399_MLLT7_CpG_17.18, X399_MLLT7_CpG_19, X399_MLLT7_CpG_20, X399_MLLT7_CpG_21, X399_MLLT7_CpG_22, X399_MLLT7_CpG_23.24, X399_MLLT7_CpG_25
X401_MSF	X401_MSF_CpG_1.2.3, X401_MSF_CpG_4.5, X401_MSF_CpG_6, X401_MSF_CpG_7.8, X401_MSF_CpG_9, X401_MSF_CpG_10.11, X401_MSF_CpG_12, X401_MSF_CpG_13.14.15, X401_MSF_CpG_16, X401_MSF_CpG_17.18.19.20, X401_MSF_CpG_21, X401_MSF_CpG_22.23, X401_MSF_CpG_24, X401_MSF_CpG_25, X401_MSF_CpG_26.27, X401_MSF_CpG_28, X401_MSF_CpG_29, X401_MSF_CpG_30.31.32, X401_MSF_CpG_33
X402_MSH2	X402_MSH2_CpG_1.2.3, X402_MSH2_CpG_4.5.6, X402_MSH2_CpG_7, X402_MSH2_CpG_8, X402_MSH2_CpG_9.10,

	X402_MSH2_CpG_11, X402_MSH2_CpG_12, X402_MSH2_CpG_13, X402_MSH2_CpG_14, X402_MSH2_CpG_15.16.17, X402_MSH2_CpG_18.19.20, X402_MSH2_CpG_21, X402_MSH2_CpG_22, X402_MSH2_CpG_23.24, X402_MSH2_CpG_25.26, X402_MSH2_CpG_27.28, X402_MSH2_CpG_29.30, X402_MSH2_CpG_31.32.33.34
X403_MSH6	X403_MSH6_01_CpG_1, X403_MSH6_01_CpG_2, X403_MSH6_01_CpG_3, X403_MSH6_01_CpG_4, X403_MSH6_01_CpG_5.6.7, X403_MSH6_01_CpG_8, X403_MSH6_01_CpG_9.10, X403_MSH6_01_CpG_11, X403_MSH6_01_CpG_12.13.14.15, X403_MSH6_01_CpG_16, X403_MSH6_01_CpG_17.18, X403_MSH6_01_CpG_19.20.21.22.23.24.25.26, X403_MSH6_01_CpG_27, X403_MSH6_01_CpG_28.29.30, X403_MSH6_01_CpG_31.32, X403_MSH6_01_CpG_33.34, X403_MSH6_01_CpG_35.36.37
X405_MSN	X405_MSN_CpG_1, X405_MSN_CpG_2, X405_MSN_CpG_3, X405_MSN_CpG_4, X405_MSN_CpG_5, X405_MSN_CpG_6, X405_MSN_CpG_7.8, X405_MSN_CpG_9, X405_MSN_CpG_10, X405_MSN_CpG_11.12, X405_MSN_CpG_13.14, X405_MSN_CpG_15.16.17.18
X406_MUTYH	X406_MUTYH_CpG_1, X406_MUTYH_CpG_2.3, X406_MUTYH_CpG_4, X406_MUTYH_CpG_5, X406_MUTYH_CpG_6.7.8.9.10, X406_MUTYH_CpG_11.12, X406_MUTYH_CpG_13.14.15.16.17, X406_MUTYH_CpG_18.19, X406_MUTYH_CpG_20.21, X406_MUTYH_CpG_22, X406_MUTYH_CpG_23.24.25, X406_MUTYH_CpG_26.27.28, X406_MUTYH_CpG_29, X406_MUTYH_CpG_30, X406_MUTYH_CpG_31, X406_MUTYH_CpG_32, X406_MUTYH_CpG_33.34, X406_MUTYH_CpG_35, X406_MUTYH_CpG_36.37, X406_MUTYH_CpG_38, X406_MUTYH_CpG_39, X406_MUTYH_CpG_40.41, X406_MUTYH_CpG_42, X406_MUTYH_CpG_43, X406_MUTYH_CpG_44, X406_MUTYH_CpG_45, X406_MUTYH_CpG_46, X406_MUTYH_CpG_47, X406_MUTYH_CpG_48, X406_MUTYH_CpG_49.50, X406_MUTYH_CpG_51, X406_MUTYH_CpG_52, X406_MUTYH_CpG_53, X406_MUTYH_CpG_54, X406_MUTYH_CpG_55, X406_MUTYH_CpG_56, X406_MUTYH_CpG_57
X408_MYCL1	X408_MYCL1_CpG_1, X408_MYCL1_CpG_2.3, X408_MYCL1_CpG_4.5, X408_MYCL1_CpG_6, X408_MYCL1_CpG_7.8, X408_MYCL1_CpG_9.10.11, X408_MYCL1_CpG_12.13, X408_MYCL1_CpG_14, X408_MYCL1_CpG_15.16.17, X408_MYCL1_CpG_18.19.20, X408_MYCL1_CpG_21, X408_MYCL1_CpG_22, X408_MYCL1_CpG_23, X408_MYCL1_CpG_24, X408_MYCL1_CpG_25
X409_MYCN	X409_MYCN_01_CpG_1, X409_MYCN_01_CpG_2.3.4.5, X409_MYCN_01_CpG_6.7.8, X409_MYCN_01_CpG_9, X409_MYCN_01_CpG_10.11.12.13, X409_MYCN_01_CpG_14.15, X409_MYCN_01_CpG_16, X409_MYCN_01_CpG_17, X409_MYCN_01_CpG_18.19.20, X409_MYCN_01_CpG_21.22.23, X409_MYCN_01_CpG_24.25.26, X409_MYCN_01_CpG_27.28.29.30.31.32.33, X409_MYCN_01_CpG_34, X409_MYCN_01_CpG_35.36.37, X409_MYCN_01_CpG_38, X409_MYCN_01_CpG_39.40.41, X409_MYCN_01_CpG_42.43, X409_MYCN_01_CpG_44.45.46, X409_MYCN_01_CpG_47, X409_MYCN_01_CpG_48.49.50.51.52.53.54, X409_MYCN_01_CpG_55, X409_MYCN_01_CpG_56.57.58.59.60, X409_MYCN_01_CpG_61.62, X409_MYCN_01_CpG_63.64.65, X409_MYCN_01_CpG_66, X409_MYCN_01_CpG_67, X409_MYCN_01_CpG_68, X409_MYCN_01_CpG_69.70, X409_MYCN_01_CpG_71.72.73, X409_MYCN_01_CpG_74
X410_MYCN	X410_MYCN_02_CpG_1.2.3, X410_MYCN_02_CpG_4, X410_MYCN_02_CpG_5, X410_MYCN_02_CpG_6.7, X410_MYCN_02_CpG_8, X410_MYCN_02_CpG_9, X410_MYCN_02_CpG_10.11, X410_MYCN_02_CpG_12.13, X410_MYCN_02_CpG_14, X410_MYCN_02_CpG_15, X410_MYCN_02_CpG_16, X410_MYCN_02_CpG_17, X410_MYCN_02_CpG_18, X410_MYCN_02_CpG_19, X410_MYCN_02_CpG_20, X410_MYCN_02_CpG_21, X410_MYCN_02_CpG_22.23
X413_MYST4	X413_MYST4_01_CpG_1.2.3, X413_MYST4_01_CpG_4.5, X413_MYST4_01_CpG_6, X413_MYST4_01_CpG_7,

	X413_MYST4_01_CpG_8, X413_MYST4_01_CpG_9.10, X413_MYST4_01_CpG_11.12.13, X413_MYST4_01_CpG_14.15, X413_MYST4_01_CpG_16, X413_MYST4_01_CpG_17, X413_MYST4_01_CpG_18, X413_MYST4_01_CpG_19, X413_MYST4_01_CpG_20, X413_MYST4_01_CpG_21.22, X413_MYST4_01_CpG_23.24.25.26.27, X413_MYST4_01_CpG_28.29.30, X413_MYST4_01_CpG_31, X413_MYST4_01_CpG_32, X413_MYST4_01_CpG_33, X413_MYST4_01_CpG_34, X413_MYST4_01_CpG_35.36, X413_MYST4_01_CpG_37.38.39.40, X413_MYST4_01_CpG_41, X413_MYST4_01_CpG_42, X413_MYST4_01_CpG_43
X414_MYST4	X414_MYST4_02_CpG_1.2, X414_MYST4_02_CpG_3.4, X414_MYST4_02_CpG_5, X414_MYST4_02_CpG_6.7, X414_MYST4_02_CpG_8, X414_MYST4_02_CpG_9, X414_MYST4_02_CpG_10, X414_MYST4_02_CpG_11.12, X414_MYST4_02_CpG_13, X414_MYST4_02_CpG_14, X414_MYST4_02_CpG_15, X414_MYST4_02_CpG_16, X414_MYST4_02_CpG_17, X414_MYST4_02_CpG_18.19.20, X414_MYST4_02_CpG_21.22, X414_MYST4_02_CpG_23
X417_NCOA2	X417_NCOA2_01_CpG_1.2.3, X417_NCOA2_01_CpG_4, X417_NCOA2_01_CpG_5.6, X417_NCOA2_01_CpG_7.8, X417_NCOA2_01_CpG_9, X417_NCOA2_01_CpG_10.11, X417_NCOA2_01_CpG_12.13, X417_NCOA2_01_CpG_14, X417_NCOA2_01_CpG_15.16, X417_NCOA2_01_CpG_17.18.19, X417_NCOA2_01_CpG_20, X417_NCOA2_01_CpG_21, X417_NCOA2_01_CpG_22.23.24, X417_NCOA2_01_CpG_25.26, X417_NCOA2_01_CpG_27.28
X418_NCOA2	X418_NCOA2_02_CpG_1, X418_NCOA2_02_CpG_2.3, X418_NCOA2_02_CpG_4, X418_NCOA2_02_CpG_5, X418_NCOA2_02_CpG_6, X418_NCOA2_02_CpG_7, X418_NCOA2_02_CpG_8, X418_NCOA2_02_CpG_9, X418_NCOA2_02_CpG_10.11.12.13.14, X418_NCOA2_02_CpG_15, X418_NCOA2_02_CpG_16.17, X418_NCOA2_02_CpG_18.19.20, X418_NCOA2_02_CpG_21.22, X418_NCOA2_02_CpG_23, X418_NCOA2_02_CpG_24, X418_NCOA2_02_CpG_25.26
X420_NF1	X420_NF1_CpG_1, X420_NF1_CpG_2, X420_NF1_CpG_3, X420_NF1_CpG_4.5, X420_NF1_CpG_6, X420_NF1_CpG_7, X420_NF1_CpG_8, X420_NF1_CpG_9, X420_NF1_CpG_10.11, X420_NF1_CpG_12.13, X420_NF1_CpG_14, X420_NF1_CpG_15, X420_NF1_CpG_16, X420_NF1_CpG_17.18.19.20.21, X420_NF1_CpG_22.23, X420_NF1_CpG_24.25, X420_NF1_CpG_26.27, X420_NF1_CpG_28.29.30.31.32, X420_NF1_CpG_33, X420_NF1_CpG_34.35.36, X420_NF1_CpG_37.38, X420_NF1_CpG_39, X420_NF1_CpG_40, X420_NF1_CpG_41.42.43.44, X420_NF1_CpG_45
X424_NPM1	X424_NPM1_CpG_1.2, X424_NPM1_CpG_3.4, X424_NPM1_CpG_5, X424_NPM1_CpG_6, X424_NPM1_CpG_7.8, X424_NPM1_CpG_9.10, X424_NPM1_CpG_11, X424_NPM1_CpG_12.13, X424_NPM1_CpG_14.15, X424_NPM1_CpG_16.17, X424_NPM1_CpG_18, X424_NPM1_CpG_19.20, X424_NPM1_CpG_21, X424_NPM1_CpG_22, X424_NPM1_CpG_23, X424_NPM1_CpG_24, X424_NPM1_CpG_25, X424_NPM1_CpG_26, X424_NPM1_CpG_27.28.29, X424_NPM1_CpG_30.31.32.33.34, X424_NPM1_CpG_35, X424_NPM1_CpG_36, X424_NPM1_CpG_37, X424_NPM1_CpG_38, X424_NPM1_CpG_39, X424_NPM1_CpG_40, X424_NPM1_CpG_41.42, X424_NPM1_CpG_43
X425_NR4A3	X425_NR4A3_CpG_1.2.3, X425_NR4A3_CpG_4.5, X425_NR4A3_CpG_6.7, X425_NR4A3_CpG_8, X425_NR4A3_CpG_9, X425_NR4A3_CpG_10, X425_NR4A3_CpG_11, X425_NR4A3_CpG_12, X425_NR4A3_CpG_13, X425_NR4A3_CpG_14, X425_NR4A3_CpG_15.16.17.18.19.20.21, X425_NR4A3_CpG_22, X425_NR4A3_CpG_23, X425_NR4A3_CpG_24, X425_NR4A3_CpG_25, X425_NR4A3_CpG_26
X429_NTRK	X429_NTRK_02_CpG_1, X429_NTRK_02_CpG_2, X429_NTRK_02_CpG_3, X429_NTRK_02_CpG_4.5.6.7, X429_NTRK_02_CpG_8, X429_NTRK_02_CpG_9.10.11.12, X429_NTRK_02_CpG_13, X429_NTRK_02_CpG_14, X429_NTRK_02_CpG_15, X429_NTRK_02_CpG_16, X429_NTRK_02_CpG_17.18, X429_NTRK_02_CpG_19.20.21, X429_NTRK_02_CpG_22, X429_NTRK_02_CpG_23, X429_NTRK_02_CpG_24
X430_NTRK3	X430_NTRK3_CpG_1.2.3, X430_NTRK3_CpG_4.5.6.7, X430_NTRK3_CpG_8, X430_NTRK3_CpG_9,

	X430_NTRK3_CpG_10, X430_NTRK3_CpG_11, X430_NTRK3_CpG_12, X430_NTRK3_CpG_13.14.15.16.17.18.19.20, X430_NTRK3_CpG_21, X430_NTRK3_CpG_22, X430_NTRK3_CpG_23.24, X430_NTRK3_CpG_25.26.27.28, X430_NTRK3_CpG_29, X430_NTRK3_CpG_30, X430_NTRK3_CpG_31, X430_NTRK3_CpG_32.33, X430_NTRK3_CpG_34.35, X430_NTRK3_CpG_36.37, X430_NTRK3_CpG_38.39.40.41, X430_NTRK3_CpG_42, X430_NTRK3_CpG_43, X430_NTRK3_CpG_44, X430_NTRK3_CpG_45, X430_NTRK3_CpG_46, X430_NTRK3_CpG_47, X430_NTRK3_CpG_48, X430_NTRK3_CpG_49, X430_NTRK3_CpG_50, X430_NTRK3_CpG_51, X430_NTRK3_CpG_52.53, X430_NTRK3_CpG_54, X430_NTRK3_CpG_55, X430_NTRK3_CpG_56.57, X430_NTRK3_CpG_58.59
X431_NUMA1	X431_NUMA1_CpG_1, X431_NUMA1_CpG_2, X431_NUMA1_CpG_3, X431_NUMA1_CpG_4.5.6.7.8, X431_NUMA1_CpG_9.10.11.12.13, X431_NUMA1_CpG_14, X431_NUMA1_CpG_15, X431_NUMA1_CpG_16.17.18, X431_NUMA1_CpG_19, X431_NUMA1_CpG_20, X431_NUMA1_CpG_21.22.23, X431_NUMA1_CpG_24.25.26, X431_NUMA1_CpG_27
X432_NUP214	X432_NUP214_CpG_1.2.3, X432_NUP214_CpG_4, X432_NUP214_CpG_5, X432_NUP214_CpG_6, X432_NUP214_CpG_7, X432_NUP214_CpG_8, X432_NUP214_CpG_9, X432_NUP214_CpG_10, X432_NUP214_CpG_11.12.13, X432_NUP214_CpG_14.15.16.17, X432_NUP214_CpG_18.19, X432_NUP214_CpG_20, X432_NUP214_CpG_21.22.23, X432_NUP214_CpG_24, X432_NUP214_CpG_25.26.27.28, X432_NUP214_CpG_29, X432_NUP214_CpG_30.31, X432_NUP214_CpG_32, X432_NUP214_CpG_33.34, X432_NUP214_CpG_35.36.37, X432_NUP214_CpG_38, X432_NUP214_CpG_39, X432_NUP214_CpG_40, X432_NUP214_CpG_41, X432_NUP214_CpG_42
X433_NUP98	X433_NUP98_01_CpG_1.2, X433_NUP98_01_CpG_3.4.5.6, X433_NUP98_01_CpG_7, X433_NUP98_01_CpG_8.9, X433_NUP98_01_CpG_10.11, X433_NUP98_01_CpG_12, X433_NUP98_01_CpG_13, X433_NUP98_01_CpG_14.15.16.17.18.19.20, X433_NUP98_01_CpG_21.22.23, X433_NUP98_01_CpG_24.25, X433_NUP98_01_CpG_26.27.28
X434_NUP98	X434_NUP98_02_CpG_1.2.3, X434_NUP98_02_CpG_4, X434_NUP98_02_CpG_5, X434_NUP98_02_CpG_6.7.8, X434_NUP98_02_CpG_9, X434_NUP98_02_CpG_10, X434_NUP98_02_CpG_11, X434_NUP98_02_CpG_12, X434_NUP98_02_CpG_13.14.15.16, X434_NUP98_02_CpG_17, X434_NUP98_02_CpG_18, X434_NUP98_02_CpG_19.20
X436_OLIG2	X436_OLIG2_CpG_1.2.3, X436_OLIG2_CpG_4, X436_OLIG2_CpG_5, X436_OLIG2_CpG_6, X436_OLIG2_CpG_7.8.9.10, X436_OLIG2_CpG_11, X436_OLIG2_CpG_12, X436_OLIG2_CpG_13, X436_OLIG2_CpG_14, X436_OLIG2_CpG_15, X436_OLIG2_CpG_16, X436_OLIG2_CpG_17, X436_OLIG2_CpG_18, X436_OLIG2_CpG_19, X436_OLIG2_CpG_20.21, X436_OLIG2_CpG_22
X438_PAX6	X438_PAX6_01_CpG_1, X438_PAX6_01_CpG_2, X438_PAX6_01_CpG_3, X438_PAX6_01_CpG_4, X438_PAX6_01_CpG_5.6, X438_PAX6_01_CpG_7.8, X438_PAX6_01_CpG_9, X438_PAX6_01_CpG_10, X438_PAX6_01_CpG_11, X438_PAX6_01_CpG_12.13, X438_PAX6_01_CpG_14.15.16, X438_PAX6_01_CpG_17.18, X438_PAX6_01_CpG_19.20.21, X438_PAX6_01_CpG_22, X438_PAX6_01_CpG_23.24, X438_PAX6_01_CpG_25, X438_PAX6_01_CpG_26, X438_PAX6_01_CpG_27, X438_PAX6_01_CpG_28.29, X438_PAX6_01_CpG_30.31.32, X438_PAX6_01_CpG_33.34.35, X438_PAX6_01_CpG_36, X438_PAX6_01_CpG_37, X438_PAX6_01_CpG_38.39, X438_PAX6_01_CpG_40, X438_PAX6_01_CpG_41, X438_PAX6_01_CpG_42, X438_PAX6_01_CpG_43, X438_PAX6_01_CpG_44, X438_PAX6_01_CpG_45
X440_PAX6	X440_PAX6_03_CpG_1.2.3, X440_PAX6_03_CpG_4, X440_PAX6_03_CpG_5, X440_PAX6_03_CpG_6, X440_PAX6_03_CpG_7, X440_PAX6_03_CpG_8, X440_PAX6_03_CpG_9, X440_PAX6_03_CpG_10, X440_PAX6_03_CpG_11.12.13.14.15.16, X440_PAX6_03_CpG_17, X440_PAX6_03_CpG_18, X440_PAX6_03_CpG_19,

	X440_PAX6_03_CpG_20, X440_PAX6_03_CpG_21
X443_PAX8	X443_PAX8_01_CpG_1.2, X443_PAX8_01_CpG_3.4, X443_PAX8_01_CpG_5, X443_PAX8_01_CpG_6.7.8.9, X443_PAX8_01_CpG_10, X443_PAX8_01_CpG_11, X443_PAX8_01_CpG_12, X443_PAX8_01_CpG_13.14, X443_PAX8_01_CpG_15.16, X443_PAX8_01_CpG_17, X443_PAX8_01_CpG_18, X443_PAX8_01_CpG_19, X443_PAX8_01_CpG_20.21.22.23, X443_PAX8_01_CpG_24.25.26.27, X443_PAX8_01_CpG_28.29, X443_PAX8_01_CpG_30.31.32.33, X443_PAX8_01_CpG_34.35, X443_PAX8_01_CpG_36, X443_PAX8_01_CpG_37.38, X443_PAX8_01_CpG_39
X444_PAX8	X444_PAX8_02_CpG_1.2, X444_PAX8_02_CpG_3.4, X444_PAX8_02_CpG_5, X444_PAX8_02_CpG_6, X444_PAX8_02_CpG_7.8.9.10.11.12.13.14, X444_PAX8_02_CpG_15, X444_PAX8_02_CpG_16.17.18.19, X444_PAX8_02_CpG_20, X444_PAX8_02_CpG_21, X444_PAX8_02_CpG_22, X444_PAX8_02_CpG_23.24, X444_PAX8_02_CpG_25, X444_PAX8_02_CpG_26, X444_PAX8_02_CpG_27, X444_PAX8_02_CpG_28, X444_PAX8_02_CpG_29, X444_PAX8_02_CpG_30, X444_PAX8_02_CpG_31
X445_PAX8	X445_PAX8_03_CpG_1.2, X445_PAX8_03_CpG_3.4, X445_PAX8_03_CpG_5, X445_PAX8_03_CpG_6, X445_PAX8_03_CpG_7.8.9.10, X445_PAX8_03_CpG_11, X445_PAX8_03_CpG_12.13, X445_PAX8_03_CpG_14, X445_PAX8_03_CpG_15, X445_PAX8_03_CpG_16, X445_PAX8_03_CpG_17, X445_PAX8_03_CpG_18, X445_PAX8_03_CpG_19.20, X445_PAX8_03_CpG_21
X447_PCM1	X447_PCM1_CpG_1.2, X447_PCM1_CpG_3.4.5, X447_PCM1_CpG_6, X447_PCM1_CpG_7.8, X447_PCM1_CpG_9, X447_PCM1_CpG_10, X447_PCM1_CpG_11, X447_PCM1_CpG_12.13.14, X447_PCM1_CpG_15, X447_PCM1_CpG_16.17, X447_PCM1_CpG_18.19, X447_PCM1_CpG_20, X447_PCM1_CpG_21.22, X447_PCM1_CpG_23.24, X447_PCM1_CpG_25.26, X447_PCM1_CpG_27.28.29, X447_PCM1_CpG_30.31, X447_PCM1_CpG_32, X447_PCM1_CpG_33
X448_PDE4DIP	X448_PDE4DIP_CpG_1.2.3.4.5.6, X448_PDE4DIP_CpG_7.8.9.10.11.12, X448_PDE4DIP_CpG_13, X448_PDE4DIP_CpG_14, X448_PDE4DIP_CpG_15, X448_PDE4DIP_CpG_16.17, X448_PDE4DIP_CpG_18, X448_PDE4DIP_CpG_19.20, X448_PDE4DIP_CpG_21, X448_PDE4DIP_CpG_22, X448_PDE4DIP_CpG_23.24.25, X448_PDE4DIP_CpG_26, X448_PDE4DIP_CpG_27, X448_PDE4DIP_CpG_28.29, X448_PDE4DIP_CpG_30.31, X448_PDE4DIP_CpG_32
X449_PDGFB	X449_PDGFB_CpG_1, X449_PDGFB_CpG_2.3, X449_PDGFB_CpG_4, X449_PDGFB_CpG_5, X449_PDGFB_CpG_6, X449_PDGFB_CpG_7.8.9, X449_PDGFB_CpG_10, X449_PDGFB_CpG_11.12.13.14.15.16.17, X449_PDGFB_CpG_18.19.20.21.22.23.24.25.26.27.28.29.30, X449_PDGFB_CpG_31.32.33.34, X449_PDGFB_CpG_35.36.37.38.39.40.41.42.43.44.45, X449_PDGFB_CpG_46, X449_PDGFB_CpG_47, X449_PDGFB_CpG_48.49, X449_PDGFB_CpG_50, X449_PDGFB_CpG_51.52.53, X449_PDGFB_CpG_54.55, X449_PDGFB_CpG_56.57.58, X449_PDGFB_CpG_59, X449_PDGFB_CpG_60.61, X449_PDGFB_CpG_62.63
X450_PDGFRA	X450_PDGFRA_CpG_1.2.3, X450_PDGFRA_CpG_4.5, X450_PDGFRA_CpG_6.7, X450_PDGFRA_CpG_8, X450_PDGFRA_CpG_9, X450_PDGFRA_CpG_10.11.12, X450_PDGFRA_CpG_13, X450_PDGFRA_CpG_14, X450_PDGFRA_CpG_15.16, X450_PDGFRA_CpG_17, X450_PDGFRA_CpG_18, X450_PDGFRA_CpG_19, X450_PDGFRA_CpG_20, X450_PDGFRA_CpG_21, X450_PDGFRA_CpG_22, X450_PDGFRA_CpG_23
X455_PIM1	X455_PIM1_01_CpG_1, X455_PIM1_01_CpG_2.3.4.5, X455_PIM1_01_CpG_6, X455_PIM1_01_CpG_7, X455_PIM1_01_CpG_8.9, X455_PIM1_01_CpG_10.11.12, X455_PIM1_01_CpG_13.14.15.16, X455_PIM1_01_CpG_17.18.19.20, X455_PIM1_01_CpG_21, X455_PIM1_01_CpG_22, X455_PIM1_01_CpG_23,

	X455_PIM1_01_CpG_24.25.26.27, X455_PIM1_01_CpG_28.29.30, X455_PIM1_01_CpG_31, X455_PIM1_01_CpG_32.33.34, X455_PIM1_01_CpG_35.36.37.38.39, X455_PIM1_01_CpG_40.41, X455_PIM1_01_CpG_42, X455_PIM1_01_CpG_43, X455_PIM1_01_CpG_44, X455_PIM1_01_CpG_45, X455_PIM1_01_CpG_46, X455_PIM1_01_CpG_47
X456_PIM1	X456_PIM1_02_CpG_1, X456_PIM1_02_CpG_2.3, X456_PIM1_02_CpG_4, X456_PIM1_02_CpG_5.6.7, X456_PIM1_02_CpG_8, X456_PIM1_02_CpG_9.10.11, X456_PIM1_02_CpG_12, X456_PIM1_02_CpG_13, X456_PIM1_02_CpG_14, X456_PIM1_02_CpG_15, X456_PIM1_02_CpG_16, X456_PIM1_02_CpG_17, X456_PIM1_02_CpG_18
X458_PMS1	X458_PMS1_01_CpG_1.2, X458_PMS1_01_CpG_3, X458_PMS1_01_CpG_4.5.6.7, X458_PMS1_01_CpG_8, X458_PMS1_01_CpG_9, X458_PMS1_01_CpG_10, X458_PMS1_01_CpG_11, X458_PMS1_01_CpG_12, X458_PMS1_01_CpG_13, X458_PMS1_01_CpG_14, X458_PMS1_01_CpG_15.16, X458_PMS1_01_CpG_17, X458_PMS1_01_CpG_18, X458_PMS1_01_CpG_19, X458_PMS1_01_CpG_20, X458_PMS1_01_CpG_21, X458_PMS1_01_CpG_22, X458_PMS1_01_CpG_23, X458_PMS1_01_CpG_24, X458_PMS1_01_CpG_25.26.27, X458_PMS1_01_CpG_28.29, X458_PMS1_01_CpG_30.31.32.33, X458_PMS1_01_CpG_34, X458_PMS1_01_CpG_35.36.37, X458_PMS1_01_CpG_38, X458_PMS1_01_CpG_39.40.41, X458_PMS1_01_CpG_42, X458_PMS1_01_CpG_43, X458_PMS1_01_CpG_44, X458_PMS1_01_CpG_45, X458_PMS1_01_CpG_46, X458_PMS1_01_CpG_47, X458_PMS1_01_CpG_48.49.50, X458_PMS1_01_CpG_51, X458_PMS1_01_CpG_52.53, X458_PMS1_01_CpG_54.55.56.57.58.59.60.61.62.63, X458_PMS1_01_CpG_64, X458_PMS1_01_CpG_65.66
X459_PMS1	X459_PMS1_02_CpG_1.2, X459_PMS1_02_CpG_3, X459_PMS1_02_CpG_4, X459_PMS1_02_CpG_5, X459_PMS1_02_CpG_6, X459_PMS1_02_CpG_7.8.9.10, X459_PMS1_02_CpG_11, X459_PMS1_02_CpG_12.13.14.15, X459_PMS1_02_CpG_16, X459_PMS1_02_CpG_17.18.19.20, X459_PMS1_02_CpG_21, X459_PMS1_02_CpG_22.23, X459_PMS1_02_CpG_24.25
X460_PMS2	X460_PMS2_CpG_1, X460_PMS2_CpG_2, X460_PMS2_CpG_3, X460_PMS2_CpG_4, X460_PMS2_CpG_5, X460_PMS2_CpG_6, X460_PMS2_CpG_7, X460_PMS2_CpG_8, X460_PMS2_CpG_9, X460_PMS2_CpG_10, X460_PMS2_CpG_11, X460_PMS2_CpG_12.13.14, X460_PMS2_CpG_15, X460_PMS2_CpG_16.17.18, X460_PMS2_CpG_19, X460_PMS2_CpG_20, X460_PMS2_CpG_21, X460_PMS2_CpG_22, X460_PMS2_CpG_23, X460_PMS2_CpG_24, X460_PMS2_CpG_25.26, X460_PMS2_CpG_27.28, X460_PMS2_CpG_29, X460_PMS2_CpG_30, X460_PMS2_CpG_31.32.33, X460_PMS2_CpG_34.35, X460_PMS2_CpG_36, X460_PMS2_CpG_37, X460_PMS2_CpG_38, X460_PMS2_CpG_39, X460_PMS2_CpG_40.41, X460_PMS2_CpG_42.43
X461_PMX1	X461_PMX1_CpG_1.2.3, X461_PMX1_CpG_4, X461_PMX1_CpG_5, X461_PMX1_CpG_6, X461_PMX1_CpG_7, X461_PMX1_CpG_8.9.10, X461_PMX1_CpG_11, X461_PMX1_CpG_12.13, X461_PMX1_CpG_14, X461_PMX1_CpG_15.16.17.18, X461_PMX1_CpG_19, X461_PMX1_CpG_20, X461_PMX1_CpG_21, X461_PMX1_CpG_22, X461_PMX1_CpG_23, X461_PMX1_CpG_24, X461_PMX1_CpG_25, X461_PMX1_CpG_26.27, X461_PMX1_CpG_28, X461_PMX1_CpG_29.30.31, X461_PMX1_CpG_32, X461_PMX1_CpG_33, X461_PMX1_CpG_34.35, X461_PMX1_CpG_36
X464_PPARG	X464_PPARG_CpG_1, X464_PPARG_CpG_2, X464_PPARG_CpG_3.4.5.6.7, X464_PPARG_CpG_8, X464_PPARG_CpG_9, X464_PPARG_CpG_10, X464_PPARG_CpG_11.12, X464_PPARG_CpG_13, X464_PPARG_CpG_14.15, X464_PPARG_CpG_16, X464_PPARG_CpG_17.18, X464_PPARG_CpG_19.20.21.22, X464_PPARG_CpG_23, X464_PPARG_CpG_24.25, X464_PPARG_CpG_26.27.28, X464_PPARG_CpG_29, X464_PPARG_CpG_30.31.32.33, X464_PPARG_CpG_34, X464_PPARG_CpG_35, X464_PPARG_CpG_36.37.38.39, X464_PPARG_CpG_40, X464_PPARG_CpG_41.42, X464_PPARG_CpG_43.44, X464_PPARG_CpG_45, X464_PPARG_CpG_46,

	X464_PPARG_CpG_47.48.49.50, X464_PPARG_CpG_51.52.53
X465_PRCC	X465_PRCC_01_CpG_1.2.3, X465_PRCC_01_CpG_4, X465_PRCC_01_CpG_5.6.7.8, X465_PRCC_01_CpG_9, X465_PRCC_01_CpG_10, X465_PRCC_01_CpG_11, X465_PRCC_01_CpG_12, X465_PRCC_01_CpG_13
X467_PRKAR1A	X467_PRKAR1A_CpG_1, X467_PRKAR1A_CpG_2.3.4.5.6, X467_PRKAR1A_CpG_7.8.9, X467_PRKAR1A_CpG_10, X467_PRKAR1A_CpG_11, X467_PRKAR1A_CpG_12.13.14.15.16, X467_PRKAR1A_CpG_17, X467_PRKAR1A_CpG_18.19.20, X467_PRKAR1A_CpG_21, X467_PRKAR1A_CpG_22, X467_PRKAR1A_CpG_23.24.25, X467_PRKAR1A_CpG_26, X467_PRKAR1A_CpG_27, X467_PRKAR1A_CpG_28, X467_PRKAR1A_CpG_29.30, X467_PRKAR1A_CpG_31, X467_PRKAR1A_CpG_32, X467_PRKAR1A_CpG_33, X467_PRKAR1A_CpG_34, X467_PRKAR1A_CpG_35, X467_PRKAR1A_CpG_36, X467_PRKAR1A_CpG_37.38, X467_PRKAR1A_CpG_39, X467_PRKAR1A_CpG_40, X467_PRKAR1A_CpG_41
X468_PRO1073	X468_PRO1073_CpG_1, X468_PRO1073_CpG_2, X468_PRO1073_CpG_3, X468_PRO1073_CpG_4, X468_PRO1073_CpG_5, X468_PRO1073_CpG_6, X468_PRO1073_CpG_7.8.9.10.11, X468_PRO1073_CpG_12.13.14, X468_PRO1073_CpG_15, X468_PRO1073_CpG_16, X468_PRO1073_CpG_17, X468_PRO1073_CpG_18, X468_PRO1073_CpG_19, X468_PRO1073_CpG_20.21, X468_PRO1073_CpG_22, X468_PRO1073_CpG_23, X468_PRO1073_CpG_24, X468_PRO1073_CpG_25.26.27, X468_PRO1073_CpG_28.29.30.31.32, X468_PRO1073_CpG_33.34.35, X468_PRO1073_CpG_36, X468_PRO1073_CpG_37.38, X468_PRO1073_CpG_39.40.41, X468_PRO1073_CpG_42
X470_PTCH	X470_PTCH_01_CpG_1, X470_PTCH_01_CpG_2, X470_PTCH_01_CpG_3.4.5, X470_PTCH_01_CpG_6, X470_PTCH_01_CpG_7.8, X470_PTCH_01_CpG_9.10.11.12.13, X470_PTCH_01_CpG_14.15.16.17, X470_PTCH_01_CpG_18.19, X470_PTCH_01_CpG_20.21.22.23.24, X470_PTCH_01_CpG_25, X470_PTCH_01_CpG_26.27, X470_PTCH_01_CpG_28.29, X470_PTCH_01_CpG_30, X470_PTCH_01_CpG_31, X470_PTCH_01_CpG_32.33, X470_PTCH_01_CpG_34, X470_PTCH_01_CpG_35, X470_PTCH_01_CpG_36, X470_PTCH_01_CpG_37.38, X470_PTCH_01_CpG_39
X471_PTCH	X471_PTCH_02_CpG_1, X471_PTCH_02_CpG_2, X471_PTCH_02_CpG_3, X471_PTCH_02_CpG_4, X471_PTCH_02_CpG_5, X471_PTCH_02_CpG_6.7, X471_PTCH_02_CpG_8, X471_PTCH_02_CpG_9, X471_PTCH_02_CpG_10, X471_PTCH_02_CpG_11.12, X471_PTCH_02_CpG_13, X471_PTCH_02_CpG_14.15.16.17, X471_PTCH_02_CpG_18, X471_PTCH_02_CpG_19, X471_PTCH_02_CpG_20, X471_PTCH_02_CpG_21, X471_PTCH_02_CpG_22, X471_PTCH_02_CpG_23, X471_PTCH_02_CpG_24
X472_PTCH	X472_PTCH_03_CpG_1, X472_PTCH_03_CpG_2, X472_PTCH_03_CpG_3.4.5, X472_PTCH_03_CpG_6.7, X472_PTCH_03_CpG_8, X472_PTCH_03_CpG_9, X472_PTCH_03_CpG_10, X472_PTCH_03_CpG_11, X472_PTCH_03_CpG_12
X474_PTEN	X474_PTEN_02_CpG_1, X474_PTEN_02_CpG_2.3, X474_PTEN_02_CpG_4, X474_PTEN_02_CpG_5.6.7.8.9.10.11.12.13.14.15.16, X474_PTEN_02_CpG_17.18.19.20.21.22.23, X474_PTEN_02_CpG_24, X474_PTEN_02_CpG_25.26.27, X474_PTEN_02_CpG_28, X474_PTEN_02_CpG_29.30, X474_PTEN_02_CpG_31.32.33.34, X474_PTEN_02_CpG_35.36, X474_PTEN_02_CpG_37, X474_PTEN_02_CpG_38, X474_PTEN_02_CpG_39, X474_PTEN_02_CpG_40, X474_PTEN_02_CpG_41, X474_PTEN_02_CpG_42, X474_PTEN_02_CpG_43.44.45.46.47.48, X474_PTEN_02_CpG_49, X474_PTEN_02_CpG_50.51, X474_PTEN_02_CpG_52.53, X474_PTEN_02_CpG_54.55.56.57.58, X474_PTEN_02_CpG_59.60.61.62.63, X474_PTEN_02_CpG_64, X474_PTEN_02_CpG_65

X475_PTPN11	X475_PTPN11_CpG_1.2.3.4.5.6.7, X475_PTPN11_CpG_8.9, X475_PTPN11_CpG_10, X475_PTPN11_CpG_11, X475_PTPN11_CpG_12, X475_PTPN11_CpG_13.14.15.16, X475_PTPN11_CpG_17, X475_PTPN11_CpG_18, X475_PTPN11_CpG_19.20, X475_PTPN11_CpG_21, X475_PTPN11_CpG_22.23.24.25.26, X475_PTPN11_CpG_27.28.29.30, X475_PTPN11_CpG_31.32, X475_PTPN11_CpG_33.34.35.36.37.38.39.40.41.42, X475_PTPN11_CpG_43.44, X475_PTPN11_CpG_45.46, X475_PTPN11_CpG_47, X475_PTPN11_CpG_48, X475_PTPN11_CpG_49.50, X475_PTPN11_CpG_51, X475_PTPN11_CpG_52, X475_PTPN11_CpG_53, X475_PTPN11_CpG_54.55, X475_PTPN11_CpG_56, X475_PTPN11_CpG_57, X475_PTPN11_CpG_58.59, X475_PTPN11_CpG_60
X477_RAD51L1	X477_RAD51L1_CpG_1.2.3.4, X477_RAD51L1_CpG_5, X477_RAD51L1_CpG_6, X477_RAD51L1_CpG_7.8, X477_RAD51L1_CpG_9, X477_RAD51L1_CpG_10.11.12.13.14, X477_RAD51L1_CpG_15, X477_RAD51L1_CpG_16.17, X477_RAD51L1_CpG_18, X477_RAD51L1_CpG_19.20, X477_RAD51L1_CpG_21, X477_RAD51L1_CpG_22, X477_RAD51L1_CpG_23, X477_RAD51L1_CpG_24.25.26.27.28.29.30.31, X477_RAD51L1_CpG_32.33, X477_RAD51L1_CpG_34.35, X477_RAD51L1_CpG_36, X477_RAD51L1_CpG_37, X477_RAD51L1_CpG_38.39.40.41.42.43.44, X477_RAD51L1_CpG_45.46.47.48, X477_RAD51L1_CpG_49.50.51, X477_RAD51L1_CpG_52, X477_RAD51L1_CpG_53.54, X477_RAD51L1_CpG_55.56, X477_RAD51L1_CpG_57, X477_RAD51L1_CpG_58.59.60, X477_RAD51L1_CpG_61, X477_RAD51L1_CpG_62, X477_RAD51L1_CpG_63.64
X480_RARA	X480_RARA_CpG_1.2.3.4.5.6.7.8, X480_RARA_CpG_9, X480_RARA_CpG_10, X480_RARA_CpG_11.12, X480_RARA_CpG_13, X480_RARA_CpG_14.15.16, X480_RARA_CpG_17, X480_RARA_CpG_18.19.20.21.22.23, X480_RARA_CpG_24.25.26, X480_RARA_CpG_27.28, X480_RARA_CpG_29.30.31.32, X480_RARA_CpG_33, X480_RARA_CpG_34, X480_RARA_CpG_35, X480_RARA_CpG_36, X480_RARA_CpG_37.38, X480_RARA_CpG_39, X480_RARA_CpG_40, X480_RARA_CpG_41, X480_RARA_CpG_42, X480_RARA_CpG_43, X480_RARA_CpG_44, X480_RARA_CpG_45.46.47
X482_RECQL4	X482_RECQL4_CpG_1.2, X482_RECQL4_CpG_3, X482_RECQL4_CpG_4, X482_RECQL4_CpG_5.6.7, X482_RECQL4_CpG_8, X482_RECQL4_CpG_9, X482_RECQL4_CpG_10.11, X482_RECQL4_CpG_12, X482_RECQL4_CpG_13, X482_RECQL4_CpG_14, X482_RECQL4_CpG_15, X482_RECQL4_CpG_16, X482_RECQL4_CpG_17.18.19.20, X482_RECQL4_CpG_21.22, X482_RECQL4_CpG_23
X489_SDHB	X489_SDHB_CpG_1, X489_SDHB_CpG_2, X489_SDHB_CpG_3, X489_SDHB_CpG_4.5, X489_SDHB_CpG_6, X489_SDHB_CpG_7.8, X489_SDHB_CpG_9, X489_SDHB_CpG_10, X489_SDHB_CpG_11.12.13.14.15, X489_SDHB_CpG_16.17.18, X489_SDHB_CpG_19.20, X489_SDHB_CpG_21, X489_SDHB_CpG_22.23.24.25, X489_SDHB_CpG_26, X489_SDHB_CpG_27, X489_SDHB_CpG_28.29, X489_SDHB_CpG_30, X489_SDHB_CpG_31.32, X489_SDHB_CpG_33
X490_SDHC	X490_SDHC_01_CpG_1.2, X490_SDHC_01_CpG_3, X490_SDHC_01_CpG_4.5.6.7, X490_SDHC_01_CpG_8, X490_SDHC_01_CpG_9, X490_SDHC_01_CpG_10, X490_SDHC_01_CpG_11.12, X490_SDHC_01_CpG_13, X490_SDHC_01_CpG_14, X490_SDHC_01_CpG_15
X491_SDHC	X491_SDHC_02_CpG_1, X491_SDHC_02_CpG_2, X491_SDHC_02_CpG_3.4.5.6.7.8.9.10, X491_SDHC_02_CpG_11, X491_SDHC_02_CpG_12, X491_SDHC_02_CpG_13, X491_SDHC_02_CpG_14.15, X491_SDHC_02_CpG_16
X492_SDHD	X492_SDHD_CpG_1.2, X492_SDHD_CpG_3.4.5, X492_SDHD_CpG_6, X492_SDHD_CpG_7, X492_SDHD_CpG_8.9, X492_SDHD_CpG_10, X492_SDHD_CpG_11, X492_SDHD_CpG_12, X492_SDHD_CpG_13, X492_SDHD_CpG_14, X492_SDHD_CpG_15.16, X492_SDHD_CpG_17, X492_SDHD_CpG_18.19, X492_SDHD_CpG_20,

	X492_SDHD_CpG_21.22.23, X492_SDHD_CpG_24, X492_SDHD_CpG_25, X492_SDHD_CpG_26, X492_SDHD_CpG_27, X492_SDHD_CpG_28.29, X492_SDHD_CpG_30
X498_SMO	X498_SMO_CpG_1.2.3.4, X498_SMO_CpG_5, X498_SMO_CpG_6.7, X498_SMO_CpG_8.9, X498_SMO_CpG_10.11.12, X498_SMO_CpG_13.14, X498_SMO_CpG_15.16.17, X498_SMO_CpG_18.19.20, X498_SMO_CpG_21.22.23, X498_SMO_CpG_24.25, X498_SMO_CpG_26.27, X498_SMO_CpG_28, X498_SMO_CpG_29, X498_SMO_CpG_30, X498_SMO_CpG_31, X498_SMO_CpG_32, X498_SMO_CpG_33.34, X498_SMO_CpG_35.36, X498_SMO_CpG_37.38, X498_SMO_CpG_39.40, X498_SMO_CpG_41, X498_SMO_CpG_42, X498_SMO_CpG_43, X498_SMO_CpG_44, X498_SMO_CpG_45, X498_SMO_CpG_46, X498_SMO_CpG_47
X499_SS18	X499_SS18_CpG_1.2.3.4.5, X499_SS18_CpG_6.7.8.9, X499_SS18_CpG_10, X499_SS18_CpG_11, X499_SS18_CpG_12.13.14, X499_SS18_CpG_15, X499_SS18_CpG_16, X499_SS18_CpG_17.18.19.20, X499_SS18_CpG_21.22, X499_SS18_CpG_23, X499_SS18_CpG_24, X499_SS18_CpG_25.26, X499_SS18_CpG_27, X499_SS18_CpG_28.29.30, X499_SS18_CpG_31, X499_SS18_CpG_32, X499_SS18_CpG_33, X499_SS18_CpG_34, X499_SS18_CpG_35.36.37, X499_SS18_CpG_38.39, X499_SS18_CpG_40, X499_SS18_CpG_41, X499_SS18_CpG_42, X499_SS18_CpG_43, X499_SS18_CpG_44.45, X499_SS18_CpG_46, X499_SS18_CpG_47, X499_SS18_CpG_48.49.50.51
X501_SSH3BP1	X501_SSH3BP1_CpG_1, X501_SSH3BP1_CpG_2.3, X501_SSH3BP1_CpG_4.5, X501_SSH3BP1_CpG_6.7, X501_SSH3BP1_CpG_8.9, X501_SSH3BP1_CpG_10.11.12.13, X501_SSH3BP1_CpG_14, X501_SSH3BP1_CpG_15, X501_SSH3BP1_CpG_16, X501_SSH3BP1_CpG_17.18.19, X501_SSH3BP1_CpG_20.21, X501_SSH3BP1_CpG_22, X501_SSH3BP1_CpG_23.24, X501_SSH3BP1_CpG_25.26.27, X501_SSH3BP1_CpG_28.29.30.31, X501_SSH3BP1_CpG_32, X501_SSH3BP1_CpG_33, X501_SSH3BP1_CpG_34, X501_SSH3BP1_CpG_35, X501_SSH3BP1_CpG_36.37.38, X501_SSH3BP1_CpG_39, X501_SSH3BP1_CpG_40
X505_STK11	X505_STK11_01_CpG_1.2, X505_STK11_01_CpG_3, X505_STK11_01_CpG_4, X505_STK11_01_CpG_5.6, X505_STK11_01_CpG_7, X505_STK11_01_CpG_8.9, X505_STK11_01_CpG_10.11.12, X505_STK11_01_CpG_13.14.15.16, X505_STK11_01_CpG_17, X505_STK11_01_CpG_18, X505_STK11_01_CpG_19, X505_STK11_01_CpG_20, X505_STK11_01_CpG_21, X505_STK11_01_CpG_22, X505_STK11_01_CpG_23, X505_STK11_01_CpG_24.25, X505_STK11_01_CpG_26.27
X506_STK11	X506_STK11_02_CpG_1, X506_STK11_02_CpG_2, X506_STK11_02_CpG_3, X506_STK11_02_CpG_4, X506_STK11_02_CpG_5, X506_STK11_02_CpG_6, X506_STK11_02_CpG_7, X506_STK11_02_CpG_8, X506_STK11_02_CpG_9.10.11, X506_STK11_02_CpG_12, X506_STK11_02_CpG_13, X506_STK11_02_CpG_14, X506_STK11_02_CpG_15, X506_STK11_02_CpG_16, X506_STK11_02_CpG_17, X506_STK11_02_CpG_18, X506_STK11_02_CpG_19, X506_STK11_02_CpG_20, X506_STK11_02_CpG_21.22.23, X506_STK11_02_CpG_24
X507_STL	X507_STL_01_CpG_1, X507_STL_01_CpG_2, X507_STL_01_CpG_3, X507_STL_01_CpG_4, X507_STL_01_CpG_5, X507_STL_01_CpG_6, X507_STL_01_CpG_7.8, X507_STL_01_CpG_9, X507_STL_01_CpG_10.11, X507_STL_01_CpG_12, X507_STL_01_CpG_13, X507_STL_01_CpG_14.15, X507_STL_01_CpG_16.17, X507_STL_01_CpG_18, X507_STL_01_CpG_19, X507_STL_01_CpG_20, X507_STL_01_CpG_21, X507_STL_01_CpG_22, X507_STL_01_CpG_23, X507_STL_01_CpG_24, X507_STL_01_CpG_25, X507_STL_01_CpG_26, X507_STL_01_CpG_27, X507_STL_01_CpG_28, X507_STL_01_CpG_29, X507_STL_01_CpG_30
X508_STL	X508_STL_02_CpG_1.2.3.4.5.6, X508_STL_02_CpG_7, X508_STL_02_CpG_8.9, X508_STL_02_CpG_10.11.12.13.14, X508_STL_02_CpG_15.16.17.18, X508_STL_02_CpG_19.20.21.22.23, X508_STL_02_CpG_24, X508_STL_02_CpG_25, X508_STL_02_CpG_26, X508_STL_02_CpG_27.28, X508_STL_02_CpG_29, X508_STL_02_CpG_30,

	X508_STL_02_CpG_31.32.33
X509_SUFU	X509_SUFU_CpG_1.2.3.4, X509_SUFU_CpG_5.6.7.8, X509_SUFU_CpG_9.10.11.12, X509_SUFU_CpG_13, X509_SUFU_CpG_14.15.16, X509_SUFU_CpG_17.18, X509_SUFU_CpG_19, X509_SUFU_CpG_20.21, X509_SUFU_CpG_22, X509_SUFU_CpG_23.24.25, X509_SUFU_CpG_26.27, X509_SUFU_CpG_28, X509_SUFU_CpG_29, X509_SUFU_CpG_30, X509_SUFU_CpG_31, X509_SUFU_CpG_32.33.34, X509_SUFU_CpG_35.36.37.38, X509_SUFU_CpG_39.40.41.42, X509_SUFU_CpG_43, X509_SUFU_CpG_44, X509_SUFU_CpG_45.46, X509_SUFU_CpG_47, X509_SUFU_CpG_48, X509_SUFU_CpG_49, X509_SUFU_CpG_50, X509_SUFU_CpG_51.52, X509_SUFU_CpG_53, X509_SUFU_CpG_54.55, X509_SUFU_CpG_56.57, X509_SUFU_CpG_58
X510_TAF15	X510_TAF15_CpG_1, X510_TAF15_CpG_2.3, X510_TAF15_CpG_4.5, X510_TAF15_CpG_6.7.8, X510_TAF15_CpG_9, X510_TAF15_CpG_10.11, X510_TAF15_CpG_12, X510_TAF15_CpG_13.14.15.16.17.18.19.20.21.22.23, X510_TAF15_CpG_24, X510_TAF15_CpG_25, X510_TAF15_CpG_26.27, X510_TAF15_CpG_28, X510_TAF15_CpG_29, X510_TAF15_CpG_30, X510_TAF15_CpG_31.32, X510_TAF15_CpG_33, X510_TAF15_CpG_34, X510_TAF15_CpG_35, X510_TAF15_CpG_36, X510_TAF15_CpG_37.38, X510_TAF15_CpG_39
X511_TAL1	X511_TAL1_CpG_1, X511_TAL1_CpG_2, X511_TAL1_CpG_3.4.5.6.7.8, X511_TAL1_CpG_9.10, X511_TAL1_CpG_11.12.13.14, X511_TAL1_CpG_15, X511_TAL1_CpG_16, X511_TAL1_CpG_17.18.19.20.21.22, X511_TAL1_CpG_23, X511_TAL1_CpG_24, X511_TAL1_CpG_25.26.27.28.29.30.31.32.33, X511_TAL1_CpG_34.35.36.37, X511_TAL1_CpG_38, X511_TAL1_CpG_39.40.41.42.43.44, X511_TAL1_CpG_45, X511_TAL1_CpG_46.47.48.49.50.51.52, X511_TAL1_CpG_53.54, X511_TAL1_CpG_55, X511_TAL1_CpG_56.57.58.59, X511_TAL1_CpG_60, X511_TAL1_CpG_61.62.63.64.65.66
X513_TCF1	X513_TCF1_CpG_1.2, X513_TCF1_CpG_3.4, X513_TCF1_CpG_5, X513_TCF1_CpG_6.7, X513_TCF1_CpG_8, X513_TCF1_CpG_9, X513_TCF1_CpG_10.11.12, X513_TCF1_CpG_13, X513_TCF1_CpG_14, X513_TCF1_CpG_15.16, X513_TCF1_CpG_17, X513_TCF1_CpG_18.19.20.21
X514_TCF12	X514_TCF12_01_CpG_1, X514_TCF12_01_CpG_2, X514_TCF12_01_CpG_3.4, X514_TCF12_01_CpG_5, X514_TCF12_01_CpG_6, X514_TCF12_01_CpG_7, X514_TCF12_01_CpG_8, X514_TCF12_01_CpG_9.10, X514_TCF12_01_CpG_11, X514_TCF12_01_CpG_12.13, X514_TCF12_01_CpG_14.15, X514_TCF12_01_CpG_16, X514_TCF12_01_CpG_17, X514_TCF12_01_CpG_18.19, X514_TCF12_01_CpG_20, X514_TCF12_01_CpG_21, X514_TCF12_01_CpG_22, X514_TCF12_01_CpG_23.24.25.26.27.28.29.30.31.32, X514_TCF12_01_CpG_33.34.35, X514_TCF12_01_CpG_36.37, X514_TCF12_01_CpG_38.39, X514_TCF12_01_CpG_40, X514_TCF12_01_CpG_41, X514_TCF12_01_CpG_42, X514_TCF12_01_CpG_43, X514_TCF12_01_CpG_44.45.46, X514_TCF12_01_CpG_47.48.49.50.51.52.53.54.55, X514_TCF12_01_CpG_56.57.58, X514_TCF12_01_CpG_59.60.61.62, X514_TCF12_01_CpG_63.64.65.66.67, X514_TCF12_01_CpG_68, X514_TCF12_01_CpG_69
X515_TCF12	X515_TCF12_02_CpG_1.2, X515_TCF12_02_CpG_3, X515_TCF12_02_CpG_4, X515_TCF12_02_CpG_5.6.7, X515_TCF12_02_CpG_8, X515_TCF12_02_CpG_9.10, X515_TCF12_02_CpG_11, X515_TCF12_02_CpG_12.13.14.15.16, X515_TCF12_02_CpG_17, X515_TCF12_02_CpG_18, X515_TCF12_02_CpG_19, X515_TCF12_02_CpG_20
X516_TCF3	X516_TCF3_01_CpG_1, X516_TCF3_01_CpG_2, X516_TCF3_01_CpG_3.4.5, X516_TCF3_01_CpG_6.7, X516_TCF3_01_CpG_8, X516_TCF3_01_CpG_9, X516_TCF3_01_CpG_10, X516_TCF3_01_CpG_11, X516_TCF3_01_CpG_12, X516_TCF3_01_CpG_13, X516_TCF3_01_CpG_14
X518_TCL1A	X518_TCL1A_01_CpG_1, X518_TCL1A_01_CpG_2, X518_TCL1A_01_CpG_3, X518_TCL1A_01_CpG_4, X518_TCL1A_01_CpG_5.6, X518_TCL1A_01_CpG_7, X518_TCL1A_01_CpG_8.9.10, X518_TCL1A_01_CpG_11,

	X518_TCL1A_01_CpG_12, X518_TCL1A_01_CpG_13, X518_TCL1A_01_CpG_14.15.16, X518_TCL1A_01_CpG_17.18, X518_TCL1A_01_CpG_19, X518_TCL1A_01_CpG_20, X518_TCL1A_01_CpG_21.22, X518_TCL1A_01_CpG_23.24.25, X518_TCL1A_01_CpG_26.27, X518_TCL1A_01_CpG_28.29, X518_TCL1A_01_CpG_30, X518_TCL1A_01_CpG_31.32, X518_TCL1A_01_CpG_33
X519_TCL1A	X519_TCL1A_02_CpG_1, X519_TCL1A_02_CpG_2.3.4, X519_TCL1A_02_CpG_5, X519_TCL1A_02_CpG_6, X519_TCL1A_02_CpG_7.8.9
X520_TEC	X520_TEC_CpG_1.2, X520_TEC_CpG_3, X520_TEC_CpG_4.5.6, X520_TEC_CpG_7.8.9, X520_TEC_CpG_10, X520_TEC_CpG_11.12, X520_TEC_CpG_13.14.15.16, X520_TEC_CpG_17.18.19, X520_TEC_CpG_20, X520_TEC_CpG_21.22.23, X520_TEC_CpG_24, X520_TEC_CpG_25, X520_TEC_CpG_26.27.28, X520_TEC_CpG_29.30, X520_TEC_CpG_31.32.33, X520_TEC_CpG_34, X520_TEC_CpG_35, X520_TEC_CpG_36, X520_TEC_CpG_37, X520_TEC_CpG_38, X520_TEC_CpG_39.40.41.42
X521_TFE3	X521_TFE3_CpG_1.2.3, X521_TFE3_CpG_4, X521_TFE3_CpG_5, X521_TFE3_CpG_6.7.8, X521_TFE3_CpG_9, X521_TFE3_CpG_10.11, X521_TFE3_CpG_12, X521_TFE3_CpG_13.14.15, X521_TFE3_CpG_16, X521_TFE3_CpG_17.18, X521_TFE3_CpG_19.20, X521_TFE3_CpG_21, X521_TFE3_CpG_22, X521_TFE3_CpG_23.24, X521_TFE3_CpG_25.26.27.28, X521_TFE3_CpG_29.30.31.32, X521_TFE3_CpG_33, X521_TFE3_CpG_34.35, X521_TFE3_CpG_36.37.38.39.40
X566_AL080059	X566_AL080059_1_01_CpG_1.2.3.4.5.6.7, X566_AL080059_1_01_CpG_8, X566_AL080059_1_01_CpG_9.10.11.12.13.14, X566_AL080059_1_01_CpG_15, X566_AL080059_1_01_CpG_16, X566_AL080059_1_01_CpG_17.18, X566_AL080059_1_01_CpG_19.20, X566_AL080059_1_01_CpG_21, X566_AL080059_1_01_CpG_22, X566_AL080059_1_01_CpG_23, X566_AL080059_1_01_CpG_24.25, X566_AL080059_1_01_CpG_26, X566_AL080059_1_01_CpG_27, X566_AL080059_1_01_CpG_28, X566_AL080059_1_01_CpG_29.30, X566_AL080059_1_01_CpG_31, X566_AL080059_1_01_CpG_32, X566_AL080059_1_01_CpG_33, X566_AL080059_1_01_CpG_34.35.36, X566_AL080059_1_01_CpG_37, X566_AL080059_1_01_CpG_38.39, X566_AL080059_1_01_CpG_40.41.42.43.44, X566_AL080059_1_01_CpG_45, X566_AL080059_1_01_CpG_46.47.48, X566_AL080059_1_01_CpG_49.50.51, X566_AL080059_1_01_CpG_52, X566_AL080059_1_01_CpG_53.54, X566_AL080059_1_01_CpG_55.56.57
X567_AL080059	X567_AL080059_2_01_CpG_1, X567_AL080059_2_01_CpG_2.3, X567_AL080059_2_01_CpG_4.5, X567_AL080059_2_01_CpG_6, X567_AL080059_2_01_CpG_7.8, X567_AL080059_2_01_CpG_9, X567_AL080059_2_01_CpG_10, X567_AL080059_2_01_CpG_11.12, X567_AL080059_2_01_CpG_13.14.15.16.17.18.19, X567_AL080059_2_01_CpG_20.21, X567_AL080059_2_01_CpG_22.23, X567_AL080059_2_01_CpG_24, X567_AL080059_2_01_CpG_25.26, X567_AL080059_2_01_CpG_27, X567_AL080059_2_01_CpG_28.29, X567_AL080059_2_01_CpG_30, X567_AL080059_2_01_CpG_31, X567_AL080059_2_01_CpG_32.33, X567_AL080059_2_01_CpG_34.35
X568_AL137718	X568_AL137718_01_CpG_1, X568_AL137718_01_CpG_2, X568_AL137718_01_CpG_3.4, X568_AL137718_01_CpG_5, X568_AL137718_01_CpG_6.7, X568_AL137718_01_CpG_8, X568_AL137718_01_CpG_9.10, X568_AL137718_01_CpG_11.12.13.14, X568_AL137718_01_CpG_15, X568_AL137718_01_CpG_16.17, X568_AL137718_01_CpG_18, X568_AL137718_01_CpG_19, X568_AL137718_01_CpG_20, X568_AL137718_01_CpG_21.22, X568_AL137718_01_CpG_23, X568_AL137718_01_CpG_24, X568_AL137718_01_CpG_25, X568_AL137718_01_CpG_26.27, X568_AL137718_01_CpG_28,

	X568_AL137718_01_CpG_29
X569_ANXA2	X569_ANXA2_01_CpG_1, X569_ANXA2_01_CpG_2, X569_ANXA2_01_CpG_3, X569_ANXA2_01_CpG_4.5.6.7, X569_ANXA2_01_CpG_8.9, X569_ANXA2_01_CpG_10.11.12.13, X569_ANXA2_01_CpG_14.15, X569_ANXA2_01_CpG_16.17, X569_ANXA2_01_CpG_18.19, X569_ANXA2_01_CpG_20.21, X569_ANXA2_01_CpG_22, X569_ANXA2_01_CpG_23.24, X569_ANXA2_01_CpG_25.26, X569_ANXA2_01_CpG_27, X569_ANXA2_01_CpG_28, X569_ANXA2_01_CpG_29.30, X569_ANXA2_01_CpG_31, X569_ANXA2_01_CpG_32
X570_APOD	X570_APOD_01_CpG_1.2, X570_APOD_01_CpG_3, X570_APOD_01_CpG_4, X570_APOD_01_CpG_5, X570_APOD_01_CpG_6.7, X570_APOD_01_CpG_8, X570_APOD_01_CpG_9, X570_APOD_01_CpG_10, X570_APOD_01_CpG_11.12, X570_APOD_01_CpG_13, X570_APOD_01_CpG_14, X570_APOD_01_CpG_15, X570_APOD_01_CpG_16.17, X570_APOD_01_CpG_18, X570_APOD_01_CpG_19, X570_APOD_01_CpG_20, X570_APOD_01_CpG_21.22, X570_APOD_01_CpG_23, X570_APOD_01_CpG_24, X570_APOD_01_CpG_25, X570_APOD_01_CpG_26.27, X570_APOD_01_CpG_28, X570_APOD_01_CpG_29, X570_APOD_01_CpG_30, X570_APOD_01_CpG_31.32, X570_APOD_01_CpG_33, X570_APOD_01_CpG_34, X570_APOD_01_CpG_35, X570_APOD_01_CpG_36
X571_ATP5A1	X571_ATP5A1_1._01_CpG_1.2.3, X571_ATP5A1_1._01_CpG_4, X571_ATP5A1_1._01_CpG_5.6.7, X571_ATP5A1_1._01_CpG_8.9, X571_ATP5A1_1._01_CpG_10, X571_ATP5A1_1._01_CpG_11, X571_ATP5A1_1._01_CpG_12, X571_ATP5A1_1._01_CpG_13, X571_ATP5A1_1._01_CpG_14, X571_ATP5A1_1._01_CpG_15, X571_ATP5A1_1._01_CpG_16, X571_ATP5A1_1._01_CpG_17.18, X571_ATP5A1_1._01_CpG_19.20.21, X571_ATP5A1_1._01_CpG_22.23.24, X571_ATP5A1_1._01_CpG_25, X571_ATP5A1_1._01_CpG_26, X571_ATP5A1_1._01_CpG_27.28, X571_ATP5A1_1._01_CpG_29, X571_ATP5A1_1._01_CpG_30, X571_ATP5A1_1._01_CpG_31, X571_ATP5A1_1._01_CpG_32, X571_ATP5A1_1._01_CpG_33
X573_ATP6V0E.	X573_ATP6V0E._01_CpG_1, X573_ATP6V0E._01_CpG_2.3, X573_ATP6V0E._01_CpG_4, X573_ATP6V0E._01_CpG_5.6.7.8, X573_ATP6V0E._01_CpG_9.10.11, X573_ATP6V0E._01_CpG_12, X573_ATP6V0E._01_CpG_13, X573_ATP6V0E._01_CpG_14.15, X573_ATP6V0E._01_CpG_16, X573_ATP6V0E._01_CpG_17, X573_ATP6V0E._01_CpG_18, X573_ATP6V0E._01_CpG_19, X573_ATP6V0E._01_CpG_20.21, X573_ATP6V0E._01_CpG_22, X573_ATP6V0E._01_CpG_23, X573_ATP6V0E._01_CpG_24.25.26, X573_ATP6V0E._01_CpG_27, X573_ATP6V0E._01_CpG_28, X573_ATP6V0E._01_CpG_29, X573_ATP6V0E._01_CpG_30.31, X573_ATP6V0E._01_CpG_32.33, X573_ATP6V0E._01_CpG_34, X573_ATP6V0E._01_CpG_35, X573_ATP6V0E._01_CpG_36, X573_ATP6V0E._01_CpG_37.38.39, X573_ATP6V0E._01_CpG_40, X573_ATP6V0E._01_CpG_41.42, X573_ATP6V0E._01_CpG_43, X573_ATP6V0E._01_CpG_44, X573_ATP6V0E._01_CpG_45
X574_Beta.NAP	X574_Beta.NAP_01_CpG_1, X574_Beta.NAP_01_CpG_2, X574_Beta.NAP_01_CpG_3, X574_Beta.NAP_01_CpG_4, X574_Beta.NAP_01_CpG_5, X574_Beta.NAP_01_CpG_6, X574_Beta.NAP_01_CpG_7, X574_Beta.NAP_01_CpG_8, X574_Beta.NAP_01_CpG_9.10, X574_Beta.NAP_01_CpG_11.12, X574_Beta.NAP_01_CpG_13, X574_Beta.NAP_01_CpG_14.15.16, X574_Beta.NAP_01_CpG_17.18, X574_Beta.NAP_01_CpG_19
X576_BIRC5	X576_BIRC5_01_CpG_1, X576_BIRC5_01_CpG_2, X576_BIRC5_01_CpG_3.4, X576_BIRC5_01_CpG_5, X576_BIRC5_01_CpG_6, X576_BIRC5_01_CpG_7, X576_BIRC5_01_CpG_8.9.10.11, X576_BIRC5_01_CpG_12.13, X576_BIRC5_01_CpG_14, X576_BIRC5_01_CpG_15.16.17, X576_BIRC5_01_CpG_18, X576_BIRC5_01_CpG_19.20.21.22,

	X576_BIRC5_01_CpG_23.24, X576_BIRC5_01_CpG_25, X576_BIRC5_01_CpG_26.27.28, X576_BIRC5_01_CpG_29.30.31.32, X576_BIRC5_01_CpG_33, X576_BIRC5_01_CpG_34.35, X576_BIRC5_01_CpG_36, X576_BIRC5_01_CpG_37.38.39, X576_BIRC5_01_CpG_40, X576_BIRC5_01_CpG_41, X576_BIRC5_01_CpG_42
X577_C2	X577_C2_1_01_CpG_1, X577_C2_1_01_CpG_2, X577_C2_1_01_CpG_3, X577_C2_1_01_CpG_4, X577_C2_1_01_CpG_5, X577_C2_1_01_CpG_6.7, X577_C2_1_01_CpG_8.9.10, X577_C2_1_01_CpG_11, X577_C2_1_01_CpG_12, X577_C2_1_01_CpG_13, X577_C2_1_01_CpG_14, X577_C2_1_01_CpG_15, X577_C2_1_01_CpG_16, X577_C2_1_01_CpG_17, X577_C2_1_01_CpG_18, X577_C2_1_01_CpG_19.20.21.22, X577_C2_1_01_CpG_23.24, X577_C2_1_01_CpG_25, X577_C2_1_01_CpG_26, X577_C2_1_01_CpG_27.28, X577_C2_1_01_CpG_29.30, X577_C2_1_01_CpG_31, X577_C2_1_01_CpG_32.33.34.35.36.37.38.39.40.41.42, X577_C2_1_01_CpG_43.44.45.46, X577_C2_1_01_CpG_47.48.49.50.51.52.53.54.55.56, X577_C2_1_01_CpG_57
X579_CA3	X579_CA3_01_CpG_1, X579_CA3_01_CpG_2, X579_CA3_01_CpG_3.4.5.6, X579_CA3_01_CpG_7, X579_CA3_01_CpG_8, X579_CA3_01_CpG_9, X579_CA3_01_CpG_10.11, X579_CA3_01_CpG_12.13, X579_CA3_01_CpG_14, X579_CA3_01_CpG_15, X579_CA3_01_CpG_16, X579_CA3_01_CpG_17, X579_CA3_01_CpG_18, X579_CA3_01_CpG_19, X579_CA3_01_CpG_20.21.22.23.24, X579_CA3_01_CpG_25, X579_CA3_01_CpG_26, X579_CA3_01_CpG_27, X579_CA3_01_CpG_28, X579_CA3_01_CpG_29, X579_CA3_01_CpG_30, X579_CA3_01_CpG_31.32, X579_CA3_01_CpG_33
X580_CA4	X580_CA4_01_CpG_1, X580_CA4_01_CpG_2, X580_CA4_01_CpG_3.4.5.6.7, X580_CA4_01_CpG_8, X580_CA4_01_CpG_9.10, X580_CA4_01_CpG_11.12.13, X580_CA4_01_CpG_14, X580_CA4_01_CpG_15.16.17, X580_CA4_01_CpG_18, X580_CA4_01_CpG_19.20.21.22.23.24.25.26.27, X580_CA4_01_CpG_28, X580_CA4_01_CpG_29.30.31, X580_CA4_01_CpG_32.33, X580_CA4_01_CpG_34, X580_CA4_01_CpG_35, X580_CA4_01_CpG_36.37.38, X580_CA4_01_CpG_39.40.41.42, X580_CA4_01_CpG_43, X580_CA4_01_CpG_44, X580_CA4_01_CpG_45.46.47, X580_CA4_01_CpG_48, X580_CA4_01_CpG_49, X580_CA4_01_CpG_50
X581_CCNA2	X581_CCNA2_01_CpG_1.2, X581_CCNA2_01_CpG_3.4, X581_CCNA2_01_CpG_5.6.7.8, X581_CCNA2_01_CpG_9.10, X581_CCNA2_01_CpG_11, X581_CCNA2_01_CpG_12.13, X581_CCNA2_01_CpG_14.15, X581_CCNA2_01_CpG_16, X581_CCNA2_01_CpG_17, X581_CCNA2_01_CpG_18, X581_CCNA2_01_CpG_19, X581_CCNA2_01_CpG_20, X581_CCNA2_01_CpG_21, X581_CCNA2_01_CpG_22.23.24, X581_CCNA2_01_CpG_25.26.27, X581_CCNA2_01_CpG_28, X581_CCNA2_01_CpG_29, X581_CCNA2_01_CpG_30, X581_CCNA2_01_CpG_31, X581_CCNA2_01_CpG_32, X581_CCNA2_01_CpG_33.34, X581_CCNA2_01_CpG_35, X581_CCNA2_01_CpG_36, X581_CCNA2_01_CpG_37.38, X581_CCNA2_01_CpG_39.40, X581_CCNA2_01_CpG_41.42, X581_CCNA2_01_CpG_43.44.45, X581_CCNA2_01_CpG_46, X581_CCNA2_01_CpG_47, X581_CCNA2_01_CpG_48, X581_CCNA2_01_CpG_49, X581_CCNA2_01_CpG_50
X582_CCNB1	X582_CCNB1_01_CpG_1, X582_CCNB1_01_CpG_2, X582_CCNB1_01_CpG_3.4, X582_CCNB1_01_CpG_5, X582_CCNB1_01_CpG_6, X582_CCNB1_01_CpG_7, X582_CCNB1_01_CpG_8, X582_CCNB1_01_CpG_9, X582_CCNB1_01_CpG_10, X582_CCNB1_01_CpG_11.12, X582_CCNB1_01_CpG_13.14.15.16, X582_CCNB1_01_CpG_17, X582_CCNB1_01_CpG_18, X582_CCNB1_01_CpG_19, X582_CCNB1_01_CpG_20, X582_CCNB1_01_CpG_21, X582_CCNB1_01_CpG_22, X582_CCNB1_01_CpG_23, X582_CCNB1_01_CpG_24.25.26.27, X582_CCNB1_01_CpG_28, X582_CCNB1_01_CpG_29.30.31, X582_CCNB1_01_CpG_32.33, X582_CCNB1_01_CpG_34.35, X582_CCNB1_01_CpG_36, X582_CCNB1_01_CpG_37.38, X582_CCNB1_01_CpG_39.40, X582_CCNB1_01_CpG_41, X582_CCNB1_01_CpG_42, X582_CCNB1_01_CpG_43, X582_CCNB1_01_CpG_44
X583_CCNC	X583_CCNC_01_CpG_1, X583_CCNC_01_CpG_2, X583_CCNC_01_CpG_3, X583_CCNC_01_CpG_4,

	X583_CCNC_01_CpG_5.6, X583_CCNC_01_CpG_7.8.9, X583_CCNC_01_CpG_10, X583_CCNC_01_CpG_11.12, X583_CCNC_01_CpG_13.14.15, X583_CCNC_01_CpG_16.17, X583_CCNC_01_CpG_18.19.20.21.22, X583_CCNC_01_CpG_23.24, X583_CCNC_01_CpG_25.26.27, X583_CCNC_01_CpG_28, X583_CCNC_01_CpG_29, X583_CCNC_01_CpG_30.31.32, X583_CCNC_01_CpG_33, X583_CCNC_01_CpG_34
X584_CCND1	X584_CCND1_1_01_CpG_1, X584_CCND1_1_01_CpG_2.3, X584_CCND1_1_01_CpG_4, X584_CCND1_1_01_CpG_5, X584_CCND1_1_01_CpG_6, X584_CCND1_1_01_CpG_7, X584_CCND1_1_01_CpG_8, X584_CCND1_1_01_CpG_9, X584_CCND1_1_01_CpG_10, X584_CCND1_1_01_CpG_11, X584_CCND1_1_01_CpG_12, X584_CCND1_1_01_CpG_13, X584_CCND1_1_01_CpG_14, X584_CCND1_1_01_CpG_15, X584_CCND1_1_01_CpG_16, X584_CCND1_1_01_CpG_17.18, X584_CCND1_1_01_CpG_19, X584_CCND1_1_01_CpG_20.21, X584_CCND1_1_01_CpG_22, X584_CCND1_1_01_CpG_23.24, X584_CCND1_1_01_CpG_25, X584_CCND1_1_01_CpG_26.27, X584_CCND1_1_01_CpG_28, X584_CCND1_1_01_CpG_29.30, X584_CCND1_1_01_CpG_31.32, X584_CCND1_1_01_CpG_33.34.35.36.37.38.39.40, X584_CCND1_1_01_CpG_41, X584_CCND1_1_01_CpG_42.43.44.45.46.47, X584_CCND1_1_01_CpG_48, X584_CCND1_1_01_CpG_49.50, X584_CCND1_1_01_CpG_51, X584_CCND1_1_01_CpG_52.53.54
X585_CCND1	X585_CCND1_2_01_CpG_1, X585_CCND1_2_01_CpG_2.3, X585_CCND1_2_01_CpG_4.5, X585_CCND1_2_01_CpG_6.7.8, X585_CCND1_2_01_CpG_9.10, X585_CCND1_2_01_CpG_11.12, X585_CCND1_2_01_CpG_13, X585_CCND1_2_01_CpG_14.15.16, X585_CCND1_2_01_CpG_17, X585_CCND1_2_01_CpG_18.19, X585_CCND1_2_01_CpG_20.21, X585_CCND1_2_01_CpG_22, X585_CCND1_2_01_CpG_23, X585_CCND1_2_01_CpG_24, X585_CCND1_2_01_CpG_25.26.27.28, X585_CCND1_2_01_CpG_29.30, X585_CCND1_2_01_CpG_31.32.33.34.35.36.37, X585_CCND1_2_01_CpG_38.39.40, X585_CCND1_2_01_CpG_41.42, X585_CCND1_2_01_CpG_43.44, X585_CCND1_2_01_CpG_45, X585_CCND1_2_01_CpG_46, X585_CCND1_2_01_CpG_47, X585_CCND1_2_01_CpG_48, X585_CCND1_2_01_CpG_49.50, X585_CCND1_2_01_CpG_51.52, X585_CCND1_2_01_CpG_53, X585_CCND1_2_01_CpG_54, X585_CCND1_2_01_CpG_55, X585_CCND1_2_01_CpG_56
X586_CCND1	X586_CCND1_3_01_CpG_1, X586_CCND1_3_01_CpG_2.3.4, X586_CCND1_3_01_CpG_5.6, X586_CCND1_3_01_CpG_7, X586_CCND1_3_01_CpG_8, X586_CCND1_3_01_CpG_9.10.11.12.13, X586_CCND1_3_01_CpG_14, X586_CCND1_3_01_CpG_15, X586_CCND1_3_01_CpG_16.17.18, X586_CCND1_3_01_CpG_19, X586_CCND1_3_01_CpG_20.21, X586_CCND1_3_01_CpG_22, X586_CCND1_3_01_CpG_23, X586_CCND1_3_01_CpG_24, X586_CCND1_3_01_CpG_25, X586_CCND1_3_01_CpG_26, X586_CCND1_3_01_CpG_27.28, X586_CCND1_3_01_CpG_29, X586_CCND1_3_01_CpG_30.31, X586_CCND1_3_01_CpG_32.33.34
X587_CCNH	X587_CCNH_1_01_CpG_1, X587_CCNH_1_01_CpG_2, X587_CCNH_1_01_CpG_3, X587_CCNH_1_01_CpG_4, X587_CCNH_1_01_CpG_5, X587_CCNH_1_01_CpG_6, X587_CCNH_1_01_CpG_7.8, X587_CCNH_1_01_CpG_9, X587_CCNH_1_01_CpG_10, X587_CCNH_1_01_CpG_11, X587_CCNH_1_01_CpG_12.13.14, X587_CCNH_1_01_CpG_15, X587_CCNH_1_01_CpG_16, X587_CCNH_1_01_CpG_17, X587_CCNH_1_01_CpG_18, X587_CCNH_1_01_CpG_19, X587_CCNH_1_01_CpG_20, X587_CCNH_1_01_CpG_21, X587_CCNH_1_01_CpG_22, X587_CCNH_1_01_CpG_23.24, X587_CCNH_1_01_CpG_25, X587_CCNH_1_01_CpG_26, X587_CCNH_1_01_CpG_27, X587_CCNH_1_01_CpG_28
X588_CCNH	X588_CCNH_2_01_CpG_1, X588_CCNH_2_01_CpG_2, X588_CCNH_2_01_CpG_3.4, X588_CCNH_2_01_CpG_5, X588_CCNH_2_01_CpG_6, X588_CCNH_2_01_CpG_7.8, X588_CCNH_2_01_CpG_9.10,

	X588_CCNH_2_01_CpG_11.12.13.14.15, X588_CCNH_2_01_CpG_16, X588_CCNH_2_01_CpG_17.18, X588_CCNH_2_01_CpG_19, X588_CCNH_2_01_CpG_20, X588_CCNH_2_01_CpG_21, X588_CCNH_2_01_CpG_22, X588_CCNH_2_01_CpG_23, X588_CCNH_2_01_CpG_24.25, X588_CCNH_2_01_CpG_26, X588_CCNH_2_01_CpG_27, X588_CCNH_2_01_CpG_28, X588_CCNH_2_01_CpG_29.30, X588_CCNH_2_01_CpG_31, X588_CCNH_2_01_CpG_32.33, X588_CCNH_2_01_CpG_34, X588_CCNH_2_01_CpG_35
X590_CD34.	X590_CD34._01_CpG_1, X590_CD34._01_CpG_2.3.4, X590_CD34._01_CpG_5.6.7.8.9.10.11, X590_CD34._01_CpG_12, X590_CD34._01_CpG_13.14, X590_CD34._01_CpG_15.16, X590_CD34._01_CpG_17.18.19.20.21, X590_CD34._01_CpG_22.23.24, X590_CD34._01_CpG_25, X590_CD34._01_CpG_26, X590_CD34._01_CpG_27, X590_CD34._01_CpG_28.29.30.31.32, X590_CD34._01_CpG_33
X591_CD38	X591_CD38_01_CpG_1, X591_CD38_01_CpG_2, X591_CD38_01_CpG_3, X591_CD38_01_CpG_4, X591_CD38_01_CpG_5.6.7, X591_CD38_01_CpG_8.9, X591_CD38_01_CpG_10.11, X591_CD38_01_CpG_12, X591_CD38_01_CpG_13.14, X591_CD38_01_CpG_15, X591_CD38_01_CpG_16.17, X591_CD38_01_CpG_18.19.20.21.22
X592_CD44	X592_CD44_01_CpG_1.2.3, X592_CD44_01_CpG_4, X592_CD44_01_CpG_5, X592_CD44_01_CpG_6, X592_CD44_01_CpG_7.8, X592_CD44_01_CpG_9.10.11.12.13.14, X592_CD44_01_CpG_15.16.17.18.19.20, X592_CD44_01_CpG_21, X592_CD44_01_CpG_22.23, X592_CD44_01_CpG_24, X592_CD44_01_CpG_25, X592_CD44_01_CpG_26.27, X592_CD44_01_CpG_28, X592_CD44_01_CpG_29.30, X592_CD44_01_CpG_31.32, X592_CD44_01_CpG_33, X592_CD44_01_CpG_34
X593_CD59	X593_CD59_01_CpG_1, X593_CD59_01_CpG_2, X593_CD59_01_CpG_3, X593_CD59_01_CpG_4, X593_CD59_01_CpG_5.6, X593_CD59_01_CpG_7, X593_CD59_01_CpG_8.9.10, X593_CD59_01_CpG_11.12, X593_CD59_01_CpG_13, X593_CD59_01_CpG_14, X593_CD59_01_CpG_15.16, X593_CD59_01_CpG_17, X593_CD59_01_CpG_18, X593_CD59_01_CpG_19, X593_CD59_01_CpG_20.21, X593_CD59_01_CpG_22, X593_CD59_01_CpG_23.24, X593_CD59_01_CpG_25, X593_CD59_01_CpG_26, X593_CD59_01_CpG_27.28.29.30, X593_CD59_01_CpG_31.32, X593_CD59_01_CpG_33.34.35, X593_CD59_01_CpG_36
X594_CDC34	X594_CDC34_01_CpG_1.2, X594_CDC34_01_CpG_3.4, X594_CDC34_01_CpG_5, X594_CDC34_01_CpG_6, X594_CDC34_01_CpG_7, X594_CDC34_01_CpG_8, X594_CDC34_01_CpG_9, X594_CDC34_01_CpG_10.11.12, X594_CDC34_01_CpG_13.14.15, X594_CDC34_01_CpG_16, X594_CDC34_01_CpG_17, X594_CDC34_01_CpG_18.19.20, X594_CDC34_01_CpG_21.22, X594_CDC34_01_CpG_23.24.25, X594_CDC34_01_CpG_26, X594_CDC34_01_CpG_27, X594_CDC34_01_CpG_28.29, X594_CDC34_01_CpG_30.31
X595_CHGA	X595_CHGA_01_CpG_1, X595_CHGA_01_CpG_2, X595_CHGA_01_CpG_3.4, X595_CHGA_01_CpG_5, X595_CHGA_01_CpG_6, X595_CHGA_01_CpG_7.8.9, X595_CHGA_01_CpG_10.11, X595_CHGA_01_CpG_12, X595_CHGA_01_CpG_13, X595_CHGA_01_CpG_14, X595_CHGA_01_CpG_15, X595_CHGA_01_CpG_16, X595_CHGA_01_CpG_17, X595_CHGA_01_CpG_18.19, X595_CHGA_01_CpG_20.21.22, X595_CHGA_01_CpG_23, X595_CHGA_01_CpG_24, X595_CHGA_01_CpG_25, X595_CHGA_01_CpG_26, X595_CHGA_01_CpG_27, X595_CHGA_01_CpG_28, X595_CHGA_01_CpG_29, X595_CHGA_01_CpG_30, X595_CHGA_01_CpG_31, X595_CHGA_01_CpG_32.33, X595_CHGA_01_CpG_34, X595_CHGA_01_CpG_35.36.37, X595_CHGA_01_CpG_38, X595_CHGA_01_CpG_39, X595_CHGA_01_CpG_40.41, X595_CHGA_01_CpG_42.43.44, X595_CHGA_01_CpG_45, X595_CHGA_01_CpG_46, X595_CHGA_01_CpG_47.48.49.50, X595_CHGA_01_CpG_51.52.53
X597_CKS2	X597_CKS2_2_01_CpG_1, X597_CKS2_2_01_CpG_2, X597_CKS2_2_01_CpG_3, X597_CKS2_2_01_CpG_4, X597_CKS2_2_01_CpG_5, X597_CKS2_2_01_CpG_6.7.8, X597_CKS2_2_01_CpG_9, X597_CKS2_2_01_CpG_10,

	X597_CKS2_2_01_CpG_11, X597_CKS2_2_01_CpG_12, X597_CKS2_2_01_CpG_13.14, X597_CKS2_2_01_CpG_15.16, X597_CKS2_2_01_CpG_17.18.19, X597_CKS2_2_01_CpG_20.21, X597_CKS2_2_01_CpG_22, X597_CKS2_2_01_CpG_23.24, X597_CKS2_2_01_CpG_25, X597_CKS2_2_01_CpG_26, X597_CKS2_2_01_CpG_27, X597_CKS2_2_01_CpG_28
X598_CKS2	X598_CKS2_3_01_CpG_1, X598_CKS2_3_01_CpG_2, X598_CKS2_3_01_CpG_3.4.5, X598_CKS2_3_01_CpG_6, X598_CKS2_3_01_CpG_7.8, X598_CKS2_3_01_CpG_9, X598_CKS2_3_01_CpG_10.11, X598_CKS2_3_01_CpG_12.13.14.15, X598_CKS2_3_01_CpG_16, X598_CKS2_3_01_CpG_17, X598_CKS2_3_01_CpG_18.19, X598_CKS2_3_01_CpG_20.21, X598_CKS2_3_01_CpG_22.23.24.25.26.27, X598_CKS2_3_01_CpG_28.29, X598_CKS2_3_01_CpG_30, X598_CKS2_3_01_CpG_31, X598_CKS2_3_01_CpG_32, X598_CKS2_3_01_CpG_33, X598_CKS2_3_01_CpG_34.35, X598_CKS2_3_01_CpG_36, X598_CKS2_3_01_CpG_37, X598_CKS2_3_01_CpG_38.39.40.41.42, X598_CKS2_3_01_CpG_43.44.45, X598_CKS2_3_01_CpG_46.47, X598_CKS2_3_01_CpG_48, X598_CKS2_3_01_CpG_49.50.51, X598_CKS2_3_01_CpG_52.53.54, X598_CKS2_3_01_CpG_55, X598_CKS2_3_01_CpG_56.57.58.59.60.61.62
X599_COL5A1	X599_COL5A1_01_CpG_1, X599_COL5A1_01_CpG_2.3.4, X599_COL5A1_01_CpG_5.6.7.8.9.10.11, X599_COL5A1_01_CpG_12.13.14.15.16.17.18, X599_COL5A1_01_CpG_19, X599_COL5A1_01_CpG_20, X599_COL5A1_01_CpG_21.22, X599_COL5A1_01_CpG_23.24.25.26.27.28.29.30.31.32, X599_COL5A1_01_CpG_33.34, X599_COL5A1_01_CpG_35.36.37.38.39, X599_COL5A1_01_CpG_40.41.42, X599_COL5A1_01_CpG_43.44.45, X599_COL5A1_01_CpG_46.47.48.49, X599_COL5A1_01_CpG_50, X599_COL5A1_01_CpG_51, X599_COL5A1_01_CpG_52, X599_COL5A1_01_CpG_53, X599_COL5A1_01_CpG_54, X599_COL5A1_01_CpG_55.56.57.58.59.60, X599_COL5A1_01_CpG_61.62.63.64.65.66, X599_COL5A1_01_CpG_67, X599_COL5A1_01_CpG_68
X600_COL5A3	X600_COL5A3_01_CpG_1, X600_COL5A3_01_CpG_2.3.4, X600_COL5A3_01_CpG_5.6, X600_COL5A3_01_CpG_7.8.9, X600_COL5A3_01_CpG_10.11, X600_COL5A3_01_CpG_12.13, X600_COL5A3_01_CpG_14, X600_COL5A3_01_CpG_15, X600_COL5A3_01_CpG_16.17.18.19.20.21, X600_COL5A3_01_CpG_22.23, X600_COL5A3_01_CpG_24.25.26.27, X600_COL5A3_01_CpG_28.29, X600_COL5A3_01_CpG_30, X600_COL5A3_01_CpG_31.32.33, X600_COL5A3_01_CpG_34, X600_COL5A3_01_CpG_35, X600_COL5A3_01_CpG_36
X601_COL6A2	X601_COL6A2_01_CpG_1, X601_COL6A2_01_CpG_2, X601_COL6A2_01_CpG_3.4, X601_COL6A2_01_CpG_5, X601_COL6A2_01_CpG_6, X601_COL6A2_01_CpG_7, X601_COL6A2_01_CpG_8, X601_COL6A2_01_CpG_9, X601_COL6A2_01_CpG_10, X601_COL6A2_01_CpG_11, X601_COL6A2_01_CpG_12, X601_COL6A2_01_CpG_13.14.15, X601_COL6A2_01_CpG_16, X601_COL6A2_01_CpG_17.18, X601_COL6A2_01_CpG_19.20, X601_COL6A2_01_CpG_21, X601_COL6A2_01_CpG_22, X601_COL6A2_01_CpG_23, X601_COL6A2_01_CpG_24
X602_COX6B1	X602_COX6B1_1_01_CpG_1, X602_COX6B1_1_01_CpG_2, X602_COX6B1_1_01_CpG_3, X602_COX6B1_1_01_CpG_4.5, X602_COX6B1_1_01_CpG_6, X602_COX6B1_1_01_CpG_7.8.9, X602_COX6B1_1_01_CpG_10.11.12, X602_COX6B1_1_01_CpG_13.14.15.16, X602_COX6B1_1_01_CpG_17.18.19, X602_COX6B1_1_01_CpG_20.21.22, X602_COX6B1_1_01_CpG_23.24.25.26, X602_COX6B1_1_01_CpG_27.28, X602_COX6B1_1_01_CpG_29, X602_COX6B1_1_01_CpG_30.31
X603_COX6B1	X603_COX6B1_2_01_CpG_1, X603_COX6B1_2_01_CpG_2, X603_COX6B1_2_01_CpG_3, X603_COX6B1_2_01_CpG_4.5, X603_COX6B1_2_01_CpG_6, X603_COX6B1_2_01_CpG_7.8.9, X603_COX6B1_2_01_CpG_10.11.12, X603_COX6B1_2_01_CpG_13.14.15.16, X603_COX6B1_2_01_CpG_17.18.19, X603_COX6B1_2_01_CpG_20.21.22,

	X603_COX6B1_2_01_CpG_23.24.25.26, X603_COX6B1_2_01_CpG_27.28
X604_COX7A2L	X604_COX7A2L_01_CpG_1.2.3, X604_COX7A2L_01_CpG_4.5, X604_COX7A2L_01_CpG_6, X604_COX7A2L_01_CpG_7, X604_COX7A2L_01_CpG_8, X604_COX7A2L_01_CpG_9, X604_COX7A2L_01_CpG_10, X604_COX7A2L_01_CpG_11, X604_COX7A2L_01_CpG_12, X604_COX7A2L_01_CpG_13, X604_COX7A2L_01_CpG_14.15, X604_COX7A2L_01_CpG_16, X604_COX7A2L_01_CpG_17.18, X604_COX7A2L_01_CpG_19, X604_COX7A2L_01_CpG_20.21.22, X604_COX7A2L_01_CpG_23, X604_COX7A2L_01_CpG_24, X604_COX7A2L_01_CpG_25, X604_COX7A2L_01_CpG_26, X604_COX7A2L_01_CpG_27
X605_CR2	X605_CR2_01_CpG_1, X605_CR2_01_CpG_2.3.4.5, X605_CR2_01_CpG_6, X605_CR2_01_CpG_7.8.9.10.11, X605_CR2_01_CpG_12.13.14.15.16.17, X605_CR2_01_CpG_18.19, X605_CR2_01_CpG_20, X605_CR2_01_CpG_21.22.23, X605_CR2_01_CpG_24.25, X605_CR2_01_CpG_26, X605_CR2_01_CpG_27, X605_CR2_01_CpG_28, X605_CR2_01_CpG_29.30.31.32, X605_CR2_01_CpG_33, X605_CR2_01_CpG_34
X608_DBI	X608_DBI_1_01_CpG_1.2.3, X608_DBI_1_01_CpG_4, X608_DBI_1_01_CpG_5, X608_DBI_1_01_CpG_6.7.8.9.10.11, X608_DBI_1_01_CpG_12, X608_DBI_1_01_CpG_13, X608_DBI_1_01_CpG_14, X608_DBI_1_01_CpG_15, X608_DBI_1_01_CpG_16.17.18, X608_DBI_1_01_CpG_19.20.21, X608_DBI_1_01_CpG_22, X608_DBI_1_01_CpG_23.24.25, X608_DBI_1_01_CpG_26.27.28.29, X608_DBI_1_01_CpG_30, X608_DBI_1_01_CpG_31
X610_DC13	X610_DC13_1_01_CpG_1, X610_DC13_1_01_CpG_2.3, X610_DC13_1_01_CpG_4.5, X610_DC13_1_01_CpG_6.7, X610_DC13_1_01_CpG_8, X610_DC13_1_01_CpG_9.10.11, X610_DC13_1_01_CpG_12, X610_DC13_1_01_CpG_13, X610_DC13_1_01_CpG_14, X610_DC13_1_01_CpG_15, X610_DC13_1_01_CpG_16, X610_DC13_1_01_CpG_17, X610_DC13_1_01_CpG_18.19, X610_DC13_1_01_CpG_20.21, X610_DC13_1_01_CpG_22, X610_DC13_1_01_CpG_23, X610_DC13_1_01_CpG_24, X610_DC13_1_01_CpG_25.26, X610_DC13_1_01_CpG_27, X610_DC13_1_01_CpG_28, X610_DC13_1_01_CpG_29.30.31.32.33.34.35, X610_DC13_1_01_CpG_36, X610_DC13_1_01_CpG_37.38, X610_DC13_1_01_CpG_39.40.41
X611_DC13	X611_DC13_2_01_CpG_1, X611_DC13_2_01_CpG_2.3, X611_DC13_2_01_CpG_4.5, X611_DC13_2_01_CpG_6.7, X611_DC13_2_01_CpG_8, X611_DC13_2_01_CpG_9, X611_DC13_2_01_CpG_10, X611_DC13_2_01_CpG_11.12.13.14, X611_DC13_2_01_CpG_15.16.17, X611_DC13_2_01_CpG_18.19.20, X611_DC13_2_01_CpG_21, X611_DC13_2_01_CpG_22.23.24.25, X611_DC13_2_01_CpG_26, X611_DC13_2_01_CpG_27.28, X611_DC13_2_01_CpG_29, X611_DC13_2_01_CpG_30, X611_DC13_2_01_CpG_31, X611_DC13_2_01_CpG_32
X612_DSTN.	X612_DSTN._01_CpG_1, X612_DSTN._01_CpG_2.3.4.5.6, X612_DSTN._01_CpG_7, X612_DSTN._01_CpG_8.9, X612_DSTN._01_CpG_10.11, X612_DSTN._01_CpG_12.13.14, X612_DSTN._01_CpG_15.16.17.18, X612_DSTN._01_CpG_19.20.21.22.23, X612_DSTN._01_CpG_24.25.26, X612_DSTN._01_CpG_27, X612_DSTN._01_CpG_28, X612_DSTN._01_CpG_29.30.31.32.33.34, X612_DSTN._01_CpG_35.36.37.38, X612_DSTN._01_CpG_39, X612_DSTN._01_CpG_40.41, X612_DSTN._01_CpG_42.43, X612_DSTN._01_CpG_44.45.46, X612_DSTN._01_CpG_47, X612_DSTN._01_CpG_48, X612_DSTN._01_CpG_49, X612_DSTN._01_CpG_50.51, X612_DSTN._01_CpG_52.53, X612_DSTN._01_CpG_54.55.56.57.58.59, X612_DSTN._01_CpG_60.61.62, X612_DSTN._01_CpG_63, X612_DSTN._01_CpG_64.65, X612_DSTN._01_CpG_66.67, X612_DSTN._01_CpG_68
X614_ECT2	X614_ECT2_2_01_CpG_1.2, X614_ECT2_2_01_CpG_3, X614_ECT2_2_01_CpG_4.5.6.7.8, X614_ECT2_2_01_CpG_9, X614_ECT2_2_01_CpG_10.11, X614_ECT2_2_01_CpG_12, X614_ECT2_2_01_CpG_13, X614_ECT2_2_01_CpG_14.15, X614_ECT2_2_01_CpG_16.17, X614_ECT2_2_01_CpG_18.19, X614_ECT2_2_01_CpG_20, X614_ECT2_2_01_CpG_21, X614_ECT2_2_01_CpG_22, X614_ECT2_2_01_CpG_23, X614_ECT2_2_01_CpG_24.25, X614_ECT2_2_01_CpG_26,

	X614_ECT2_2_01_CpG_27.28, X614_ECT2_2_01_CpG_29, X614_ECT2_2_01_CpG_30, X614_ECT2_2_01_CpG_31.32, X614_ECT2_2_01_CpG_33
X623_FLT1	X623_FLT1_3_01_CpG_1.2, X623_FLT1_3_01_CpG_3, X623_FLT1_3_01_CpG_4, X623_FLT1_3_01_CpG_5, X623_FLT1_3_01_CpG_6, X623_FLT1_3_01_CpG_7, X623_FLT1_3_01_CpG_8.9, X623_FLT1_3_01_CpG_10, X623_FLT1_3_01_CpG_11, X623_FLT1_3_01_CpG_12.13, X623_FLT1_3_01_CpG_14, X623_FLT1_3_01_CpG_15.16, X623_FLT1_3_01_CpG_17, X623_FLT1_3_01_CpG_18, X623_FLT1_3_01_CpG_19.20, X623_FLT1_3_01_CpG_21.22, X623_FLT1_3_01_CpG_23, X623_FLT1_3_01_CpG_24.25.26, X623_FLT1_3_01_CpG_27.28, X623_FLT1_3_01_CpG_29.30, X623_FLT1_3_01_CpG_31, X623_FLT1_3_01_CpG_32, X623_FLT1_3_01_CpG_33, X623_FLT1_3_01_CpG_34.35
X624_FOXK2	X624_FOXK2_01_CpG_1, X624_FOXK2_01_CpG_2, X624_FOXK2_01_CpG_3, X624_FOXK2_01_CpG_4.5, X624_FOXK2_01_CpG_6.7.8.9, X624_FOXK2_01_CpG_10, X624_FOXK2_01_CpG_11.12, X624_FOXK2_01_CpG_13.14.15.16.17.18.19.20, X624_FOXK2_01_CpG_21, X624_FOXK2_01_CpG_22.23, X624_FOXK2_01_CpG_24.25.26.27.28.29
X625_G3PD	X625_G3PD_01_CpG_1, X625_G3PD_01_CpG_2.3, X625_G3PD_01_CpG_4.5.6.7.8, X625_G3PD_01_CpG_9, X625_G3PD_01_CpG_10.11.12, X625_G3PD_01_CpG_13, X625_G3PD_01_CpG_14.15, X625_G3PD_01_CpG_16.17, X625_G3PD_01_CpG_18, X625_G3PD_01_CpG_19, X625_G3PD_01_CpG_20, X625_G3PD_01_CpG_21.22, X625_G3PD_01_CpG_23, X625_G3PD_01_CpG_24.25.26.27.28.29.30, X625_G3PD_01_CpG_31.32, X625_G3PD_01_CpG_33, X625_G3PD_01_CpG_34.35.36, X625_G3PD_01_CpG_37.38.39, X625_G3PD_01_CpG_40, X625_G3PD_01_CpG_41.42, X625_G3PD_01_CpG_43, X625_G3PD_01_CpG_44, X625_G3PD_01_CpG_45, X625_G3PD_01_CpG_46, X625_G3PD_01_CpG_47.48.49, X625_G3PD_01_CpG_50.51, X625_G3PD_01_CpG_52.53, X625_G3PD_01_CpG_54, X625_G3PD_01_CpG_55.56, X625_G3PD_01_CpG_57
X626_GDI2.	X626_GDI2._01_CpG_1, X626_GDI2._01_CpG_2.3, X626_GDI2._01_CpG_4.5, X626_GDI2._01_CpG_6, X626_GDI2._01_CpG_7.8, X626_GDI2._01_CpG_9.10.11.12, X626_GDI2._01_CpG_13.14.15, X626_GDI2._01_CpG_16.17.18, X626_GDI2._01_CpG_19.20, X626_GDI2._01_CpG_21.22, X626_GDI2._01_CpG_23.24.25.26.27, X626_GDI2._01_CpG_28, X626_GDI2._01_CpG_29.30.31, X626_GDI2._01_CpG_32, X626_GDI2._01_CpG_33.34.35.36, X626_GDI2._01_CpG_37.38, X626_GDI2._01_CpG_39, X626_GDI2._01_CpG_40.41, X626_GDI2._01_CpG_42.43.44.45.46, X626_GDI2._01_CpG_47.48, X626_GDI2._01_CpG_49.50.51.52.53.54.55.56.57, X626_GDI2._01_CpG_58.59, X626_GDI2._01_CpG_60, X626_GDI2._01_CpG_61.62, X626_GDI2._01_CpG_63.64.65, X626_GDI2._01_CpG_66
X627_GLI	X627_GLI_01_CpG_1, X627_GLI_01_CpG_2, X627_GLI_01_CpG_3, X627_GLI_01_CpG_4, X627_GLI_01_CpG_5, X627_GLI_01_CpG_6.7.8.9, X627_GLI_01_CpG_10, X627_GLI_01_CpG_11.12.13.14.15.16.17.18.19, X627_GLI_01_CpG_20, X627_GLI_01_CpG_21.22.23, X627_GLI_01_CpG_24, X627_GLI_01_CpG_25.26, X627_GLI_01_CpG_27, X627_GLI_01_CpG_28, X627_GLI_01_CpG_29
X628_GNAZ	X628_GNAZ_01_CpG_1.2.3.4.5, X628_GNAZ_01_CpG_6.7.8.9.10.11.12.13, X628_GNAZ_01_CpG_14.15.16, X628_GNAZ_01_CpG_17.18.19.20.21.22.23.24.25.26.27.28.29.30, X628_GNAZ_01_CpG_31.32, X628_GNAZ_01_CpG_33.34.35.36.37.38.39.40.41.42.43, X628_GNAZ_01_CpG_44.45, X628_GNAZ_01_CpG_46.47, X628_GNAZ_01_CpG_48.49.50.51.52, X628_GNAZ_01_CpG_53.54.55.56.57.58.59.60, X628_GNAZ_01_CpG_61, X628_GNAZ_01_CpG_62, X628_GNAZ_01_CpG_63.64.65.66.67.68.69.70.71.72, X628_GNAZ_01_CpG_73, X628_GNAZ_01_CpG_74.75, X628_GNAZ_01_CpG_76, X628_GNAZ_01_CpG_77.78.79.80.81.82.83,

	X628_GNAZ_01_CpG_84, X628_GNAZ_01_CpG_85.86
X629_GNB2L1	X629_GNB2L1_01_CpG_1, X629_GNB2L1_01_CpG_2, X629_GNB2L1_01_CpG_3, X629_GNB2L1_01_CpG_4.5, X629_GNB2L1_01_CpG_6, X629_GNB2L1_01_CpG_7.8.9.10, X629_GNB2L1_01_CpG_11, X629_GNB2L1_01_CpG_12, X629_GNB2L1_01_CpG_13, X629_GNB2L1_01_CpG_14, X629_GNB2L1_01_CpG_15.16, X629_GNB2L1_01_CpG_17.18, X629_GNB2L1_01_CpG_19, X629_GNB2L1_01_CpG_20, X629_GNB2L1_01_CpG_21.22.23, X629_GNB2L1_01_CpG_24, X629_GNB2L1_01_CpG_25.26, X629_GNB2L1_01_CpG_27, X629_GNB2L1_01_CpG_28.29, X629_GNB2L1_01_CpG_30, X629_GNB2L1_01_CpG_31, X629_GNB2L1_01_CpG_32, X629_GNB2L1_01_CpG_33, X629_GNB2L1_01_CpG_34, X629_GNB2L1_01_CpG_35, X629_GNB2L1_01_CpG_36, X629_GNB2L1_01_CpG_37
X630_HAL	X630_HAL_01_CpG_1, X630_HAL_01_CpG_2.3.4, X630_HAL_01_CpG_5, X630_HAL_01_CpG_6, X630_HAL_01_CpG_7, X630_HAL_01_CpG_8.9, X630_HAL_01_CpG_10.11, X630_HAL_01_CpG_12.13, X630_HAL_01_CpG_14, X630_HAL_01_CpG_15, X630_HAL_01_CpG_16, X630_HAL_01_CpG_17.18, X630_HAL_01_CpG_19.20, X630_HAL_01_CpG_21, X630_HAL_01_CpG_22, X630_HAL_01_CpG_23, X630_HAL_01_CpG_24
X631_hB23	X631_hB23_1_01_CpG_1.2, X631_hB23_1_01_CpG_3.4, X631_hB23_1_01_CpG_5, X631_hB23_1_01_CpG_6, X631_hB23_1_01_CpG_7.8, X631_hB23_1_01_CpG_9.10, X631_hB23_1_01_CpG_11, X631_hB23_1_01_CpG_12.13, X631_hB23_1_01_CpG_14.15, X631_hB23_1_01_CpG_16.17, X631_hB23_1_01_CpG_18, X631_hB23_1_01_CpG_19.20, X631_hB23_1_01_CpG_21, X631_hB23_1_01_CpG_22, X631_hB23_1_01_CpG_23, X631_hB23_1_01_CpG_24, X631_hB23_1_01_CpG_25, X631_hB23_1_01_CpG_26, X631_hB23_1_01_CpG_27.28.29, X631_hB23_1_01_CpG_30.31.32.33.34, X631_hB23_1_01_CpG_35, X631_hB23_1_01_CpG_36, X631_hB23_1_01_CpG_37, X631_hB23_1_01_CpG_38, X631_hB23_1_01_CpG_39, X631_hB23_1_01_CpG_40, X631_hB23_1_01_CpG_41.42, X631_hB23_1_01_CpG_43
X632_hB23	X632_hB23_2_01_CpG_1.2, X632_hB23_2_01_CpG_3.4, X632_hB23_2_01_CpG_5, X632_hB23_2_01_CpG_6, X632_hB23_2_01_CpG_7.8, X632_hB23_2_01_CpG_9.10, X632_hB23_2_01_CpG_11, X632_hB23_2_01_CpG_12.13, X632_hB23_2_01_CpG_14.15, X632_hB23_2_01_CpG_16.17, X632_hB23_2_01_CpG_18, X632_hB23_2_01_CpG_19.20, X632_hB23_2_01_CpG_21, X632_hB23_2_01_CpG_22, X632_hB23_2_01_CpG_23, X632_hB23_2_01_CpG_24, X632_hB23_2_01_CpG_25, X632_hB23_2_01_CpG_26, X632_hB23_2_01_CpG_27.28.29, X632_hB23_2_01_CpG_30.31.32.33.34, X632_hB23_2_01_CpG_35, X632_hB23_2_01_CpG_36, X632_hB23_2_01_CpG_37, X632_hB23_2_01_CpG_38, X632_hB23_2_01_CpG_39, X632_hB23_2_01_CpG_40, X632_hB23_2_01_CpG_41.42, X632_hB23_2_01_CpG_43
X633_HDAC3.	X633_HDAC3_01_CpG_1, X633_HDAC3_01_CpG_2, X633_HDAC3_01_CpG_3, X633_HDAC3_01_CpG_4, X633_HDAC3_01_CpG_5.6.7, X633_HDAC3_01_CpG_8, X633_HDAC3_01_CpG_9.10, X633_HDAC3_01_CpG_11, X633_HDAC3_01_CpG_12.13.14.15.16.17.18.19, X633_HDAC3_01_CpG_20.21.22.23, X633_HDAC3_01_CpG_24, X633_HDAC3_01_CpG_25.26, X633_HDAC3_01_CpG_27.28.29, X633_HDAC3_01_CpG_30, X633_HDAC3_01_CpG_31.32.33, X633_HDAC3_01_CpG_34, X633_HDAC3_01_CpG_35.36
X636_HSPA8	X636_HSPA8_1_01_CpG_1.2, X636_HSPA8_1_01_CpG_3, X636_HSPA8_1_01_CpG_4, X636_HSPA8_1_01_CpG_5, X636_HSPA8_1_01_CpG_6.7.8, X636_HSPA8_1_01_CpG_9.10, X636_HSPA8_1_01_CpG_11, X636_HSPA8_1_01_CpG_12, X636_HSPA8_1_01_CpG_13, X636_HSPA8_1_01_CpG_14, X636_HSPA8_1_01_CpG_15.16, X636_HSPA8_1_01_CpG_17, X636_HSPA8_1_01_CpG_18, X636_HSPA8_1_01_CpG_19.20.21, X636_HSPA8_1_01_CpG_22, X636_HSPA8_1_01_CpG_23, X636_HSPA8_1_01_CpG_24, X636_HSPA8_1_01_CpG_25
X637_HSPA8	X637_HSPA8_2_01_CpG_1, X637_HSPA8_2_01_CpG_2.3, X637_HSPA8_2_01_CpG_4.5, X637_HSPA8_2_01_CpG_6,

	X637_HSPA8_2_01_CpG_7.8.9, X637_HSPA8_2_01_CpG_10.11.12, X637_HSPA8_2_01_CpG_13, X637_HSPA8_2_01_CpG_14, X637_HSPA8_2_01_CpG_15, X637_HSPA8_2_01_CpG_16, X637_HSPA8_2_01_CpG_17.18.19, X637_HSPA8_2_01_CpG_20.21, X637_HSPA8_2_01_CpG_22, X637_HSPA8_2_01_CpG_23, X637_HSPA8_2_01_CpG_24.25.26.27, X637_HSPA8_2_01_CpG_28.29, X637_HSPA8_2_01_CpG_30, X637_HSPA8_2_01_CpG_31, X637_HSPA8_2_01_CpG_32, X637_HSPA8_2_01_CpG_33.34, X637_HSPA8_2_01_CpG_35, X637_HSPA8_2_01_CpG_36
X638_ICAM1	X638_ICAM1_01_CpG_1, X638_ICAM1_01_CpG_2, X638_ICAM1_01_CpG_3.4, X638_ICAM1_01_CpG_5.6, X638_ICAM1_01_CpG_7, X638_ICAM1_01_CpG_8, X638_ICAM1_01_CpG_9.10.11, X638_ICAM1_01_CpG_12, X638_ICAM1_01_CpG_13.14.15, X638_ICAM1_01_CpG_16, X638_ICAM1_01_CpG_17, X638_ICAM1_01_CpG_18.19, X638_ICAM1_01_CpG_20, X638_ICAM1_01_CpG_21.22, X638_ICAM1_01_CpG_23, X638_ICAM1_01_CpG_24, X638_ICAM1_01_CpG_25.26.27, X638_ICAM1_01_CpG_28, X638_ICAM1_01_CpG_29.30.31, X638_ICAM1_01_CpG_32.33, X638_ICAM1_01_CpG_34, X638_ICAM1_01_CpG_35
X639_IFITM1	X639_IFITM1_01_CpG_1, X639_IFITM1_01_CpG_2.3, X639_IFITM1_01_CpG_4, X639_IFITM1_01_CpG_5, X639_IFITM1_01_CpG_6, X639_IFITM1_01_CpG_7.8.9, X639_IFITM1_01_CpG_10, X639_IFITM1_01_CpG_11, X639_IFITM1_01_CpG_12, X639_IFITM1_01_CpG_13.14, X639_IFITM1_01_CpG_15.16.17.18.19
X641_IL10RA	X641_IL10RA_01_CpG_1, X641_IL10RA_01_CpG_2, X641_IL10RA_01_CpG_3, X641_IL10RA_01_CpG_4.5.6, X641_IL10RA_01_CpG_7, X641_IL10RA_01_CpG_8.9.10, X641_IL10RA_01_CpG_11, X641_IL10RA_01_CpG_12, X641_IL10RA_01_CpG_13, X641_IL10RA_01_CpG_14.15, X641_IL10RA_01_CpG_16, X641_IL10RA_01_CpG_17, X641_IL10RA_01_CpG_18, X641_IL10RA_01_CpG_19.20.21.22.23, X641_IL10RA_01_CpG_24, X641_IL10RA_01_CpG_25.26.27, X641_IL10RA_01_CpG_28, X641_IL10RA_01_CpG_29
X644_KCNMB1	X644_KCNMB1_01_CpG_1, X644_KCNMB1_01_CpG_2.3, X644_KCNMB1_01_CpG_4, X644_KCNMB1_01_CpG_5, X644_KCNMB1_01_CpG_6, X644_KCNMB1_01_CpG_7, X644_KCNMB1_01_CpG_8
X646_KIAA0683.	X646_KIAA0683._01_CpG_1, X646_KIAA0683._01_CpG_2, X646_KIAA0683._01_CpG_3.4.5, X646_KIAA0683._01_CpG_6.7, X646_KIAA0683._01_CpG_8.9.10.11.12, X646_KIAA0683._01_CpG_13, X646_KIAA0683._01_CpG_14.15, X646_KIAA0683._01_CpG_16, X646_KIAA0683._01_CpG_17, X646_KIAA0683._01_CpG_18, X646_KIAA0683._01_CpG_19, X646_KIAA0683._01_CpG_20, X646_KIAA0683._01_CpG_21.22.23, X646_KIAA0683._01_CpG_24.25, X646_KIAA0683._01_CpG_26.27.28.29.30
X649_KSRP	X649_KSRP_1_01_CpG_1.2, X649_KSRP_1_01_CpG_3.4.5, X649_KSRP_1_01_CpG_6, X649_KSRP_1_01_CpG_7, X649_KSRP_1_01_CpG_8, X649_KSRP_1_01_CpG_9.10, X649_KSRP_1_01_CpG_11, X649_KSRP_1_01_CpG_12, X649_KSRP_1_01_CpG_13
X650_KSRP	X650_KSRP_2_01_CpG_1.2, X650_KSRP_2_01_CpG_3.4.5, X650_KSRP_2_01_CpG_6, X650_KSRP_2_01_CpG_7, X650_KSRP_2_01_CpG_8, X650_KSRP_2_01_CpG_9.10, X650_KSRP_2_01_CpG_11, X650_KSRP_2_01_CpG_12, X650_KSRP_2_01_CpG_13
X651_LDH.A	X651_LDH.A_01_CpG_1, X651_LDH.A_01_CpG_2, X651_LDH.A_01_CpG_3, X651_LDH.A_01_CpG_4, X651_LDH.A_01_CpG_5, X651_LDH.A_01_CpG_6.7.8.9.10, X651_LDH.A_01_CpG_11, X651_LDH.A_01_CpG_12.13, X651_LDH.A_01_CpG_14, X651_LDH.A_01_CpG_15.16, X651_LDH.A_01_CpG_17.18.19.20, X651_LDH.A_01_CpG_21, X651_LDH.A_01_CpG_22.23, X651_LDH.A_01_CpG_24.25.26, X651_LDH.A_01_CpG_27, X651_LDH.A_01_CpG_28.29.30, X651_LDH.A_01_CpG_31, X651_LDH.A_01_CpG_32.33, X651_LDH.A_01_CpG_34, X651_LDH.A_01_CpG_35, X651_LDH.A_01_CpG_36, X651_LDH.A_01_CpG_37.38, X651_LDH.A_01_CpG_39.40, X651_LDH.A_01_CpG_41

X652_LEP	X652_LEP_01_CpG_1, X652_LEP_01_CpG_2.3.4, X652_LEP_01_CpG_5, X652_LEP_01_CpG_6, X652_LEP_01_CpG_7, X652_LEP_01_CpG_8.9, X652_LEP_01_CpG_10, X652_LEP_01_CpG_11, X652_LEP_01_CpG_12, X652_LEP_01_CpG_13.14.15, X652_LEP_01_CpG_16.17, X652_LEP_01_CpG_18.19.20.21.22.23, X652_LEP_01_CpG_24, X652_LEP_01_CpG_25.26.27, X652_LEP_01_CpG_28, X652_LEP_01_CpG_29.30.31.32.33.34, X652_LEP_01_CpG_35, X652_LEP_01_CpG_36.37, X652_LEP_01_CpG_38, X652_LEP_01_CpG_39.40, X652_LEP_01_CpG_41.42, X652_LEP_01_CpG_43.44, X652_LEP_01_CpG_45, X652_LEP_01_CpG_46.47.48, X652_LEP_01_CpG_49, X652_LEP_01_CpG_50.51, X652_LEP_01_CpG_52, X652_LEP_01_CpG_53, X652_LEP_01_CpG_54, X652_LEP_01_CpG_55, X652_LEP_01_CpG_56, X652_LEP_01_CpG_57.58.59
X653_LIAS	X653_LIAS_01_CpG_1, X653_LIAS_01_CpG_2, X653_LIAS_01_CpG_3, X653_LIAS_01_CpG_4.5, X653_LIAS_01_CpG_6, X653_LIAS_01_CpG_7, X653_LIAS_01_CpG_8, X653_LIAS_01_CpG_9, X653_LIAS_01_CpG_10, X653_LIAS_01_CpG_11, X653_LIAS_01_CpG_12, X653_LIAS_01_CpG_13, X653_LIAS_01_CpG_14.15, X653_LIAS_01_CpG_16, X653_LIAS_01_CpG_17, X653_LIAS_01_CpG_18, X653_LIAS_01_CpG_19.20, X653_LIAS_01_CpG_21.22
X654_LLPL	X654_LLPL_01_CpG_1.2.3, X654_LLPL_01_CpG_4, X654_LLPL_01_CpG_5, X654_LLPL_01_CpG_6.7, X654_LLPL_01_CpG_8, X654_LLPL_01_CpG_9, X654_LLPL_01_CpG_10, X654_LLPL_01_CpG_11, X654_LLPL_01_CpG_12.13.14, X654_LLPL_01_CpG_15.16.17, X654_LLPL_01_CpG_18.19, X654_LLPL_01_CpG_20, X654_LLPL_01_CpG_21, X654_LLPL_01_CpG_22.23, X654_LLPL_01_CpG_24.25, X654_LLPL_01_CpG_26, X654_LLPL_01_CpG_27.28
X655_LRP2	X655_LRP2_01_CpG_1.2, X655_LRP2_01_CpG_3.4, X655_LRP2_01_CpG_5, X655_LRP2_01_CpG_6.7, X655_LRP2_01_CpG_8.9, X655_LRP2_01_CpG_10, X655_LRP2_01_CpG_11, X655_LRP2_01_CpG_12, X655_LRP2_01_CpG_13, X655_LRP2_01_CpG_14, X655_LRP2_01_CpG_15.16.17.18.19, X655_LRP2_01_CpG_20, X655_LRP2_01_CpG_21, X655_LRP2_01_CpG_22.23.24.25.26, X655_LRP2_01_CpG_27, X655_LRP2_01_CpG_28.29.30.31, X655_LRP2_01_CpG_32, X655_LRP2_01_CpG_33, X655_LRP2_01_CpG_34
X657_MKI67	X657_MKI67_01_CpG_1.2.3.4.5.6.7, X657_MKI67_01_CpG_8.9, X657_MKI67_01_CpG_10, X657_MKI67_01_CpG_11.12, X657_MKI67_01_CpG_13, X657_MKI67_01_CpG_14
X658_mpp5.	X658_mpp5._01_CpG_1, X658_mpp5._01_CpG_2, X658_mpp5._01_CpG_3.4, X658_mpp5._01_CpG_5.6, X658_mpp5._01_CpG_7, X658_mpp5._01_CpG_8.9.10, X658_mpp5._01_CpG_11, X658_mpp5._01_CpG_12, X658_mpp5._01_CpG_13, X658_mpp5._01_CpG_14.15, X658_mpp5._01_CpG_16.17.18.19.20, X658_mpp5._01_CpG_21.22, X658_mpp5._01_CpG_23.24, X658_mpp5._01_CpG_25.26.27.28, X658_mpp5._01_CpG_29.30
X659_MRPL3.	X659_MRPL3._01_CpG_1, X659_MRPL3._01_CpG_2, X659_MRPL3._01_CpG_3.4, X659_MRPL3._01_CpG_5, X659_MRPL3._01_CpG_6.7, X659_MRPL3._01_CpG_8, X659_MRPL3._01_CpG_9, X659_MRPL3._01_CpG_10, X659_MRPL3._01_CpG_11, X659_MRPL3._01_CpG_12, X659_MRPL3._01_CpG_13.14.15, X659_MRPL3._01_CpG_16, X659_MRPL3._01_CpG_17, X659_MRPL3._01_CpG_18, X659_MRPL3._01_CpG_19, X659_MRPL3._01_CpG_20, X659_MRPL3._01_CpG_21, X659_MRPL3._01_CpG_22.23, X659_MRPL3._01_CpG_24.25.26.27, X659_MRPL3._01_CpG_28, X659_MRPL3._01_CpG_29, X659_MRPL3._01_CpG_30.31, X659_MRPL3._01_CpG_32.33, X659_MRPL3._01_CpG_34, X659_MRPL3._01_CpG_35, X659_MRPL3._01_CpG_36.37, X659_MRPL3._01_CpG_38, X659_MRPL3._01_CpG_39
X660_MYBL2	X660_MYBL2_1_01_CpG_1.2, X660_MYBL2_1_01_CpG_3.4.5.6, X660_MYBL2_1_01_CpG_7.8.9.10.11, X660_MYBL2_1_01_CpG_12.13.14, X660_MYBL2_1_01_CpG_15.16.17, X660_MYBL2_1_01_CpG_18.19.20.21.22, X660_MYBL2_1_01_CpG_23, X660_MYBL2_1_01_CpG_24, X660_MYBL2_1_01_CpG_25.26, X660_MYBL2_1_01_CpG_27,

	X660_MYBL2_1_01_CpG_28.29, X660_MYBL2_1_01_CpG_30.31.32.33, X660_MYBL2_1_01_CpG_34.35, X660_MYBL2_1_01_CpG_36, X660_MYBL2_1_01_CpG_37.38.39.40.41.42.43.44, X660_MYBL2_1_01_CpG_45.46.47.48.49.50, X660_MYBL2_1_01_CpG_51.52, X660_MYBL2_1_01_CpG_53.54, X660_MYBL2_1_01_CpG_55, X660_MYBL2_1_01_CpG_56, X660_MYBL2_1_01_CpG_57
X661_MYBL2	X661_MYBL2_2_01_CpG_1.2, X661_MYBL2_2_01_CpG_3.4.5.6, X661_MYBL2_2_01_CpG_7.8.9.10.11, X661_MYBL2_2_01_CpG_12.13.14, X661_MYBL2_2_01_CpG_15.16.17, X661_MYBL2_2_01_CpG_18.19.20.21.22, X661_MYBL2_2_01_CpG_23, X661_MYBL2_2_01_CpG_24, X661_MYBL2_2_01_CpG_25.26, X661_MYBL2_2_01_CpG_27, X661_MYBL2_2_01_CpG_28.29, X661_MYBL2_2_01_CpG_30.31.32.33, X661_MYBL2_2_01_CpG_34.35, X661_MYBL2_2_01_CpG_36, X661_MYBL2_2_01_CpG_37.38.39.40.41.42.43.44, X661_MYBL2_2_01_CpG_45.46.47.48.49.50, X661_MYBL2_2_01_CpG_51.52, X661_MYBL2_2_01_CpG_53.54, X661_MYBL2_2_01_CpG_55, X661_MYBL2_2_01_CpG_56, X661_MYBL2_2_01_CpG_57
X662_NDUFA6	X662_NDUFA6_01_CpG_1, X662_NDUFA6_01_CpG_2.3, X662_NDUFA6_01_CpG_4.5, X662_NDUFA6_01_CpG_6, X662_NDUFA6_01_CpG_7, X662_NDUFA6_01_CpG_8, X662_NDUFA6_01_CpG_9, X662_NDUFA6_01_CpG_10.11, X662_NDUFA6_01_CpG_12.13.14.15, X662_NDUFA6_01_CpG_16, X662_NDUFA6_01_CpG_17, X662_NDUFA6_01_CpG_18, X662_NDUFA6_01_CpG_19, X662_NDUFA6_01_CpG_20.21.22, X662_NDUFA6_01_CpG_23, X662_NDUFA6_01_CpG_24.25.26, X662_NDUFA6_01_CpG_27, X662_NDUFA6_01_CpG_28, X662_NDUFA6_01_CpG_29, X662_NDUFA6_01_CpG_30, X662_NDUFA6_01_CpG_31.32, X662_NDUFA6_01_CpG_33.34, X662_NDUFA6_01_CpG_35.36, X662_NDUFA6_01_CpG_37, X662_NDUFA6_01_CpG_38, X662_NDUFA6_01_CpG_39, X662_NDUFA6_01_CpG_40, X662_NDUFA6_01_CpG_41.42.43, X662_NDUFA6_01_CpG_44.45.46, X662_NDUFA6_01_CpG_47.48.49
X663_NEDD5	X663_NEDD5_1_01_CpG_1.2, X663_NEDD5_1_01_CpG_3.4.5.6.7, X663_NEDD5_1_01_CpG_8, X663_NEDD5_1_01_CpG_9.10, X663_NEDD5_1_01_CpG_11.12, X663_NEDD5_1_01_CpG_13, X663_NEDD5_1_01_CpG_14, X663_NEDD5_1_01_CpG_15.16, X663_NEDD5_1_01_CpG_17, X663_NEDD5_1_01_CpG_18.19.20, X663_NEDD5_1_01_CpG_21, X663_NEDD5_1_01_CpG_22, X663_NEDD5_1_01_CpG_23.24.25, X663_NEDD5_1_01_CpG_26, X663_NEDD5_1_01_CpG_27.28.29.30.31.32.33, X663_NEDD5_1_01_CpG_34, X663_NEDD5_1_01_CpG_35.36, X663_NEDD5_1_01_CpG_37.38
X664_NEDD5	X664_NEDD5_2_01_CpG_1, X664_NEDD5_2_01_CpG_2.3, X664_NEDD5_2_01_CpG_4, X664_NEDD5_2_01_CpG_5.6.7.8.9.10.11, X664_NEDD5_2_01_CpG_12, X664_NEDD5_2_01_CpG_13.14, X664_NEDD5_2_01_CpG_15.16.17.18.19.20.21.22.23.24.25, X664_NEDD5_2_01_CpG_26.27, X664_NEDD5_2_01_CpG_28, X664_NEDD5_2_01_CpG_29.30, X664_NEDD5_2_01_CpG_31, X664_NEDD5_2_01_CpG_32.33.34.35, X664_NEDD5_2_01_CpG_36.37.38.39.40.41, X664_NEDD5_2_01_CpG_42.43, X664_NEDD5_2_01_CpG_44, X664_NEDD5_2_01_CpG_45.46.47.48, X664_NEDD5_2_01_CpG_49.50, X664_NEDD5_2_01_CpG_51, X664_NEDD5_2_01_CpG_52, X664_NEDD5_2_01_CpG_53.54.55, X664_NEDD5_2_01_CpG_56, X664_NEDD5_2_01_CpG_57, X664_NEDD5_2_01_CpG_58.59.60.61.62, X664_NEDD5_2_01_CpG_63.64, X664_NEDD5_2_01_CpG_65
X665_Nm23	X665_Nm23_01_CpG_1, X665_Nm23_01_CpG_2.3, X665_Nm23_01_CpG_4.5, X665_Nm23_01_CpG_6, X665_Nm23_01_CpG_7, X665_Nm23_01_CpG_8, X665_Nm23_01_CpG_9, X665_Nm23_01_CpG_10.11.12, X665_Nm23_01_CpG_13, X665_Nm23_01_CpG_14.15.16.17.18.19, X665_Nm23_01_CpG_20, X665_Nm23_01_CpG_21, X665_Nm23_01_CpG_22.23, X665_Nm23_01_CpG_24.25, X665_Nm23_01_CpG_26, X665_Nm23_01_CpG_27,

	X665_Nm23_01_CpG_28.29.30, X665_Nm23_01_CpG_31, X665_Nm23_01_CpG_32, X665_Nm23_01_CpG_33, X665_Nm23_01_CpG_34.35.36.37, X665_Nm23_01_CpG_38.39, X665_Nm23_01_CpG_40
X666_NMU	X666_NMU_01_CpG_1, X666_NMU_01_CpG_2.3, X666_NMU_01_CpG_4, X666_NMU_01_CpG_5, X666_NMU_01_CpG_6.7.8, X666_NMU_01_CpG_9, X666_NMU_01_CpG_10, X666_NMU_01_CpG_11.12, X666_NMU_01_CpG_13.14, X666_NMU_01_CpG_15, X666_NMU_01_CpG_16, X666_NMU_01_CpG_17.18, X666_NMU_01_CpG_19, X666_NMU_01_CpG_20.21, X666_NMU_01_CpG_22, X666_NMU_01_CpG_23.24.25.26, X666_NMU_01_CpG_27, X666_NMU_01_CpG_28.29.30, X666_NMU_01_CpG_31, X666_NMU_01_CpG_32, X666_NMU_01_CpG_33.34.35, X666_NMU_01_CpG_36.37.38, X666_NMU_01_CpG_39, X666_NMU_01_CpG_40, X666_NMU_01_CpG_41.42.43, X666_NMU_01_CpG_44, X666_NMU_01_CpG_45.46.47, X666_NMU_01_CpG_48.49
X667_N.MYC	X667_N.MYC_1_01_CpG_1, X667_N.MYC_1_01_CpG_2, X667_N.MYC_1_01_CpG_3, X667_N.MYC_1_01_CpG_4, X667_N.MYC_1_01_CpG_5, X667_N.MYC_1_01_CpG_6, X667_N.MYC_1_01_CpG_7, X667_N.MYC_1_01_CpG_8, X667_N.MYC_1_01_CpG_9, X667_N.MYC_1_01_CpG_10.11, X667_N.MYC_1_01_CpG_12, X667_N.MYC_1_01_CpG_13.14, X667_N.MYC_1_01_CpG_15.16.17, X667_N.MYC_1_01_CpG_18.19, X667_N.MYC_1_01_CpG_20, X667_N.MYC_1_01_CpG_21.22, X667_N.MYC_1_01_CpG_23, X667_N.MYC_1_01_CpG_24, X667_N.MYC_1_01_CpG_25, X667_N.MYC_1_01_CpG_26.27, X667_N.MYC_1_01_CpG_28.29.30, X667_N.MYC_1_01_CpG_31, X667_N.MYC_1_01_CpG_32, X667_N.MYC_1_01_CpG_33.34, X667_N.MYC_1_01_CpG_35, X667_N.MYC_1_01_CpG_36.37, X667_N.MYC_1_01_CpG_38
X668_N.MYC	X668_N.MYC_2_01_CpG_1.2, X668_N.MYC_2_01_CpG_3, X668_N.MYC_2_01_CpG_4, X668_N.MYC_2_01_CpG_5, X668_N.MYC_2_01_CpG_6.7, X668_N.MYC_2_01_CpG_8.9.10, X668_N.MYC_2_01_CpG_11, X668_N.MYC_2_01_CpG_12, X668_N.MYC_2_01_CpG_13.14, X668_N.MYC_2_01_CpG_15, X668_N.MYC_2_01_CpG_16, X668_N.MYC_2_01_CpG_17, X668_N.MYC_2_01_CpG_18, X668_N.MYC_2_01_CpG_19.20.21, X668_N.MYC_2_01_CpG_22.23, X668_N.MYC_2_01_CpG_24.25, X668_N.MYC_2_01_CpG_26.27.28, X668_N.MYC_2_01_CpG_29
X669_Notch4	X669_Notch4_01_CpG_1, X669_Notch4_01_CpG_2.3.4, X669_Notch4_01_CpG_5, X669_Notch4_01_CpG_6, X669_Notch4_01_CpG_7, X669_Notch4_01_CpG_8, X669_Notch4_01_CpG_9.10, X669_Notch4_01_CpG_11.12.13, X669_Notch4_01_CpG_14, X669_Notch4_01_CpG_15, X669_Notch4_01_CpG_16, X669_Notch4_01_CpG_17.18.19, X669_Notch4_01_CpG_20, X669_Notch4_01_CpG_21, X669_Notch4_01_CpG_22, X669_Notch4_01_CpG_23, X669_Notch4_01_CpG_24, X669_Notch4_01_CpG_25.26, X669_Notch4_01_CpG_27.28, X669_Notch4_01_CpG_29, X669_Notch4_01_CpG_30, X669_Notch4_01_CpG_31, X669_Notch4_01_CpG_32.33.34.35.36, X669_Notch4_01_CpG_37.38.39.40, X669_Notch4_01_CpG_41
X670_NPD017.	X670_NPD017._01_CpG_1, X670_NPD017._01_CpG_2, X670_NPD017._01_CpG_3, X670_NPD017._01_CpG_4, X670_NPD017._01_CpG_5, X670_NPD017._01_CpG_6, X670_NPD017._01_CpG_7.8, X670_NPD017._01_CpG_9, X670_NPD017._01_CpG_10, X670_NPD017._01_CpG_11, X670_NPD017._01_CpG_12, X670_NPD017._01_CpG_13, X670_NPD017._01_CpG_14, X670_NPD017._01_CpG_15, X670_NPD017._01_CpG_16, X670_NPD017._01_CpG_17, X670_NPD017._01_CpG_18, X670_NPD017._01_CpG_19.20.21, X670_NPD017._01_CpG_22, X670_NPD017._01_CpG_23.24
X671_OXCT	X671_OXCT_01_CpG_1, X671_OXCT_01_CpG_2.3, X671_OXCT_01_CpG_4, X671_OXCT_01_CpG_5, X671_OXCT_01_CpG_6.7, X671_OXCT_01_CpG_8, X671_OXCT_01_CpG_9, X671_OXCT_01_CpG_10, X671_OXCT_01_CpG_11, X671_OXCT_01_CpG_12.13, X671_OXCT_01_CpG_14, X671_OXCT_01_CpG_15.16.17, X671_OXCT_01_CpG_18.19.20.21, X671_OXCT_01_CpG_22, X671_OXCT_01_CpG_23.24, X671_OXCT_01_CpG_25,

	X671_OXCT_01_CpG_26.27.28, X671_OXCT_01_CpG_29.30.31, X671_OXCT_01_CpG_32, X671_OXCT_01_CpG_33, X671_OXCT_01_CpG_34.35.36, X671_OXCT_01_CpG_37.38.39, X671_OXCT_01_CpG_40.41, X671_OXCT_01_CpG_42.43, X671_OXCT_01_CpG_44, X671_OXCT_01_CpG_45, X671_OXCT_01_CpG_46, X671_OXCT_01_CpG_47, X671_OXCT_01_CpG_48, X671_OXCT_01_CpG_49.50
X672_PAK.3.	X672_PAK.3._01_CpG_1, X672_PAK.3._01_CpG_2, X672_PAK.3._01_CpG_3.4, X672_PAK.3._01_CpG_5.6.7, X672_PAK.3._01_CpG_8, X672_PAK.3._01_CpG_9, X672_PAK.3._01_CpG_10.11, X672_PAK.3._01_CpG_12.13, X672_PAK.3._01_CpG_14.15.16.17.18.19.20, X672_PAK.3._01_CpG_21, X672_PAK.3._01_CpG_22.23, X672_PAK.3._01_CpG_24, X672_PAK.3._01_CpG_25, X672_PAK.3._01_CpG_26.27, X672_PAK.3._01_CpG_28, X672_PAK.3._01_CpG_29.30
X673_PECAM1	X673_PECAM1_01_CpG_1, X673_PECAM1_01_CpG_2, X673_PECAM1_01_CpG_3.4.5.6, X673_PECAM1_01_CpG_7, X673_PECAM1_01_CpG_8, X673_PECAM1_01_CpG_9, X673_PECAM1_01_CpG_10, X673_PECAM1_01_CpG_11.12, X673_PECAM1_01_CpG_13, X673_PECAM1_01_CpG_14
X674_PIK3CG	X674_PIK3CG_01_CpG_1, X674_PIK3CG_01_CpG_2, X674_PIK3CG_01_CpG_3.4.5, X674_PIK3CG_01_CpG_6, X674_PIK3CG_01_CpG_7, X674_PIK3CG_01_CpG_8, X674_PIK3CG_01_CpG_9, X674_PIK3CG_01_CpG_10, X674_PIK3CG_01_CpG_11, X674_PIK3CG_01_CpG_12, X674_PIK3CG_01_CpG_13, X674_PIK3CG_01_CpG_14, X674_PIK3CG_01_CpG_15.16, X674_PIK3CG_01_CpG_17, X674_PIK3CG_01_CpG_18.19, X674_PIK3CG_01_CpG_20, X674_PIK3CG_01_CpG_21, X674_PIK3CG_01_CpG_22, X674_PIK3CG_01_CpG_23, X674_PIK3CG_01_CpG_24, X674_PIK3CG_01_CpG_25.26.27, X674_PIK3CG_01_CpG_28.29, X674_PIK3CG_01_CpG_30, X674_PIK3CG_01_CpG_31.32, X674_PIK3CG_01_CpG_33, X674_PIK3CG_01_CpG_34, X674_PIK3CG_01_CpG_35, X674_PIK3CG_01_CpG_36
X675_PLOD	X675_PLOD_01_CpG_1.2, X675_PLOD_01_CpG_3, X675_PLOD_01_CpG_4.5.6.7, X675_PLOD_01_CpG_8, X675_PLOD_01_CpG_9, X675_PLOD_01_CpG_10.11.12.13, X675_PLOD_01_CpG_14, X675_PLOD_01_CpG_15.16.17.18.19, X675_PLOD_01_CpG_20, X675_PLOD_01_CpG_21, X675_PLOD_01_CpG_22, X675_PLOD_01_CpG_23, X675_PLOD_01_CpG_24, X675_PLOD_01_CpG_25, X675_PLOD_01_CpG_26, X675_PLOD_01_CpG_27, X675_PLOD_01_CpG_28, X675_PLOD_01_CpG_29.30, X675_PLOD_01_CpG_31.32, X675_PLOD_01_CpG_33.34, X675_PLOD_01_CpG_35, X675_PLOD_01_CpG_36, X675_PLOD_01_CpG_37, X675_PLOD_01_CpG_38, X675_PLOD_01_CpG_39.40
X676_PRDM1	X676_PRDM1_01_CpG_1, X676_PRDM1_01_CpG_2, X676_PRDM1_01_CpG_3, X676_PRDM1_01_CpG_4.5, X676_PRDM1_01_CpG_6, X676_PRDM1_01_CpG_7, X676_PRDM1_01_CpG_8, X676_PRDM1_01_CpG_9, X676_PRDM1_01_CpG_10, X676_PRDM1_01_CpG_11, X676_PRDM1_01_CpG_12.13, X676_PRDM1_01_CpG_14.15, X676_PRDM1_01_CpG_16.17.18.19.20.21, X676_PRDM1_01_CpG_22, X676_PRDM1_01_CpG_23, X676_PRDM1_01_CpG_24.25, X676_PRDM1_01_CpG_26.27.28, X676_PRDM1_01_CpG_29, X676_PRDM1_01_CpG_30.31, X676_PRDM1_01_CpG_32
X677_PSMB6	X677_PSMB6_01_CpG_1, X677_PSMB6_01_CpG_2, X677_PSMB6_01_CpG_3, X677_PSMB6_01_CpG_4, X677_PSMB6_01_CpG_5, X677_PSMB6_01_CpG_6, X677_PSMB6_01_CpG_7.8, X677_PSMB6_01_CpG_9, X677_PSMB6_01_CpG_10, X677_PSMB6_01_CpG_11, X677_PSMB6_01_CpG_12, X677_PSMB6_01_CpG_13, X677_PSMB6_01_CpG_14, X677_PSMB6_01_CpG_15, X677_PSMB6_01_CpG_16.17, X677_PSMB6_01_CpG_18, X677_PSMB6_01_CpG_19, X677_PSMB6_01_CpG_20, X677_PSMB6_01_CpG_21, X677_PSMB6_01_CpG_22.23
X678_PSME2	X678_PSME2_01_CpG_1, X678_PSME2_01_CpG_2, X678_PSME2_01_CpG_3, X678_PSME2_01_CpG_4.5,

	X678_PSME2_01_CpG_6, X678_PSME2_01_CpG_7, X678_PSME2_01_CpG_8, X678_PSME2_01_CpG_9, X678_PSME2_01_CpG_10, X678_PSME2_01_CpG_11, X678_PSME2_01_CpG_12.13.14, X678_PSME2_01_CpG_15, X678_PSME2_01_CpG_16, X678_PSME2_01_CpG_17, X678_PSME2_01_CpG_18.19
X680_PTPRN2	X680_PTPRN2_2_01_CpG_1, X680_PTPRN2_2_01_CpG_2.3.4.5.6.7.8, X680_PTPRN2_2_01_CpG_9, X680_PTPRN2_2_01_CpG_10, X680_PTPRN2_2_01_CpG_11, X680_PTPRN2_2_01_CpG_12, X680_PTPRN2_2_01_CpG_13, X680_PTPRN2_2_01_CpG_14.15.16.17, X680_PTPRN2_2_01_CpG_18, X680_PTPRN2_2_01_CpG_19.20.21.22, X680_PTPRN2_2_01_CpG_23, X680_PTPRN2_2_01_CpG_24, X680_PTPRN2_2_01_CpG_25, X680_PTPRN2_2_01_CpG_26, X680_PTPRN2_2_01_CpG_27.28.29.30.31.32, X680_PTPRN2_2_01_CpG_33.34
X681_RAD51	X681_RAD51_1_01_CpG_1, X681_RAD51_1_01_CpG_2, X681_RAD51_1_01_CpG_3, X681_RAD51_1_01_CpG_4, X681_RAD51_1_01_CpG_5.6, X681_RAD51_1_01_CpG_7.8.9, X681_RAD51_1_01_CpG_10, X681_RAD51_1_01_CpG_11.12, X681_RAD51_1_01_CpG_13, X681_RAD51_1_01_CpG_14.15, X681_RAD51_1_01_CpG_16, X681_RAD51_1_01_CpG_17, X681_RAD51_1_01_CpG_18, X681_RAD51_1_01_CpG_19, X681_RAD51_1_01_CpG_20.21, X681_RAD51_1_01_CpG_22.23, X681_RAD51_1_01_CpG_24, X681_RAD51_1_01_CpG_25, X681_RAD51_1_01_CpG_26.27.28, X681_RAD51_1_01_CpG_29.30, X681_RAD51_1_01_CpG_31.32, X681_RAD51_1_01_CpG_33
X682_RAD51	X682_RAD51_2_01_CpG_1, X682_RAD51_2_01_CpG_2, X682_RAD51_2_01_CpG_3, X682_RAD51_2_01_CpG_4.5.6.7.8.9, X682_RAD51_2_01_CpG_10.11.12, X682_RAD51_2_01_CpG_13, X682_RAD51_2_01_CpG_14.15, X682_RAD51_2_01_CpG_16.17, X682_RAD51_2_01_CpG_18, X682_RAD51_2_01_CpG_19, X682_RAD51_2_01_CpG_20.21.22.23, X682_RAD51_2_01_CpG_24.25, X682_RAD51_2_01_CpG_26, X682_RAD51_2_01_CpG_27.28.29, X682_RAD51_2_01_CpG_30, X682_RAD51_2_01_CpG_31, X682_RAD51_2_01_CpG_32.33.34.35, X682_RAD51_2_01_CpG_36, X682_RAD51_2_01_CpG_37
X683_rhoC.	X683_rhoC._01_CpG_1, X683_rhoC._01_CpG_2, X683_rhoC._01_CpG_3.4, X683_rhoC._01_CpG_5, X683_rhoC._01_CpG_6.7.8, X683_rhoC._01_CpG_9.10.11.12, X683_rhoC._01_CpG_13.14, X683_rhoC._01_CpG_15.16.17.18, X683_rhoC._01_CpG_19.20, X683_rhoC._01_CpG_21.22.23.24.25.26.27.28, X683_rhoC._01_CpG_29, X683_rhoC._01_CpG_30.31, X683_rhoC._01_CpG_32, X683_rhoC._01_CpG_33, X683_rhoC._01_CpG_34, X683_rhoC._01_CpG_35, X683_rhoC._01_CpG_36, X683_rhoC._01_CpG_37.38, X683_rhoC._01_CpG_39, X683_rhoC._01_CpG_40, X683_rhoC._01_CpG_41
X001_SEPT6	X001_SEPT6_001_CpG_1.2.3.4.5.6.7, X001_SEPT6_001_CpG_8, X001_SEPT6_001_CpG_9.10.11.12.13, X001_SEPT6_001_CpG_14.15, X001_SEPT6_001_CpG_16, X001_SEPT6_001_CpG_17, X001_SEPT6_001_CpG_18.19, X001_SEPT6_001_CpG_20, X001_SEPT6_001_CpG_21.22.23.24, X001_SEPT6_001_CpG_25, X001_SEPT6_001_CpG_26.27, X001_SEPT6_001_CpG_28.29, X001_SEPT6_001_CpG_30, X001_SEPT6_001_CpG_31.32, X001_SEPT6_001_CpG_33, X001_SEPT6_001_CpG_34, X001_SEPT6_001_CpG_35, X001_SEPT6_001_CpG_36.37, X001_SEPT6_001_CpG_38, X001_SEPT6_001_CpG_39.40, X001_SEPT6_001_CpG_41, X001_SEPT6_001_CpG_42.43.44, X001_SEPT6_001_CpG_45.46.47.48.49, X001_SEPT6_001_CpG_50.51
X002_ATM	X002_ATM_001_CpG_1, X002_ATM_001_CpG_2.3.4, X002_ATM_001_CpG_5.6, X002_ATM_001_CpG_7.8, X002_ATM_001_CpG_9.10, X002_ATM_001_CpG_11, X002_ATM_001_CpG_12.13.14, X002_ATM_001_CpG_15, X002_ATM_001_CpG_16, X002_ATM_001_CpG_17, X002_ATM_001_CpG_18, X002_ATM_001_CpG_19,

	X002_ATM_001_CpG_20, X002_ATM_001_CpG_21.22.23, X002_ATM_001_CpG_24, X002_ATM_001_CpG_25, X002_ATM_001_CpG_26, X002_ATM_001_CpG_27.28.29, X002_ATM_001_CpG_30, X002_ATM_001_CpG_31.32, X002_ATM_001_CpG_33, X002_ATM_001_CpG_34.35, X002_ATM_001_CpG_36.37, X002_ATM_001_CpG_38
X003_BCL11A	X003_BCL11A_001_CpG_1, X003_BCL11A_001_CpG_2.3.4.5, X003_BCL11A_001_CpG_6, X003_BCL11A_001_CpG_7.8.9, X003_BCL11A_001_CpG_10.11, X003_BCL11A_001_CpG_12.13.14, X003_BCL11A_001_CpG_15, X003_BCL11A_001_CpG_16, X003_BCL11A_001_CpG_17.18.19.20.21.22, X003_BCL11A_001_CpG_23.24, X003_BCL11A_001_CpG_25.26, X003_BCL11A_001_CpG_27, X003_BCL11A_001_CpG_28, X003_BCL11A_001_CpG_29, X003_BCL11A_001_CpG_30.31.32
X004_BCL11B	X004_BCL11B_001_CpG_1, X004_BCL11B_001_CpG_2, X004_BCL11B_001_CpG_3, X004_BCL11B_001_CpG_4, X004_BCL11B_001_CpG_5, X004_BCL11B_001_CpG_6, X004_BCL11B_001_CpG_7.8.9.10.11.12, X004_BCL11B_001_CpG_13, X004_BCL11B_001_CpG_14, X004_BCL11B_001_CpG_15, X004_BCL11B_001_CpG_16, X004_BCL11B_001_CpG_17, X004_BCL11B_001_CpG_18.19.20, X004_BCL11B_001_CpG_21, X004_BCL11B_001_CpG_22.23, X004_BCL11B_001_CpG_24, X004_BCL11B_001_CpG_25
X007_BCL5	X007_BCL5_001_CpG_1, X007_BCL5_001_CpG_2.3.4, X007_BCL5_001_CpG_5, X007_BCL5_001_CpG_6, X007_BCL5_001_CpG_7, X007_BCL5_001_CpG_8.9, X007_BCL5_001_CpG_10, X007_BCL5_001_CpG_11, X007_BCL5_001_CpG_12.13, X007_BCL5_001_CpG_14, X007_BCL5_001_CpG_15.16, X007_BCL5_001_CpG_17, X007_BCL5_001_CpG_18.19
X009_BUB1B	X009_BUB1B_001_CpG_1.2, X009_BUB1B_001_CpG_3.4, X009_BUB1B_001_CpG_5.6, X009_BUB1B_001_CpG_7, X009_BUB1B_001_CpG_8.9, X009_BUB1B_001_CpG_10.11, X009_BUB1B_001_CpG_12, X009_BUB1B_001_CpG_13.14, X009_BUB1B_001_CpG_15, X009_BUB1B_001_CpG_16, X009_BUB1B_001_CpG_17, X009_BUB1B_001_CpG_18.19, X009_BUB1B_001_CpG_20.21.22, X009_BUB1B_001_CpG_23, X009_BUB1B_001_CpG_24, X009_BUB1B_001_CpG_25, X009_BUB1B_001_CpG_26, X009_BUB1B_001_CpG_27.28, X009_BUB1B_001_CpG_29, X009_BUB1B_001_CpG_30, X009_BUB1B_001_CpG_31
X010_CARS	X010_CARS_001_CpG_1.2.3, X010_CARS_001_CpG_4.5, X010_CARS_001_CpG_6.7.8.9, X010_CARS_001_CpG_10.11.12, X010_CARS_001_CpG_13, X010_CARS_001_CpG_14.15.16, X010_CARS_001_CpG_17, X010_CARS_001_CpG_18.19.20, X010_CARS_001_CpG_21.22.23, X010_CARS_001_CpG_24, X010_CARS_001_CpG_25, X010_CARS_001_CpG_26.27, X010_CARS_001_CpG_28, X010_CARS_001_CpG_29, X010_CARS_001_CpG_30.31
X011_CBFA2T3	X011_CBFA2T3_001_CpG_1, X011_CBFA2T3_001_CpG_2.3.4, X011_CBFA2T3_001_CpG_5.6, X011_CBFA2T3_001_CpG_7, X011_CBFA2T3_001_CpG_8, X011_CBFA2T3_001_CpG_9, X011_CBFA2T3_001_CpG_10, X011_CBFA2T3_001_CpG_11, X011_CBFA2T3_001_CpG_12, X011_CBFA2T3_001_CpG_13.14, X011_CBFA2T3_001_CpG_15, X011_CBFA2T3_001_CpG_16, X011_CBFA2T3_001_CpG_17, X011_CBFA2T3_001_CpG_18, X011_CBFA2T3_001_CpG_19, X011_CBFA2T3_001_CpG_20, X011_CBFA2T3_001_CpG_21, X011_CBFA2T3_001_CpG_22.23, X011_CBFA2T3_001_CpG_24, X011_CBFA2T3_001_CpG_25.26, X011_CBFA2T3_001_CpG_27.28.29, X011_CBFA2T3_001_CpG_30, X011_CBFA2T3_001_CpG_31.32, X011_CBFA2T3_001_CpG_33, X011_CBFA2T3_001_CpG_34.35, X011_CBFA2T3_001_CpG_36
X012_CCND2	X012_CCND2_001_CpG_1, X012_CCND2_001_CpG_2, X012_CCND2_001_CpG_3, X012_CCND2_001_CpG_4, X012_CCND2_001_CpG_5, X012_CCND2_001_CpG_6.7, X012_CCND2_001_CpG_8, X012_CCND2_001_CpG_9, X012_CCND2_001_CpG_10, X012_CCND2_001_CpG_11, X012_CCND2_001_CpG_12, X012_CCND2_001_CpG_13,

	X012_CCND2_001_CpG_14.15, X012_CCND2_001_CpG_16, X012_CCND2_001_CpG_17.18, X012_CCND2_001_CpG_19.20, X012_CCND2_001_CpG_21, X012_CCND2_001_CpG_22, X012_CCND2_001_CpG_23, X012_CCND2_001_CpG_24.25, X012_CCND2_001_CpG_26, X012_CCND2_001_CpG_27, X012_CCND2_001_CpG_28, X012_CCND2_001_CpG_29, X012_CCND2_001_CpG_30
X013_CCND2	X013_CCND2_002_CpG_1, X013_CCND2_002_CpG_2, X013_CCND2_002_CpG_3.4.5.6, X013_CCND2_002_CpG_7.8, X013_CCND2_002_CpG_9, X013_CCND2_002_CpG_10.11.12.13.14, X013_CCND2_002_CpG_15, X013_CCND2_002_CpG_16, X013_CCND2_002_CpG_17, X013_CCND2_002_CpG_18, X013_CCND2_002_CpG_19.20.21, X013_CCND2_002_CpG_22.23, X013_CCND2_002_CpG_24, X013_CCND2_002_CpG_25, X013_CCND2_002_CpG_26, X013_CCND2_002_CpG_27, X013_CCND2_002_CpG_28.29, X013_CCND2_002_CpG_30, X013_CCND2_002_CpG_31, X013_CCND2_002_CpG_32, X013_CCND2_002_CpG_33, X013_CCND2_002_CpG_34.35
X014_CCND3	X014_CCND3_001_CpG_1, X014_CCND3_001_CpG_2, X014_CCND3_001_CpG_3, X014_CCND3_001_CpG_4.5, X014_CCND3_001_CpG_6.7.8, X014_CCND3_001_CpG_9.10, X014_CCND3_001_CpG_11.12, X014_CCND3_001_CpG_13.14.15.16.17, X014_CCND3_001_CpG_18.19.20, X014_CCND3_001_CpG_21, X014_CCND3_001_CpG_22, X014_CCND3_001_CpG_23, X014_CCND3_001_CpG_24, X014_CCND3_001_CpG_25, X014_CCND3_001_CpG_26.27.28, X014_CCND3_001_CpG_29, X014_CCND3_001_CpG_30, X014_CCND3_001_CpG_31, X014_CCND3_001_CpG_32, X014_CCND3_001_CpG_33, X014_CCND3_001_CpG_34
X015_CDH1	X015_CDH1_001_CpG_1, X015_CDH1_001_CpG_2, X015_CDH1_001_CpG_3.4, X015_CDH1_001_CpG_5, X015_CDH1_001_CpG_6, X015_CDH1_001_CpG_7.8.9.10.11.12, X015_CDH1_001_CpG_13, X015_CDH1_001_CpG_14.15, X015_CDH1_001_CpG_16, X015_CDH1_001_CpG_17, X015_CDH1_001_CpG_18, X015_CDH1_001_CpG_19.20, X015_CDH1_001_CpG_21.22, X015_CDH1_001_CpG_23.24.25, X015_CDH1_001_CpG_26, X015_CDH1_001_CpG_27, X015_CDH1_001_CpG_28, X015_CDH1_001_CpG_29, X015_CDH1_001_CpG_30.31.32.33, X015_CDH1_001_CpG_34, X015_CDH1_001_CpG_35.36, X015_CDH1_001_CpG_37, X015_CDH1_001_CpG_38, X015_CDH1_001_CpG_39.40.41.42, X015_CDH1_001_CpG_43.44.45.46.47.48.49, X015_CDH1_001_CpG_50
X017_CDK6	X017_CDK6_001_CpG_1, X017_CDK6_001_CpG_2, X017_CDK6_001_CpG_3, X017_CDK6_001_CpG_4.5.6, X017_CDK6_001_CpG_7, X017_CDK6_001_CpG_8, X017_CDK6_001_CpG_9, X017_CDK6_001_CpG_10.11.12.13, X017_CDK6_001_CpG_14, X017_CDK6_001_CpG_15, X017_CDK6_001_CpG_16.17.18, X017_CDK6_001_CpG_19, X017_CDK6_001_CpG_20, X017_CDK6_001_CpG_21.22, X017_CDK6_001_CpG_23, X017_CDK6_001_CpG_24.25, X017_CDK6_001_CpG_26.27, X017_CDK6_001_CpG_28, X017_CDK6_001_CpG_29, X017_CDK6_001_CpG_30.31, X017_CDK6_001_CpG_32, X017_CDK6_001_CpG_33, X017_CDK6_001_CpG_34, X017_CDK6_001_CpG_35, X017_CDK6_001_CpG_36, X017_CDK6_001_CpG_37, X017_CDK6_001_CpG_38.39, X017_CDK6_001_CpG_40, X017_CDK6_001_CpG_41.42
X018_CHEK2	X018_CHEK2_001_CpG_1, X018_CHEK2_001_CpG_2.3, X018_CHEK2_001_CpG_4, X018_CHEK2_001_CpG_5.6, X018_CHEK2_001_CpG_7.8, X018_CHEK2_001_CpG_9, X018_CHEK2_001_CpG_10, X018_CHEK2_001_CpG_11, X018_CHEK2_001_CpG_12.13, X018_CHEK2_001_CpG_14, X018_CHEK2_001_CpG_15.16.17, X018_CHEK2_001_CpG_18, X018_CHEK2_001_CpG_19, X018_CHEK2_001_CpG_20.21, X018_CHEK2_001_CpG_22, X018_CHEK2_001_CpG_23, X018_CHEK2_001_CpG_24.25, X018_CHEK2_001_CpG_26.27
X020_CLTC	X020_CLTC_001_CpG_1, X020_CLTC_001_CpG_2, X020_CLTC_001_CpG_3, X020_CLTC_001_CpG_4, X020_CLTC_001_CpG_5, X020_CLTC_001_CpG_6.7.8.9, X020_CLTC_001_CpG_10, X020_CLTC_001_CpG_11, X020_CLTC_001_CpG_12, X020_CLTC_001_CpG_13, X020_CLTC_001_CpG_14, X020_CLTC_001_CpG_15.16,

	X020_CLTC_001_CpG_17.18, X020_CLTC_001_CpG_19.20.21.22.23.24.25.26, X020_CLTC_001_CpG_27, X020_CLTC_001_CpG_28, X020_CLTC_001_CpG_29, X020_CLTC_001_CpG_30.31, X020_CLTC_001_CpG_32, X020_CLTC_001_CpG_33.34, X020_CLTC_001_CpG_35.36.37.38, X020_CLTC_001_CpG_39, X020_CLTC_001_CpG_40.41, X020_CLTC_001_CpG_42, X020_CLTC_001_CpG_43, X020_CLTC_001_CpG_44.45
X021_CLTCL1	X021_CLTCL1_001_CpG_1, X021_CLTCL1_001_CpG_2, X021_CLTCL1_001_CpG_3, X021_CLTCL1_001_CpG_4.5.6.7.8, X021_CLTCL1_001_CpG_9, X021_CLTCL1_001_CpG_10.11, X021_CLTCL1_001_CpG_12.13.14, X021_CLTCL1_001_CpG_15.16, X021_CLTCL1_001_CpG_17.18, X021_CLTCL1_001_CpG_19, X021_CLTCL1_001_CpG_20, X021_CLTCL1_001_CpG_21.22, X021_CLTCL1_001_CpG_23.24.25.26, X021_CLTCL1_001_CpG_27.28.29.30.31.32.33.34.35.36.37.38, X021_CLTCL1_001_CpG_39.40.41, X021_CLTCL1_001_CpG_42.43, X021_CLTCL1_001_CpG_44.45.46, X021_CLTCL1_001_CpG_47.48, X021_CLTCL1_001_CpG_49, X021_CLTCL1_001_CpG_50, X021_CLTCL1_001_CpG_51.52, X021_CLTCL1_001_CpG_53, X021_CLTCL1_001_CpG_54, X021_CLTCL1_001_CpG_55, X021_CLTCL1_001_CpG_56
X022_CMKOR1	X022_CMKOR1_001_CpG_1, X022_CMKOR1_001_CpG_2, X022_CMKOR1_001_CpG_3, X022_CMKOR1_001_CpG_4, X022_CMKOR1_001_CpG_5, X022_CMKOR1_001_CpG_6, X022_CMKOR1_001_CpG_7, X022_CMKOR1_001_CpG_8, X022_CMKOR1_001_CpG_9.10, X022_CMKOR1_001_CpG_11.12, X022_CMKOR1_001_CpG_13.14.15, X022_CMKOR1_001_CpG_16, X022_CMKOR1_001_CpG_17, X022_CMKOR1_001_CpG_18, X022_CMKOR1_001_CpG_19, X022_CMKOR1_001_CpG_20.21
X023_COL1A1	X023_COL1A1_001_CpG_1.2.3, X023_COL1A1_001_CpG_4, X023_COL1A1_001_CpG_5, X023_COL1A1_001_CpG_6.7.8.9, X023_COL1A1_001_CpG_10.11.12, X023_COL1A1_001_CpG_13.14.15.16, X023_COL1A1_001_CpG_17, X023_COL1A1_001_CpG_18.19, X023_COL1A1_001_CpG_20, X023_COL1A1_001_CpG_21, X023_COL1A1_001_CpG_22.23, X023_COL1A1_001_CpG_24.25.26, X023_COL1A1_001_CpG_27, X023_COL1A1_001_CpG_28.29, X023_COL1A1_001_CpG_30.31, X023_COL1A1_001_CpG_32.33, X023_COL1A1_001_CpG_34.35, X023_COL1A1_001_CpG_36
X024_COPEB	X024_COPEB_001_CpG_1, X024_COPEB_001_CpG_2, X024_COPEB_001_CpG_3, X024_COPEB_001_CpG_4, X024_COPEB_001_CpG_5.6.7, X024_COPEB_001_CpG_8, X024_COPEB_001_CpG_9, X024_COPEB_001_CpG_10, X024_COPEB_001_CpG_11, X024_COPEB_001_CpG_12.13.14.15.16.17, X024_COPEB_001_CpG_18.19, X024_COPEB_001_CpG_20, X024_COPEB_001_CpG_21, X024_COPEB_001_CpG_22, X024_COPEB_001_CpG_23, X024_COPEB_001_CpG_24.25.26.27.28.29, X024_COPEB_001_CpG_30.31.32.33, X024_COPEB_001_CpG_34, X024_COPEB_001_CpG_35.36, X024_COPEB_001_CpG_37.38, X024_COPEB_001_CpG_39
X025_COX6C	X025_COX6C_001_CpG_1, X025_COX6C_001_CpG_2, X025_COX6C_001_CpG_3, X025_COX6C_001_CpG_4, X025_COX6C_001_CpG_5, X025_COX6C_001_CpG_6, X025_COX6C_001_CpG_7.8.9.10, X025_COX6C_001_CpG_11.12.13.14.15, X025_COX6C_001_CpG_16, X025_COX6C_001_CpG_17, X025_COX6C_001_CpG_18, X025_COX6C_001_CpG_19
X026_CREBBP	X026_CREBBP_001_CpG_1, X026_CREBBP_001_CpG_2, X026_CREBBP_001_CpG_3.4, X026_CREBBP_001_CpG_5.6, X026_CREBBP_001_CpG_7.8.9.10.11.12.13, X026_CREBBP_001_CpG_14, X026_CREBBP_001_CpG_15, X026_CREBBP_001_CpG_16.17.18.19.20.21.22, X026_CREBBP_001_CpG_23.24, X026_CREBBP_001_CpG_25.26.27, X026_CREBBP_001_CpG_28.29.30, X026_CREBBP_001_CpG_31.32, X026_CREBBP_001_CpG_33.34.35, X026_CREBBP_001_CpG_36.37, X026_CREBBP_001_CpG_38, X026_CREBBP_001_CpG_39, X026_CREBBP_001_CpG_40.41, X026_CREBBP_001_CpG_42, X026_CREBBP_001_CpG_43,

	X026_CREBBP_001_CpG_44.45, X026_CREBBP_001_CpG_46
X027_DDX10	X027_DDX10_001_CpG_1, X027_DDX10_001_CpG_2, X027_DDX10_001_CpG_3, X027_DDX10_001_CpG_4.5.6.7, X027_DDX10_001_CpG_8.9, X027_DDX10_001_CpG_10.11, X027_DDX10_001_CpG_12, X027_DDX10_001_CpG_13, X027_DDX10_001_CpG_14.15.16, X027_DDX10_001_CpG_17.18, X027_DDX10_001_CpG_19.20, X027_DDX10_001_CpG_21.22, X027_DDX10_001_CpG_23, X027_DDX10_001_CpG_24, X027_DDX10_001_CpG_25, X027_DDX10_001_CpG_26.27.28.29.30, X027_DDX10_001_CpG_31, X027_DDX10_001_CpG_32.33, X027_DDX10_001_CpG_34, X027_DDX10_001_CpG_35, X027_DDX10_001_CpG_36.37, X027_DDX10_001_CpG_38
X028_DDX6	X028_DDX6_001_CpG_1, X028_DDX6_001_CpG_2, X028_DDX6_001_CpG_3.4, X028_DDX6_001_CpG_5.6, X028_DDX6_001_CpG_7, X028_DDX6_001_CpG_8.9, X028_DDX6_001_CpG_10, X028_DDX6_001_CpG_11, X028_DDX6_001_CpG_12, X028_DDX6_001_CpG_13.14, X028_DDX6_001_CpG_15.16, X028_DDX6_001_CpG_17, X028_DDX6_001_CpG_18.19.20.21.22.23, X028_DDX6_001_CpG_24.25, X028_DDX6_001_CpG_26.27, X028_DDX6_001_CpG_28.29.30, X028_DDX6_001_CpG_31.32.33.34.35.36, X028_DDX6_001_CpG_37.38, X028_DDX6_001_CpG_39.40.41.42.43.44.45.46.47, X028_DDX6_001_CpG_48.49, X028_DDX6_001_CpG_50.51, X028_DDX6_001_CpG_52, X028_DDX6_001_CpG_53.54.55.56, X028_DDX6_001_CpG_57.58.59.60
X030_ELL	X030_ELL_001_CpG_1, X030_ELL_001_CpG_2, X030_ELL_001_CpG_3, X030_ELL_001_CpG_4, X030_ELL_001_CpG_5, X030_ELL_001_CpG_6.7, X030_ELL_001_CpG_8, X030_ELL_001_CpG_9.10, X030_ELL_001_CpG_11, X030_ELL_001_CpG_12, X030_ELL_001_CpG_13, X030_ELL_001_CpG_14, X030_ELL_001_CpG_15, X030_ELL_001_CpG_16, X030_ELL_001_CpG_17, X030_ELL_001_CpG_18.19, X030_ELL_001_CpG_20, X030_ELL_001_CpG_21.22.23.24, X030_ELL_001_CpG_25, X030_ELL_001_CpG_26, X030_ELL_001_CpG_27.28.29.30, X030_ELL_001_CpG_31, X030_ELL_001_CpG_32
X031_ERG.	X031_ERG._001_CpG_1.2.3, X031_ERG._001_CpG_4, X031_ERG._001_CpG_5.6, X031_ERG._001_CpG_7, X031_ERG._001_CpG_8, X031_ERG._001_CpG_9.10, X031_ERG._001_CpG_11.12, X031_ERG._001_CpG_13, X031_ERG._001_CpG_14.15, X031_ERG._001_CpG_16, X031_ERG._001_CpG_17, X031_ERG._001_CpG_18, X031_ERG._001_CpG_19, X031_ERG._001_CpG_20
X032_ETV1	X032_ETV1_001_CpG_1, X032_ETV1_001_CpG_2.3, X032_ETV1_001_CpG_4, X032_ETV1_001_CpG_5.6.7.8, X032_ETV1_001_CpG_9.10, X032_ETV1_001_CpG_11, X032_ETV1_001_CpG_12, X032_ETV1_001_CpG_13, X032_ETV1_001_CpG_14, X032_ETV1_001_CpG_15, X032_ETV1_001_CpG_16, X032_ETV1_001_CpG_17.18, X032_ETV1_001_CpG_19
X034_FBXW7	X034_FBXW7_001_CpG_1.2, X034_FBXW7_001_CpG_3, X034_FBXW7_001_CpG_4.5.6.7, X034_FBXW7_001_CpG_8, X034_FBXW7_001_CpG_9, X034_FBXW7_001_CpG_10, X034_FBXW7_001_CpG_11.12.13, X034_FBXW7_001_CpG_14.15.16, X034_FBXW7_001_CpG_17, X034_FBXW7_001_CpG_18.19.20, X034_FBXW7_001_CpG_21.22.23, X034_FBXW7_001_CpG_24.25, X034_FBXW7_001_CpG_26, X034_FBXW7_001_CpG_27
X035_FGFR3	X035_FGFR3_001_CpG_1, X035_FGFR3_001_CpG_2.3.4, X035_FGFR3_001_CpG_5, X035_FGFR3_001_CpG_6, X035_FGFR3_001_CpG_7.8.9, X035_FGFR3_001_CpG_10.11, X035_FGFR3_001_CpG_12.13, X035_FGFR3_001_CpG_14, X035_FGFR3_001_CpG_15.16, X035_FGFR3_001_CpG_17.18, X035_FGFR3_001_CpG_19.20.21, X035_FGFR3_001_CpG_22.23, X035_FGFR3_001_CpG_24, X035_FGFR3_001_CpG_25, X035_FGFR3_001_CpG_26, X035_FGFR3_001_CpG_27.28, X035_FGFR3_001_CpG_29, X035_FGFR3_001_CpG_30, X035_FGFR3_001_CpG_31, X035_FGFR3_001_CpG_32.33, X035_FGFR3_001_CpG_34, X035_FGFR3_001_CpG_35, X035_FGFR3_001_CpG_36.37,

	X035_FGFR3_001_CpG_38, X035_FGFR3_001_CpG_39.40, X035_FGFR3_001_CpG_41, X035_FGFR3_001_CpG_42, X035_FGFR3_001_CpG_43, X035_FGFR3_001_CpG_44.45, X035_FGFR3_001_CpG_46, X035_FGFR3_001_CpG_47.48.49, X035_FGFR3_001_CpG_50.51.52
X037_FSTL3	X037_FSTL3_001_CpG_1.2.3.4, X037_FSTL3_001_CpG_5, X037_FSTL3_001_CpG_6.7, X037_FSTL3_001_CpG_8, X037_FSTL3_001_CpG_9.10, X037_FSTL3_001_CpG_11, X037_FSTL3_001_CpG_12, X037_FSTL3_001_CpG_13, X037_FSTL3_001_CpG_14.15.16.17.18
X038_FVT1	X038_FVT1_001_CpG_1, X038_FVT1_001_CpG_2, X038_FVT1_001_CpG_3.4.5.6.7, X038_FVT1_001_CpG_8.9, X038_FVT1_001_CpG_10, X038_FVT1_001_CpG_11, X038_FVT1_001_CpG_12.13.14, X038_FVT1_001_CpG_15.16.17, X038_FVT1_001_CpG_18.19, X038_FVT1_001_CpG_20.21
X039_GAS7	X039_GAS7_001_CpG_1.2.3.4, X039_GAS7_001_CpG_5, X039_GAS7_001_CpG_6.7, X039_GAS7_001_CpG_8.9.10.11.12, X039_GAS7_001_CpG_13.14.15, X039_GAS7_001_CpG_16.17.18.19.20.21, X039_GAS7_001_CpG_22, X039_GAS7_001_CpG_23, X039_GAS7_001_CpG_24, X039_GAS7_001_CpG_25.26, X039_GAS7_001_CpG_27.28.29.30.31, X039_GAS7_001_CpG_32.33.34.35, X039_GAS7_001_CpG_36, X039_GAS7_001_CpG_37.38.39, X039_GAS7_001_CpG_40, X039_GAS7_001_CpG_41.42.43, X039_GAS7_001_CpG_44.45.46, X039_GAS7_001_CpG_47.48, X039_GAS7_001_CpG_49.50, X039_GAS7_001_CpG_51.52, X039_GAS7_001_CpG_53, X039_GAS7_001_CpG_54.55.56.57.58.59, X039_GAS7_001_CpG_60, X039_GAS7_001_CpG_61
X040_GOPC	X040_GOPC_001_CpG_1.2.3.4.5, X040_GOPC_001_CpG_6, X040_GOPC_001_CpG_7.8.9, X040_GOPC_001_CpG_10, X040_GOPC_001_CpG_11, X040_GOPC_001_CpG_12, X040_GOPC_001_CpG_13, X040_GOPC_001_CpG_14.15.16, X040_GOPC_001_CpG_17, X040_GOPC_001_CpG_18.19, X040_GOPC_001_CpG_20, X040_GOPC_001_CpG_21, X040_GOPC_001_CpG_22, X040_GOPC_001_CpG_23, X040_GOPC_001_CpG_24, X040_GOPC_001_CpG_25, X040_GOPC_001_CpG_26, X040_GOPC_001_CpG_27, X040_GOPC_001_CpG_28, X040_GOPC_001_CpG_29, X040_GOPC_001_CpG_30, X040_GOPC_001_CpG_31.32, X040_GOPC_001_CpG_33, X040_GOPC_001_CpG_34.35, X040_GOPC_001_CpG_36.37, X040_GOPC_001_CpG_38, X040_GOPC_001_CpG_39, X040_GOPC_001_CpG_40
X041_HCMOGT.1	X041_HCMOGT.1_001_CpG_1, X041_HCMOGT.1_001_CpG_2.3.4.5.6.7, X041_HCMOGT.1_001_CpG_8, X041_HCMOGT.1_001_CpG_9.10.11, X041_HCMOGT.1_001_CpG_12, X041_HCMOGT.1_001_CpG_13, X041_HCMOGT.1_001_CpG_14.15.16, X041_HCMOGT.1_001_CpG_17.18.19, X041_HCMOGT.1_001_CpG_20.21, X041_HCMOGT.1_001_CpG_22, X041_HCMOGT.1_001_CpG_23.24, X041_HCMOGT.1_001_CpG_25, X041_HCMOGT.1_001_CpG_26.27, X041_HCMOGT.1_001_CpG_28, X041_HCMOGT.1_001_CpG_29.30, X041_HCMOGT.1_001_CpG_31, X041_HCMOGT.1_001_CpG_32, X041_HCMOGT.1_001_CpG_33.34, X041_HCMOGT.1_001_CpG_35, X041_HCMOGT.1_001_CpG_36.37, X041_HCMOGT.1_001_CpG_38, X041_HCMOGT.1_001_CpG_39.40, X041_HCMOGT.1_001_CpG_41, X041_HCMOGT.1_001_CpG_42.43.44.45.46, X041_HCMOGT.1_001_CpG_47, X041_HCMOGT.1_001_CpG_48, X041_HCMOGT.1_001_CpG_49.50.51.52.53.54, X041_HCMOGT.1_001_CpG_55, X041_HCMOGT.1_001_CpG_56
X042_HEAB	X042_HEAB_001_CpG_1, X042_HEAB_001_CpG_2.3.4, X042_HEAB_001_CpG_5.6, X042_HEAB_001_CpG_7, X042_HEAB_001_CpG_8, X042_HEAB_001_CpG_9.10.11, X042_HEAB_001_CpG_12, X042_HEAB_001_CpG_13, X042_HEAB_001_CpG_14, X042_HEAB_001_CpG_15, X042_HEAB_001_CpG_16, X042_HEAB_001_CpG_17, X042_HEAB_001_CpG_18, X042_HEAB_001_CpG_19, X042_HEAB_001_CpG_20, X042_HEAB_001_CpG_21, X042_HEAB_001_CpG_22.23.24, X042_HEAB_001_CpG_25.26.27, X042_HEAB_001_CpG_28.29,

	X042_HEAB_001_CpG_30, X042_HEAB_001_CpG_31, X042_HEAB_001_CpG_32.33.34.35, X042_HEAB_001_CpG_36, X042_HEAB_001_CpG_37, X042_HEAB_001_CpG_38
X043_HLXB9	X043_HLXB9_001_CpG_1.2, X043_HLXB9_001_CpG_3, X043_HLXB9_001_CpG_4.5, X043_HLXB9_001_CpG_6, X043_HLXB9_001_CpG_7.8.9, X043_HLXB9_001_CpG_10.11, X043_HLXB9_001_CpG_12.13, X043_HLXB9_001_CpG_14.15.16.17.18.19, X043_HLXB9_001_CpG_20.21, X043_HLXB9_001_CpG_22.23, X043_HLXB9_001_CpG_24, X043_HLXB9_001_CpG_25, X043_HLXB9_001_CpG_26.27, X043_HLXB9_001_CpG_28.29, X043_HLXB9_001_CpG_30, X043_HLXB9_001_CpG_31, X043_HLXB9_001_CpG_32, X043_HLXB9_001_CpG_33, X043_HLXB9_001_CpG_34, X043_HLXB9_001_CpG_35, X043_HLXB9_001_CpG_36, X043_HLXB9_001_CpG_37, X043_HLXB9_001_CpG_38, X043_HLXB9_001_CpG_39, X043_HLXB9_001_CpG_40.41
X045_HMGA2	X045_HMGA2_001_CpG_1, X045_HMGA2_001_CpG_2, X045_HMGA2_001_CpG_3.4, X045_HMGA2_001_CpG_5, X045_HMGA2_001_CpG_6, X045_HMGA2_001_CpG_7.8.9.10, X045_HMGA2_001_CpG_11, X045_HMGA2_001_CpG_12.13, X045_HMGA2_001_CpG_14.15.16.17.18.19, X045_HMGA2_001_CpG_20, X045_HMGA2_001_CpG_21, X045_HMGA2_001_CpG_22.23.24.25, X045_HMGA2_001_CpG_26, X045_HMGA2_001_CpG_27, X045_HMGA2_001_CpG_28, X045_HMGA2_001_CpG_29, X045_HMGA2_001_CpG_30.31, X045_HMGA2_001_CpG_32
X047_HOXC13	X047_HOXC13_001_CpG_1, X047_HOXC13_001_CpG_2.3, X047_HOXC13_001_CpG_4, X047_HOXC13_001_CpG_5.6.7.8.9, X047_HOXC13_001_CpG_10.11, X047_HOXC13_001_CpG_12, X047_HOXC13_001_CpG_13.14, X047_HOXC13_001_CpG_15.16.17, X047_HOXC13_001_CpG_18.19.20, X047_HOXC13_001_CpG_21, X047_HOXC13_001_CpG_22, X047_HOXC13_001_CpG_23, X047_HOXC13_001_CpG_24, X047_HOXC13_001_CpG_25.26.27, X047_HOXC13_001_CpG_28, X047_HOXC13_001_CpG_29, X047_HOXC13_001_CpG_30.31, X047_HOXC13_001_CpG_32, X047_HOXC13_001_CpG_33.34.35.36, X047_HOXC13_001_CpG_37, X047_HOXC13_001_CpG_38, X047_HOXC13_001_CpG_39, X047_HOXC13_001_CpG_40, X047_HOXC13_001_CpG_41, X047_HOXC13_001_CpG_42.43.44, X047_HOXC13_001_CpG_45, X047_HOXC13_001_CpG_46, X047_HOXC13_001_CpG_47.48, X047_HOXC13_001_CpG_49, X047_HOXC13_001_CpG_50, X047_HOXC13_001_CpG_51.52
X049_HOXD13	X049_HOXD13_001_CpG_1, X049_HOXD13_001_CpG_2.3, X049_HOXD13_001_CpG_4.5.6.7, X049_HOXD13_001_CpG_8.9.10.11.12, X049_HOXD13_001_CpG_13.14, X049_HOXD13_001_CpG_15, X049_HOXD13_001_CpG_16, X049_HOXD13_001_CpG_17.18.19, X049_HOXD13_001_CpG_20.21, X049_HOXD13_001_CpG_22
X050_HRAS	X050_HRAS_001_CpG_1, X050_HRAS_001_CpG_2.3.4, X050_HRAS_001_CpG_5, X050_HRAS_001_CpG_6, X050_HRAS_001_CpG_7, X050_HRAS_001_CpG_8, X050_HRAS_001_CpG_9, X050_HRAS_001_CpG_10, X050_HRAS_001_CpG_11.12, X050_HRAS_001_CpG_13, X050_HRAS_001_CpG_14, X050_HRAS_001_CpG_15, X050_HRAS_001_CpG_16.17.18.19.20.21, X050_HRAS_001_CpG_22, X050_HRAS_001_CpG_23.24.25.26.27.28, X050_HRAS_001_CpG_29.30.31.32, X050_HRAS_001_CpG_33.34.35, X050_HRAS_001_CpG_36, X050_HRAS_001_CpG_37.38, X050_HRAS_001_CpG_39.40, X050_HRAS_001_CpG_41.42.43, X050_HRAS_001_CpG_44.45.46.47, X050_HRAS_001_CpG_48.49.50.51.52.53.54.55.56.57, X050_HRAS_001_CpG_58, X050_HRAS_001_CpG_59, X050_HRAS_001_CpG_60, X050_HRAS_001_CpG_61
X051_HRAS	X051_HRAS_002_CpG_1, X051_HRAS_002_CpG_2, X051_HRAS_002_CpG_3, X051_HRAS_002_CpG_4.5, X051_HRAS_002_CpG_6, X051_HRAS_002_CpG_7.8, X051_HRAS_002_CpG_9.10, X051_HRAS_002_CpG_11.12.13,

	X051_HRAS_002_CpG_14.15.16.17, X051_HRAS_002_CpG_18, X051_HRAS_002_CpG_19, X051_HRAS_002_CpG_20.21.22, X051_HRAS_002_CpG_23, X051_HRAS_002_CpG_24.25, X051_HRAS_002_CpG_26.27, X051_HRAS_002_CpG_28
X052_HRPT2	X052_HRPT2_001_CpG_1.2.3, X052_HRPT2_001_CpG_4.5.6.7.8.9, X052_HRPT2_001_CpG_10.11.12.13.14.15.16.17, X052_HRPT2_001_CpG_18, X052_HRPT2_001_CpG_19.20.21, X052_HRPT2_001_CpG_22.23.24, X052_HRPT2_001_CpG_25, X052_HRPT2_001_CpG_26, X052_HRPT2_001_CpG_27, X052_HRPT2_001_CpG_28, X052_HRPT2_001_CpG_29.30.31.32.33, X052_HRPT2_001_CpG_34, X052_HRPT2_001_CpG_35, X052_HRPT2_001_CpG_36.37.38, X052_HRPT2_001_CpG_39.40.41, X052_HRPT2_001_CpG_42.43.44.45
X053_HSPCA	X053_HSPCA_001_CpG_1.2.3.4, X053_HSPCA_001_CpG_5, X053_HSPCA_001_CpG_6, X053_HSPCA_001_CpG_7, X053_HSPCA_001_CpG_8, X053_HSPCA_001_CpG_9, X053_HSPCA_001_CpG_10, X053_HSPCA_001_CpG_11, X053_HSPCA_001_CpG_12, X053_HSPCA_001_CpG_13, X053_HSPCA_001_CpG_14, X053_HSPCA_001_CpG_15, X053_HSPCA_001_CpG_16.17.18, X053_HSPCA_001_CpG_19, X053_HSPCA_001_CpG_20.21, X053_HSPCA_001_CpG_22, X053_HSPCA_001_CpG_23, X053_HSPCA_001_CpG_24, X053_HSPCA_001_CpG_25, X053_HSPCA_001_CpG_26.27, X053_HSPCA_001_CpG_28, X053_HSPCA_001_CpG_29.30, X053_HSPCA_001_CpG_31, X053_HSPCA_001_CpG_32, X053_HSPCA_001_CpG_33, X053_HSPCA_001_CpG_34.35, X053_HSPCA_001_CpG_36
X054_HSPCB	X054_HSPCB_001_CpG_1, X054_HSPCB_001_CpG_2, X054_HSPCB_001_CpG_3, X054_HSPCB_001_CpG_4.5.6, X054_HSPCB_001_CpG_7, X054_HSPCB_001_CpG_8, X054_HSPCB_001_CpG_9.10.11.12.13, X054_HSPCB_001_CpG_14, X054_HSPCB_001_CpG_15, X054_HSPCB_001_CpG_16.17, X054_HSPCB_001_CpG_18.19.20, X054_HSPCB_001_CpG_21, X054_HSPCB_001_CpG_22.23.24, X054_HSPCB_001_CpG_25
X055_IRF4	X055_IRF4_001_CpG_1, X055_IRF4_001_CpG_2, X055_IRF4_001_CpG_3, X055_IRF4_001_CpG_4, X055_IRF4_001_CpG_5.6.7, X055_IRF4_001_CpG_8, X055_IRF4_001_CpG_9, X055_IRF4_001_CpG_10.11.12.13.14, X055_IRF4_001_CpG_15.16.17.18.19.20.21, X055_IRF4_001_CpG_22, X055_IRF4_001_CpG_23.24, X055_IRF4_001_CpG_25.26.27, X055_IRF4_001_CpG_28.29, X055_IRF4_001_CpG_30.31.32.33.34.35, X055_IRF4_001_CpG_36, X055_IRF4_001_CpG_37.38.39.40, X055_IRF4_001_CpG_41, X055_IRF4_001_CpG_42, X055_IRF4_001_CpG_43.44, X055_IRF4_001_CpG_45, X055_IRF4_001_CpG_46, X055_IRF4_001_CpG_47, X055_IRF4_001_CpG_48
X056_JAK2	X056_JAK2_001_CpG_1.2, X056_JAK2_001_CpG_3.4, X056_JAK2_001_CpG_5, X056_JAK2_001_CpG_6, X056_JAK2_001_CpG_7.8, X056_JAK2_001_CpG_9, X056_JAK2_001_CpG_10.11.12, X056_JAK2_001_CpG_13.14.15, X056_JAK2_001_CpG_16.17, X056_JAK2_001_CpG_18, X056_JAK2_001_CpG_19, X056_JAK2_001_CpG_20.21.22.23.24.25, X056_JAK2_001_CpG_26.27.28.29.30.31, X056_JAK2_001_CpG_32, X056_JAK2_001_CpG_33.34, X056_JAK2_001_CpG_35.36, X056_JAK2_001_CpG_37.38.39.40, X056_JAK2_001_CpG_41.42, X056_JAK2_001_CpG_43, X056_JAK2_001_CpG_44, X056_JAK2_001_CpG_45, X056_JAK2_001_CpG_46.47, X056_JAK2_001_CpG_48.49.50.51, X056_JAK2_001_CpG_52.53, X056_JAK2_001_CpG_54.55.56
X058_KIT	X058_KIT_001_CpG_1, X058_KIT_001_CpG_2, X058_KIT_001_CpG_3.4.5.6.7.8, X058_KIT_001_CpG_9.10, X058_KIT_001_CpG_11.12, X058_KIT_001_CpG_13.14.15, X058_KIT_001_CpG_16, X058_KIT_001_CpG_17.18.19.20, X058_KIT_001_CpG_21, X058_KIT_001_CpG_22.23.24.25, X058_KIT_001_CpG_26, X058_KIT_001_CpG_27.28.29.30.31.32.33.34, X058_KIT_001_CpG_35, X058_KIT_001_CpG_36, X058_KIT_001_CpG_37,

	X058_KIT_001_CpG_38, X058_KIT_001_CpG_39.40, X058_KIT_001_CpG_41.42.43.44, X058_KIT_001_CpG_45, X058_KIT_001_CpG_46.47, X058_KIT_001_CpG_48.49, X058_KIT_001_CpG_50, X058_KIT_001_CpG_51.52, X058_KIT_001_CpG_53.54
X059_KTN1	X059_KTN1_001_CpG_1, X059_KTN1_001_CpG_2, X059_KTN1_001_CpG_3.4.5, X059_KTN1_001_CpG_6, X059_KTN1_001_CpG_7, X059_KTN1_001_CpG_8, X059_KTN1_001_CpG_9, X059_KTN1_001_CpG_10, X059_KTN1_001_CpG_11, X059_KTN1_001_CpG_12, X059_KTN1_001_CpG_13.14.15, X059_KTN1_001_CpG_16, X059_KTN1_001_CpG_17, X059_KTN1_001_CpG_18, X059_KTN1_001_CpG_19.20, X059_KTN1_001_CpG_21, X059_KTN1_001_CpG_22, X059_KTN1_001_CpG_23.24, X059_KTN1_001_CpG_25.26.27, X059_KTN1_001_CpG_28.29.30, X059_KTN1_001_CpG_31.32.33.34.35, X059_KTN1_001_CpG_36, X059_KTN1_001_CpG_37.38.39.40.41.42, X059_KTN1_001_CpG_43.44.45, X059_KTN1_001_CpG_46.47.48, X059_KTN1_001_CpG_49, X059_KTN1_001_CpG_50, X059_KTN1_001_CpG_51.52.53.54.55.56.57.58.59.60, X059_KTN1_001_CpG_61.62.63, X059_KTN1_001_CpG_64.65.66.67.68.69.70.71
X060_LAF4	X060_LAF4_001_CpG_1, X060_LAF4_001_CpG_2.3, X060_LAF4_001_CpG_4.5.6.7, X060_LAF4_001_CpG_8, X060_LAF4_001_CpG_9, X060_LAF4_001_CpG_10, X060_LAF4_001_CpG_11, X060_LAF4_001_CpG_12, X060_LAF4_001_CpG_13.14, X060_LAF4_001_CpG_15.16.17.18.19, X060_LAF4_001_CpG_20, X060_LAF4_001_CpG_21.22.23.24.25.26.27.28.29.30.31.32, X060_LAF4_001_CpG_33.34, X060_LAF4_001_CpG_35, X060_LAF4_001_CpG_36, X060_LAF4_001_CpG_37
X061_LASP1	X061_LASP1_001_CpG_1.2, X061_LASP1_001_CpG_3, X061_LASP1_001_CpG_4, X061_LASP1_001_CpG_5.6.7.8, X061_LASP1_001_CpG_9.10.11, X061_LASP1_001_CpG_12.13.14, X061_LASP1_001_CpG_15.16.17.18.19.20.21.22, X061_LASP1_001_CpG_23.24.25, X061_LASP1_001_CpG_26, X061_LASP1_001_CpG_27, X061_LASP1_001_CpG_28, X061_LASP1_001_CpG_29.30.31, X061_LASP1_001_CpG_32.33.34.35, X061_LASP1_001_CpG_36.37, X061_LASP1_001_CpG_38.39.40, X061_LASP1_001_CpG_41.42, X061_LASP1_001_CpG_43, X061_LASP1_001_CpG_44.45.46, X061_LASP1_001_CpG_47, X061_LASP1_001_CpG_48, X061_LASP1_001_CpG_49, X061_LASP1_001_CpG_50, X061_LASP1_001_CpG_51.52, X061_LASP1_001_CpG_53, X061_LASP1_001_CpG_54, X061_LASP1_001_CpG_55.56, X061_LASP1_001_CpG_57.58
X062_LMO2	X062_LMO2_001_CpG_1, X062_LMO2_001_CpG_2.3, X062_LMO2_001_CpG_4.5, X062_LMO2_001_CpG_6.7, X062_LMO2_001_CpG_8, X062_LMO2_001_CpG_9, X062_LMO2_001_CpG_10, X062_LMO2_001_CpG_11.12.13, X062_LMO2_001_CpG_14.15.16, X062_LMO2_001_CpG_17, X062_LMO2_001_CpG_18, X062_LMO2_001_CpG_19.20, X062_LMO2_001_CpG_21.22.23, X062_LMO2_001_CpG_24.25, X062_LMO2_001_CpG_26.27.28.29.30, X062_LMO2_001_CpG_31.32, X062_LMO2_001_CpG_33.34, X062_LMO2_001_CpG_35, X062_LMO2_001_CpG_36, X062_LMO2_001_CpG_37
X063_LMO2	X063_LMO2_002_CpG_1.2.3.4, X063_LMO2_002_CpG_5.6.7.8.9.10.11.12.13.14.15.16, X063_LMO2_002_CpG_17.18.19.20.21, X063_LMO2_002_CpG_22, X063_LMO2_002_CpG_23.24.25.26.27.28.29.30.31, X063_LMO2_002_CpG_32.33, X063_LMO2_002_CpG_34, X063_LMO2_002_CpG_35.36.37.38, X063_LMO2_002_CpG_39, X063_LMO2_002_CpG_40, X063_LMO2_002_CpG_41, X063_LMO2_002_CpG_42
X064_LPP	X064_LPP_001_CpG_1.2.3.4.5.6.7.8.9.10.11.12, X064_LPP_001_CpG_13.14.15.16, X064_LPP_001_CpG_17, X064_LPP_001_CpG_18, X064_LPP_001_CpG_19.20.21.22.23.24.25.26, X064_LPP_001_CpG_27.28.29, X064_LPP_001_CpG_30.31.32.33, X064_LPP_001_CpG_34.35.36, X064_LPP_001_CpG_37.38, X064_LPP_001_CpG_39, X064_LPP_001_CpG_40.41.42.43.44, X064_LPP_001_CpG_45.46.47, X064_LPP_001_CpG_48, X064_LPP_001_CpG_49

X065_LYL1	X065_LYL1_001_CpG_1, X065_LYL1_001_CpG_2.3, X065_LYL1_001_CpG_4, X065_LYL1_001_CpG_5.6.7.8.9.10, X065_LYL1_001_CpG_11, X065_LYL1_001_CpG_12.13, X065_LYL1_001_CpG_14.15.16.17.18.19.20.21, X065_LYL1_001_CpG_22.23, X065_LYL1_001_CpG_24.25, X065_LYL1_001_CpG_26.27, X065_LYL1_001_CpG_28, X065_LYL1_001_CpG_29.30, X065_LYL1_001_CpG_31.32.33.34, X065_LYL1_001_CpG_35.36, X065_LYL1_001_CpG_37.38, X065_LYL1_001_CpG_39.40, X065_LYL1_001_CpG_41, X065_LYL1_001_CpG_42, X065_LYL1_001_CpG_43, X065_LYL1_001_CpG_44
X067_MAFB	X067_MAFB_001_CpG_1.2, X067_MAFB_001_CpG_3, X067_MAFB_001_CpG_4, X067_MAFB_001_CpG_5, X067_MAFB_001_CpG_6.7.8.9, X067_MAFB_001_CpG_10.11.12, X067_MAFB_001_CpG_13.14.15, X067_MAFB_001_CpG_16.17, X067_MAFB_001_CpG_18, X067_MAFB_001_CpG_19, X067_MAFB_001_CpG_20, X067_MAFB_001_CpG_21, X067_MAFB_001_CpG_22.23.24.25, X067_MAFB_001_CpG_26.27.28.29.30.31, X067_MAFB_001_CpG_32, X067_MAFB_001_CpG_33, X067_MAFB_001_CpG_34.35, X067_MAFB_001_CpG_36.37, X067_MAFB_001_CpG_38.39, X067_MAFB_001_CpG_40, X067_MAFB_001_CpG_41.42.43, X067_MAFB_001_CpG_44.45, X067_MAFB_001_CpG_46.47, X067_MAFB_001_CpG_48.49.50, X067_MAFB_001_CpG_51.52, X067_MAFB_001_CpG_53.54, X067_MAFB_001_CpG_55.56.57.58, X067_MAFB_001_CpG_59
X068_MAP2K4	X068_MAP2K4_001_CpG_1, X068_MAP2K4_001_CpG_2, X068_MAP2K4_001_CpG_3.4.5, X068_MAP2K4_001_CpG_6.7, X068_MAP2K4_001_CpG_8.9, X068_MAP2K4_001_CpG_10.11.12.13.14.15, X068_MAP2K4_001_CpG_16.17.18.19, X068_MAP2K4_001_CpG_20, X068_MAP2K4_001_CpG_21, X068_MAP2K4_001_CpG_22.23.24.25, X068_MAP2K4_001_CpG_26, X068_MAP2K4_001_CpG_27.28.29.30.31.32, X068_MAP2K4_001_CpG_33.34, X068_MAP2K4_001_CpG_35, X068_MAP2K4_001_CpG_36.37.38.39.40.41, X068_MAP2K4_001_CpG_42, X068_MAP2K4_001_CpG_43, X068_MAP2K4_001_CpG_44.45, X068_MAP2K4_001_CpG_46.47, X068_MAP2K4_001_CpG_48.49
X069_MAP2K4	X069_MAP2K4_002_CpG_1.2, X069_MAP2K4_002_CpG_3.4, X069_MAP2K4_002_CpG_5.6.7.8.9.10.11.12, X069_MAP2K4_002_CpG_13, X069_MAP2K4_002_CpG_14.15, X069_MAP2K4_002_CpG_16, X069_MAP2K4_002_CpG_17, X069_MAP2K4_002_CpG_18, X069_MAP2K4_002_CpG_19, X069_MAP2K4_002_CpG_20, X069_MAP2K4_002_CpG_21, X069_MAP2K4_002_CpG_22
X070_MDS1	X070_MDS1_001_CpG_1.2, X070_MDS1_001_CpG_3.4, X070_MDS1_001_CpG_5.6, X070_MDS1_001_CpG_7.8, X070_MDS1_001_CpG_9.10, X070_MDS1_001_CpG_11.12.13, X070_MDS1_001_CpG_14, X070_MDS1_001_CpG_15.16, X070_MDS1_001_CpG_17.18, X070_MDS1_001_CpG_19.20, X070_MDS1_001_CpG_21.22.23, X070_MDS1_001_CpG_24.25.26.27, X070_MDS1_001_CpG_28, X070_MDS1_001_CpG_29, X070_MDS1_001_CpG_30, X070_MDS1_001_CpG_31, X070_MDS1_001_CpG_32.33.34.35, X070_MDS1_001_CpG_36.37.38.39, X070_MDS1_001_CpG_40.41.42, X070_MDS1_001_CpG_43.44.45.46.47, X070_MDS1_001_CpG_48, X070_MDS1_001_CpG_49, X070_MDS1_001_CpG_50, X070_MDS1_001_CpG_51, X070_MDS1_001_CpG_52.53, X070_MDS1_001_CpG_54
X071_MET	X071_MET_001_CpG_1.2, X071_MET_001_CpG_3, X071_MET_001_CpG_4.5, X071_MET_001_CpG_6.7, X071_MET_001_CpG_8.9.10.11, X071_MET_001_CpG_12, X071_MET_001_CpG_13.14, X071_MET_001_CpG_15.16, X071_MET_001_CpG_17.18, X071_MET_001_CpG_19, X071_MET_001_CpG_20.21, X071_MET_001_CpG_22.23, X071_MET_001_CpG_24, X071_MET_001_CpG_25, X071_MET_001_CpG_26.27.28, X071_MET_001_CpG_29.30.31.32.33.34.35.36.37.38.39, X071_MET_001_CpG_40
X072_MKL1	X072_MKL1_001_CpG_1, X072_MKL1_001_CpG_2.3.4.5.6.7.8.9.10, X072_MKL1_001_CpG_11,

	X072_MKL1_001_CpG_12.13.14.15, X072_MKL1_001_CpG_16.17, X072_MKL1_001_CpG_18, X072_MKL1_001_CpG_19.20, X072_MKL1_001_CpG_21, X072_MKL1_001_CpG_22, X072_MKL1_001_CpG_23, X072_MKL1_001_CpG_24.25.26.27.28.29, X072_MKL1_001_CpG_30.31.32, X072_MKL1_001_CpG_33, X072_MKL1_001_CpG_34.35, X072_MKL1_001_CpG_36.37.38, X072_MKL1_001_CpG_39, X072_MKL1_001_CpG_40.41.42, X072_MKL1_001_CpG_43.44, X072_MKL1_001_CpG_45.46, X072_MKL1_001_CpG_47.48, X072_MKL1_001_CpG_49, X072_MKL1_001_CpG_50, X072_MKL1_001_CpG_51.52, X072_MKL1_001_CpG_53, X072_MKL1_001_CpG_54.55, X072_MKL1_001_CpG_56, X072_MKL1_001_CpG_57.58, X072_MKL1_001_CpG_59, X072_MKL1_001_CpG_60, X072_MKL1_001_CpG_61.62, X072_MKL1_001_CpG_63, X072_MKL1_001_CpG_64, X072_MKL1_001_CpG_65, X072_MKL1_001_CpG_66, X072_MKL1_001_CpG_67.68, X072_MKL1_001_CpG_69, X072_MKL1_001_CpG_70, X072_MKL1_001_CpG_71.72, X072_MKL1_001_CpG_73, X072_MKL1_001_CpG_74, X072_MKL1_001_CpG_75, X072_MKL1_001_CpG_76
X073_MLF1	X073_MLF1_001_CpG_1, X073_MLF1_001_CpG_2.3.4, X073_MLF1_001_CpG_5, X073_MLF1_001_CpG_6, X073_MLF1_001_CpG_7.8, X073_MLF1_001_CpG_9.10, X073_MLF1_001_CpG_11, X073_MLF1_001_CpG_12, X073_MLF1_001_CpG_13, X073_MLF1_001_CpG_14.15, X073_MLF1_001_CpG_16.17.18.19.20, X073_MLF1_001_CpG_21.22.23, X073_MLF1_001_CpG_24.25.26.27.28, X073_MLF1_001_CpG_29, X073_MLF1_001_CpG_30.31.32
X074_MLH1	X074_MLH1_001_CpG_1, X074_MLH1_001_CpG_2, X074_MLH1_001_CpG_3, X074_MLH1_001_CpG_4, X074_MLH1_001_CpG_5.6.7.8.9.10, X074_MLH1_001_CpG_11.12, X074_MLH1_001_CpG_13, X074_MLH1_001_CpG_14, X074_MLH1_001_CpG_15, X074_MLH1_001_CpG_16.17.18.19.20, X074_MLH1_001_CpG_21, X074_MLH1_001_CpG_22.23, X074_MLH1_001_CpG_24.25, X074_MLH1_001_CpG_26, X074_MLH1_001_CpG_27.28, X074_MLH1_001_CpG_29.30, X074_MLH1_001_CpG_31, X074_MLH1_001_CpG_32, X074_MLH1_001_CpG_33, X074_MLH1_001_CpG_34, X074_MLH1_001_CpG_35, X074_MLH1_001_CpG_36.37, X074_MLH1_001_CpG_38.39
X076_MSI2	X076_MSI2_001_CpG_1, X076_MSI2_001_CpG_2.3, X076_MSI2_001_CpG_4, X076_MSI2_001_CpG_5.6, X076_MSI2_001_CpG_7, X076_MSI2_001_CpG_8, X076_MSI2_001_CpG_9, X076_MSI2_001_CpG_10, X076_MSI2_001_CpG_11, X076_MSI2_001_CpG_12.13.14, X076_MSI2_001_CpG_15.16, X076_MSI2_001_CpG_17.18.19.20.21.22, X076_MSI2_001_CpG_23.24.25.26.27.28.29, X076_MSI2_001_CpG_30.31.32, X076_MSI2_001_CpG_33.34.35.36, X076_MSI2_001_CpG_37.38, X076_MSI2_001_CpG_39.40, X076_MSI2_001_CpG_41, X076_MSI2_001_CpG_42, X076_MSI2_001_CpG_43, X076_MSI2_001_CpG_44, X076_MSI2_001_CpG_45, X076_MSI2_001_CpG_46.47.48
X077_MTCP1	X077_MTCP1_001_CpG_1, X077_MTCP1_001_CpG_2.3.4.5, X077_MTCP1_001_CpG_6, X077_MTCP1_001_CpG_7, X077_MTCP1_001_CpG_8.9, X077_MTCP1_001_CpG_10, X077_MTCP1_001_CpG_11.12, X077_MTCP1_001_CpG_13.14, X077_MTCP1_001_CpG_15, X077_MTCP1_001_CpG_16, X077_MTCP1_001_CpG_17.18.19.20, X077_MTCP1_001_CpG_21.22.23, X077_MTCP1_001_CpG_24.25.26.27.28.29, X077_MTCP1_001_CpG_30.31, X077_MTCP1_001_CpG_32.33.34, X077_MTCP1_001_CpG_35.36.37, X077_MTCP1_001_CpG_38, X077_MTCP1_001_CpG_39, X077_MTCP1_001_CpG_40.41.42.43, X077_MTCP1_001_CpG_44.45.46, X077_MTCP1_001_CpG_47.48.49.50, X077_MTCP1_001_CpG_51.52.53.54.55, X077_MTCP1_001_CpG_56, X077_MTCP1_001_CpG_57.58, X077_MTCP1_001_CpG_59, X077_MTCP1_001_CpG_60.61.62.63, X077_MTCP1_001_CpG_64, X077_MTCP1_001_CpG_65, X077_MTCP1_001_CpG_66.67, X077_MTCP1_001_CpG_68.69, X077_MTCP1_001_CpG_70

X078_MUC1	X078_MUC1_001_CpG_1, X078_MUC1_001_CpG_2, X078_MUC1_001_CpG_3, X078_MUC1_001_CpG_4.5.6, X078_MUC1_001_CpG_7.8, X078_MUC1_001_CpG_9.10, X078_MUC1_001_CpG_11, X078_MUC1_001_CpG_12, X078_MUC1_001_CpG_13.14, X078_MUC1_001_CpG_15, X078_MUC1_001_CpG_16, X078_MUC1_001_CpG_17, X078_MUC1_001_CpG_18, X078_MUC1_001_CpG_19, X078_MUC1_001_CpG_20.21.22, X078_MUC1_001_CpG_23
X079_MYH11	X079_MYH11_001_CpG_1, X079_MYH11_001_CpG_2, X079_MYH11_001_CpG_3, X079_MYH11_001_CpG_4, X079_MYH11_001_CpG_5, X079_MYH11_001_CpG_6.7.8, X079_MYH11_001_CpG_9, X079_MYH11_001_CpG_10, X079_MYH11_001_CpG_11.12, X079_MYH11_001_CpG_13, X079_MYH11_001_CpG_14.15.16.17.18, X079_MYH11_001_CpG_19, X079_MYH11_001_CpG_20.21, X079_MYH11_001_CpG_22, X079_MYH11_001_CpG_23.24, X079_MYH11_001_CpG_25, X079_MYH11_001_CpG_26, X079_MYH11_001_CpG_27, X079_MYH11_001_CpG_28, X079_MYH11_001_CpG_29, X079_MYH11_001_CpG_30, X079_MYH11_001_CpG_31, X079_MYH11_001_CpG_32, X079_MYH11_001_CpG_33.34, X079_MYH11_001_CpG_35.36, X079_MYH11_001_CpG_37, X079_MYH11_001_CpG_38, X079_MYH11_001_CpG_39, X079_MYH11_001_CpG_40.41.42, X079_MYH11_001_CpG_43.44
X080_MYH9	X080_MYH9_001_CpG_1, X080_MYH9_001_CpG_2.3, X080_MYH9_001_CpG_4.5, X080_MYH9_001_CpG_6, X080_MYH9_001_CpG_7.8.9.10.11.12, X080_MYH9_001_CpG_13.14, X080_MYH9_001_CpG_15, X080_MYH9_001_CpG_16.17.18, X080_MYH9_001_CpG_19, X080_MYH9_001_CpG_20.21, X080_MYH9_001_CpG_22, X080_MYH9_001_CpG_23, X080_MYH9_001_CpG_24, X080_MYH9_001_CpG_25, X080_MYH9_001_CpG_26, X080_MYH9_001_CpG_27.28, X080_MYH9_001_CpG_29, X080_MYH9_001_CpG_30, X080_MYH9_001_CpG_31, X080_MYH9_001_CpG_32, X080_MYH9_001_CpG_33.34, X080_MYH9_001_CpG_35.36.37, X080_MYH9_001_CpG_38.39.40.41, X080_MYH9_001_CpG_42, X080_MYH9_001_CpG_43
X081_NBS1	X081_NBS1_001_CpG_1.2, X081_NBS1_001_CpG_3.4.5, X081_NBS1_001_CpG_6.7.8, X081_NBS1_001_CpG_9, X081_NBS1_001_CpG_10, X081_NBS1_001_CpG_11.12.13, X081_NBS1_001_CpG_14.15, X081_NBS1_001_CpG_16.17, X081_NBS1_001_CpG_18, X081_NBS1_001_CpG_19.20, X081_NBS1_001_CpG_21, X081_NBS1_001_CpG_22, X081_NBS1_001_CpG_23, X081_NBS1_001_CpG_24, X081_NBS1_001_CpG_25, X081_NBS1_001_CpG_26, X081_NBS1_001_CpG_27.28.29.30, X081_NBS1_001_CpG_31.32, X081_NBS1_001_CpG_33, X081_NBS1_001_CpG_34, X081_NBS1_001_CpG_35.36, X081_NBS1_001_CpG_37, X081_NBS1_001_CpG_38, X081_NBS1_001_CpG_39.40, X081_NBS1_001_CpG_41.42.43.44, X081_NBS1_001_CpG_45, X081_NBS1_001_CpG_46.47.48.49, X081_NBS1_001_CpG_50, X081_NBS1_001_CpG_51, X081_NBS1_001_CpG_52, X081_NBS1_001_CpG_53.54
X082_NCOA4	X082_NCOA4_001_CpG_1, X082_NCOA4_001_CpG_2.3, X082_NCOA4_001_CpG_4, X082_NCOA4_001_CpG_5, X082_NCOA4_001_CpG_6.7, X082_NCOA4_001_CpG_8, X082_NCOA4_001_CpG_9.10.11, X082_NCOA4_001_CpG_12, X082_NCOA4_001_CpG_13.14, X082_NCOA4_001_CpG_15, X082_NCOA4_001_CpG_16, X082_NCOA4_001_CpG_17.18, X082_NCOA4_001_CpG_19, X082_NCOA4_001_CpG_20, X082_NCOA4_001_CpG_21, X082_NCOA4_001_CpG_22, X082_NCOA4_001_CpG_23, X082_NCOA4_001_CpG_24.25, X082_NCOA4_001_CpG_26.27, X082_NCOA4_001_CpG_28, X082_NCOA4_001_CpG_29.30, X082_NCOA4_001_CpG_31.32, X082_NCOA4_001_CpG_33.34, X082_NCOA4_001_CpG_35
X083_NF2	X083_NF2_001_CpG_1, X083_NF2_001_CpG_2, X083_NF2_001_CpG_3, X083_NF2_001_CpG_4, X083_NF2_001_CpG_5, X083_NF2_001_CpG_6.7.8.9.10, X083_NF2_001_CpG_11, X083_NF2_001_CpG_12.13, X083_NF2_001_CpG_14, X083_NF2_001_CpG_15.16.17.18.19.20, X083_NF2_001_CpG_21, X083_NF2_001_CpG_22.23.24.25.26, X083_NF2_001_CpG_27.28.29, X083_NF2_001_CpG_30.31.32, X083_NF2_001_CpG_33.34, X083_NF2_001_CpG_35.36.37, X083_NF2_001_CpG_38.39, X083_NF2_001_CpG_40.41, X083_NF2_001_CpG_42.43,

	X083_NF2_001_CpG_44.45, X083_NF2_001_CpG_46, X083_NF2_001_CpG_47.48.49, X083_NF2_001_CpG_50, X083_NF2_001_CpG_51, X083_NF2_001_CpG_52, X083_NF2_001_CpG_53, X083_NF2_001_CpG_54, X083_NF2_001_CpG_55.56, X083_NF2_001_CpG_57, X083_NF2_001_CpG_58.59, X083_NF2_001_CpG_60.61.62, X083_NF2_001_CpG_63
X085_NFKB2	X085_NFKB2_002_CpG_1, X085_NFKB2_002_CpG_2.3.4, X085_NFKB2_002_CpG_5.6, X085_NFKB2_002_CpG_7, X085_NFKB2_002_CpG_8, X085_NFKB2_002_CpG_9.10.11, X085_NFKB2_002_CpG_12, X085_NFKB2_002_CpG_13, X085_NFKB2_002_CpG_14, X085_NFKB2_002_CpG_15.16, X085_NFKB2_002_CpG_17, X085_NFKB2_002_CpG_18, X085_NFKB2_002_CpG_19, X085_NFKB2_002_CpG_20, X085_NFKB2_002_CpG_21, X085_NFKB2_002_CpG_22.23
X086_NFKB2	X086_NFKB2_003_CpG_1.2, X086_NFKB2_003_CpG_3.4, X086_NFKB2_003_CpG_5, X086_NFKB2_003_CpG_6, X086_NFKB2_003_CpG_7, X086_NFKB2_003_CpG_8, X086_NFKB2_003_CpG_9.10.11.12, X086_NFKB2_003_CpG_13, X086_NFKB2_003_CpG_14, X086_NFKB2_003_CpG_15.16.17, X086_NFKB2_003_CpG_18, X086_NFKB2_003_CpG_19, X086_NFKB2_003_CpG_20, X086_NFKB2_003_CpG_21, X086_NFKB2_003_CpG_22, X086_NFKB2_003_CpG_23, X086_NFKB2_003_CpG_24, X086_NFKB2_003_CpG_25, X086_NFKB2_003_CpG_26, X086_NFKB2_003_CpG_27, X086_NFKB2_003_CpG_28, X086_NFKB2_003_CpG_29.30
X087_NFKB2	X087_NFKB2_004_CpG_1.2.3, X087_NFKB2_004_CpG_4.5.6, X087_NFKB2_004_CpG_7.8, X087_NFKB2_004_CpG_9, X087_NFKB2_004_CpG_10, X087_NFKB2_004_CpG_11, X087_NFKB2_004_CpG_12, X087_NFKB2_004_CpG_13.14, X087_NFKB2_004_CpG_15, X087_NFKB2_004_CpG_16, X087_NFKB2_004_CpG_17.18, X087_NFKB2_004_CpG_19, X087_NFKB2_004_CpG_20.21.22, X087_NFKB2_004_CpG_23, X087_NFKB2_004_CpG_24.25, X087_NFKB2_004_CpG_26, X087_NFKB2_004_CpG_27, X087_NFKB2_004_CpG_28, X087_NFKB2_004_CpG_29
X088_NFKB2	X088_NFKB2_005_CpG_1, X088_NFKB2_005_CpG_2, X088_NFKB2_005_CpG_3, X088_NFKB2_005_CpG_4.5, X088_NFKB2_005_CpG_6, X088_NFKB2_005_CpG_7, X088_NFKB2_005_CpG_8, X088_NFKB2_005_CpG_9.10, X088_NFKB2_005_CpG_11, X088_NFKB2_005_CpG_12.13, X088_NFKB2_005_CpG_14, X088_NFKB2_005_CpG_15, X088_NFKB2_005_CpG_16, X088_NFKB2_005_CpG_17, X088_NFKB2_005_CpG_18.19, X088_NFKB2_005_CpG_20, X088_NFKB2_005_CpG_21, X088_NFKB2_005_CpG_22, X088_NFKB2_005_CpG_23, X088_NFKB2_005_CpG_24, X088_NFKB2_005_CpG_25, X088_NFKB2_005_CpG_26, X088_NFKB2_005_CpG_27.28, X088_NFKB2_005_CpG_29, X088_NFKB2_005_CpG_30, X088_NFKB2_005_CpG_31, X088_NFKB2_005_CpG_32, X088_NFKB2_005_CpG_33
X089_NIN	X089_NIN_001_CpG_1, X089_NIN_001_CpG_2, X089_NIN_001_CpG_3.4, X089_NIN_001_CpG_5, X089_NIN_001_CpG_6, X089_NIN_001_CpG_7, X089_NIN_001_CpG_8, X089_NIN_001_CpG_9, X089_NIN_001_CpG_10.11, X089_NIN_001_CpG_12, X089_NIN_001_CpG_13, X089_NIN_001_CpG_14, X089_NIN_001_CpG_15
X090_NONO	X090_NONO_001_CpG_1, X090_NONO_001_CpG_2, X090_NONO_001_CpG_3, X090_NONO_001_CpG_4.5.6.7.8.9.10.11.12, X090_NONO_001_CpG_13, X090_NONO_001_CpG_14, X090_NONO_001_CpG_15.16.17, X090_NONO_001_CpG_18, X090_NONO_001_CpG_19, X090_NONO_001_CpG_20, X090_NONO_001_CpG_21, X090_NONO_001_CpG_22, X090_NONO_001_CpG_23.24
X091_NOTCH1	X091_NOTCH1_001_CpG_1.2, X091_NOTCH1_001_CpG_3.4.5.6.7.8, X091_NOTCH1_001_CpG_9, X091_NOTCH1_001_CpG_10, X091_NOTCH1_001_CpG_11.12, X091_NOTCH1_001_CpG_13, X091_NOTCH1_001_CpG_14.15, X091_NOTCH1_001_CpG_16, X091_NOTCH1_001_CpG_17.18.19.20, X091_NOTCH1_001_CpG_21, X091_NOTCH1_001_CpG_22.23
X092_NTRK1	X092_NTRK1_001_CpG_1, X092_NTRK1_001_CpG_2, X092_NTRK1_001_CpG_3.4.5.6.7.8, X092_NTRK1_001_CpG_9, X092_NTRK1_001_CpG_10, X092_NTRK1_001_CpG_11, X092_NTRK1_001_CpG_12, X092_NTRK1_001_CpG_13.14,

	X092_NTRK1_001_CpG_15, X092_NTRK1_001_CpG_16.17.18.19.20, X092_NTRK1_001_CpG_21, X092_NTRK1_001_CpG_22, X092_NTRK1_001_CpG_23.24.25, X092_NTRK1_001_CpG_26.27, X092_NTRK1_001_CpG_28.29.30, X092_NTRK1_001_CpG_31, X092_NTRK1_001_CpG_32.33, X092_NTRK1_001_CpG_34, X092_NTRK1_001_CpG_35, X092_NTRK1_001_CpG_36.37, X092_NTRK1_001_CpG_38.39.40.41.42, X092_NTRK1_001_CpG_43, X092_NTRK1_001_CpG_44.45, X092_NTRK1_001_CpG_46
X093_PAFAH1B2	X093_PAFAH1B2_001_CpG_1, X093_PAFAH1B2_001_CpG_2, X093_PAFAH1B2_001_CpG_3.4, X093_PAFAH1B2_001_CpG_5, X093_PAFAH1B2_001_CpG_6, X093_PAFAH1B2_001_CpG_7, X093_PAFAH1B2_001_CpG_8, X093_PAFAH1B2_001_CpG_9.10, X093_PAFAH1B2_001_CpG_11.12, X093_PAFAH1B2_001_CpG_13, X093_PAFAH1B2_001_CpG_14.15, X093_PAFAH1B2_001_CpG_16.17, X093_PAFAH1B2_001_CpG_18, X093_PAFAH1B2_001_CpG_19, X093_PAFAH1B2_001_CpG_20, X093_PAFAH1B2_001_CpG_21, X093_PAFAH1B2_001_CpG_22, X093_PAFAH1B2_001_CpG_23, X093_PAFAH1B2_001_CpG_24, X093_PAFAH1B2_001_CpG_25, X093_PAFAH1B2_001_CpG_26.27.28, X093_PAFAH1B2_001_CpG_29, X093_PAFAH1B2_001_CpG_30, X093_PAFAH1B2_001_CpG_31, X093_PAFAH1B2_001_CpG_32, X093_PAFAH1B2_001_CpG_33, X093_PAFAH1B2_001_CpG_34, X093_PAFAH1B2_001_CpG_35, X093_PAFAH1B2_001_CpG_36.37, X093_PAFAH1B2_001_CpG_38.39, X093_PAFAH1B2_001_CpG_40, X093_PAFAH1B2_001_CpG_41.42, X093_PAFAH1B2_001_CpG_43
X094_PAX3	X094_PAX3_001_CpG_1, X094_PAX3_001_CpG_2, X094_PAX3_001_CpG_3.4.5, X094_PAX3_001_CpG_6, X094_PAX3_001_CpG_7, X094_PAX3_001_CpG_8.9, X094_PAX3_001_CpG_10.11.12, X094_PAX3_001_CpG_13.14, X094_PAX3_001_CpG_15, X094_PAX3_001_CpG_16.17, X094_PAX3_001_CpG_18, X094_PAX3_001_CpG_19, X094_PAX3_001_CpG_20, X094_PAX3_001_CpG_21.22.23, X094_PAX3_001_CpG_24, X094_PAX3_001_CpG_25, X094_PAX3_001_CpG_26, X094_PAX3_001_CpG_27, X094_PAX3_001_CpG_28.29, X094_PAX3_001_CpG_30, X094_PAX3_001_CpG_31, X094_PAX3_001_CpG_32, X094_PAX3_001_CpG_33, X094_PAX3_001_CpG_34, X094_PAX3_001_CpG_35, X094_PAX3_001_CpG_36, X094_PAX3_001_CpG_37, X094_PAX3_001_CpG_38
X095_PAX5	X095_PAX5_001_CpG_1, X095_PAX5_001_CpG_2, X095_PAX5_001_CpG_3.4.5, X095_PAX5_001_CpG_6, X095_PAX5_001_CpG_7.8, X095_PAX5_001_CpG_9, X095_PAX5_001_CpG_10, X095_PAX5_001_CpG_11, X095_PAX5_001_CpG_12.13.14, X095_PAX5_001_CpG_15.16.17, X095_PAX5_001_CpG_18.19, X095_PAX5_001_CpG_20, X095_PAX5_001_CpG_21.22.23.24, X095_PAX5_001_CpG_25.26, X095_PAX5_001_CpG_27.28, X095_PAX5_001_CpG_29.30.31, X095_PAX5_001_CpG_32, X095_PAX5_001_CpG_33, X095_PAX5_001_CpG_34.35.36
X096_PAX7	X096_PAX7_001_CpG_1, X096_PAX7_001_CpG_2, X096_PAX7_001_CpG_3, X096_PAX7_001_CpG_4, X096_PAX7_001_CpG_5.6, X096_PAX7_001_CpG_7, X096_PAX7_001_CpG_8, X096_PAX7_001_CpG_9, X096_PAX7_001_CpG_10.11, X096_PAX7_001_CpG_12, X096_PAX7_001_CpG_13.14, X096_PAX7_001_CpG_15
X097_PAX7	X097_PAX7_002_CpG_1, X097_PAX7_002_CpG_2, X097_PAX7_002_CpG_3, X097_PAX7_002_CpG_4, X097_PAX7_002_CpG_5, X097_PAX7_002_CpG_6, X097_PAX7_002_CpG_7, X097_PAX7_002_CpG_8.9.10.11, X097_PAX7_002_CpG_12.13, X097_PAX7_002_CpG_14, X097_PAX7_002_CpG_15, X097_PAX7_002_CpG_16.17.18, X097_PAX7_002_CpG_19, X097_PAX7_002_CpG_20, X097_PAX7_002_CpG_21, X097_PAX7_002_CpG_22.23.24, X097_PAX7_002_CpG_25.26.27, X097_PAX7_002_CpG_28, X097_PAX7_002_CpG_29, X097_PAX7_002_CpG_30.31.32.33.34, X097_PAX7_002_CpG_35, X097_PAX7_002_CpG_36.37.38

X098_PBX1	X098_PBX1_001_CpG_1.2, X098_PBX1_001_CpG_3, X098_PBX1_001_CpG_4, X098_PBX1_001_CpG_5.6, X098_PBX1_001_CpG_7, X098_PBX1_001_CpG_8, X098_PBX1_001_CpG_9.10, X098_PBX1_001_CpG_11, X098_PBX1_001_CpG_12.13, X098_PBX1_001_CpG_14.15.16.17.18.19.20.21.22, X098_PBX1_001_CpG_23, X098_PBX1_001_CpG_24, X098_PBX1_001_CpG_25.26.27.28.29, X098_PBX1_001_CpG_30, X098_PBX1_001_CpG_31, X098_PBX1_001_CpG_32, X098_PBX1_001_CpG_33.34, X098_PBX1_001_CpG_35.36.37, X098_PBX1_001_CpG_38.39, X098_PBX1_001_CpG_40, X098_PBX1_001_CpG_41, X098_PBX1_001_CpG_42, X098_PBX1_001_CpG_43.44.45.46.47, X098_PBX1_001_CpG_48, X098_PBX1_001_CpG_49, X098_PBX1_001_CpG_50.51
X100_PER1	X100_PER1_001_CpG_1, X100_PER1_001_CpG_2, X100_PER1_001_CpG_3, X100_PER1_001_CpG_4.5, X100_PER1_001_CpG_6, X100_PER1_001_CpG_7, X100_PER1_001_CpG_8, X100_PER1_001_CpG_9, X100_PER1_001_CpG_10, X100_PER1_001_CpG_11.12.13.14, X100_PER1_001_CpG_15, X100_PER1_001_CpG_16, X100_PER1_001_CpG_17.18.19, X100_PER1_001_CpG_20, X100_PER1_001_CpG_21, X100_PER1_001_CpG_22, X100_PER1_001_CpG_23, X100_PER1_001_CpG_24, X100_PER1_001_CpG_25.26, X100_PER1_001_CpG_27.28, X100_PER1_001_CpG_29.30, X100_PER1_001_CpG_31
X101_PHOX2B	X101_PHOX2B_001_CpG_1, X101_PHOX2B_001_CpG_2, X101_PHOX2B_001_CpG_3, X101_PHOX2B_001_CpG_4, X101_PHOX2B_001_CpG_5.6, X101_PHOX2B_001_CpG_7.8, X101_PHOX2B_001_CpG_9.10.11, X101_PHOX2B_001_CpG_12.13, X101_PHOX2B_001_CpG_14, X101_PHOX2B_001_CpG_15, X101_PHOX2B_001_CpG_16, X101_PHOX2B_001_CpG_17.18, X101_PHOX2B_001_CpG_19, X101_PHOX2B_001_CpG_20.21.22.23, X101_PHOX2B_001_CpG_24.25.26, X101_PHOX2B_001_CpG_27, X101_PHOX2B_001_CpG_28.29.30
X103_PICALM	X103_PICALM_002_CpG_1, X103_PICALM_002_CpG_2, X103_PICALM_002_CpG_3, X103_PICALM_002_CpG_4.5, X103_PICALM_002_CpG_6, X103_PICALM_002_CpG_7, X103_PICALM_002_CpG_8.9, X103_PICALM_002_CpG_10, X103_PICALM_002_CpG_11, X103_PICALM_002_CpG_12.13.14.15.16.17.18.19.20, X103_PICALM_002_CpG_21.22, X103_PICALM_002_CpG_23.24, X103_PICALM_002_CpG_25, X103_PICALM_002_CpG_26, X103_PICALM_002_CpG_27, X103_PICALM_002_CpG_28, X103_PICALM_002_CpG_29
X104_PIK3CA	X104_PIK3CA_001_CpG_1.2, X104_PIK3CA_001_CpG_3, X104_PIK3CA_001_CpG_4.5.6.7.8.9.10, X104_PIK3CA_001_CpG_11, X104_PIK3CA_001_CpG_12.13, X104_PIK3CA_001_CpG_14.15, X104_PIK3CA_001_CpG_16, X104_PIK3CA_001_CpG_17.18.19.20, X104_PIK3CA_001_CpG_21.22, X104_PIK3CA_001_CpG_23.24, X104_PIK3CA_001_CpG_25.26, X104_PIK3CA_001_CpG_27.28, X104_PIK3CA_001_CpG_29.30
X105_PLAG1	X105_PLAG1_001_CpG_1.2.3.4, X105_PLAG1_001_CpG_5, X105_PLAG1_001_CpG_6.7.8.9.10, X105_PLAG1_001_CpG_11, X105_PLAG1_001_CpG_12.13, X105_PLAG1_001_CpG_14.15.16.17, X105_PLAG1_001_CpG_18.19.20, X105_PLAG1_001_CpG_21, X105_PLAG1_001_CpG_22.23.24, X105_PLAG1_001_CpG_25, X105_PLAG1_001_CpG_26
X106_PML	X106_PML_001_CpG_1.2, X106_PML_001_CpG_3, X106_PML_001_CpG_4, X106_PML_001_CpG_5.6, X106_PML_001_CpG_7.8.9, X106_PML_001_CpG_10, X106_PML_001_CpG_11, X106_PML_001_CpG_12, X106_PML_001_CpG_13.14, X106_PML_001_CpG_15, X106_PML_001_CpG_16, X106_PML_001_CpG_17, X106_PML_001_CpG_18, X106_PML_001_CpG_19, X106_PML_001_CpG_20, X106_PML_001_CpG_21.22, X106_PML_001_CpG_23, X106_PML_001_CpG_24, X106_PML_001_CpG_25, X106_PML_001_CpG_26, X106_PML_001_CpG_27
X107_PRDM1	X107_PRDM16_001_CpG_1.2.3.4, X107_PRDM16_001_CpG_5.6, X107_PRDM16_001_CpG_7,

6	X107_PRDM16_001_CpG_8, X107_PRDM16_001_CpG_9, X107_PRDM16_001_CpG_10, X107_PRDM16_001_CpG_11, X107_PRDM16_001_CpG_12, X107_PRDM16_001_CpG_13.14.15, X107_PRDM16_001_CpG_16.17.18.19.20.21.22.23.24, X107_PRDM16_001_CpG_25, X107_PRDM16_001_CpG_26.27, X107_PRDM16_001_CpG_28, X107_PRDM16_001_CpG_29
X108_PSIP2	X108_PSIP2_001_CpG_1, X108_PSIP2_001_CpG_2, X108_PSIP2_001_CpG_3.4, X108_PSIP2_001_CpG_5, X108_PSIP2_001_CpG_6, X108_PSIP2_001_CpG_7, X108_PSIP2_001_CpG_8.9.10.11.12.13, X108_PSIP2_001_CpG_14, X108_PSIP2_001_CpG_15, X108_PSIP2_001_CpG_16, X108_PSIP2_001_CpG_17, X108_PSIP2_001_CpG_18.19, X108_PSIP2_001_CpG_20.21.22, X108_PSIP2_001_CpG_23.24.25.26.27, X108_PSIP2_001_CpG_28.29.30.31, X108_PSIP2_001_CpG_32.33, X108_PSIP2_001_CpG_34, X108_PSIP2_001_CpG_35, X108_PSIP2_001_CpG_36, X108_PSIP2_001_CpG_37, X108_PSIP2_001_CpG_38.39, X108_PSIP2_001_CpG_40, X108_PSIP2_001_CpG_41.42.43.44.45.46.47, X108_PSIP2_001_CpG_48.49.50.51.52.53.54.55, X108_PSIP2_001_CpG_56.57, X108_PSIP2_001_CpG_58, X108_PSIP2_001_CpG_59.60, X108_PSIP2_001_CpG_61, X108_PSIP2_001_CpG_62, X108_PSIP2_001_CpG_63, X108_PSIP2_001_CpG_64
X109_RANBP17	X109_RANBP17_001_CpG_1.2.3.4.5.6, X109_RANBP17_001_CpG_7, X109_RANBP17_001_CpG_8.9, X109_RANBP17_001_CpG_10.11, X109_RANBP17_001_CpG_12, X109_RANBP17_001_CpG_13, X109_RANBP17_001_CpG_14.15, X109_RANBP17_001_CpG_16, X109_RANBP17_001_CpG_17.18.19, X109_RANBP17_001_CpG_20, X109_RANBP17_001_CpG_21, X109_RANBP17_001_CpG_22.23, X109_RANBP17_001_CpG_24, X109_RANBP17_001_CpG_25.26, X109_RANBP17_001_CpG_27.28, X109_RANBP17_001_CpG_29, X109_RANBP17_001_CpG_30.31, X109_RANBP17_001_CpG_32, X109_RANBP17_001_CpG_33.34, X109_RANBP17_001_CpG_35.36, X109_RANBP17_001_CpG_37.38, X109_RANBP17_001_CpG_39.40.41.42.43.44.45, X109_RANBP17_001_CpG_46, X109_RANBP17_001_CpG_47.48.49.50.51.52.53.54, X109_RANBP17_001_CpG_55, X109_RANBP17_001_CpG_56, X109_RANBP17_001_CpG_57, X109_RANBP17_001_CpG_58, X109_RANBP17_001_CpG_59.60, X109_RANBP17_001_CpG_61
X110_RAP1GDS1	X110_RAP1GDS1_001_CpG_1, X110_RAP1GDS1_001_CpG_2.3.4.5, X110_RAP1GDS1_001_CpG_6.7, X110_RAP1GDS1_001_CpG_8.9.10.11.12.13.14.15, X110_RAP1GDS1_001_CpG_16.17.18.19, X110_RAP1GDS1_001_CpG_20.21, X110_RAP1GDS1_001_CpG_22.23.24.25.26.27.28.29.30.31.32.33.34.35, X110_RAP1GDS1_001_CpG_36.37.38.39.40.41, X110_RAP1GDS1_001_CpG_42, X110_RAP1GDS1_001_CpG_43.44.45.46, X110_RAP1GDS1_001_CpG_47.48.49.50, X110_RAP1GDS1_001_CpG_51, X110_RAP1GDS1_001_CpG_52.53, X110_RAP1GDS1_001_CpG_54, X110_RAP1GDS1_001_CpG_55.56
X111_RB1	X111_RB1_001_CpG_1, X111_RB1_001_CpG_2, X111_RB1_001_CpG_3.4.5.6.7, X111_RB1_001_CpG_8, X111_RB1_001_CpG_9, X111_RB1_001_CpG_10, X111_RB1_001_CpG_11.12, X111_RB1_001_CpG_13, X111_RB1_001_CpG_14, X111_RB1_001_CpG_15.16.17.18, X111_RB1_001_CpG_19.20, X111_RB1_001_CpG_21, X111_RB1_001_CpG_22.23.24.25, X111_RB1_001_CpG_26.27.28, X111_RB1_001_CpG_29.30.31, X111_RB1_001_CpG_32.33, X111_RB1_001_CpG_34.35.36, X111_RB1_001_CpG_37, X111_RB1_001_CpG_38, X111_RB1_001_CpG_39, X111_RB1_001_CpG_40.41.42, X111_RB1_001_CpG_43.44.45.46.47.48.49.50, X111_RB1_001_CpG_51.52.53.54, X111_RB1_001_CpG_55, X111_RB1_001_CpG_56, X111_RB1_001_CpG_57, X111_RB1_001_CpG_58.59, X111_RB1_001_CpG_60.61.62.63.64.65, X111_RB1_001_CpG_66, X111_RB1_001_CpG_67.68.69.70

X112_RBM15	X112_RBM15_001_CpG_1, X112_RBM15_001_CpG_2, X112_RBM15_001_CpG_3.4, X112_RBM15_001_CpG_5, X112_RBM15_001_CpG_6.7, X112_RBM15_001_CpG_8, X112_RBM15_001_CpG_9, X112_RBM15_001_CpG_10, X112_RBM15_001_CpG_11.12, X112_RBM15_001_CpG_13.14, X112_RBM15_001_CpG_15.16, X112_RBM15_001_CpG_17.18, X112_RBM15_001_CpG_19.20, X112_RBM15_001_CpG_21, X112_RBM15_001_CpG_22, X112_RBM15_001_CpG_23, X112_RBM15_001_CpG_24, X112_RBM15_001_CpG_25.26, X112_RBM15_001_CpG_27, X112_RBM15_001_CpG_28.29.30, X112_RBM15_001_CpG_31, X112_RBM15_001_CpG_32.33, X112_RBM15_001_CpG_34, X112_RBM15_001_CpG_35
X113_REL	X113_REL_001_CpG_1, X113_REL_001_CpG_2, X113_REL_001_CpG_3, X113_REL_001_CpG_4.5.6.7.8, X113_REL_001_CpG_9.10, X113_REL_001_CpG_11.12, X113_REL_001_CpG_13.14.15, X113_REL_001_CpG_16.17.18, X113_REL_001_CpG_19.20.21, X113_REL_001_CpG_22.23.24.25.26.27.28.29.30.31.32, X113_REL_001_CpG_33.34, X113_REL_001_CpG_35.36, X113_REL_001_CpG_37.38, X113_REL_001_CpG_39, X113_REL_001_CpG_40.41, X113_REL_001_CpG_42, X113_REL_001_CpG_43.44, X113_REL_001_CpG_45.46.47.48, X113_REL_001_CpG_49, X113_REL_001_CpG_50.51, X113_REL_001_CpG_52, X113_REL_001_CpG_53, X113_REL_001_CpG_54, X113_REL_001_CpG_55, X113_REL_001_CpG_56
X114_RET	X114_RET_001_CpG_1.2, X114_RET_001_CpG_3.4, X114_RET_001_CpG_5.6, X114_RET_001_CpG_7, X114_RET_001_CpG_8.9.10, X114_RET_001_CpG_11.12, X114_RET_001_CpG_13.14.15, X114_RET_001_CpG_16, X114_RET_001_CpG_17, X114_RET_001_CpG_18.19, X114_RET_001_CpG_20
X115_RPN1	X115_RPN1_001_CpG_1.2.3, X115_RPN1_001_CpG_4, X115_RPN1_001_CpG_5.6.7.8.9, X115_RPN1_001_CpG_10.11.12, X115_RPN1_001_CpG_13, X115_RPN1_001_CpG_14, X115_RPN1_001_CpG_15, X115_RPN1_001_CpG_16, X115_RPN1_001_CpG_17.18.19, X115_RPN1_001_CpG_20, X115_RPN1_001_CpG_21, X115_RPN1_001_CpG_22, X115_RPN1_001_CpG_23.24, X115_RPN1_001_CpG_25, X115_RPN1_001_CpG_26, X115_RPN1_001_CpG_27.28, X115_RPN1_001_CpG_29, X115_RPN1_001_CpG_30.31, X115_RPN1_001_CpG_32, X115_RPN1_001_CpG_33, X115_RPN1_001_CpG_34.35.36, X115_RPN1_001_CpG_37.38.39.40, X115_RPN1_001_CpG_41.42.43, X115_RPN1_001_CpG_44, X115_RPN1_001_CpG_45, X115_RPN1_001_CpG_46, X115_RPN1_001_CpG_47.48.49, X115_RPN1_001_CpG_50.51, X115_RPN1_001_CpG_52
X116_RUNX1	X116_RUNX1_001_CpG_1.2.3.4.5.6.7, X116_RUNX1_001_CpG_8, X116_RUNX1_001_CpG_9.10.11, X116_RUNX1_001_CpG_12.13.14, X116_RUNX1_001_CpG_15, X116_RUNX1_001_CpG_16, X116_RUNX1_001_CpG_17, X116_RUNX1_001_CpG_18, X116_RUNX1_001_CpG_19, X116_RUNX1_001_CpG_20, X116_RUNX1_001_CpG_21, X116_RUNX1_001_CpG_22, X116_RUNX1_001_CpG_23, X116_RUNX1_001_CpG_24
X117_SBDS	X117_SBDS_001_CpG_1, X117_SBDS_001_CpG_2, X117_SBDS_001_CpG_3, X117_SBDS_001_CpG_4, X117_SBDS_001_CpG_5, X117_SBDS_001_CpG_6, X117_SBDS_001_CpG_7.8, X117_SBDS_001_CpG_9, X117_SBDS_001_CpG_10, X117_SBDS_001_CpG_11.12.13, X117_SBDS_001_CpG_14, X117_SBDS_001_CpG_15, X117_SBDS_001_CpG_16, X117_SBDS_001_CpG_17, X117_SBDS_001_CpG_18.19, X117_SBDS_001_CpG_20, X117_SBDS_001_CpG_21, X117_SBDS_001_CpG_22, X117_SBDS_001_CpG_23, X117_SBDS_001_CpG_24, X117_SBDS_001_CpG_25.26, X117_SBDS_001_CpG_27.28, X117_SBDS_001_CpG_29.30.31, X117_SBDS_001_CpG_32.33.34, X117_SBDS_001_CpG_35, X117_SBDS_001_CpG_36, X117_SBDS_001_CpG_37.38.39.40, X117_SBDS_001_CpG_41.42.43.44.45, X117_SBDS_001_CpG_46
X118_SET	X118_SET_001_CpG_1.2.3, X118_SET_001_CpG_4, X118_SET_001_CpG_5, X118_SET_001_CpG_6, X118_SET_001_CpG_7, X118_SET_001_CpG_8

X119_SFPQ	X119_SFPQ_001_CpG_1.2.3.4.5, X119_SFPQ_001_CpG_6, X119_SFPQ_001_CpG_7.8.9, X119_SFPQ_001_CpG_10.11, X119_SFPQ_001_CpG_12.13, X119_SFPQ_001_CpG_14.15.16, X119_SFPQ_001_CpG_17, X119_SFPQ_001_CpG_18, X119_SFPQ_001_CpG_19.20, X119_SFPQ_001_CpG_21, X119_SFPQ_001_CpG_22, X119_SFPQ_001_CpG_23.24.25.26, X119_SFPQ_001_CpG_27, X119_SFPQ_001_CpG_28.29.30, X119_SFPQ_001_CpG_31.32.33.34.35
X120_SFRS3	X120_SFRS3_001_CpG_1, X120_SFRS3_001_CpG_2, X120_SFRS3_001_CpG_3.4, X120_SFRS3_001_CpG_5, X120_SFRS3_001_CpG_6.7.8.9, X120_SFRS3_001_CpG_10, X120_SFRS3_001_CpG_11, X120_SFRS3_001_CpG_12.13, X120_SFRS3_001_CpG_14, X120_SFRS3_001_CpG_15.16, X120_SFRS3_001_CpG_17.18.19.20, X120_SFRS3_001_CpG_21, X120_SFRS3_001_CpG_22
X121_SIL	X121_SIL_001_CpG_1, X121_SIL_001_CpG_2.3, X121_SIL_001_CpG_4, X121_SIL_001_CpG_5, X121_SIL_001_CpG_6, X121_SIL_001_CpG_7.8, X121_SIL_001_CpG_9.10, X121_SIL_001_CpG_11.12.13, X121_SIL_001_CpG_14, X121_SIL_001_CpG_15.16, X121_SIL_001_CpG_17.18, X121_SIL_001_CpG_19, X121_SIL_001_CpG_20, X121_SIL_001_CpG_21, X121_SIL_001_CpG_22.23, X121_SIL_001_CpG_24.25.26, X121_SIL_001_CpG_27, X121_SIL_001_CpG_28, X121_SIL_001_CpG_29.30, X121_SIL_001_CpG_31.32.33
X122_SS18L1	X122_SS18L1_001_CpG_1.2, X122_SS18L1_001_CpG_3.4.5, X122_SS18L1_001_CpG_6.7, X122_SS18L1_001_CpG_8, X122_SS18L1_001_CpG_9, X122_SS18L1_001_CpG_10, X122_SS18L1_001_CpG_11, X122_SS18L1_001_CpG_12.13.14, X122_SS18L1_001_CpG_15, X122_SS18L1_001_CpG_16.17, X122_SS18L1_001_CpG_18, X122_SS18L1_001_CpG_19, X122_SS18L1_001_CpG_20.21.22, X122_SS18L1_001_CpG_23.24.25.26.27.28, X122_SS18L1_001_CpG_29.30.31.32, X122_SS18L1_001_CpG_33.34.35.36.37
X123_SS18L1	X123_SS18L1_002_CpG_1.2, X123_SS18L1_002_CpG_3, X123_SS18L1_002_CpG_4.5, X123_SS18L1_002_CpG_6.7.8, X123_SS18L1_002_CpG_9.10.11, X123_SS18L1_002_CpG_12.13, X123_SS18L1_002_CpG_14.15.16, X123_SS18L1_002_CpG_17.18, X123_SS18L1_002_CpG_19.20.21.22, X123_SS18L1_002_CpG_23, X123_SS18L1_002_CpG_24.25, X123_SS18L1_002_CpG_26, X123_SS18L1_002_CpG_27, X123_SS18L1_002_CpG_28.29, X123_SS18L1_002_CpG_30, X123_SS18L1_002_CpG_31, X123_SS18L1_002_CpG_32.33.34, X123_SS18L1_002_CpG_35, X123_SS18L1_002_CpG_36, X123_SS18L1_002_CpG_37, X123_SS18L1_002_CpG_38.39, X123_SS18L1_002_CpG_40, X123_SS18L1_002_CpG_41.42, X123_SS18L1_002_CpG_43.44, X123_SS18L1_002_CpG_45.46, X123_SS18L1_002_CpG_47, X123_SS18L1_002_CpG_48, X123_SS18L1_002_CpG_49.50, X123_SS18L1_002_CpG_51, X123_SS18L1_002_CpG_52, X123_SS18L1_002_CpG_53, X123_SS18L1_002_CpG_54, X123_SS18L1_002_CpG_55
X124_SUZ12	X124_SUZ12_001_CpG_1, X124_SUZ12_001_CpG_2.3, X124_SUZ12_001_CpG_4, X124_SUZ12_001_CpG_5.6, X124_SUZ12_001_CpG_7.8, X124_SUZ12_001_CpG_9.10.11.12, X124_SUZ12_001_CpG_13, X124_SUZ12_001_CpG_14.15, X124_SUZ12_001_CpG_16, X124_SUZ12_001_CpG_17.18.19.20, X124_SUZ12_001_CpG_21.22.23, X124_SUZ12_001_CpG_24, X124_SUZ12_001_CpG_25.26, X124_SUZ12_001_CpG_27.28.29.30.31.32.33.34, X124_SUZ12_001_CpG_35.36.37, X124_SUZ12_001_CpG_38, X124_SUZ12_001_CpG_39, X124_SUZ12_001_CpG_40.41, X124_SUZ12_001_CpG_42, X124_SUZ12_001_CpG_43
X125_SYK	X125_SYK_001_CpG_1, X125_SYK_001_CpG_2, X125_SYK_001_CpG_3.4.5, X125_SYK_001_CpG_6, X125_SYK_001_CpG_7, X125_SYK_001_CpG_8, X125_SYK_001_CpG_9, X125_SYK_001_CpG_10.11, X125_SYK_001_CpG_12.13, X125_SYK_001_CpG_14, X125_SYK_001_CpG_15.16.17, X125_SYK_001_CpG_18.19.20.21.22, X125_SYK_001_CpG_23, X125_SYK_001_CpG_24, X125_SYK_001_CpG_25, X125_SYK_001_CpG_26.27, X125_SYK_001_CpG_28, X125_SYK_001_CpG_29.30.31.32, X125_SYK_001_CpG_33.34.35.36.37

X126_TCEA1	X126_TCEA1_001_CpG_1, X126_TCEA1_001_CpG_2, X126_TCEA1_001_CpG_3, X126_TCEA1_001_CpG_4.5, X126_TCEA1_001_CpG_6, X126_TCEA1_001_CpG_7, X126_TCEA1_001_CpG_8, X126_TCEA1_001_CpG_9, X126_TCEA1_001_CpG_10.11.12, X126_TCEA1_001_CpG_13, X126_TCEA1_001_CpG_14, X126_TCEA1_001_CpG_15, X126_TCEA1_001_CpG_16, X126_TCEA1_001_CpG_17.18.19.20.21.22.23.24.25.26, X126_TCEA1_001_CpG_27, X126_TCEA1_001_CpG_28, X126_TCEA1_001_CpG_29.30.31.32, X126_TCEA1_001_CpG_33, X126_TCEA1_001_CpG_34, X126_TCEA1_001_CpG_35, X126_TCEA1_001_CpG_36, X126_TCEA1_001_CpG_37, X126_TCEA1_001_CpG_38.39.40, X126_TCEA1_001_CpG_41.42, X126_TCEA1_001_CpG_43, X126_TCEA1_001_CpG_44.45.46.47, X126_TCEA1_001_CpG_48.49, X126_TCEA1_001_CpG_50.51.52, X126_TCEA1_001_CpG_53, X126_TCEA1_001_CpG_54, X126_TCEA1_001_CpG_55.56, X126_TCEA1_001_CpG_57, X126_TCEA1_001_CpG_58, X126_TCEA1_001_CpG_59
X127_TFEB	X127_TFEB_001_CpG_1, X127_TFEB_001_CpG_2.3.4.5, X127_TFEB_001_CpG_6, X127_TFEB_001_CpG_7, X127_TFEB_001_CpG_8, X127_TFEB_001_CpG_9.10, X127_TFEB_001_CpG_11.12, X127_TFEB_001_CpG_13.14.15.16.17, X127_TFEB_001_CpG_18, X127_TFEB_001_CpG_19.20.21, X127_TFEB_001_CpG_22.23, X127_TFEB_001_CpG_24.25.26.27, X127_TFEB_001_CpG_28.29, X127_TFEB_001_CpG_30.31.32.33, X127_TFEB_001_CpG_34, X127_TFEB_001_CpG_35.36.37, X127_TFEB_001_CpG_38.39.40, X127_TFEB_001_CpG_41.42.43.44.45, X127_TFEB_001_CpG_46, X127_TFEB_001_CpG_47.48.49.50, X127_TFEB_001_CpG_51.52, X127_TFEB_001_CpG_53, X127_TFEB_001_CpG_54
X128_TFG	X128_TFG_001_CpG_1, X128_TFG_001_CpG_2, X128_TFG_001_CpG_3.4.5.6.7.8, X128_TFG_001_CpG_9, X128_TFG_001_CpG_10.11, X128_TFG_001_CpG_12, X128_TFG_001_CpG_13, X128_TFG_001_CpG_14, X128_TFG_001_CpG_15, X128_TFG_001_CpG_16.17, X128_TFG_001_CpG_18.19.20.21, X128_TFG_001_CpG_22, X128_TFG_001_CpG_23, X128_TFG_001_CpG_24.25.26.27, X128_TFG_001_CpG_28, X128_TFG_001_CpG_29, X128_TFG_001_CpG_30.31.32, X128_TFG_001_CpG_33, X128_TFG_001_CpG_34.35.36, X128_TFG_001_CpG_37, X128_TFG_001_CpG_38, X128_TFG_001_CpG_39.40.41.42.43, X128_TFG_001_CpG_44, X128_TFG_001_CpG_45.46.47.48, X128_TFG_001_CpG_49, X128_TFG_001_CpG_50, X128_TFG_001_CpG_51.52, X128_TFG_001_CpG_53.54.55, X128_TFG_001_CpG_56
X129_TFPT	X129_TFPT_001_CpG_1.2, X129_TFPT_001_CpG_3.4, X129_TFPT_001_CpG_5.6.7.8, X129_TFPT_001_CpG_9, X129_TFPT_001_CpG_10, X129_TFPT_001_CpG_11, X129_TFPT_001_CpG_12, X129_TFPT_001_CpG_13.14, X129_TFPT_001_CpG_15.16, X129_TFPT_001_CpG_17, X129_TFPT_001_CpG_18.19, X129_TFPT_001_CpG_20, X129_TFPT_001_CpG_21.22.23, X129_TFPT_001_CpG_24, X129_TFPT_001_CpG_25, X129_TFPT_001_CpG_26, X129_TFPT_001_CpG_27, X129_TFPT_001_CpG_28.29, X129_TFPT_001_CpG_30, X129_TFPT_001_CpG_31
X130_TFRC	X130_TFRC_001_CpG_1, X130_TFRC_001_CpG_2.3, X130_TFRC_001_CpG_4, X130_TFRC_001_CpG_5, X130_TFRC_001_CpG_6, X130_TFRC_001_CpG_7, X130_TFRC_001_CpG_8.9.10.11, X130_TFRC_001_CpG_12, X130_TFRC_001_CpG_13, X130_TFRC_001_CpG_14, X130_TFRC_001_CpG_15, X130_TFRC_001_CpG_16, X130_TFRC_001_CpG_17.18, X130_TFRC_001_CpG_19.20, X130_TFRC_001_CpG_21, X130_TFRC_001_CpG_22, X130_TFRC_001_CpG_23.24.25, X130_TFRC_001_CpG_26.27.28, X130_TFRC_001_CpG_29.30.31, X130_TFRC_001_CpG_32.33, X130_TFRC_001_CpG_34, X130_TFRC_001_CpG_35.36.37, X130_TFRC_001_CpG_38, X130_TFRC_001_CpG_39, X130_TFRC_001_CpG_40, X130_TFRC_001_CpG_41.42.43, X130_TFRC_001_CpG_44, X130_TFRC_001_CpG_45.46, X130_TFRC_001_CpG_47
X131_THRAP3	X131_THRAP3_001_CpG_1, X131_THRAP3_001_CpG_2.3.4, X131_THRAP3_001_CpG_5, X131_THRAP3_001_CpG_6,

	X131_THRAP3_001_CpG_7.8, X131_THRAP3_001_CpG_9, X131_THRAP3_001_CpG_10.11, X131_THRAP3_001_CpG_12, X131_THRAP3_001_CpG_13.14, X131_THRAP3_001_CpG_15, X131_THRAP3_001_CpG_16.17, X131_THRAP3_001_CpG_18.19, X131_THRAP3_001_CpG_20, X131_THRAP3_001_CpG_21, X131_THRAP3_001_CpG_22, X131_THRAP3_001_CpG_23, X131_THRAP3_001_CpG_24.25.26.27.28.29, X131_THRAP3_001_CpG_30, X131_THRAP3_001_CpG_31.32.33.34.35, X131_THRAP3_001_CpG_36.37.38, X131_THRAP3_001_CpG_39
X133_TLX1	X133_TLX1_001_CpG_1.2, X133_TLX1_001_CpG_3, X133_TLX1_001_CpG_4, X133_TLX1_001_CpG_5.6, X133_TLX1_001_CpG_7, X133_TLX1_001_CpG_8, X133_TLX1_001_CpG_9, X133_TLX1_001_CpG_10, X133_TLX1_001_CpG_11, X133_TLX1_001_CpG_12.13.14.15.16, X133_TLX1_001_CpG_17, X133_TLX1_001_CpG_18, X133_TLX1_001_CpG_19, X133_TLX1_001_CpG_20, X133_TLX1_001_CpG_21, X133_TLX1_001_CpG_22
X134_TLX3	X134_TLX3_001_CpG_1.2.3, X134_TLX3_001_CpG_4, X134_TLX3_001_CpG_5, X134_TLX3_001_CpG_6.7, X134_TLX3_001_CpG_8.9.10.11, X134_TLX3_001_CpG_12, X134_TLX3_001_CpG_13.14.15, X134_TLX3_001_CpG_16, X134_TLX3_001_CpG_17, X134_TLX3_001_CpG_18, X134_TLX3_001_CpG_19, X134_TLX3_001_CpG_20.21, X134_TLX3_001_CpG_22, X134_TLX3_001_CpG_23, X134_TLX3_001_CpG_24, X134_TLX3_001_CpG_25.26.27.28, X134_TLX3_001_CpG_29, X134_TLX3_001_CpG_30, X134_TLX3_001_CpG_31, X134_TLX3_001_CpG_32.33, X134_TLX3_001_CpG_34.35, X134_TLX3_001_CpG_36.37, X134_TLX3_001_CpG_38
X135_TMPRSS2	X135_TMPRSS2_001_CpG_1.2.3, X135_TMPRSS2_001_CpG_4, X135_TMPRSS2_001_CpG_5.6.7.8, X135_TMPRSS2_001_CpG_9.10, X135_TMPRSS2_001_CpG_11, X135_TMPRSS2_001_CpG_12, X135_TMPRSS2_001_CpG_13, X135_TMPRSS2_001_CpG_14, X135_TMPRSS2_001_CpG_15.16.17.18, X135_TMPRSS2_001_CpG_19, X135_TMPRSS2_001_CpG_20, X135_TMPRSS2_001_CpG_21.22, X135_TMPRSS2_001_CpG_23, X135_TMPRSS2_001_CpG_24, X135_TMPRSS2_001_CpG_25.26, X135_TMPRSS2_001_CpG_27, X135_TMPRSS2_001_CpG_28, X135_TMPRSS2_001_CpG_29, X135_TMPRSS2_001_CpG_30
X136_TNFRSF6	X136_TNFRSF6_001_CpG_1, X136_TNFRSF6_001_CpG_2, X136_TNFRSF6_001_CpG_3, X136_TNFRSF6_001_CpG_4, X136_TNFRSF6_001_CpG_5, X136_TNFRSF6_001_CpG_6.7.8, X136_TNFRSF6_001_CpG_9.10, X136_TNFRSF6_001_CpG_11, X136_TNFRSF6_001_CpG_12.13, X136_TNFRSF6_001_CpG_14, X136_TNFRSF6_001_CpG_15, X136_TNFRSF6_001_CpG_16, X136_TNFRSF6_001_CpG_17, X136_TNFRSF6_001_CpG_18.19.20.21, X136_TNFRSF6_001_CpG_22.23, X136_TNFRSF6_001_CpG_24.25, X136_TNFRSF6_001_CpG_26.27, X136_TNFRSF6_001_CpG_28, X136_TNFRSF6_001_CpG_29, X136_TNFRSF6_001_CpG_30.31, X136_TNFRSF6_001_CpG_32.33.34, X136_TNFRSF6_001_CpG_35.36.37, X136_TNFRSF6_001_CpG_38, X136_TNFRSF6_001_CpG_39.40.41, X136_TNFRSF6_001_CpG_42
X137_TOP1	X137_TOP1_001_CpG_1.2.3.4, X137_TOP1_001_CpG_5.6.7.8, X137_TOP1_001_CpG_9, X137_TOP1_001_CpG_10, X137_TOP1_001_CpG_11.12, X137_TOP1_001_CpG_13.14, X137_TOP1_001_CpG_15, X137_TOP1_001_CpG_16.17.18, X137_TOP1_001_CpG_19.20.21.22, X137_TOP1_001_CpG_23.24.25.26.27.28.29.30.31, X137_TOP1_001_CpG_32, X137_TOP1_001_CpG_33.34, X137_TOP1_001_CpG_35.36, X137_TOP1_001_CpG_37.38.39.40, X137_TOP1_001_CpG_41.42, X137_TOP1_001_CpG_43, X137_TOP1_001_CpG_44.45, X137_TOP1_001_CpG_46, X137_TOP1_001_CpG_47, X137_TOP1_001_CpG_48.49, X137_TOP1_001_CpG_50.51, X137_TOP1_001_CpG_52.53, X137_TOP1_001_CpG_54, X137_TOP1_001_CpG_55.56, X137_TOP1_001_CpG_57
X138_TP53	X138_TP53_001_CpG_1, X138_TP53_001_CpG_2.3.4, X138_TP53_001_CpG_5.6, X138_TP53_001_CpG_7,

	X138_TP53_001_CpG_8, X138_TP53_001_CpG_9.10, X138_TP53_001_CpG_11, X138_TP53_001_CpG_12, X138_TP53_001_CpG_13, X138_TP53_001_CpG_14.15.16.17.18.19.20.21, X138_TP53_001_CpG_22, X138_TP53_001_CpG_23.24, X138_TP53_001_CpG_25, X138_TP53_001_CpG_26, X138_TP53_001_CpG_27.28, X138_TP53_001_CpG_29, X138_TP53_001_CpG_30, X138_TP53_001_CpG_31.32, X138_TP53_001_CpG_33.34.35.36
X139_TPM3	X139_TPM3_001_CpG_1, X139_TPM3_001_CpG_2.3, X139_TPM3_001_CpG_4.5.6.7.8.9, X139_TPM3_001_CpG_10, X139_TPM3_001_CpG_11, X139_TPM3_001_CpG_12, X139_TPM3_001_CpG_13.14, X139_TPM3_001_CpG_15.16.17, X139_TPM3_001_CpG_18, X139_TPM3_001_CpG_19
X140_TPM4	X140_TPM4_001_CpG_1.2.3.4.5.6, X140_TPM4_001_CpG_7, X140_TPM4_001_CpG_8, X140_TPM4_001_CpG_9, X140_TPM4_001_CpG_10, X140_TPM4_001_CpG_11.12, X140_TPM4_001_CpG_13, X140_TPM4_001_CpG_14, X140_TPM4_001_CpG_15, X140_TPM4_001_CpG_16.17.18.19.20, X140_TPM4_001_CpG_21.22, X140_TPM4_001_CpG_23, X140_TPM4_001_CpG_24, X140_TPM4_001_CpG_25.26, X140_TPM4_001_CpG_27, X140_TPM4_001_CpG_28, X140_TPM4_001_CpG_29, X140_TPM4_001_CpG_30, X140_TPM4_001_CpG_31.32.33.34, X140_TPM4_001_CpG_35, X140_TPM4_001_CpG_36.37.38.39, X140_TPM4_001_CpG_40, X140_TPM4_001_CpG_41.42
X141_TPR	X141_TPR_001_CpG_1.2, X141_TPR_001_CpG_3, X141_TPR_001_CpG_4, X141_TPR_001_CpG_5, X141_TPR_001_CpG_6.7.8, X141_TPR_001_CpG_9.10.11.12.13.14.15.16.17, X141_TPR_001_CpG_18.19.20, X141_TPR_001_CpG_21, X141_TPR_001_CpG_22, X141_TPR_001_CpG_23, X141_TPR_001_CpG_24.25.26, X141_TPR_001_CpG_27, X141_TPR_001_CpG_28.29.30, X141_TPR_001_CpG_31, X141_TPR_001_CpG_32, X141_TPR_001_CpG_33, X141_TPR_001_CpG_34, X141_TPR_001_CpG_35
X142_TRIM33	X142_TRIM33_001_CpG_1, X142_TRIM33_001_CpG_2, X142_TRIM33_001_CpG_3, X142_TRIM33_001_CpG_4, X142_TRIM33_001_CpG_5.6.7, X142_TRIM33_001_CpG_8.9.10.11.12, X142_TRIM33_001_CpG_13.14.15.16, X142_TRIM33_001_CpG_17.18, X142_TRIM33_001_CpG_19, X142_TRIM33_001_CpG_20.21.22, X142_TRIM33_001_CpG_23, X142_TRIM33_001_CpG_24
X143_TRIP11	X143_TRIP11_001_CpG_1, X143_TRIP11_001_CpG_2, X143_TRIP11_001_CpG_3.4.5, X143_TRIP11_001_CpG_6.7, X143_TRIP11_001_CpG_8, X143_TRIP11_001_CpG_9, X143_TRIP11_001_CpG_10.11.12.13, X143_TRIP11_001_CpG_14.15, X143_TRIP11_001_CpG_16.17, X143_TRIP11_001_CpG_18.19, X143_TRIP11_001_CpG_20.21, X143_TRIP11_001_CpG_22, X143_TRIP11_001_CpG_23.24, X143_TRIP11_001_CpG_25, X143_TRIP11_001_CpG_26, X143_TRIP11_001_CpG_27, X143_TRIP11_001_CpG_28.29
X144_TSC1	X144_TSC1_001_CpG_1, X144_TSC1_001_CpG_2, X144_TSC1_001_CpG_3.4.5, X144_TSC1_001_CpG_6, X144_TSC1_001_CpG_7, X144_TSC1_001_CpG_8.9, X144_TSC1_001_CpG_10.11.12.13, X144_TSC1_001_CpG_14.15, X144_TSC1_001_CpG_16, X144_TSC1_001_CpG_17.18.19, X144_TSC1_001_CpG_20, X144_TSC1_001_CpG_21.22, X144_TSC1_001_CpG_23.24.25, X144_TSC1_001_CpG_26, X144_TSC1_001_CpG_27.28, X144_TSC1_001_CpG_29.30, X144_TSC1_001_CpG_31.32.33.34.35, X144_TSC1_001_CpG_36, X144_TSC1_001_CpG_37, X144_TSC1_001_CpG_38.39
X145_TSC2	X145_TSC2_001_CpG_1.2.3, X145_TSC2_001_CpG_4, X145_TSC2_001_CpG_5, X145_TSC2_001_CpG_6.7.8.9.10.11.12, X145_TSC2_001_CpG_13.14.15.16.17.18, X145_TSC2_001_CpG_19.20.21.22.23.24, X145_TSC2_001_CpG_25, X145_TSC2_001_CpG_26, X145_TSC2_001_CpG_27, X145_TSC2_001_CpG_28, X145_TSC2_001_CpG_29, X145_TSC2_001_CpG_30, X145_TSC2_001_CpG_31, X145_TSC2_001_CpG_32.33, X145_TSC2_001_CpG_34.35, X145_TSC2_001_CpG_36, X145_TSC2_001_CpG_37, X145_TSC2_001_CpG_38, X145_TSC2_001_CpG_39.40, X145_TSC2_001_CpG_41, X145_TSC2_001_CpG_42.43
X146_TSHR	X146_TSHR_001_CpG_1, X146_TSHR_001_CpG_2.3, X146_TSHR_001_CpG_4.5, X146_TSHR_001_CpG_6,

	X146_TSHR_001_CpG_7.8, X146_TSHR_001_CpG_9, X146_TSHR_001_CpG_10, X146_TSHR_001_CpG_11, X146_TSHR_001_CpG_12, X146_TSHR_001_CpG_13.14.15, X146_TSHR_001_CpG_16.17, X146_TSHR_001_CpG_18.19, X146_TSHR_001_CpG_20.21.22, X146_TSHR_001_CpG_23.24, X146_TSHR_001_CpG_25.26, X146_TSHR_001_CpG_27
X148_WHSC1L1	X148_WHSC1L1_001_CpG_1.2, X148_WHSC1L1_001_CpG_3.4.5, X148_WHSC1L1_001_CpG_6, X148_WHSC1L1_001_CpG_7, X148_WHSC1L1_001_CpG_8, X148_WHSC1L1_001_CpG_9.10.11.12.13.14.15, X148_WHSC1L1_001_CpG_16.17, X148_WHSC1L1_001_CpG_18, X148_WHSC1L1_001_CpG_19.20.21.22.23.24.25, X148_WHSC1L1_001_CpG_26, X148_WHSC1L1_001_CpG_27, X148_WHSC1L1_001_CpG_28, X148_WHSC1L1_001_CpG_29.30.31, X148_WHSC1L1_001_CpG_32, X148_WHSC1L1_001_CpG_33.34, X148_WHSC1L1_001_CpG_35.36, X148_WHSC1L1_001_CpG_37.38, X148_WHSC1L1_001_CpG_39, X148_WHSC1L1_001_CpG_40.41, X148_WHSC1L1_001_CpG_42.43.44.45, X148_WHSC1L1_001_CpG_46, X148_WHSC1L1_001_CpG_47, X148_WHSC1L1_001_CpG_48, X148_WHSC1L1_001_CpG_49, X148_WHSC1L1_001_CpG_50, X148_WHSC1L1_001_CpG_51, X148_WHSC1L1_001_CpG_52, X148_WHSC1L1_001_CpG_53, X148_WHSC1L1_001_CpG_54
X149_WT1	X149_WT1_001_CpG_1.2.3.4.5.6, X149_WT1_001_CpG_7.8.9.10.11, X149_WT1_001_CpG_12, X149_WT1_001_CpG_13, X149_WT1_001_CpG_14, X149_WT1_001_CpG_15.16.17, X149_WT1_001_CpG_18.19, X149_WT1_001_CpG_20.21.22.23, X149_WT1_001_CpG_24.25.26, X149_WT1_001_CpG_27.28, X149_WT1_001_CpG_29.30, X149_WT1_001_CpG_31, X149_WT1_001_CpG_32.33, X149_WT1_001_CpG_34, X149_WT1_001_CpG_35, X149_WT1_001_CpG_36.37.38.39, X149_WT1_001_CpG_40, X149_WT1_001_CpG_41.42.43.44, X149_WT1_001_CpG_45.46.47
X150_WT1	X150_WT1_002_CpG_1, X150_WT1_002_CpG_2, X150_WT1_002_CpG_3, X150_WT1_002_CpG_4.5.6, X150_WT1_002_CpG_7.8, X150_WT1_002_CpG_9, X150_WT1_002_CpG_10.11, X150_WT1_002_CpG_12.13, X150_WT1_002_CpG_14, X150_WT1_002_CpG_15.16, X150_WT1_002_CpG_17, X150_WT1_002_CpG_18, X150_WT1_002_CpG_19, X150_WT1_002_CpG_20, X150_WT1_002_CpG_21, X150_WT1_002_CpG_22, X150_WT1_002_CpG_23.24.25.26.27, X150_WT1_002_CpG_28
X152_ZNF198	X152_ZNF198_001_CpG_1, X152_ZNF198_001_CpG_2, X152_ZNF198_001_CpG_3, X152_ZNF198_001_CpG_4.5.6.7.8, X152_ZNF198_001_CpG_9, X152_ZNF198_001_CpG_10, X152_ZNF198_001_CpG_11.12, X152_ZNF198_001_CpG_13, X152_ZNF198_001_CpG_14, X152_ZNF198_001_CpG_15, X152_ZNF198_001_CpG_16.17, X152_ZNF198_001_CpG_18.19, X152_ZNF198_001_CpG_20, X152_ZNF198_001_CpG_21.22.23.24
X153_ZNF278	X153_ZNF278_001_CpG_1, X153_ZNF278_001_CpG_2, X153_ZNF278_001_CpG_3.4, X153_ZNF278_001_CpG_5, X153_ZNF278_001_CpG_6, X153_ZNF278_001_CpG_7, X153_ZNF278_001_CpG_8, X153_ZNF278_001_CpG_9, X153_ZNF278_001_CpG_10, X153_ZNF278_001_CpG_11, X153_ZNF278_001_CpG_12, X153_ZNF278_001_CpG_13.14.15, X153_ZNF278_001_CpG_16, X153_ZNF278_001_CpG_17, X153_ZNF278_001_CpG_18, X153_ZNF278_001_CpG_19.20, X153_ZNF278_001_CpG_21, X153_ZNF278_001_CpG_22.23, X153_ZNF278_001_CpG_24, X153_ZNF278_001_CpG_25, X153_ZNF278_001_CpG_26, X153_ZNF278_001_CpG_27, X153_ZNF278_001_CpG_28.29.30
X154_ZNF331	X154_ZNF331_001_CpG_1, X154_ZNF331_001_CpG_2.3, X154_ZNF331_001_CpG_4, X154_ZNF331_001_CpG_5, X154_ZNF331_001_CpG_6.7, X154_ZNF331_001_CpG_8, X154_ZNF331_001_CpG_9, X154_ZNF331_001_CpG_10, X154_ZNF331_001_CpG_11.12, X154_ZNF331_001_CpG_13.14, X154_ZNF331_001_CpG_15.16, X154_ZNF331_001_CpG_17, X154_ZNF331_001_CpG_18, X154_ZNF331_001_CpG_19.20, X154_ZNF331_001_CpG_21, X154_ZNF331_001_CpG_22.23, X154_ZNF331_001_CpG_24

X155_ZNF384	X155_ZNF384_001_CpG_1, X155_ZNF384_001_CpG_2, X155_ZNF384_001_CpG_3.4, X155_ZNF384_001_CpG_5, X155_ZNF384_001_CpG_6, X155_ZNF384_001_CpG_7, X155_ZNF384_001_CpG_8, X155_ZNF384_001_CpG_9, X155_ZNF384_001_CpG_10.11.12, X155_ZNF384_001_CpG_13.14, X155_ZNF384_001_CpG_15, X155_ZNF384_001_CpG_16.17, X155_ZNF384_001_CpG_18, X155_ZNF384_001_CpG_19, X155_ZNF384_001_CpG_20, X155_ZNF384_001_CpG_21.22, X155_ZNF384_001_CpG_23, X155_ZNF384_001_CpG_24, X155_ZNF384_001_CpG_25, X155_ZNF384_001_CpG_26.27
X156_ZNF9	X156_ZNF9_001_CpG_1, X156_ZNF9_001_CpG_2.3, X156_ZNF9_001_CpG_4, X156_ZNF9_001_CpG_5.6.7, X156_ZNF9_001_CpG_8.9.10, X156_ZNF9_001_CpG_11.12, X156_ZNF9_001_CpG_13.14.15.16, X156_ZNF9_001_CpG_17.18.19, X156_ZNF9_001_CpG_20, X156_ZNF9_001_CpG_21.22.23.24.25.26.27, X156_ZNF9_001_CpG_28.29.30.31.32.33.34, X156_ZNF9_001_CpG_35.36, X156_ZNF9_001_CpG_37.38.39, X156_ZNF9_001_CpG_40.41
X003_IGF2R	X003_IGF2R_003_CpG_1, X003_IGF2R_003_CpG_2, X003_IGF2R_003_CpG_3.4, X003_IGF2R_003_CpG_5, X003_IGF2R_003_CpG_6, X003_IGF2R_003_CpG_7.8, X003_IGF2R_003_CpG_9, X003_IGF2R_003_CpG_10, X003_IGF2R_003_CpG_11, X003_IGF2R_003_CpG_12, X003_IGF2R_003_CpG_13, X003_IGF2R_003_CpG_14, X003_IGF2R_003_CpG_15.16, X003_IGF2R_003_CpG_17.18, X003_IGF2R_003_CpG_19.20, X003_IGF2R_003_CpG_21, X003_IGF2R_003_CpG_22.23, X003_IGF2R_003_CpG_24, X003_IGF2R_003_CpG_25, X003_IGF2R_003_CpG_26.27, X003_IGF2R_003_CpG_28, X003_IGF2R_003_CpG_29, X003_IGF2R_003_CpG_30.31, X003_IGF2R_003_CpG_32, X003_IGF2R_003_CpG_33, X003_IGF2R_003_CpG_34.35, X003_IGF2R_003_CpG_36, X003_IGF2R_003_CpG_37, X003_IGF2R_003_CpG_38.39, X003_IGF2R_003_CpG_40, X003_IGF2R_003_CpG_41.42, X003_IGF2R_003_CpG_43, X003_IGF2R_003_CpG_44, X003_IGF2R_003_CpG_45
X005_SLC22A2	X005_SLC22A2_001_CpG_1, X005_SLC22A2_001_CpG_2, X005_SLC22A2_001_CpG_3, X005_SLC22A2_001_CpG_4.5, X005_SLC22A2_001_CpG_6.7, X005_SLC22A2_001_CpG_8, X005_SLC22A2_001_CpG_9, X005_SLC22A2_001_CpG_10, X005_SLC22A2_001_CpG_11, X005_SLC22A2_001_CpG_12, X005_SLC22A2_001_CpG_13.14, X005_SLC22A2_001_CpG_15, X005_SLC22A2_001_CpG_16, X005_SLC22A2_001_CpG_17, X005_SLC22A2_001_CpG_18, X005_SLC22A2_001_CpG_19, X005_SLC22A2_001_CpG_20.21, X005_SLC22A2_001_CpG_22
X006_SLC22A3	X006_SLC22A3_001_CpG_1, X006_SLC22A3_001_CpG_2, X006_SLC22A3_001_CpG_3.4, X006_SLC22A3_001_CpG_5, X006_SLC22A3_001_CpG_6, X006_SLC22A3_001_CpG_7.8.9.10.11.12.13, X006_SLC22A3_001_CpG_14, X006_SLC22A3_001_CpG_15.16, X006_SLC22A3_001_CpG_17, X006_SLC22A3_001_CpG_18, X006_SLC22A3_001_CpG_19, X006_SLC22A3_001_CpG_20
X009_SGCE	X009_SGCE_001_CpG_1, X009_SGCE_001_CpG_2.3, X009_SGCE_001_CpG_4.5, X009_SGCE_001_CpG_6.7, X009_SGCE_001_CpG_8, X009_SGCE_001_CpG_9, X009_SGCE_001_CpG_10.11.12, X009_SGCE_001_CpG_13.14.15.16, X009_SGCE_001_CpG_17.18, X009_SGCE_001_CpG_19.20, X009_SGCE_001_CpG_21, X009_SGCE_001_CpG_22
X011_PON1	X011_PON1_001_CpG_1, X011_PON1_001_CpG_2, X011_PON1_001_CpG_3, X011_PON1_001_CpG_4, X011_PON1_001_CpG_5, X011_PON1_001_CpG_6, X011_PON1_001_CpG_7, X011_PON1_001_CpG_8, X011_PON1_001_CpG_9.10, X011_PON1_001_CpG_11.12.13.14.15, X011_PON1_001_CpG_16, X011_PON1_001_CpG_17.18, X011_PON1_001_CpG_19, X011_PON1_001_CpG_20
X013_PON2	X013_PON2_001_CpG_1.2, X013_PON2_001_CpG_3, X013_PON2_001_CpG_4.5, X013_PON2_001_CpG_6.7,

	X013_PON2_001_CpG_8, X013_PON2_001_CpG_9.10, X013_PON2_001_CpG_11.12.13, X013_PON2_001_CpG_14, X013_PON2_001_CpG_15, X013_PON2_001_CpG_16.17, X013_PON2_001_CpG_18, X013_PON2_001_CpG_19.20, X013_PON2_001_CpG_21.22.23.24.25, X013_PON2_001_CpG_26.27, X013_PON2_001_CpG_28.29, X013_PON2_001_CpG_30.31.32.33.34.35, X013_PON2_001_CpG_36, X013_PON2_001_CpG_37.38.39.40, X013_PON2_001_CpG_41
X018_MESTIT1	X018_MESTIT1_001_CpG_1.2, X018_MESTIT1_001_CpG_3.4, X018_MESTIT1_001_CpG_5, X018_MESTIT1_001_CpG_6.7, X018_MESTIT1_001_CpG_8, X018_MESTIT1_001_CpG_9, X018_MESTIT1_001_CpG_10.11.12, X018_MESTIT1_001_CpG_13.14, X018_MESTIT1_001_CpG_15.16, X018_MESTIT1_001_CpG_17, X018_MESTIT1_001_CpG_18, X018_MESTIT1_001_CpG_19.20, X018_MESTIT1_001_CpG_21, X018_MESTIT1_001_CpG_22, X018_MESTIT1_001_CpG_23.24, X018_MESTIT1_001_CpG_25, X018_MESTIT1_001_CpG_26.27, X018_MESTIT1_001_CpG_28, X018_MESTIT1_001_CpG_29, X018_MESTIT1_001_CpG_30.31, X018_MESTIT1_001_CpG_32, X018_MESTIT1_001_CpG_33, X018_MESTIT1_001_CpG_34
X019_COPG2	X019_COPG2_001_CpG_1, X019_COPG2_001_CpG_2, X019_COPG2_001_CpG_3.4.5, X019_COPG2_001_CpG_6.7.8.9, X019_COPG2_001_CpG_10, X019_COPG2_001_CpG_11, X019_COPG2_001_CpG_12, X019_COPG2_001_CpG_13, X019_COPG2_001_CpG_14
X023_SYTB	X023_SYTB_001_CpG_1, X023_SYTB_001_CpG_2, X023_SYTB_001_CpG_3, X023_SYTB_001_CpG_4, X023_SYTB_001_CpG_5, X023_SYTB_001_CpG_6, X023_SYTB_001_CpG_7, X023_SYTB_001_CpG_8, X023_SYTB_001_CpG_9, X023_SYTB_001_CpG_10, X023_SYTB_001_CpG_11, X023_SYTB_001_CpG_12, X023_SYTB_001_CpG_13, X023_SYTB_001_CpG_14, X023_SYTB_001_CpG_15, X023_SYTB_001_CpG_16.17.18
X025_LSP1	X025_LSP1_002_CpG_1, X025_LSP1_002_CpG_2.3, X025_LSP1_002_CpG_4.5, X025_LSP1_002_CpG_6, X025_LSP1_002_CpG_7, X025_LSP1_002_CpG_8.9.10, X025_LSP1_002_CpG_11.12.13.14, X025_LSP1_002_CpG_15, X025_LSP1_002_CpG_16, X025_LSP1_002_CpG_17.18, X025_LSP1_002_CpG_19
X026_TNNT3	X026_TNNT3_001_CpG_1.2.3, X026_TNNT3_001_CpG_4.5.6, X026_TNNT3_001_CpG_7, X026_TNNT3_001_CpG_8.9, X026_TNNT3_001_CpG_10, X026_TNNT3_001_CpG_11, X026_TNNT3_001_CpG_12, X026_TNNT3_001_CpG_13, X026_TNNT3_001_CpG_14.15.16.17, X026_TNNT3_001_CpG_18, X026_TNNT3_001_CpG_19, X026_TNNT3_001_CpG_20
X027_TNNT3	X027_TNNT3_002_CpG_1, X027_TNNT3_002_CpG_2.3.4, X027_TNNT3_002_CpG_5, X027_TNNT3_002_CpG_6.7, X027_TNNT3_002_CpG_8, X027_TNNT3_002_CpG_9, X027_TNNT3_002_CpG_10, X027_TNNT3_002_CpG_11, X027_TNNT3_002_CpG_12, X027_TNNT3_002_CpG_13.14.15, X027_TNNT3_002_CpG_16, X027_TNNT3_002_CpG_17, X027_TNNT3_002_CpG_18, X027_TNNT3_002_CpG_19, X027_TNNT3_002_CpG_20, X027_TNNT3_002_CpG_21.22
X028_TNNT3	X028_TNNT3_003_CpG_1, X028_TNNT3_003_CpG_2, X028_TNNT3_003_CpG_3, X028_TNNT3_003_CpG_4, X028_TNNT3_003_CpG_5, X028_TNNT3_003_CpG_6.7, X028_TNNT3_003_CpG_8.9.10
X030_MRPL23	X030_MRPL23_001_CpG_1.2.3, X030_MRPL23_001_CpG_4, X030_MRPL23_001_CpG_5.6.7, X030_MRPL23_001_CpG_8, X030_MRPL23_001_CpG_9.10, X030_MRPL23_001_CpG_11, X030_MRPL23_001_CpG_12, X030_MRPL23_001_CpG_13, X030_MRPL23_001_CpG_14.15, X030_MRPL23_001_CpG_16.17, X030_MRPL23_001_CpG_18, X030_MRPL23_001_CpG_19.20, X030_MRPL23_001_CpG_21, X030_MRPL23_001_CpG_22.23.24.25
X031_MRPL23	X031_MRPL23_002_CpG_1, X031_MRPL23_002_CpG_2.3, X031_MRPL23_002_CpG_4, X031_MRPL23_002_CpG_5, X031_MRPL23_002_CpG_6, X031_MRPL23_002_CpG_7, X031_MRPL23_002_CpG_8, X031_MRPL23_002_CpG_9, X031_MRPL23_002_CpG_10, X031_MRPL23_002_CpG_11, X031_MRPL23_002_CpG_12.13.14,

	X031_MRPL23_002_CpG_15, X031_MRPL23_002_CpG_16, X031_MRPL23_002_CpG_17
X032_MRPL23	X032_MRPL23_003_CpG_1, X032_MRPL23_003_CpG_2, X032_MRPL23_003_CpG_3, X032_MRPL23_003_CpG_4.5, X032_MRPL23_003_CpG_6, X032_MRPL23_003_CpG_7, X032_MRPL23_003_CpG_8, X032_MRPL23_003_CpG_9.10.11.12.13, X032_MRPL23_003_CpG_14, X032_MRPL23_003_CpG_15, X032_MRPL23_003_CpG_16.17
X034_MRPL23	X034_MRPL23_005_CpG_1.2, X034_MRPL23_005_CpG_3, X034_MRPL23_005_CpG_4, X034_MRPL23_005_CpG_5, X034_MRPL23_005_CpG_6, X034_MRPL23_005_CpG_7, X034_MRPL23_005_CpG_8, X034_MRPL23_005_CpG_9, X034_MRPL23_005_CpG_10, X034_MRPL23_005_CpG_11, X034_MRPL23_005_CpG_12
X035_MRPL23	X035_MRPL23_006_CpG_1, X035_MRPL23_006_CpG_2.3, X035_MRPL23_006_CpG_4.5.6.7.8.9, X035_MRPL23_006_CpG_10.11.12.13.14.15, X035_MRPL23_006_CpG_16, X035_MRPL23_006_CpG_17, X035_MRPL23_006_CpG_18, X035_MRPL23_006_CpG_19, X035_MRPL23_006_CpG_20, X035_MRPL23_006_CpG_21, X035_MRPL23_006_CpG_22, X035_MRPL23_006_CpG_23, X035_MRPL23_006_CpG_24.25, X035_MRPL23_006_CpG_26.27
X036_MRPL23	X036_MRPL23_007_CpG_1, X036_MRPL23_007_CpG_2, X036_MRPL23_007_CpG_3, X036_MRPL23_007_CpG_4, X036_MRPL23_007_CpG_5, X036_MRPL23_007_CpG_6.7, X036_MRPL23_007_CpG_8, X036_MRPL23_007_CpG_9, X036_MRPL23_007_CpG_10, X036_MRPL23_007_CpG_11.12, X036_MRPL23_007_CpG_13
X040_H19	X040_H19_004_CpG_1, X040_H19_004_CpG_2, X040_H19_004_CpG_3, X040_H19_004_CpG_4, X040_H19_004_CpG_5, X040_H19_004_CpG_6, X040_H19_004_CpG_7, X040_H19_004_CpG_8, X040_H19_004_CpG_9, X040_H19_004_CpG_10, X040_H19_004_CpG_11, X040_H19_004_CpG_12, X040_H19_004_CpG_13, X040_H19_004_CpG_14, X040_H19_004_CpG_15, X040_H19_004_CpG_16, X040_H19_004_CpG_17, X040_H19_004_CpG_18, X040_H19_004_CpG_19, X040_H19_004_CpG_20, X040_H19_004_CpG_21, X040_H19_004_CpG_22, X040_H19_004_CpG_23, X040_H19_004_CpG_24, X040_H19_004_CpG_25, X040_H19_004_CpG_26, X040_H19_004_CpG_27, X040_H19_004_CpG_28, X040_H19_004_CpG_29, X040_H19_004_CpG_30, X040_H19_004_CpG_31, X040_H19_004_CpG_32, X040_H19_004_CpG_33, X040_H19_004_CpG_34, X040_H19_004_CpG_35, X040_H19_004_CpG_36, X040_H19_004_CpG_37, X040_H19_004_CpG_38
X042_IGF2	X042_IGF2_001_CpG_1, X042_IGF2_001_CpG_2, X042_IGF2_001_CpG_3, X042_IGF2_001_CpG_4.5, X042_IGF2_001_CpG_6.7, X042_IGF2_001_CpG_8, X042_IGF2_001_CpG_9, X042_IGF2_001_CpG_10.11.12, X042_IGF2_001_CpG_13, X042_IGF2_001_CpG_14, X042_IGF2_001_CpG_15.16, X042_IGF2_001_CpG_17, X042_IGF2_001_CpG_18, X042_IGF2_001_CpG_19.20, X042_IGF2_001_CpG_21, X042_IGF2_001_CpG_22, X042_IGF2_001_CpG_23, X042_IGF2_001_CpG_24
X044_IGF2	X044_IGF2_003_CpG_1.2, X044_IGF2_003_CpG_3, X044_IGF2_003_CpG_4.5.6.7, X044_IGF2_003_CpG_8.9.10, X044_IGF2_003_CpG_11, X044_IGF2_003_CpG_12, X044_IGF2_003_CpG_13, X044_IGF2_003_CpG_14.15.16.17, X044_IGF2_003_CpG_18, X044_IGF2_003_CpG_19.20.21, X044_IGF2_003_CpG_22, X044_IGF2_003_CpG_23, X044_IGF2_003_CpG_24.25, X044_IGF2_003_CpG_26, X044_IGF2_003_CpG_27.28, X044_IGF2_003_CpG_29.30.31.32.33.34, X044_IGF2_003_CpG_35.36, X044_IGF2_003_CpG_37.38
X047_ASCL2	X047_ASCL2_001_CpG_1.2.3.4, X047_ASCL2_001_CpG_5.6, X047_ASCL2_001_CpG_7, X047_ASCL2_001_CpG_8.9.10.11.12, X047_ASCL2_001_CpG_13.14.15, X047_ASCL2_001_CpG_16.17.18.19.20.21.22.23.24.25.26, X047_ASCL2_001_CpG_27, X047_ASCL2_001_CpG_28, X047_ASCL2_001_CpG_29.30.31.32, X047_ASCL2_001_CpG_33, X047_ASCL2_001_CpG_34,

	X047_ASCL2_001_CpG_35.36, X047_ASCL2_001_CpG_37.38, X047_ASCL2_001_CpG_39.40, X047_ASCL2_001_CpG_41.42, X047_ASCL2_001_CpG_43.44, X047_ASCL2_001_CpG_45.46.47.48, X047_ASCL2_001_CpG_49, X047_ASCL2_001_CpG_50, X047_ASCL2_001_CpG_51, X047_ASCL2_001_CpG_52, X047_ASCL2_001_CpG_53.54.55, X047_ASCL2_001_CpG_56.57, X047_ASCL2_001_CpG_58, X047_ASCL2_001_CpG_59
X051_BC050616	X051_BC050616_001_CpG_1.2, X051_BC050616_001_CpG_3, X051_BC050616_001_CpG_4, X051_BC050616_001_CpG_5, X051_BC050616_001_CpG_6, X051_BC050616_001_CpG_7, X051_BC050616_001_CpG_8.9, X051_BC050616_001_CpG_10, X051_BC050616_001_CpG_11, X051_BC050616_001_CpG_12, X051_BC050616_001_CpG_13.14, X051_BC050616_001_CpG_15, X051_BC050616_001_CpG_16.17, X051_BC050616_001_CpG_18, X051_BC050616_001_CpG_19, X051_BC050616_001_CpG_20, X051_BC050616_001_CpG_21.22.23, X051_BC050616_001_CpG_24, X051_BC050616_001_CpG_25.26.27.28.29, X051_BC050616_001_CpG_30, X051_BC050616_001_CpG_31, X051_BC050616_001_CpG_32, X051_BC050616_001_CpG_33
X052_TRPM5	X052_TRPM5_001_CpG_1.2.3, X052_TRPM5_001_CpG_4, X052_TRPM5_001_CpG_5.6, X052_TRPM5_001_CpG_7, X052_TRPM5_001_CpG_8, X052_TRPM5_001_CpG_9, X052_TRPM5_001_CpG_10, X052_TRPM5_001_CpG_11.12, X052_TRPM5_001_CpG_13.14.15, X052_TRPM5_001_CpG_16, X052_TRPM5_001_CpG_17, X052_TRPM5_001_CpG_18, X052_TRPM5_001_CpG_19, X052_TRPM5_001_CpG_20.21, X052_TRPM5_001_CpG_22.23, X052_TRPM5_001_CpG_24, X052_TRPM5_001_CpG_25.26, X052_TRPM5_001_CpG_27, X052_TRPM5_001_CpG_28, X052_TRPM5_001_CpG_29, X052_TRPM5_001_CpG_30, X052_TRPM5_001_CpG_31, X052_TRPM5_001_CpG_32
X053_TRPM5	X053_TRPM5_002_CpG_1.2, X053_TRPM5_002_CpG_3.4, X053_TRPM5_002_CpG_5.6, X053_TRPM5_002_CpG_7, X053_TRPM5_002_CpG_8.9.10, X053_TRPM5_002_CpG_11, X053_TRPM5_002_CpG_12, X053_TRPM5_002_CpG_13.14, X053_TRPM5_002_CpG_15, X053_TRPM5_002_CpG_16.17, X053_TRPM5_002_CpG_18.19, X053_TRPM5_002_CpG_20, X053_TRPM5_002_CpG_21, X053_TRPM5_002_CpG_22, X053_TRPM5_002_CpG_23, X053_TRPM5_002_CpG_24, X053_TRPM5_002_CpG_25.26, X053_TRPM5_002_CpG_27.28, X053_TRPM5_002_CpG_29.30
X054_KCNQ1	X054_KCNQ1_001_CpG_1, X054_KCNQ1_001_CpG_2, X054_KCNQ1_001_CpG_3, X054_KCNQ1_001_CpG_4, X054_KCNQ1_001_CpG_5.6.7, X054_KCNQ1_001_CpG_8.9.10, X054_KCNQ1_001_CpG_11.12, X054_KCNQ1_001_CpG_13.14, X054_KCNQ1_001_CpG_15, X054_KCNQ1_001_CpG_16, X054_KCNQ1_001_CpG_17.18.19.20.21, X054_KCNQ1_001_CpG_22, X054_KCNQ1_001_CpG_23, X054_KCNQ1_001_CpG_24, X054_KCNQ1_001_CpG_25
X055_KCNQ1	X055_KCNQ1_002_CpG_1, X055_KCNQ1_002_CpG_2.3, X055_KCNQ1_002_CpG_4, X055_KCNQ1_002_CpG_5, X055_KCNQ1_002_CpG_6, X055_KCNQ1_002_CpG_7.8, X055_KCNQ1_002_CpG_9, X055_KCNQ1_002_CpG_10.11, X055_KCNQ1_002_CpG_12, X055_KCNQ1_002_CpG_13
X056_KCNQ1	X056_KCNQ1_003_CpG_1, X056_KCNQ1_003_CpG_2.3.4, X056_KCNQ1_003_CpG_5, X056_KCNQ1_003_CpG_6.7, X056_KCNQ1_003_CpG_8, X056_KCNQ1_003_CpG_9.10, X056_KCNQ1_003_CpG_11, X056_KCNQ1_003_CpG_12.13, X056_KCNQ1_003_CpG_14.15, X056_KCNQ1_003_CpG_16, X056_KCNQ1_003_CpG_17, X056_KCNQ1_003_CpG_18, X056_KCNQ1_003_CpG_19
X057_KCNQ1	X057_KCNQ1_004_CpG_1, X057_KCNQ1_004_CpG_2.3, X057_KCNQ1_004_CpG_4, X057_KCNQ1_004_CpG_5, X057_KCNQ1_004_CpG_6.7, X057_KCNQ1_004_CpG_8, X057_KCNQ1_004_CpG_9, X057_KCNQ1_004_CpG_10, X057_KCNQ1_004_CpG_11.12.13, X057_KCNQ1_004_CpG_14.15, X057_KCNQ1_004_CpG_16
X058_KCNQ1	X058_KCNQ1_005_CpG_1, X058_KCNQ1_005_CpG_2, X058_KCNQ1_005_CpG_3, X058_KCNQ1_005_CpG_4.5,

	X058_KCNQ1_005_CpG_6.7, X058_KCNQ1_005_CpG_8, X058_KCNQ1_005_CpG_9, X058_KCNQ1_005_CpG_10, X058_KCNQ1_005_CpG_11, X058_KCNQ1_005_CpG_12, X058_KCNQ1_005_CpG_13, X058_KCNQ1_005_CpG_14, X058_KCNQ1_005_CpG_15, X058_KCNQ1_005_CpG_16.17, X058_KCNQ1_005_CpG_18, X058_KCNQ1_005_CpG_19.20, X058_KCNQ1_005_CpG_21, X058_KCNQ1_005_CpG_22, X058_KCNQ1_005_CpG_23, X058_KCNQ1_005_CpG_24
X059_KCNQ1	X059_KCNQ1_006_CpG_1, X059_KCNQ1_006_CpG_2, X059_KCNQ1_006_CpG_3, X059_KCNQ1_006_CpG_4, X059_KCNQ1_006_CpG_5, X059_KCNQ1_006_CpG_6.7.8, X059_KCNQ1_006_CpG_9.10, X059_KCNQ1_006_CpG_11, X059_KCNQ1_006_CpG_12, X059_KCNQ1_006_CpG_13, X059_KCNQ1_006_CpG_14, X059_KCNQ1_006_CpG_15.16.17, X059_KCNQ1_006_CpG_18, X059_KCNQ1_006_CpG_19.20.21, X059_KCNQ1_006_CpG_22
X060_KCNQ1	X060_KCNQ1_007_CpG_1, X060_KCNQ1_007_CpG_2.3.4.5, X060_KCNQ1_007_CpG_6, X060_KCNQ1_007_CpG_7, X060_KCNQ1_007_CpG_8, X060_KCNQ1_007_CpG_9, X060_KCNQ1_007_CpG_10, X060_KCNQ1_007_CpG_11, X060_KCNQ1_007_CpG_12.13, X060_KCNQ1_007_CpG_14, X060_KCNQ1_007_CpG_15.16.17, X060_KCNQ1_007_CpG_18
X061_KCNQ1	X061_KCNQ1_008_CpG_1, X061_KCNQ1_008_CpG_2, X061_KCNQ1_008_CpG_3.4.5, X061_KCNQ1_008_CpG_6, X061_KCNQ1_008_CpG_7, X061_KCNQ1_008_CpG_8.9, X061_KCNQ1_008_CpG_10.11.12, X061_KCNQ1_008_CpG_13.14, X061_KCNQ1_008_CpG_15, X061_KCNQ1_008_CpG_16, X061_KCNQ1_008_CpG_17.18, X061_KCNQ1_008_CpG_19, X061_KCNQ1_008_CpG_20, X061_KCNQ1_008_CpG_21, X061_KCNQ1_008_CpG_22, X061_KCNQ1_008_CpG_23, X061_KCNQ1_008_CpG_24, X061_KCNQ1_008_CpG_25, X061_KCNQ1_008_CpG_26.27
X063_KCNQ1	X063_KCNQ1_010_CpG_1.2, X063_KCNQ1_010_CpG_3.4.5, X063_KCNQ1_010_CpG_6, X063_KCNQ1_010_CpG_7, X063_KCNQ1_010_CpG_8.9, X063_KCNQ1_010_CpG_10.11, X063_KCNQ1_010_CpG_12.13.14, X063_KCNQ1_010_CpG_15, X063_KCNQ1_010_CpG_16, X063_KCNQ1_010_CpG_17.18, X063_KCNQ1_010_CpG_19, X063_KCNQ1_010_CpG_20, X063_KCNQ1_010_CpG_21, X063_KCNQ1_010_CpG_22
X068_CDKN1C	X068_CDKN1C_001_CpG_1, X068_CDKN1C_001_CpG_2, X068_CDKN1C_001_CpG_3, X068_CDKN1C_001_CpG_4.5, X068_CDKN1C_001_CpG_6.7.8, X068_CDKN1C_001_CpG_9, X068_CDKN1C_001_CpG_10, X068_CDKN1C_001_CpG_11, X068_CDKN1C_001_CpG_12.13.14, X068_CDKN1C_001_CpG_15
X070_SLC22A18	X070_SLC22A18_001_CpG_1, X070_SLC22A18_001_CpG_2, X070_SLC22A18_001_CpG_3.4, X070_SLC22A18_001_CpG_5, X070_SLC22A18_001_CpG_6, X070_SLC22A18_001_CpG_7, X070_SLC22A18_001_CpG_8, X070_SLC22A18_001_CpG_9, X070_SLC22A18_001_CpG_10, X070_SLC22A18_001_CpG_11, X070_SLC22A18_001_CpG_12, X070_SLC22A18_001_CpG_13, X070_SLC22A18_001_CpG_14, X070_SLC22A18_001_CpG_15, X070_SLC22A18_001_CpG_16.17, X070_SLC22A18_001_CpG_18.19, X070_SLC22A18_001_CpG_20.21, X070_SLC22A18_001_CpG_22, X070_SLC22A18_001_CpG_23, X070_SLC22A18_001_CpG_24, X070_SLC22A18_001_CpG_25, X070_SLC22A18_001_CpG_26, X070_SLC22A18_001_CpG_27, X070_SLC22A18_001_CpG_28
X071_SLC22A18	X071_SLC22A18_002_CpG_1, X071_SLC22A18_002_CpG_2.3, X071_SLC22A18_002_CpG_4, X071_SLC22A18_002_CpG_5, X071_SLC22A18_002_CpG_6, X071_SLC22A18_002_CpG_7.8, X071_SLC22A18_002_CpG_9, X071_SLC22A18_002_CpG_10.11, X071_SLC22A18_002_CpG_12, X071_SLC22A18_002_CpG_13.14.15.16.17.18, X071_SLC22A18_002_CpG_19.20, X071_SLC22A18_002_CpG_21.22, X071_SLC22A18_002_CpG_23.24, X071_SLC22A18_002_CpG_25.26.27.28, X071_SLC22A18_002_CpG_29, X071_SLC22A18_002_CpG_30, X071_SLC22A18_002_CpG_31, X071_SLC22A18_002_CpG_32.33, X071_SLC22A18_002_CpG_34, X071_SLC22A18_002_CpG_35, X071_SLC22A18_002_CpG_36.37.38.39

X074_NAP1L4	X074_NAP1L4_001_CpG_1, X074_NAP1L4_001_CpG_2, X074_NAP1L4_001_CpG_3, X074_NAP1L4_001_CpG_4, X074_NAP1L4_001_CpG_5, X074_NAP1L4_001_CpG_6.7, X074_NAP1L4_001_CpG_8.9, X074_NAP1L4_001_CpG_10.11, X074_NAP1L4_001_CpG_12.13.14, X074_NAP1L4_001_CpG_15, X074_NAP1L4_001_CpG_16, X074_NAP1L4_001_CpG_17, X074_NAP1L4_001_CpG_18, X074_NAP1L4_001_CpG_19, X074_NAP1L4_001_CpG_20
X076_CARS	X076_CARS_001_CpG_1.2, X076_CARS_001_CpG_3, X076_CARS_001_CpG_4.5, X076_CARS_001_CpG_6, X076_CARS_001_CpG_7, X076_CARS_001_CpG_8.9, X076_CARS_001_CpG_10, X076_CARS_001_CpG_11, X076_CARS_001_CpG_12.13, X076_CARS_001_CpG_14.15, X076_CARS_001_CpG_16.17, X076_CARS_001_CpG_18, X076_CARS_001_CpG_19, X076_CARS_001_CpG_20, X076_CARS_001_CpG_21, X076_CARS_001_CpG_22.23, X076_CARS_001_CpG_24, X076_CARS_001_CpG_25, X076_CARS_001_CpG_26, X076_CARS_001_CpG_27.28.29.30, X076_CARS_001_CpG_31
X077_OSBPL5	X077_OSBPL5_001_CpG_1, X077_OSBPL5_001_CpG_2, X077_OSBPL5_001_CpG_3, X077_OSBPL5_001_CpG_4, X077_OSBPL5_001_CpG_5, X077_OSBPL5_001_CpG_6, X077_OSBPL5_001_CpG_7.8, X077_OSBPL5_001_CpG_9, X077_OSBPL5_001_CpG_10, X077_OSBPL5_001_CpG_11, X077_OSBPL5_001_CpG_12, X077_OSBPL5_001_CpG_13, X077_OSBPL5_001_CpG_14.15.16, X077_OSBPL5_001_CpG_17, X077_OSBPL5_001_CpG_18, X077_OSBPL5_001_CpG_19, X077_OSBPL5_001_CpG_20, X077_OSBPL5_001_CpG_21
X080_OSBPL5	X080_OSBPL5_004_CpG_1, X080_OSBPL5_004_CpG_2.3.4, X080_OSBPL5_004_CpG_5.6, X080_OSBPL5_004_CpG_7, X080_OSBPL5_004_CpG_8, X080_OSBPL5_004_CpG_9.10, X080_OSBPL5_004_CpG_11.12.13, X080_OSBPL5_004_CpG_14.15, X080_OSBPL5_004_CpG_16.17.18, X080_OSBPL5_004_CpG_19.20.21.22.23, X080_OSBPL5_004_CpG_24.25.26.27.28, X080_OSBPL5_004_CpG_29.30.31.32.33.34.35.36.37.38, X080_OSBPL5_004_CpG_39, X080_OSBPL5_004_CpG_40.41.42.43.44.45.46, X080_OSBPL5_004_CpG_47.48.49, X080_OSBPL5_004_CpG_50.51.52.53.54.55.56, X080_OSBPL5_004_CpG_57.58.59
X084_OSBPL5	X084_OSBPL5_008_CpG_1, X084_OSBPL5_008_CpG_2, X084_OSBPL5_008_CpG_3, X084_OSBPL5_008_CpG_4, X084_OSBPL5_008_CpG_5, X084_OSBPL5_008_CpG_6, X084_OSBPL5_008_CpG_7, X084_OSBPL5_008_CpG_8, X084_OSBPL5_008_CpG_9, X084_OSBPL5_008_CpG_10, X084_OSBPL5_008_CpG_11, X084_OSBPL5_008_CpG_12, X084_OSBPL5_008_CpG_13, X084_OSBPL5_008_CpG_14, X084_OSBPL5_008_CpG_15, X084_OSBPL5_008_CpG_16.17
X085_ZNF195	X085_ZNF195_001_CpG_1, X085_ZNF195_001_CpG_2, X085_ZNF195_001_CpG_3, X085_ZNF195_001_CpG_4.5, X085_ZNF195_001_CpG_6, X085_ZNF195_001_CpG_7.8, X085_ZNF195_001_CpG_9, X085_ZNF195_001_CpG_10, X085_ZNF195_001_CpG_11.12, X085_ZNF195_001_CpG_13, X085_ZNF195_001_CpG_14.15, X085_ZNF195_001_CpG_16, X085_ZNF195_001_CpG_17, X085_ZNF195_001_CpG_18, X085_ZNF195_001_CpG_19, X085_ZNF195_001_CpG_20, X085_ZNF195_001_CpG_21
X086_ZNF195	X086_ZNF195_002_CpG_1, X086_ZNF195_002_CpG_2.3, X086_ZNF195_002_CpG_4.5, X086_ZNF195_002_CpG_6, X086_ZNF195_002_CpG_7, X086_ZNF195_002_CpG_8.9, X086_ZNF195_002_CpG_10.11, X086_ZNF195_002_CpG_12.13, X086_ZNF195_002_CpG_14, X086_ZNF195_002_CpG_15, X086_ZNF195_002_CpG_16.17, X086_ZNF195_002_CpG_18, X086_ZNF195_002_CpG_19, X086_ZNF195_002_CpG_20
X088_DLK1	X088_DLK1_002_CpG_1, X088_DLK1_002_CpG_2, X088_DLK1_002_CpG_3, X088_DLK1_002_CpG_4, X088_DLK1_002_CpG_5.6, X088_DLK1_002_CpG_7, X088_DLK1_002_CpG_8, X088_DLK1_002_CpG_9, X088_DLK1_002_CpG_10.11, X088_DLK1_002_CpG_12
X091_DLK1	X091_DLK1_005_CpG_1, X091_DLK1_005_CpG_2, X091_DLK1_005_CpG_3, X091_DLK1_005_CpG_4, X091_DLK1_005_CpG_5, X091_DLK1_005_CpG_6, X091_DLK1_005_CpG_7, X091_DLK1_005_CpG_8.9,

	X091_DLK1_005_CpG_10, X091_DLK1_005_CpG_11, X091_DLK1_005_CpG_12, X091_DLK1_005_CpG_13, X091_DLK1_005_CpG_14, X091_DLK1_005_CpG_15
X092_MEG3	X092_MEG3_001_CpG_1, X092_MEG3_001_CpG_2, X092_MEG3_001_CpG_3, X092_MEG3_001_CpG_4, X092_MEG3_001_CpG_5.6, X092_MEG3_001_CpG_7, X092_MEG3_001_CpG_8.9.10.11, X092_MEG3_001_CpG_12, X092_MEG3_001_CpG_13.14.15.16, X092_MEG3_001_CpG_17, X092_MEG3_001_CpG_18.19.20, X092_MEG3_001_CpG_21.22.23, X092_MEG3_001_CpG_24, X092_MEG3_001_CpG_25
X093_MEG3	X093_MEG3_002_CpG_1, X093_MEG3_002_CpG_2, X093_MEG3_002_CpG_3, X093_MEG3_002_CpG_4, X093_MEG3_002_CpG_5, X093_MEG3_002_CpG_6, X093_MEG3_002_CpG_7.8, X093_MEG3_002_CpG_9.10.11.12.13, X093_MEG3_002_CpG_14, X093_MEG3_002_CpG_15, X093_MEG3_002_CpG_16, X093_MEG3_002_CpG_17, X093_MEG3_002_CpG_18, X093_MEG3_002_CpG_19
X094_MEG3	X094_MEG3_003_CpG_1, X094_MEG3_003_CpG_2, X094_MEG3_003_CpG_3, X094_MEG3_003_CpG_4, X094_MEG3_003_CpG_5, X094_MEG3_003_CpG_6.7, X094_MEG3_003_CpG_8.9, X094_MEG3_003_CpG_10, X094_MEG3_003_CpG_11, X094_MEG3_003_CpG_12, X094_MEG3_003_CpG_13
X095_MEG3	X095_MEG3_004_CpG_1, X095_MEG3_004_CpG_2, X095_MEG3_004_CpG_3, X095_MEG3_004_CpG_4, X095_MEG3_004_CpG_5.6, X095_MEG3_004_CpG_7, X095_MEG3_004_CpG_8, X095_MEG3_004_CpG_9.10, X095_MEG3_004_CpG_11.12.13, X095_MEG3_004_CpG_14.15.16
X097_MEG3	X097_MEG3_001_CpG_1.2.3, X097_MEG3_001_CpG_4, X097_MEG3_001_CpG_5, X097_MEG3_001_CpG_6.7, X097_MEG3_001_CpG_8, X097_MEG3_001_CpG_9, X097_MEG3_001_CpG_10, X097_MEG3_001_CpG_11, X097_MEG3_001_CpG_12, X097_MEG3_001_CpG_13, X097_MEG3_001_CpG_14, X097_MEG3_001_CpG_15, X097_MEG3_001_CpG_16, X097_MEG3_001_CpG_17, X097_MEG3_001_CpG_18, X097_MEG3_001_CpG_19.20, X097_MEG3_001_CpG_21, X097_MEG3_001_CpG_22, X097_MEG3_001_CpG_23, X097_MEG3_001_CpG_24, X097_MEG3_001_CpG_25, X097_MEG3_001_CpG_26.27, X097_MEG3_001_CpG_28
X101_NDN	X101_NDN_004_CpG_1.2, X101_NDN_004_CpG_3, X101_NDN_004_CpG_4, X101_NDN_004_CpG_5, X101_NDN_004_CpG_6, X101_NDN_004_CpG_7.8.9, X101_NDN_004_CpG_10, X101_NDN_004_CpG_11, X101_NDN_004_CpG_12.13, X101_NDN_004_CpG_14, X101_NDN_004_CpG_15.16, X101_NDN_004_CpG_17.18, X101_NDN_004_CpG_19, X101_NDN_004_CpG_20, X101_NDN_004_CpG_21.22, X101_NDN_004_CpG_23
X102_NDN	X102_NDN_005_CpG_1.2.3, X102_NDN_005_CpG_4, X102_NDN_005_CpG_5, X102_NDN_005_CpG_6, X102_NDN_005_CpG_7, X102_NDN_005_CpG_8, X102_NDN_005_CpG_9.10, X102_NDN_005_CpG_11, X102_NDN_005_CpG_12.13, X102_NDN_005_CpG_14, X102_NDN_005_CpG_15, X102_NDN_005_CpG_16.17.18.19, X102_NDN_005_CpG_20.21.22, X102_NDN_005_CpG_23.24.25, X102_NDN_005_CpG_26, X102_NDN_005_CpG_27, X102_NDN_005_CpG_28, X102_NDN_005_CpG_29
X105_SNRPN	X105_SNRPN_003_CpG_1, X105_SNRPN_003_CpG_2.3, X105_SNRPN_003_CpG_4, X105_SNRPN_003_CpG_5, X105_SNRPN_003_CpG_6, X105_SNRPN_003_CpG_7.8, X105_SNRPN_003_CpG_9, X105_SNRPN_003_CpG_10.11.12.13.14.15, X105_SNRPN_003_CpG_16.17, X105_SNRPN_003_CpG_18.19.20.21, X105_SNRPN_003_CpG_22, X105_SNRPN_003_CpG_23, X105_SNRPN_003_CpG_24.25.26, X105_SNRPN_003_CpG_27, X105_SNRPN_003_CpG_28
X107_SNRPN	X107_SNRPN_005_CpG_1, X107_SNRPN_005_CpG_2, X107_SNRPN_005_CpG_3, X107_SNRPN_005_CpG_4.5.6, X107_SNRPN_005_CpG_7, X107_SNRPN_005_CpG_8, X107_SNRPN_005_CpG_9.10.11.12.13.14, X107_SNRPN_005_CpG_15, X107_SNRPN_005_CpG_16.17.18, X107_SNRPN_005_CpG_19, X107_SNRPN_005_CpG_20,

	X107_SNRPN_005_CpG_21, X107_SNRPN_005_CpG_22, X107_SNRPN_005_CpG_23
X109_UBE3A	X109_UBE3A_001_CpG_1.2, X109_UBE3A_001_CpG_3, X109_UBE3A_001_CpG_4, X109_UBE3A_001_CpG_5.6.7.8, X109_UBE3A_001_CpG_9, X109_UBE3A_001_CpG_10.11.12.13, X109_UBE3A_001_CpG_14, X109_UBE3A_001_CpG_15.16, X109_UBE3A_001_CpG_17.18.19.20.21, X109_UBE3A_001_CpG_22.23.24, X109_UBE3A_001_CpG_25.26, X109_UBE3A_001_CpG_27, X109_UBE3A_001_CpG_28, X109_UBE3A_001_CpG_29.30, X109_UBE3A_001_CpG_31.32, X109_UBE3A_001_CpG_33, X109_UBE3A_001_CpG_34, X109_UBE3A_001_CpG_35, X109_UBE3A_001_CpG_36.37.38.39.40, X109_UBE3A_001_CpG_41, X109_UBE3A_001_CpG_42.43, X109_UBE3A_001_CpG_44, X109_UBE3A_001_CpG_45.46.47.48.49.50.51, X109_UBE3A_001_CpG_52, X109_UBE3A_001_CpG_53.54, X109_UBE3A_001_CpG_55.56, X109_UBE3A_001_CpG_57.58.59, X109_UBE3A_001_CpG_60.61.62.63.64.65.66.67.68.69.70.71.72, X109_UBE3A_001_CpG_73
X110_UBE3A	X110_UBE3A_002_CpG_1, X110_UBE3A_002_CpG_2, X110_UBE3A_002_CpG_3, X110_UBE3A_002_CpG_4, X110_UBE3A_002_CpG_5, X110_UBE3A_002_CpG_6.7, X110_UBE3A_002_CpG_8.9, X110_UBE3A_002_CpG_10, X110_UBE3A_002_CpG_11.12, X110_UBE3A_002_CpG_13.14, X110_UBE3A_002_CpG_15, X110_UBE3A_002_CpG_16, X110_UBE3A_002_CpG_17, X110_UBE3A_002_CpG_18.19, X110_UBE3A_002_CpG_20, X110_UBE3A_002_CpG_21.22, X110_UBE3A_002_CpG_23, X110_UBE3A_002_CpG_24.25, X110_UBE3A_002_CpG_26, X110_UBE3A_002_CpG_27, X110_UBE3A_002_CpG_28, X110_UBE3A_002_CpG_29
X111_ATP10A	X111_ATP10A_001_CpG_1, X111_ATP10A_001_CpG_2, X111_ATP10A_001_CpG_3, X111_ATP10A_001_CpG_4.5, X111_ATP10A_001_CpG_6, X111_ATP10A_001_CpG_7, X111_ATP10A_001_CpG_8, X111_ATP10A_001_CpG_9, X111_ATP10A_001_CpG_10, X111_ATP10A_001_CpG_11, X111_ATP10A_001_CpG_12, X111_ATP10A_001_CpG_13, X111_ATP10A_001_CpG_14, X111_ATP10A_001_CpG_15.16.17, X111_ATP10A_001_CpG_18, X111_ATP10A_001_CpG_19.20, X111_ATP10A_001_CpG_21, X111_ATP10A_001_CpG_22, X111_ATP10A_001_CpG_23.24, X111_ATP10A_001_CpG_25, X111_ATP10A_001_CpG_26.27, X111_ATP10A_001_CpG_28, X111_ATP10A_001_CpG_29
X112_ATP10A	X112_ATP10A_002_CpG_1.2, X112_ATP10A_002_CpG_3, X112_ATP10A_002_CpG_4.5, X112_ATP10A_002_CpG_6.7, X112_ATP10A_002_CpG_8, X112_ATP10A_002_CpG_9, X112_ATP10A_002_CpG_10, X112_ATP10A_002_CpG_11, X112_ATP10A_002_CpG_12, X112_ATP10A_002_CpG_13, X112_ATP10A_002_CpG_14.15, X112_ATP10A_002_CpG_16.17, X112_ATP10A_002_CpG_18.19, X112_ATP10A_002_CpG_20
X113_ATP10A	X113_ATP10A_003_CpG_1, X113_ATP10A_003_CpG_2, X113_ATP10A_003_CpG_3.4.5, X113_ATP10A_003_CpG_6, X113_ATP10A_003_CpG_7.8, X113_ATP10A_003_CpG_9.10.11.12, X113_ATP10A_003_CpG_13.14.15, X113_ATP10A_003_CpG_16, X113_ATP10A_003_CpG_17.18.19, X113_ATP10A_003_CpG_20.21.22.23.24.25.26, X113_ATP10A_003_CpG_27, X113_ATP10A_003_CpG_28.29, X113_ATP10A_003_CpG_30, X113_ATP10A_003_CpG_31.32, X113_ATP10A_003_CpG_33, X113_ATP10A_003_CpG_34, X113_ATP10A_003_CpG_35.36, X113_ATP10A_003_CpG_37, X113_ATP10A_003_CpG_38.39, X113_ATP10A_003_CpG_40.41.42, X113_ATP10A_003_CpG_43
X114_ATP10A	X114_ATP10A_004_CpG_1, X114_ATP10A_004_CpG_2, X114_ATP10A_004_CpG_3, X114_ATP10A_004_CpG_4, X114_ATP10A_004_CpG_5.6, X114_ATP10A_004_CpG_7, X114_ATP10A_004_CpG_8, X114_ATP10A_004_CpG_9.10.11, X114_ATP10A_004_CpG_12, X114_ATP10A_004_CpG_13, X114_ATP10A_004_CpG_14, X114_ATP10A_004_CpG_15, X114_ATP10A_004_CpG_16.17, X114_ATP10A_004_CpG_18, X114_ATP10A_004_CpG_19, X114_ATP10A_004_CpG_20, X114_ATP10A_004_CpG_21.22.23

X115_ATP10A	X115_ATP10A_005_CpG_1, X115_ATP10A_005_CpG_2, X115_ATP10A_005_CpG_3.4, X115_ATP10A_005_CpG_5.6, X115_ATP10A_005_CpG_7.8.9.10.11, X115_ATP10A_005_CpG_12, X115_ATP10A_005_CpG_13, X115_ATP10A_005_CpG_14, X115_ATP10A_005_CpG_15, X115_ATP10A_005_CpG_16
X116_GABRB3	X116_GABRB3_001_CpG_1, X116_GABRB3_001_CpG_2, X116_GABRB3_001_CpG_3, X116_GABRB3_001_CpG_4, X116_GABRB3_001_CpG_5, X116_GABRB3_001_CpG_6, X116_GABRB3_001_CpG_7.8, X116_GABRB3_001_CpG_9, X116_GABRB3_001_CpG_10.11, X116_GABRB3_001_CpG_12, X116_GABRB3_001_CpG_13.14, X116_GABRB3_001_CpG_15.16, X116_GABRB3_001_CpG_17, X116_GABRB3_001_CpG_18, X116_GABRB3_001_CpG_19, X116_GABRB3_001_CpG_20.21.22.23.24, X116_GABRB3_001_CpG_25, X116_GABRB3_001_CpG_26
X117_GABRB3	X117_GABRB3_002_CpG_1, X117_GABRB3_002_CpG_2, X117_GABRB3_002_CpG_3, X117_GABRB3_002_CpG_4.5, X117_GABRB3_002_CpG_6, X117_GABRB3_002_CpG_7, X117_GABRB3_002_CpG_8, X117_GABRB3_002_CpG_9.10, X117_GABRB3_002_CpG_11.12, X117_GABRB3_002_CpG_13, X117_GABRB3_002_CpG_14, X117_GABRB3_002_CpG_15.16.17, X117_GABRB3_002_CpG_18
X118_GABRB3	X118_GABRB3_003_CpG_1, X118_GABRB3_003_CpG_2, X118_GABRB3_003_CpG_3, X118_GABRB3_003_CpG_4, X118_GABRB3_003_CpG_5.6, X118_GABRB3_003_CpG_7, X118_GABRB3_003_CpG_8, X118_GABRB3_003_CpG_9.10, X118_GABRB3_003_CpG_11, X118_GABRB3_003_CpG_12, X118_GABRB3_003_CpG_13
X119_ZIM2	X119_ZIM2_001_CpG_1.2, X119_ZIM2_001_CpG_3, X119_ZIM2_001_CpG_4, X119_ZIM2_001_CpG_5.6, X119_ZIM2_001_CpG_7, X119_ZIM2_001_CpG_8, X119_ZIM2_001_CpG_9.10, X119_ZIM2_001_CpG_11.12, X119_ZIM2_001_CpG_13
X120_ZIM2	X120_ZIM2_002_CpG_1.2.3.4, X120_ZIM2_002_CpG_5, X120_ZIM2_002_CpG_6, X120_ZIM2_002_CpG_7, X120_ZIM2_002_CpG_8, X120_ZIM2_002_CpG_9, X120_ZIM2_002_CpG_10, X120_ZIM2_002_CpG_11, X120_ZIM2_002_CpG_12, X120_ZIM2_002_CpG_13.14.15.16.17.18, X120_ZIM2_002_CpG_19, X120_ZIM2_002_CpG_20, X120_ZIM2_002_CpG_21, X120_ZIM2_002_CpG_22.23, X120_ZIM2_002_CpG_24.25, X120_ZIM2_002_CpG_26, X120_ZIM2_002_CpG_27, X120_ZIM2_002_CpG_28.29, X120_ZIM2_002_CpG_30
X121_ZIM2	X121_ZIM2_003_CpG_1, X121_ZIM2_003_CpG_2.3, X121_ZIM2_003_CpG_4, X121_ZIM2_003_CpG_5.6, X121_ZIM2_003_CpG_7, X121_ZIM2_003_CpG_8, X121_ZIM2_003_CpG_9.10, X121_ZIM2_003_CpG_11, X121_ZIM2_003_CpG_12.13, X121_ZIM2_003_CpG_14.15, X121_ZIM2_003_CpG_16, X121_ZIM2_003_CpG_17, X121_ZIM2_003_CpG_18.19.20, X121_ZIM2_003_CpG_21, X121_ZIM2_003_CpG_22.23.24, X121_ZIM2_003_CpG_25.26, X121_ZIM2_003_CpG_27
X123_ZIM2	X123_ZIM2_005_CpG_1.2, X123_ZIM2_005_CpG_3, X123_ZIM2_005_CpG_4, X123_ZIM2_005_CpG_5.6, X123_ZIM2_005_CpG_7, X123_ZIM2_005_CpG_8, X123_ZIM2_005_CpG_9
X124_ZIM2	X124_ZIM2_006_CpG_1.2, X124_ZIM2_006_CpG_3, X124_ZIM2_006_CpG_4, X124_ZIM2_006_CpG_5, X124_ZIM2_006_CpG_6.7, X124_ZIM2_006_CpG_8.9.10, X124_ZIM2_006_CpG_11, X124_ZIM2_006_CpG_12.13, X124_ZIM2_006_CpG_14, X124_ZIM2_006_CpG_15, X124_ZIM2_006_CpG_16.17, X124_ZIM2_006_CpG_18, X124_ZIM2_006_CpG_19, X124_ZIM2_006_CpG_20, X124_ZIM2_006_CpG_21, X124_ZIM2_006_CpG_22.23, X124_ZIM2_006_CpG_24, X124_ZIM2_006_CpG_25.26.27, X124_ZIM2_006_CpG_28.29.30
X125_USP29	X125_USP29_001_CpG_1, X125_USP29_001_CpG_2.3, X125_USP29_001_CpG_4.5.6.7, X125_USP29_001_CpG_8, X125_USP29_001_CpG_9.10, X125_USP29_001_CpG_11, X125_USP29_001_CpG_12, X125_USP29_001_CpG_13, X125_USP29_001_CpG_14, X125_USP29_001_CpG_15, X125_USP29_001_CpG_16.17, X125_USP29_001_CpG_18.19.20,

	X125_USP29_001_CpG_21, X125_USP29_001_CpG_22.23.24.25, X125_USP29_001_CpG_26, X125_USP29_001_CpG_27, X125_USP29_001_CpG_28, X125_USP29_001_CpG_29, X125_USP29_001_CpG_30, X125_USP29_001_CpG_31
X127_USP29	X127_USP29_003_CpG_1, X127_USP29_003_CpG_2.3.4, X127_USP29_003_CpG_5.6, X127_USP29_003_CpG_7.8.9.10, X127_USP29_003_CpG_11, X127_USP29_003_CpG_12.13, X127_USP29_003_CpG_14.15, X127_USP29_003_CpG_16, X127_USP29_003_CpG_17, X127_USP29_003_CpG_18, X127_USP29_003_CpG_19, X127_USP29_003_CpG_20, X127_USP29_003_CpG_21, X127_USP29_003_CpG_22.23.24, X127_USP29_003_CpG_25, X127_USP29_003_CpG_26.27
X128_ZIM3	X128_ZIM3_001_CpG_1, X128_ZIM3_001_CpG_2.3.4, X128_ZIM3_001_CpG_5.6.7, X128_ZIM3_001_CpG_8.9.10, X128_ZIM3_001_CpG_11, X128_ZIM3_001_CpG_12.13.14.15, X128_ZIM3_001_CpG_16, X128_ZIM3_001_CpG_17.18.19, X128_ZIM3_001_CpG_20, X128_ZIM3_001_CpG_21, X128_ZIM3_001_CpG_22.23.24
X129_ZNF264	X129_ZNF264_001_CpG_1.2.3, X129_ZNF264_001_CpG_4, X129_ZNF264_001_CpG_5.6, X129_ZNF264_001_CpG_7, X129_ZNF264_001_CpG_8.9.10, X129_ZNF264_001_CpG_11.12, X129_ZNF264_001_CpG_13.14, X129_ZNF264_001_CpG_15.16, X129_ZNF264_001_CpG_17.18, X129_ZNF264_001_CpG_19, X129_ZNF264_001_CpG_20.21.22, X129_ZNF264_001_CpG_23.24, X129_ZNF264_001_CpG_25, X129_ZNF264_001_CpG_26.27.28, X129_ZNF264_001_CpG_29.30, X129_ZNF264_001_CpG_31, X129_ZNF264_001_CpG_32, X129_ZNF264_001_CpG_33, X129_ZNF264_001_CpG_34, X129_ZNF264_001_CpG_35.36, X129_ZNF264_001_CpG_37, X129_ZNF264_001_CpG_38, X129_ZNF264_001_CpG_39, X129_ZNF264_001_CpG_40, X129_ZNF264_001_CpG_41, X129_ZNF264_001_CpG_42, X129_ZNF264_001_CpG_43.44.45.46, X129_ZNF264_001_CpG_47, X129_ZNF264_001_CpG_48.49
X131_AURKC	X131_AURKC_002_CpG_1.2, X131_AURKC_002_CpG_3, X131_AURKC_002_CpG_4, X131_AURKC_002_CpG_5, X131_AURKC_002_CpG_6, X131_AURKC_002_CpG_7.8, X131_AURKC_002_CpG_9.10, X131_AURKC_002_CpG_11.12.13.14.15, X131_AURKC_002_CpG_16, X131_AURKC_002_CpG_17, X131_AURKC_002_CpG_18.19.20, X131_AURKC_002_CpG_21, X131_AURKC_002_CpG_22, X131_AURKC_002_CpG_23, X131_AURKC_002_CpG_24
X132_ZNF272	X132_ZNF272_001_CpG_1.2.3.4, X132_ZNF272_001_CpG_5, X132_ZNF272_001_CpG_6, X132_ZNF272_001_CpG_7.8, X132_ZNF272_001_CpG_9, X132_ZNF272_001_CpG_10.11, X132_ZNF272_001_CpG_12, X132_ZNF272_001_CpG_13.14, X132_ZNF272_001_CpG_15.16.17.18, X132_ZNF272_001_CpG_19, X132_ZNF272_001_CpG_20, X132_ZNF272_001_CpG_21.22.23.24, X132_ZNF272_001_CpG_25.26, X132_ZNF272_001_CpG_27, X132_ZNF272_001_CpG_28.29.30.31, X132_ZNF272_001_CpG_32, X132_ZNF272_001_CpG_33.34, X132_ZNF272_001_CpG_35, X132_ZNF272_001_CpG_36.37.38, X132_ZNF272_001_CpG_39, X132_ZNF272_001_CpG_40, X132_ZNF272_001_CpG_41, X132_ZNF272_001_CpG_42, X132_ZNF272_001_CpG_43.44
X133_RAI17	X133_RAI17_001_CpG_1, X133_RAI17_001_CpG_2, X133_RAI17_001_CpG_3, X133_RAI17_001_CpG_4.5, X133_RAI17_001_CpG_6.7, X133_RAI17_001_CpG_8, X133_RAI17_001_CpG_9, X133_RAI17_001_CpG_10, X133_RAI17_001_CpG_11, X133_RAI17_001_CpG_12
X134_FRAT1	X134_FRAT1_001_CpG_1, X134_FRAT1_001_CpG_2, X134_FRAT1_001_CpG_3, X134_FRAT1_001_CpG_4.5, X134_FRAT1_001_CpG_6.7, X134_FRAT1_001_CpG_8, X134_FRAT1_001_CpG_9, X134_FRAT1_001_CpG_10, X134_FRAT1_001_CpG_11, X134_FRAT1_001_CpG_12.13, X134_FRAT1_001_CpG_14, X134_FRAT1_001_CpG_15.16, X134_FRAT1_001_CpG_17.18, X134_FRAT1_001_CpG_19.20.21.22, X134_FRAT1_001_CpG_23
X135_ZNF215	X135_ZNF215_001_CpG_1.2.3, X135_ZNF215_001_CpG_4.5, X135_ZNF215_001_CpG_6.7, X135_ZNF215_001_CpG_8, X135_ZNF215_001_CpG_9, X135_ZNF215_001_CpG_10.11, X135_ZNF215_001_CpG_12, X135_ZNF215_001_CpG_13,

	X135_ZNF215_001_CpG_14, X135_ZNF215_001_CpG_15.16, X135_ZNF215_001_CpG_17, X135_ZNF215_001_CpG_18, X135_ZNF215_001_CpG_19, X135_ZNF215_001_CpG_20, X135_ZNF215_001_CpG_21.22, X135_ZNF215_001_CpG_23.24, X135_ZNF215_001_CpG_25.26, X135_ZNF215_001_CpG_27, X135_ZNF215_001_CpG_28, X135_ZNF215_001_CpG_29, X135_ZNF215_001_CpG_30, X135_ZNF215_001_CpG_31, X135_ZNF215_001_CpG_32, X135_ZNF215_001_CpG_33.34, X135_ZNF215_001_CpG_35, X135_ZNF215_001_CpG_36.37, X135_ZNF215_001_CpG_38, X135_ZNF215_001_CpG_39, X135_ZNF215_001_CpG_40, X135_ZNF215_001_CpG_41.42, X135_ZNF215_001_CpG_43
X136_WT1	X136_WT1_001_CpG_1.2, X136_WT1_001_CpG_3, X136_WT1_001_CpG_4, X136_WT1_001_CpG_5, X136_WT1_001_CpG_6, X136_WT1_001_CpG_7, X136_WT1_001_CpG_8, X136_WT1_001_CpG_9.10.11, X136_WT1_001_CpG_12, X136_WT1_001_CpG_13.14, X136_WT1_001_CpG_15, X136_WT1_001_CpG_16, X136_WT1_001_CpG_17, X136_WT1_001_CpG_18, X136_WT1_001_CpG_19
X137_SDHD	X137_SDHD_001_CpG_1.2, X137_SDHD_001_CpG_3.4.5, X137_SDHD_001_CpG_6, X137_SDHD_001_CpG_7, X137_SDHD_001_CpG_8.9, X137_SDHD_001_CpG_10, X137_SDHD_001_CpG_11, X137_SDHD_001_CpG_12, X137_SDHD_001_CpG_13, X137_SDHD_001_CpG_14, X137_SDHD_001_CpG_15.16, X137_SDHD_001_CpG_17, X137_SDHD_001_CpG_18.19, X137_SDHD_001_CpG_20, X137_SDHD_001_CpG_21.22.23, X137_SDHD_001_CpG_24, X137_SDHD_001_CpG_25, X137_SDHD_001_CpG_26, X137_SDHD_001_CpG_27, X137_SDHD_001_CpG_28.29, X137_SDHD_001_CpG_30
X138_SLC38A4	X138_SLC38A4_001_CpG_1, X138_SLC38A4_001_CpG_2.3.4.5.6, X138_SLC38A4_001_CpG_7, X138_SLC38A4_001_CpG_8, X138_SLC38A4_001_CpG_9.10.11, X138_SLC38A4_001_CpG_12.13.14, X138_SLC38A4_001_CpG_15, X138_SLC38A4_001_CpG_16.17, X138_SLC38A4_001_CpG_18, X138_SLC38A4_001_CpG_19, X138_SLC38A4_001_CpG_20.21.22, X138_SLC38A4_001_CpG_23.24, X138_SLC38A4_001_CpG_25.26, X138_SLC38A4_001_CpG_27, X138_SLC38A4_001_CpG_28, X138_SLC38A4_001_CpG_29
X139_HTR2A	X139_HTR2A_001_CpG_1, X139_HTR2A_001_CpG_2, X139_HTR2A_001_CpG_3, X139_HTR2A_001_CpG_4, X139_HTR2A_001_CpG_5, X139_HTR2A_001_CpG_6, X139_HTR2A_001_CpG_7, X139_HTR2A_001_CpG_8, X139_HTR2A_001_CpG_9
X140_CR601144	X140_CR601144_001_CpG_1, X140_CR601144_001_CpG_2.3, X140_CR601144_001_CpG_4, X140_CR601144_001_CpG_5, X140_CR601144_001_CpG_6, X140_CR601144_001_CpG_7.8.9, X140_CR601144_001_CpG_10, X140_CR601144_001_CpG_11, X140_CR601144_001_CpG_12, X140_CR601144_001_CpG_13, X140_CR601144_001_CpG_14.15, X140_CR601144_001_CpG_16, X140_CR601144_001_CpG_17.18, X140_CR601144_001_CpG_19, X140_CR601144_001_CpG_20, X140_CR601144_001_CpG_21.22, X140_CR601144_001_CpG_23
X141_DI03	X141_DI03_001_CpG_1.2, X141_DI03_001_CpG_3.4, X141_DI03_001_CpG_5, X141_DI03_001_CpG_6, X141_DI03_001_CpG_7, X141_DI03_001_CpG_8, X141_DI03_001_CpG_9.10.11.12, X141_DI03_001_CpG_13, X141_DI03_001_CpG_14.15.16, X141_DI03_001_CpG_17, X141_DI03_001_CpG_18.19.20, X141_DI03_001_CpG_21, X141_DI03_001_CpG_22.23.24.25, X141_DI03_001_CpG_26.27.28, X141_DI03_001_CpG_29.30.31.32, X141_DI03_001_CpG_33, X141_DI03_001_CpG_34, X141_DI03_001_CpG_35.36.37.38.39.40, X141_DI03_001_CpG_41.42, X141_DI03_001_CpG_43.44, X141_DI03_001_CpG_45, X141_DI03_001_CpG_46, X141_DI03_001_CpG_47, X141_DI03_001_CpG_48.49

X144_IMPACT	X144_IMPACT_001_CpG_1, X144_IMPACT_001_CpG_2.3, X144_IMPACT_001_CpG_4, X144_IMPACT_001_CpG_5, X144_IMPACT_001_CpG_6, X144_IMPACT_001_CpG_7.8.9, X144_IMPACT_001_CpG_10, X144_IMPACT_001_CpG_11.12, X144_IMPACT_001_CpG_13.14, X144_IMPACT_001_CpG_15, X144_IMPACT_001_CpG_16, X144_IMPACT_001_CpG_17, X144_IMPACT_001_CpG_18, X144_IMPACT_001_CpG_19.20, X144_IMPACT_001_CpG_21, X144_IMPACT_001_CpG_22.23.24.25.26, X144_IMPACT_001_CpG_27.28.29.30.31, X144_IMPACT_001_CpG_32.33, X144_IMPACT_001_CpG_34, X144_IMPACT_001_CpG_35.36.37.38.39, X144_IMPACT_001_CpG_40.41
X145_TCEB3C	X145_TCEB3C_001_CpG_1, X145_TCEB3C_001_CpG_2, X145_TCEB3C_001_CpG_3.4, X145_TCEB3C_001_CpG_5, X145_TCEB3C_001_CpG_6, X145_TCEB3C_001_CpG_7, X145_TCEB3C_001_CpG_8.9, X145_TCEB3C_001_CpG_10.11.12, X145_TCEB3C_001_CpG_13, X145_TCEB3C_001_CpG_14, X145_TCEB3C_001_CpG_15, X145_TCEB3C_001_CpG_16.17.18, X145_TCEB3C_001_CpG_19, X145_TCEB3C_001_CpG_20, X145_TCEB3C_001_CpG_21.22.23.24, X145_TCEB3C_001_CpG_25, X145_TCEB3C_001_CpG_26, X145_TCEB3C_001_CpG_27.28
X146_NNAT	X146_NNAT_001_CpG_1, X146_NNAT_001_CpG_2.3.4, X146_NNAT_001_CpG_5, X146_NNAT_001_CpG_6.7.8, X146_NNAT_001_CpG_9.10.11, X146_NNAT_001_CpG_12, X146_NNAT_001_CpG_13, X146_NNAT_001_CpG_14.15, X146_NNAT_001_CpG_16, X146_NNAT_001_CpG_17, X146_NNAT_001_CpG_18, X146_NNAT_001_CpG_19.20, X146_NNAT_001_CpG_21, X146_NNAT_001_CpG_22, X146_NNAT_001_CpG_23, X146_NNAT_001_CpG_24
X147_GNAS	X147_GNAS_001_CpG_1, X147_GNAS_001_CpG_2, X147_GNAS_001_CpG_3, X147_GNAS_001_CpG_4, X147_GNAS_001_CpG_5, X147_GNAS_001_CpG_6, X147_GNAS_001_CpG_7, X147_GNAS_001_CpG_8, X147_GNAS_001_CpG_9, X147_GNAS_001_CpG_10, X147_GNAS_001_CpG_11, X147_GNAS_001_CpG_12, X147_GNAS_001_CpG_13, X147_GNAS_001_CpG_14, X147_GNAS_001_CpG_15, X147_GNAS_001_CpG_16, X147_GNAS_001_CpG_17, X147_GNAS_001_CpG_18.19.20, X147_GNAS_001_CpG_21, X147_GNAS_001_CpG_22, X147_GNAS_001_CpG_23, X147_GNAS_001_CpG_24, X147_GNAS_001_CpG_25, X147_GNAS_001_CpG_26, X147_GNAS_001_CpG_27.28.29.30
X148_TPD52L2	X148_TPD52L2_001_CpG_1.2, X148_TPD52L2_001_CpG_3.4.5, X148_TPD52L2_001_CpG_6.7, X148_TPD52L2_001_CpG_8, X148_TPD52L2_001_CpG_9, X148_TPD52L2_001_CpG_10, X148_TPD52L2_001_CpG_11, X148_TPD52L2_001_CpG_12, X148_TPD52L2_001_CpG_13, X148_TPD52L2_001_CpG_14.15, X148_TPD52L2_001_CpG_16.17.18, X148_TPD52L2_001_CpG_19, X148_TPD52L2_001_CpG_20, X148_TPD52L2_001_CpG_21, X148_TPD52L2_001_CpG_22
X149_F2R	X149_F2R_001_CpG_1, X149_F2R_001_CpG_2, X149_F2R_001_CpG_3, X149_F2R_001_CpG_4, X149_F2R_001_CpG_5, X149_F2R_001_CpG_6, X149_F2R_001_CpG_7, X149_F2R_001_CpG_8, X149_F2R_001_CpG_9, X149_F2R_001_CpG_10, X149_F2R_001_CpG_11.12, X149_F2R_001_CpG_13, X149_F2R_001_CpG_14, X149_F2R_001_CpG_15, X149_F2R_001_CpG_16.17.18, X149_F2R_001_CpG_19, X149_F2R_001_CpG_20.21, X149_F2R_001_CpG_22, X149_F2R_001_CpG_23.24, X149_F2R_001_CpG_25, X149_F2R_001_CpG_26, X149_F2R_001_CpG_27.28
X150_U2AF1RS1	X150_U2AF1RS1_001_CpG_1, X150_U2AF1RS1_001_CpG_2, X150_U2AF1RS1_001_CpG_3, X150_U2AF1RS1_001_CpG_4.5, X150_U2AF1RS1_001_CpG_6
HOXA1_AB01	HOXA1_AB01_CpG_1, HOXA1_AB01_CpG_2.3, HOXA1_AB01_CpG_4, HOXA1_AB01_CpG_5, HOXA1_AB01_CpG_6.7.8.9.10, HOXA1_AB01_CpG_11, HOXA1_AB01_CpG_12.13, HOXA1_AB01_CpG_14, HOXA1_AB01_CpG_15, HOXA1_AB01_CpG_16, HOXA1_AB01_CpG_17, HOXA1_AB01_CpG_18

HOXA1_SQ05	HOXA1_SQ05_CpG_1.2, HOXA1_SQ05_CpG_3, HOXA1_SQ05_CpG_4.5, HOXA1_SQ05_CpG_6, HOXA1_SQ05_CpG_7, HOXA1_SQ05_CpG_8.9, HOXA1_SQ05_CpG_10, HOXA1_SQ05_CpG_11, HOXA1_SQ05_CpG_12, HOXA1_SQ05_CpG_13, HOXA1_SQ05_CpG_14.15, HOXA1_SQ05_CpG_16.17, HOXA1_SQ05_CpG_18.19.20, HOXA1_SQ05_CpG_21, HOXA1_SQ05_CpG_22.23, HOXA1_SQ05_CpG_24
HOXA3_AB01	HOXA3_AB01_CpG_1, HOXA3_AB01_CpG_2.3, HOXA3_AB01_CpG_4, HOXA3_AB01_CpG_5, HOXA3_AB01_CpG_6.7, HOXA3_AB01_CpG_8, HOXA3_AB01_CpG_9, HOXA3_AB01_CpG_10, HOXA3_AB01_CpG_11, HOXA3_AB01_CpG_12.13.14, HOXA3_AB01_CpG_15, HOXA3_AB01_CpG_16.17, HOXA3_AB01_CpG_18.19.20, HOXA3_AB01_CpG_21, HOXA3_AB01_CpG_22, HOXA3_AB01_CpG_23.24, HOXA3_AB01_CpG_25.26
HOXA3_SQ01	HOXA3_SQ01_CpG_1, HOXA3_SQ01_CpG_2, HOXA3_SQ01_CpG_3, HOXA3_SQ01_CpG_4.5.6, HOXA3_SQ01_CpG_7.8, HOXA3_SQ01_CpG_9.10.11.12, HOXA3_SQ01_CpG_13.14, HOXA3_SQ01_CpG_15.16, HOXA3_SQ01_CpG_17, HOXA3_SQ01_CpG_18, HOXA3_SQ01_CpG_19, HOXA3_SQ01_CpG_20, HOXA3_SQ01_CpG_21.22, HOXA3_SQ01_CpG_23, HOXA3_SQ01_CpG_24, HOXA3_SQ01_CpG_25.26, HOXA3_SQ01_CpG_27, HOXA3_SQ01_CpG_28, HOXA3_SQ01_CpG_29, HOXA3_SQ01_CpG_30, HOXA3_SQ01_CpG_31.32.33, HOXA3_SQ01_CpG_34, HOXA3_SQ01_CpG_35.36, HOXA3_SQ01_CpG_37.38.39, HOXA3_SQ01_CpG_40, HOXA3_SQ01_CpG_41, HOXA3_SQ01_CpG_42.43, HOXA3_SQ01_CpG_44.45
HOXA4_AB01	HOXA4_AB01_CpG_1, HOXA4_AB01_CpG_2.3, HOXA4_AB01_CpG_4.5.6.7.8.9.10.11, HOXA4_AB01_CpG_12.13.14, HOXA4_AB01_CpG_15, HOXA4_AB01_CpG_16, HOXA4_AB01_CpG_17
HOXA4_SQ02	HOXA4_SQ02_CpG_1, HOXA4_SQ02_CpG_2.3, HOXA4_SQ02_CpG_4, HOXA4_SQ02_CpG_5.6.7.8, HOXA4_SQ02_CpG_9.10.11.12, HOXA4_SQ02_CpG_13.14.15.16, HOXA4_SQ02_CpG_17.18.19, HOXA4_SQ02_CpG_20.21, HOXA4_SQ02_CpG_22.23, HOXA4_SQ02_CpG_24.25.26.27.28.29.30.31.32.33.34.35, HOXA4_SQ02_CpG_36.37.38, HOXA4_SQ02_CpG_39.40, HOXA4_SQ02_CpG_41.42, HOXA4_SQ02_CpG_43.44.45.46.47.48.49.50, HOXA4_SQ02_CpG_51.52.53.54.55
HOXA5_AB01	HOXA5_AB01_CpG_1, HOXA5_AB01_CpG_2, HOXA5_AB01_CpG_3.4.5.6.7.8.9.10.11, HOXA5_AB01_CpG_12.13, HOXA5_AB01_CpG_14, HOXA5_AB01_CpG_15, HOXA5_AB01_CpG_16, HOXA5_AB01_CpG_17, HOXA5_AB01_CpG_18, HOXA5_AB01_CpG_19, HOXA5_AB01_CpG_20, HOXA5_AB01_CpG_21.22, HOXA5_AB01_CpG_23, HOXA5_AB01_CpG_24, HOXA5_AB01_CpG_25, HOXA5_AB01_CpG_26.27.28.29.30
HOXA5_SQ03	HOXA5_SQ03_CpG_1, HOXA5_SQ03_CpG_2, HOXA5_SQ03_CpG_3, HOXA5_SQ03_CpG_4, HOXA5_SQ03_CpG_5, HOXA5_SQ03_CpG_6, HOXA5_SQ03_CpG_7, HOXA5_SQ03_CpG_8.9.10.11.12.13.14.15.16, HOXA5_SQ03_CpG_17.18, HOXA5_SQ03_CpG_19, HOXA5_SQ03_CpG_20, HOXA5_SQ03_CpG_21, HOXA5_SQ03_CpG_22, HOXA5_SQ03_CpG_23, HOXA5_SQ03_CpG_24, HOXA5_SQ03_CpG_25, HOXA5_SQ03_CpG_26.27, HOXA5_SQ03_CpG_28, HOXA5_SQ03_CpG_29, HOXA5_SQ03_CpG_30, HOXA5_SQ03_CpG_31.32.33.34.35, HOXA5_SQ03_CpG_36, HOXA5_SQ03_CpG_37, HOXA5_SQ03_CpG_38, HOXA5_SQ03_CpG_39
HOXA6_AB01	HOXA6_AB01_CpG_1, HOXA6_AB01_CpG_2, HOXA6_AB01_CpG_3, HOXA6_AB01_CpG_4, HOXA6_AB01_CpG_5, HOXA6_AB01_CpG_6, HOXA6_AB01_CpG_7.8, HOXA6_AB01_CpG_9, HOXA6_AB01_CpG_10.11, HOXA6_AB01_CpG_12, HOXA6_AB01_CpG_13.14, HOXA6_AB01_CpG_15, HOXA6_AB01_CpG_16, HOXA6_AB01_CpG_17.18
HOXA7_AB01	HOXA7_AB01_CpG_1, HOXA7_AB01_CpG_2.3, HOXA7_AB01_CpG_4, HOXA7_AB01_CpG_5.6.7.8.9, HOXA7_AB01_CpG_10, HOXA7_AB01_CpG_11.12, HOXA7_AB01_CpG_13.14, HOXA7_AB01_CpG_15.16, HOXA7_AB01_CpG_17, HOXA7_AB01_CpG_18, HOXA7_AB01_CpG_19, HOXA7_AB01_CpG_20, HOXA7_AB01_CpG_21, HOXA7_AB01_CpG_22.23, HOXA7_AB01_CpG_24, HOXA7_AB01_CpG_25, HOXA7_AB01_CpG_26.27,

	HOXA7_AB01_CpG_28.29, HOXA7_AB01_CpG_30, HOXA7_AB01_CpG_31
HOXA7_SQ03	HOXA7_SQ03_CpG_1, HOXA7_SQ03_CpG_2.3.4.5.6.7.8.9.10, HOXA7_SQ03_CpG_11.12, HOXA7_SQ03_CpG_13, HOXA7_SQ03_CpG_14, HOXA7_SQ03_CpG_15, HOXA7_SQ03_CpG_16, HOXA7_SQ03_CpG_17, HOXA7_SQ03_CpG_18.19, HOXA7_SQ03_CpG_20, HOXA7_SQ03_CpG_21.22.23
HOXA9_AB01	HOXA9_AB01_CpG_1, HOXA9_AB01_CpG_2.3.4.5, HOXA9_AB01_CpG_6, HOXA9_AB01_CpG_7, HOXA9_AB01_CpG_8.9.10.11, HOXA9_AB01_CpG_12.13.14, HOXA9_AB01_CpG_15.16, HOXA9_AB01_CpG_17.18, HOXA9_AB01_CpG_19, HOXA9_AB01_CpG_20, HOXA9_AB01_CpG_21, HOXA9_AB01_CpG_22.23, HOXA9_AB01_CpG_24, HOXA9_AB01_CpG_25, HOXA9_AB01_CpG_26
HOXA9_SQ03	HOXA9_SQ03_CpG_1, HOXA9_SQ03_CpG_2, HOXA9_SQ03_CpG_3, HOXA9_SQ03_CpG_4, HOXA9_SQ03_CpG_5.6, HOXA9_SQ03_CpG_7, HOXA9_SQ03_CpG_8.9, HOXA9_SQ03_CpG_10, HOXA9_SQ03_CpG_11.12.13.14.15.16, HOXA9_SQ03_CpG_17.18, HOXA9_SQ03_CpG_19, HOXA9_SQ03_CpG_20, HOXA9_SQ03_CpG_21, HOXA9_SQ03_CpG_22.23.24.25.26, HOXA9_SQ03_CpG_27, HOXA9_SQ03_CpG_28, HOXA9_SQ03_CpG_29.30, HOXA9_SQ03_CpG_31, HOXA9_SQ03_CpG_32.33, HOXA9_SQ03_CpG_34.35.36.37, HOXA9_SQ03_CpG_38.39, HOXA9_SQ03_CpG_40, HOXA9_SQ03_CpG_41, HOXA9_SQ03_CpG_42.43.44.45.46, HOXA9_SQ03_CpG_47, HOXA9_SQ03_CpG_48
HOXA10_AB01	HOXA10_AB01_CpG_1, HOXA10_AB01_CpG_2, HOXA10_AB01_CpG_3.4.5.6.7, HOXA10_AB01_CpG_8, HOXA10_AB01_CpG_9.10.11, HOXA10_AB01_CpG_12, HOXA10_AB01_CpG_13.14.15.16, HOXA10_AB01_CpG_17, HOXA10_AB01_CpG_18.19, HOXA10_AB01_CpG_20, HOXA10_AB01_CpG_21, HOXA10_AB01_CpG_22, HOXA10_AB01_CpG_23
HOXA10_SQ02	HOXA10_SQ02_CpG_1, HOXA10_SQ02_CpG_2, HOXA10_SQ02_CpG_3.4.5.6.7, HOXA10_SQ02_CpG_8, HOXA10_SQ02_CpG_9.10.11, HOXA10_SQ02_CpG_12, HOXA10_SQ02_CpG_13.14.15.16, HOXA10_SQ02_CpG_17, HOXA10_SQ02_CpG_18.19, HOXA10_SQ02_CpG_20, HOXA10_SQ02_CpG_21, HOXA10_SQ02_CpG_22, HOXA10_SQ02_CpG_23, HOXA10_SQ02_CpG_24, HOXA10_SQ02_CpG_25.26, HOXA10_SQ02_CpG_27, HOXA10_SQ02_CpG_28, HOXA10_SQ02_CpG_29, HOXA10_SQ02_CpG_30.31, HOXA10_SQ02_CpG_32.33, HOXA10_SQ02_CpG_34, HOXA10_SQ02_CpG_35, HOXA10_SQ02_CpG_36.37.38, HOXA10_SQ02_CpG_39.40
HOXA11_SQ01	HOXA11_SQ01_CpG_1, HOXA11_SQ01_CpG_2, HOXA11_SQ01_CpG_3, HOXA11_SQ01_CpG_4, HOXA11_SQ01_CpG_5.6, HOXA11_SQ01_CpG_7.8.9.10.11, HOXA11_SQ01_CpG_12, HOXA11_SQ01_CpG_13.14, HOXA11_SQ01_CpG_15, HOXA11_SQ01_CpG_16, HOXA11_SQ01_CpG_17, HOXA11_SQ01_CpG_18, HOXA11_SQ01_CpG_19.20.21, HOXA11_SQ01_CpG_22, HOXA11_SQ01_CpG_23, HOXA11_SQ01_CpG_24.25, HOXA11_SQ01_CpG_26, HOXA11_SQ01_CpG_27, HOXA11_SQ01_CpG_28
HOXA13_SQ01	HOXA13_SQ01_CpG_1, HOXA13_SQ01_CpG_2, HOXA13_SQ01_CpG_3.4.5, HOXA13_SQ01_CpG_6, HOXA13_SQ01_CpG_7, HOXA13_SQ01_CpG_8, HOXA13_SQ01_CpG_9, HOXA13_SQ01_CpG_10, HOXA13_SQ01_CpG_11, HOXA13_SQ01_CpG_12, HOXA13_SQ01_CpG_13, HOXA13_SQ01_CpG_14.15.16, HOXA13_SQ01_CpG_17.18.19, HOXA13_SQ01_CpG_20
HOXA13_SQ03	HOXA13_SQ03_CpG_1.2.3.4.5.6.7, HOXA13_SQ03_CpG_8, HOXA13_SQ03_CpG_9, HOXA13_SQ03_CpG_10.11.12.13.14.15.16, HOXA13_SQ03_CpG_17, HOXA13_SQ03_CpG_18.19, HOXA13_SQ03_CpG_20.21, HOXA13_SQ03_CpG_22, HOXA13_SQ03_CpG_23.24.25.26, HOXA13_SQ03_CpG_27, HOXA13_SQ03_CpG_28.29.30, HOXA13_SQ03_CpG_31.32.33, HOXA13_SQ03_CpG_34, HOXA13_SQ03_CpG_35.36.37.38.39, HOXA13_SQ03_CpG_40.41.42.43.44, HOXA13_SQ03_CpG_45,

	HOXA13_SQ03_CpG_46.47, HOXA13_SQ03_CpG_48.49, HOXA13_SQ03_CpG_50.51.52, HOXA13_SQ03_CpG_53.54.55, HOXA13_SQ03_CpG_56, HOXA13_SQ03_CpG_57.58.59, HOXA13_SQ03_CpG_60.61, HOXA13_SQ03_CpG_62.63.64.65, HOXA13_SQ03_CpG_66.67, HOXA13_SQ03_CpG_68, HOXA13_SQ03_CpG_69, HOXA13_SQ03_CpG_70, HOXA13_SQ03_CpG_71, HOXA13_SQ03_CpG_72
X005_ERalpha	X005_ERalpha_02_CpG_1, X005_ERalpha_02_CpG_2.3, X005_ERalpha_02_CpG_4.5, X005_ERalpha_02_CpG_6.7, X005_ERalpha_02_CpG_8, X005_ERalpha_02_CpG_9.10, X005_ERalpha_02_CpG_11, X005_ERalpha_02_CpG_12.13.14.15.16, X005_ERalpha_02_CpG_17.18, X005_ERalpha_02_CpG_19, X005_ERalpha_02_CpG_20, X005_ERalpha_02_CpG_21.22, X005_ERalpha_02_CpG_23.24.25, X005_ERalpha_02_CpG_26, X005_ERalpha_02_CpG_27.28, X005_ERalpha_02_CpG_29, X005_ERalpha_02_CpG_30.31.32, X005_ERalpha_02_CpG_33, X005_ERalpha_02_CpG_34
ESR1_01	ESR1_01_01_CpG_1, ESR1_01_01_CpG_2, ESR1_01_01_CpG_3.4, ESR1_01_01_CpG_5.6.7.8, ESR1_01_01_CpG_9, ESR1_01_01_CpG_10, ESR1_01_01_CpG_11, ESR1_01_01_CpG_12, ESR1_01_01_CpG_13.14.15.16, ESR1_01_01_CpG_17.18.19, ESR1_01_01_CpG_20, ESR1_01_01_CpG_21.22, ESR1_01_01_CpG_23, ESR1_01_01_CpG_24, ESR1_01_01_CpG_25.26, ESR1_01_01_CpG_27
MYOD_01	MYOD_01_02_CpG_1.2, MYOD_01_02_CpG_3, MYOD_01_02_CpG_4, MYOD_01_02_CpG_5.6, MYOD_01_02_CpG_7.8.9, MYOD_01_02_CpG_10, MYOD_01_02_CpG_11, MYOD_01_02_CpG_12.13.14, MYOD_01_02_CpG_15, MYOD_01_02_CpG_16.17, MYOD_01_02_CpG_18, MYOD_01_02_CpG_19, MYOD_01_02_CpG_20, MYOD_01_02_CpG_21, MYOD_01_02_CpG_22.23, MYOD_01_02_CpG_24, MYOD_01_02_CpG_25.26, MYOD_01_02_CpG_27.28, MYOD_01_02_CpG_29.30.31, MYOD_01_02_CpG_32, MYOD_01_02_CpG_33, MYOD_01_02_CpG_34.35.36, MYOD_01_02_CpG_37.38.39, MYOD_01_02_CpG_40, MYOD_01_02_CpG_41, MYOD_01_02_CpG_42.43.44, MYOD_01_02_CpG_45, MYOD_01_02_CpG_46.47
X002_E.cad	X002_E.cad_02_CpG_1, X002_E.cad_02_CpG_2.3.4, X002_E.cad_02_CpG_5.6.7, X002_E.cad_02_CpG_8, X002_E.cad_02_CpG_9.10.11.12.13.14, X002_E.cad_02_CpG_15, X002_E.cad_02_CpG_16.17, X002_E.cad_02_CpG_18, X002_E.cad_02_CpG_19.20.21, X002_E.cad_02_CpG_22, X002_E.cad_02_CpG_23, X002_E.cad_02_CpG_24
RASSF1_CpG	RASSF1_CpG_1.2, RASSF1_CpG_3.4.5, RASSF1_CpG_6.7.8, RASSF1_CpG_9, RASSF1_CpG_10, RASSF1_CpG_11, RASSF1_CpG_12, RASSF1_CpG_13, RASSF1_CpG_14.15.16.17.18, RASSF1_CpG_19, RASSF1_CpG_20, RASSF1_CpG_21, RASSF1_CpG_22.23.24.25.26, RASSF1_CpG_27, RASSF1_CpG_28.29, RASSF1_CpG_30, RASSF1_CpG_31.32, RASSF1_CpG_33.34, RASSF1_CpG_35, RASSF1_CpG_36, RASSF1_CpG_37, RASSF1_CpG_38.39.40.41, RASSF1_CpG_42.43.44.45, RASSF1_CpG_46.47, RASSF1_CpG_48, RASSF1_CpG_49.50, RASSF1_CpG_51.52
p53_03	p53_03_CpG_1, p53_03_CpG_2.3.4.5.6.7.8.9, p53_03_CpG_10, p53_03_CpG_11.12, p53_03_CpG_13, p53_03_CpG_14, p53_03_CpG_15.16, p53_03_CpG_17, p53_03_CpG_18, p53_03_CpG_19.20
X007_RAR.beta	X007_RAR.beta_01_CpG_1, X007_RAR.beta_01_CpG_2, X007_RAR.beta_01_CpG_3.4, X007_RAR.beta_01_CpG_5, X007_RAR.beta_01_CpG_6, X007_RAR.beta_01_CpG_7.8, X007_RAR.beta_01_CpG_9, X007_RAR.beta_01_CpG_10, X007_RAR.beta_01_CpG_11, X007_RAR.beta_01_CpG_12.13, X007_RAR.beta_01_CpG_14, X007_RAR.beta_01_CpG_15
LINE.1_CpG	LINE.1_CpG_1, LINE.1_CpG_2, LINE.1_CpG_3, LINE.1_CpG_4, LINE.1_CpG_5, LINE.1_CpG_6, LINE.1_CpG_7, LINE.1_CpG_8.9, LINE.1_CpG_10, LINE.1_CpG_11, LINE.1_CpG_12, LINE.1_CpG_13, LINE.1_CpG_14, LINE.1_CpG_15, LINE.1_CpG_16, LINE.1_CpG_17, LINE.1_CpG_18, LINE.1_CpG_19, LINE.1_CpG_20.21, LINE.1_CpG_22, LINE.1_CpG_23.24, LINE.1_CpG_25.26, LINE.1_CpG_27, LINE.1_CpG_28, LINE.1_CpG_29, LINE.1_CpG_30,

	LINE.1_CpG_31.32, LINE.1_CpG_33, LINE.1_CpG_34, LINE.1_CpG_35, LINE.1_CpG_36, LINE.1_CpG_37, LINE.1_CpG_38, LINE.1_CpG_39, LINE.1_CpG_40, LINE.1_CpG_41
ALU.M1_CpG	ALU.M1_CpG_1, ALU.M1_CpG_2, ALU.M1_CpG_3, ALU.M1_CpG_4, ALU.M1_CpG_5, ALU.M1_CpG_6, ALU.M1_CpG_7, ALU.M1_CpG_8, ALU.M1_CpG_9, ALU.M1_CpG_10, ALU.M1_CpG_11.12.13.14, ALU.M1_CpG_15, ALU.M1_CpG_16, ALU.M1_CpG_17, ALU.M1_CpG_18, ALU.M1_CpG_19, ALU.M1_CpG_20, ALU.M1_CpG_21, ALU.M1_CpG_22, ALU.M1_CpG_23
ALU.cons_CpG	ALU.cons_CpG_1, ALU.cons_CpG_2, ALU.cons_CpG_3, ALU.cons_CpG_4, ALU.cons_CpG_5, ALU.cons_CpG_6, ALU.cons_CpG_7, ALU.cons_CpG_8.9, ALU.cons_CpG_10, ALU.cons_CpG_11, ALU.cons_CpG_12, ALU.cons_CpG_13, ALU.cons_CpG_14.15.16, ALU.cons_CpG_17, ALU.cons_CpG_18, ALU.cons_CpG_19, ALU.cons_CpG_20, ALU.cons_CpG_21.22, ALU.cons_CpG_23, ALU.cons_CpG_24.25, ALU.cons_CpG_26
SATalpha_CpG	SATalpha_CpG_1, SATalpha_CpG_2, SATalpha_CpG_3, SATalpha_CpG_4, SATalpha_CpG_5, SATalpha_CpG_6, SATalpha_CpG_7, SATalpha_CpG_8, SATalpha_CpG_9, SATalpha_CpG_10, SATalpha_CpG_11, SATalpha_CpG_12, SATalpha_CpG_13, SATalpha_CpG_14, SATalpha_CpG_15, SATalpha_CpG_16, SATalpha_CpG_17, SATalpha_CpG_18, SATalpha_CpG_19, SATalpha_CpG_20, SATalpha_CpG_21.22
seq.GSTP1.300.100_01	seq.GSTP1.300.100_01_CpG_1.2.3, seq.GSTP1.300.100_01_CpG_4.5, seq.GSTP1.300.100_01_CpG_6.7, seq.GSTP1.300.100_01_CpG_8, seq.GSTP1.300.100_01_CpG_9, seq.GSTP1.300.100_01_CpG_10.11.12, seq.GSTP1.300.100_01_CpG_13, seq.GSTP1.300.100_01_CpG_14.15.16, seq.GSTP1.300.100_01_CpG_17.18, seq.GSTP1.300.100_01_CpG_19.20.21.22.23, seq.GSTP1.300.100_01_CpG_24.25, seq.GSTP1.300.100_01_CpG_26.27.28.29, seq.GSTP1.300.100_01_CpG_30, seq.GSTP1.300.100_01_CpG_31.32, seq.GSTP1.300.100_01_CpG_33, seq.GSTP1.300.100_01_CpG_34.35, seq.GSTP1.300.100_01_CpG_36, seq.GSTP1.300.100_01_CpG_37.38.39, seq.GSTP1.300.100_01_CpG_40, seq.GSTP1.300.100_01_CpG_41.42.43.44.45.46, seq.GSTP1.300.100_01_CpG_47
X14_RUNX3	X14_RUNX3_01_01_CpG_1, X14_RUNX3_01_01_CpG_2, X14_RUNX3_01_01_CpG_3.4, X14_RUNX3_01_01_CpG_5, X14_RUNX3_01_01_CpG_6, X14_RUNX3_01_01_CpG_7, X14_RUNX3_01_01_CpG_8, X14_RUNX3_01_01_CpG_9.10.11.12, X14_RUNX3_01_01_CpG_13.14, X14_RUNX3_01_01_CpG_15, X14_RUNX3_01_01_CpG_16, X14_RUNX3_01_01_CpG_17, X14_RUNX3_01_01_CpG_18, X14_RUNX3_01_01_CpG_19.20, X14_RUNX3_01_01_CpG_21, X14_RUNX3_01_01_CpG_22.23.24, X14_RUNX3_01_01_CpG_25.26, X14_RUNX3_01_01_CpG_27.28, X14_RUNX3_01_01_CpG_29, X14_RUNX3_01_01_CpG_30, X14_RUNX3_01_01_CpG_31, X14_RUNX3_01_01_CpG_32, X14_RUNX3_01_01_CpG_33.34, X14_RUNX3_01_01_CpG_35, X14_RUNX3_01_01_CpG_36
X15_RUNX3	X15_RUNX3_02_01_CpG_1.2.3.4.5.6.7, X15_RUNX3_02_01_CpG_8.9.10.11.12, X15_RUNX3_02_01_CpG_13, X15_RUNX3_02_01_CpG_14.15.16, X15_RUNX3_02_01_CpG_17.18, X15_RUNX3_02_01_CpG_19.20, X15_RUNX3_02_01_CpG_21.22.23.24, X15_RUNX3_02_01_CpG_25.26, X15_RUNX3_02_01_CpG_27, X15_RUNX3_02_01_CpG_28, X15_RUNX3_02_01_CpG_29, X15_RUNX3_02_01_CpG_30, X15_RUNX3_02_01_CpG_31.32, X15_RUNX3_02_01_CpG_33, X15_RUNX3_02_01_CpG_34, X15_RUNX3_02_01_CpG_35.36, X15_RUNX3_02_01_CpG_37, X15_RUNX3_02_01_CpG_38.39.40.41, X15_RUNX3_02_01_CpG_42.43, X15_RUNX3_02_01_CpG_44.45.46.47.48

The entirety of each patent, patent application, publication and document referenced herein hereby is incorporated by reference, including all tables, drawings, and figures. All patents and publications are herein incorporated by reference to the same extent as if each was specifically and individually indicated to be incorporated by reference. Citation of the above patents, patent applications, publications and documents is not an admission that any of the foregoing is pertinent prior art, nor does it constitute any admission as to the contents or date of these publications or documents. All patents and publications mentioned herein are indicative of the skill levels of those of ordinary skill in the art to which the invention pertains.

Modifications may be made to the foregoing without departing from the scope, spirit and basic aspects of the invention. Although the invention has been described in substantial detail with reference to one or more specific embodiments, those of ordinary skill in the art will recognize that changes may be made to the embodiments specifically disclosed in this application, and yet these modifications and improvements are within the scope and spirit of the invention. One skilled in the art readily appreciates that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The examples provided herein are representative of specific embodiments, are exemplary, and are not intended as limitations on the scope of the invention.

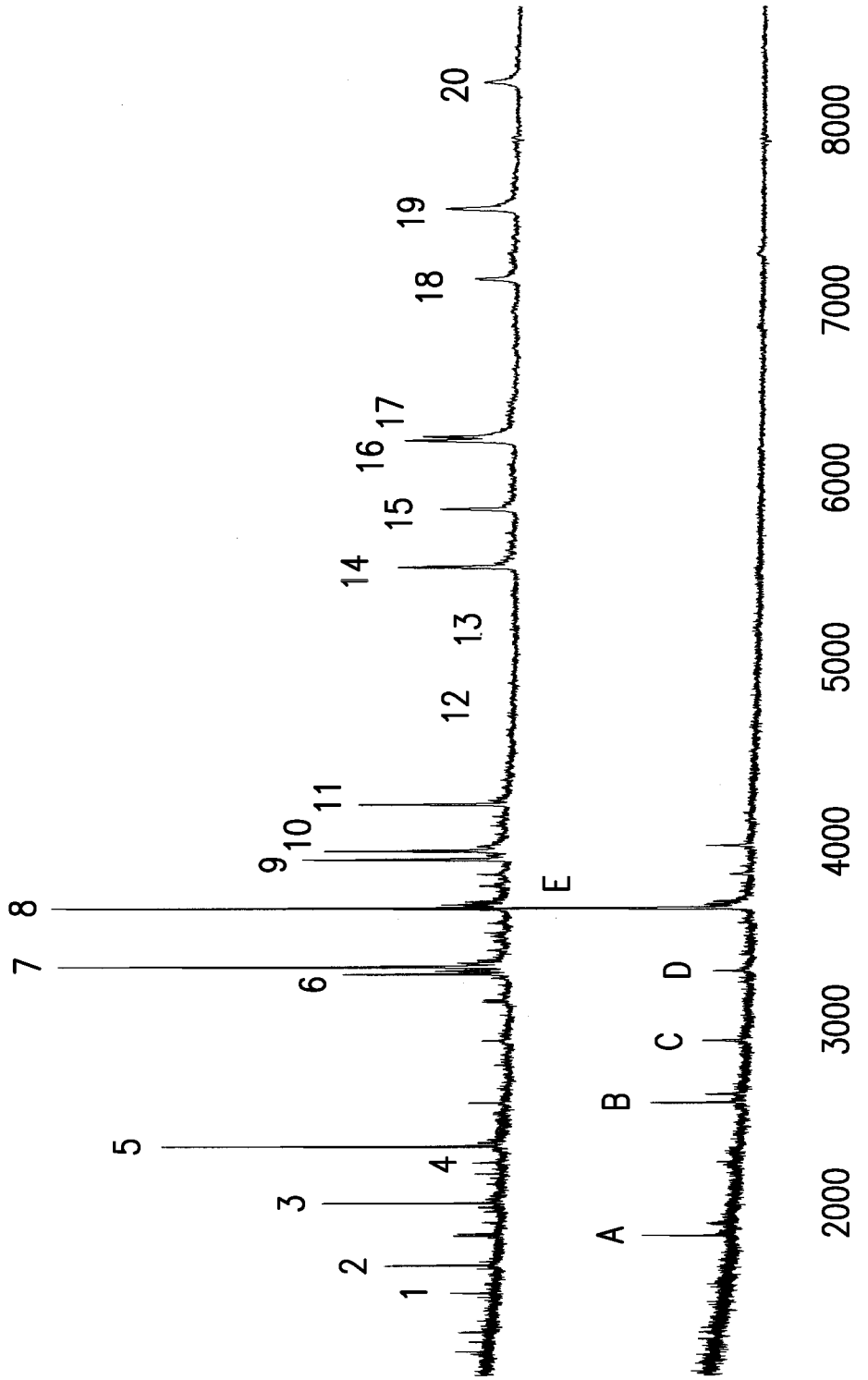
The invention illustratively described herein suitably may be practiced in the absence of any element(s) not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" may be replaced with either of the other two terms. Thus, the terms and expressions which have been employed are used as terms of description and not of limitation, equivalents of the features shown and described, or portions thereof, are not excluded, and it is recognized that various modifications are possible within the scope of the invention. Embodiments of the invention are set forth in the following claims.

What is claimed is:

1. A composition comprising a probe that binds specifically to the PRC2 binding site of one or more nucleic acid target genes provided in Table 9, which blocks the binding of a PRC2 complex to the one or more target genes.

2. A method for treating, detecting or preventing cancer in a subject, which comprises: determining the methylation status of one or one or more nucleic acid target gene regions, wherein the one or one or more nucleic acid target gene regions comprises one or more PRC2 binding sites and is disclosed in Table 9, and administering a cancer treatment or cancer preventative procedure or cancer detection procedure to a subject in need thereof based upon the methylation status of one or one or more nucleic acid target gene regions.

3. The method of claim 2, wherein the cancer treatment targets one or more of the PRC2 binding sites.


1
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20
A
B
C
D
E
2000
3000
4000
5000
6000
7000
8000

FIG.1A

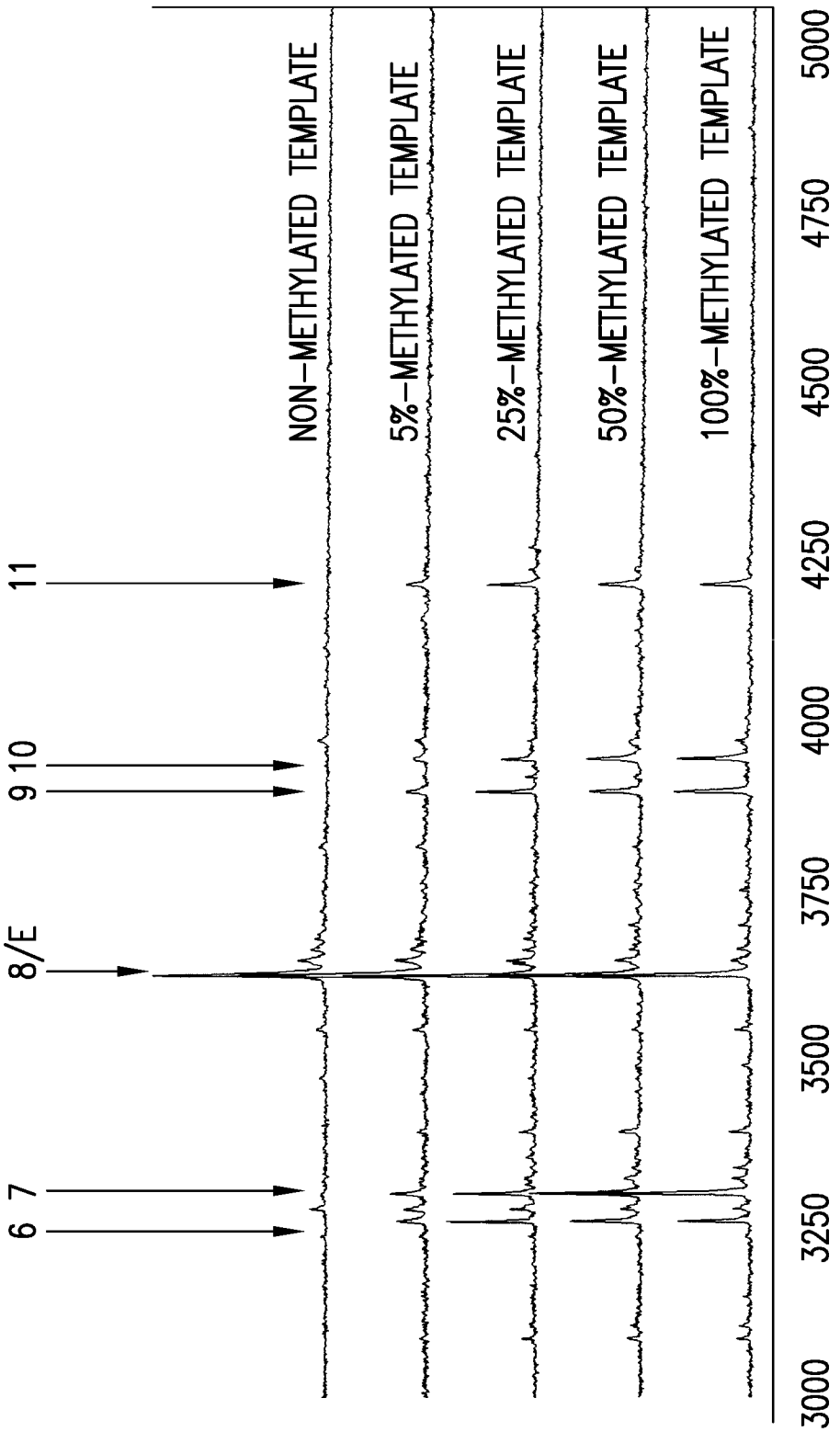
NON-METHYLATED TEMPLATE
5%-METHYLATED TEMPLATE
25%-METHYLATED TEMPLATE
50%-METHYLATED TEMPLATE
100%-METHYLATED TEMPLATE
6 7
8/E
9 10
11
3000
3250
3500
3750
4000
4250
4500
4750
5000

FIG.2

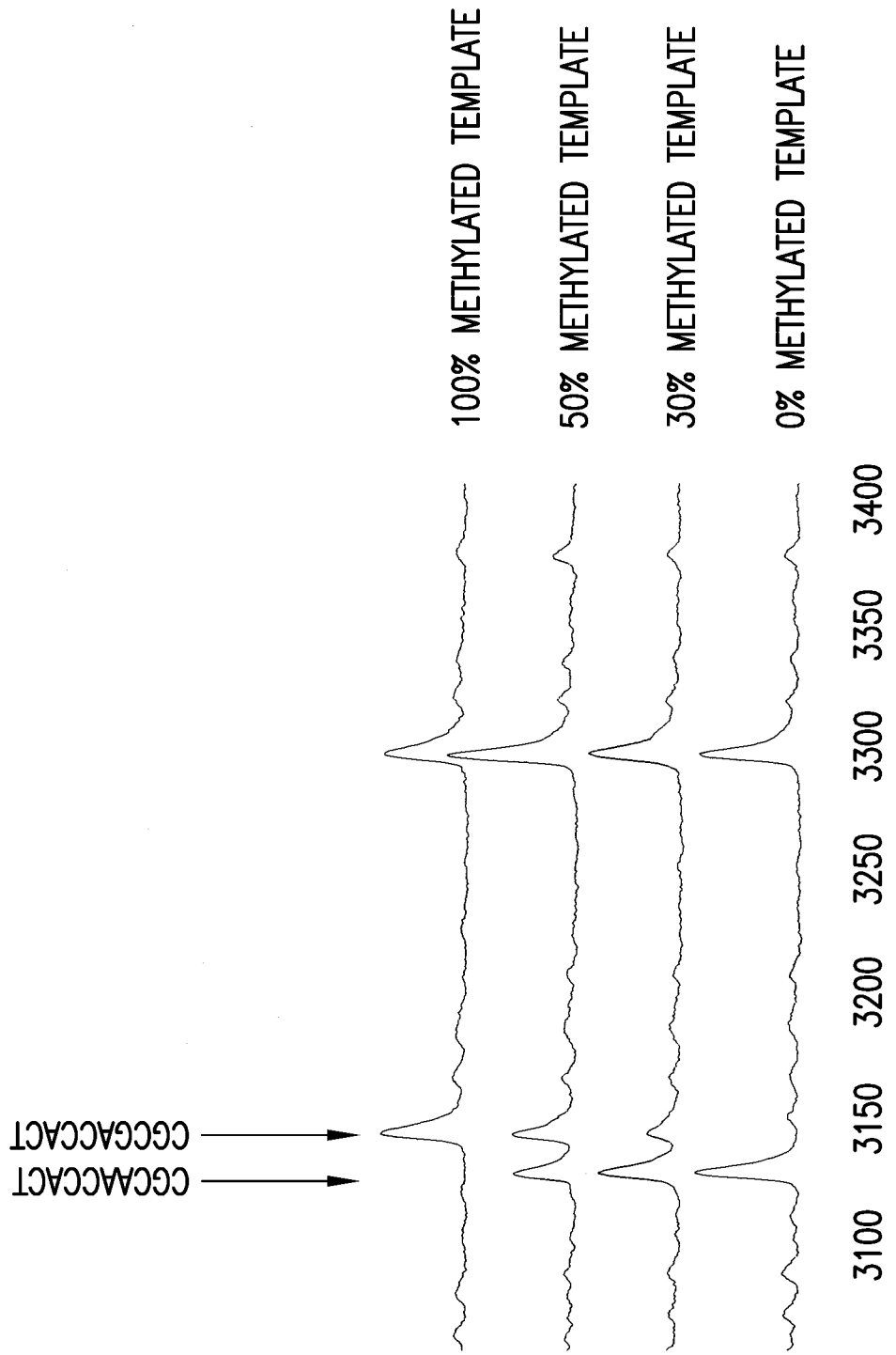
100% METHYLATED TEMPLATE
50% METHYLATED TEMPLATE
30% METHYLATED TEMPLATE
0% METHYLATED TEMPLATE
CGCGACCACT
CGCAACCACT
3100
3150
3200
3250
3300
3350
3400

FIG.3A

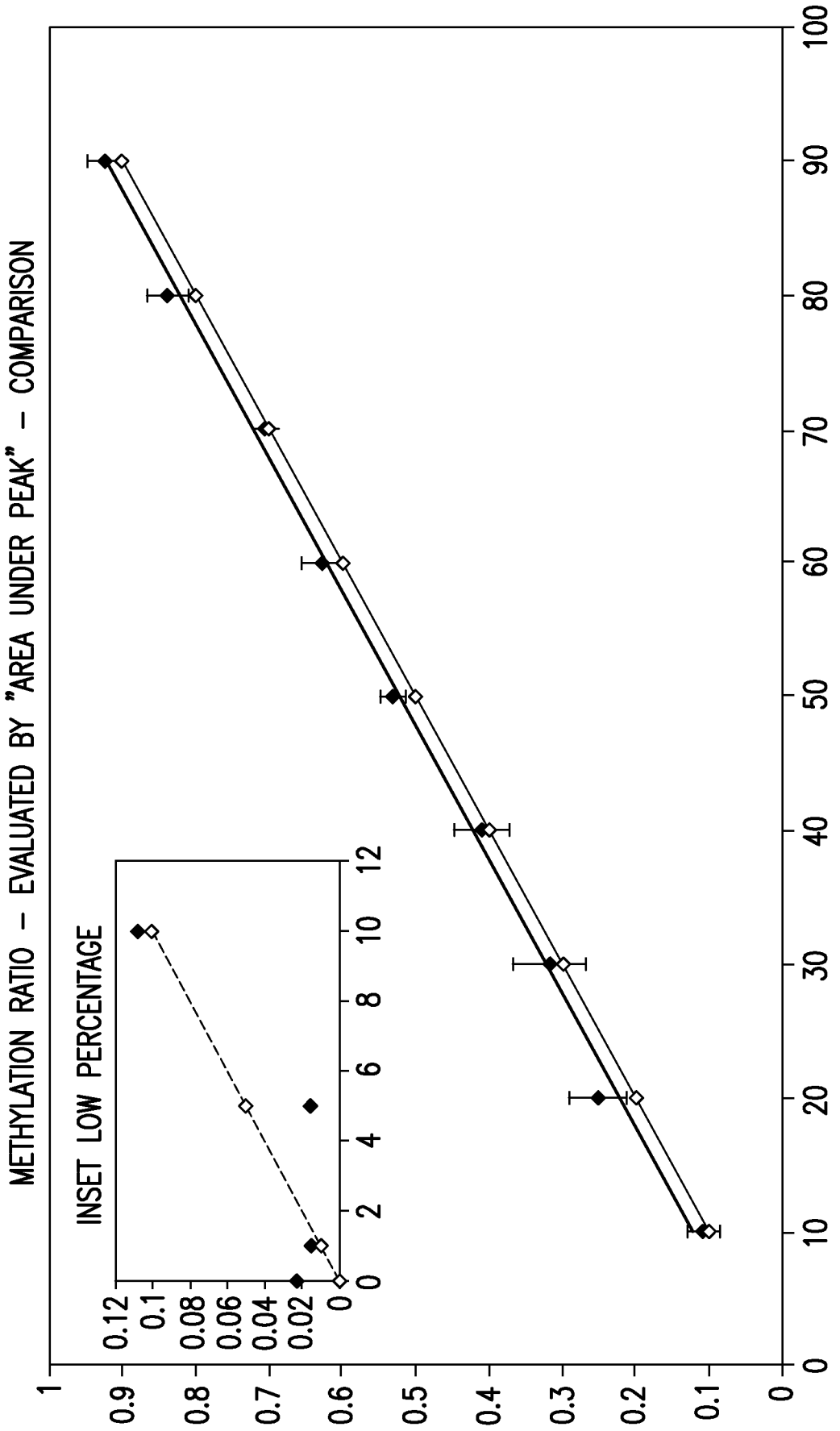
METHYLATION RATIO – EVALUATED BY "AREA UNDER PEAK" – COMPARISON
INSET LOW PERCENTAGE
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
0.9
1
0
10
20
30
40
50
60
70
80
90
100
0
0.02
0.04
0.06
0.08
0.1
0.12
0
2
4
6
8
10
12

FIG.3B

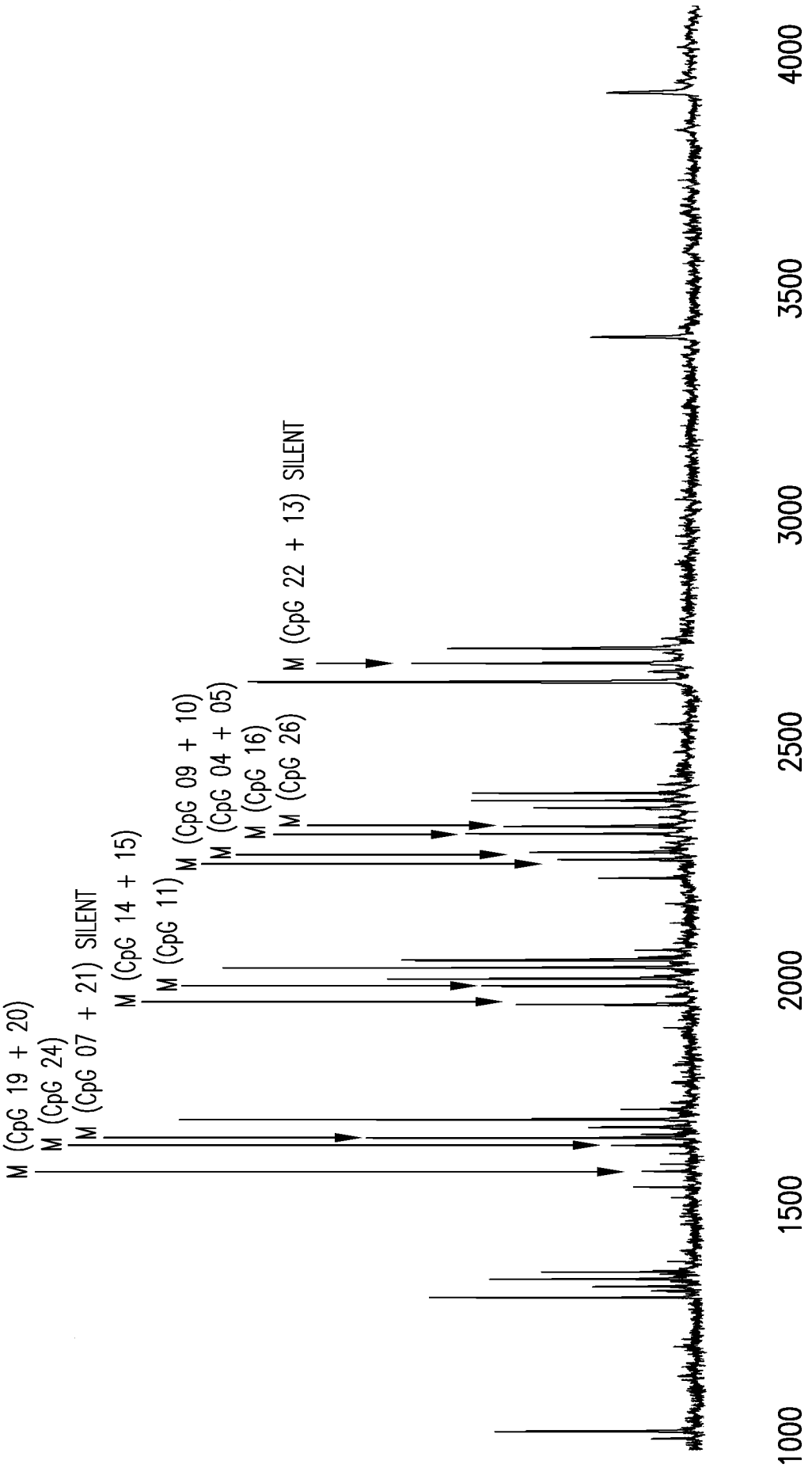
M (CpG 19 + 20)
M (CpG 24)
M (CpG 07 + 21) SILENT
M (CpG 14 + 15)
M (CpG 11)
M (CpG 09 + 10)
M (CpG 04 + 05)
M (CpG 16)
M (CpG 26)
M (CpG 22 + 13) SILENT
1000
1500
2000
2500
3000
3500
4000

FIG.4

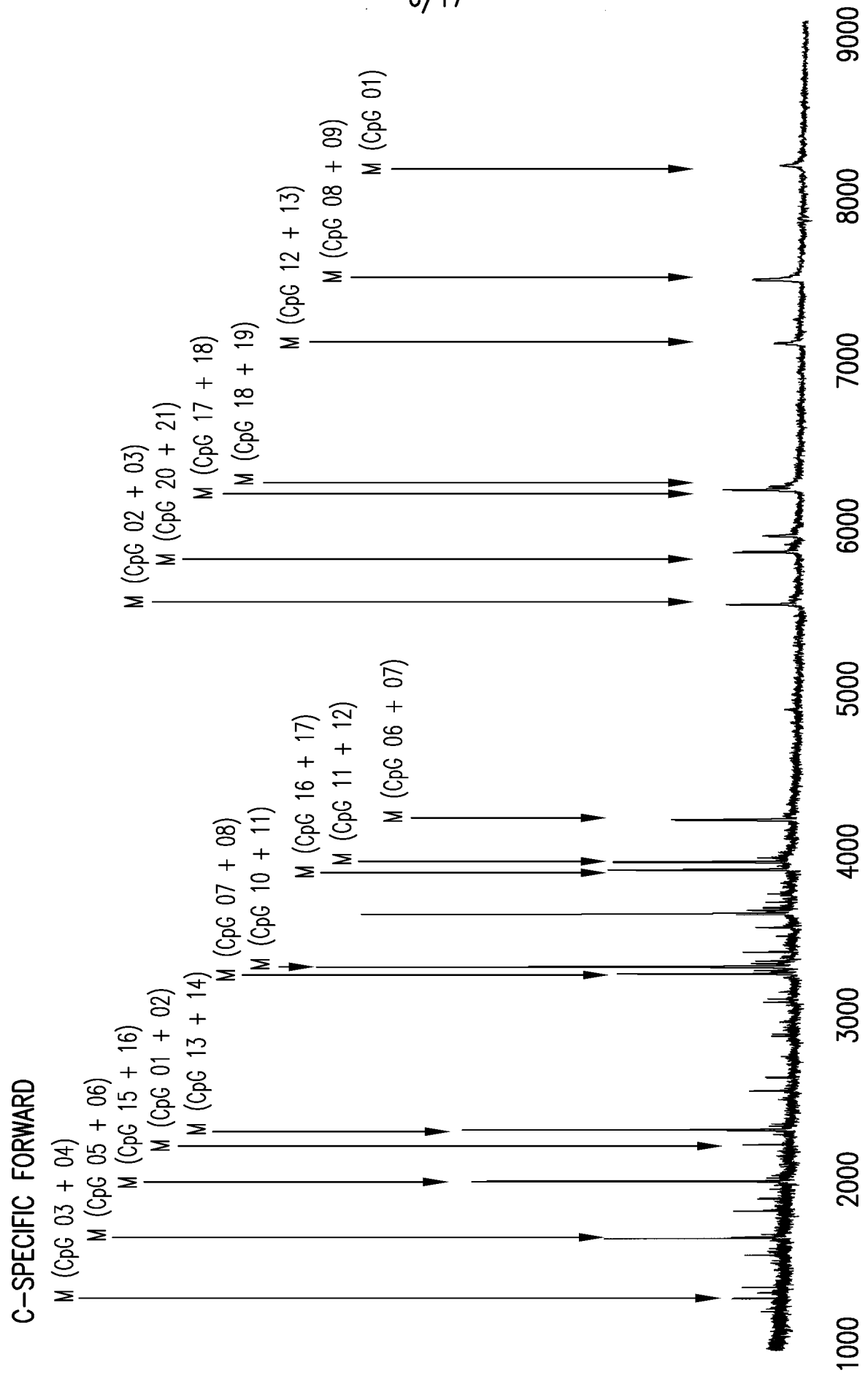
C-SPECIFIC FORWARD
M (CpG 03 + 04)
M (CpG 05 + 06)
M (CpG 15 + 16)
M (CpG 01 + 02)
M (CpG 13 + 14)
M (CpG 07 + 08)
M (CpG 10 + 11)
M (CpG 16 + 17)
M (CpG 11 + 12)
M (CpG 06 + 07)
M (CpG 02 + 03)
M (CpG 20 + 21)
M (CpG 17 + 18)
M (CpG 18 + 19)
M (CpG 12 + 13)
M (CpG 08 + 09)
M (CpG 01)
1000
2000
3000
4000
5000
6000
7000
8000
9000

FIG.4-1

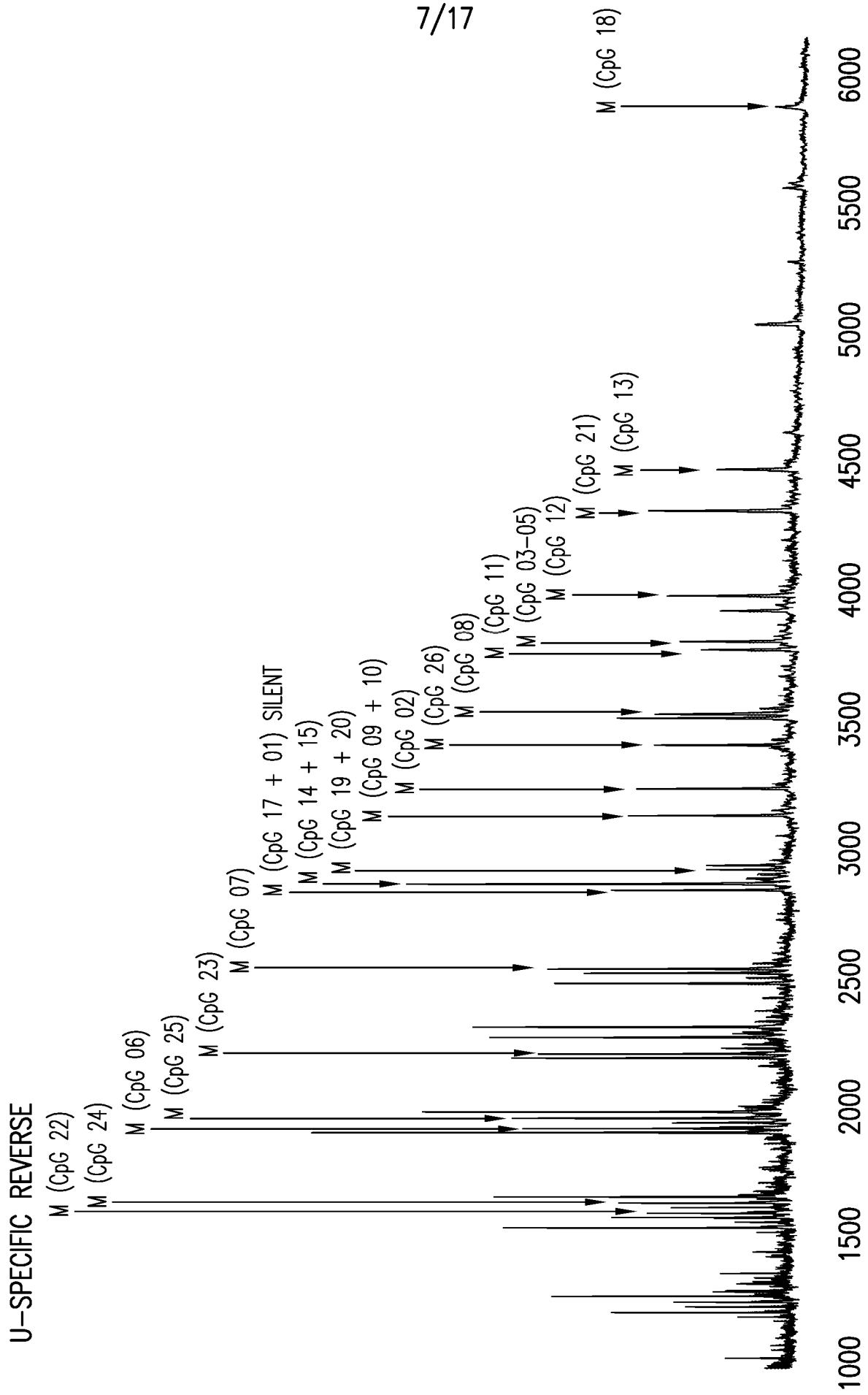
U–SPECIFIC REVERSE
M (CpG 22)
M (CpG 24)
M (CpG 06)
M (CpG 25)
M (CpG 23)
M (CpG 07)
M (CpG 17 + 01) SILENT
M (CpG 14 + 15)
M (CpG 19 + 20)
M (CpG 09 + 10)
M (CpG 02)
M (CpG 26)
M (CpG 08)
M (CpG 11)
M (CpG 03–05)
M (CpG 12)
M (CpG 21)
M (CpG 13)
M (CpG 18)
1000
1500
2000
2500
3000
3500
4000
4500
5000
5500
6000

FIG.4-2

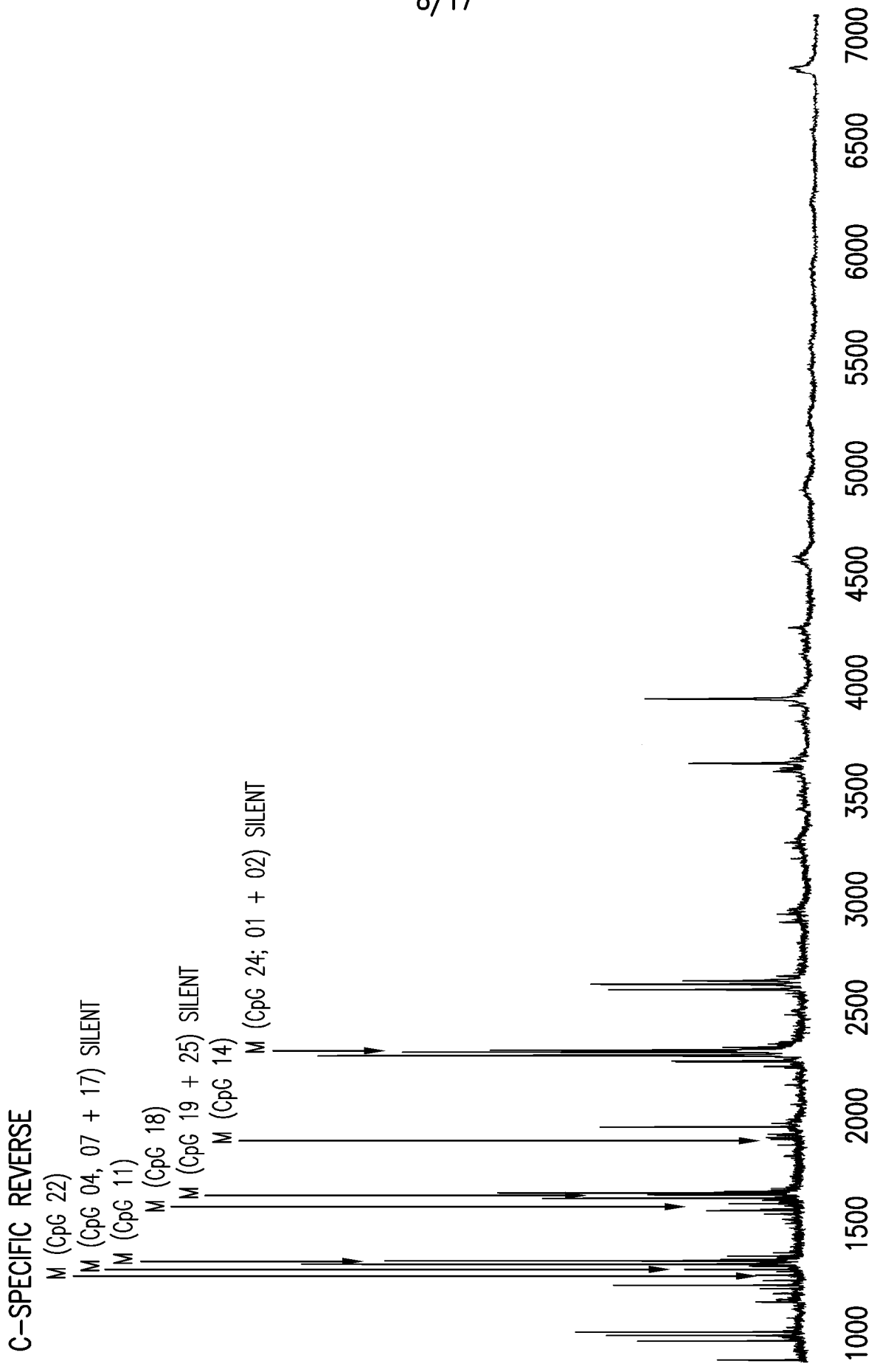
C-SPECIFIC REVERSE
M (CpG 22)
M (CpG 04, 07 + 17) SILENT
M (CpG 11)
M (CpG 18)
M (CpG 19 + 25) SILENT
M (CpG 14)
M (CpG 24; 01 + 02) SILENT
1000
1500
2000
2500
3000
3500
4000
4500
5000
5500
6000
6500
7000

FIG.4-3

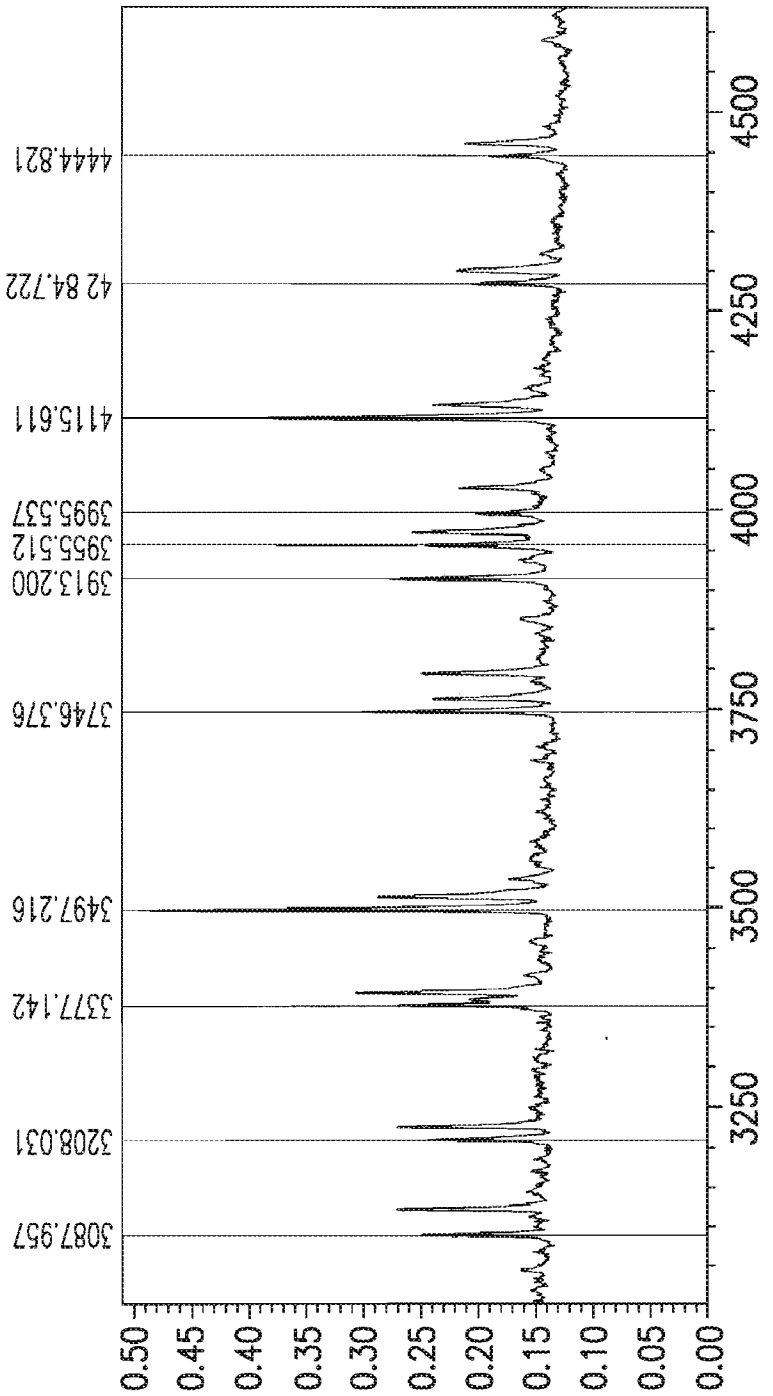
4444.821
4284.722
4115.611
3995.537
3955.512
3913.200
3746.376
3497.216
3377.142
3208.031
3087.957
4500
4250
4000
3750
3500
3250
0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00

FIG. 5

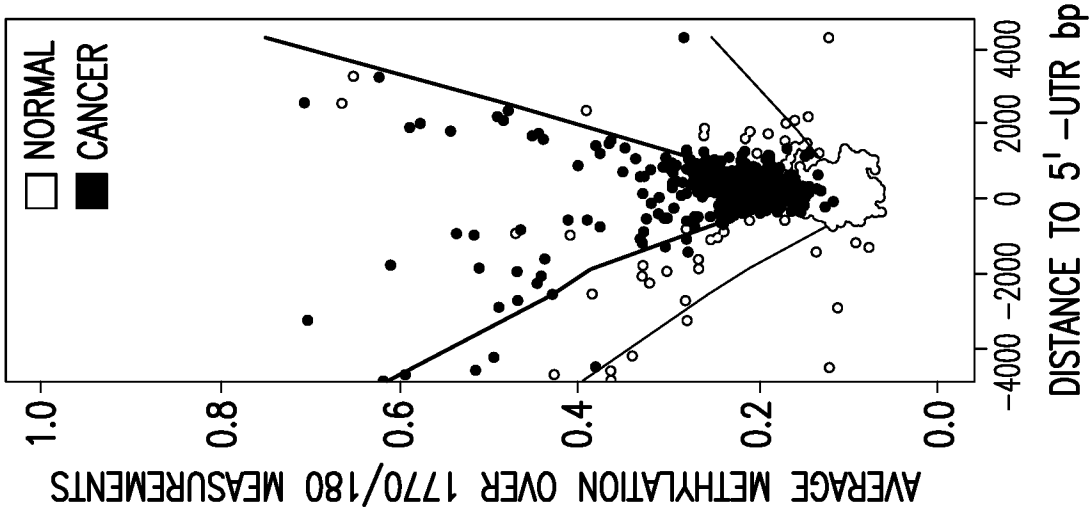

FIG.6E

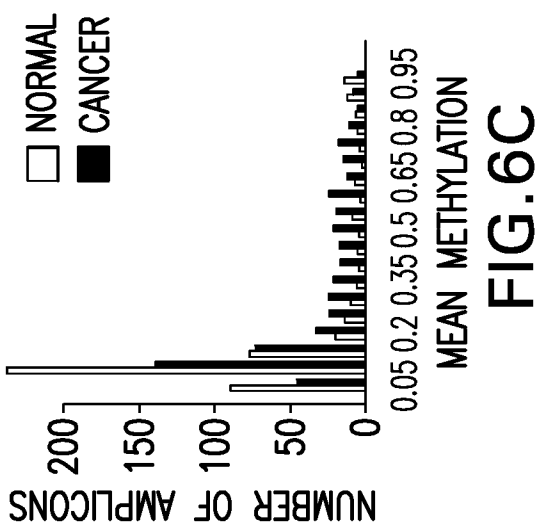

FIG.6C

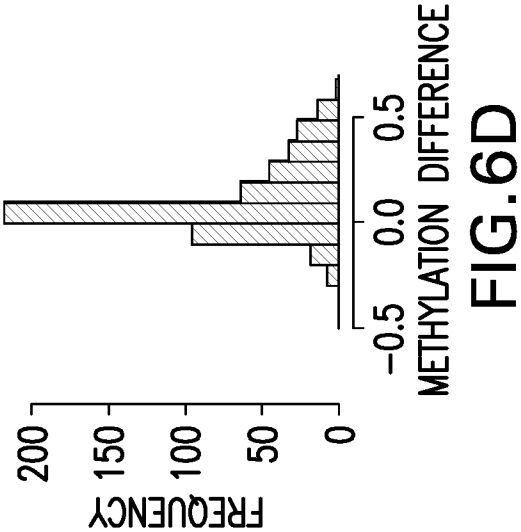

FIG.6D

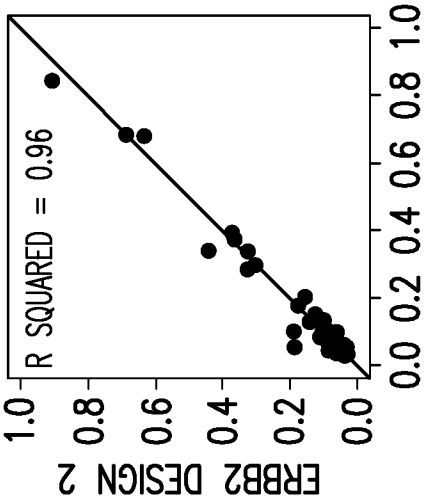

FIG.6A

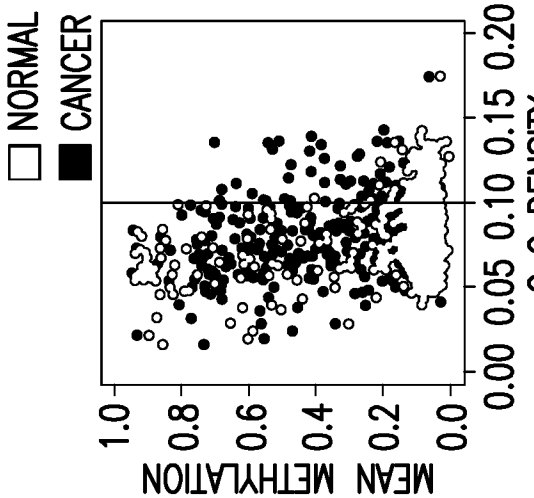

FIG.6B

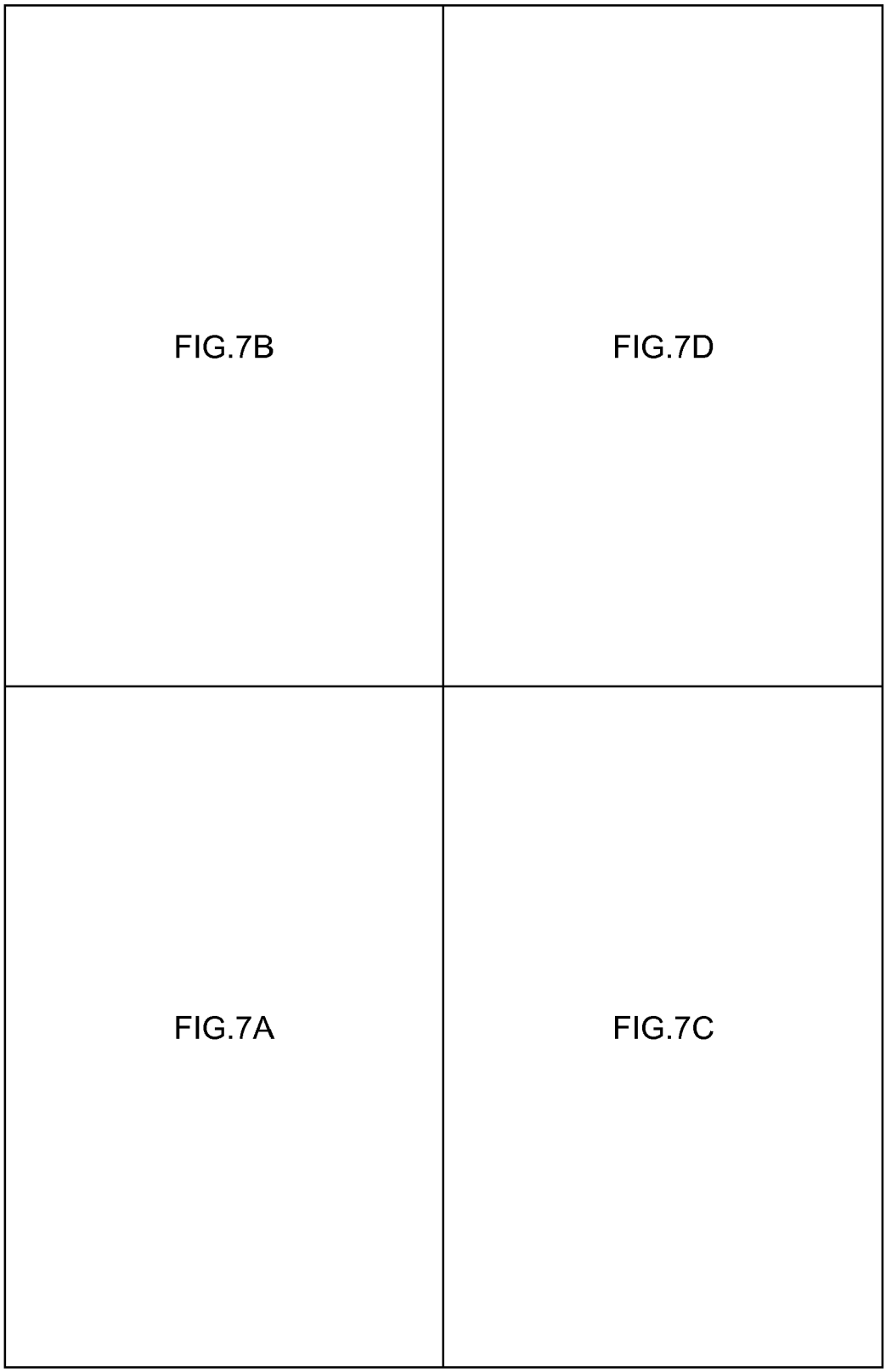

FIG.7

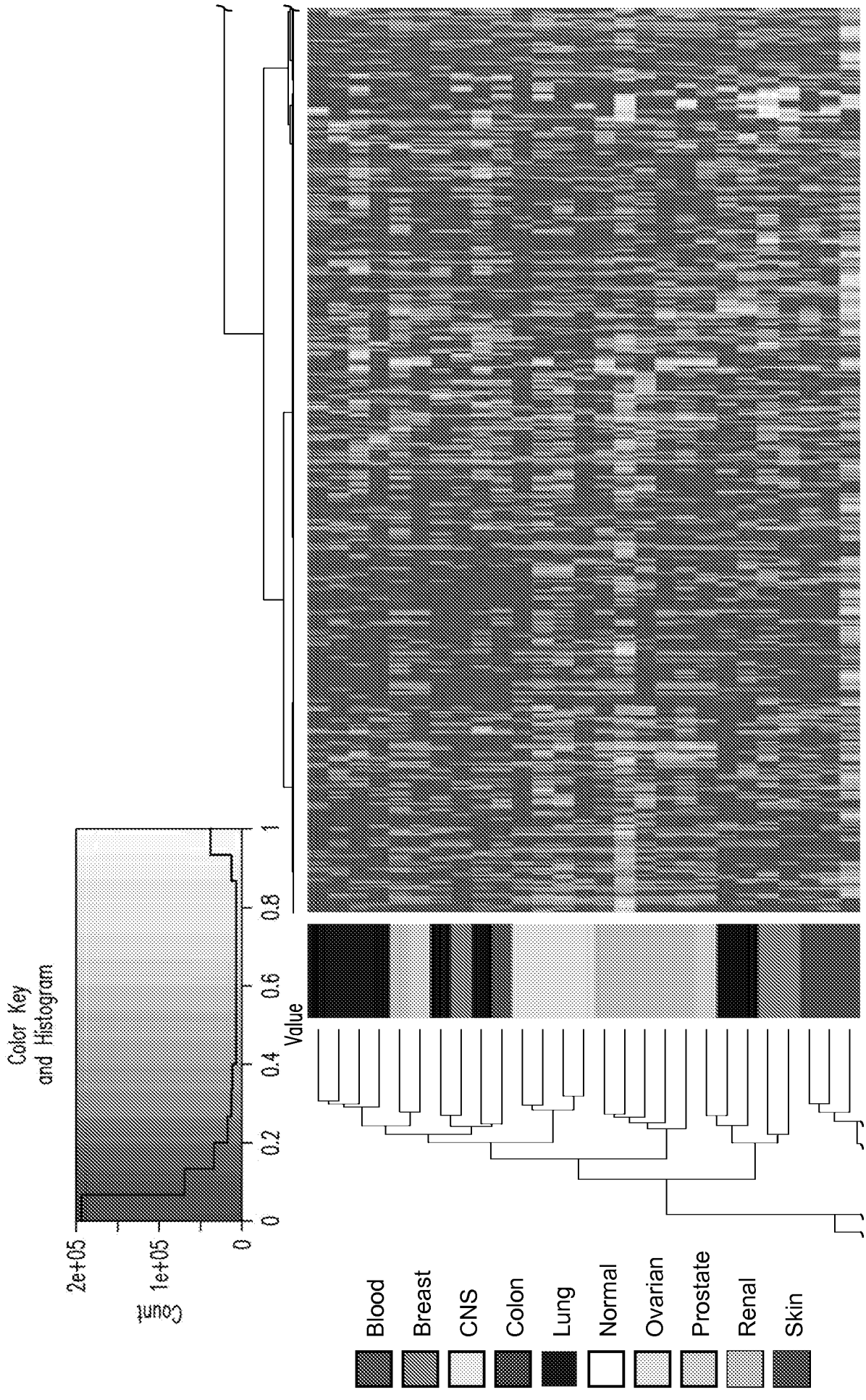
Color Key
and Histogram
Count
2e+05
1e+05
0
0
0.2
0.4
0.6
0.8
1
Value
Blood
Breast
CNS
Colon
Lung
Normal
Ovarian
Prostate
Renal
Skin

FIG. 7A

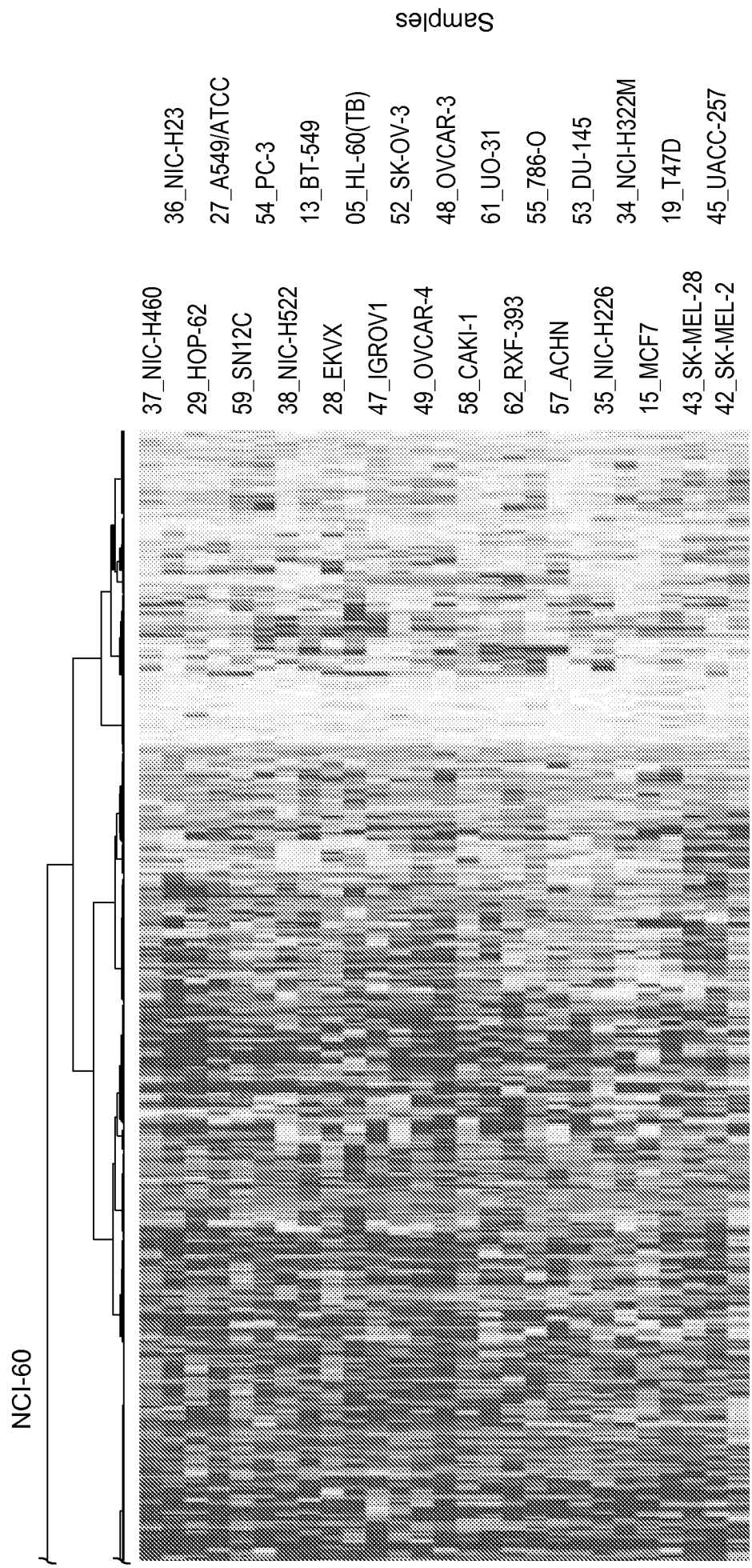
Samples
36_NIC-H23
27_A549/ATCC
54_PC-3
13_BT-549
05_HL-60(TB)
52_SK-OV-3
48_OVCAR-3
61_UO-31
55_786-O
53_DU-145
34_NCI-H322M
19_T47D
45_UACC-257
37_NIC-H460
29_HOP-62
59_SN12C
38_NIC-H522
28_EKVX
47_IGROV1
49_OVCAR-4
58_CAKI-1
62_RXF-393
57_ACHN
35_NIC-H226
15_MCF7
43_SK-MEL-28
42_SK-MEL-2
NCI-60

FIG. 7B

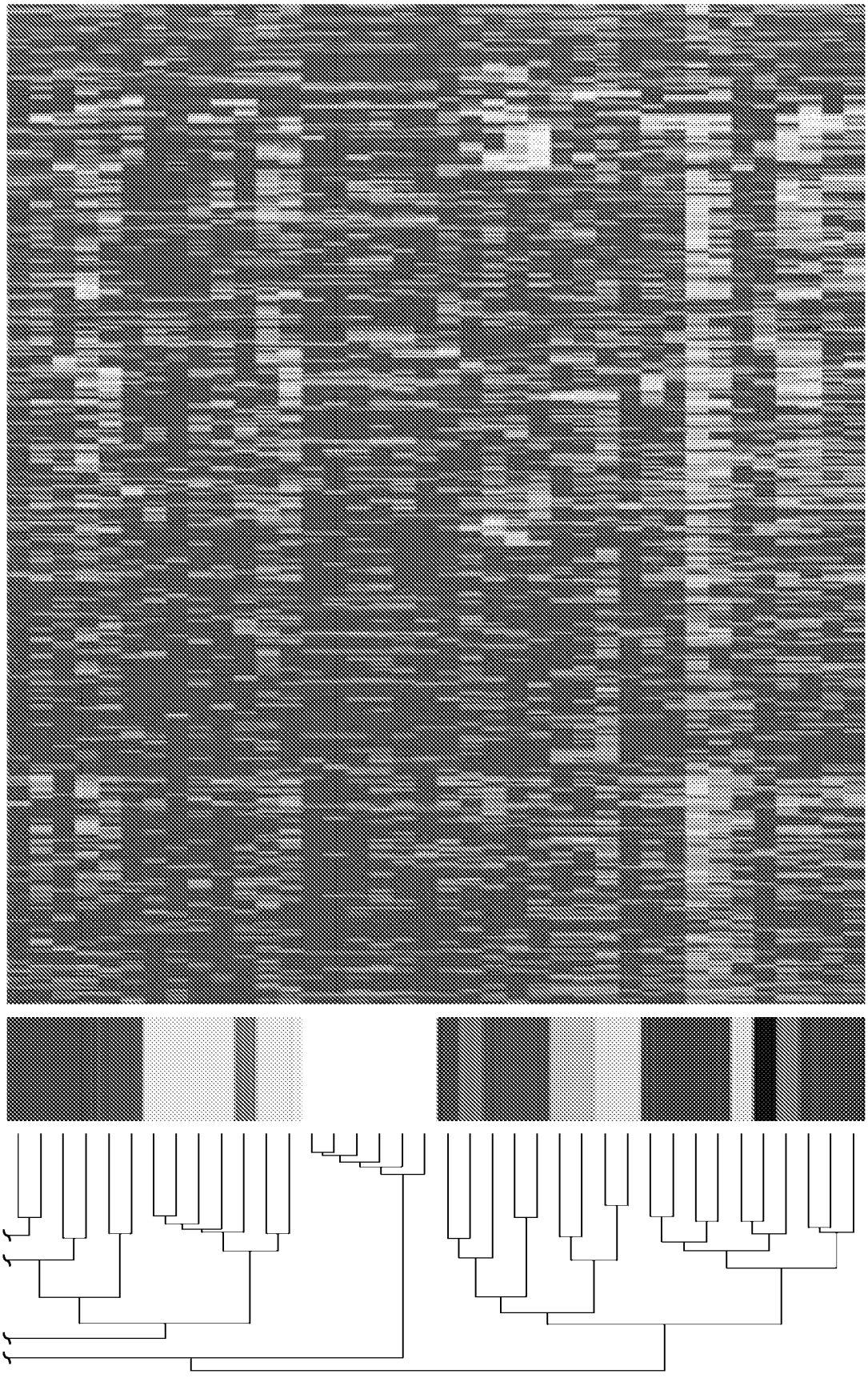

FIG.7C

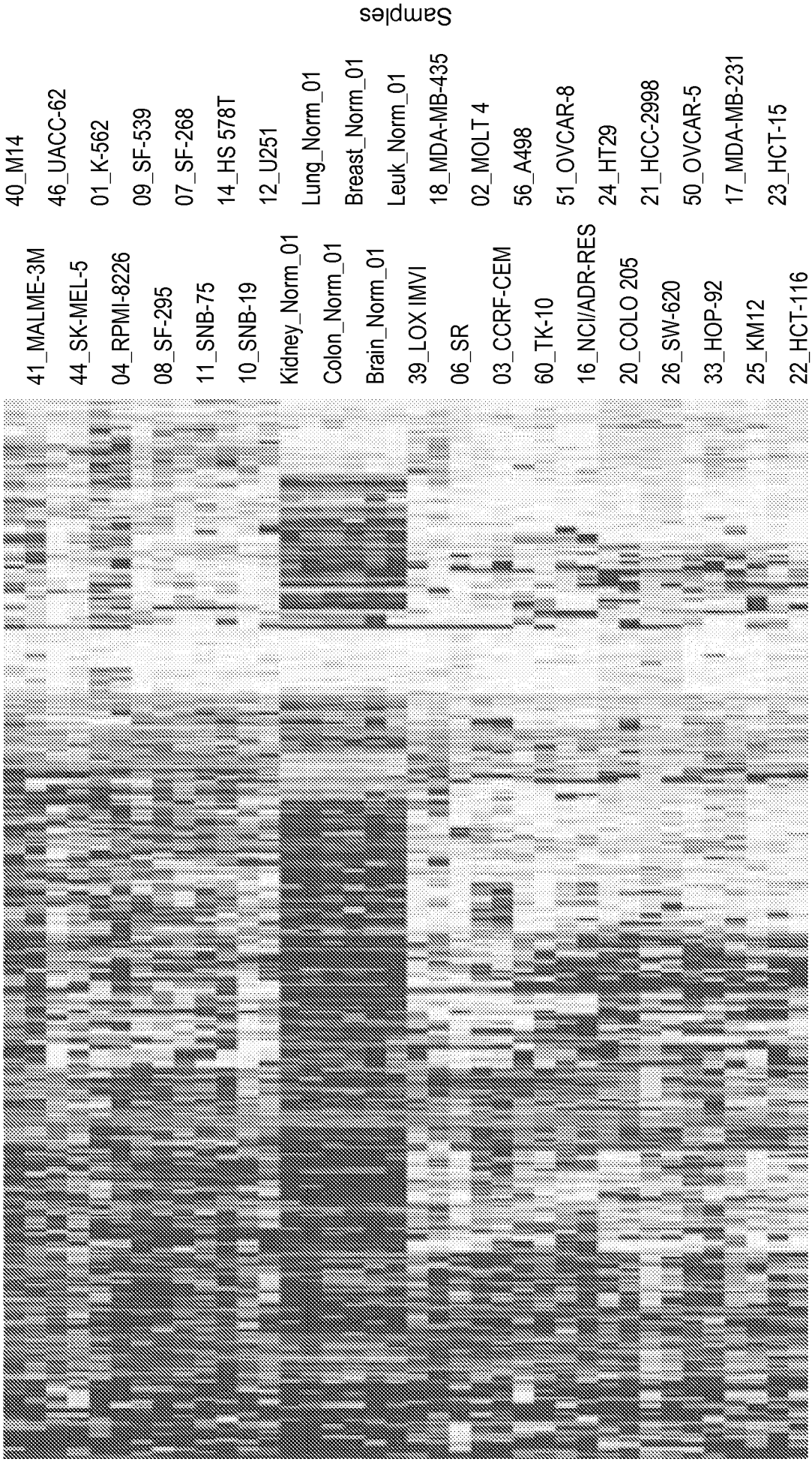
Samples
40_M14
46_UACC-62
01_K-562
09_SF-539
07_SF-268
14_HS 578T
12_U251
Lung_Norm_01
Breast_Norm_01
Leuk_Norm_01
18_MDA-MB-435
02_MOLT 4
56_A498
51_OVCAR-8
24_HT29
21_HCC-2998
50_OVCAR-5
17_MDA-MB-231
23_HCT-15
41_MALME-3M
44_SK-MEL-5
04_RPMI-8226
08_SF-295
11_SNB-75
10_SNB-19
Kidney_Norm_01
Colon_Norm_01
Brain_Norm_01
39_LOX IMVI
06_SR
03_CCRF-CEM
60_TK-10
16_NCI/ADR-RES
20_COLO 205
26_SW-620
33_HOP-92
25_KM12
22_HCT-116
CpG Units

FIG. 7D

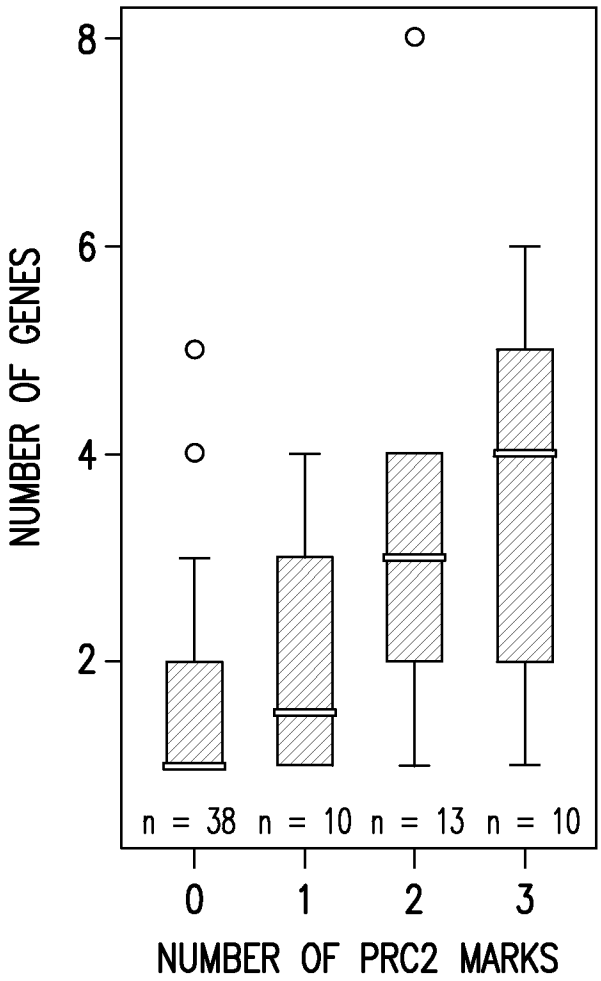
8
6
4
2
NUMBER OF GENES
n = 38
n = 10
n = 13
n = 10
0
1
2
3
NUMBER OF PRC2 MARKS

FIG.8

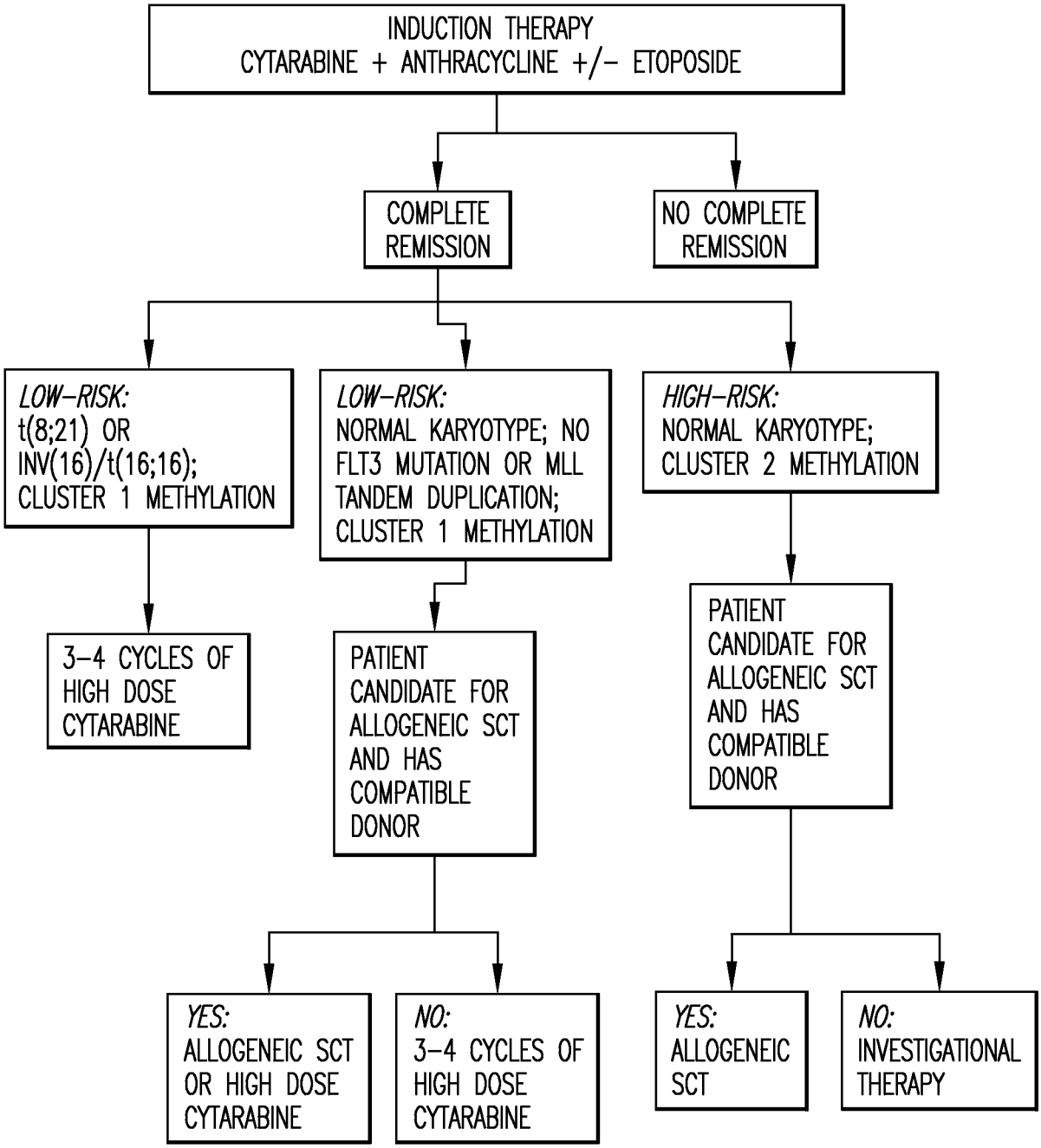
INDUCTION THERAPY
CYTARABINE + ANTHRACYCLINE +/- ETOPOSIDE
COMPLETE REMISSION
NO COMPLETE REMISSION
LOW-RISK:
t(8;21) OR
INV(16)/t(16;16);
CLUSTER 1 METHYLATION
LOW-RISK:
NORMAL KARYOTYPE; NO
FLT3 MUTATION OR MLL
TANDEM DUPLICATION;
CLUSTER 1 METHYLATION
HIGH-RISK:
NORMAL KARYOTYPE;
CLUSTER 2 METHYLATION
3-4 CYCLES OF
HIGH DOSE
CYTARABINE
PATIENT
CANDIDATE FOR
ALLOGENEIC SCT
AND HAS
COMPATIBLE
DONOR
PATIENT
CANDIDATE FOR
ALLOGENEIC SCT
AND HAS
COMPATIBLE
DONOR
YES:
ALLOGENEIC SCT
OR HIGH DOSE
CYTARABINE
NO:
3-4 CYCLES OF
HIGH DOSE
CYTARABINE
YES:
ALLOGENEIC
SCT
NO:
INVESTIGATIONAL
THERAPY

FIG.9