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## DESCRIPTION

**[0001]** The discovery that tumor cells release tumor-derived DNA into the blood stream has sparked the development of non-invasive methods capable of determining the presence, location and/or type of tumor in a subject using cell-free samples (e.g., plasma). Many tumors can be treatable if detected early in their development. However, current methods can lack the sensitivity and/or specificity to detect a tumor at an early stage and can return a large number of false positive or false negative results. For example, certain viruses are associated with cancer, but viral DNA can be detected in subjects that do not have cancer, thereby causing false positive results.

**[0002]** The sensitivity of a test can refer to the likelihood that a subject that is positive for a condition tests positive for the condition. The specificity of a test can refer to the likelihood that a subject that is negative for a condition tests negative for that condition. The problems of sensitivity and specificity can be exaggerated in assays for the early detection of tumors, e.g., because samples on which such tumor detection methods are performed can have relatively small amounts of tumor-derived DNA and because the condition itself can have a relatively low prevalence among individuals tested in the early stage. Accordingly, there is a clinical need for methods having higher sensitivity and/or specificity for the detection of tumors. US 2015/361505 A1 (SONG WEI [US] ET AL) describes a method of detecting the presence or absence of hepatitis B virus (HBV)-associated hepatocellular carcinoma (HCC) in a mammal, comprising quantifying the methylation level of one or more regions of HBV DNA in the DNA from one or more body fluids from said mammal. KANAKRY J. A. ET AL (BLOOD, vol. 122, no. 21, 4232-4232, 15 November 2013) describes differential methylation of EBV DNA in different EBV-related tumours.

**[0003]** According to the present invention, there is provided a method of analyzing a biological sample of a subject that is an animal, the biological sample including a mixture of cell-free DNA molecules from a genome of the subject and from one or more other genomes, the method comprising: analyzing a plurality of cell-free DNA molecules from the biological sample, wherein analyzing one of the plurality of cell-free DNA molecules includes: identifying a location of the cell-free DNA molecule in a particular viral genome; and determining whether the cell-free DNA molecule is methylated at one or more sites of the particular viral genome; measuring a mixture methylation level based on amounts of the plurality of cell-free DNA molecules methylated at a set of sites of the particular viral genome, wherein the set of sites are across a plurality of regions; comparing the mixture methylation level to one or more reference methylation levels determined from at least two cohorts of other subjects, wherein the at least two cohorts have different classifications associated with the particular viral genome, the different classifications including a first condition; and determining a first classification of whether the subject has the first condition based on the comparing..

**[0004]** Embodiments provide systems, apparatuses, and methods for analyzing a biological sample of a subject, e.g., in the animal kingdom, such as a human. Cell-free DNA molecules in

a mixture of the biological sample can be analyzed to detect viral DNA, e.g., by determining a location in a particular viral genome. A methylation status of the viral DNA at one or more sites in the viral genome can be determined. Mixture methylation level(s) can be measured based on one or more amounts of the plurality of cell-free DNA molecules methylated at a set of site(s) of the particular viral genome. The mixture methylation level(s) can be determined in various ways, e.g., as a percentage/density of cell-free DNA molecules that are methylated at a particular site or across multiple sites, and potentially across multiple regions, each including one or more sites.

**[0005]** The mixture methylation level(s) can be compared to reference methylation level(s), e.g., determined from at least two cohorts of other subjects. The cohorts can have different classifications (including the first condition) associated with the particular viral genome. Other cohort(s) can correspond to other condition(s). The comparison can be performed in a variety of ways, e.g., by forming a multidimensional point of N methylation levels and determining differences from N reference methylation levels. A first classification of whether the subject has the first condition can be determined based on the comparing.

**[0006]** These and other embodiments of the disclosure are described in detail below. For example, other embodiments are directed to systems, devices, and computer readable media associated with methods described herein.

**[0007]** A better understanding of the nature and advantages of embodiments of the present disclosure may be gained with reference to the following detailed description and the accompanying drawings, in which:

FIG. 1 shows the design of capture probes for targeted bisulfite sequencing according to embodiments of the present disclosure.

FIG. 2 shows the methylation densities of CpG sites across the Epstein-Barr virus (EBV) genome in patients with infectious mononucleosis, nasopharyngeal carcinoma (NPC) and Natural killer (NK)-T cell lymphoma according to embodiments of the present disclosure.

FIG. 3 shows the methylation profiles of plasma EBV DNA in a patient (AL038) from a screening cohort with early stage NPC (Stage I) according to embodiments of the present disclosure.

FIG. 4 shows the differences in methylation densities of CpG sites across the EBV genome between two patients with different conditions according to embodiments of the present disclosure.

FIG. 5 shows the differences in methylation densities of CpG sites across the EBV genome between two patients with NPC (TBR1392 and TBR1416) according to embodiments of the present disclosure.

FIG. 6 shows the differences in the methylation patterns of plasma EBV DNA between a patient with early stage NPC (AO050) and a subject with false positive result of plasma EBV DNA

(HB002) according to embodiments of the present disclosure.

FIGS. 7A-7C are dot plots showing the methylation density of a CpG site across the EBV genome in one patient (on the x-axis) and the corresponding methylation density of the same CpG site in the other patient (on the y-axis) according to embodiments of the present disclosure.

FIG. 8 shows the methylation percentages of plasma EBV DNA based on CpG sites in the EBV genome in subjects with infectious mononucleosis (IM) (n=2), EBV-associated lymphoma (n=3), transiently positive plasma EBV DNA (n=3), persistently positive plasma EBV DNA (n=3) and NPC (n=6) according to embodiments of the present disclosure.

FIG. 9 illustrates the mining of differentially methylated regions (DMRs) fulfilling first selection criteria according to embodiments of the present disclosure.

FIG. 10 is a table listing the genomic coordinates of the differentially methylated regions fulfilling the criteria described in FIG. 9.

FIG. 11 shows the methylation percentages of plasma EBV DNA based on the 821 CpG sites within the 39 DMRs described in FIG. 10 in the subjects with infectious mononucleosis (IM) (n=2), EBV-associated lymphoma (n=3), transiently positive plasma EBV DNA (n=3), persistently positive plasma EBV DNA (n=3), and NPC (n=6) according to embodiments of the present disclosure.

FIG. 12 illustrates the mining of differentially methylated regions (DMRs) fulfilling the second selection criteria according to embodiments of the present disclosure.

FIG. 13 shows the methylation percentages of plasma EBV DNA based on the 46 DMRs defined in FIG. 12 in the non-NPC subjects with transiently positive plasma EBV DNA, non-NPC subjects with persistently positive plasma EBV DNA, and NPC patients according to embodiments of the present disclosure.

FIG. 14 illustrates the mining of representative methylation consensus regions fulfilling third selection criteria according to embodiments of the present disclosure.

FIG. 15 shows the methylation percentages of plasma EBV DNA based on the 'representative' CpG sites described in FIG. 12 in the same group of subjects with infectious mononucleosis (IM) (n=2), EBV-associated lymphoma (n=3), transiently positive plasma EBV DNA (n=3), persistently positive plasma EBV DNA (n=3), and NPC (n=6) according to embodiments of the present disclosure.

FIG. 16 shows examples of CpG sites with the methylation percentages over the sites greater than 80% in the pooled sequencing data of the 3 cases with persistently positive plasma EBV DNA and an average of less than 20% in the 3 subjects with NPC according to embodiments of the present disclosure.

FIG. 17 shows examples of CpG sites with the methylation percentages over the sites less than 20% in the pooled sequencing data of the 3 cases with persistently positive plasma EBV

DNA and greater than 80% in the 3 subjects with NPC according to embodiments of the present disclosure.

FIG. 18 shows a cluster dendrogram with the hierarchical clustering analysis based on methylation pattern analysis of plasma EBV DNA for 6 patients with NPC (including 4 patients with early stage disease from our screening cohort), 2 patients with extranodal NK-T cell lymphoma, and 2 patients with infectious mononucleosis according to embodiments of the present disclosure.

FIG. 19 shows a cluster dendrogram with the hierarchical clustering analysis based on methylation pattern analysis of plasma EBV DNA for 6 patients with NPC (including 4 patients with early stage NPC from our screening cohort) and 3 non-NPC subjects with persistently positive plasma EBV DNA according to embodiments of the present disclosure.

FIG. 20 shows a heatmap 2000 illustrating the methylation levels of all the non-overlapping 500-bp regions in the whole EBV genome for patients with nasopharyngeal carcinoma, NK-T cell lymphoma, and infectious mononucleosis.

FIG. 21 shows the size profiles of size distribution of sequenced plasma DNA fragments mapped to the EBV genome and human genome in 2 patients with NPC (TBR1392 and TBR1416) and 2 patients with infectious mononucleosis (TBR1610 and TBR1661), and 3 non-NPC subjects with persistently positive plasma EBV DNA on serial analysis (AF091, HB002 and HF020) according to embodiments of the present disclosure.

FIG. 22 shows the size ratio in 6 patients with NPC and 3 subjects that are persistently positive for plasma EBV DNA according to embodiments of the present disclosure.

FIG. 23 shows the EBV DNA size ratios in the non-NPC subjects with transiently positive plasma EBV DNA, non-NPC subjects with persistently positive plasma EBV DNA, and NPC patients according to embodiments of the present disclosure.

FIG. 24 shows the proportion of plasma EBV DNA reads (plasma DNA reads mapped to the EBV genome) among all sequenced plasma DNA reads in the non-NPC subjects with transiently positive plasma EBV DNA, non-NPC subjects with persistently positive plasma EBV DNA, and NPC patients according to embodiments of the present disclosure.

FIG. 25 is a plot of the proportions of the plasma EBV DNA reads and corresponding size ratio values for the NPC patients, non-NPC subjects with transiently positive, and persistently positive plasma EBV DNA according to embodiments of the present disclosure.

FIG. 26 is a plot of the proportions of the plasma EBV DNA reads and corresponding methylation percentage values for the NPC patients, non-NPC subjects with transiently positive, and persistently positive plasma EBV DNA according to embodiments of the present disclosure.

FIGS. 27A and 27B show a 3-dimensional plot of the proportions of the plasma EBV DNA reads and corresponding size ratio and methylation percentage values for the NPC patients,

non-NPC subjects with transiently positive, and persistently positive plasma EBV DNA according to embodiments of the present disclosure.

FIGS. 28A and 28B show a receiver operator characteristics (ROC) curve analysis for various combinations of count-based, size-based, and methylation-based analyses according to embodiments of the present disclosure.

FIG. 29 shows the clinical stage of the 5 cases of HPV positive-head and neck squamous cell carcinoma (HPV+ve HNSCC).

FIG. 30 shows the methylation profiles of plasma HPV DNA in individual patients with HPV positive head and neck squamous cell carcinoma (HPV+ve HNSCC) according to embodiments of the present disclosure.

FIG. 31 shows the methylation level of all the CpG sites across the HPV genome in two patients with HPV+ve HNSCC according to embodiments of the present disclosure.

FIGS. 32A and 32B shows the proportions of hepatitis B virus (HBV) DNA reads (plasma DNA reads mapped to the HBV genome) and the methylation percentages of all the CpG sites across the HBV genome for 9 patients with chronic hepatitis B infection (HBV) and 10 patients with hepatocellular carcinoma (HCC) according to embodiments of the present disclosure.

FIG. 33 is a flowchart illustrating a method of analyzing a biological sample of a subject that is an animal to determine a classification of a first condition according to embodiments of the present disclosure.

FIG. 34 illustrates a system according to an embodiment of the present invention.

FIG. 35 shows a block diagram of an example computer system usable with system and methods according to embodiments of the present invention.

**[0008]** Appendix A shows the list of individual CpG sites across the EBV genome with differential methylation levels, when the differences in the methylation percentages over these CpG sites between the pooled sequencing data of 3 subjects with persistently positive EBV DNA and the 3 patients with NPC are greater than 20%. Those sites marked with \* have a difference in methylation percentages greater than 40%, \*\* have a difference greater than 60%, and \*\*\* have a difference greater than 80%.

**[0009]** The term "sample", "biological sample" or "patient sample" is meant to include any tissue or material derived from a living or dead subject. A biological sample may be a cell-free sample, which may include a mixture of nucleic acid molecules from the subject and potentially nucleic acid molecules from a pathogen, e.g., a virus. A biological sample generally comprises a nucleic acid (e.g., DNA or RNA) or a fragment thereof. The term "nucleic acid" may generally refer to deoxyribonucleic acid (DNA), ribonucleic acid (RNA) or any hybrid or fragment thereof. The nucleic acid in the sample may be a cell-free nucleic acid. A sample may be a liquid

sample or a solid sample (e.g., a cell or tissue sample). The biological sample can be a bodily fluid, such as blood, plasma, serum, urine, vaginal fluid, fluid from a hydrocele (e.g., of the testis), vaginal flushing fluids, pleural fluid, ascitic fluid, cerebrospinal fluid, saliva, sweat, tears, sputum, bronchoalveolar lavage fluid, discharge fluid from the nipple, aspiration fluid from different parts of the body (e.g., thyroid, breast), etc. Stool samples can also be used. In various embodiments, the majority of DNA in a biological sample that has been enriched for cell-free DNA (e.g., a plasma sample obtained via a centrifugation protocol) can be cell-free (e.g., greater than 50%, 60%, 70%, 80%, 90%, 95%, or 99% of the DNA can be cell-free). The centrifugation protocol can include, for example, 3,000 g × 10 minutes, obtaining the fluid part, and re-centrifuging at, for example, 30,000 g for another 10 minutes to remove residual cells.

**[0010]** The term "fragment" (e.g., a DNA fragment), as used herein, can refer to a portion of a polynucleotide or polypeptide sequence that comprises at least 3 consecutive nucleotides. A nucleic acid fragment can retain the biological activity and/or some characteristics of the parent polypeptide. A nucleic acid fragment can be double-stranded or single-stranded, methylated or unmethylated, intact or nicked, complexed or not complexed with other macromolecules, e.g. lipid particles, proteins. In an example, nasopharyngeal cancer cells can release fragments of Epstein- Barr Virus (EBV) DNA into the blood stream of a subject, e.g., a patient. These fragments can comprise one or more BamHI-W sequence fragments, which can be used to detect the level of tumor-derived DNA in the plasma. The BamHI-W sequence fragment corresponds to a sequence that can be recognized and/or digested using the Bam-HI restriction enzyme. The BamHI-W sequence can refer to the sequence 5'-GGATCC-3'.

**[0011]** A tumor-derived nucleic acid can refer to any nucleic acid released from a tumor cell, including pathogen nucleic acids from pathogens in a tumor cell. For example, Epstein-Barr virus (EBV) DNA can be released from a cancer cell of a subject with nasopharyngeal carcinoma (NPC).

**[0012]** The term "assay" generally refers to a technique for determining a property of a nucleic acid. An assay (e.g., a first assay or a second assay) generally refers to a technique for determining the quantity of nucleic acids in a sample, genomic identity of nucleic acids in a sample, the copy number variation of nucleic acids in a sample, the methylation status of nucleic acids in a sample, the fragment size distribution of nucleic acids in a sample, the mutational status of nucleic acids in a sample, or the fragmentation pattern of nucleic acids in a sample. Any assay known to a person having ordinary skill in the art may be used to detect any of the properties of nucleic acids mentioned herein. Properties of nucleic acids include a sequence, quantity, genomic identity, copy number, a methylation state at one or more nucleotide positions, a size of the nucleic acid, a mutation in the nucleic acid at one or more nucleotide positions, and the pattern of fragmentation of a nucleic acid (e.g., the nucleotide position(s) at which a nucleic acid fragments). The term "assay" may be used interchangeably with the term "method". An assay or method can have a particular sensitivity and/or specificity, and their relative usefulness as a diagnostic tool can be measured using ROC-AUC statistics.

**[0013]** The term "random sequencing," as used herein, generally refers to sequencing

whereby the nucleic acid fragments sequenced have not been specifically identified or predetermined before the sequencing procedure. Sequence-specific primers to target specific gene loci are not required. In some embodiments, adapters are added to the end of a fragment, and the primers for sequencing attached to the adapters. Thus, any fragment can be sequenced with the same primer that attaches to a same universal adapter, and thus the sequencing can be random. Massively parallel sequencing may be performed using random sequencing.

**[0014]** A "*sequence read*" generally refers to a string of nucleotides sequenced from any part or all of a nucleic acid molecule. For example, a sequence read may be a short string of nucleotides (e.g., 20-150 bases) sequenced from a nucleic acid fragment, a short string of nucleotides at one or both ends of a nucleic acid fragment, or the sequencing of the entire nucleic acid fragment that exists in the biological sample. A sequence read may be obtained in a variety of ways, e.g., using sequencing techniques or using probes, e.g., in hybridization arrays or capture probes, or amplification techniques, such as the polymerase chain reaction (PCR) or linear amplification using a single primer or isothermal amplification, or based on biophysical measurements, such as mass spectrometry.

**[0015]** A "*methylome*" provides a measure of an amount of DNA methylation at a plurality of sites or loci in a genome (e.g., a human or other animal genome or a viral genome). The methylome may correspond to all of the genome, a substantial part of the genome, or relatively small portion(s) of the genome. Examples of methylomes of interest are the methylomes of tumor cells (e.g. nasopharyngeal carcinoma, hepatocellular carcinoma, cervical carcinoma), viral methylomes (e.g., of EBV resident within healthy or tumor cells of a subject); bacterial methylomes, and organs (e.g. methylomes of brain cells, bones, the lungs, the heart, the muscles and the kidneys, etc.) that can contribute DNA into a bodily fluid (e.g. plasma, serum, sweat, saliva, urine, genital secretions, semen, stools fluid, diarrheal fluid, cerebrospinal fluid, secretions of the gastrointestinal tract, ascitic fluid, pleural fluid, intraocular fluid, fluid from a hydrocele (e.g. of the testis), fluid from a cyst, pancreatic secretions, intestinal secretions, sputum, tears, aspiration fluids from breast and thyroid, etc.). The organs may be transplanted organs. The methylome of a fetus is another example.

**[0016]** A "*plasma methylome*" is a methylome determined from the plasma or serum of an animal (e.g., a human). The plasma methylome is an example of a cell-free methylome since plasma and serum include cell-free DNA. The plasma methylome is also an example of a mixed methylome since it is a mixture of fetal/maternal methylome, tumor/patient methylome, DNA derived from different tissues or organs, donor/recipient methylome in the context or organ transplantation, and/or mixture of DNA from different genomes (e.g., animal genome and bacterial/viral genomes).

**[0017]** A "*site*" (also called a "*genomic site*") corresponds to a single site, which may be a single base position or a group of correlated base positions, e.g., a CpG site or larger group of correlated base positions. A "*locus*" may correspond to a region that includes multiple sites. A locus can include just one site, which would make the locus equivalent to a site in that context.

**[0018]** The "*methylation index*" for each genomic site (e.g., a CpG site) can refer to the proportion of DNA fragments (e.g., as determined from sequence reads or probes) showing methylation at the site over the total number of reads covering that site. A "read" can correspond to information (e.g., methylation status at a site) obtained from a DNA fragment. A read can be obtained using reagents (e.g. primers or probes) that preferentially hybridize to DNA fragments of a particular methylation status. Typically, such reagents are applied after treatment with a process that differentially modifies or differentially recognizes DNA molecules depending of their methylation status, e.g. bisulfite conversion, or methylation-sensitive restriction enzyme, or methylation binding proteins, or anti-methylcytosine antibodies. In another embodiment, single molecule sequencing techniques that recognize methylcytosines and hydroxymethylcytosines can be used for elucidating the methylation status and for determining a methylation index.

**[0019]** The "*methylation density*" of a region can refer to the number of reads at sites within the region showing methylation divided by the total number of reads covering the sites in the region. The sites may have specific characteristics, e.g., being CpG sites. Thus, the "CpG methylation density" of a region can refer to the number of reads showing CpG methylation divided by the total number of reads covering CpG sites in the region (e.g., a particular CpG site, CpG sites within a CpG island, or a larger region). For example, the methylation density for each 100-kb bin in the human genome can be determined from the total number of cytosines not converted after bisulfite treatment (which corresponds to methylated cytosine) at CpG sites as a proportion of all CpG sites covered by sequence reads mapped to the 100-kb region. This analysis can also be performed for other bin sizes, e.g. 500 bp, 5 kb, 10 kb, 50-kb or 1-Mb, etc. A region could be the entire genome or a chromosome or part of a chromosome (e.g. a chromosomal arm). The methylation index of a CpG site is the same as the methylation density for a region when the region only includes that CpG site. The "proportion of methylated cytosines" can refer to the number of cytosine sites, "C's", that are shown to be methylated (for example unconverted after bisulfite conversion) over the total number of analyzed cytosine residues, i.e. including cytosines outside of the CpG context, in the region. The methylation index, methylation density, and proportion of methylated cytosines are examples of "*methylation levels*," which may include other ratios involving counts of methylated reads at sites. Apart from bisulfite conversion, other processes known to those skilled in the art can be used to interrogate the methylation status of DNA molecules, including, but not limited to enzymes sensitive to the methylation status (e.g. methylation-sensitive restriction enzymes), methylation binding proteins, single molecule sequencing using a platform sensitive to the methylation status (e.g. nanopore sequencing (Schreiber et al. Proc Natl Acad Sci 2013; 110: 18910-18915) and by the Pacific Biosciences single molecule real time analysis (Flusberg et al. Nat Methods 2010; 7: 461-465)).

**[0020]** A "*methylation profile*" (also called methylation status) includes information related to DNA methylation for a region. Information related to DNA methylation can include, but not limited to, a methylation index of a CpG site, a methylation density of CpG sites in a region, a distribution of CpG sites over a contiguous region, a pattern or level of methylation for each

individual CpG site within a region that contains more than one CpG site, and non-CpG methylation. A methylation profile of a substantial part (e.g., covering more than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90%) of the genome can be considered equivalent to the methylome. "*DNA methylation*" in mammalian genomes typically refers to the addition of a methyl group to the 5' carbon of cytosine residues (i.e. 5-methylcytosines) among CpG dinucleotides. DNA methylation may occur in cytosines in other contexts, for example CHG and CHH, where H is adenine, cytosine or thymine. Cytosine methylation may also be in the form of 5-hydroxymethylcytosine. Non-cytosine methylation, such as N<sup>6</sup>-methyladenine, has also been reported.

**[0021]** "*Methylation-aware sequencing*" refers to any sequencing method that allows one to ascertain the methylation status of a DNA molecule during a sequencing process, including, but not limited to bisulfite sequencing, or sequencing preceded by methylation-sensitive restriction enzyme digestion, immunoprecipitation using anti-methylcytosine antibody or methylation binding protein, or single molecule sequencing that allows elucidation of the methylation status. A "*methylation-aware assay*" or "*methylation-sensitive assay*" can include both sequencing and non-sequencing based methods, such as MSP, probe based interrogation, hybridization, restriction enzyme digestion followed by density measurements, anti-methylcytosine immunoassays, mass spectrometry interrogation of proportion of methylated cytosines or hydroxymethylcytosines, immunoprecipitation not followed by sequencing, etc.

**[0022]** A "tissue" corresponds to a group of cells that group together as a functional unit. More than one type of cells can be found in a single tissue. Different types of tissue may consist of different types of cells (e.g., hepatocytes, alveolar cells or blood cells), but also may correspond to tissue from different organisms (host vs. virus) or to healthy cells vs. tumor cells. The term "tissue" can generally refer to any group of cells found in the human body (e.g., heart tissue, lung tissue, kidney tissue, nasopharyngeal tissue, oropharyngeal tissue). In some aspects, the term "tissue" or "tissue type" may be used to refer to a tissue from which a cell-free nucleic acid originates. In one example, viral nucleic acid fragments may be derived from blood tissue, e.g., for Epstein- Barr Virus (EBV). In another example, viral nucleic acid fragments may be derived from tumor tissue, e.g., EBV or Human papillomavirus infection (HPV).

**[0023]** A "*separation value*" (or relative abundance) corresponds to a difference or a ratio involving two values, e.g., two amounts of DNA molecules, two fractional contributions, or two methylation levels, such as a sample (mixture) methylation level and a reference methylation level. The separation value could be a simple difference or ratio. As examples, a direct ratio of  $x/y$  is a separation value, as well as  $x/(x+y)$ . The separation value can include other factors, e.g., multiplicative factors. As other examples, a difference or ratio of functions of the values can be used, e.g., a difference or ratio of the natural logarithms ( $\ln$ ) of the two values. A separation value can include a difference and/or a ratio. A methylation level is an example of a relative abundance, e.g., between methylated DNA molecules (e.g., at particular sites) and other DNA molecules (e.g., all other DNA molecules at particular sites or just unmethylated

DNA molecules). The amount of other DNA molecules can act as a normalization factor. As another example, an intensity of methylated DNA molecules (e.g., fluorescent or electrical intensity) relative to intensity of all or unmethylated DNA molecules can be determined. The relative abundance can also include an intensity per volume.

**[0024]** The term "*classification*" as used herein refers to any number(s) or other character(s) that are associated with a particular property of a sample. For example, a "+" symbol (or the word "positive") could signify that a sample is classified as having a particular level of a condition (e.g., cancer). The classification can be binary (e.g., positive or negative) or have more levels of classification (e.g., a scale from 1 to 10 or 0 to 1).

**[0025]** The terms "*cutoff*," "*threshold*," or reference level can refer to a predetermined number used in an operation. A threshold or reference value may be a value above or below which a particular classification applies, e.g., a classification of a condition, such as whether a subject has a condition or a severity of the condition. A cutoff may be predetermined with or without reference to the characteristics of the sample or the subject. For example, cutoffs may be chosen based on the age or sex of the tested subject. A cutoff may be chosen after and based on output of the test data. For example, certain cutoffs may be used when the sequencing of a sample reaches a certain depth. As another example, reference subjects with known classifications of one or more conditions and measured characteristic values (e.g., a methylation level) can be used to determine reference levels to discriminate between the different conditions and/or classifications of a condition (e.g., whether the subject has the condition). Any of these terms can be used in any of these contexts.

**[0026]** The terms "control", "control sample", "reference", "reference sample", "normal", and "normal sample" may be interchangeably used to generally describe a sample that does not have a particular condition, or is otherwise healthy. In an example, a method as disclosed herein may be performed on a subject having a tumor, where the reference sample is a sample taken from a healthy tissue of the subject. In another example, the reference sample is a sample taken from a subject with the disease, e.g. cancer or a particular stage of cancer. A reference sample may be obtained from the subject, or from a database. The reference generally refers to a reference genome that is used to map sequence reads obtained from sequencing a sample from the subject. A reference genome generally refers to a haploid or diploid genome to which sequence reads from the biological sample and the constitutional sample can be aligned and compared. For a haploid genome, there is only one nucleotide at each locus. For a diploid genome, heterozygous loci can be identified, with such a locus having two alleles, where either allele can allow a match for alignment to the locus. A reference genome may correspond to a virus, e.g., by including one or more viral genomes.

**[0027]** The phrase "healthy," as used herein, generally refers to a subject possessing good health. Such a subject demonstrates an absence of any malignant or non-malignant disease. A "healthy individual" may have other diseases or conditions, unrelated to the condition being assayed, that may normally not be considered "healthy".

**[0028]** The terms "cancer" or "tumor" may be used interchangeably and generally refer to an abnormal mass of tissue wherein the growth of the mass surpasses and is not coordinated with the growth of normal tissue. A cancer or tumor may be defined as "benign" or "malignant" depending on the following characteristics: degree of cellular differentiation including morphology and functionality, rate of growth, local invasion, and metastasis. A "benign" tumor is generally well differentiated, has characteristically slower growth than a malignant tumor, and remains localized to the site of origin. In addition, a benign tumor does not have the capacity to infiltrate, invade, or metastasize to distant sites. A "malignant" tumor is generally poorly differentiated (anaplasia), has characteristically rapid growth accompanied by progressive infiltration, invasion, and destruction of the surrounding tissue. Furthermore, a malignant tumor has the capacity to metastasize to distant sites. "Stage" can be used to describe how advanced a malignant tumor is. Early stage cancer or malignancy is associated with less tumor burden in the body, generally with less symptoms, with better prognosis, and with better treatment outcome than a late stage malignancy. Late or advanced stage cancer or malignancy is often associated with distant metastases and/or lymphatic spread.

**[0029]** The term "*level of cancer*" (or more generally "*level of disease*" or "*level of condition*") can refer to whether cancer exists (i.e., presence or absence), a stage of a cancer, a size of tumor, whether there is metastasis, the total tumor burden of the body, the cancer's response to treatment, and/or other measure of a severity of a cancer (e.g. recurrence of cancer). The level of cancer may be a number or other indicia, such as symbols, alphabet letters, and colors. The level may be zero. The level of cancer may also include premalignant or precancerous conditions (states). The level of cancer can be used in various ways. For example, screening can check if cancer is present in someone who is not known previously to have cancer. Assessment can investigate someone who has been diagnosed with cancer to monitor the progress of cancer over time, study the effectiveness of therapies or to determine the prognosis. In one embodiment, the prognosis can be expressed as the chance of a patient dying of cancer, or the chance of the cancer progressing after a specific duration or time, or the chance of cancer metastasizing. Detection can mean 'screening' or can mean checking if someone, with suggestive features of cancer (e.g. symptoms or other positive tests), has cancer. A "level of pathology" can refer to level of pathology associated with a pathogen, where the level can be as described above for cancer. The level of diseases/condition can also be as described above for cancer. When the cancer is associated with a pathogen, a level of cancer can be a type of a level of pathology.

**[0030]** The terms "size profile" and "size distribution" generally relate to the sizes of DNA fragments in a biological sample. A size profile may be a histogram that provides a distribution of an amount of DNA fragments at a variety of sizes. Various statistical parameters (also referred to as size parameters or just parameter) can distinguish one size profile to another. One parameter is the percentage of DNA fragment of a particular size or range of sizes relative to all DNA fragments or relative to DNA fragments of another size or range.

**[0031]** The term "false positive" (FP) can refer to subjects not having a condition. False positive generally refers to subjects not having a tumor, a cancer, a pre-cancerous condition

(e.g., a precancerous lesion), a localized or a metastasized cancer, a non-malignant disease, or are otherwise healthy. The term false positive generally refers to subjects not having a condition, but are identified as having the condition by an assay or method of the present disclosure.

**[0032]** The terms "sensitivity" or "true positive rate" (TPR) can refer to the number of true positives divided by the sum of the number of true positives and false negatives. Sensitivity may characterize the ability of an assay or method to correctly identify a proportion of the population that truly has a condition. For example, sensitivity may characterize the ability of a method to correctly identify the number of subjects within a population having cancer. In another example, sensitivity may characterize the ability of a method to correctly identify one or more markers indicative of cancer.

**[0033]** The terms "specificity" or "true negative rate" (TNR) can refer to the number of true negatives divided by the sum of the number of true negatives and false positives. Specificity may characterize the ability of an assay or method to correctly identify a proportion of the population that truly does not have a condition. For example, specificity may characterize the ability of a method to correctly identify the number of subjects within a population not having cancer. In another example, specificity may characterize the ability of a method to correctly identify one or more markers indicative of cancer.

**[0034]** The term "ROC" or "ROC curve" can refer to the receiver operator characteristic curve. The ROC curve can be a graphical representation of the performance of a binary classifier system. For any given method, an ROC curve may be generated by plotting the sensitivity against the specificity at various threshold settings. The sensitivity and specificity of a method for detecting the presence of a tumor in a subject may be determined at various concentrations of tumor-derived nucleic acid in the plasma sample of the subject. Furthermore, provided at least one of the three parameters (e.g., sensitivity, specificity, and the threshold setting), and ROC curve may determine the value or expected value for any unknown parameter. The unknown parameter may be determined using a curve fitted to the ROC curve. The term "AUC" or "ROC-AUC" generally refers to the area under a receiver operator characteristic curve. This metric can provide a measure of diagnostic utility of a method, taking into account both the sensitivity and specificity of the method. Generally, ROC-AUC ranges from 0.5 to 1.0, where a value closer to 0.5 indicates the method has limited diagnostic utility (e.g., lower sensitivity and/or specificity) and a value closer to 1.0 indicates the method has greater diagnostic utility (e.g., higher sensitivity and/or specificity). See, e.g., Pepe et al, "Limitations of the Odds Ratio in Gauging the Performance of a Diagnostic, Prognostic, or Screening Marker," *Am. J. Epidemiol* 2004, 159 (9): 882-890. Additional approaches for characterizing diagnostic utility using likelihood functions, odds ratios, information theory, predictive values, calibration (including goodness-of-fit), and reclassification measurements are summarized according to Cook, "Use and Misuse of the Receiver Operating Characteristic Curve in Risk Prediction," *Circulation* 2007, 115: 928-935.

**[0035]** The term "about" or "approximately" can mean within an acceptable error range for the

particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, i.e., the limitations of the measurement system. For example, "about" can mean within 1 or more than 1 standard deviation, per the practice in the art. Alternatively, "about" can mean a range of up to 20%, up to 10%, up to 5%, or up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term "about" or "approximately" can mean within an order of magnitude, within 5-fold, and more preferably within 2-fold, of a value. Where particular values are described in the application and claims, unless otherwise stated the term "about" meaning within an acceptable error range for the particular value should be assumed. The term "about" can have the meaning as commonly understood by one of ordinary skill in the art. The term "about" can refer to  $\pm 10\%$ . The term "about" can refer to  $\pm 5\%$ .

**[0036]** The terminology used herein is for the purpose of describing particular cases only and is not intended to be limiting. As used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. The use of "or" is intended to mean an "inclusive or," and not an "exclusive or" unless specifically indicated to the contrary. The term "based on" is intended to mean "based at least in part on." Furthermore, to the extent that the terms "including", "includes", "having", "has", "with", or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term "comprising."

**[0037]** In the present disclosure, we describe an approach to differentiate among different EBV-associated diseases, malignancies, states or completely healthy individuals based on the analysis of methylation patterns of circulating EBV DNA fragments in blood. There are a number of applications or utilities for the analysis of methylation patterns of cell-free EBV DNA molecules. The feasibility of methylation analysis of cell-free viral molecules in a noninvasive manner would enhance the clinical applications in the context of screening, predictive medicine, risk stratification, surveillance and prognostication.

**[0038]** Embodiments can differentiate subjects with different virus-associated conditions (e.g., patients with NPC) and apparently healthy subjects with detectable plasma EBV DNA, with even a single time-point analysis, e.g., from a single blood draw. Embodiments can also be used for screening or detecting if a subject has a disease or cancer, for disease monitoring in a cancer patient, for prognostication and for disease or cancer risk prediction (i.e., for predicting if a subject may develop a disease or cancer in the future). This approach can also be generalized to viruses other than EBV. This approach is thus a general approach for identifying viral DNA-based biomarkers.

## **I. CANCER AND VIRUSES**

**[0039]** Both DNA and RNA viruses have been shown to be capable of causing cancer in humans. In some embodiments, a subject may have a cancer caused by a virus (e.g., an oncovirus). In some embodiments, a subject may have a cancer, and the cancer may be

detectable using viral DNA. For analysis of RNA, the nucleic acids would exist as complementary DNA (cDNA), which is copied from the RNA and is the medium for replication in the host cells. These cDNA could have methylation and be used in embodiments.

**[0040]** Various viral infections are associated with various cancers or other pathological conditions. For example, EBV infection is closely associated with NPC and natural killer (NK) T-cell lymphoma, Hodgkin lymphoma, gastric cancer, and infectious mononucleosis. Hepatitis B virus (HBV) infection and hepatitis C virus (HCV) infection are associated with increased risks of developing hepatocellular carcinoma (HCC). Human papillomavirus infection (HPV) are associated with increased risks of developing cervical cancer (CC) and head and neck squamous cell carcinoma (HNSCC). Although examples focus more on EBV, techniques are equally applicable for cancer and other conditions relating to HPV, HBV, and other viruses, particularly those associated with cancer.

#### **A. EBV**

**[0041]** It has been estimated that 95% of the world's population have an asymptomatic lifelong Epstein-Barr virus (EBV) infection, whereby the virus remains latent in the memory B cells of healthy individuals and persists in the body (Young et al. *Nat Rev Cancer* 2016 16(12):789-802). A small proportion of subjects develop a symptomatic infection, presenting as infectious mononucleosis with the viral infection. EBV is also regarded as an oncogenic virus for its association with a number of malignancies or cancer-like syndromes of epithelial and hematological origins, including nasopharyngeal carcinoma (NPC), gastric carcinoma, Burkitt's lymphoma, Hodgkin's lymphoma, natural killer-T cell (NK-T cell) lymphoma and post-transplant lymphoproliferative disorder (PTLD).

**[0042]** Circulating EBV DNA has been explored for its diagnostic and prognostic role in patients with EBV-associated malignancies. In this regard, plasma EBV DNA has been established as a biomarker of NPC (Lo et al. *Cancer Res* 1999; 59:1188-91). Regular surveillance with plasma EBV DNA is recommended for patients with a confirmed diagnosis of NPC for detection of residual disease and recurrence (Lo et al. *Cancer Res* 1999; 59:5452-5, Chan et al. *J Natl Cancer Inst* 2002;94:1614-9, Leung et al. *Cancer* 2003, 98(2), 288-91 & Leung et al. *Ann Oncol* 2014; 25(6):1204-8). Plasma EBV DNA has also been shown to have prognostic significance in other EBV-associated malignancies, including Hodgkin's lymphoma (Kanakry et al. *Blood* 2013; 121(18): 3547-3553), extranodal NK-T cell lymphoma (Wang et al. *Oncotarget* 2015; 6(30):30317-26, Kwong et al. *Leukemia* 2014; 28(4):865-870) and PTLN (Gulley and Tang. *Clin Microbiol Rev* 2010; 23(2): 350-66).

**[0043]** However, not all subjects that have such an infection will get an associated cancer. The source of the plasma EBV DNA must be different in persons without NPC. Unlike the persistent release of EBV DNA into the circulation from NPC cells, the source of EBV DNA only contributes such DNA transiently in the persons without NPC

### ***B. False Positives***

**[0044]** In the context of cancer screening, we have recently conducted a large-scale prospective study on NPC screening using plasma EBV DNA analysis by quantitative PCR (qPCR) (Chan et al. N Engl J Med 2017;377:513-522). We analyzed the plasma EBV DNA level in all recruited subjects (screening cohort) who were asymptomatic for NPC upon enrollment. Subjects with detectable amount of plasma EBV DNA were retested for EBV DNA at 4 weeks after the initial test. Among 20,174 subjects recruited, 1,112 had detectable plasma EBV DNA on their first test. There were 309 subjects who were persistently positive on the follow-up test based on a measure of an amount of plasma EBV DNA. Subsequently, 34 subjects with persistently positive plasma EBV DNA results were confirmed to have NPC by endoscopy and magnetic resonance imaging (MRI). As mentioned, plasma EBV DNA could be detected in apparently healthy individuals without NPC or other EBV-associated malignancies.

**[0045]** In the 20,174 subjects undergone NPC screening, the false plasma EBV DNA positive rate was approximately 5% based on single time-point analysis ( $(1112-34) / (20174-34) = 5.3\%$ ). The false positive rate was lowered to 1.5% with serial EBV DNA analysis on two occasions. However, the sequential testing of plasma EBV DNA requires the collection of an additional blood sample from subjects with initial positive results, which can present logistical challenges. Also, a substantial proportion of subjects who have positive plasma EBV DNA results do not have NPC (96% of subjects showing positive results on single time-point analysis do not have NPC, determined as  $(1112-34)/1112$ ). Subjects with false positive results would need serial assessment and unnecessary investigations including endoscopy and MRI for definitive diagnosis. All these would lead to patient anxiety and higher follow-up costs. Therefore, we aim to distinguish patients with NPC from subjects with false positive plasma EBV DNA results with a single time-point blood analysis. In this example, a false plasma EBV DNA positive rate can be considered a non-NPC positive rate or also referred to as a one-time positive rate.

### ***C. Use of Methylation***

**[0046]** Previous studies have described different types of viral latency (Types 0, I, II and III), which are defined by latency-associated viral gene transcription patterns, found in different EBV-associated malignancies (Young et al. Nat Rev Cancer 2016; 16(12):789-802). Viral latency is defined by the latency-associated gene transcription patterns. Therefore, viruses in different types of viral latency have different patterns of viral gene transcription. Different EBV-associated diseases or conditions with the same type of viral latency can have similar viral gene transcription patterns.

**[0047]** Among the different types of latency, there are different viral gene expression profiles and different methylation status of different viral gene promoters, including the origin of

replication, C-promoter, W-promoter, Q-promoter and LMP1/2 promoters (Woeller et al. *Curr Opin Virol* 2013;3(3):260-5). It has been suggested that DNA methylation contributes to regulate the gene expression and that there are latency-specific methylation patterns (Lieberman. *Nat Rev Microbiol* 2013;11(12):863-75). In one example, a previous study found a methylated state of C promoter, which is compatible with latency type II-specific methylation pattern, in EBV DNA from nasopharyngeal brush cytology samples of patients with NPC using methylation-specific PCR (Ramayanti et al. *Int J Cancer* 140,149-162). However, different EBV-associated diseases or conditions may have the same type of viral latency and would therefore have similar viral gene transcription patterns (examples described in the next paragraph). Thus, viral latency has no correlation with the stage of disease or cancer.

**[0048]** It is expected that different EBV-associated diseases with the same type of viral latency would have similar methylation patterns (Tempera et al. *Semin Cancer Biol* 2014;26:22-9, Fejer et al. *J Gen Virol* 2008;89:1364-70). In one example, a previous study has shown a similar methylation pattern across the viral promoter regions of EBV in both B cells from healthy EBV-seropositive individuals and tumor tissues from EBV-positive lymphomas, which both exhibit type I latency, using methylation-specific PCR (Paulson et al. *J Virol* 1999;73:9959-68).

**[0049]** A previous study has also attempted to study the methylation profiles of EBV by amplicon sequencing of bisulfite-converted DNA from cell lines and tissue samples of different EBV-associated diseases (Fernandex et al. *Genome Res* 2009;19(3):438-51). The 77 amplicons designed covered the transcription start sites of 94 different EBV latent and lytic genes and two structural RNAs, *FBFR1* and *EBER2*. The methylation status, either methylated or unmethylated, of the transcription start sites across the EBV genome was assessed. These results only demonstrated that the free viral DNA was devoid of DNA methylation as opposed to quantification, and the viral DNA from the cell lines or tissue samples of EBV-associated malignancies had a large number of methylated EBV transcription start sites. Importantly, samples with different malignant conditions (i.e. NPC and different lymphomas) were clustered together with the clustering analysis based on the methylation patterns of the transcription start sites, and transiently positive or persistently positive subjects were not identified. Based on their methylation patterns, the different malignant conditions could not be differentiated.

**[0050]** Most of the previous studies have focused on the analysis of the viral methylation profiles in tumor and cell line samples. These tumor samples need to be obtained through invasive procedures, for example surgical biopsies. This may limit the diagnostic applications e.g., for screening and serial monitoring. And, previous studies have been focused on qualitative aspects, and not quantitative results.

**[0051]** Despite the above reported data, we investigate the feasibility of differentiating among different EBV-associated diseases that exhibit the same type of viral latency. In contrast to the reported data above, we describe methods based on the analysis of the methylation profiles of plasma EBV DNA sequences that could differentiate between different EBV-related diseases or stage of diseases. For example, instead of only analyzing the methylation status (either

methylated or unmethylated) of the viral gene promoters, we studied the methylation level of each CpG site of cell-free EBV DNA molecules at a higher resolution in a genomewide manner. Remarkably, our data reveal that we could differentiate among different EBV-associated conditions and malignancies with the same latency type based on the methylation analysis of cell-free EBV DNA molecules. Our data thus provide new information on cell-free EBV DNA methylation patterns beyond that of latency type-specific variability.

**[0052]** Embodiments can analyze the methylation patterns of cell-free EBV DNA molecules in blood (e.g. in plasma or serum). Embodiments of the present disclosure can also be used in other bodily fluids containing cell-free EBV DNA molecules, e.g. urine (Chan et al. Clin Cancer Res 2008; 14(15):4809-13), serum, vaginal fluid, uterine or vaginal flushing fluids, plural fluid, ascitic fluid, cerebrospinal fluid, saliva, sweat, tears, sputum, bronchoalveolar lavage fluid, etc. Stool samples can also be used. The technical challenges are the low abundance and fragmented nature of viral molecules, when compared to analysis of tumoral DNA in tissue samples. Our present disclosure demonstrates the feasibility of methylation analysis of cell-free viral molecules in a noninvasive manner.

## II. MEASURING METHYLATION OF CELL-FREE EBV DNA MOLECULES

**[0053]** Methylation level(s) can be measured at various sites in a genome, e.g., animal (such as human), viral, or other. Methylation levels can be determined using methylation information at one or more sites, e.g., CpG sites. The methylation information can include counts of DNA molecules methylated at a given site or intensity signals corresponding to an amount of methylated/unmethylated DNA molecules. The methylation level can provide a relative abundance between methylated DNA molecules and unmethylated DNA molecules, e.g., where the amount of all or unmethylated DNA molecules at sites can act as a normalization factor.

**[0054]** For a viral genome, the mean methylated CpG density (also called methylation density, MD) of specific loci across the viral genome in the plasma can be calculated using the equation:

$$MD = \frac{M}{M + U}$$

where M is the count of methylated viral reads and U is the count of unmethylated viral reads at the CpG sites within the genetic locus across the viral genome. If there is more than one CpG site within a locus, then M and U correspond to the counts of methylated and unmethylated reads, respectively, across the sites. As examples, such counts of individual DNA fragments being methylated or unmethylated can be determined using sequencing or digital PCR. As another example, the methylation density can also be determined using real-time PCR to obtain a ratio of intensity of signals (e.g., a ratio a methylated intensity vs. unmethylated intensity), as opposed to counting specific numbers of reads. Thus, the analysis of nucleic acids can be performed collectively, where an intensity signal corresponds to multiple nucleic acids. The particular form for the methylation level can vary, e.g., a proportion as above

or a ratio between M and U.

#### **A. Various techniques for assessing methylation levels**

**[0055]** Different approaches can be used for determining the methylation levels, e.g., to determine a methylation profile spanning all or a substantial part of a genome, e.g., a human genome or a viral genome. To interrogate a methylation profile comprehensively, example embodiments can use massively parallel sequencing (MPS) of bisulfite-converted DNA to provide genomewide information and quantitative assessment of the level of methylation on a per nucleotide and per allele basis. Any methylation-sensitive assay could be used to determine the methylation levels of the selected CpG sites. Other example techniques include single molecule sequencing (e.g. nanopore sequencing (Simpson et al. Nat Methods 2017;14(4):407-410)), methylation-specific PCR (Herman et al. Proc Natl Acad Sci USA 1996;93(18):9821-9826), treatment with enzymes that differentially modify DNA molecules based on their methylation status (e.g. methylation-sensitive restriction enzymes), methylation binding proteins (e.g. antibodies), or mass spectrometry based methods (e.g. Lin et al. Anal Chem 2016;88(2):1083-7).

**[0056]** Various types of methylation can be analyzed. In some embodiments, we have used 5-methylation of cytosine residues as an example. Other types of DNA methylation changes can also be used, e.g. hydroxymethylation or methylation of adenine. Hence, technologies for detecting hydroxymethylation can also be used, e.g. oxidative bisulfite sequencing (Booth et al. Science 2012;336(6083):934-7) and Tet-assisted bisulfite sequencing (Nat Protoc 2012;7(12):2159-70). Further details for determination and use of a methylation profile can be found in U.S. Patent Publications 2015/0011403 and 2016/0017419, and 2017/0029900.

**[0057]** During bisulfite modification, unmethylated cytosines are converted to uracils and subsequently thymines after PCR amplification while the methylated cytosines would remain intact (Frommer M, et al. Proc Natl Acad Sci USA 1992; 89:1827-31). After sequencing and alignment, the methylation of an individual CpG site could thus be inferred from the count of methylated sequence reads 'M' (methylated) and the count of unmethylated sequence reads 'U' (unmethylated) at the cytosine residue of the CpG site. Using bisulfite sequencing data, viral methylomes from the plasma of subjects with different virus-associated conditions could be constructed.

**[0058]** As described above, methylation profiling can be performed using massively parallel sequencing (MPS) of bisulfite converted DNA. The MPS of the bisulfite converted DNA can be performed in a random or shotgun fashion, or in a targeted fashion. For example, region(s) of interest in the bisulfite converted DNA can be captured using a solution-phase or solid-phase hybridization-based process, followed by the MPS.

**[0059]** The MPS can be performed using a sequencing-by-synthesis platform (e.g., the Illumina HiSeq or NextSeq or NovaSeq platform), a sequencing-by-ligation platform (e.g., the

SOLiD platform from Life Technologies), a semiconductor-based sequencing system (e.g., the Ion Torrent or Ion Proton platforms from Life Technologies), the GenapSys Gene Electronic Nano-Integrated Ultra-Sensitive (GENIUS) technology, single molecule sequencing system (e.g., the Helicos system or the Pacific Biosciences system) or a nanopore-based sequencing system (e.g. from Oxford Nanopore Technologies or the Genia platform from Roche ([sequencing.roche.com/research---development/nanopore-sequencing.html](http://sequencing.roche.com/research---development/nanopore-sequencing.html))). Nanopore-based sequencing including nanopores that are constructed using lipid bilayers and protein nanopore, and solid-state nanopores (such as those that are graphene-based). As selected single molecule sequencing platforms would allow the methylation status of DNA molecules (including N6-methyladenine, 5-methylcytosine and 5-hydroxymethylcytosine) to be elucidated directly without bisulfite conversion (B.A. Flusberg et al. 2010 Nat Methods; 7:461-465; J. Shim et al. 2013 Sci Rep: 3: 1389. doi: 10.1038/srep01389), the use of such platforms would allow the methylation status of non-bisulfite converted sample DNA (e.g. plasma or serum DNA) to be analyzed. The sequence may include paired-end sequencing or provide a single sequence read for the entire DNA molecule.

**[0060]** Besides sequencing, other techniques can be used, e.g., as mentioned above. In one embodiment, methylation profiling can be done by methylation-specific PCR or methylation-sensitive restriction enzyme digestion followed by PCR or ligase chain reaction followed by PCR. In yet other embodiments, the PCR is a form of single molecule or digital PCR (B. Vogelstein et al. 1999 Proc Natl Acad Sci USA; 96:9236-9241). In yet further embodiments, the PCR can be a real-time PCR (Lo et al. Cancer Res 1999;59(16):3899-903 and Eads et al. Nucleic Acids Res 2000;28(8):E32). In other embodiments, the PCR can be a multiplex PCR. In one embodiment, methylation profiling can be done by using microarray-based technologies.

**[0061]** After sequencing, the sequence reads can be processed in *Methyl-Pipe*, a methylation data-analysis pipeline (Jiang et al. PLoS One 2014;9:e100360) and mapped to an artificially combined reference sequence that consists of the whole human genome (hg19), the whole EBV genome (AJ507799.2), the whole HBV genome, and the whole HPV genome. Different reference sequences can be used, and the mapping can be performed to each of the genomes separately, as opposed to combining into one reference sequence. Sequenced reads mapping to unique position in the combined genomic sequence can be used for downstream analysis.

### ***B. Targeted bisulfite sequencing using capture probes***

**[0062]** Certain embodiments can interrogate specific regions for the methylation patterns of plasma EBV DNA molecules. In one embodiment, targeted bisulfite sequencing with capture enrichment can be used to analyze the cell-free viral DNA molecules in the circulation of subjects with different EBV-associated diseases or conditions. For example, capture probes may be designed to cover all or some of the CpG sites of the EBV genome. This approach can also be used for other viruses. Hence, capture probes can also be designed to cover all or some of the CpG sites of the hepatitis B virus (HBV) genome, the human papillomavirus (HPV)

genome, and other viral/bacterial genomes. In the same analysis, capture probes can also be included to target genomic regions in the human genome.

**[0063]** In some embodiments, to take into account of the differences in size between a viral genome and the human genome, more probes can be designed to hybridize to viral genomic sequences than human genomic regions of interest may be used. In another embodiment, one can target whole viral genomes, e.g., designing on average 200 hybridizing probes covering each viral genomic region with ~200 bp in size (e.g., 200X tiling capturing probes). In one embodiment and as an example, for the regions of interest in the human genome, we designed on average 5 hybridizing probes covering each region with ~200 bp in size (e.g., 5X tiling capturing probes). As an illustration, the capture probes may be designed according to FIG. 1.

**[0064]** FIG. 1 shows the design of capture probes for targeted bisulfite sequencing according to embodiments of the present disclosure. FIG. 1 provides information about capture probes, e.g., size of capturing regions and the amount of tiling covered by the probes. The capture probes can be various lengths and overlap with each other. Such capture probes can use the SeqCap-Epi system (Nimblegen). Other embodiments may not use such capture probes.

**[0065]** Column 101 identifies the type of sequence, i.e., autosomes of the human or viral targets. Column 102 identifies the particular sequence (e.g., of a chromosome or of a particular viral genome). Column 103 provides the total length in base pairs (bp) that the capture probes cover. The capture probes may not cover the entire sequence (e.g. as shown for the autosomes), but may cover the entire sequence, e.g., for a viral genome. Column 104 provides the capture probe depth, also referred to as probe tiling fold. These numbers convey the number of probes covering any given position. For the autosomes, the capture probes provide 5x tiling on average. For the viral targets, the capture probes provide 200x tiling on average. Thus, the number of probes for the viral is a higher percentage/proportion per unit length than the autosomes. Such a higher level of concentration of capture probes for the viral targets can help maximize the chance of capturing the viral DNA.

### III. METHYLATION LEVELS OF PLASMA EBV DNA FOR VARIOUS CONDITIONS

**[0066]** We have analyzed the methylation patterns of plasma EBV DNA molecules in patients with various EBV-associated diseases/condition, e.g., NPC, infectious mononucleosis, Hodgkin's lymphoma, NK-T cell lymphoma, and apparently healthy individuals with detectable plasma EBV DNA. Those apparently healthy subjects with detectable plasma EBV DNA were retrieved from a subject cohort recruited for the screening of NPC and were classified into 2 groups. The first group included those subjects who had detectable plasma EBV DNA levels on the initial test, but undetectable levels on the follow-up test and were denoted as 'transiently positive'. The second group included those subjects who had detectable plasma EBV DNA levels on both the initial and follow-up tests and were denoted as 'persistently positive'.

**[0067]** Targeted bisulfite sequencing with capture enrichment by specifically designed capture probes was used. For each plasma sample analyzed, DNA was extracted from 4 mL plasma using the QIAamp DSP DNA blood mini kit. For each case, all extracted DNA was used for the preparation of sequencing library using the KAPA library preparation kit (Roche) or TruSeq DNA PCR-free library preparation kit (Illumina). The adapter-ligated DNA products were subjected to two rounds of bisulfite treatment using an EpiTect Bisulfite Kit (Qiagen). Twelve to fifteen cycles of PCR amplification were performed on the bisulfite-converted samples using the KAPA HiFi HotStart Uracil+ ReadyMix PCR kit (Roche). The first PCR amplification can increase the quantity of DNA for the target capture. An input amount of DNA can be suggested for the target capture reaction. The input DNA amount from plasma (without amplification) may not be sufficient for target capture.

**[0068]** The amplification products were then captured with the SeqCap-Epi system (Nimblegen) using the custom-designed probes covering the viral and human genomic regions stated above (FIG. 1). Substantial 'loss of DNA' can occur the capturing step. The amount of DNA after target capture reaction may be less than required for sequencing. Therefore, a second amplification stage (e.g., using PCR) can amplify the DNA amount for subsequent sequencing step. Thus, in some embodiments, after the target capture, the captured products were enriched by 14 cycles of PCR to generate DNA libraries. The DNA libraries were sequenced on a NextSeq platform (Illumina). For each sequencing run, four to six samples with unique sample barcodes were sequenced using the paired-end mode. From each DNA fragment, 75 nucleotides were sequenced from each of the two ends, but other numbers of nucleotides can be sequenced.

#### ***A. Methylation profiles of plasma EBV DNA in different EBV-associated conditions***

**[0069]** FIG. 2 shows the methylation densities of CpG sites across the EBV genome in patients with infectious mononucleosis, NPC, and NK-T cell lymphoma according to embodiments of the present disclosure. The methylation profiles of EBV DNA were generated through targeted capture bisulfite sequencing of plasma EBV DNA fragments. The horizontal axis provides the genomic coordinates in the EBV reference genome. The vertical axis provides the methylation density at a single CpG site resolution.

**[0070]** The methylation densities of the CpG sites across the EBV genome were derived with the formula described above:

$$MD = \frac{M}{M+U}$$

We could observe different patterns of methylation density of plasma EBV DNA amongst different subjects. These differences in the profiles of DNA methylation could be analyzed on a global or locus-specific level. For example, on a global level, we observed a total lower methylation level in the patient with infectious mononucleosis (TBR1610) (methylation density of 57.3%) than the two patients with NPC (TBR1392 and TBR1416) (methylation densities of 83.8% and 81.3%). The global methylation level uses methylation measurements for sites

across the genome to determine a single value.

**[0071]** Also on a relatively macroscopic level, the patient with NK-T cell lymphoma (TBR1629) exhibited a greater heterogeneity in the methylation levels across the EBV genome than the two patients with NPC (TBR1392 and TBR1416), for example, between genomic coordinates 50000 to 100000. The heterogeneity shows up as dips in the methylation density plot. The NPC patients have relatively uniform density, whereas the lymphoma patient show many tiny valleys where the density drops significantly, thereby giving a comb-like structure.

**[0072]** Patterns of DNA methylation could also be analyzed on a locus-specific or region-specific level. These loci could be of any size and of at least 1 CpG site. These loci may or may not associated with any annotated viral genes. Such region-specific methylation levels can have similar values across different subject with the same condition, but have different values relative to other subjects with a different condition.

**[0073]** In FIG. 2, we define 4 genomic regions, namely region 201 (7,000-13,000), region 202 (138,000-139,000), region 203 (143,000-145,000), and region 204 (169,000-170,000). The region-specific methylation densities in regions 201 and 204 were higher in the two cases of NPC (TBR 1392 and TBR 1416) than the case of infectious mononucleosis (TBR 1610). The region-specific methylation density in region 203 was, on the contrary, lower in the two cases of NPC than the case of infectious mononucleosis. The region-specific DNA methylation density in region 203 was highest in the case of NK-T cell lymphoma (TBR 1629) than the other cases of NPC and infectious mononucleosis. Such results demonstrate that there are different patterns of methylation profiles of plasma EBV DNA fragments on a global and locus-specific level in patients with different EBV-associated conditions.

**[0074]** Accordingly, a low methylation level in region 201 can indicate that a subject has infectious mononucleosis. A high methylation level in region 204 can indicate the subject has NPC. And, a high methylation level in region 203 can indicate the subject has NK-T cell lymphoma. The specific values for threshold defining what is high or low (or an intermediate range) can be determined for each region based on measurements of the type shown in FIG. 2. Such regions can be selected by analyzing the methylation profiles of subjects with the different conditions and choosing regions that have different methylation densities for different conditions. Further, measurements from multiple regions may be combined, e.g., via clustering techniques or a decision tree.

### ***B. Early stage NPC***

**[0075]** FIG. 3 shows the methylation profiles of plasma EBV DNA in a patient (AL 038) from our screening cohort with early stage NPC (Stage I) and a low concentration of plasma EBV DNA (8 copies/mL plasma as measured by quantitative PCR). Plasma DNA was extracted from the initial blood sample. Subjects with a positive initial (baseline) test were be retested 4 weeks later, and that was regarded as a follow-up test. This patient did not have symptoms of NPC at

the time of blood sampling, and the cancer was detected through screening using real-time PCR analysis of plasma EBV DNA with a two stage analysis. Subjects with persistently positive plasma EBV DNA by real-time PCR were further confirmed using nasal endoscopy and MRI.

**[0076]** FIG. 3 shows that the signal is more noisy, e.g., some sites have 100% methylation density and some sites have very low methylation density, such as zero. To remove such noisy behavior, embodiments can use region methylation levels that are measured using the combined methylation density of all the sequence reads at sites within the window. For example, a 200 bp window can be used, which can reduce the noise and provide smoother data. Accordingly, even with low EBV DNA sequence concentration in the sample, methylation levels can be measured and used to distinguish different conditions. More data showing such ability to distinguish conditions is provided below.

**[0077]** In this patient, the amount of plasma EBV DNA fragments being captured was comparatively lower than the other two patients (TBR1392 and TBR1416) with advanced stage NPC and high concentrations of plasma EBV DNA. As mentioned above, this illustrates a case where methylation level(s) can still be used to identify a particular condition-NPC in this case-even though the EBV concentration is low. Further, the amount of plasma EBV can be used as part of determining a level of disease (e.g., a level of cancer).

### ***C. Difference values in methylation profiles among patients***

**[0078]** A difference in the methylation profiles can provide a comparison between patients with NPC and infectious mononucleosis. As shown earlier in FIG. 2, there are different methylation patterns of plasma EBV DNA among patients with different EBV-associated conditions. We analyze the difference in the methylation patterns by comparing the methylation densities of CpG sites across the EBV genome between these different patients.

#### **1. Different conditions**

**[0079]** FIG. 4 shows the differences in methylation densities of the CpG sites across the EBV genome between two patients with different conditions according to embodiments of the present disclosure. The horizontal axis is the genomic coordinate in the EBV genome. The vertical axis shows the per-site difference in the methylation between the two patients. The median methylation difference between NPC (TBR1392) and infectious mononucleosis (TBR1610) was 23.9% (IQR (interquartile range): 14.8-39.3%), suggesting the NPC methylation level across CpG sites in EBV genome was systematically higher in NPC than in infectious mononucleosis. Similar patterns of methylation difference (median: 22.9%; IQR: 13.3-37.8%) were observed in another comparison between NPC (TBR1416) and infectious mononucleosis (TBR1610).

**[0080]** The upper diagram shows the differences in methylation densities between a patient with NPC (TBR1392) and a patient with infectious mononucleosis (TBR1610). A positive value at one CpG site indicates a higher methylation density in case TBR1392 than case TBR1610 at that particular site. A negative value indicates a lower methylation density in case TBR1392 than case TBR1610 at that CpG site.

**[0081]** The lower diagram shows the differences in methylation densities between another patient with NPC (TBR1416) and the same patient with infectious mononucleosis (TBR1610). This graphical presentation illustrates one example of analysis and comparison of methylation patterns of plasma EBV DNA in different EBV-associated conditions.

**[0082]** In general, the NPC patients have higher methylation, and the differences in methylation have significant values. Such difference values can be quantified in various ways, e.g., by summing to get a global difference value. This global difference value can act as a distance between two subjects, as may be used in clustering, where each methylation value (e.g., as an index per site or a level per region) is one data point in a multidimensional data point.

## **2. Same condition**

**[0083]** FIG. 5 shows the differences in methylation densities of the CpG sites across the EBV genome between two patients with the same diagnosis of NPC (TBR1392 and TBR1416) according to embodiments of the present disclosure. In general, there are smaller differences in methylation densities across the EBV genomes, compared to previous analyses for patients with two different diseases (FIG. 4). The median methylation difference between two NPC subjects (TBR1392 vs. TBR1416) was 0.3% (IQR: -1.2-2.5%). This suggests that patients with the same diagnosis of EBV-associated disease would have similar methylation patterns of plasma EBV DNA. The difference in methylation densities could have implications on some disease characteristics specific to the particular case and provide additional diagnostic or prognostic information.

## **3. NPC and false positive**

**[0084]** FIG. 6 shows the differences in the methylation patterns of plasma EBV DNA between a patient with early stage NPC (AO050) and a subject with false positive result of plasma EBV DNA (HB002) according to embodiments of the present disclosure. This comparison shows the methylation patterns of plasma EBV DNA between a patient with early stage NPC and a subject without NPC, but who was persistently positive for plasma EBV DNA on serial tests. Both of them were from our screening cohort. The plasma DNA was extracted from their initial blood samples upon recruitment.

**[0085]** As shown in FIG. 6, there are differences in the methylation patterns of plasma EBV DNA between the patient with early stage NPC (AO050) and the subject with false positive result of plasma EBV DNA (HB002). But, the number and size of the differences is less than in the plots of FIG. 4, between an NPC subject and an IM subject. Thus, the fact that there are differences between the NPC subject and the false positive subject indicates an ability to increase the accuracy of cancer screening. And, the fact that the differences are of a different scale than for the IM subject indicates any ability to distinguish subjects having any of the three conditions. Based on this observation, we explored the diagnostic utility to differentiate the two groups (subjects with early-stage NPC and false positive results) using plasma EBV DNA methylation patterns, for which data is provide in a later section.

#### ***D. Correlation between methylation densities of similar and different patients***

**[0086]** Besides analyzing the difference values between methylation densities at different sites, the methylation densities can be plotted together to identify a correlation or lack therefore. For example, each data point in a two dimensional plot can include the two methylation densities from two subjects at a same site. If the methylation densities are correlated (e.g., the two subjects have the same condition), then the plot will exhibit linear behavior. If the methylation densities are not correlated (e.g., the two subjects have the same condition), then the plot will not exhibit linear behavior.

**[0087]** FIGS. 7A-7C illustrate the differences in methylation profiles of plasma EBV DNA between two clinical cases. In FIGS. 7A-7C, each data point in the three graphs represents the methylation density of a CpG site across the EBV genome in one patient (on the x-axis) and the corresponding methylation density of the same CpG site in the other patient (on the y-axis).

**[0088]** FIG. 7A and 7B show the methylation densities between two patients of different diseases (one NPC and one infectious mononucleosis). As can be seen, the methylation densities are not correlated. The NPC subjects consistently have a high methylation density (e.g., above 80%) that is not matched by the IM subject, thereby causing a horizontal band along the top. Such behavior indicates that the two subject are different, e.g., different conditions. Different conditions can include one with disease and the other without disease.

**[0089]** FIG. 7C shows the methylation densities between two different patients with NPC. In FIG. 7C, we can observe a diagonal trend line (slope being approximately equal to 1), suggesting that the methylation density of each CpG site is similar between two different patients with NPC. This graphical pattern is not observed in FIG. 7A and 7B. These results again suggest that patients with different EBV-associated diseases have different methylation profiles of plasma EBV DNA fragments. Embodiments can use such different methylation properties of the sites (or of regions of sites) to identify sites/regions that have different methylation densities between different conditions, and use those sites/regions to determine a methylation level(s) for discriminating between the conditions.

#### IV. DISCRIMINATING AMONG EBV-ASSOCIATED CONDITIONS USING METHYLATION PATTERNS OF PLASMA EBV DNA

**[0090]** For a systematic comparison of the methylation profiles of plasma EBV DNA in different EBV-associated conditions, we used a 'methylation percentage' (one example of a type of 'methylation density'), for each case. The methylation percentage of plasma EBV DNA fragments can be derived using the equation:

$$\text{Methylation \%} = \frac{M'}{M' + U'}$$

where  $M'$  is the count of methylated reads and  $U'$  is the count of unmethylated reads at one or more CpG sites, which may be pre-selected. The methylation percentage can be calculated based on all CpG sites or some CpG sites within the EBV genome covered by our capture probes. Other examples of methylation levels can also be used.

##### **A. Genomewide aggregated methylation level**

**[0091]** As one example of a single methylation level across the EBV genome can be determined. The aggregate number of methylated EBV DNA molecules at a specific set of CpG sites can be used to determine the methylation percentage as a genomewide methylation level, with a normalization by a measured amount including other DNA molecules, e.g., as a measure of volume, an intensity corresponding to the other DNA molecules, or a count of the other DNA molecules. In one embodiment, we calculated the methylation percentage of plasma EBV DNA molecules based on the CpG sites within the EBV genome covered by our capture probes.

**[0092]** FIG. 8 shows the methylation percentages of plasma EBV DNA based on all CpG sites covered in subjects with infectious mononucleosis (IM) (number of patients  $n=2$ ), EBV-associated lymphoma ( $n=3$ ), transiently positive plasma EBV DNA ( $n=3$ ), persistently positive plasma EBV DNA ( $n=3$ ), and NPC ( $n=6$ ) according to embodiments of the present disclosure. FIG. 8 shows box and whisker plots for the five different conditions. As can be seen, the median values are sufficiently separated to discriminate between the different conditions. For example, a reference level of about 79% can discriminate between patients that are persistently positive for EBV and those that have NPC.

**[0093]** Overall, we could differentiate among different EBV-associated diseases/conditions through analysis of genomewide aggregated methylation percentage of plasma EBV DNA ( $p$ -value =  $8.52e-05$ , one-way ANOVA test). Four out of the six patients with NPC were from the screening cohort and had early stage NPC (stage I or II). Thus, even early stages of a condition can be discriminated from subjects not having the condition (e.g., even the persistently positive subjects). Different reference levels can be used to discriminate between different conditions, e.g., lower than about 57% can be used to identify IM and between 57%

and 63% can be used to identify transiently positive subjects. In some embodiments, more than one condition out of a larger set of conditions can be identified for a given methylation level (e.g., lymphoma and transiently positive could be identified in the range 57% to 63%). In such a situation, a probability can be assigned to each of the conditions. For example, the methylation of a tested subject can be compared to two groups of reference subjects, one group suffering from condition A (e.g. lymphoma) and the other suffering from condition B (e.g. infectious mononucleosis). The number of standard deviations from the means of the two groups of reference subjects can be determined. Based on the number of standard deviations, the probabilities of suffering from the two conditions can be computed. These probabilities can be used to determine the relative likelihood of suffering from these two conditions.

**[0094]** The specific reference value(s) selected can depend on the specific manner in which the methylation level is determined. For example, a methylation percentage would have different reference levels than if the number of methylated DNA molecules  $M$  (e.g., as determined using a number of reads or an intensity) is divided by the number of unmethylated DNA molecules  $U$  (e.g., as determined using a number of reads or an intensity), e.g.,  $M/U$ . Other scaling factors or additive factors would change the particular reference values. As long as a methylation level of a current sample is determined in a same manner as the methylation levels of the reference samples, then the selected reference levels will be applicable. The reference levels can also depend on the sites selected for measuring the methylation level, as shown in later results.

**[0095]** The ability to discriminate between different conditions using a methylation level can depend on the number of DNA molecules detected at the sites, but the results presented herein show that the number of EBV DNA molecules can be relatively low. For example, in FIG. 8, the 5<sup>th</sup> percentile of plasma EBV DNA molecules analyzed in the different subjects is 44, with the minimum being 26. In various embodiments, the number of cell-free viral DNA molecules can include at least 10 cell-free DNA molecules, e.g., 20, 30, 40, 50, 100, or 500). In other embodiments, the total number of cell-free DNA molecules analyzed for the subject and the particular viral genome can be at least 1,000 cell-free DNA molecules or more (e.g., at least 10,000, at least 100,000, or at least 1,000,000).

### ***B. Differentially methylated regions (DMRs)***

**[0096]** Instead of using all sites covered by the capture probes, only certain sites may be used. These sites may be determined by analyzing all the sites and then selecting ones having a certain properties, e.g., having different methylation levels among between certain conditions. The sites can be analyzed individually or collectively by regions, e.g., more than one site can be allocated to a region and a methylation level determined for that region. The sites and regions can be genomewide by spanning the viral genome, e.g., not restricted to just one site/region. For example, at least one site/region can be used for every 1 kb, 2 kb, 5 kb, or 10 kb.

**[0097]** Accordingly, some embodiments can calculate the methylation percentages based on CpG sites within differentially methylated regions (DMRs). We have shown earlier that the methylation patterns of plasma EBV DNA are different in different EBV-associated diseases. Therefore, there should exist DMRs within which the methylation levels are different between different diseases/conditions. Besides using individual sites, non-overlapping windows of different sizes can be used. For example, the sizes of the non-overlapping regions could be set at, but not limited to, 50 bp, 100 bp, 200 bp, 300 bp, 400 bp, 500 bp, 600 bp, 800 bp and 1000 bp. In another example, each CpG site can be analyzed separately, e.g., without use of regions combining sites.

**[0098]** The DMRs can be selected to have particular methylation levels in subjects have different conditions. For example, the DMR could be defined if the methylation percentages of the CpG sites within the region are less than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% in one or more cases of a disease/condition and greater than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% in one case of another disease/condition. In yet another embodiment, more than one case per disease can be used to define the DMR. And, cutoff criteria for more than two diseases/conditions can be used, e.g., different ranges of methylation levels for each of the conditions.

#### **1. DMRs using IM<50% and NPC>80%**

**[0099]** To demonstrate the mining of such DMRs, we randomly selected one patient with infectious mononucleosis (TBR1610) and one patient with NPC (TBR1392). Here, we first set non-overlapping windows of 500 base pairs (bp) in size across the EBV genome, e.g., bins of positions 1-500, 501-1000, etc.. Within the 500-bp regions, we calculated the average methylation percentages of all the CpG sites within the region in the patient with IM (TBR1610) and NPC (TBR1392). In this example, the 500-bp region would fulfil a first selection criteria for DMR if the average methylation percentages of all the CpG sites within the region are less than 50% in the case of infectious mononucleosis (TBR1610) and greater than 80% in the case of NPC (TBR1392).

**[0100]** FIG. 9 illustrates the mining of differentially methylated regions (DMRs) fulfilling the first selection criteria according to embodiments of the present disclosure. FIG. 9 corresponds to the two cases shown in FIG. 7A. Each data point in FIG. 9 represents the methylation percentage of a 500-bp region across the EBV genome in the IM subject (on the x-axis) and the corresponding methylation percentage of the same 500-bp region in the NPC subject (on the y-axis). With this first selection criteria defined above, we identified a total of 39 DMRs that comprised of 821 CpG sites (approximately 10% of the total CpG sites within the EBV genome being captured with our probes). These 39 DMRs are those within the upper left corner of FIG. 9.

**[0101]** In FIG. 9, the methylation percentage for the NPC subject is shown on the vertical axis,

and the methylation percentage for the IM subject is shown on the horizontal axis. Vertical line 901 shows the cutoff of 50% for the methylation percentage in the case of IM. Horizontal line 902 shows the cutoff of 80% in the case of NPC. Thus, the regions in the upper left section (generally marked as 910) correspond to the DMRs for this example.

**[0102]** FIG. 10 is a table listing the genomic coordinates of the 39 differentially methylated regions fulfilling the criteria described in FIG. 9. Column 1001 lists the viral genome, which is EBV for this example. Column 1002 provides the starting genomic coordinate in the reference EBV genome. Column 1003 provides the ending genomic coordinate in the reference EBV genome. Column 1004 the methylation density in the IM subject and in the NPC subject.

**[0103]** These DMRs can then be used to determine methylation level(s) in other subjects. In one embodiment, the methylation status of each sequence read covering a site in one of this set of DMRs is used to determine a methylation percentage that corresponds to the set of DMRs. This methylation percentage can be determined in a similar manner as in FIG. 8, but a subset of the sequence reads are used, namely those corresponding to the sites in the set of DMRs. In other embodiments, individual methylation levels can be determined for each of the DMRs. The methylation levels for a subject can form a multidimensional data point, e.g., where clustering techniques or reference planes (hyperplanes in the multidimensional space) can separate subjects with different conditions or different classifications/levels of a condition. Other analytical methods for differentiating these conditions can be used, for example but not limited to, Naive Bayes, random forest, decision tree, support vector machines, k-nearest neighbors, K-means clustering, Gaussian mixture model (GMM), density-based spatial clustering, hierarchical Clustering, logistic regression classifiers, and other supervised and unsupervised classification or regression methods.

**[0104]** FIG. 11 shows the methylation percentages of plasma EBV DNA based on the 821 CpG sites within the 39 DMRs defined above (FIG. 8) in the same group of subjects with infectious mononucleosis (IM) (n=2), EBV-associated lymphoma (n=3), transiently positive plasma EBV DNA (n=3), persistently positive plasma EBV DNA (n=3) and NPC (n=6) according to embodiments of the present disclosure. These are the same subjects used in FIG. 8. The methylation percentages are determined as a single value using sequence reads that correspond (e.g., align) to the 821 sites in the set of 39 DMRs.

**[0105]** FIG. 11 shows box and whisker plots for the five different conditions. As can be seen, the median values can discriminate between the different conditions. For example, a reference level of about 75% can discriminate between patients that are persistently positive for EBV and those that have NPC. We could observe a statistically significant difference in the methylation percentages among the different groups (p-value =  $1.83e-05$ , one-way ANOVA test), which is better than FIG. 8.

**[0106]** FIG. 11 has some differences than FIG. 8. For example, the spread in values for IM and NPC are smaller, resulting from the DMRs being specifically select to be in a particular range for those subjects. Such a result indicates that criteria of different ranges of methylation

levels indicative of different conditions can provide more selective techniques discriminating among different classifications of subjects. Additionally, the difference between NPC subjects and persistently positive subjects is larger than in FIG. 8.

## 2. DMRs using IM<80% and NPC>90%

**[0107]** As in the previous section, we performed an analysis for the use methylation percentages based on differentiated methylated regions to distinguish patients with early NPC and non-NPC subjects with detectable plasma EBV DNA. All the NPC patients and non-NPC subjects analyzed were identified through a prospective screening cohort (Chan et al. N Engl J Med 2017; 377:513-522). To mine the DMRs, we randomly selected two patients with NPC (TBR1416 and FD089) and one patient with infectious mononucleosis (TBR1748). In yet another embodiment, other EBV-associated disease or condition, including non-EBV subject with detectable plasma EBV DNA, could be used for mining of DMRs. We set non-overlapping windows of 500 base pairs (bp) in size across the EBV genome.

**[0108]** FIG. 12 illustrates the mining of differentially methylated regions (DMRs) fulfilling the second selection criteria according to embodiments of the present disclosure. In contrast to the previous section, we have included more than one case per disease (NPC in this analysis) for mining of the DMRs. The second selection criteria corresponds to: (1) non-overlapping, contiguous window of 500 bp in size and (2) methylation percentages of the CpG sites within the region less than 80% in the selected case of infectious mononucleosis (TBR1748) and greater than 90% in both cases of nasopharyngeal carcinoma (TBR1416 and FD089). Each data point in FIG. 12 represents the average methylation percentage of all the CpG site within the 500-bp regions across the EBV genome in the IM subject (on the x-axis) and the corresponding average methylation percentage of the same region in the two NPC subjects (on the y-axis).

**[0109]** In FIG. 12, the methylation percentage for the NPC subject is shown on the vertical axis, and the methylation percentage for the IM subject is shown on the horizontal axis. Vertical line 1201 shows the cutoff of 80% for the methylation percentage in the case of IM. Horizontal line 902 shows the cutoff of 90% in the case of NPC. With this second selection criteria defined above, we identified a total of 46 DMRs which comprised of 1,520 CpG sites (approximately 20% of the total CpG sites within the EBV genome being captured with our probes). The 46 DMRs are shown in the upper left section (generally marked as region 1210).

**[0110]** FIG. 13 shows the methylation percentages of plasma EBV DNA based on the 46 DMRs defined in FIG. 12 in the non-NPC subjects with transiently positive plasma EBV DNA, non-NPC subjects with persistently positive plasma EBV DNA, and NPC patients according to embodiments of the present disclosure. Each data point corresponds to a different subject. The classifications of transiently positive and persistently positive are determined as described above, i.e., based on numbers of EBV DNA reads taken from samples at two times.

**[0111]** We analyzed 117 non-NPC subjects with transiently positive plasma EBV DNA, 39 non-NPC subjects with persistently positive plasma EBV DNA, and 30 NPC patients by targeted bisulfite sequencing. All the non-NPC subjects and NPC patients were recruited from the prospective screening cohort. We compared the methylation percentages of plasma EBV DNA based on the DMRs defined above (FIG. 12) among the three groups. The methylation percentages are determined as a single value using sequence reads that correspond (e.g., align) to the 1,520 sites in the set of 46 DMRs.

**[0112]** In one embodiment, different weighting could be assigned to the various DMRs for the calculation of the aggregated methylation percentage. Such weightings can be implemented in various ways, e.g., a scaling factor for each methylated sequence read at a site (e.g., multiplying by a factor greater than 1 when a region is to be weighted higher) or a scaling factor can be applied to region methylation percentages, thereby providing a weighted average of region methylation percentages. In this example, we applied equal weighting for all the DMRs defined.

**[0113]** The mean methylation percentage of plasma EBV DNA based on the 46 DMRs for the NPC group (mean = 88.3%) was significantly higher than the mean methylation percentages of the other two non-NPC groups with transiently positive (mean = 65.3%) and persistently positive (mean = 71.1%) plasma EBV DNA ( $p < 0.0001$ , Kruskal-Wallis test). Accordingly, NPC patients could be differentiated from non-NPC subjects with detectable plasma EBV DNA (transiently or persistently positive) based on the difference in the methylation profiles of plasma EBV DNA (e.g., as represented by methylation percentages of plasma EBV DNA based on DMRs).

**[0114]** In this example and in other embodiments described herein, the reference levels for discriminating between classifications can be determined in various ways. In one embodiment, the cutoff value (reference level) used to discriminate between a subject having NPC and not having NPC can be the lowest value in the EBV DNA methylation percentages among the NPC patients being analyzed (training set). In other embodiments, the cutoff values can be determined, for example, as the mean EBV DNA methylation percentages of the NPC patients minus one standard deviation (SD), mean minus two SD, mean minus three SD. In yet other embodiments, the cutoff can be determined using Receiver Operator Characteristics (ROC) curves or by nonparametric methods, for example but not limited to including 100%, 95%, 90%, 85%, 80% of the NPC patients being analyzed.

**[0115]** In the current example, a cutoff value of 80% in the methylation percentage can be set to achieve a sensitivity of greater than 95% for NPC detection. Using this cutoff value of 80%, 29 out of the 30 patients with NPC, 16 out of 119 non-NPC subjects with transiently positive plasma EBV DNA, and 6 out of 39 non-NPC subjects with persistently positive plasma EBV DNA had their methylation percentages of plasma EBV DNA, determined within the 46 defined DMRs by targeted bisulfite sequencing, higher than the cutoff value (80%). The calculated sensitivity, specificity, and positive predictive value were 96.7%, 85.9% and 58.5% respectively.

### ***C. Representative methylation consensus regions of same condition***

**[0116]** In the examples below, we aimed to identify regions that have similar methylation densities across subjects with a same condition. We define such regions to be representative methylation consensus regions for a condition. In some implementations, such a criteria can also be combined with criteria of differential methylation among conditions.

**[0117]** To demonstrate the identification of 'representative' methylation consensus regions, we randomly selected two patients with NPC (TBR1392 and TBR1416). Here, we divided the EBV genome into non-overlapping regions of 500 bp. In other embodiments, different sizes of overlapping regions could be set. For examples, the sizes of the overlapping regions could be set at 50 bp, 100 bp, 200 bp, 300 bp, 400 bp, 600 bp, 800 bp and 1000 bp. Within the 500-bp regions, we calculated the average methylation percentages of all CpG sites within the region in the two patients with NPC (TBR1392 and TBR1416).

**[0118]** FIG. 14 illustrates the mining of representative methylation consensus regions fulfilling third selection criteria according to embodiments of the present disclosure. The third selection criteria corresponds to: (1) non-overlapping, contiguous window of 500 bp in size, (2) differences in the overall methylation density of the region less than 1% between the two cases of NPC, and (3) overall methylation density of the region greater than 80% for both cases.

**[0119]** In other embodiments, the 'representative' methylation consensus region could be defined if the differences in methylation percentages between the two NPC patients are less than 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or 10% between the two NPC cases and the methylation percentages are greater than 10%, 20%, 30%, 40%, 50%, 60%, 70% or 90%. More than two subjects per disease can be used to define the 'representative' methylation consensus regions, e.g., the methylation percentages for each of the subjects being within the specified similarity cutoff (e.g., 1%) and being within a specified range for methylation percentage (e.g., greater than 80%).

**[0120]** Each data point in FIG. 14 represents the methylation percentage of a 500-bp region across the EBV genome in on NPC subject (on the x-axis) and the corresponding methylation percentage of the same region in the other NPC subject (on the y-axis). With the selection criteria defined above, we have identified 79 regions. These 79 DMRs can be found in region 1410 in FIG. 14.

**[0121]** In FIG. 14, the methylation percentage for the first NPC subject is shown on the vertical axis, and the methylation percentage for the second NPC subject is shown on the horizontal axis. Vertical line 1401 shows the cutoff of 80% for the methylation percentage in the case of IM. Horizontal line 1402 shows the cutoff of 80% in the case of NPC. Thus, the regions in the upper right section (generally marked as region 1410) correspond to the DMRs for this example.

**[0122]** FIG. 15 shows the methylation densities of plasma EBV DNA based on the 'representative' methylation consensus regions defined above (FIG. 12) in the same group of subjects with infectious mononucleosis (IM) (n=2), EBV-associated lymphoma (n=3), transiently positive plasma EBV DNA (n=3), persistently positive plasma EBV DNA (n=3), and NPC (n=6) according to embodiments of the present disclosure. We could observe a statistically significant difference in the methylation percentages among the groups (p-value = 0.00371, one-way ANOVA test). Based on these data, one can determine the status of a tested sample by analyzing the methylation densities of the plasma DNA for the representative methylation consensus regions. For example, a methylation density of 90% would indicate that the sample is collected from a patient with NPC whereas a methylation of density of 80% is suggestive that the sample is from a patient with EBV-positive lymphoma.

#### ***D. Single CpG site analysis***

**[0123]** Besides calculating an aggregate methylation level based on a set of sites (e.g., as described in sections above), embodiments can calculate the methylation percentage based on individual CpG sites within the EBV genome. To identify individual CpG sites with differential methylation levels in different EBV-associated diseases, we pooled the sequencing data of plasma DNA reads of 3 subjects with persistently positive EBV DNA, but without NPC, giving a sequencing depth of 7x. We then compared the methylation percentages of all the CpG sites between the pooled sequencing data of 3 subjects with persistently positive EBV DNA and 3 patients with NPC (AO050, TBR1392 and TBR1416). The pooling of the sequencing data means that the methylation percentage was determined as if all the sequence reads were from a same subject.

**[0124]** In various embodiments, these individual CpG sites with differential methylation levels could be defined if the methylation percentages of the CpG sites are less than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% in one case (subject) of a disease and greater than 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 90% in one case of another disease. The criteria can apply to more than one case per disease to define the DMR, e.g., as described above for examples using regions, as may be done with different ranges for different conditions as well as specific separations between subjects with a different (greater than) or a same condition (within a threshold).

**[0125]** Appendix A shows the list of individual CpG sites across the EBV genome with differential methylation levels, when the differences in the methylation percentages over these CpG sites between the pooled sequencing data of 3 subjects with persistently positive EBV DNA and the 3 patients with NPC are greater than 20%. Those sites marked with \* have a difference greater than 40%, \*\* have a difference greater than 60% and \*\*\* have a difference greater than 80%. In other embodiments, the CpG sites with differential methylation levels could be defined with the difference in methylation percentages larger than 20%, 30%, 50%, 70% or 90%. Some example sites having a difference greater than 60% are now analyzed.

**[0126]** FIG. 16 shows examples of CpG sites with the methylation percentages over the sites greater than 80% in the pooled sequencing data of the 3 cases with persistently positive plasma EBV DNA and an average of less than 20% in the 3 subjects with NPC according to embodiments of the present disclosure. The methylation percentages over these sites of two patients with infectious mononucleosis were also included. The methylation percentages are provided on the vertical axis, and the horizontal axis lists 8 separate sites satisfying the criteria. The sites are labeled with sequential numbers.

**[0127]** As can be seen, all of the sites provide a good separation between the non-NPC subjects (including persistently positive and IM) and two of the NPC subjects (TBR1416 and TBR1392). For NPC subject AO050, sites 1-4, 7, and 8 provide good separation, but sites 5 and 6 do not. Thus, individual differentially methylated sites (e.g., not just as a region) determined to discriminate between two conditions can also be used to discriminate between one condition (NPC) and two or more conditions.

**[0128]** FIG. 17 shows examples of CpG sites with the methylation percentages over the sites less than 20% in the pooled sequencing data of the 3 cases with persistently positive plasma EBV DNA and greater than 80% in the 3 subjects with NPC according to embodiments of the present disclosure. The methylation percentages over these sites of two patients with infectious mononucleosis are also shown. This criteria is the opposite of those used for FIG. 16. The methylation percentages are provided on the vertical axis, and the horizontal axis lists 22 separate sites satisfying the criteria. The sites are labeled with sequential numbers.

**[0129]** As can be seen, all of the sites provide a good separation between the non-NPC subjects (including persistently positive and IM) and the NPC subjects. This shows that individual sites can be used to discriminate between classifications. And, sites can be selected from across the viral genome, as opposed to being within a same contiguous region of a specified length. More sites can be selected to provide greater statistical accuracy, e.g., so that more EBV DNA fragments can be detected.

**[0130]** In one embodiment, multiple CpG sites with differential methylation levels (e.g., those defined in Appendix A and FIGS. 16 and 17) are chosen to be within a specified distance to each other. In this manner, individual viral DNA fragments may each cover the multiple sites. For example, the specified distance can be 150 bp because this is approximately the representative size of a plasma DNA molecule. In such situation, targeted amplification of the particular region with multiple differentially methylated CpG sites by PCR amplification would be possible. This targeted analysis would be of lower cost than using genome-wide analysis approach.

**[0131]** Accordingly, in various embodiments, the analysis of methylation pattern can be based on the genomic regions of the whole viral genome or individual CpG sites. In such a region analysis, the viral genome can be divided into different regions based on the genomic coordinates, with each region including all the CpG sites within such a region. Alternatively, differentially methylated CpG sites can first be selected and then merged within a region to

form a DMR. In another example, all CpG sites may be included in the calculation of the methylation density of the region without prior selection of the informative ones.

#### ***E. Hierarchical clustering analysis***

**[0132]** Some embodiments may use more than methylation level to discriminate between classifications. In one example, clustering techniques may be used. In such clustering techniques, multiple methylation levels can be determined for each subject, e.g., methylation levels for different regions (each including one or more sites), methylation levels for individual sites, or combinations thereof. In some embodiments, the clustering can be hierarchical.

**[0133]** The set of methylation levels can form a vector that represents a multidimensional data point having a length that equals the number of methylation levels. The regions (bins) can be of various sizes, as described herein. And, the clustering analysis can be based on non-overlapping contiguous bins of different sizes. For examples, the sizes of bins could be defined at 50 bp, 100 bp, 200 bp, 300 bp, 400 bp, 500 bp, 600 bp, 700 bp, 800 bp, 900 bp or 1000 bp. Accordingly, the clustering analysis can be based on comparisons of the methylation levels for different sites/bins to corresponding methylation levels among the different subjects.

**[0134]** FIG. 18 shows a cluster dendrogram with the hierarchical clustering analysis based on methylation pattern analysis of plasma EBV DNA for 6 patients with NPC (including 4 patients with early stage disease from our screening cohort), 2 patients with extranodal NK-T cell lymphoma, and 2 patients with infectious mononucleosis according to embodiments of the present disclosure. In this example, the hierarchical clustering analysis was based on comparison of the methylation percentages of the CpG sites within non-overlapping contiguous regions of 500 bp in size. The clustering groups the different subject based on differences in the methylation percentages for the different regions, where the differences can be combined to provide a distance.

**[0135]** In FIG. 18, the distance is shown along the top horizontal axis. The distance can be determined as a sum of differences between each of the methylation densities (percentages), e.g., when the methylation densities at different loci corresponds to a vector representing a multi-dimensional point, where the distance is between two multi-dimensional points. Two subjects are combined at a point equal to the distance between them. When a new patient is tested, the new multidimensional point of methylation percentages (or other level) is used to determine a closest one of the reference subjects (e.g., those shown in FIG. 18) or a closest subgroup, as depicted at a node, e.g., nodes 1801 or 1802. The identification of a closest reference subject or reference node can provide the classification.

**[0136]** Cluster dendrogram 1800 shows that the NPC subject are incrementally clustered together, with all of the NPC subject being clustered into a subgroup at node 1803, which does not include subjects with other conditions. This shows an ability to discriminate the NPC subjects from the IM subjects and the lymphoma subjects. Similarly, the IM subjects are

grouped together. Of note, the two NK-T cell lymphoma patients were not clustered together. Patient 1629 had stage IV disease and patient 1713 had stage I disease. This may indicate that the methylation pattern would progress across different stage of the same disease. One potential application of this would be using the methylation profile for staging and prognosticating the patients.

**[0137]** We have demonstrated the feasibility of differentiating among different EBV-associated diseases based on clustering analysis through methylation patterns of plasma EBV DNA. For example, after a certain pattern is identified, embodiments can rule-in or rule-out a disease. Other classification algorithms including but not limited to principle component analysis, linear discriminant analysis, logistic regression, machine learning models, k-means clustering, k-nearest neighbors and random decision forests could also be used.

**[0138]** FIG. 19 shows a cluster dendrogram with the hierarchical clustering analysis based on methylation pattern analysis of plasma EBV DNA for 6 patients with NPC (including 4 patients with early stage NPC from our screening cohort) and 3 non-NPC subjects with persistently positive plasma EBV DNA according to embodiments of the present disclosure. The plasma DNA was extracted from their first blood samples upon recruitment. In this example, the hierarchical clustering analysis was based on comparison of the methylation percentages of the CpG sites within non-overlapping contiguous bins of 500 bp in size.

**[0139]** In FIG. 19, the distance is also shown along the top horizontal axis. The distance can be determined as described above. Similar to FIG. 18, two subjects can be combined at a point equal to the distance between them. As shown, the NPC subjects are clustered with other NPC subjects, e.g., at nodes 1901 and 1902. Cluster dendrogram 1900 shows that the NPC subject are incrementally clustered together, with all of the NPC subject being clustered into a subgroup at node 1903, which does not include subjects with other conditions (i.e., persistently positive for this example). Similarly, the persistently positive subjects are grouped together first. This shows an ability to discriminate the NPC subjects from the persistently positive subjects.

**[0140]** Accordingly, we have demonstrated the feasibility of differentiating the patients with early stage NPC from the non-NPC subjects with false positive plasma EBV DNA results based on methylation pattern analysis of plasma EBV DNA from the first blood sample without the need for serial analysis. That is, an accurate classification can be made with a single measurement, as opposed to requiring multiple measurements at different times. This would potentially save the medical costs in the logistic arrangement for serial blood tests and further investigations for confirmatory purpose.

**[0141]** FIG. 20 shows a heatmap 2000 illustrating the methylation levels of all the non-overlapping 500-bp regions in the whole EBV genome for patients with nasopharyngeal carcinoma, NK-T cell lymphoma, and infectious mononucleosis. The methylation level of each window was calculated as the average of the methylation densities of all CpG sites (without selection) within the window. We analyzed the methylation patterns of plasma EBV DNA for 5 patients with NPC, 3 patients with NK-T cell lymphoma and 3 patients with infectious

mononucleosis. In the current example, the methylation pattern is analyzed through the methylation percentages over all 500-bp non-overlapping windows. Color key/histogram 2050 shows different colors for different methylation percentages, with white being near zero, yellow (light gray) being low (e.g., ~ 20%), orange (medium gray) being medium (e.g., ~ 50%), and red (dark gray) being high (e.g., ~ 80% and higher). Color key/histogram 2050 also shows a histogram for the number of regions having a particular methylation level.

**[0142]** Heatmap 2000 shows the methylation levels across all the non-overlapping 500-bp window on EBV genome for all the cases. Each row represents one 500-bp region and the color represents its methylation level. Each column represents one case. Cluster dendrogram 2010 shows clustering of the different cases. Different cases with the same diagnosis were clustered together. For example, the NPC cases are all clustered on the right, and exhibit high methylation levels, as evidenced by the dark red (dark gray). The lymphoma subjects are clustered in the middle and have a mix between yellow (light gray) (low methylation levels) and red (dark gray) (high methylation levels). The cluster of infectious mononucleosis samples are shown on the left and exhibit relatively low methylation levels, as evidenced by the light yellow (light gray).

**[0143]** FIG. 20 demonstrates the feasibility of predicting the EBV-associated diseases through the analysis of the methylation patterns of plasma EBV DNA. Further, greater accuracy is seen using the DMRs as opposed to all regions spanning the EBV genome.

**[0144]** In other embodiments, the methylation patterns can be derived through the methylation percentages over all the CpG sites across the EBV genome (as genomewide analysis), e.g., on a per site bases. In another embodiment, different weighting could be assigned to any individual CpG site(s) and/or DMR(s) for prediction of the EBV-associated diseases or conditions. Such weightings can be implemented in various ways, as is described above, e.g., applying scaling factors (weights) to intermediate methylation levels to obtain a weighted average for a region or genomewide. Here, we assigned equal weighting for all the CpG sites being analyzed.

## V. USE OF COUNTS AND SIZE

**[0145]** In addition to using methylation levels of cell-free viral DNA fragments in a cell-free sample to discriminate among subjects with different conditions and/or levels of a condition, some embodiments can use sizes of cell-free viral DNA fragments in a cell-free sample. Some embodiments can also use a number (e.g., a proportion) of cell-free viral DNA fragments in a cell-free sample. Various embodiments can use combinations of different techniques, e.g., by requiring a same classification for a subject using each of the techniques. For example, any combination of a) the proportion of plasma DNA fragments aligning to the EBV, b) the size profile of the plasma EBV DNA fragments, and c) the methylation profile of plasma EBV DNA, can be used for the classification. Different thresholds can be adopted for the classification when different techniques are combined to achieve the desired diagnostic sensitivity and

specificity.

#### **A. Size profile analysis of plasma EBV DNA fragments**

**[0146]** In addition to the feasibility of methylation analysis of plasma EBV DNA fragments, the size of each plasma EBV DNA fragment was deduced based on the coordinates of the outmost nucleotide at the two ends in the EBV genome. The size distributions of cell-free EBV DNA fragments varies for different conditions (i.e., different patterns), thereby allowing discrimination among subjects with different conditions, and thus levels of a condition. These different size patterns can be quantified in various size metrics, e.g., size ratios of an amount of viral DNA at one size (e.g. a first size range) relative to an amount of viral DNA at another size (e.g., a second size range). For example, a size ratio can be used to compare the proportion of plasma EBV DNA reads within a certain size range (e.g., between 80 and 110 base pairs) normalized to the amount of autosomal DNA fragments within the same size range among subjects with different conditions.

**[0147]** FIG. 21 shows the size profiles of size distribution of sequenced plasma DNA fragments mapped to the EBV genome and human genome in 2 patients with NPC (TBR1392 and TBR1416) and 2 patients with infectious mononucleosis (TBR1610 and TBR1661), and 3 non-NPC subjects with persistently positive plasma EBV DNA on serial analysis (AF091, HB002 and HF020) according to embodiments of the present disclosure. The plots show a sizes (bp) along the horizontal axis and frequency (proportion) of DNA at a given size in the vertical axis. The size distributions of the human genomic DNA is shown in blue (gray), e.g., in size distribution 2104. The EBV size distributions are shown in red (black), e.g., size distribution 2103.

**[0148]** A difference in the size profile pattern of plasma EBV DNA fragments aligned to the EBV genome and those aligned to the autosomal genome were observed. For example, the NPC subjects have a shift to smaller cell-free EBV DNA fragments at the peak around 160 bp with a similar amount of fragments at the lower end as human DNA, while IM subjects have a larger amount of EBV DNA than human DNA below 100 bp. The persistently positive subjects have significant fluctuations up and down as size increases, as well as a more pronounced shift of the peak relative to the NPC subjects. These differences can be used to differentiate subjects with different conditions, e.g., differentiate subjects with NPC from subjects with false-positive plasma EBV DNA results.

**[0149]** To compare the proportion of plasma EBV DNA reads within a certain size range (e.g., between 80 and 110 bp) among individuals, the amount of plasma EBV DNA fragments can be normalized to the amount of autosomal DNA fragments within the same size range. This metric is an example of a size ratio. A size ratio can be defined by the proportion of plasma EBV DNA fragments within a certain size range divided by the proportion of a reference set of sequences (e.g., DNA fragments from the human autosomes) within the corresponding size range. Various size ratios may be used. For example, a size ratio of fragments between 80 and 110 base pairs would be:

$$\text{Size ratio}_{80-110bp} = \frac{\text{Proportion of EBV DNA fragments within 80 – 110bp}}{\text{Proportion of autosomal DNA fragments within 80 – 110bp}}$$

**[0150]** FIG. 22 shows the size ratio in 6 patients with NPC and 3 subjects that are persistently positive for plasma EBV DNA according to embodiments of the present disclosure. We could observe a statistically significant difference between the size ratio of the two groups of subjects (p-value=0.02, Mann-Whitney test). Example reference size values for discriminating between NPC subjects and persistently positive subjects can be between 2-4 (e.g., 3) for this particular size ratio.

**[0151]** FIG. 23 shows the EBV DNA size ratios in the non-NPC subjects with transiently positive plasma EBV DNA, non-NPC subjects with persistently positive plasma EBV DNA, and NPC patients according to embodiments of the present disclosure. The mean EBV DNA size ratio (80-110 bp) for the NPC group (mean=1.9) was significantly lower than the median size ratios of the other two non-NPC groups with transiently positive (mean=4.3) and persistently positive (mean=4.8) plasma EBV DNA (p<0.0001, Kruskal-Wallis test).

**[0152]** Accordingly, NPC patients could be differentiated from non-NPC subjects with detectable plasma EBV DNA (transiently or persistently positive) based on the difference in the size profiles of plasma EBV DNA, e.g., as represented by EBV DNA size ratios. In the current example, a cutoff value of 3 was used to achieve a detection sensitivity of 90%. Using a cutoff value of 3, 27 out of 30 patients with NPC, 23 out of 117 non-NPC subjects with transiently positive plasma EBV DNA, and 7 out of 39 non-NPC subjects with persistently positive plasma EBV DNA passed the cutoff and had their size ratios of plasma EBV DNA lower than the cutoff value. The calculated sensitivity, specificity and positive predictive value were 90%, 80.8% and 49.2% respectively.

**[0153]** The selection of the cutoff (reference) value can be determined in various ways. In one embodiment, a cutoff value for the EBV DNA size ratios can be selected as any value above the highest value in the EBV DNA size ratios among the NPC patients being analyzed (e.g., in a training set). In other embodiments, a cutoff values can be determined, for example, as the mean EBV DNA size ratios of the NPC patients plus one standard deviation (SD), mean plus two SD, mean plus three SD. In yet other embodiments, the cutoff can be determined using Receiver Operator Characteristics (ROC) curves or by nonparametric methods, for example, including 100%, 95%, 90%, 85%, 80% of the NPC patients being analyzed.

**[0154]** Other definitions of a size ratio or other statistical values of the size distribution would result in different values for each of the subjects, and thus have different reference values for discriminating among subjects. For example, a different size range can be used, or a subset of chromosomes can be used for the autosomal DNA fragments, or no autosomal DNA at all. Various statistical values of a size distribution of nucleic acid fragments can be determined. For example, an average, mode, median, or mean of a size distribution can be used. Other statistical values can be used, e.g., a cumulative frequency for a given size or various ratios of

amount of nucleic acid fragments of different sizes. A cumulative frequency can correspond to a proportion (e.g., a percentage) of DNA fragments that are of a given size or smaller, or larger than a given size. Accordingly, any normalization factor (if one is used) in the denominator can be for an amount of EBV DNA for a different size range. The statistical values provide information about the distribution of the sizes of DNA fragments for comparison against one or more size thresholds for healthy control subjects or other conditions. One skilled in the art will know how to determine such thresholds based on the present disclosure. Other examples of size ratios can be found in U.S. Patent Publications 2011/0276277, 2013/0237431, and 2016/0217251.

### **B. Count**

**[0155]** In addition to the analysis of methylation percentages of plasma EBV DNA, we analyzed the proportion of plasma EBV DNA reads from targeted bisulfite sequencing. The proportion of cell-free EBV DNA reads can be determined in various ways, e.g., as a proportion of all DNA reads in the human genome and several viral genomes or just of the human genome and the viral genome being analyzed. In the former example, a combined reference sequence can comprise the whole human genome (hg19), the whole EBV genome (AJ507799.2), the whole HBV genome, and the whole HPV genome. In various examples, the proportion can be determined based on counts of reads that align to the viral genome being analysed relative to the all the other DNA reads or just the ones that could be aligned (e.g., uniquely or with a specified number of mismatches). Using a reference genome of the human genome and several viral genomes, we compared the proportion of plasma EBV DNA reads among the three groups of NPC patients, non-NPC subjects with transiently positive and non-NPC subjects with persistently positive plasma EBV DNA.

**[0156]** FIG. 24 shows the proportion of plasma EBV DNA reads (plasma DNA reads mapped to the EBV genome) among all sequenced plasma DNA reads in the non-NPC subjects with transiently positive plasma EBV DNA, non-NPC subjects with persistently positive plasma EBV DNA, and NPC patients according to embodiments of the present disclosure. The mean proportion of plasma EBV DNA reads for the NPC group (mean = 0.075%) was significantly higher than the mean proportions of the other two non-NPC groups with transiently positive (mean = 0.003%) and persistently positive (mean = 0.052%) plasma EBV DNA ( $p < 0.0001$ , Kruskal-Wallis test). Accordingly, NPC patients could be differentiated from non-NPC subjects with detectable plasma EBV DNA (transiently or persistently positive) based on the difference in the quantity of plasma EBV DNA (i.e. proportion of plasma EBV DNA).

**[0157]** In the current example, using a cutoff value of  $4.5 \times 10^{-6}$ , all the 30 patients with NPC, 79 out of 119 non-NPC subjects with transiently positive plasma EBV DNA and 34 out of 39 non-NPC subjects with persistently positive plasma EBV DNA had their proportions of plasma EBV DNA by targeted bisulfite sequencing higher than this cutoff value. The calculated sensitivity, specificity, and positive predictive value were 100%, 27.6% and 22.1% respectively

**[0158]** The selection of the cutoff (reference) value can be determined in various ways. In one embodiment, the cutoff value for the proportion of plasma EBV DNA can be selected as any value below the lowest value in the proportion among the NPC patients being analyzed. The cutoff can be set to capture all the NPC patients and achieve the maximal sensitivity. In other embodiments, the cutoff values can be determined, for example, as the mean proportion of plasma EBV DNA reads of the NPC patients minus one standard deviation (SD), mean minus two SD, mean minus three SD. In the current example, a cutoff value was set at the mean of the proportions of plasma EBV DNA reads among all NPC patients minus three SD. In yet other embodiments, the cutoff can be determined after the logarithmic transformation of the proportion of plasma DNA fragments mapped to the EBV genome and then selected in a similar manner (e.g., using a mean, etc.). In yet other embodiments, the cutoff can be determined using Receiver Operator Characteristics (ROC) curves or by nonparametric methods, for example, including 100%, 95%, 90%, 85%, 80% of the NPC patients being analyzed.

### ***C. Combined analysis***

**[0159]** These three techniques can be combined to provide increased accuracy. For example, the metrics for each of the techniques—each technique potentially including multiple metrics, e.g., multiple methylation levels—can be compared to respective reference values to classify a subject, e.g., as may be done in a decision tree or to identify the subject as corresponding to a particular section (quadrant) of a plot of training values. Clustering techniques may also be used, e.g., as described above.

**[0160]** We assessed the value of combining the analyses for plasma EBV DNA proportions (quantification) and size ratios for NPC identification. We also assessed the value of combining the analyses for plasma EBV DNA proportions (quantification) and methylation percentages for NPC identification, and then all three together.

**[0161]** FIG. 25 is a plot of the proportions of the plasma EBV DNA reads and corresponding size ratio values for the NPC patients, non-NPC subjects with transiently positive, and persistently positive plasma EBV DNA according to embodiments of the present disclosure. The same cutoff values in EBV DNA size ratios and the proportion of plasma EBV DNA reads defined in FIGS. 23 and 24 are denoted by the grey dotted lines. The oval highlights the quadrant 2510 that passed the combined analyses.

**[0162]** In this combined analysis, a plasma sample was deemed to be positive if its sequencing data concurrently passed the cutoffs in both the analyses for the proportions and size ratios of plasma EBV DNA. Using the cutoffs defined above, the sensitivity, specificity and positive predictive value for NPC detection were 90%, 88.5% and 61.7%, respectively.

**[0163]** FIG. 26 is a plot of the proportions of the plasma EBV DNA reads and corresponding

methylation percentage values for the NPC patients, non-NPC subjects with transiently positive, and persistently positive plasma EBV DNA according to embodiments of the present disclosure. The same cutoff values in the EBV DNA methylation percentages within the 46 DMRs and the proportion of plasma EBV DNA reads as respectively defined in FIGS. 13 and 24 are denoted by the grey dotted lines. The oval highlights the quadrant 2610 that passed the combined analyses.

**[0164]** In this combined analysis, a plasma sample was deemed to be positive if its sequencing data concurrently passed the cutoffs in both the analyses for the proportions and methylation percentages of plasma EBV DNA (based on the DMR defined in FIG.). Using the cutoffs defined above, the sensitivity, specificity, and positive predictive value for NPC detection were 96.7%, 89.1% and 64.6%, respectively.

**[0165]** FIGS. 27A and 27B show a 3-dimensional plot of the proportions of the plasma EBV DNA reads and corresponding size ratio and methylation percentage values for the NPC patients, non-NPC subjects with transiently positive, and persistently positive plasma EBV DNA according to embodiments of the present disclosure. We assessed the value of combining all the three parameters, plasma EBV DNA proportions (quantification), size ratios, and methylation percentages for NPC identification. The proportions were determined in a same manner as FIG. 24. The size ratios were determined in a same manner as FIG. 23. And, the methylation levels are determined using the 46 DMRs used for FIG. 13.

**[0166]** In FIG. 27A, the purple surface 2710 denotes a fitted 3-D surface that differentiates the NPC patients from the non-NPC subjects with transiently and persistently positive plasma EBV DNA in the 3-dimensional space. The use of a fitted surface illustrates that the reference values for differentiating among subjects can be more complex than constant values. For example, in FIG. 26, the cutoff for the methylation percentage could vary with the proportion of sequence reads. Such flexibility in determining classification can provide for greater accuracy. The fitting can be selected to optimized various accuracy metrics, e.g., specificity, sensitivity, or some average of both. Such fitting can be performed using support vector machines. FIG. 27B shows the same data as in FIG. 27A, but without surface 2710, and with the axes labeled in a box around the data.

**[0167]** FIGS. 28A and 28B show a receiver operator characteristics (ROC) curve analysis for various combinations of count-based, size-based, and methylation-based analyses according to embodiments of the present disclosure. The accuracy is for the correct classification of NPC subjects and non-NPC subjects. The parameters (i.e., proportions, size ratios, and methylation levels) were determined in a same manner as for FIGS. 27A and 27B. Cutoff value were varied, thereby causing a change in sensitivity and specificity. FIG. 27A shows a comparison of the three techniques used individually. The area under the curve (AUC) values are shown. The AUC values were 0.905, 0.942 and 0.979 respectively for count-only, size-only, and methylation-only. Methylation provides the best results. FIG. 28B shows a comparison of three combined techniques. The AUC value for count and size is 0.97. The AUC value for count and methylation is 0.985. Using all three techniques provides the best accuracy with 0.989.

## VI. OTHER VIRAL EXAMPLES

**[0168]** Other viruses are also associated with cancer. For example, plasma human papillomavirus (HPV) is associated with head and neck squamous cell carcinoma (HNSCC). And, hepatitis B virus (HBV) is associated with hepatocellular carcinoma (HCC). The results below show that embodiments can use methylation level(s) for other cell-free viral DNA to classify levels of a condition in a similar manner that methylation level(s) were used for cell-free EBV DNA.

### A. HPV

**[0169]** FIG. 29 shows the clinical stage of the 5 cases of HPV positive-head and neck squamous cell carcinoma (HPV+ve HNSCC). The cases were staged according to the 8<sup>th</sup> Edition of AJCC Cancer Staging Manual. We have analyzed the methylation profiles of plasma human papillomavirus (HPV) DNA reads from these 5 patients with HPV positive-head and neck squamous cell carcinoma (HPV+ve HNSCC) by target bisulfite sequencing of plasma DNA. All the 5 patients had early stage (stage I or II) diseases. All of them had detectable HPV DNA fragments in their plasma DNA samples.

**[0170]** For each clinical case, plasma DNA was extracted from 4 mL plasma using the QIAamp DSP DNA blood mini kit. For each case, all extracted DNA was used for the preparation of sequencing library using TruSeq DNA PCR-free library preparation kit (Illumina). The adapter-ligated DNA products were subjected to two rounds of bisulfite treatment using an EpiTect Bisulfite Kit (Qiagen). Twelve to fifteen cycles of PCR amplification were performed on the bisulfite-converted samples using the KAPA HiFi HotStart Uracil+ ReadyMix PCR kit (Roche). The amplification products were then captured with the SeqCap-Epi system (Nimblegen) using the custom-designed probes covering the viral and human genomic regions stated above (FIG. 1).

**[0171]** After the target capture, the captured products were enriched by 14 cycles of PCR to generate DNA libraries. The DNA libraries were sequenced on a NextSeq platform (Illumina). For each sequencing run, four to six samples with unique sample barcodes were sequenced using the paired-end mode. For each DNA fragment, 75 nucleotides were sequenced from each of the two ends. After sequencing, the sequence reads were processed in *Methyl-Pipe*, a methylation data-analysis pipeline (Jiang et al. PLoS One 2014;9:e1 00360), and mapped to an artificially combined reference sequence comprising the whole human genome (hg19), the whole EBV genome (AJ507799.2), the whole HBV genome, and the whole HPV genome. Sequenced reads mapping to unique positions (although mismatches may be allowed in other embodiments) in the combined genomic sequence were used for downstream analysis.

**[0172]** FIG. 30 shows the methylation profiles of plasma HPV DNA in individual patients with HPV positive head and neck squamous cell carcinoma (HPV+ve HNSCC) according to embodiments of the present disclosure. The methylation profiles of HPV DNA were generated through targeted capture bisulfite sequencing of plasma DNA from these patients. FIG. 30 shows that HPV16 (HPV serotype 16) methylation can be detected in plasma HPV16 DNA molecules of HNSCC patients. The methylation density of all the CpG sites across the HPV genome was determined.

**[0173]** The methylation density MD of specific loci across the viral genome in the plasma can be calculated using the equation:  $MD=M/(M+U)$ , where M is the count of methylated viral reads and U is the count of unmethylated viral reads at the CpG sites within the genetic locus across the viral genome. On a locus-specific level, these loci could be of any size and of at least 1 CpG site (1bp). If there is more than one CpG site within a locus, then M and U corresponds to the counts across the sites. These loci could be and could be not associated with any annotated viral genes.

**[0174]** We could observe similar patterns of the methylation profiles of plasma HPV DNA among different patients. Usually there are no HPV in the non-cancer subjects. We defined two genomic regions, namely region 3001 and region 3002. The region-specific methylation density in region 3001 was consistently higher than that in region 3002 for all 5 cases of HPV+ve HNSCC. These similarities in the patterns among subjects with the same condition and differences in the patterns among subjects with different conditions of methylation profiles could be analyzed on a global or locus-specific level. The methylation densities of such pre-defined regions could predict the clinical presentation, for example, for cancer stage, response to treatment, and recurrence risk.

**[0175]** FIG. 31 shows the methylation level of all the CpG sites across the HPV genome in two patients with HPV+ve HNSCC according to embodiments of the present disclosure. A first patient is shown in black and is on the bottom, as depicted at 3101. A second patient is in gray, and when larger can be seen, as in 3102. As can be seen, the two patients have appreciable methylation levels at similar loci, and many loci have similar values for the methylation levels. By comparing the methylation level on a global or locus-specific level among cases, embodiments can identify a subject as having HNSCC.

## ***B. HBV***

**[0176]** Targeted bisulfite sequencing of plasma DNA was performed for 9 patients with chronic hepatitis B infection and 10 patients with HCC. We also analyzed the methylation profile of plasma HBV reads from these patients with chronic hepatitis B infection and HCC.

**[0177]** FIGS. 32A and 32B shows the proportions of hepatitis B virus (HBV) DNA reads (plasma DNA reads mapped to the HBV genome) and the methylation percentages of all the CpG sites across the HBV genome for 9 patients with chronic hepatitis B infection (HBV) and

10 patients with hepatocellular carcinoma (HCC) according to embodiments of the present disclosure.

**[0178]** In FIG. 32A, the percentage of DNA fragments that aligned to the HBV genome relative to the human genome was determined. In this particular example, the number of cell-free DNA fragments uniquely aligning to the HBV genome was divided by the number of cell-free DNA fragments that uniquely aligned to a combined reference genome comprising the genomes of human, HBV, HPV and EBV as listed in FIG. 1. A higher average proportion of HBV DNA reads was observed in patients with HCC (mean = 0.006%) than patients with chronic HBV infection (mean = 0.03%), but a statistical significance was not achieved ( $p=0.07$ , Student's t-test). As one can see visually, the means of the HCC subjects and the HBV subjects are similar. Thus, a count-based technique has a relatively low predictive capability.

**[0179]** In FIG. 32B, the HBV methylation percentage was determined as a global methylation level across all the CpG sites in the HBV genome. We observed a significantly higher methylation percentage of plasma HBV DNA for patients with HCC (mean = 1.7 %) than patients with chronic hepatitis B infection (mean = 23%) ( $p=0.03$ , Student's t-test). Such a separation indicates an increased ability to discriminate between subjects that have HBV but without HCC, and those subjects that have HCC. Thus, embodiments can classify levels of the HCC condition (e.g., HCC or no HCC). Accordingly, embodiments could predict the risk of HCC based on the genomewide methylation level of plasma HBV DNA in the sample.

**[0180]** Other embodiments can implement other types of methylation levels, e.g., as described herein. For example, the classification could be based on the methylation levels within differentiated methylated regions with pre-defined criteria.

## VII. METHOD USING METHYLATION OF CELL-FREE VIRAL DNA

**[0181]** As described above, embodiments can measure one or more methylation levels in a sample of cell-free DNA, including cell-free viral DNA and cell-free genomic human DNA. The methylation levels can classify a level of a condition by analyzing the methylation level(s) for DNA from a particular virus that is associated with the condition. Count-based and size-based techniques can also be used to supplement the methylation techniques.

**[0182]** As examples, the level of the condition may be whether the condition exists, a severity of a condition, a stage of the condition, an outlook for the condition, the condition's response to treatment, or another measure of severity or progression of the condition. As examples for cancer, the level of cancer may be whether cancer exists, a stage of cancer (e.g., early stage and late stage), a size of tumor, the cancer's response to treatment, or another measure of a severity or progression of cancer.

**[0183]** For EBV, example conditions can include infectious mononucleosis (IM), nasopharyngeal carcinoma (NPC), natural killer (NK)-T cell lymphoma, and subjects without

these conditions, but who may show appreciable numbers of cell-free EBV DNA fragments in the sample. For HPV, example conditions can include head and neck squamous cell carcinoma (HNSCC) and subject that have an appreciable amount of cell-free HPV DNA fragments, but do not have HNSCC. For HBV, example conditions can include hepatocellular carcinoma (HCC) and subjects that have an appreciable amount of cell-free HBV DNA fragments, but do not have HCC.

***A. Using methylation levels to classify condition***

**[0184]** FIG. 33 is a flowchart illustrating a method 3300 of analyzing a biological sample of a subject that is an animal to determine a classification of a first condition according to embodiments of the present disclosure. The sample can include a mixture of DNA molecules from the subject and potentially DNA molecules from a virus. Method 3300 can include clinical, laboratory, and in silico (computer) steps. Method 3300 can be performed as part of a screening of subjects, e.g., to screen for cancer. Thus, the subject may be asymptomatic for the condition.

**[0185]** At block 3310, the biological sample is obtained from the subject. As examples, the biological sample can be blood, plasma, serum, urine, saliva, sweat, tears, and sputum, as well as other examples provided herein. The biological sample can include a mixture of cell-free DNA molecules from a genome of the subject and from one or more other genomes. For example, the one or more other genomes can include viral genomes, such as, EBV, HPV, and/or HBV genomes. In some embodiments (e.g., for blood), the biological sample can be purified for the mixture of cell-free DNA molecules, e.g., centrifuging blood to obtain plasma.

**[0186]** At block 3320, a plurality of cell-free DNA molecules are analyzed from the biological sample. The analysis of a cell-free DNA molecule can include identifying a location of the cell-free DNA molecule in a particular viral genome and determining whether the cell-free DNA molecule is methylated at one or more sites of the particular viral genome. Various numbers of cell-free DNA molecules can be analyzed (human and virus), e.g., at least 1,000, with various numbers being identified as from the particular viral genome (e.g., 10, 20, 30, 50, 100, 200, 500, or a 1,000 or more).

**[0187]** The methylation status of sites of the sequence read can be obtained as described herein. For example, the DNA molecules can be analyzed using sequence reads of the DNA molecules, where the sequencing is methylation-aware. Other methylation-aware assays can also be used. The sequence reads can each include a methylation status of cell-free DNA molecules from the biological sample. The methylation status can include whether a particular cytosine residue is 5-methylcytosine or 5-hydroxymethylcytosine. The sequence reads can be obtained in various ways, each as various sequencing techniques, PCR techniques (e.g., real-time or digital), arrays, and other suitable techniques for identifying sequences of fragments. Real-time PCR is an example of analyzing a group of DNA collectively, e.g., as an intensity signal proportional to the number of DNA methylated at a site. A sequence read can cover

more than one site depending on the proximity of the two sites to each other and the length of the sequence read.

**[0188]** The analysis can be performed by receiving sequence reads from a methylation-aware sequencing, and thus the analysis can be performed just on data previously obtained from the DNA. In other embodiments, the analysis can include the actual sequencing or other active steps for performing the measurements of the properties of the DNA molecules. The sequencing may be performed in a variety of ways, e.g., using massively parallel sequencing or next-generation sequencing, using single molecule sequencing, and/or using double- or single-stranded DNA sequencing library preparation protocols, and other techniques described herein. As part of the sequencing, it is possible that some of the sequence reads may correspond to cellular nucleic acids.

**[0189]** The sequencing may be targeted sequencing, e.g., as described herein. For example, biological sample can be enriched for nucleic acid molecules from the virus. The enriching of the biological sample for nucleic acid molecules from the virus can include using capture probes that bind to a portion of, or an entire genome of, the virus. Other embodiments can use primers specific to a particular locus of the virus. The biological sample can be enriched for nucleic acid molecules from a portion of a human genome, e.g., regions of autosomes. FIG. 1 provides examples of such capture probes. In other embodiments, the sequencing can include random sequencing.

**[0190]** After sequencing by a sequencing device, the sequence reads may be received by a computer system, which may be communicably coupled to a sequencing device that performed the sequencing, e.g., via wired or wireless communications or via a detachable memory device. In some embodiments, one or more sequence reads that include both ends of the nucleic acid fragment can be received. The location of a DNA molecule can be determined by mapping (aligning) the one or more sequence reads of the DNA molecule to respective parts of the human genome, e.g., to specific regions, such as differentially methylation regions (DMRs). In one implementation, if a read does not map to a region of interest, then the read can be ignored. In other embodiments, a particular probe (e.g., following PCR or other amplification) can indicate a location, such as via a particular fluorescent color. The identification can be that the cell-free DNA molecule corresponds to one of the set of one or more sites, i.e., the particular site may not be known, as the amount of DNA methylated at one or more sites is all that is needed.

**[0191]** At block 3330, one or more mixture methylation levels are measured based on one or more amounts of the plurality of cell-free DNA molecules methylated at a set of one or more sites of the particular viral genome. A mixture methylation level may be a methylation density or percentage (e.g., as described herein) for the cell-free DNA molecules of the set of site(s) or a subset of the site(s). For example, the methylation level can correspond to a methylation density that is determined based on the number of DNA molecules corresponding to the set of sites and the number methylated. The number may be determined based on alignment of sequence reads to the viral genome, in combination with the methylation status for a given

sequence read at one or more sites.

**[0192]** A respective number of DNA molecules that are methylated at the site can be determined for each of the set of sites. In one embodiment, the sites are CpG sites, and may be only certain CpG sites, as selected using one or more criteria mentioned herein. The number of DNA molecules that are methylated is equivalent to determining the number that are unmethylated once normalization is performed using a total number of DNA molecules analyzed at a particular site, e.g., a total number of sequence reads. For example, an increase in the CpG methylation density of a region is equivalent to a decrease in the density of unmethylated CpGs of the same region.

**[0193]** When the set of one or more sites includes at least two sites, one mixture methylation level can be determined across the at least two sites. For example, the methylation level can be computed as a total methylation density for all of the cell-free DNA molecules of the first set. In another example, separate methylation densities can be computed for each site or region(s) of one or more sites, thereby providing N (e.g., integer of 2 or more) mixture methylation levels as multidimensional point, e.g., as described in sections IV.B-IV.E. The separate methylation densities can be combined to obtain the mixture methylation level, e.g., an average of the separate methylation densities.

**[0194]** In other embodiments, the separate methylation levels may be kept for later analysis, e.g., using clustering and other techniques described herein. For example, the multidimensional point (N mixture methylation levels) can be compared to N reference methylation levels to obtain N differences, which can be used to determine whether the subject belongs to one of the at least two cohorts. FIGS. 18-20 provide such examples for hierarchical clustering analysis. The regions may be predetermined, e.g., as described above for predetermined regions having a size between 50 bases and 1,000 bases, with the sizes being the same or varying among regions.

**[0195]** If more than one mixture methylation level is determined, the different levels can correspond to different subset of the set of sites. For example, methylation levels can be determined for different regions, each of which may include one or more sites. The regions can span the entire viral genome or correspond to only parts, e.g., as may be done when particular regions are selected. Such regions may be selected for being differentially methylated according to one or more criteria, e.g., as described herein. Such criteria can correspond to methylation levels in a cohort of subjects having a same condition being within a specific range, and potentially having a difference within a threshold from other subjects of the cohort. Thus, the criteria for the regions or for each of the sites may include (1) a difference in methylation level among multiple subjects of a same cohort and/or (2) a difference in methylation level between a subject of one cohort and a subject of another cohort.

**[0196]** At block 3340, the one or more mixture methylation levels are compared to one or more reference methylation levels determined from at least two cohorts of other subjects. The at least two cohorts can have different classifications associated with the particular viral genome,

where the different classifications include a first condition. Examples of such conditions are provided above, e.g., NPC, IM, lymphoma, and non-NPC states related to transient or persistently positive for the number of EBV DNA molecules. Examples of cohorts and reference methylation levels are provided in FIGS. 8, 11, 13, 15, and 18-20.

**[0197]** The comparison can take various forms. For example, a separation value can be determined, such as a ratio or a difference between a mixture methylation level and a reference methylation level. Various separation values can be defined, include definitions that includes ratios and differences, and functions of both. The comparison can further include a comparison of the separation value to a cutoff value to determine a statistically significant difference. For example, the reference methylation level can be an average for a cohort, and a difference between the mixture methylation level of a sample and the average for the cohort can be compared to a cutoff value, which may be determined based on a standard deviation of the measured methylation levels for the reference samples used in the cohort.

**[0198]** In some embodiments involving multiple methylation levels and multiple reference levels, the multiple methylation levels can correspond to a sample multidimensional point (e.g., N levels forming a vector) with the multiple reference levels corresponding to surface (e.g., a hyperplane) of N-1 dimensions, where the surface may be a closed surface, e.g., like a sphere in which the data points correspond to a same condition. As another example, the comparison of multiple methylation levels to reference levels can be implemented by determining a distance between the sample multidimensional point to a representative (reference) multidimensional point of a reference subject. The reference multidimensional point can correspond to a single reference subject, e.g., patient AL038. As another example, the representative (reference) multidimensional point can be a centroid of a cluster of reference multidimensional points from subjects with the same condition.

**[0199]** As another example, the comparing of mixture methylation level(s) to reference methylation level(s) can include inputting the one or more mixture methylation levels into a machine learning model that was trained using the one or more reference methylation levels determined from the at least two cohorts of other subjects. For example, the reference levels can be the methylation levels measured for the other subjects, and a clustering model can be trained using those reference levels. For instance, a centroid can be selected for the cluster of subjects corresponding to a particular cohort.

**[0200]** At block 3350, a first classification of whether the subject has the first condition is determined based on the comparing. The first classification can take various forms, e.g., a binary result or a probability value. In some embodiments, the first classification can provide a level of the first condition, e.g., a size of a tumor, a severity, or a stage of cancer.

**[0201]** The different classifications of the at least two cohorts can also include a second condition, where the comparison to the one or more reference levels can determine a second classification of whether the subject has the second condition. For example, a single reference level can discriminate between IM and lymphoma, or between NPC and persistently positive

subjects.

**[0202]** The one or more mixture methylation levels can be compared to a plurality of reference methylation levels. As an example of using one methylation level but multiple reference methylation levels, different reference levels can discriminate between different conditions. For example, first reference methylation level can determine the first classification of whether the subject has the first condition (e.g., discriminate between IM and not having IM), and second reference methylation level can determine the second classification of whether the subject has the second condition (e.g., discriminate between NPC and not having NPC), e.g., as depicted in FIGS. 8, 11, and 15. Thus, embodiments can use a different reference level to determine a second classification of whether the subject has a second condition based on the comparing.

**[0203]** The method may further include treating the subject for the condition responsive to the classification being that the subject has the condition, thereby improving the condition (e.g., to remove the condition or reduce severity). If the condition is cancer, the treatment may include surgery, radiation therapy, chemotherapy, immunotherapy, targeted therapy, hormone therapy, stem cell transplant, or precision medicine. Based on the determined level of condition, a treatment plan can be developed to decrease the risk of harm to the subject. Methods may further include treating the subject according to the treatment plan.

**[0204]** Biological samples can be obtained at various time points and analyzed independently at those time points, or in conjunction with the measurements and classifications at the other time points. Examples of such time points include before and after treatment of cancer (e.g. targeted therapy, immunotherapy, chemotherapy, surgery), different time points following the diagnosis of cancer, before and after progression of cancer, before and after development of metastasis, before and after increased severity of disease, or before and after development of complications.

### ***B. Using methylation levels in combination with sizecount***

**[0205]** As described in section V, count-based and/or size-based techniques can be used in combination with methylation techniques. Such techniques can be implemented independently, e.g., each providing a separate classification. Each of such independent classifications can be required to provide a same result in order to provide a final classification of that result. In other embodiments, the reference values for the different techniques can depend on the metrics from another technique, e.g., the size reference value can depend on a methylation level measured for the given sample, as was described above for FIG. 27. In some implementations, each metric (e.g., a methylation level) can be a different element in a vector, thereby creating a multidimensional data point out of the metrics for a given sample. Each of the metrics can be determined from the same sample or separate samples, e.g., which may be obtained from the subject at around the same time.

**[0206]** In some embodiments, the size-based technique can be implemented as follows to

analyze a biological sample of the subject. The sample can be the same or different sample as the one used for the methylation analysis. The biological sample can include a mixture of cell-free DNA molecules from a genome of the subject and from one or more other genomes (e.g., a viral genome). For each of a plurality of cell-free DNA molecules in the biological sample, a size and a location can be determined, e.g., as described herein. For instance, both ends of the DNA molecules can be sequenced (e.g., to provide one sequence read for the entire DNA molecule or a pair of sequence reads for the two ends) and the sequence read(s) aligned to a reference genome to determine size. Thus, embodiments can measure a size of the DNA molecule and identify a location of the DNA molecule in the particular viral genome. These cell-free DNA molecules can be the same as were used for the methylation analysis, e.g., where methylation-aware sequencing is used. The sizes of the plurality of DNA molecules can form a size distribution.

**[0207]** A statistical value (e.g., a size ratio) of the size distribution can be determined. The statistical value can be compared to a reference size value determined from at least two cohorts of other subjects, which may be the same two cohorts used for the methylation analysis. The at least two cohorts can have different classifications associated with the particular viral genome, including a first condition. A size-based classification of whether the subject has the first condition can be determined based on the comparing. The size-based classification and the methylation-based classification can be used together to provide a final classification. Example reference size values are provided in FIGS. 22, 23, 25, and 27.

**[0208]** In some embodiments, the count-based technique can be implemented as follows to analyze a biological sample of the subject. The sample can be the same or different as the one used for the methylation analysis. The biological sample can include a mixture of cell-free DNA molecules from a genome of the subject and from one or more other genomes (e.g., a viral genome).

**[0209]** An amount of cell-free DNA molecules derived from the particular viral genome in a sample can be determined. In some embodiments, for each of a plurality of cell-free DNA molecules in the biological sample, it is determined whether the molecule is derived from the particular viral genome, e.g., using sequencing or probes, potentially along with amplifications, such as PCR. For instance, a location can be determined, e.g., whether from a human genome or from a particular viral genome. The location can be determined using a plurality of sequence reads obtained from a sequencing of the mixture of cell-free DNA. An amount of the plurality of sequence reads aligning to the particular viral genome can be determined. For example, a proportion of sequence reads aligned to the viral genome relative to a total number of sequence reads can be determined. The total number of sequence reads can be a sum of the sequence reads that aligned to a reference genome corresponding to the virus and the sequence reads that aligned to a human genome. Other ratios described herein can also be used, e.g., amount of reads from the particular viral genome divided by the amount of human reads.

**[0210]** The amount of sequence reads aligning to the reference genome can be compared to

a reference value determined from at least two cohorts of other subjects, which may be the same two cohorts used for the methylation and/or size analysis. The at least two cohorts can have different classifications associated with the particular viral genome, including a first condition. A count-based classification of whether the subject has the first condition can be determined based on the comparing. The count-based classification and the methylation-based classification can be used together to provide a final classification. Example reference count values are provided in FIGS. 24-27 and 32A.

## VIII. EXAMPLE SYSTEMS

**[0211]** FIG. 34 illustrates a system 3400 according to an embodiment of the present invention. The system as shown includes a sample 3405, such as cell-free DNA molecules within a sample holder 3410, where sample 3405 can be contacted with an assay 3408 to provide a signal of a physical characteristic 3415. An example of a sample holder can be a flow cell that includes probes and/or primers of an assay or a tube through which a droplet moves (with the droplet including the assay). Physical characteristic 3415, such as a fluorescence intensity value, from the sample is detected by detector 3420. Detector 3420 can take a measurement at intervals (e.g., periodic intervals) to obtain data points that make up a data signal. In one embodiment, an analog to digital converter converts an analog signal from the detector into digital form at a plurality of times. Sample holder 3410 and detector 3420 can form an assay device, e.g., a sequencing device that performs sequencing according to embodiments described herein. A data signal 3425 is sent from detector 3420 to logic system 3430. Data signal 3425 may be stored in a local memory 3435, an external memory 3440, or a storage device 3445.

**[0212]** Logic system 3430 may be, or may include, a computer system, ASIC, microprocessor, etc. It may also include or be coupled with a display (e.g., monitor, LED display, etc.) and a user input device (e.g., mouse, keyboard, buttons, etc.). Logic system 3430 and the other components may be part of a stand-alone or network connected computer system, or they may be directly attached to or incorporated in a thermal cycler device. Logic system 3430 may also include optimization software that executes in a processor 3450. Logic system 3430 may include a computer readable medium storing instructions for controlling system 3400 to perform any of the methods described herein.

**[0213]** Any of the computer systems mentioned herein may utilize any suitable number of subsystems. Examples of such subsystems are shown in FIG. 35 in computer system 10. In some embodiments, a computer system includes a single computer apparatus, where the subsystems can be the components of the computer apparatus. In other embodiments, a computer system can include multiple computer apparatuses, each being a subsystem, with internal components. A computer system can include desktop and laptop computers, tablets, mobile phones and other mobile devices.

**[0214]** The subsystems shown in FIG. 35 are interconnected via a system bus 75. Additional

subsystems such as a printer 74, keyboard 78, storage device(s) 79, monitor 76, which is coupled to display adapter 82, and others are shown. Peripherals and input/output (I/O) devices, which couple to I/O controller 71, can be connected to the computer system by any number of means known in the art such as input/output (I/O) port 77 (e.g., USB, FireWire<sup>®</sup>). For example, I/O port 77 or external interface 81 (e.g. Ethernet, Wi-Fi, etc.) can be used to connect computer system 10 to a wide area network such as the Internet, a mouse input device, or a scanner. The interconnection via system bus 75 allows the central processor 73 to communicate with each subsystem and to control the execution of a plurality of instructions from system memory 72 or the storage device(s) 79 (e.g., a fixed disk, such as a hard drive, or optical disk), as well as the exchange of information between subsystems. The system memory 72 and/or the storage device(s) 79 may embody a computer readable medium. Another subsystem is a data collection device 85, such as a camera, microphone, accelerometer, and the like. Any of the data mentioned herein can be output from one component to another component and can be output to the user.

**[0215]** A computer system can include a plurality of the same components or subsystems, e.g., connected together by external interface 81, by an internal interface, or via removable storage devices that can be connected and removed from one component to another component. In some embodiments, computer systems, subsystem, or apparatuses can communicate over a network. In such instances, one computer can be considered a client and another computer a server, where each can be part of a same computer system. A client and a server can each include multiple systems, subsystems, or components.

**[0216]** Aspects of embodiments can be implemented in the form of control logic using hardware circuitry (e.g. an application specific integrated circuit or field programmable gate array) and/or using computer software with a generally programmable processor in a modular or integrated manner. As used herein, a processor can include a single-core processor, multi-core processor on a same integrated chip, or multiple processing units on a single circuit board or networked, as well as dedicated hardware. Based on the disclosure and teachings provided herein, a person of ordinary skill in the art will know and appreciate other ways and/or methods to implement embodiments of the present invention using hardware and a combination of hardware and software.

**[0217]** Any of the software components or functions described in this application may be implemented as software code to be executed by a processor using any suitable computer language such as, for example, Java, C, C++, C#, Objective-C, Swift, or scripting language such as Perl or Python using, for example, conventional or object-oriented techniques. The software code may be stored as a series of instructions or commands on a computer readable medium for storage and/or transmission. A suitable non-transitory computer readable medium can include random access memory (RAM), a read only memory (ROM), a magnetic medium such as a hard-drive or a floppy disk, or an optical medium such as a compact disk (CD) or DVD (digital versatile disk), flash memory, and the like. The computer readable medium may be any combination of such storage or transmission devices.

**[0218]** Such programs may also be encoded and transmitted using carrier signals adapted for transmission via wired, optical, and/or wireless networks conforming to a variety of protocols, including the Internet. As such, a computer readable medium may be created using a data signal encoded with such programs. Computer readable media encoded with the program code may be packaged with a compatible device or provided separately from other devices (e.g., via Internet download). Any such computer readable medium may reside on or within a single computer product (e.g. a hard drive, a CD, or an entire computer system), and may be present on or within different computer products within a system or network. A computer system may include a monitor, printer, or other suitable display for providing any of the results mentioned herein to a user.

**[0219]** Any of the methods described herein may be totally or partially performed with a computer system including one or more processors, which can be configured to perform the steps. Thus, embodiments can be directed to computer systems configured to perform the steps of any of the methods described herein, potentially with different components performing a respective step or a respective group of steps. Although presented as numbered steps, steps of methods herein can be performed at a same time or at different times or in a different order. Additionally, portions of these steps may be used with portions of other steps from other methods. Also, all or portions of a step may be optional. Additionally, any of the steps of any of the methods can be performed with modules, units, circuits, or other means of a system for performing these steps.

**[0220]** The embodiments of the invention may be directed to specific embodiments relating to each individual aspect, or specific combinations of these individual aspects.

**[0221]** The above description of example embodiments of the invention has been presented for the purposes of illustration and description. It is not intended to be exhaustive or to limit the invention to the precise form described, and many modifications and variations are possible in light of the teaching above. The invention is however limited by the content of the appended claims.

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PATENTKRAV

1. Fremgangsmåde til analyse af en biologisk prøve fra et individ, der er et dyr, hvilken biologisk prøve indbefatter en blanding af cellefrie DNA-molekyler fra et genom fra individet og fra ét eller flere andre genomer, hvilken fremgangsmåde  
5 omfatter:

analyse af en flerhed af cellefrie DNA-molekyler fra den biologiske prøve, hvor analyse af ét af flerheden af cellefrie DNA-molekyler indbefatter:

identificering af en placering af det cellefrie DNA-molekyle i et specifikt, viralt genom; og

10 bestemmelse af, hvorvidt det cellefrie DNA-molekyle er methyleret ved ét eller flere steder af det specifikke, virale genom;

måling af et blandingsmethyleringsniveau baseret på mængder af flerheden af cellefrie DNA-molekyler methyleret ved et sæt af steder af det specifikke, virale genom, hvor sættet af steder er over en flerhed af områder;

15 sammenligning af blandingsmethyleringsniveauet med ét eller flere referencemethyleringsniveauer bestemt fra mindst to kohorter af andre individer, hvor de mindst to kohorter har forskellige klassifikationer forbundet med det specifikke, virale genom, hvilke forskellige klassifikationer indbefatter en første tilstand; og

20 bestemmelse af en første klassifikation af, hvorvidt individet har den første tilstand baseret på sammenligningen.

2. Fremgangsmåde ifølge krav 1, hvor de forskellige klassifikationer af de mindst to kohorter endvidere indbefatter en anden tilstand, hvilken fremgangsmåde endvidere omfatter:

25 bestemmelse af en anden klassifikation af, hvorvidt individet har den anden tilstand baseret på sammenligningen.

3. Fremgangsmåde ifølge krav 2, hvor blandingsmethyleringsniveauet sammenlignes med en flerhed af referencemethyleringsniveauer, der indbefatter et første referencemethyleringsniveau og et andet referencemethyleringsniveau, hvor

det første referencemetyleringsniveau anvendes til at bestemme den første klassifikation af, hvorvidt individet har den første tilstand, og hvor det andet referencemetyleringsniveau anvendes til at bestemme den anden klassifikation af, hvorvidt individet har den anden tilstand.

5           **4.** Fremgangsmåde ifølge krav 3, hvor det specifikke, virale genom er fra Epstein-Barr-virus, og individet er et menneske, hvor den første tilstand er nasopharynxcancer, og hvor den anden tilstand er infektiøs mononukleose.

**5.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor det specifikke, virale genom er fra Epstein-Barr-virus, og individet er et menneske,  
10           og hvor den første tilstand er nasopharynxcancer.

**6.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor trinnet med måling af et blandingsmetyleringsniveau omfatter måling af N blandingsmetyleringsniveauer, hvor N er et heltal, der er større end én, hvor blandingsmetyleringsniveauet er ét af de N blandingsmetyleringsniveauer, hvor  
15           hvert af de N blandingsmetyleringsniveauer måles ved hjælp af et tilsvarende sæt af steder over en tilsvarende flerhed af områder, og

              trinnet med sammenligning af blandingsmetyleringsniveauet med ét eller flere referencemetyleringsniveauer omfatter sammenligning af de N blandingsmetyleringsniveauer med N referencemetyleringsniveauer ved:

20           måling af forskelle mellem de N blandingsmetyleringsniveauer og N referencemetyleringsniveauer; og

              bestemmelse af, hvorvidt individet hører til den ende af de mindst to kohorter ved hjælp af forskellene.

**7.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor  
25           sættet af steder ligger i en flerhed af områder, der hvert opfylder ét eller flere kriterier indbefattende (1) en forskel i metyleringsniveau blandt flere individer fra en samme kohorte og/eller (2) en forskel i metyleringsniveau mellem et individ fra én kohorte og et individ fra en anden kohorte.

**8.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor  
30           sammenligning af blandingsmetyleringsniveauet med det ene eller flere

referencemetyleringsniveauer bestemt fra mindst to kohorter af andre individet omfatter:

indlæsning af blandingsmetyleringsniveauet i en maskinlæringsmodel, der er trænet ved hjælp af det ene eller flere referencemetyleringsniveauer bestemt fra de mindst to kohorter af andre individer.

**9.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, og som endvidere omfatter:

for hvert sted af sættet af steder:

bestemmelse af et tilsvarende antal af DNA-molekyler, der methyleres på stedet, hvorved mængderne af flerheden af cellefrie DNA-molekyler methyleret ved sættet af steder af det specifikke, virale genom bestemmes, og hvor fremgangsmåde endvidere omfatter:

udførelse af metyleringsbevidst sekvensering af flerheden af cellefrie DNA-molekyler for at opnå sekvenslæsninger; og

alignment af sekvenslæsningerne med det specifikke, virale genom for at bestemme det tilsvarende antal af DNA-molekyler, der er methyleret ved hvert sted af sættet af steder.

**10.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor en gruppe af flerheden af cellefrie DNA-molekyler analyseres kollektivt for at bestemme mængderne af flerheden af cellefrie DNA-molekyler methyleret ved sættet af steder af det specifikke, virale genom.

**11.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, hvor det specifikke, virale genom svarer til Epstein-Barr-virus, human papillomavirus eller hepatitis B-virus.

**12.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, og som endvidere omfatter:

for hvert af et sæt af cellefrie DNA-molekyler i en prøve:

måling af en størrelse på det cellefrie DNA-molekyle og

identificering af en placering af det cellefrie DNA-molekyle i det specifikke, virale genom, hvor størrelserne på sættet af cellefrie DNA-molekyler danner en størrelsesfordeling, hvilken prøve er den biologiske prøve eller en forskellig prøve indbefattende en blanding af cellefrie DNA-molekyler fra individets genom og fra det ene eller flere andre genomer;

bestemmelse af en statistisk værdi af størrelsesfordelingen;

sammenligning af den statistiske værdi med en referencestørrelsesværdi bestemt fra de mindst to kohorter af andre individer;

bestemmelse af en anden klassifikation af, hvorvidt individet har den første tilstand baseret på sammenligningen af den statistiske værdi med referencestørrelsesværdien; og

bestemmelse af en endelig klassifikation ved hjælp af den første klassifikation og den anden klassifikation.

**13.** Fremgangsmåde ifølge et hvilket som helst af de foregående krav, og som endvidere omfatter:

bestemmelse af en mængde cellefrie DNA-molekyler afledt af det specifikke, virale genom i en prøve, hvilken prøve er den biologiske prøve eller en forskellig prøve indbefattende en blanding af cellefrie DNA-molekyler fra individets genom og fra det ene eller flere andre genomer;

sammenligning af mængden med en referenceværdi bestemt fra de mindst to kohorter af andre individer;

bestemmelse af en anden klassifikation af, hvorvidt individet har den første tilstand baseret på sammenligningen af mængden med referenceværdien; og

bestemmelse af en endelig klassifikation ved hjælp af den første klassifikation og den anden klassifikation.

**14.** Computerprogram omfattende en flerhed af instruktioner, der kan udføres af et computersystem, der, når det således udføres, styrer computersystemet til at udføre de computerimplementerede trin fra fremgangsmåden ifølge et hvilket som helst af de foregående krav.

## DRAWINGS

101	102	103	104
	Chromosomes	Sizes of capturing regions (bp)	Probe tiling fold
Autosomes	chr1	2018178	5x tiling capturing probes
	chr2	959395	
	chr3	1143882	
	chr4	1035300	
	chr5	464688	
	chr6	693162	
	chr7	696688	
	chr8	889727	
	chr9	1257194	
	chr10	383650	
	chr11	1410412	
	chr12	1463254	
	chr13	570007	
	chr14	213784	
	chr15	468290	
	chr16	1115989	
	chr17	843909	
	chr18	971357	
	chr19	1157954	
	chr20	1028902	
	chr21	806977	
	Viral targets	chr22	
EBV		171326	
HBV		2741	
HPV16		7902	
HPV18		7847	
HPV31		7902	
HPV33		7899	
HPV35		7837	
HPV39		7823	
HPV45		7841	
HPV51		7809	
HPV52		7905	
HPV56		7817	
HPV58		7819	
HPV66		7815	
HPV68	7836		
HPV70	7895		

FIG. 1

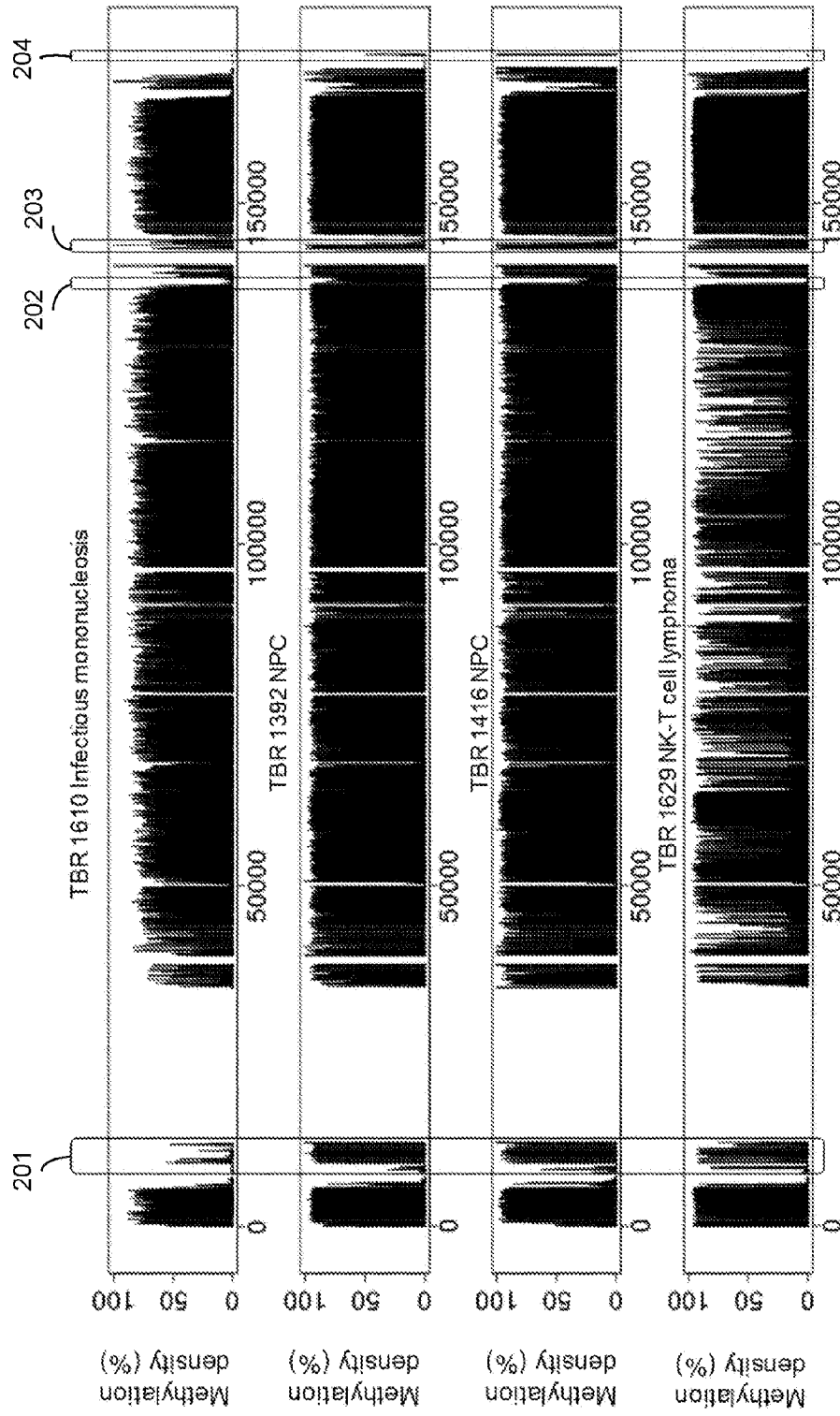


FIG. 2

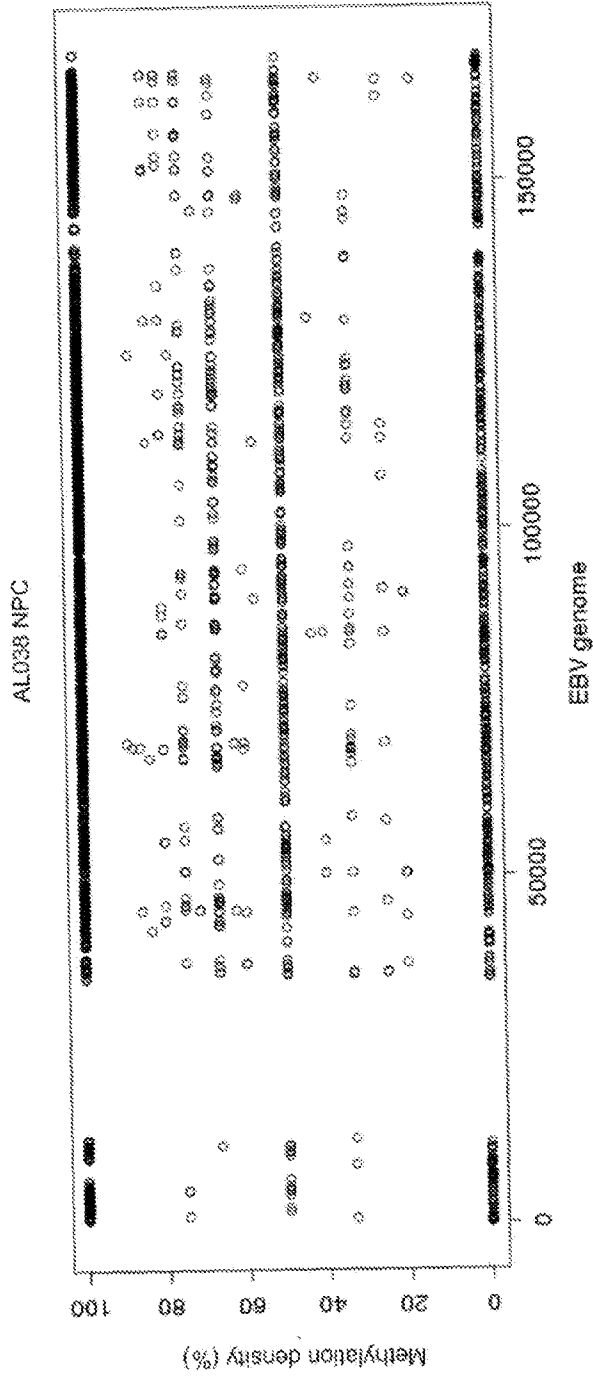


FIG. 3

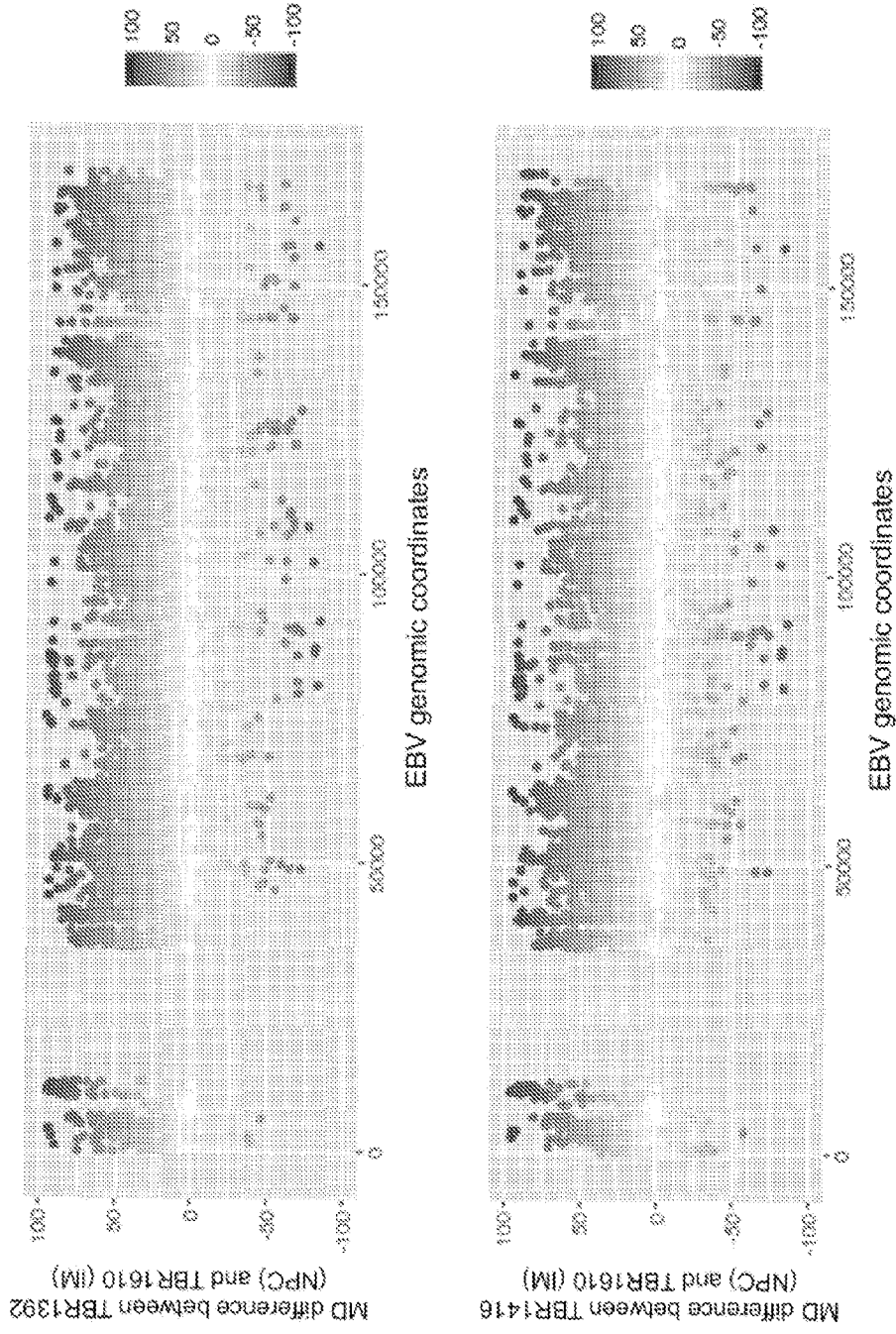


FIG. 4

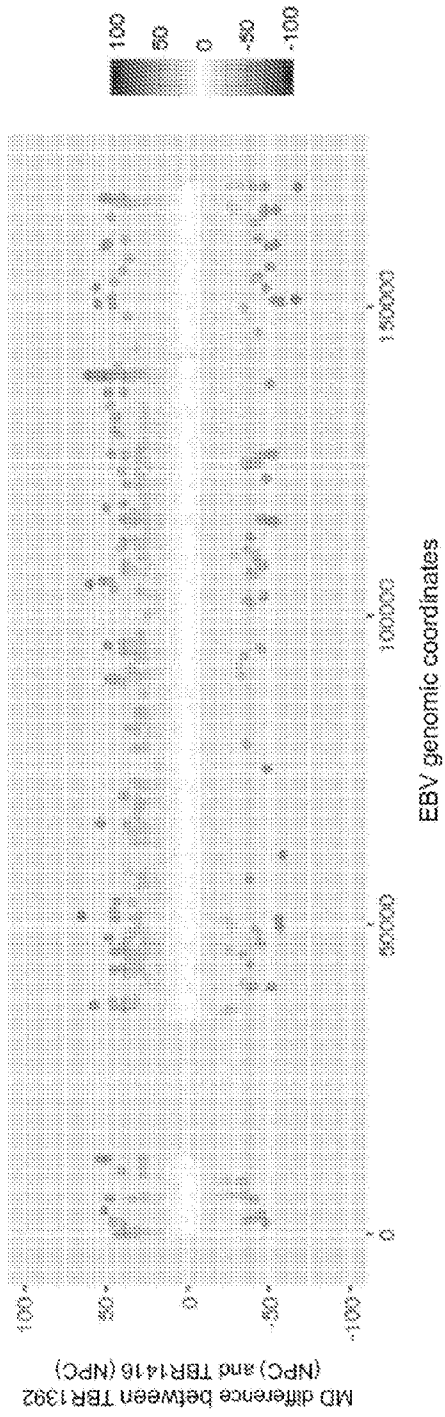


FIG. 5

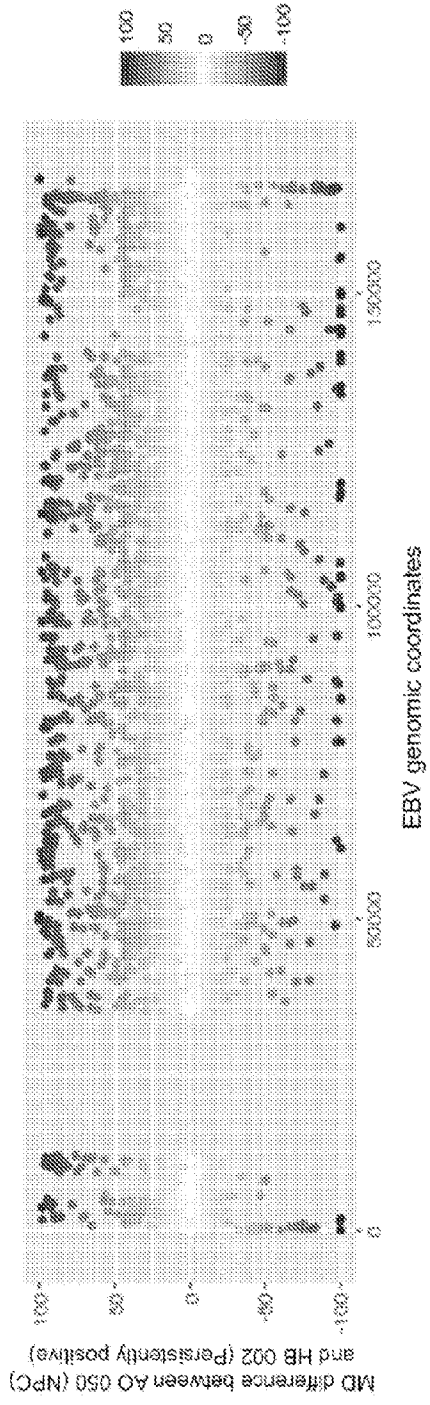


FIG. 6

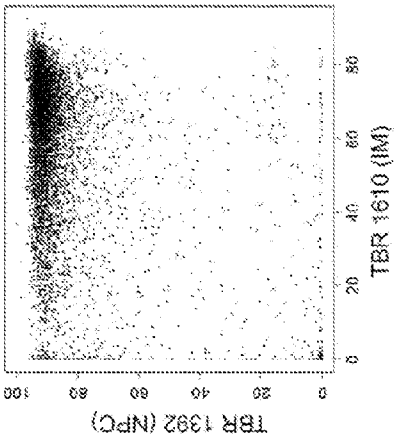


FIG. 7A

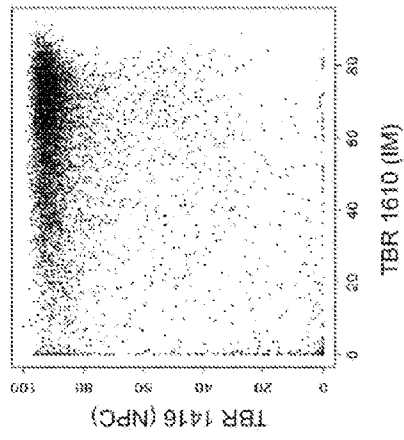


FIG. 7B

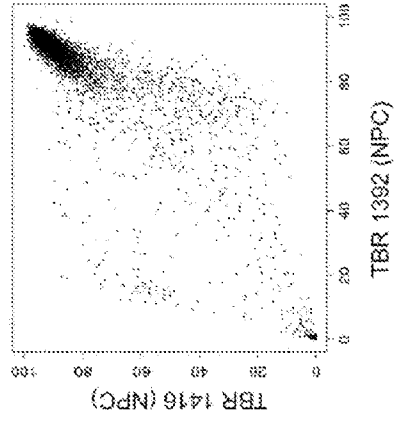
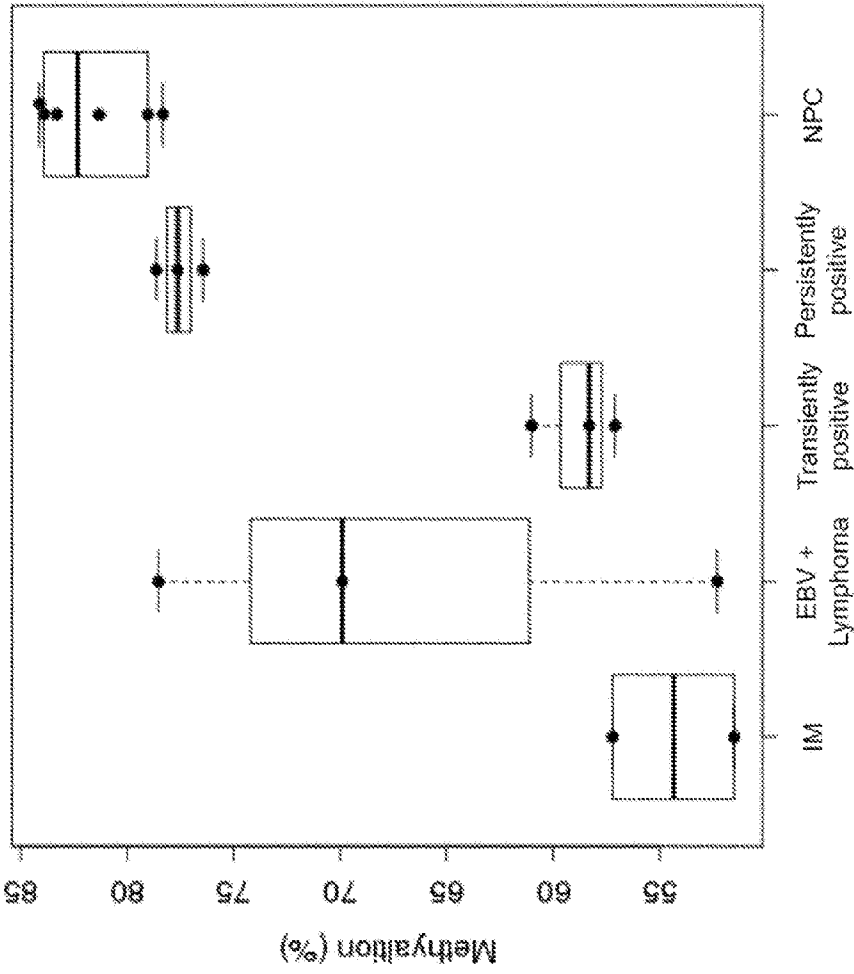


FIG. 7C



All CpG sites  
P-value: 8.52e-05

FIG. 8

Infectious mononucleosis (IM) TBR1610 vs. NPC TBR1392

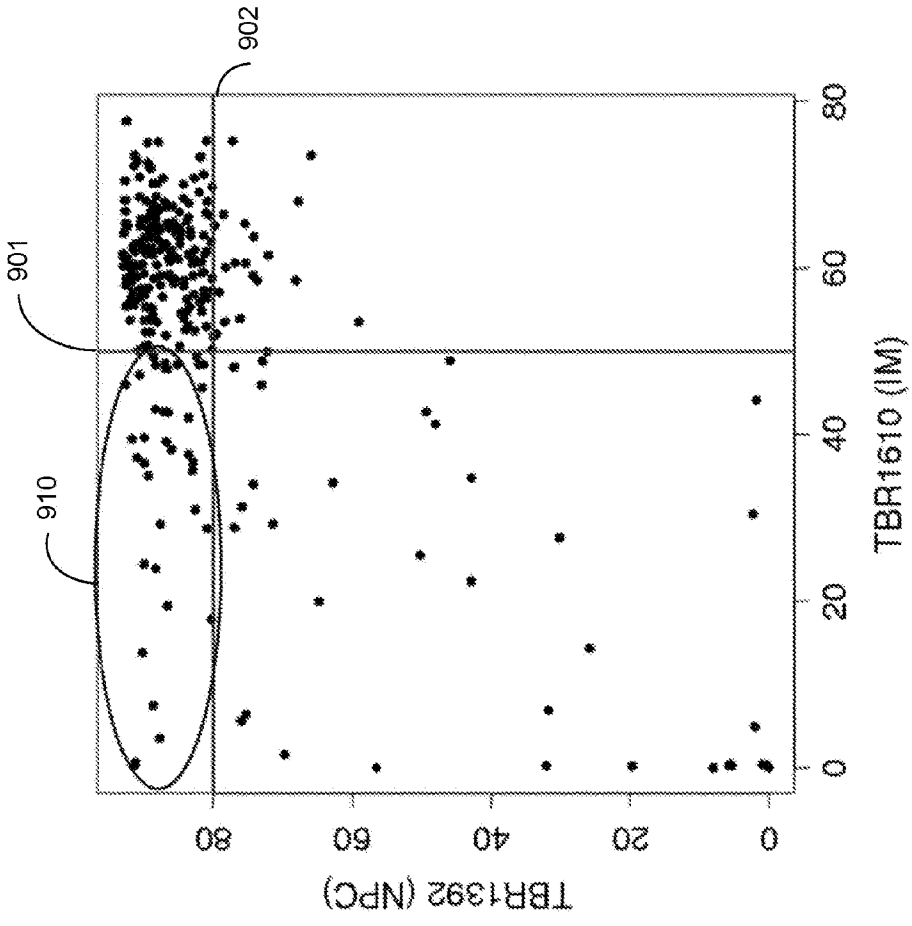


FIG. 9

1001 Virus genome	1002 start	1003 end	Methylation density (%) — 1004	
			Infectious mononucleosis (TBR1610)	NPC (TBR1392)
EBV	10000	10500	7.5	88.7
EBV	10500	11000	0.6	91.3
EBV	11000	11500	3.5	87.7
EBV	114500	115000	42.7	87.1
EBV	11500	12000	0.3	91.3
EBV	115000	115500	31.0	82.6
EBV	12000	12500	19.5	86.6
EBV	137000	137500	42.0	83.5
EBV	137500	138000	39.4	91.7
EBV	139000	139500	29.3	87.6
EBV	139500	140000	46.0	92.6
EBV	140000	140500	24.4	90.0
EBV	140500	141000	47.2	90.6
EBV	143000	143500	37.2	91.0
EBV	143500	144000	13.8	90.2
EBV	165000	165500	35.7	83.0
EBV	168000	168500	42.7	86.5
EBV	36500	37000	39.6	90.0
EBV	37000	37500	36.7	82.9
EBV	37500	38000	39.1	86.8
EBV	38000	38500	36.6	89.9
EBV	39500	40000	17.8	80.2
EBV	40000	40500	28.7	80.9
EBV	41000	41500	37.6	83.5
EBV	41500	42000	35.1	89.4
EBV	42500	43000	45.6	81.6
EBV	43000	43500	48.0	86.9
EBV	45000	45500	48.5	81.4
EBV	51000	51500	38.2	86.0
EBV	51500	52000	50.0	89.0
EBV	58000	58500	48.4	88.3
EBV	59500	60000	49.4	88.6
EBV	61000	61500	43.0	88.3
EBV	63500	64000	48.0	86.6
EBV	73500	74000	48.6	87.0
EBV	79500	80000	48.4	82.1
EBV	82000	82500	48.4	85.2
EBV	84500	85000	49.5	82.4
EBV	9500	10000	23.9	88.3

FIG. 10

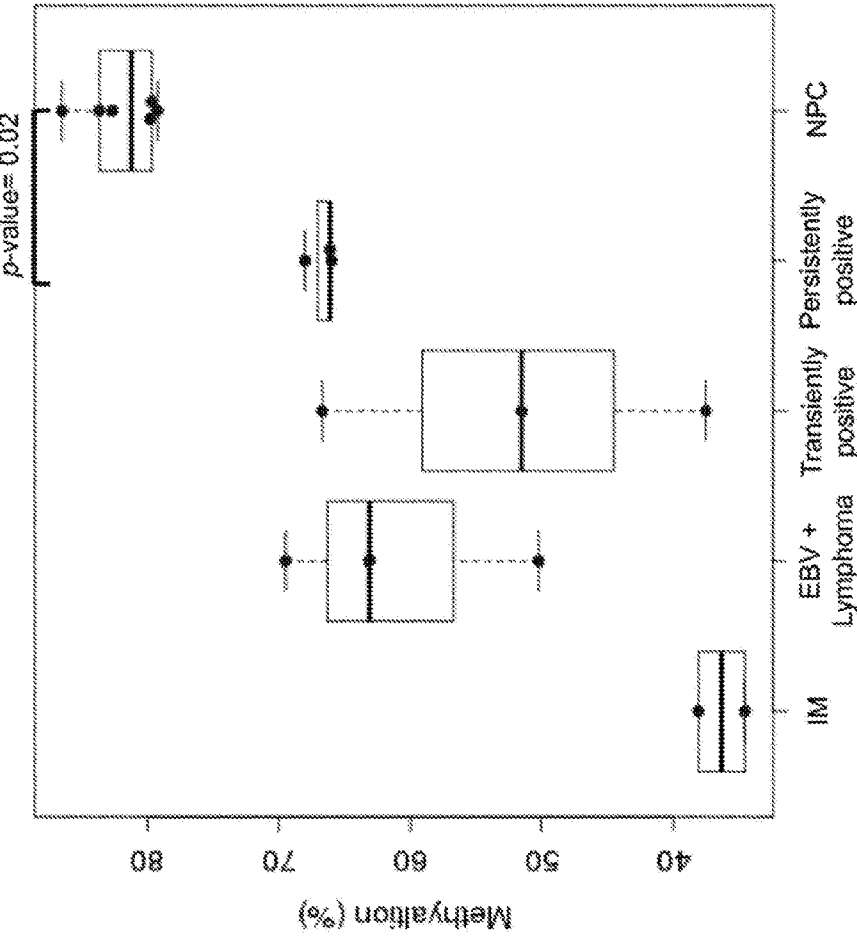


FIG. 11

DMRs  
P-value: 1.83e-05  
(one-way ANOVA test)

NPC vs. Infectious mononucleosis (IM)

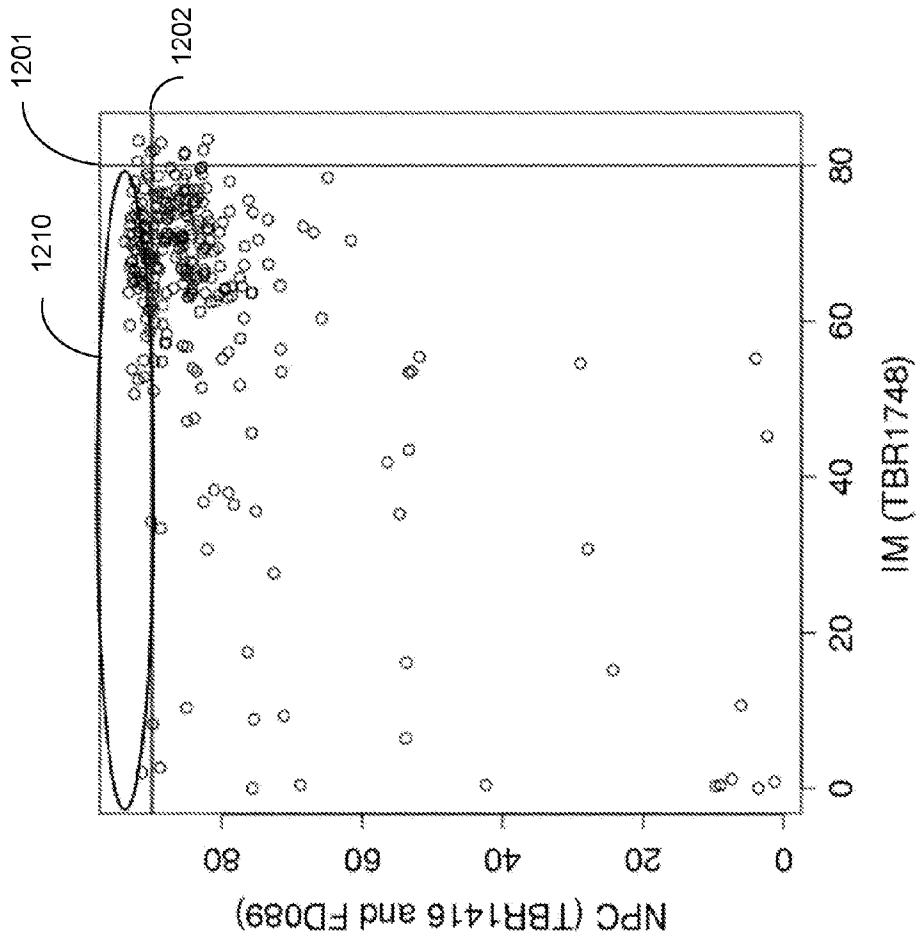


FIG. 12

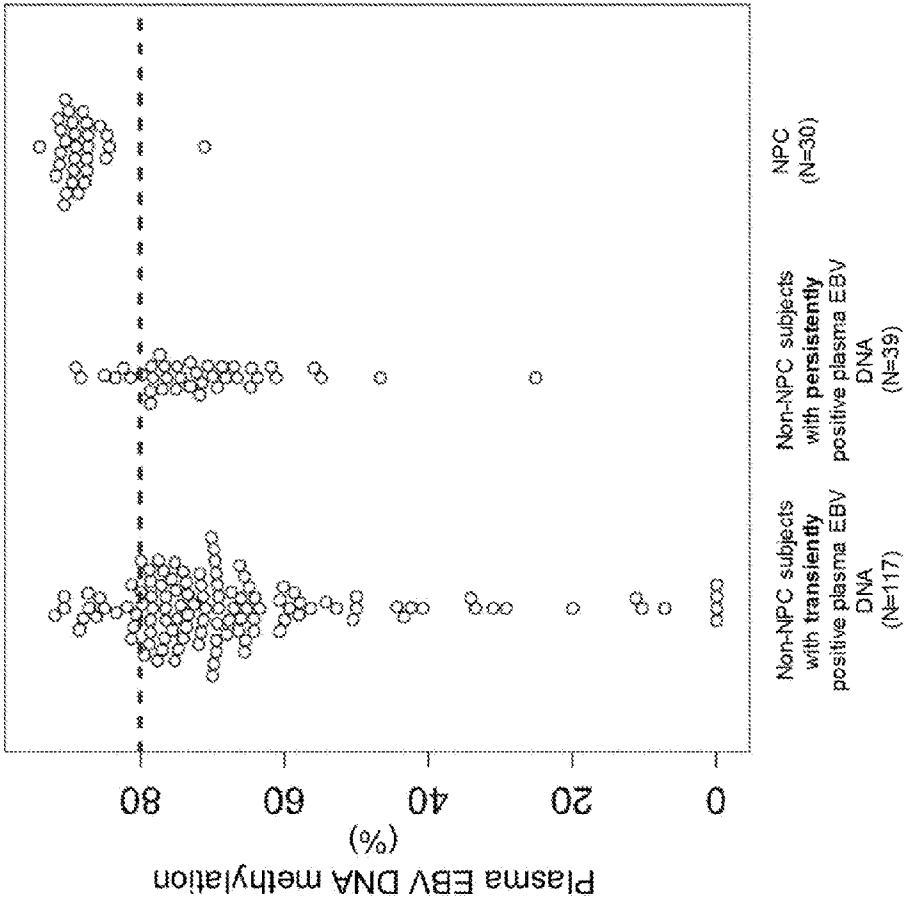


FIG. 13

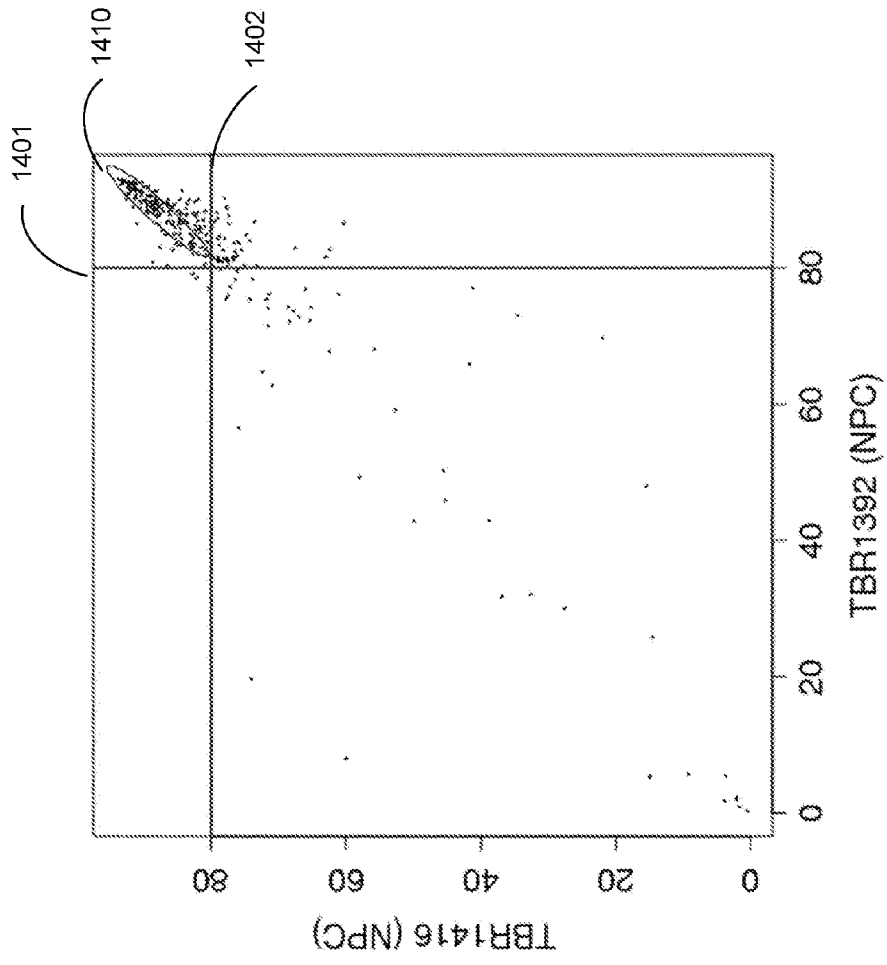
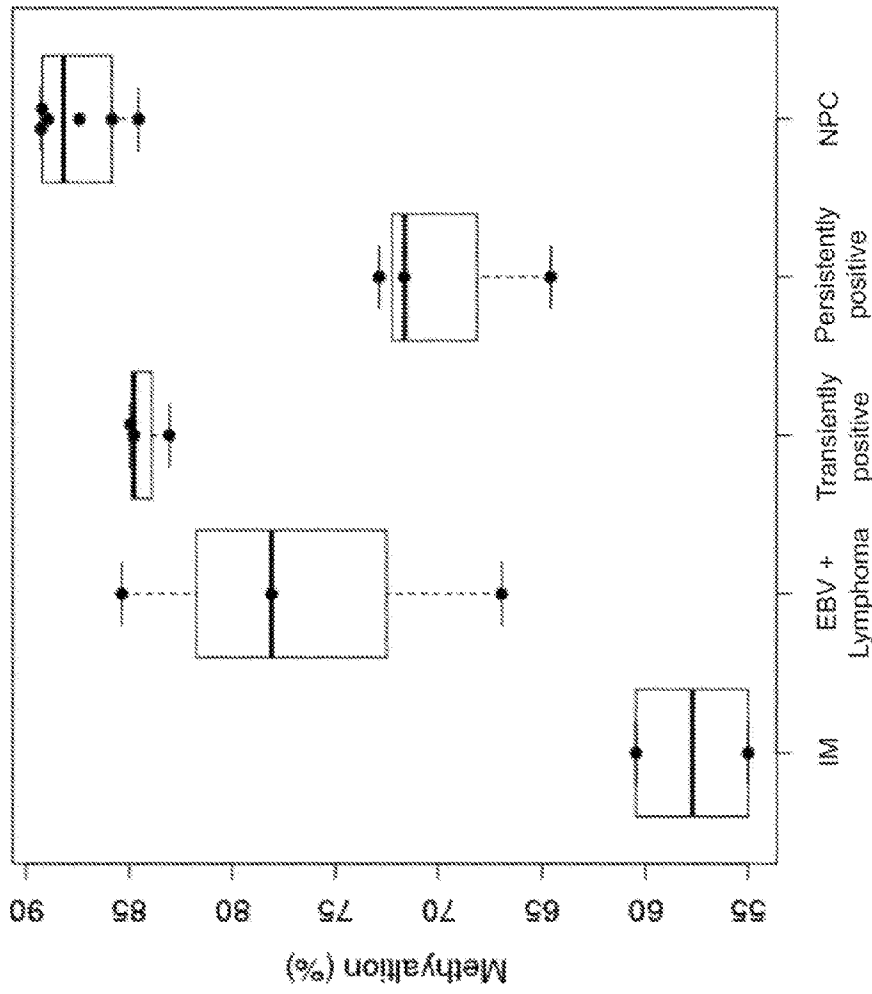


FIG. 14



Representative CpG sites:  
P-value: 0.00371

FIG. 15

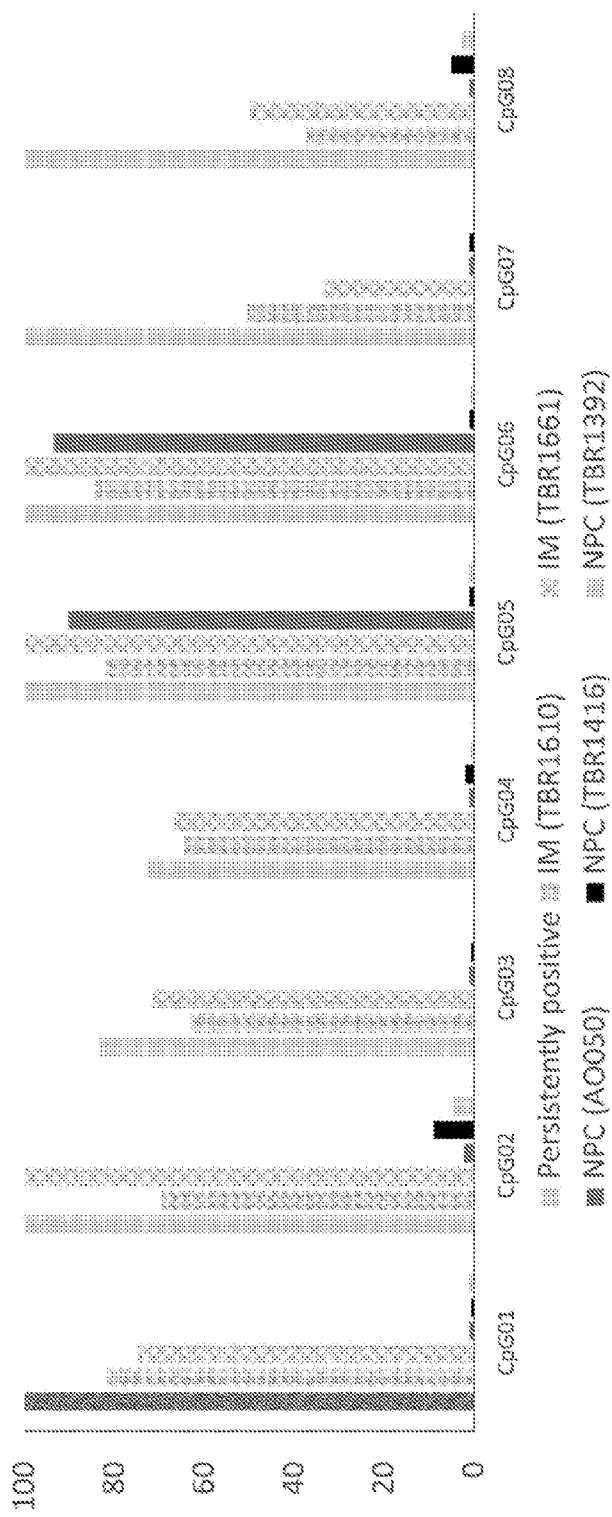


FIG. 16

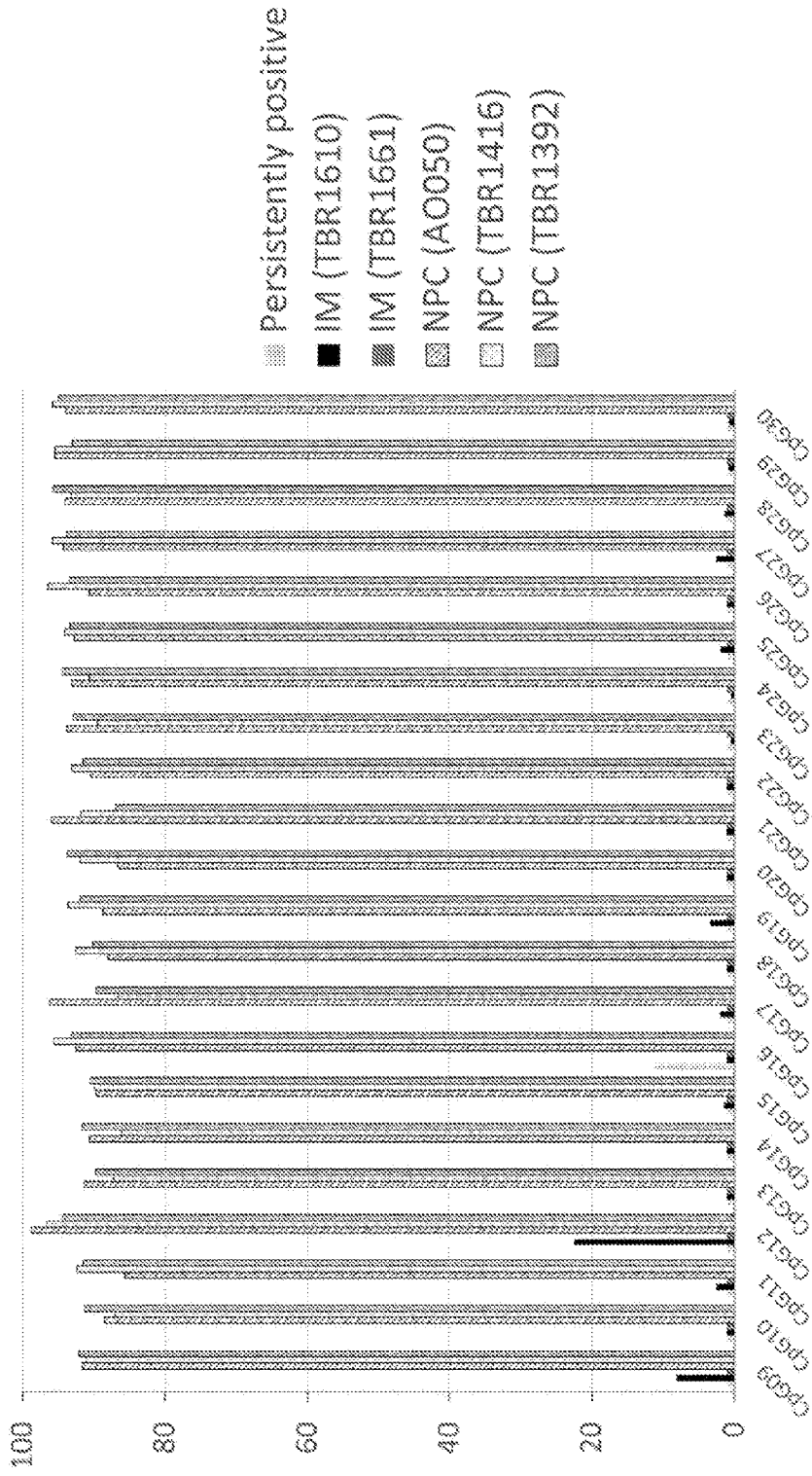


FIG. 17

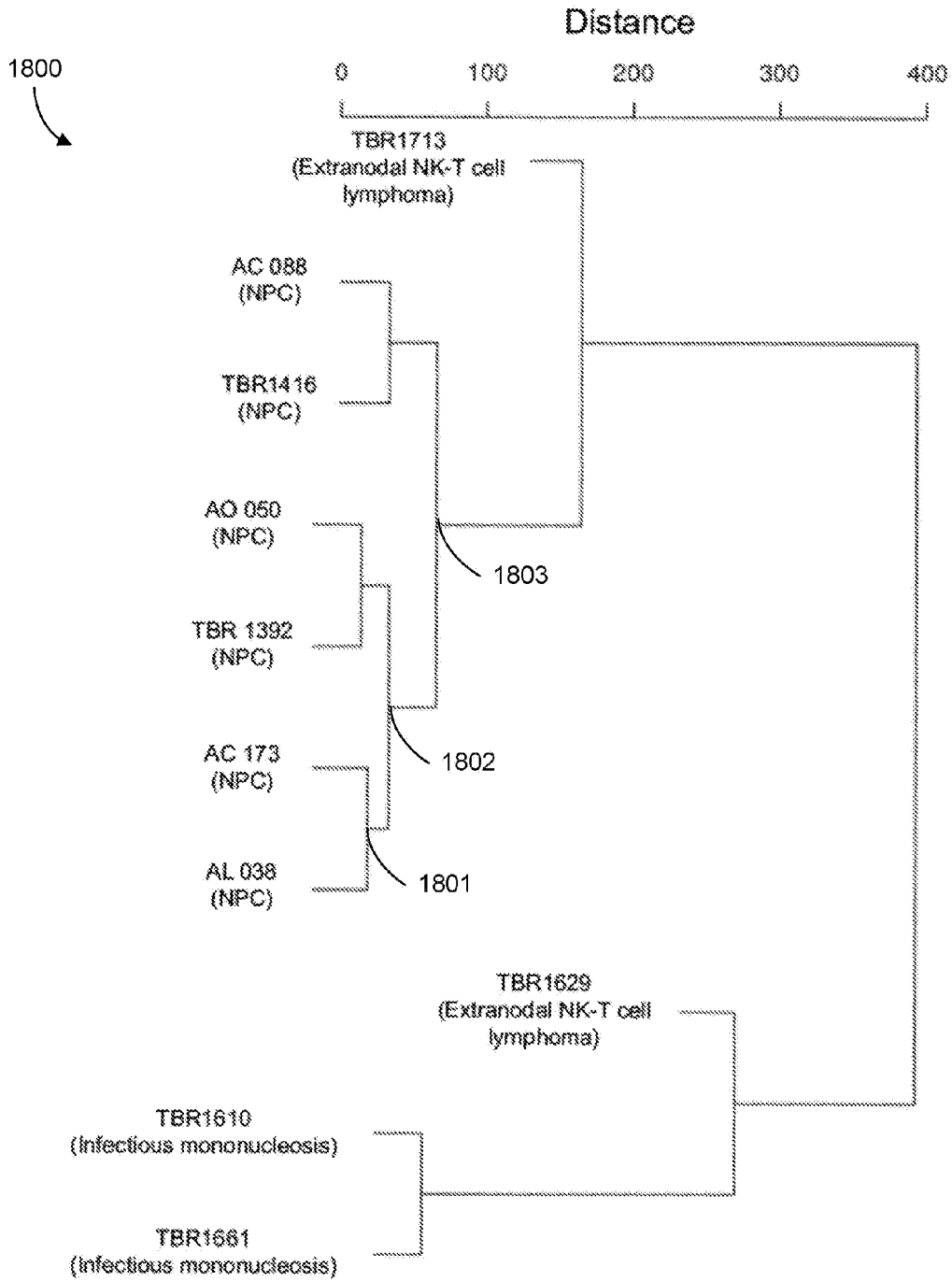


FIG. 18



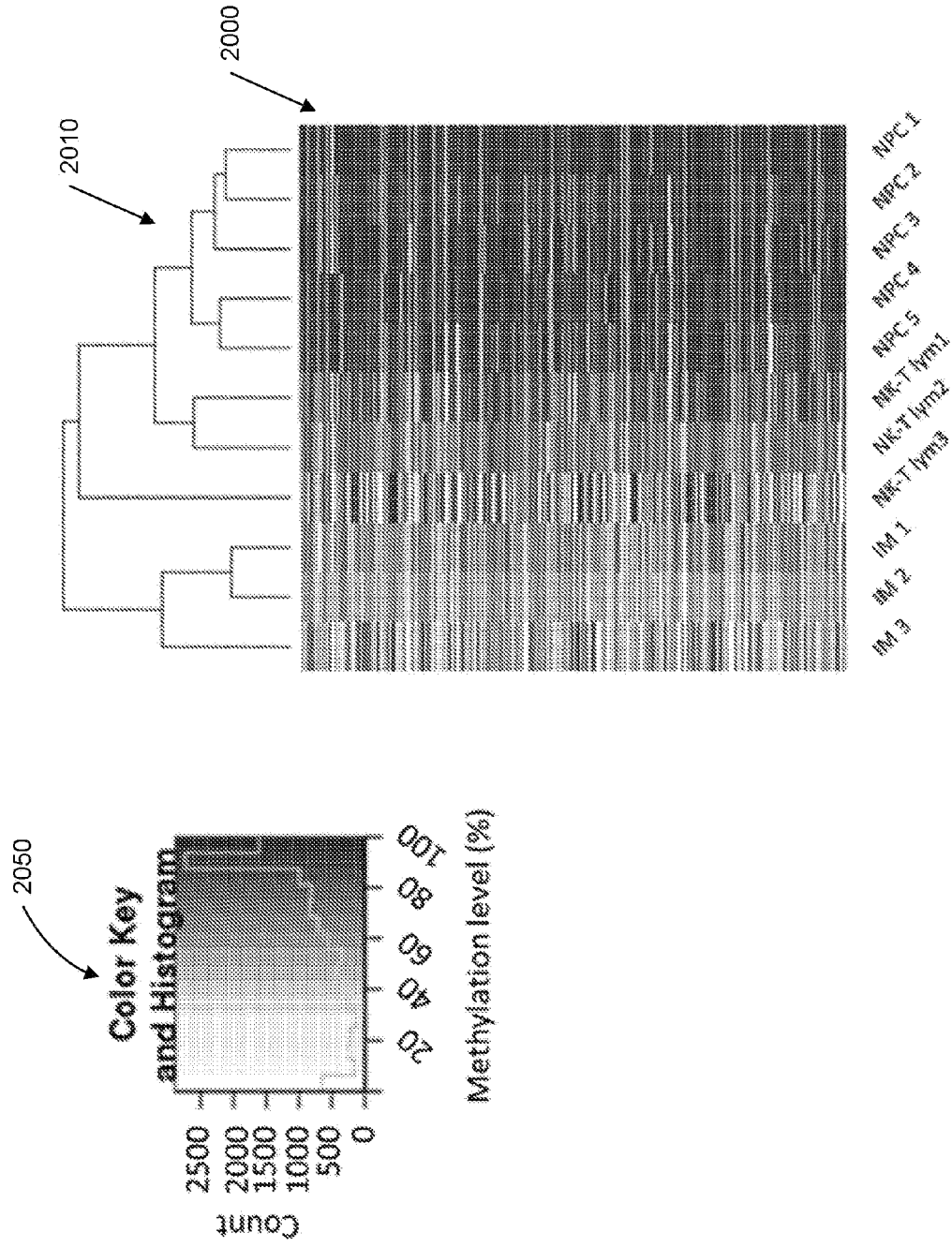


FIG. 20

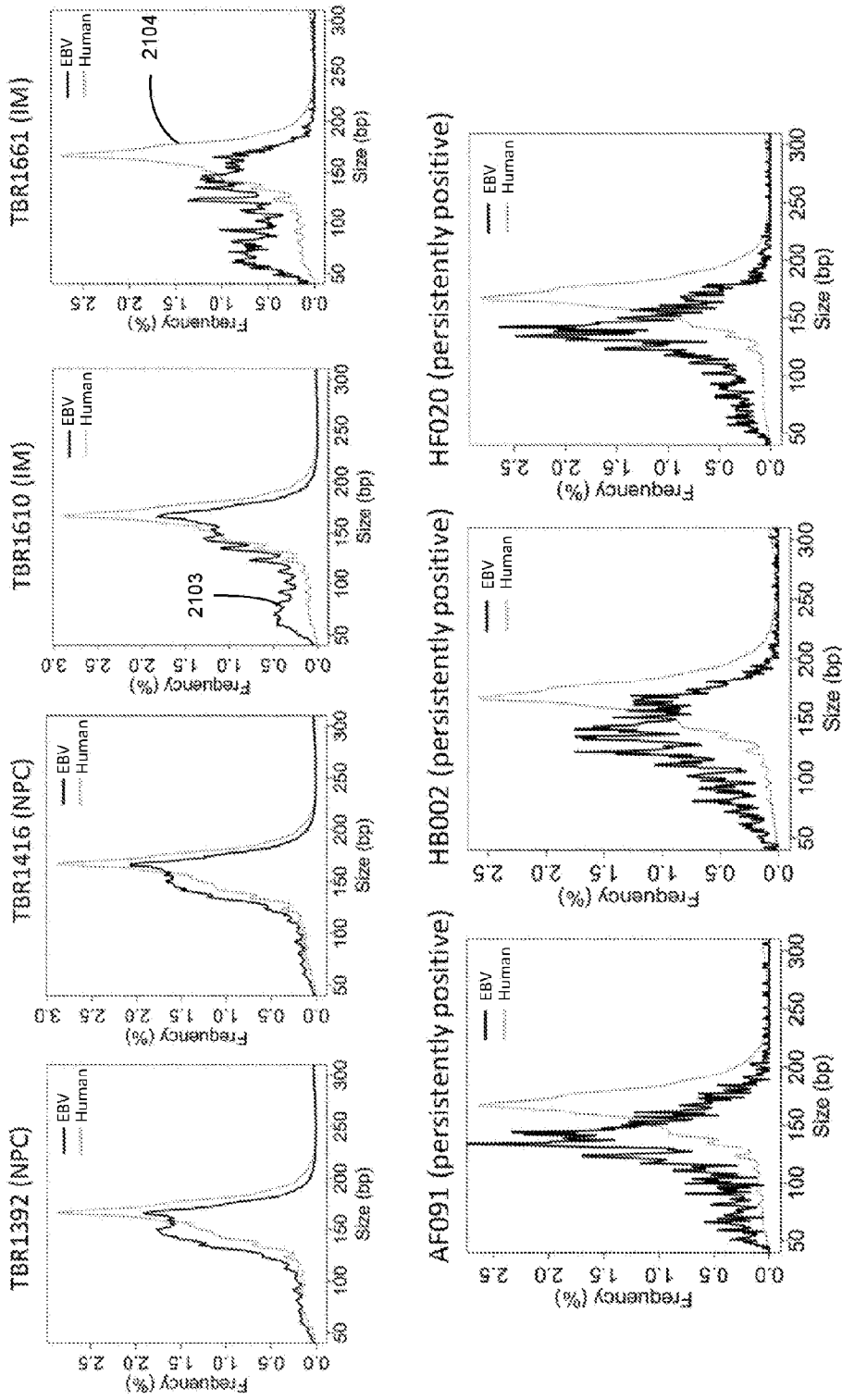


FIG. 21

$p\text{-value} = 0.02$

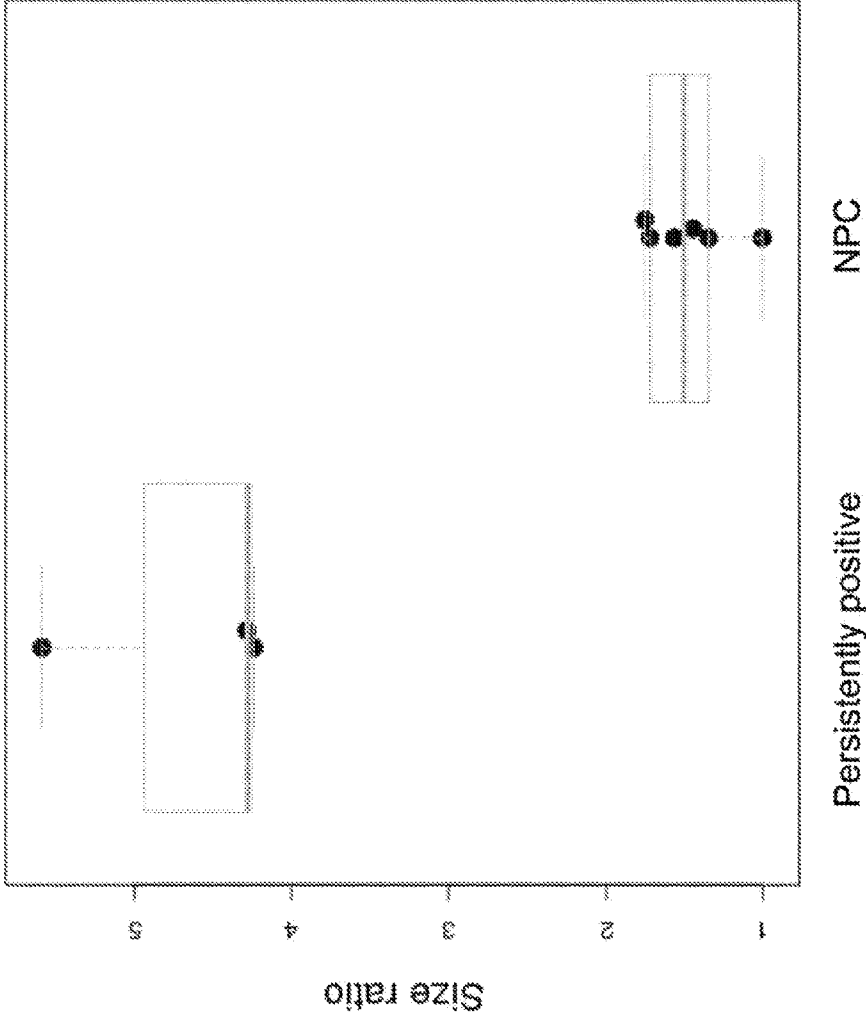


FIG. 22

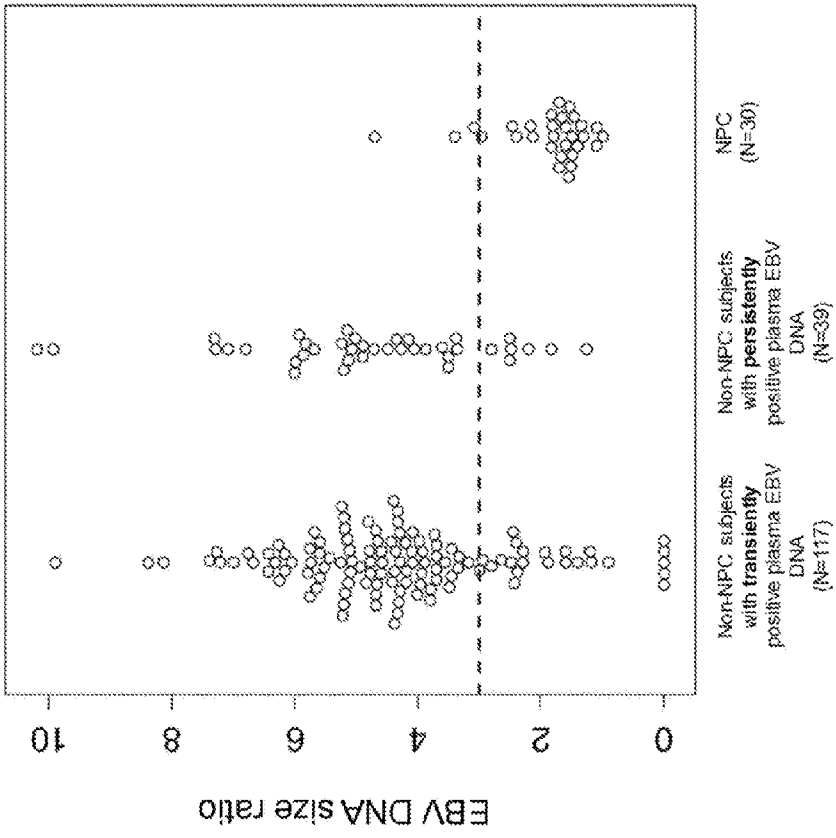


FIG. 23

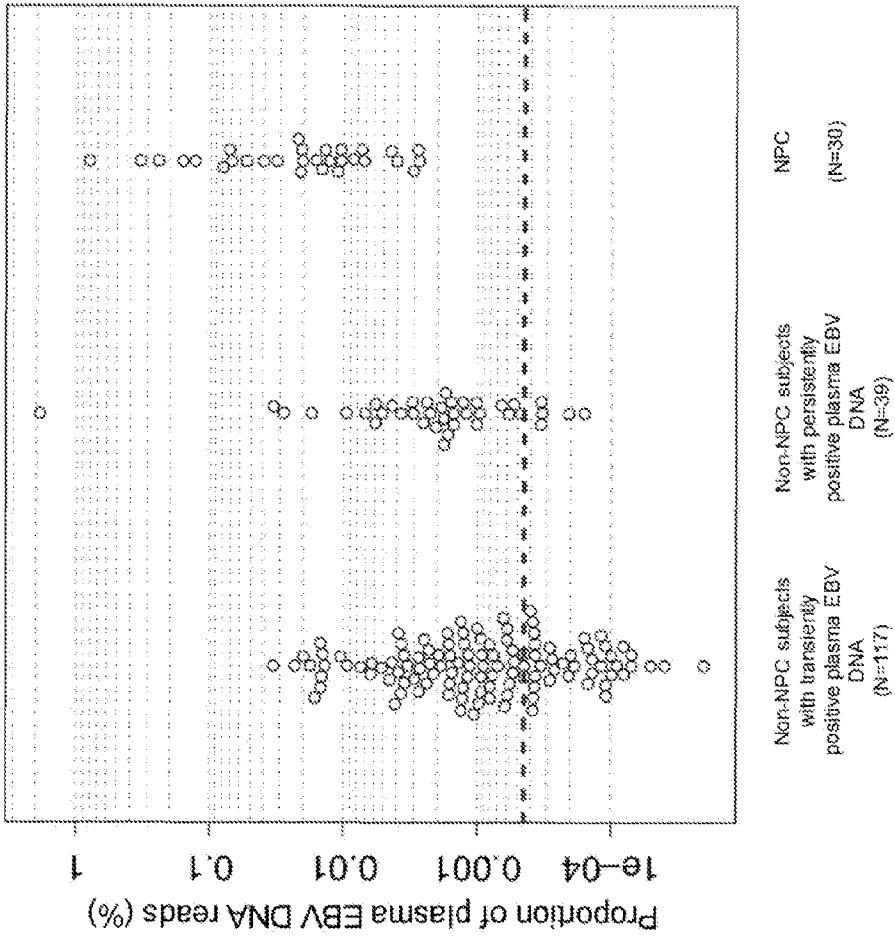


FIG. 24

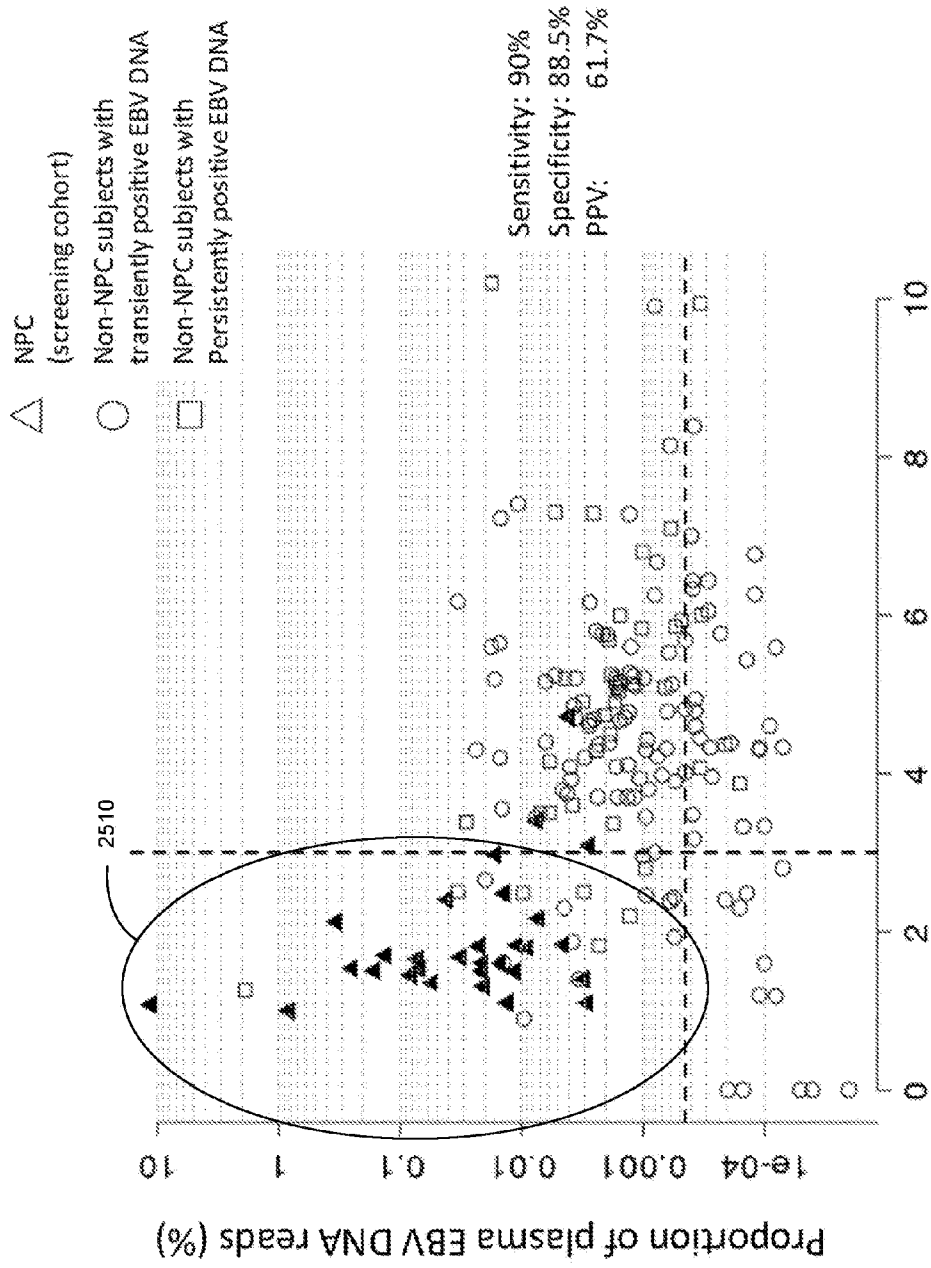


FIG. 25

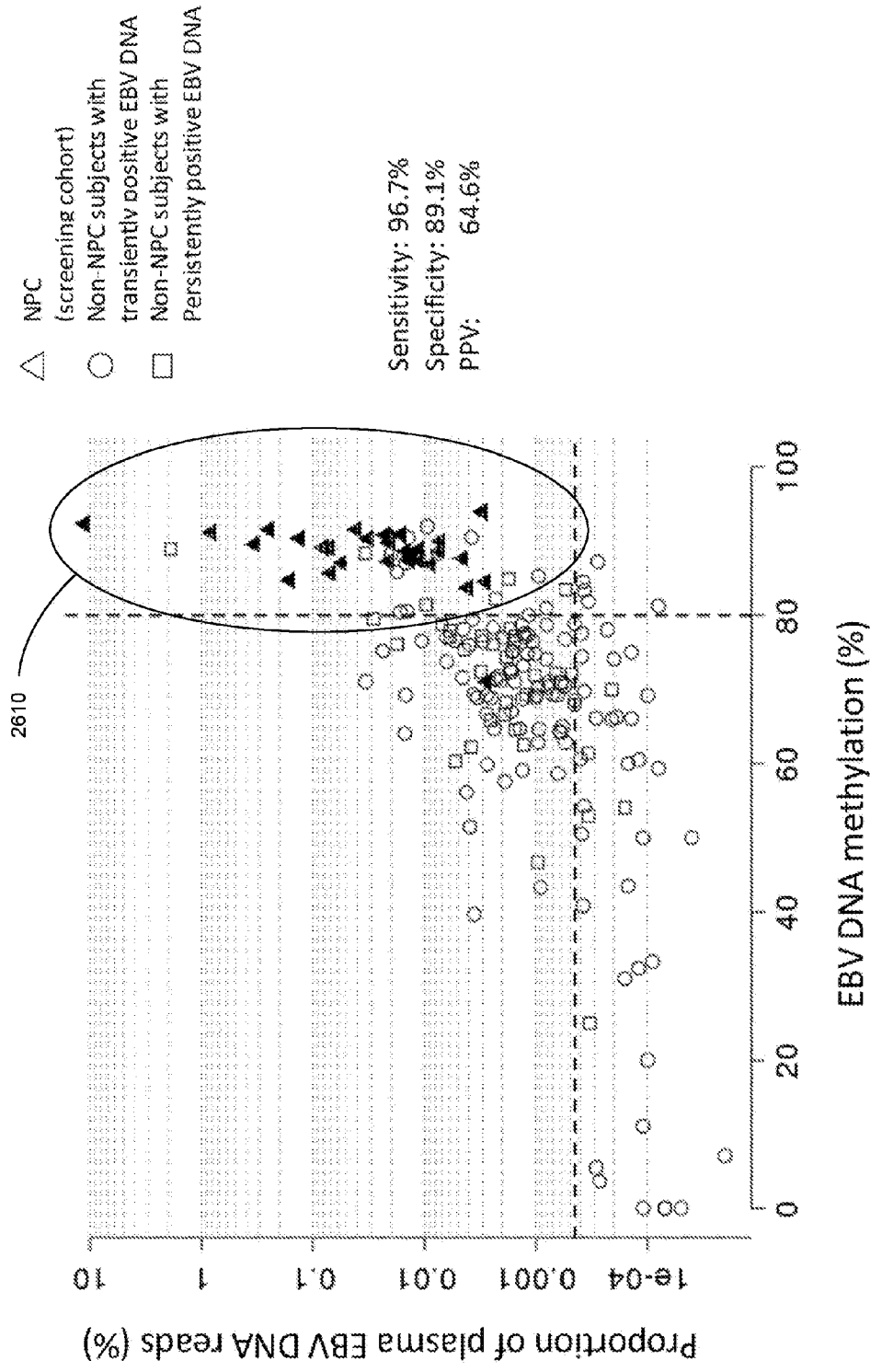


FIG. 26

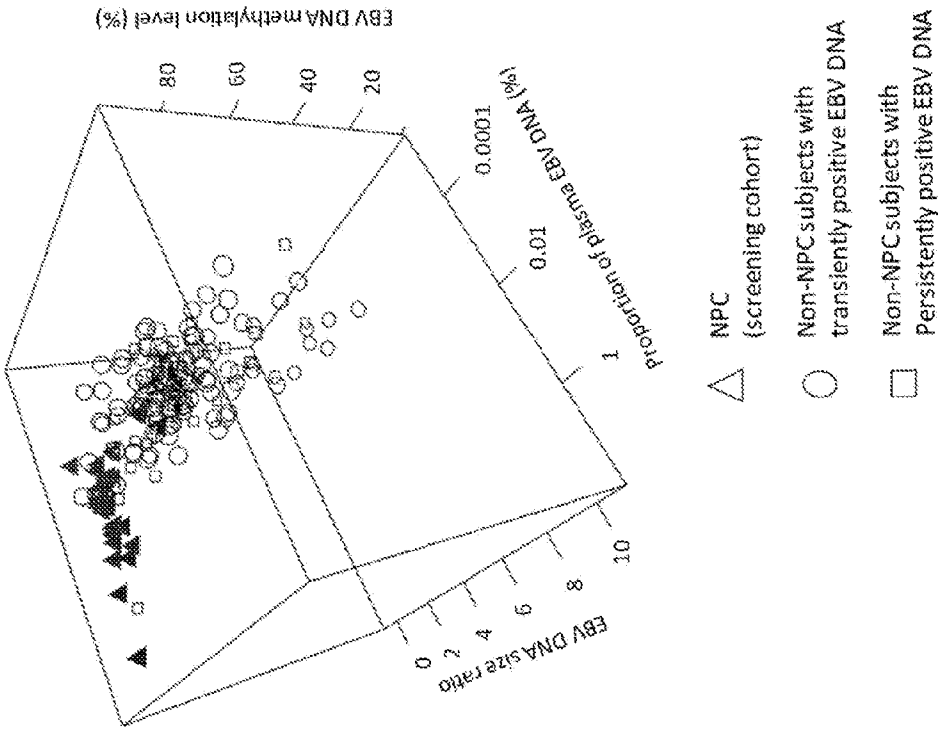


FIG. 27B

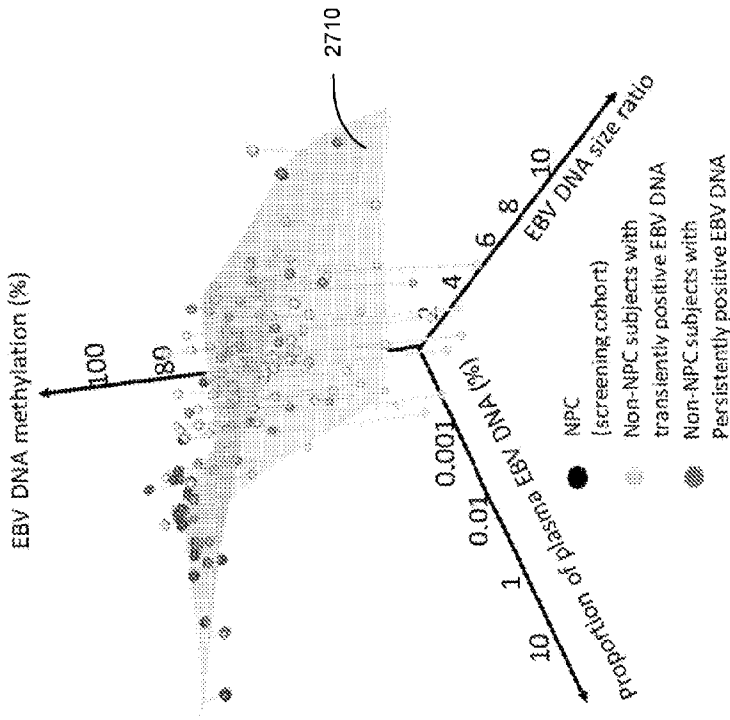


FIG. 27A

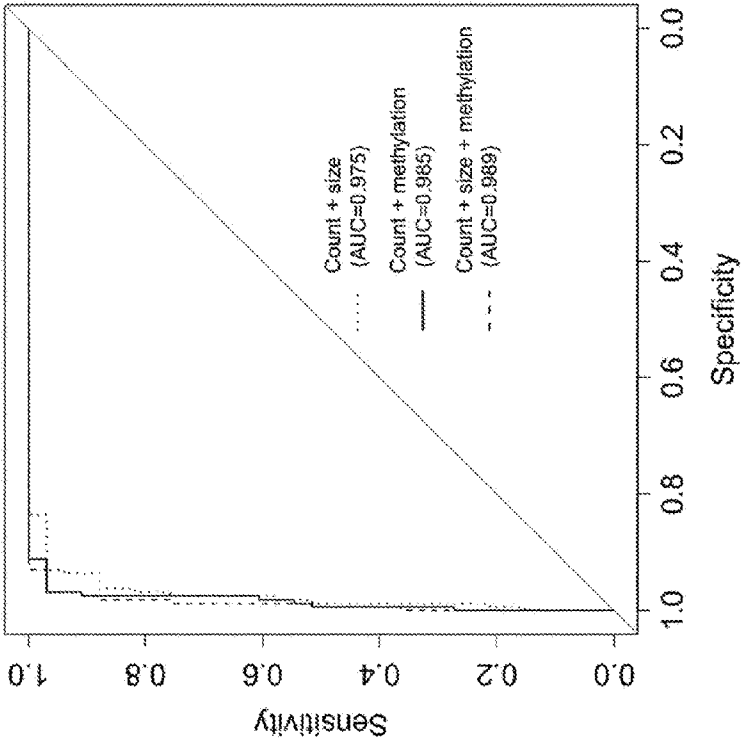


FIG. 28B

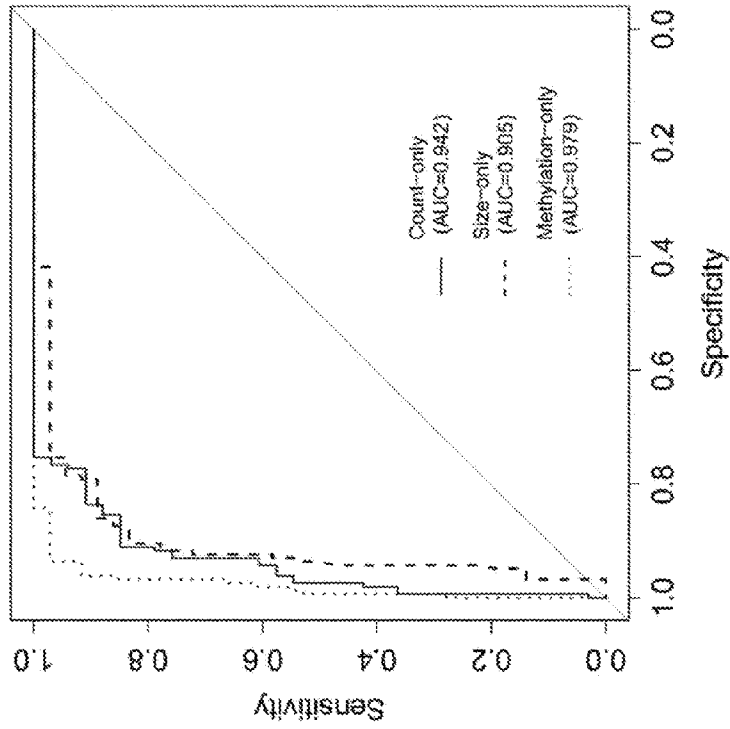
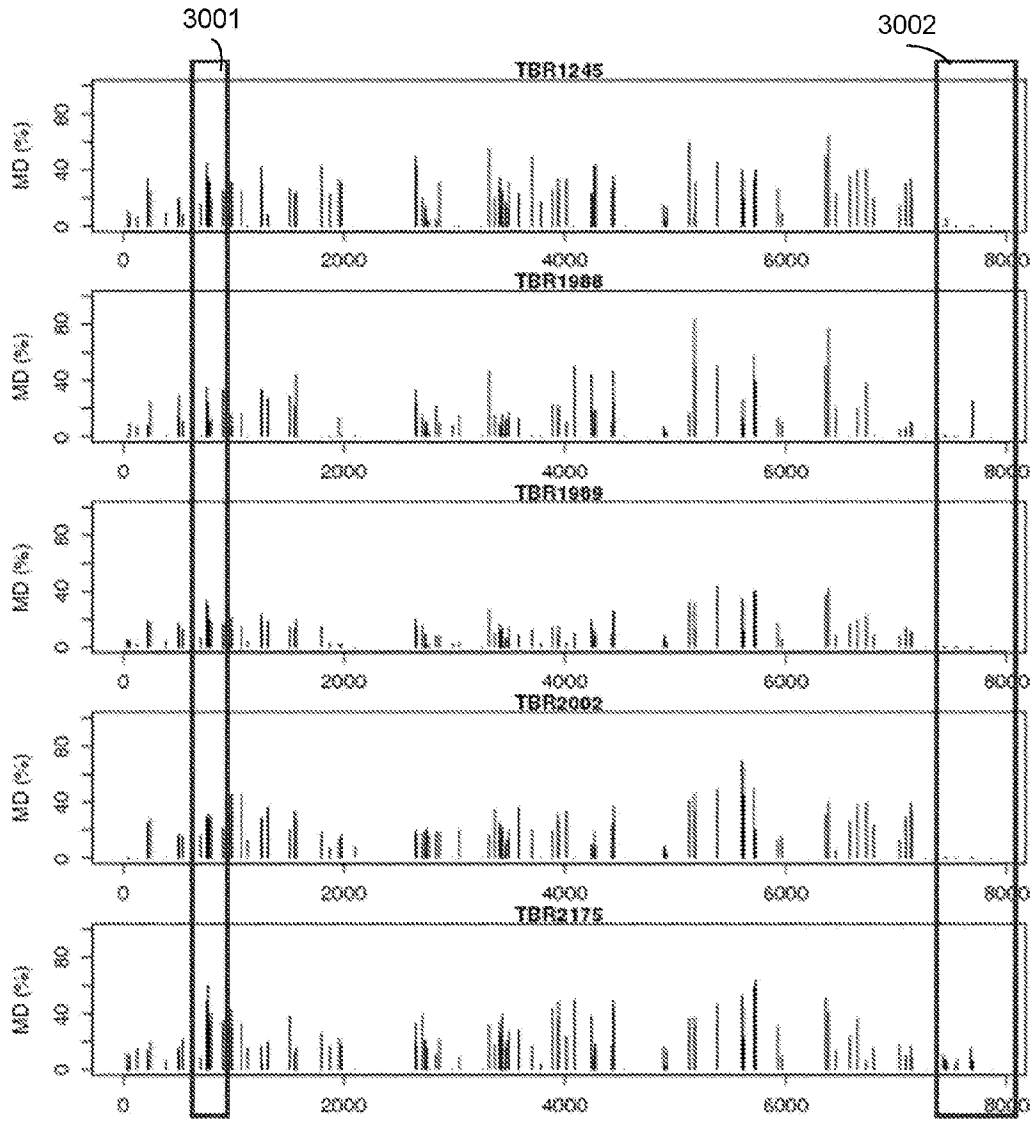


FIG. 28A

Type	Sample	Stage
HNSCC	TBR1245	I
HNSCC	TBR1988	I
HNSCC	TBR1989	II
HNSCC	TBR2002	I
HNSCC	TBR2175	II

FIG. 29



HPV16

FIG. 30

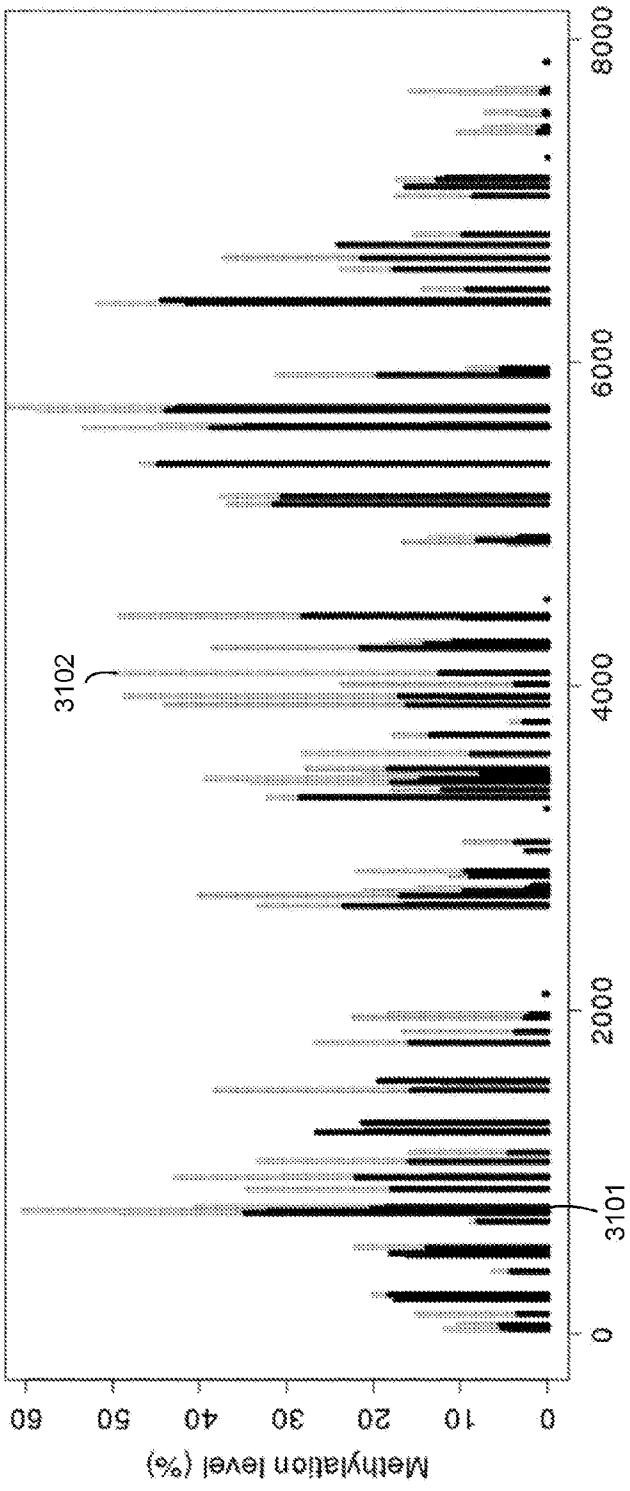


FIG. 31

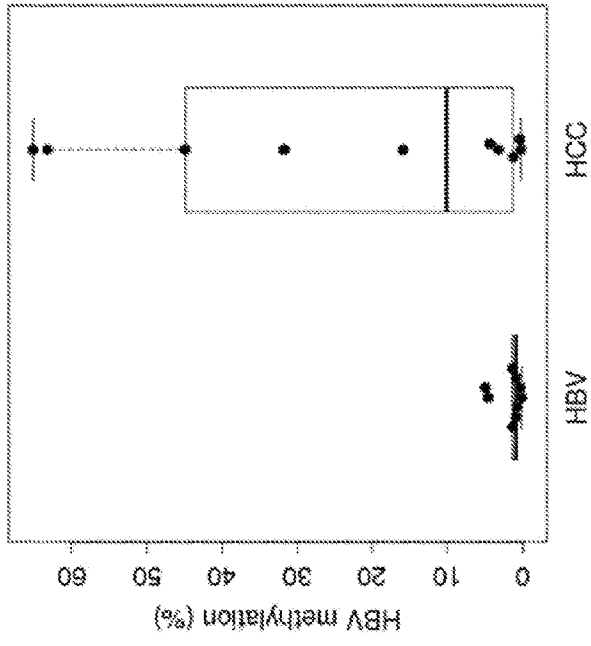


FIG. 32B

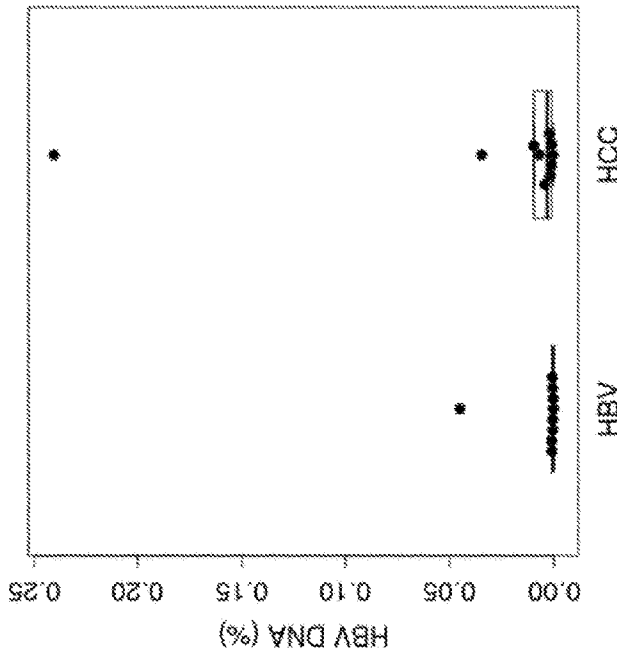


FIG. 32A

3300

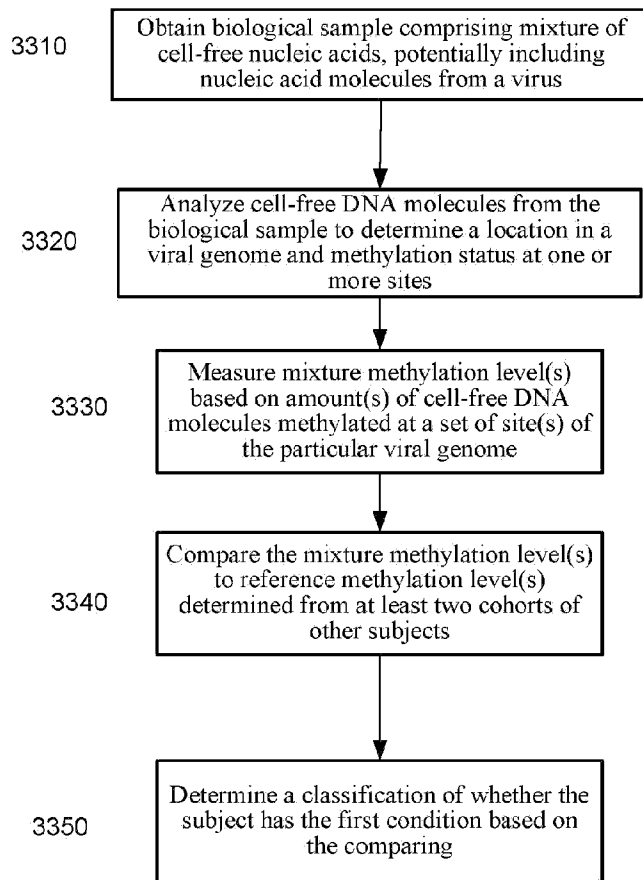


FIG. 33

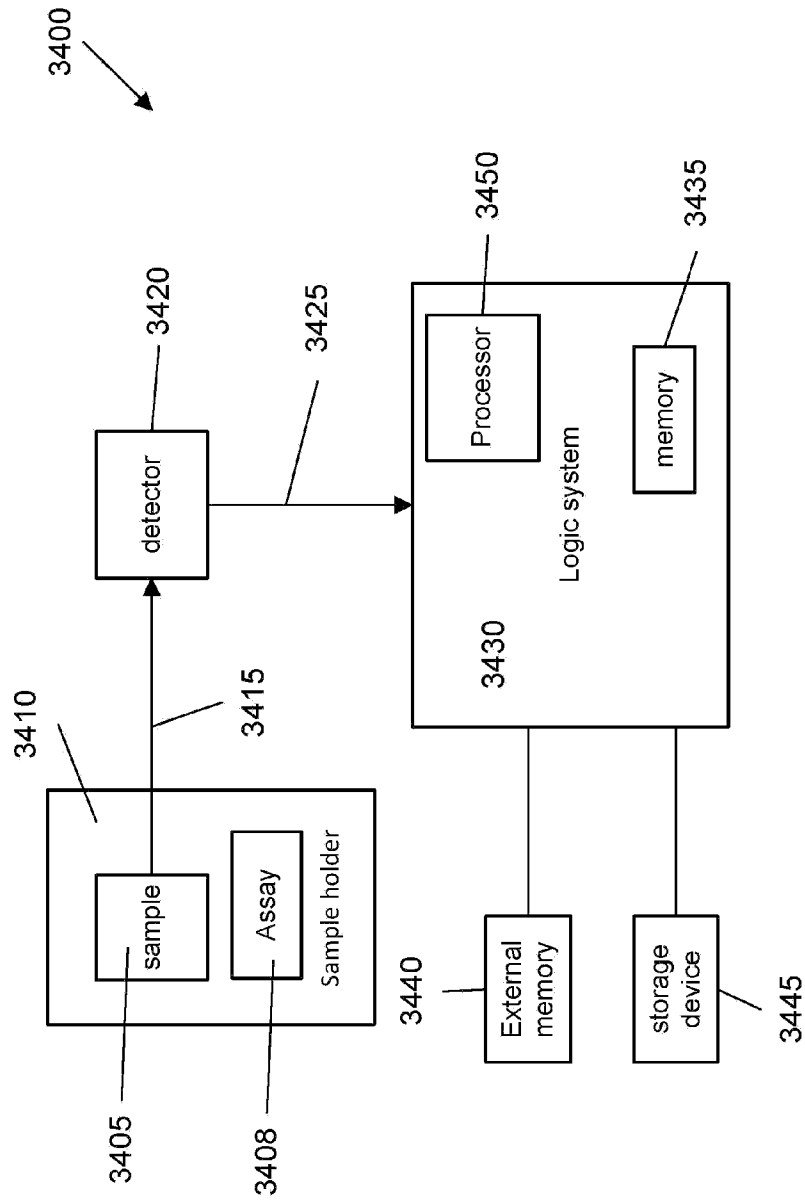


FIG. 34

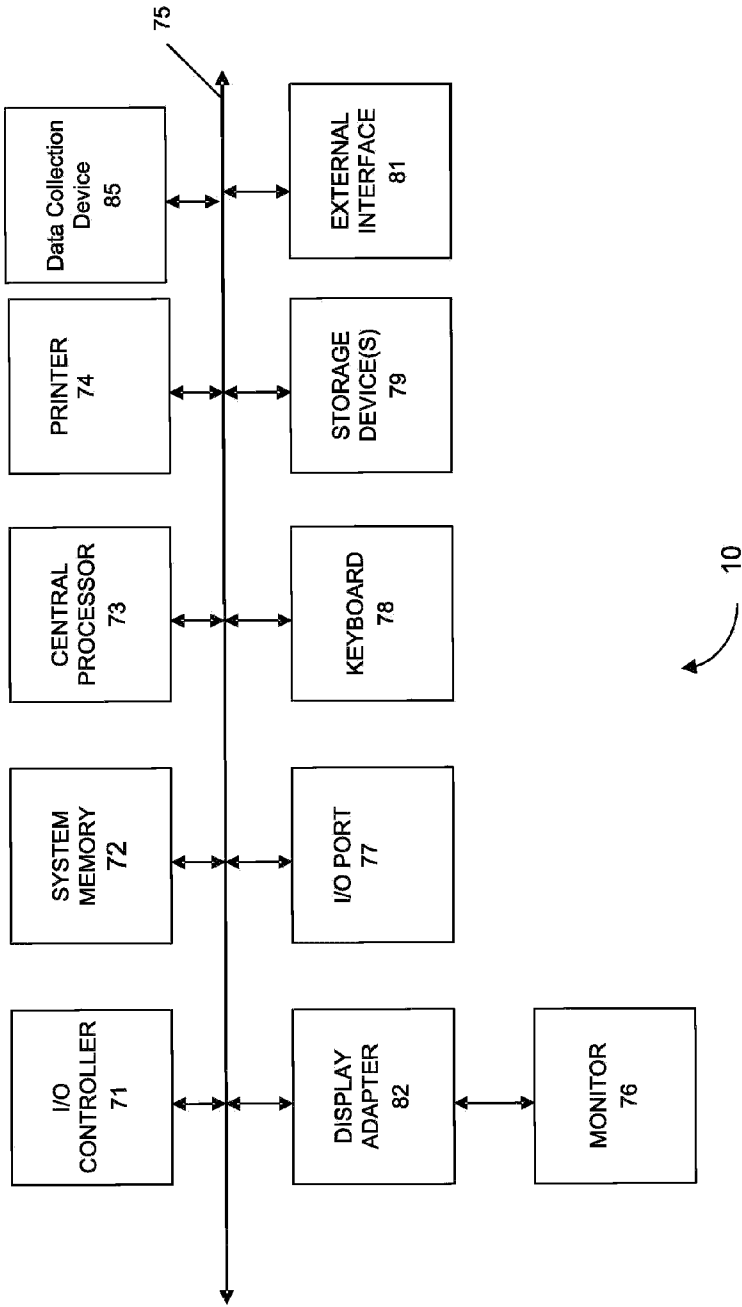


FIG. 35

## Appendix A

EBV	start	end	Remarks
EBV	89	90	
EBV	125	126	
EBV	134	135	
EBV	165	166	
EBV	216	217	
EBV	260	261	
EBV	429	430	
EBV	438	439	
EBV	456	457	
EBV	642	643	
EBV	645	646	*
EBV	648	649	
EBV	701	702	
EBV	995	996	
EBV	1046	1047	
EBV	1084	1085	
EBV	1125	1126	
EBV	1127	1128	
EBV	1264	1265	
EBV	1307	1308	
EBV	1412	1413	*
EBV	1415	1416	
EBV	1429	1430	
EBV	1647	1648	
EBV	1654	1655	*
EBV	1665	1666	
EBV	1714	1715	
EBV	1881	1882	
EBV	1892	1893	*
EBV	1933	1934	
EBV	1947	1948	
EBV	1992	1993	
EBV	2016	2017	
EBV	2121	2122	
EBV	2143	2144	
EBV	2159	2160	
EBV	2172	2173	*
EBV	2199	2200	*
EBV	2215	2216	*
EBV	2227	2228	
EBV	2275	2276	
EBV	2283	2284	*
EBV	2289	2290	*
EBV	2331	2332	*
EBV	2343	2344	
EBV	2351	2352	*
EBV	2421	2422	*

start	end	Remarks
2424	2425	
2462	2463	
2527	2528	
2565	2566	*
2567	2568	
2608	2609	
2619	2620	
2634	2635	
2654	2655	
2676	2677	
2682	2683	*
2688	2689	
2708	2709	
2713	2714	
2716	2717	
2850	2851	
2946	2947	
2954	2955	*
2963	2964	
3000	3001	
3008	3009	
3015	3016	
3026	3027	
3038	3039	**
3062	3063	
3071	3072	
3090	3091	
3165	3166	
3171	3172	
3185	3186	
3294	3295	*
3368	3369	
3378	3379	*
3426	3427	
3459	3460	
3473	3474	
3500	3501	
3519	3520	
3539	3540	
3546	3547	
3563	3564	
3603	3604	*
3672	3673	**
3695	3696	
3701	3702	
3714	3715	*
3744	3745	

start	end	Remarks
3781	3782	
3816	3817	
3828	3829	*
3846	3847	
3881	3882	*
3923	3924	*
3933	3934	**
3959	3960	
3998	3999	
4000	4001	
4016	4017	
4020	4021	
4037	4038	
4040	4041	
4053	4054	
4055	4056	
4057	4058	
4134	4135	
4225	4226	
4256	4257	**
4278	4279	*
4281	4282	
4289	4290	
4297	4298	
4305	4305	
4310	4311	
4333	4334	
4365	4366	*
4431	4432	
4438	4439	*
4460	4461	
4481	4482	*
4503	4504	*
4528	4529	
4533	4534	
4558	4559	
4577	4578	
4587	4588	
4591	4592	
4635	4636	
4790	4791	*
4816	4817	
4843	4844	*
4857	4858	*
4866	4867	
4871	4872	*
4945	4946	

EBV	4947	4948	**
EBV	4964	4965	
EBV	5043	5044	
EBV	5166	5167	**
EBV	5241	5245	
EBV	5323	5324	
EBV	5421	5422	
EBV	5489	5490	*
EBV	5523	5524	
EBV	5598	5599	
EBV	5615	5616	**
EBV	5673	5674	
EBV	5677	5678	*
EBV	5685	5686	*
EBV	5751	5752	
EBV	6154	6155	
EBV	6270	6271	*
EBV	6299	6300	*
EBV	6326	6327	*
EBV	6347	6348	*
EBV	6352	6353	*
EBV	6388	6389	*
EBV	6401	6402	
EBV	6407	6408	
EBV	8432	8433	
EBV	8441	8442	
EBV	8444	8445	
EBV	8606	8607	
EBV	8887	8888	
EBV	9445	9446	*
EBV	9516	9517	**
EBV	9518	9519	**
EBV	9527	9528	
EBV	9579	9580	**
EBV	9800	9801	**
EBV	9829	9830	*
EBV	10010	10011	
EBV	10016	10017	
EBV	10022	10023	*
EBV	10044	10045	*
EBV	10242	10243	**
EBV	10301	10302	**
EBV	10330	10331	***
EBV	10365	10366	***
EBV	10378	10379	***
EBV	10391	10392	***
EBV	10440	10441	***
EBV	10464	10465	**

10489	10490	***
10546	10547	***
10559	10560	***
10569	10570	***
10583	10584	***
10607	10608	***
10644	10645	***
10665	10666	**
10668	10669	**
10681	10682	*
10691	10692	**
10701	10702	*
10705	10706	
10712	10713	***
10716	10717	*
10721	10722	*
10864	10865	***
10954	10955	***
10957	10958	***
10983	10984	***
10986	10987	***
11028	11029	***
11043	11044	**
11061	11062	***
11064	11065	*
11093	11094	**
11102	11103	**
11120	11121	***
11144	11145	***
11169	11170	***
11192	11193	**
11196	11197	*
11208	11209	*
11219	11220	
11236	11237	*
11242	11243	*
11274	11275	*
11363	11364	**
11385	11386	**
11438	11439	**
11478	11479	***
11648	11649	***
11765	11766	***
11771	11772	***
11777	11778	***
11851	11852	***
12018	12019	*
12039	12040	**

12056	12057	**
12110	12111	
12137	12138	**
12153	12154	*
35239	35240	
35478	35479	
35484	35485	
35490	35491	
35502	35503	
35766	35767	
35813	35814	*
35829	35830	**
35838	35839	**
35870	35871	
35972	35973	*
35978	35979	*
36050	36051	
36092	36093	*
36111	36112	
36118	36119	
36183	36184	
36185	36186	
36234	36235	
36273	36274	*
36291	36292	*
36312	36313	*
36381	36382	
36564	36565	*
36577	36578	
36580	36581	*
36608	36609	*
36647	36648	*
36656	36657	
36731	36732	
36735	36736	
36849	36850	*
36903	36904	
36922	36923	*
36950	36951	
37144	37145	*
37170	37171	**
37198	37199	*
37307	37308	
37315	37316	***
37381	37382	
37438	37439	
37444	37445	
37477	37478	*

EBV	37537	37538	**
EBV	37567	37568	
EBV	37661	37562	
EBV	37888	37889	*
EBV	37893	37891	*
EBV	38092	38093	*
EBV	38099	38100	
EBV	38121	38122	
EBV	38124	38125	
EBV	38149	38150	*
EBV	38225	38226	
EBV	38229	38230	
EBV	38248	38249	*
EBV	38290	38291	
EBV	38309	38310	*
EBV	39935	39936	*
EBV	39972	39973	
EBV	39989	39990	*
EBV	39994	39995	*
EBV	40006	40007	*
EBV	40025	40026	
EBV	40030	40031	**
EBV	40051	40052	
EBV	40101	40102	***
EBV	40332	40333	**
EBV	40334	40335	**
EBV	40338	40339	**
EBV	40354	40355	*
EBV	40372	40373	*
EBV	40383	40384	
EBV	40441	40442	*
EBV	40452	40453	*
EBV	40457	40458	*
EBV	40491	40492	
EBV	40494	40495	
EBV	40505	40506	
EBV	40510	40511	
EBV	40515	40516	*
EBV	40680	40681	
EBV	40704	40705	*
EBV	40706	40707	*
EBV	40722	40723	*
EBV	40780	40781	**
EBV	40785	40786	**
EBV	40858	40859	
EBV	41269	41270	
EBV	41315	41316	*
EBV	41322	41323	

41374	41375		
41397	41398		
41462	41463	**	
41488	41489	**	
41515	41516	*	
41594	41595	**	
41604	41605	**	
41664	41665	*	
41669	41670	**	
41692	41693		
41709	41710		
41807	41808	*	
41935	41936		
42138	42139		
42231	42232		
42264	42265	*	
42314	42315		
42363	42364	*	
42384	42385		
42386	42387		
42477	42478	*	
42497	42498		
42711	42712	*	
42800	42801		
42838	42839		
42896	42897		
42970	42971		
43004	43005		
43014	43015		
43021	43022	*	
43103	43104	*	
43566	43567		
43662	43663	*	
43794	43795		
43819	43820		
43869	43870		
44022	44023		
44037	44038		
44241	44242	**	
44304	44305		
44339	44340		
44393	44394	*	
44435	44436	*	
44450	44451		
44515	44516		
44533	44534		
44548	44549		
44599	44600		

44647	44648	*	
44706	44707		
44946	44947		
45084	45085		
45132	45133		
45136	45137	*	
45147	45148	*	
45156	45157		
45176	45177		
45277	45278		
45291	45292		
45303	45304	*	
45312	45313	*	
45336	45337		
45384	45385		
45423	45424		
45449	45450		
45498	45499	**	
45501	45502		
45604	45605		
45704	45705	*	
45903	45904		
45990	45991		
46018	46019		
46020	46021	*	
46065	46066	*	
46089	46090		
46191	46192	*	
46308	46309	*	
46357	46358		
46470	46471	*	
46501	46502		
46514	46515		
46562	46563		
46576	46577		
46612	46613		
46643	46644		
46697	46698		
46742	46743		
46856	46857		
46889	46890		
46894	46895		
46897	46898		
46942	46943		
47061	47062		
47082	47083		
47089	47090		
47120	47121		

EBV	47136	47137	
EBV	47178	47179	*
EBV	47192	47193	*
EBV	47204	47205	
EBV	47240	47241	
EBV	47251	47252	*
EBV	47273	47274	
EBV	47283	47284	
EBV	47285	47286	*
EBV	47324	47325	*
EBV	47365	47366	
EBV	47371	47372	
EBV	47378	47379	
EBV	47383	47384	
EBV	47386	47387	*
EBV	47389	47390	
EBV	47405	47406	
EBV	47454	47455	
EBV	47469	47470	**
EBV	47480	47481	
EBV	47496	47497	
EBV	47523	47524	
EBV	47535	47536	
EBV	47537	47538	
EBV	47556	47557	
EBV	47633	47634	
EBV	47812	47813	*
EBV	47825	47826	
EBV	47911	47912	*
EBV	47944	47945	
EBV	48040	48041	
EBV	48050	48051	**
EBV	48055	48056	*
EBV	48071	48072	
EBV	48100	48101	
EBV	48161	48162	*
EBV	48189	48190	*
EBV	48216	48217	
EBV	48222	48223	
EBV	48250	48251	
EBV	48256	48257	
EBV	48262	48263	
EBV	48269	48270	*
EBV	48297	48298	
EBV	48330	48331	
EBV	48420	48421	*
EBV	48460	48461	
EBV	48483	48484	

48493	48494	*	
48508	48509		
48536	48537	*	
48547	48548		
48552	48553		
48556	48557		
48563	48564		
48576	48577		
48589	48590		
48598	48599	*	
48600	48601		
48645	48646		
48657	48658	*	
48676	48677	*	
48694	48695		
48841	48842		
48849	48850	*	
48852	48853		
48908	48909	*	
48943	48944		
48997	48998	*	
49001	49002		
49013	49014		
49017	49018		
49028	49029	*	
49038	49039		
49067	49068		
49123	49124		
49127	49128	*	
49129	49130	*	
49199	49200		
49214	49215		
49224	49225		
49227	49228		
49264	49265		
49338	49339		
49422	49423	*	
49425	49426		
49431	49432		
49493	49494		
49567	49568		
49570	49571		
49576	49577		
49636	49637		
49648	49649		
49676	49677	*	
49685	49686		
49889	49890	*	

50584	50585	**	
50637	50638	*	
50641	50642	*	
50644	50645	*	
50653	50654		
50658	50659	*	
50662	50663		
50673	50674		
50685	50686	*	
50688	50689	*	
50691	50692		
50700	50701	*	
50704	50705	*	
50708	50709	**	
50714	50715	*	
50721	50722	*	
50724	50725	*	
50728	50729	*	
50738	50739		
50745	50746		
50753	50754		
50761	50762		
50763	50764	**	
50872	50873	*	
50911	50912		
50914	50915	**	
50922	50923	*	
51010	51011	*	
51019	51020		
51051	51052		
51164	51165		
51177	51178		
51198	51199		
51221	51222		
51270	51271	*	
51275	51276	*	
51434	51435	*	
51438	51439		
51448	51449	*	
51474	51475		
51480	51481	*	
51492	51493	*	
51516	51517	*	
51534	51535	*	
51547	51548		
51568	51569		
51585	51586		
51615	51616		

EBV	51619	51520	
EBV	51626	51527	*
EBV	51660	51561	
EBV	51677	51678	
EBV	51759	51760	
EBV	51771	51772	
EBV	51783	51784	
EBV	51785	51786	
EBV	51795	51796	
EBV	51828	51829	
EBV	51837	51838	*
EBV	51846	51847	
EBV	51871	51872	*
EBV	51893	51894	
EBV	51912	51913	
EBV	51915	51916	
EBV	51936	51937	**
EBV	52004	52005	
EBV	52008	52009	
EBV	52018	52019	
EBV	52157	52158	
EBV	52167	52168	
EBV	52177	52178	
EBV	52199	52200	*
EBV	52224	52225	
EBV	52245	52246	*
EBV	52249	52250	**
EBV	52261	52262	*
EBV	52296	52297	
EBV	52310	52311	
EBV	52343	52344	
EBV	52348	52349	
EBV	52398	52399	*
EBV	52403	52404	**
EBV	52425	52426	
EBV	52446	52447	*
EBV	52458	52459	*
EBV	52461	52462	
EBV	52466	52467	
EBV	52472	52473	
EBV	52481	52482	
EBV	52486	52487	
EBV	52497	52498	
EBV	52500	52501	
EBV	52509	52510	*
EBV	52511	52512	*
EBV	52539	52540	*
EBV	52648	52649	

52692	52693	
52715	52716	**
52739	52740	
52782	52783	
52858	52859	
52866	52867	
52874	52875	*
52887	52888	
52890	52891	
52905	52906	*
52929	52930	
52935	52936	
52941	52942	
53028	53029	
53067	53068	*
53149	53150	*
53163	53164	**
53221	53222	*
53240	53241	*
53245	53246	
53278	53279	
53284	53285	*
53331	53332	
53377	53378	
53428	53429	
53482	53483	*
53524	53525	*
53576	53577	
53585	53586	
53601	53602	
53620	53621	
53622	53623	
53627	53628	
53641	53642	*
53743	53744	
53799	53800	
53814	53815	
53831	53832	
53877	53878	
53887	53888	
53894	53895	
53910	53911	
53938	53939	
53967	53968	
53982	53983	
54013	54014	
54029	54030	
54040	54041	

54058	54059	
54080	54081	
54097	54098	
54101	54102	
54108	54109	
54112	54113	
54117	54118	*
54123	54124	*
54136	54137	
54151	54152	
54168	54169	
54173	54174	
54179	54180	
54217	54218	
54238	54239	
54324	54325	
54357	54358	
54365	54366	
54384	54385	
54395	54396	
54406	54407	*
54408	54409	
54427	54428	*
54439	54440	
54454	54455	*
54490	54491	
54494	54495	
54504	54505	
54508	54509	
54511	54512	*
54519	54520	
54521	54522	
54534	54535	
54547	54548	*
54583	54584	*
54585	54586	
54594	54595	
54603	54604	
54630	54631	*
54648	54649	
54655	54656	
54657	54658	
54676	54677	
54693	54694	
54704	54705	
54727	54728	*
54781	54782	
54799	54800	

EBV	54802	54803	
EBV	54811	54812	
EBV	54813	54814	
EBV	54867	54868	*
EBV	54871	54872	
EBV	54904	54905	
EBV	54934	54935	*
EBV	54941	54942	
EBV	54943	54944	
EBV	54947	54948	
EBV	55095	55096	
EBV	55116	55117	
EBV	55161	55162	*
EBV	55339	55340	
EBV	55342	55343	*
EBV	55344	55345	
EBV	55348	55349	
EBV	55472	55473	
EBV	55507	55508	
EBV	55517	55518	
EBV	55668	55669	
EBV	55674	55675	
EBV	55729	55730	*
EBV	55731	55732	
EBV	55750	55751	
EBV	55758	55759	*
EBV	55767	55768	
EBV	55797	55798	
EBV	55822	55823	
EBV	55854	55855	*
EBV	55905	55906	
EBV	55924	55925	
EBV	55926	55927	*
EBV	55965	55966	
EBV	55979	55980	
EBV	56001	56002	
EBV	56019	56020	
EBV	56040	56041	
EBV	56069	56070	
EBV	56094	56095	
EBV	56133	56134	
EBV	56187	56188	
EBV	56194	56195	
EBV	56197	56198	
EBV	56271	56272	
EBV	56433	56434	
EBV	56436	56437	**
EBV	56526	56527	

56555	56556	
56583	56584	
56592	56593	
56713	56714	
56815	56816	
56854	56855	
56886	56887	
56948	56949	
57021	57022	
57087	57088	*
57109	57110	*
57127	57128	
57159	57160	
57192	57193	
57318	57319	
57343	57344	
57360	57361	*
57364	57365	*
57485	57486	
57586	57587	
57749	57750	*
57774	57775	*
57790	57791	
57805	57806	*
57813	57814	
57857	57858	
57875	57876	
57888	57889	*
58015	58016	*
58293	58294	
58333	58334	
58346	58347	*
58354	58355	*
58386	58387	*
58446	58447	*
58452	58453	
58527	58528	*
58593	58594	*
58633	58634	*
58639	58640	*
58689	58690	
58705	58706	*
58707	58708	
58716	58717	
58746	58747	*
58758	58759	
58770	58771	
58792	58793	*

58800	58801	
58821	58822	
58837	58838	
58840	58841	
58844	58845	
58857	58858	*
58859	58860	
58866	58867	
58881	58882	*
58893	58894	
58914	58915	
58932	58933	
58958	58959	
58960	58961	
58980	58981	
59013	59014	
59055	59056	
59104	59105	*
59123	59124	
59145	59146	
59151	59152	
59181	59182	
59183	59184	
59187	59188	*
59193	59194	
59201	59202	**
59207	59208	
59226	59227	
59229	59230	*
59245	59246	
59253	59254	
59262	59263	
59270	59271	
59286	59287	*
59305	59306	
59308	59309	*
59315	59316	
59318	59319	*
59336	59337	**
59409	59410	
59411	59412	
59418	59419	*
59636	59637	
59652	59653	
59661	59662	
59664	59665	
59672	59673	*
59674	59675	

EBV	59683	59584	
EBV	59702	59703	
EBV	59704	59705	*
EBV	59716	59717	*
EBV	59727	59728	*
EBV	59735	59736	
EBV	59741	59742	*
EBV	59767	59768	*
EBV	59770	59771	*
EBV	59780	59781	
EBV	59785	59786	*
EBV	59805	59806	*
EBV	59810	59811	**
EBV	59814	59815	*
EBV	59824	59825	
EBV	59827	59828	
EBV	59834	59835	*
EBV	59867	59868	
EBV	59884	59885	
EBV	59918	59919	
EBV	59920	59921	
EBV	59935	59936	*
EBV	60026	60027	*
EBV	60033	60034	*
EBV	60178	60179	
EBV	60208	60209	*
EBV	60223	60224	
EBV	60235	60236	
EBV	60246	60247	
EBV	60256	60257	
EBV	60284	60285	
EBV	60286	60287	*
EBV	60294	60295	*
EBV	60341	60342	*
EBV	60346	60347	
EBV	60350	60351	
EBV	60381	60382	
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EBV	60485	60486	
EBV	60503	60504	
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EBV	60541	60542	*

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60920	60921	**
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61347	61348	*
61356	61357	
61435	61436	**
61446	61447	*
61459	61460	*
61542	61543	
61545	61546	**
61551	61552	
61561	61562	*

61567	61568	*
61574	61575	
61578	61579	
61602	61603	*
61625	61626	*
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EBV	62375	62376	***
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EBV	63066	63067	*

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66092	66093	
66107	66108	
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66223	66224	
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71508	71509	
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77373	77374	
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77455	77456	
77515	77516	**
77561	77562	
77564	77565	
77594	77595	
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78641	78642	
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78755	78756	
78917	78918	
78995	78996	***
79047	79048	
79121	79122	
79141	79142	
79298	79299	
79513	79514	**
79649	79650	**
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80486	80487	
80542	80543	*
80545	80546	*
80596	80597	**
80634	80635	**
80683	80684	
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EBV	81854	81855	
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EBV	84295	84296	*
EBV	84348	84349	

84507	84508	
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84886	84887	*
84917	84918	**
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84970	84971	**
84981	84982	
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85240	85241	
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87334	87335	
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87776	87777	
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88333	88334	
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88533	88534	*

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EBV	91437	91438	**
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92967	92968	**
93003	93004	**
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96780	96781	**
96786	96787	
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96952	96953	
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97065	97066	**
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97463	97464	*
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97516	97517	*
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EBV	98807	98808	
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EBV	98866	98867	*
EBV	99057	99058	
EBV	99084	99085	*
EBV	99092	99093	*
EBV	99172	99173	
EBV	99230	99231	
EBV	99244	99245	
EBV	99250	99251	*
EBV	99260	99261	
EBV	99269	99270	
EBV	99276	99277	*
EBV	99278	99279	*
EBV	99281	99282	
EBV	99367	99368	*
EBV	99394	99395	
EBV	99582	99583	
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EBV	99595	99596	
EBV	99597	99598	
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EBV	99696	99697	
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EBV	99879	99880	
EBV	99917	99918	
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EBV	99969	99970	

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100221	100222	
100225	100226	
100257	100258	
100268	100269	
100294	100295	*
100302	100303	
100386	100387	
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100470	100471	
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100631	100632	
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100657	100658	
100674	100675	*
100695	100696	
100749	100750	**
100779	100780	*
100791	100792	
100801	100802	
100847	100848	*
100849	100850	*
100851	100852	
100856	100857	
100866	100867	*
100914	100915	*
100934	100935	
100954	100955	
100983	100984	*
100995	100996	*
101017	101018	
101025	101026	**
101070	101071	*
101121	101122	
101128	101129	
101130	101131	
101223	101224	
101253	101254	
101273	101274	
101328	101329	
101364	101365	
101373	101374	
101446	101447	
101525	101526	
101528	101529	
101561	101562	

101645	101646	
101670	101671	
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101727	101728	
101752	101753	
101797	101798	*
101806	101807	
101853	101854	
101855	101856	
101858	101859	
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101898	101899	
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101929	101930	
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101956	101957	
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101994	101995	
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102166	102167	*
102204	102205	
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102215	102216	*
102221	102222	
102235	102236	**
102240	102241	**
102249	102250	*
102265	102266	*
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102311	102312	
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102546	102547	
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EBV	103864	103865	
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EBV	104055	104056	**
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104793	104794	
104803	104804	*
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104896	104897	*
104918	104919	*
104941	104942	
104980	104981	**
104986	104987	*
104988	104989	*
104991	104992	*
105003	105004	*
105015	105016	
105022	105023	*
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105071	105072	
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105162	105163	*
105189	105190	*
105196	105197	*
105198	105199	
105216	105217	
105327	105328	
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105348	105349	
105351	105352	
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105374	105375	
105377	105378	*
105398	105399	*
105410	105411	*
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105433	105434	
105444	105445	*
105468	105469	
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105501	105502	*
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105609	105610	
105637	105638	
105664	105665	
105671	105672	*
105674	105675	*

105686	105687	
105688	105689	*
105690	105691	
105693	105694	*
105708	105709	
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105765	105766	*
105775	105776	
105779	105780	*
105793	105794	
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105879	105880	
105972	105973	
106005	106006	
106056	106057	*
106071	106072	
106083	106084	
106155	106156	*
106164	106165	*
106190	106191	*
106209	106210	
106275	106276	
106281	106282	*
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106461	106462	*
106467	106468	
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106557	106558	*
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106677	106678	
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109245	109246	
109471	109472	
109506	109507	*
109685	109686	
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110169	110170	
110327	110328	
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110389	110390	
110464	110465	
110477	110478	*
110589	110590	
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110782	110783	
110989	110990	
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111784	111785	*
111817	111818	
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112143	112144	
112342	112343	
112503	112504	
112620	112621	
112746	112747	*
112969	112970	
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113719	113720	
113730	113731	*
113784	113785	*
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113837	113838	**
113850	113851	
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113927	113928	*
113936	113937	
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114335	114336	*
114467	114468	*
114547	114548	
114559	114560	*
114570	114571	*
114572	114573	*
114575	114576	
114587	114588	
114612	114613	**
114679	114680	
114708	114709	
114771	114772	**
114790	114791	*
114841	114842	
114844	114845	**
114899	114900	**
114919	114920	**
114953	114954	
115067	115068	**
115200	115201	*
115250	115251	*
115259	115260	*
115262	115263	*
115291	115292	
115303	115304	*
115308	115309	*
115323	115324	
115337	115338	*
115347	115348	**
115359	115360	*
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115389	115390	
115429	115430	
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115446	115447	*

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118097	118098	
118104	118105	
118106	118107	
118237	118238	*
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118679	118680	
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118688	118689	*
118780	118781	
118802	118803	
118867	118868	
118908	118909	*
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118981	118982	
119003	119004	
119157	119158	
119169	119170	
119341	119342	
119381	119382	***
119415	119416	
119447	119448	
119629	119630	
119696	119697	
119698	119699	
119790	119791	
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119915	119916	
119955	119956	
119961	119962	
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120070	120071	
120094	120095	
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120156	120157	*
120317	120318	**
120444	120445	**
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120524	120525	
120650	120651	
120788	120789	
120806	120807	

120845	120846	
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121869	121870	
121886	121887	
121892	121893	
121929	121930	*
121931	121932	
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121951	121952	
122030	122031	
122141	122142	
122159	122160	
122163	122164	
122165	122166	
122185	122186	*
122197	122198	
122245	122246	
122260	122261	
122305	122306	*
122307	122308	*
122339	122340	
122360	122361	*
122365	122366	
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122546	122547	
122586	122587	
122606	122607	
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122763	122764	
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122813	122814	*
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125383	125384	
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125660	125661	
125686	125687	
125754	125755	
125758	125759	
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125853	125854	
125929	125930	
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126287	126288	
126301	126302	**
126309	126310	*
126314	126315	*
126369	126370	
126391	126392	*
126442	126443	
126554	126555	
126664	126665	
126696	126697	*
126698	126699	*
126719	126720	
126769	126770	**
126774	126775	
126803	126804	
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126921	126922	
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126949	126950	
126961	126962	
126991	126992	
127081	127082	
127146	127147	
127175	127176	
127203	127204	
127207	127208	
127234	127235	

127239	127240	
127253	127254	*
127321	127322	
127324	127325	
127354	127355	
127459	127460	*
127473	127474	*
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127572	127573	
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127831	127832	*
127867	127868	
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127880	127881	*
127885	127886	
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127916	127917	
127936	127937	
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128010	128011	
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128116	128117	
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128401	128402	
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129003	129004	
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129477	129478	
129603	129604	
129606	129607	
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130196	130197	
130292	130293	
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130476	130477	
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EBV	133338	133339	
EBV	133348	133349	*
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EBV	133378	133379	
EBV	133448	133449	***
EBV	133456	133457	**

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133547	133548		
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133835	133836	*	
133922	133923		
133968	133969		
133995	133996		
134009	134010	*	
134011	134012		
134064	134065	*	
134066	134067		
134114	134115		
134117	134118		
134123	134124		
134130	134131		
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134144	134145		
134149	134150	*	
134155	134156		
134170	134171	*	
134175	134176		
134233	134234		
134247	134248		
134253	134254		
134276	134277		
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134330	134331		
134390	134391		
134394	134395		
134468	134469	**	
134474	134475		
134511	134512	**	
134586	134587		
134640	134641		
134645	134646		
134688	134689		
134694	134695		
134697	134698		
134700	134701		
134723	134724		
134740	134741		
134755	134756		

134785	134786		
134822	134823	*	
134891	134892		
134895	134896		
134915	134916		
134945	134946	*	
134972	134973		
134996	134997		
135082	135083		
135088	135089	**	
135148	135149		
135188	135189		
135320	135321		
135325	135326		
135339	135340	*	
135352	135353	*	
135364	135365	*	
135421	135422		
135440	135441		
135448	135449		
135521	135522		
135523	135524		
135569	135570		
135602	135603		
135629	135630		
135672	135673		
135687	135688		
135729	135730		
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135897	135898	*	
135903	135904		
135963	135964		
136078	136079	*	
136081	136082		
136083	136084		
136091	136092		
136148	136149		
136155	136156		
136158	136159		
136176	136177		
136200	136201		
136208	136209	*	
136232	136233	*	
136254	136255		
136276	136277	*	
136278	136279	**	
136323	136324		
136328	136329		

EBV	136344	136345	
EBV	136347	136348	*
EBV	136352	136353	
EBV	136394	136395	
EBV	136431	136432	
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EBV	136472	136473	*
EBV	136491	136492	
EBV	136544	136545	
EBV	136547	136548	
EBV	136571	136572	*
EBV	136689	136690	**
EBV	136695	136696	***
EBV	136697	136698	***
EBV	136701	136702	
EBV	136709	136710	*
EBV	136724	136725	
EBV	136766	136767	*
EBV	136784	136785	
EBV	136809	136810	
EBV	136824	136825	
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EBV	136854	136855	
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EBV	136864	136865	
EBV	136876	136877	
EBV	136890	136891	*
EBV	136922	136923	
EBV	136932	136933	*
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EBV	136958	136959	
EBV	136994	136995	
EBV	137008	137009	
EBV	137011	137012	*
EBV	137018	137019	
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EBV	137081	137082	*
EBV	137091	137092	*
EBV	137115	137116	*
EBV	137130	137131	
EBV	137256	137257	
EBV	137272	137273	*
EBV	137304	137305	*
EBV	137317	137318	*
EBV	137319	137320	
EBV	137345	137346	

137349	137350	
137445	137446	
137514	137515	
137528	137529	
137570	137571	*
137631	137632	*
137641	137642	*
137675	137676	
137682	137683	
137697	137698	*
137787	137788	
137802	137803	
137821	137822	
137857	137858	*
137894	137895	*
137912	137913	
137944	137945	*
137998	137999	*
138016	138017	**
138034	138035	***
138058	138059	***
138072	138073	**
138082	138083	*
138087	138088	*
138095	138096	*
138112	138113	*
138148	138149	**
138454	138455	
138489	138490	
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138551	138552	
138573	138574	
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138862	138863	
138875	138876	
138880	138881	
138894	138895	
139013	139014	
139148	139149	
139272	139273	*
139306	139307	

139320	139321	*
139341	139342	*
139365	139366	
139392	139393	
139409	139410	
139413	139414	
139449	139450	
139458	139459	
139511	139512	
139696	139697	*
139699	139700	
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139714	139715	*
139722	139723	
139757	139758	
139767	139768	
139875	139876	*
139892	139893	*
139922	139923	*
139979	139980	
140071	140072	**
140078	140079	***
140345	140346	*
140379	140380	*
140397	140398	*
140409	140410	
140479	140480	
140495	140496	*
140605	140606	
140612	140613	
140628	140629	
140685	140686	**
140726	140727	
140775	140776	
143290	143291	*
143301	143302	*
143327	143328	
143329	143330	*
143336	143337	
143356	143357	**
143359	143360	
143370	143371	*
143375	143376	*
143397	143398	*
143401	143402	
143409	143410	
143412	143413	
143433	143434	

EBV	144234	144235	**
EBV	144241	144242	***
EBV	144311	144312	
EBV	144316	144317	
EBV	144322	144323	**
EBV	144375	144376	**
EBV	144402	144403	*
EBV	144417	144418	
EBV	144575	144576	
EBV	144648	144649	
EBV	144666	144667	
EBV	144670	144671	
EBV	145646	145647	
EBV	145706	145707	*
EBV	145708	145709	*
EBV	145938	145939	*
EBV	146243	146244	
EBV	146266	146267	
EBV	146506	146507	
EBV	146550	146551	
EBV	146755	146756	
EBV	146773	146774	
EBV	146823	146824	*
EBV	147093	147094	
EBV	147316	147317	
EBV	147465	147466	
EBV	147505	147506	
EBV	147650	147651	
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EBV	147816	147817	
EBV	147903	147904	
EBV	148009	148010	
EBV	148017	148018	
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EBV	148050	148051	
EBV	148055	148056	
EBV	148064	148065	
EBV	148071	148072	
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EBV	148488	148489	*
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EBV	148528	148529	
EBV	148533	148534	
EBV	148540	148541	
EBV	148548	148549	
EBV	148578	148579	

148585	148586		
148612	148613		
148615	148616		
148628	148629		
148691	148692		
148756	148757		
148806	148807		
148829	148830		
148843	148844		
148846	148847		
148936	148937		
148939	148940	*	
149155	149156		
149198	149199		
149244	149245	*	
149328	149329		
149348	149349		
149354	149355	***	
149358	149359		
149471	149472		
149618	149619		
149620	149621	**	
149668	149669		
149694	149695		
149703	149704		
149792	149793	*	
149926	149927		
149948	149949		
149972	149973		
149996	149997		
150024	150025	*	
150030	150031		
150047	150048		
150057	150058		
150105	150106		
150267	150268		
150334	150335		
150337	150338	**	
150363	150364		
150367	150368	*	
150370	150371		
150375	150376		
150417	150418		
150421	150422		
150424	150425		
150441	150442		
150445	150446		
150449	150450		

150461	150462		
150555	150556	*	
150617	150618		
150707	150708		
150765	150766	*	
150769	150770	*	
150781	150782	*	
150799	150800		
150817	150818	**	
150847	150848		
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150900	150901	*	
150922	150923		
150939	150940		
150966	150967	*	
150971	150972	*	
150973	150974	**	
150977	150978		
150980	150981		
150995	150996		
151662	151663	*	
151989	151990		
152037	152038		
152085	152086	**	
152089	152090		
152148	152149		
152151	152152		
152251	152252		
152255	152256		
152284	152285		
152441	152442		
152529	152530		
152560	152561		
152610	152611	***	
152619	152620	*	
152788	152789		
152826	152827		
152861	152862		
152870	152871	*	
152886	152887	*	
152914	152915		
153080	153081		
153168	153169		
153171	153172		
153184	153185	*	
153192	153193	*	
153290	153291	*	
153347	153348		

EBV	153386	153387	*
EBV	153396	153397	
EBV	153469	153470	*
EBV	153503	153504	
EBV	153616	153617	
EBV	153736	153737	
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EBV	153839	153840	
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EBV	154052	154053	
EBV	154065	154066	
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EBV	154178	154179	
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EBV	154370	154371	
EBV	154407	154408	
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EBV	154604	154605	
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EBV	154754	154755	
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EBV	154817	154818	
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EBV	154835	154836	*
EBV	154842	154843	
EBV	154855	154856	
EBV	154951	154952	
EBV	154958	154959	
EBV	154970	154971	*

154985	154986	
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155041	155042	
155051	155052	*
155057	155058	*
155150	155151	
155159	155160	
155174	155175	
155204	155205	
155261	155262	
155300	155301	
155316	155317	
155357	155358	
155396	155397	
155402	155403	
155443	155444	*
155446	155447	
155486	155487	
155489	155490	
155493	155494	
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155575	155576	
155580	155581	
155608	155609	
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155634	155635	*
155642	155643	
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155702	155703	
155722	155723	
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155761	155762	*
155765	155766	*
155786	155787	
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155987	155988	
155996	155997	
156048	156049	
156064	156065	
156111	156112	
156173	156174	
156322	156323	

156340	156341	
156372	156373	
156464	156465	
156550	156551	
156556	156557	*
156596	156597	
156605	156606	*
156635	156636	***
156661	156662	
156664	156665	
156725	156726	*
156796	156797	**
156860	156861	
156879	156880	
156904	156905	
156915	156916	
156922	156923	
156964	156965	
157021	157022	*
157045	157046	*
157054	157055	
157063	157064	
157069	157070	
157141	157142	
157174	157175	
157203	157204	
157205	157206	**
157248	157249	
157258	157259	*
157273	157274	
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157333	157334	
157443	157444	
157455	157456	
157458	157459	
157468	157469	
157489	157490	
157495	157496	
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157532	157533	*
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157578	157579	
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157591	157592	*

EBV	157608	157609	*
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EBV	157631	157632	**
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EBV	158206	158207	*
EBV	158290	158291	*
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EBV	158335	158336	*
EBV	158386	158387	
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EBV	158574	158575	*
EBV	158585	158586	**
EBV	158695	158696	
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EBV	158856	158857	
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EBV	159006	159007	*
EBV	159008	159009	*
EBV	159016	159017	
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159062	159063	*
159071	159072	*
159077	159078	
159079	159080	*
159125	159126	
159131	159132	
159167	159168	
159171	159172	
159176	159177	
159233	159234	
159236	159237	
159247	159248	
159260	159261	*
159330	159331	
159336	159337	
159338	159339	
159351	159352	
159419	159420	*
159422	159423	
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159484	159485	
159506	159507	
159518	159519	
159520	159521	
159590	159591	**
159604	159605	*
159622	159623	
159630	159631	*
159632	159633	
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159651	159652	
159656	159657	
159664	159665	
159700	159701	
159753	159754	*
159801	159802	
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160016	160017	
160035	160036	
160043	160044	*
160055	160056	
160158	160159	
160173	160174	*
160181	160182	
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160235	160236	
160242	160243	
160249	160250	
160272	160273	
160278	160279	
160284	160285	
160335	160336	*
160416	160417	
160468	160469	
160514	160515	
160571	160572	*
160636	160637	*
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160665	160666	
160667	160668	*
160683	160684	
160753	160754	
160778	160779	
160790	160791	
160806	160807	*
160837	160838	*
160902	160903	
160908	160909	
160933	160934	*
160939	160940	
160948	160949	
160978	160979	**
161011	161012	
161024	161025	
161027	161028	
161029	161030	
161050	161051	
161077	161078	*
161113	161114	
161153	161154	*
161215	161216	
161354	161355	
161356	161357	*
161367	161368	
161370	161371	*

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EBV	161434	161435	*
EBV	161458	161459	**
EBV	161490	161491	
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EBV	161788	161789	
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EBV	162208	162209	
EBV	162216	162217	*
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162936	162937	
162943	162944	
162992	162993	*
162998	162999	
163004	163005	*
163056	163057	
163108	163109	
163118	163119	
163123	163124	
163132	163133	
163138	163139	
163157	163158	*
163170	163171	**
163173	163174	*
163213	163214	*
163258	163259	*
163268	163269	
163291	163292	**
163321	163322	
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163799	163800	
163833	163834	
163849	163850	
163862	163863	*
163894	163895	
163910	163911	
163945	163946	
163987	163988	*
163994	163995	***
164077	164078	
164089	164090	**
164129	164130	
164156	164157	*
164180	164181	
164182	164183	
164188	164189	*
164261	164262	*
164373	164374	
164438	164439	

164462	164463	
164545	164546	*
164574	164575	
164579	164580	*
164616	164617	
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164629	164630	
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164673	164674	
164677	164678	
164681	164682	
164695	164696	
164701	164702	
164808	164809	*
164819	164820	
164821	164822	*
164866	164867	*
164870	164871	
164873	164874	*
164876	164877	*
164882	164883	
164884	164885	*
164891	164892	
164896	164897	
164900	164901	
164950	164951	
164965	164966	*
164994	164995	*
165014	165015	*
165016	165017	*
165059	165060	
165095	165096	
165126	165127	
165164	165165	
165228	165229	
165239	165240	**
165320	165321	**
165341	165342	
165357	165358	*
165371	165372	
165377	165378	**
165404	165405	*
165421	165422	**
165437	165438	
165485	165486	*
165509	165510	**
165527	165528	***
165533	165534	***

EBV	165542	165543	**
EBV	165553	165554	**
EBV	165563	165564	**
EBV	165647	165648	*
EBV	165677	165678	**
EBV	165703	165704	***
EBV	165712	165713	**
EBV	165764	165765	*
EBV	165778	165779	**
EBV	165780	165781	**
EBV	165785	165786	*
EBV	165799	165800	**
EBV	165810	165811	***
EBV	165953	165954	
EBV	165987	165988	**
EBV	165990	165991	*
EBV	165992	165993	*
EBV	166035	166036	**
EBV	166048	166049	**
EBV	166077	166078	
EBV	166089	166090	
EBV	166149	166150	**
EBV	166152	166153	*
EBV	166160	166161	***
EBV	166170	166171	***
EBV	166176	166177	***
EBV	166235	166236	**
EBV	166239	166240	*
EBV	166274	166275	*
EBV	166738	166739	*
EBV	166792	166793	
EBV	166802	166803	*
EBV	166831	166832	
EBV	166916	166917	
EBV	166956	166957	*
EBV	167008	167009	
EBV	167053	167054	
EBV	167112	167113	*
EBV	167183	167184	*
EBV	167331	167332	*
EBV	167435	167436	
EBV	167444	167445	
EBV	167457	167458	
EBV	167519	167520	
EBV	167928	167929	*
EBV	167947	167948	+
EBV	168162	168163	*
EBV	168165	168166	+

168168	168169	*
168180	168181	
168201	168202	
168237	168238	
168256	168257	*
168270	168271	+
168634	168635	*
168691	168692	
169511	169512	*
169514	169515	*
169521	169522	*
169533	169534	*